



(51) International Patent Classification:

C12N 1/20 (2006.01) A23K 50/80 (2016.01)

(21) International Application Number:

PCT/IB2019/059131

(22) International Filing Date:

24 October 2019 (24.10.2019)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

115101 24 October 2018 (24.10.2018) PT

(71) Applicants: **CIIMAR - CENTRO INTERDISCIPLINAR DE INVESTIGAÇÃO MARINHA E AMBIENTAL** [PT/PT]; Novo Edifício Do Terminal De Cruzeiros Do Porto De Leixõesavenida General, Norton De Matos, S/N, 4450-208 Matosinhos (PT). **UNIVERSIDADE DO PORTO** [PT/PT]; Praça Gomes Teixeira, S/N, 4º, S. 463, 4099-002 Porto (PT).

(72) Inventors: **DOS REIS SERRA, Claudia Alexandra**; CIIMAR - Terminal De Cruzeiros Do Porto De Leixões, Avenida General Norton De, Matos, S/N, 4450-208 Matosinhos (PT). **ENES OLIVEIRA DA SILVA, Paula Cristina**; CIIMAR - Terminal De Cruzeiros Do Porto De Leixões, Avenida General Norton De, Matos, S/N, 4450-208 Matosinhos (PT). **OLIVA TELES, Aires**; FCUP-Departamento De Biologia, Faculdade De Ciências, Universidade Do Porto, Rua, Do Campo Alegre S/N, 4169-007 Porto (PT). **TAVARES, Fernando**; FCUP-DEPARTAMENTO DE BIOLOGIA, FACULDADE DE CIÊNCIAS, UNIVERSIDADE DO PORTO, RUA, DO CAMPO ALEGRE S/N, 4169-007 PORTO (PT).

(74) Agent: **PATENTREE**; Association 669, Rua de Salazares, 842, Edf. NET, 4149-002 Porto (PT).

(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

- without international search report and to be republished upon receipt of that report (Rule 48.2(g))
- with (an) indication(s) in relation to deposited biological material furnished under Rule 13bis separately from the description (Rules 13bis.4(d)(i) and 48.2(a)(viii))
- with sequence listing part of description (Rule 5.2(a))
- in black and white; the international application as filed contained color or greyscale and is available for download from PATENTSCOPE

(54) Title: SPOREFORMING PROBIOTIC STRAINS, METHODS AND USES THEREOF

(57) Abstract: The present disclosure relates to the isolation, identification and characterization of novel sporeforming probiotic strain(s) with NSPase (Non-Starch Polysaccharides-active hydrolases) activity isolated from fish gut microbiota, methods and uses thereof. The sporeforming probiotic strain(s) with NSPase activity now disclosed are able of producing carbohydrate-active enzymes (CAZymes) that hydrolyse non-starch polysaccharides (NSPs) and accesses their potential as probiotics (PRO) for use in particular in aquafeeds.



D E S C R I P T I O N

SPOREFORMING PROBIOTIC STRAINS, METHODS AND USES THEREOF

TECHNICAL FIELD

[0001] The present disclosure relates to the isolation, identification and characterization of novel sporeforming probiotic strain(s) with NSPase (Non-Starch Polysaccharides-active hydrolases) activity isolated from fish gut microbiota, methods and uses thereof.

[0002] The sporeforming probiotic strain(s) with NSPase activity now disclosed are able of producing carbohydrate-active enzymes (CAZymes) that hydrolyse non-starch polysaccharides (NSPs) and accesses their potential as probiotics (PRO) for use in particular in aquafeeds.

BACKGROUND ART

[0003] The gastrointestinal microbial community plays a critical role on vertebrates' health and metabolism, impacting host metabolism, immune status and health/disease balance. In the last decade, this relationship has received increased attention particularly in humans, where it is known to control local (at the gut level) health status as well as systemic health. The gut microbiota of vertebrates, ranging from mammals to teleost fish, is involved in host appetite control and obesity development [1], protection against pathogens, immunity enhancement or inflammatory processes [2]. Additionally, gut microorganisms respond to a wide range of factors, including dietary composition, and harbor a relevant and diversified enzymatic repertoire that might interfere with host metabolism [3, 4]. This is particularly important in fish nutrition, because fish do not possess all of the necessary enzymes to cope with the current aquaculture dietary challenges [4].

[0004] A main difficulty within fish nutrition is its dependence on fish meal (FM), an unsustainable commodity and a source of organic pollutants. The most obvious sustainable alternatives to fish meal are plant feedstuffs, but their nutritive value is limited by the presence of high levels of non-starch polysaccharides (NSPs) which are not metabolized by fish.

[0005] These facts are disclosed to illustrate the technical problem addressed by the present disclosure.

GENERAL DESCRIPTION

[0006] Aquaculture output is growing rapidly and has already surpassed fisheries in terms of providing food to meet the growing human population [5]. Aquaculture is greatly dependent on FM, an unsustainable commodity and a source of organic pollutants, almost exclusively provided by fisheries. This is particularly obvious in carnivorous fish production due to their high dietary protein requirement (40-

50%), which is mainly provided by FM. Plant feedstuffs (PF) are sustainable alternatives to FM, and among them, soybean meal (SBM), rapeseed meal (RSM), and sunflower meal (SFM), have been acknowledged as the most promising due to their high protein level, world-wide availability, and reasonable price. However, the nutritive value of PF is limited by the presence of several anti-nutritional factors, including high levels of non-starch polysaccharides (NSPs) which are not digested by fish [6]. NSPs content in SBM, RSM, and SFM averages 22-24% and the major NSPs components are pectic polysaccharides with arabinose, galactose, and xylose residues predominating. Yet, the proportion of these sugar residues varies between PF with galactose being predominant in SBM, arabinose in RSM, and xylose in SFM.

[0007] In fish, the carbohydrate-active enzymes (CAZymes) able to hydrolyze the β -glycosidic bonds of NSPs are scarce or non-existent. Thus, dietary NSPs remain indigestible and cannot be used as energy source. Moreover, indigestible NSPs might have detrimental effects on fish performance and nutrient digestibility and on fish health [7]. These adverse effects are associated with the viscous nature of NSPs and their interaction with gut epithelium, mucus, and microbiota, which ultimately result on physiological and inflammatory imbalances [7]. Additionally, and contrary to other animal species, such as pigs and poultry, the supplementation of PF based diets with exogenous carbohydrases does not necessarily translate into an effective strategy for improving NSPs utilization, as diverging results on their impact on fish growth performance and feed utilization have been reported. Therefore, gut microorganisms characterized by a rich secretome are a potential source of *in loco* carbohydrases that may help fish to overcome the mentioned constraints.

[0008] Live microorganisms that confer a health benefit to the host when administered in adequate amounts are denominated probiotics (PRO) [8]. In particular, PRO decrease the incidence of diseases by competing with pathogens for adhesion sites/nutrients; produce natural antimicrobial compounds that inhibit pathogens growth; contribute to a balanced gut microbiota; improve host growth; enhance host immune system and gastrointestinal histomorphology. PRO have also been implicated in bioremediation and water quality improvement by reducing antibiotic usage, contributing to aquaculture sustainability.

[0009] Among the bacterial species currently used as PRO, sporeformers show critical advantages: bacterial spores are remarkably resistant dormant structures [9], permitting good shelf-storage; spores are easily produced in large scale and can be dehydrated, facilitating feed incorporation without losing characteristics. Importantly, spores survive gut transit since they are acid and bile tolerant and become successfully established in the gut [10]. In particular, *Bacillus subtilis* spores, which enjoy GRAS (Generally Regarded As Safe) status from the U.S. Food and Drug Administration (FDA) and are included in the European Food Safety Authority (EFSA) list of Qualified Presumption of Safety (QPS) [11], experience exponentially growing applications in biomedicine and biotechnology (as oral vaccines, disinfectants, PRO or display systems) [12]. In fact, different sporeformers are nowadays used as human and animal PRO [12-

13], but within European Union (EU) just one PRO has been authorised for use in aquaculture (Bactocell®, LALLEMAND Inc., Canada).

[0010] The role of gut microbiota in shaping human and animal health is well established, and the potential health benefit of manipulating the gut ecosystem using PRO is increasingly being accepted. In carnivorous fish, such as European sea bass, an ideal PRO should not only enhance resistance to pathogens, i.e. by competitive exclusion, the most common criteria for selection of PRO strains, but also help fish in their current dietary challenges, including the utilization of PF. In this disclosure, the application of a PF-based dietary pressure to modulate European sea bass gut microbiota composition and corresponding metabolic functions revealed to be a successful strategy to find carbohydrate-active bacteria with PRO potential. In particular, it was targeted and isolated spore-forming Bacilli, commonly used in PRO preparations, mainly due to their extreme resistance characteristics and indefinitely survival, advantageous for industrial applications [9-10, 12-13, 17].

[0011] The composition of the gut microbial communities of fish have been demonstrated to adapt when the host is fed different dietary ingredients [1, 3, 4]. Thus, a selective pressure of plant-based diets on fish gut microbiota, can be a beneficial strategy for an enrichment of bacteria with a secretome able to mobilize the dietary NSPs. By targeting bacterial sporulating isolates with diverse carbohydrase activities from the gut of European sea bass (*Dicentrarchus labrax*), isolates with high probiotic potential were obtained. By inferring the adaptive fitness to the fish gut and the amenability to industrial processing, the best two candidates were identified to become industrially valuable PRO for improvement of fish health and utilization of dietary NSPs, contributing for sustainable and more cost-effective aquaculture practices.

[0012] Thus, the present disclosure relates to screening fish gut microbiota for bacteria capable of producing extracellular digestive enzymes that hydrolyse NSPs present in PF, in particular mannans, glucans, xylans, arabinans, and galactans.

[0013] Gut microbiota isolates showing promising metabolic traits and absence of safety concerns can be used as PRO in cost-effective and environmental-friendly diets by allowing the host to obtain energy from otherwise indigestible dietary constituents. In fact, native bacteria with PRO potential will be more apt to become established and persist in the fish gut environment after withdrawal from the diet.

[0014] The present disclosure provides several advantages, namely: it solves the incapability of fish to efficiently digest and utilize PF as alternative protein source to FM; compared to exogenous purified enzymes (the only available technology, with poor results in fish), this disclosure has the added value of being also an autochthonous PRO that besides helping fish with the digestive challenges also contributes to fish health and welfare by antagonizing fish pathogens, having a dual positive effect on fish performance. Additionally, this product, by being a sporeformer, is more robust and resistant than the other PRO in EU market, allowing feed incorporation without losing characteristics and storage without refrigeration.

[0015] The present disclosure relates to ABP1 which was received on 08.06.2018 and accepted for deposit for patent purposes at the Colección Española de Cultivos Tipo (CECT) - International Depositary Authority under the Budapest Treaty - under the accession number CECT 9675.

[0016] The present disclosure also relates to ABP2 which was received on 08.06.2018 and accepted for deposit for patent purposes at the Colección Española de Cultivos Tipo (CECT) - International Depositary Authority under the Budapest Treaty - under the accession number CECT 9676.

[0017] The present disclosure therefore relates to a bacterial strain selected from ABP1 with a deposit under the accession number CECT 9675, of 08.06.2018, at Colección Española de Cultivos Tipo, and/or from ABP2 with a deposit under the accession number CECT 9676, of 08.06.2018, at Colección Española de Cultivos Tipo.

[0018] Furthermore, the present disclosure also relates to a composition for aquatic animal feed comprising a bacterial strain selected from ABP1 with a deposit under the accession number CECT 9675, of 08.06.2018, at Colección Española de Cultivos Tipo, and/or from ABP2 with a deposit under the accession number CECT 9676, of 08.06.2018, at Colección Española de Cultivos Tipo.

[0019] In an embodiment, said composition may comprise 1×10^5 - 1×10^{12} of colony forming units of the bacterial strain per gram of the composition, preferably said composition may comprise 1×10^7 - 1×10^{10} colony forming units of the bacterial strain per gram of the composition, more preferably said composition may comprise 2×10^9 colony forming units of the bacterial strain per gram of the composition.

[0020] In an embodiment, said composition may further comprise a preservative.

[0021] In an embodiment, said composition may be a granulate form, a powdered form or a pellet.

[0022] In an embodiment, said composition may be a granulate form wherein the granulate form is coated, in particular wherein the coating comprises a salt and/or wax and/or a flour.

[0023] The present disclosure also relates to a method for feeding an aquatic animal present in an aquaculture comprising the step of feeding the aquatic animal with the composition now disclosed.

[0024] In an embodiment, the step of feeding the aquatic animal may be carried out during the life span of the aquatic animal.

[0025] In an embodiment, the aquatic animal may be selected from the following list: a shellfish, fish, amberjack, arapaima, barb, bass, bluefish, bocachico, bream, bullhead, cachama, carp, catfish, catla, chanos, char, cichlid, cobia, cod, crappie, dorada, drum, eel, goby, goldfish, gourami, grouper, guapote, halibut, java, labeo, lai, loach, mackerel, milkfish, mojarra, mudfish, mullet, paco, pearlspot, pejerrey, perch, pike, pompano, roach, Atlantic salmon, salmon, sampa, sauger, sea bass, European sea bass, seabream, gilthead seabream, white seabream, shiner, sleeper, snakehead, snapper, snook, sole,

spinefoot, sturgeon, sunfish, sweetfish, tench, terror, tilapia, trout, tuna, turbot, vendace, walleye, halibut, whitefish or shrimp.

[0026] This disclosure also relates to the use of a bacterial strain selected from ABP1 with a deposit under the accession number CECT 9675, of 08.06.2018, at Colección Espanola de Cultivos Tipo, and/or from ABP2 with a deposit under the accession number CECT 9676, of 08.06.2018, at Colección Espanola de Cultivos Tipo, as a probiotic.

[0027] This disclosure also relates to the use of a bacterial strain selected from ABP1 with a deposit under the accession number CECT 9675, of 08.06.2018, at Colección Espanola de Cultivos Tipo, and/or from ABP2 with a deposit under the accession number CECT 9676, of 08.06.2018, at Colección Espanola de Cultivos Tipo, as a supplement to feedstuff, preferably as a supplement to feedstuff for fish or shellfish.

[0028] Furthermore, the present disclosure also relates to an isolated polynucleotide or polypeptide from ABP1 with a deposit under the accession number CECT 9675, of 08.06.2018, at Colección Espanola de Cultivos Tipo, wherein the isolated polynucleotide is selected from the following list: SEQ. ID. No. 19 (ABP10666), SEQ. ID. No. 20 (ABP10667), SEQ. ID. No. 7 (ABP10654), SEQ. ID. No. 24 (ABP10671), SEQ. ID. No. 36 (ABP10829), SEQ. ID. No. 37 (ABP10830), or combinations thereof, wherein the isolated polynucleotide encodes for a polypeptide that hydrolyses a non-starch polysaccharide, preferably non-starch polysaccharides present in plant feedstuffs, preferably wherein the non-starch polysaccharide is mannan, glucan, xylan, arabinan, and/or galactan.

[0029] The present disclosure also relates to an isolated polynucleotide or polypeptide from ABP2 with a deposit under the accession number CECT 9676, of 08.06.2018, at Colección Espanola de Cultivos Tipo, wherein the isolated polynucleotide is selected from the following list: SEQ. ID. No. 160 (ABP24564), SEQ. ID. No. 161 (ABP24565), SEQ. ID. No. 162 (ABP24566), SEQ. ID. No. 163 (ABP24567) or combinations thereof, wherein the isolated polynucleotide encodes for a polypeptide that hydrolyses a non-starch polysaccharide, preferably non-starch polysaccharides present in plant feedstuffs, preferably wherein the non-starch polysaccharide is mannan, glucan, xylan, arabinan, and/or galactan.

BRIEF DESCRIPTION OF THE DRAWINGS

[0030] The following figures provide preferred embodiments for illustrating the description and should not be seen as limiting the scope of the present disclosure.

[0031] **Figure 1.** Morphological diversity (Panels A-J) of representative sporeforming fish isolates obtained from European sea bass gut contents. Photographs of colonies grown 24 h in LB (Luria-Bertani) agar medium, are at the same scale defined in Panel J (0.5 cm). Panel K depicts a representative image of the different development stages of sporulation [(a) vegetative cell, (b) sporulating cell (forespore engulfed by the mother cell) and (c) free spore] that were observed in each sporeforming isolate by phase-

contrast microscopy. Sporulation was induced by nutrient exhaustion in solid Difco Sporulation Medium (DSM).

[0032] **Figure 2. (A)** Diversity of sporeforming genera obtained from European sea bass digesta samples. **(B)** Distribution of bacterial species within the *Bacillus* genus depicted in panel A.

[0033] **Figure 3.** Carbohydrolytic profile of representative sporeformers (A-L) isolated from the gut of European sea bass, when cultured on solid minimal medium (M9) alone or supplemented with D-glucose (Gluc), D-fructose (Fruct), D-xylose (Xyl), L-arabinose (Arab), D-galactose (Galact), D-mannose (Mann), Xylooligosaccharides (XOS) and Galactooligosaccharides (GOS).

[0034] **Figure 4. (A)** Carbohydrolytic profile of the best 11 sporeformers (codes in the x axis) isolated from European sea bass gut, when cultured in liquid minimal medium supplemented with D-glucose, D-fructose, D-xylose, L-arabinose, D-galactose, D-mannose, Xylooligosaccharides (XOS) and Galactooligosaccharides (GOS) for 24 h at 37 °C with agitation. Growth was quantified by measuring the optical density (OD) at an absorbance of 600 nm. The results presented are the average of three independent experiments with error bars representing the standard deviation. **(B)** PCR detection of genes coding for β -glucanase (*bgIS*), levanase or β -D-fructofuranosidase (*sacC*), mannan endo-1,4- β -mannosidase (*gmuG*), endo-1,5- α -L-arabinanase (*abnA*) and arabinoxylan arabinofuranohydrolase (*xynD*) carbohydrases in the genome of fish isolates (FI numbers on top of the figure). The amplicon size, in base pairs (bp) is depicted on the right.

[0035] **Figure 5.** Titer of viable cells present in 24 h DSM (Difco Sporulation Medium) cultures of each sporeformer fish isolate (codes in x axis) before (grey, total cells) and after (black, sporulating or heat resistant cells) a 20 min heat treatment at 80 °C. Sporulation was induced by nutrient exhaustion in liquid DSM at 37 °C, 150 rpm. Numbers on top of the panel correspond to the percentages (%) of sporulation calculated as the ratio between sporulating cells and total cells. *Bacillus subtilis* 168 was used as control and the results are the average of three independent experiments with error bars representing the standard deviation.

[0036] **Figure 6.** Viability of spores from each sporeformer isolate (codes in x axis) when exposed for 4 h (T4, dark grey) to simulated stomach conditions (0.85% NaCl, pH 2, containing 3 mg ml⁻¹ pepsin) followed by 24 h (T24, black) exposition to simulated gut condition (Luria-Bertani, LB, pH 8 containing 1 mg ml⁻¹ pancreatin and 0.3% bile salts). The initial viable counts (time 0 or T0) are depicted in light grey. *B. subtilis* 168 was used as control and the results are the average of three independent experiments with error bars representing the standard deviation.

[0037] **Figure 7.** Antimicrobial activity of sporeforming fish isolates ABP1, ABP20, ABP27 and ABP2 against different fish pathogens (*Staphylococcus aureus*, *Photobacterium damsela*, *Vibrio harveyi*, *Aeromonas bivalvium* and *Tenacibaculum maritimum*). **(A)** Growth inhibition screened by a colony overlay

assay, where the producer strains were inoculated as spots on Luria-Bertani agar plates, grown for 24 h and then covered by Soft Marine Agar (for *Tenacibaculum maritimum*) or Soft Brain Heart Infusion Agar (for all the other) inoculated with indicator pathogenic strains. **(B)** Growth Inhibition screened by a cell-free supernatant assay in which a Marine Agar plate seeded with *Tenacibaculum maritimum* was perforated with 0.5 cm holes and filled with 100 µl of filtered culture medium from overnight grown sporeforming isolates. *B. subtilis* 168 (*Bsub*) was used as control. All photographs are to scale.

[0038] **Figure 8.** Germination of populations of purified spores of sporeformers fish isolates ABP7, ABP1, ABP20, ABP27, ABP34 and ABP2 at 37 °C in 50 mM Tris-HCl, pH7.5 (control, black circles) or in response to the addition of 100 mM L-alanine (dark grey circles) or a mixture of 100 mM KCl, 56 mM glucose, 56 mM fructose and 33 mM L-asparagine (AGFK, light grey circles). *B. subtilis* 168 was used as control.

DETAILED DESCRIPTION

[0039] The present disclosure relates to the isolation, identification and characterization of novel sporeforming probiotic strain(s) with NSPase (Non-Starch Polysaccharides-active hydrolases) activity isolated from fish gut microbiota, methods and uses thereof.

[0040] In an embodiment, sporeformers were isolated from the gut of European sea bass juveniles challenged with PF diets based on SBM, RSM or SFM, which have different NSPs profiles. European sea bass was the model species chosen due to its high commercial importance in European aquaculture and its carnivorous feeding habits, thus being more challenging to cope with PF-based diets. However, other models could be equally used such as gilthead seabream (*Sparus aurata*) or white seabream (*Diplodus sargus*) or Atlantic salmon (*Salmo salar*).

[0041] Providing fish with self-gut bacteria capable of producing carbohydrate-active extracellular enzymes that hydrolyse NSPs emerge as a strategy with enormous potential to overcome PF-diets limitations. The bacterial strains now disclosed were isolated with this purpose and their genome sequences support their view as potential NSPs-hydrolyzers that might help aquaculture fish on using high PF-diets.

[0042] Having in mind the enhanced adaptability of gut microbial communities, a selective pressure of plant-based diets on fish gut microbiota was carried out for an enrichment of bacteria with a secretome able to mobilize the dietary NSPs. By targeting bacterial spores, remarkably resistant dormant structures with increasing applications in animal health, namely as vaccines or PRO, it was possible to isolate carbohydrate-active gut bacterial strains, from European sea bass, with PRO potential. By inferring the adaptive fitness to the fish gut and the amenability to industrial processing, the best candidates were identified to become industrially valuable PRO for improvement of fish health and utilization of dietary NSPs, contributing for sustainable and more cost-effective aquaculture practices.

[0043] In an embodiment, the PRO were isolated and purified, identified to the species level, fully characterised, namely its safety following EFSA guidelines, NSPase activity, antimicrobial activity against important fish-pathogens, adaptive fitness to the fish gut and the amenability to industrial processing. The complete genome has been sequenced.

[0044] In an embodiment, there is a need for further research namely addressing the *in vivo* efficacy in improving PF utilization by fish and disease resistance in bacterial infection models. A preliminary assay using challenging plant-based diets (CTR-), revealed that supplementation with ABP1, or ABP1 and ABP2 (Mix) has a positive effect on the final body weight, the weight gain, the feed efficiency and the protein efficiency ratio of European sea bass juveniles, with a tendency to get closer to a FM- based diet (CTR+) (**Table 1**). Future analyses including digestive enzymes activity and gut microbiota modulation, might help explain the results obtained. Furthermore, a comprehensive screening of ABP1 and ABP2 genomes will potentially allow the identification of new carbohydrases or antimicrobial molecules.

[0045] **Table 1.** Growth performance and feed utilization efficiency of European sea bass fed the experimental diets¹.

	Diets				
	CTR-	ABP1	ABP2	Mix	CTR+
Final body weight (g)	74.0 ± 4.8 ^a	83.0 ± 1.6 ^{ab}	73.7 ± 6.8 ^a	80.0 ± 12.0 ^{ab}	97.0 ± 2.0 ^b
Weight gain (%IBW [†])	155.4 ± 16.6 ^a	185.3 ± 5.4 ^{ab}	160.5 ± 23.2 ^a	176.0 ± 41.3 ^{ab}	233.8 ± 6.7 ^b
Daily growth index ²	17.3 ± 0.1	19.8 ± 0.0	17.7 ± 0.2	18.9 ± 0.3	23.4 ± 0.1
Feed intake (g kg ABW ^{-1.5} day ⁻¹)	15.4 ± 1.4	16.7 ± 0.3	15.6 ± 0.2	15.8 ± 1.3	17.5 ± 0.1
Feed efficiency ³	0.82 ± 0.03 ^a	0.86 ± 0.02 ^{ab}	0.84 ± 0.03 ^{ab}	0.87 ± 0.06 ^{ab}	0.94 ± 0.01 ^b
Protein efficiency ratio ⁴	1.82 ± 0.08 ^a	1.86 ± 0.05 ^{ab}	1.84 ± 0.07 ^a	1.88 ± 0.12 ^{ab}	2.09 ± 0.02 ^b

[†]IBW: initial body weight.

⁵ABW: average body weight (initial body weight + final body weight) / 2.

¹Mean values and standard deviation (± SD) are presented for each parameter (n=3).

Significant differences within the diets are indicated by different letters (Tukey test, P < 0.05).

²DGI: ((final body weight^{1/3} - initial body weight^{1/3}) / time in days) × 100.

³FE: (wet weight gain / dry feed intake).

⁴PER: (wet weight gain / crude protein intake).

[0046] In an embodiment, the fermentation of the strains can be easily reproduced by another practitioner. Furthermore, regarding commercial applications, companies within the aquaculture and feed industry may be potentially interested in acquiring these strains for the development of new PRO with digestive added-value.

[0047] In an embodiment, diet composition was formulated. Three experimental diets were formulated to be isonitrogenous (47% crude protein), isolipidic (17% crude lipid) and to contain 30% of soy bean meal (SBM diet), 30% of rapeseed meal (RSM diet) or 30% of sunflower meal (SFM diet). A FM-based diet was used as the control diet (CTR diet). Fish oil and pregelatinized maize starch were the main lipid and carbohydrate sources, respectively. Bicalcium phosphate was added to adjust dietary phosphorus level.

All diet ingredients were thoroughly mixed and dry-pelleted in a laboratory pellet mill (California Pellet Mill, CPM Crawfordsville, IN, USA), through a 3.0 mm die. Pellets were dried in an oven at 50 °C for 24 h, and then stored at -20 °C until used. Ingredients and proximate composition of the experimental diets are presented in **Table 2**.

[0048] **Table 2.** Ingredients composition and proximate analysis of experimental diets

Diets ^a	CTR	SBM	RSM	SFM
<i>Ingredients (% dry weight)</i>				
Fish meal ^b	60.2	38.7	45.2	48.1
Soy bean meal ^c	—	30.0	—	—
Rapeseed meal ^d	—	—	30.0	—
Sunflower meal ^e	—	—	—	30.0
Pregelatinized maize starch ^f	23.2	11.6	8.0	4.8
Fish oil	12.1	13.6	12.4	13.0
Bicalcium phosphate ^g	1.0	2.6	1.0	0.6
Choline chloride (50 %)	0.5	0.5	0.5	0.5
Vitamin premix ^h	1.0	1.0	1.0	1.0
Mineral premix ⁱ	1.0	1.0	1.0	1.0
Binder ^j	1.0	1.0	1.0	1.0
<i>Proximate analysis (% dry weight)</i>				
Dry matter	91.5	92.4	92.7	93.5
Crude protein	46.9	46.5	46.3	46.4
Crude lipids	17.3	16.1	16.6	16.8
Ash	11.3	11.7	11.3	11.1

DM dry matter, CP crude protein, CL crude lipid

^a CTR, control fishmeal-based diet; SBM, soybean meal-based diet; RSM, rapeseed meal-based diet; SFM, sunflower meal-based diet

^b Steam Dried LT fish meal, Pesquera Diamante, Austral Group, S.A Perú (CP: 74.7 % DM; GL: 9.8 % DM)

^c Sorgal, S.A. Ovar, Portugal (CP: 53.7 % DM; GL: 2.1 % DM)

^d Sorgal, S.A. Ovar, Portugal (CP: 37.5 % DM; GL: 4.0 % DM)

^e Sorgal, S.A. Ovar, Portugal (CP: 30.3 % DM; GL: 1.0 % DM)

^f C-Gel Instant-12016, Cerestar, Mechelen, Belgium

^g Premix, Portugal (Calcium: 24 %; Total phosphorus: 18 %)

^h Vitamins (mg kg⁻¹ diet): retinol acetate, 18,000 (IU kg⁻¹ diet); cholecalciferol, 2000 (IU kg⁻¹ diet); alfa tocopherol acetate, 35; sodium menadione bisulphate, 10; thiamine-HCl, 15; riboflavin, 25; calcium pantothenate, 50; nicotinic acid, 200; pyridoxine HCl, 5; folic acid, 10; cyanocobalamin, 0.02; biotin, 1.5; ascorbic acid, 50; inositol, 400

ⁱ Minerals (mg kg⁻¹ diet): cobalt sulphate, 1.91; copper sulphate, 19.6; iron sulphate, 200; sodium fluoride, 2.21; potassium iodide, 0.78; magnesium oxide, 830; manganese oxide, 26; sodium selenite, 0.66; zinc oxide, 37.5; dibasic calcium phosphate, 8.02 (g kg⁻¹ diet); potassium chloride, 1.15 (g kg⁻¹ diet); sodium chloride, 0.44 (g kg⁻¹ diet)

^j Aquacube (guar gum, polymethyl carbamide, manioc starch blend, hydrate calcium sulphate) Agil, UK.

[0049] In an embodiment, the animal experiment was performed at the Marine Zoology Station, Porto University, Portugal, with European sea bass, juveniles obtained from a commercial fish farm (Maresa S.A., Ayamonte, Huelva, Spain). After transportation to the experimental facilities fish were first submitted to a quarantine period of 30 days before transfer to the experimental system where they were allowed to adapt for 15 days. Before the experimental period, fish were fed a commercial diet (48% protein, 11% lipids, 5% starch). The trial was performed in a recirculating water system equipped with 12 cylindrical fiberglass tanks of 100 l water capacity and thermo-regulated to 22.0 ± 1.0 °C. Tanks were supplied with continuous flow of filtered seawater (2.5-3.5 l min⁻¹) of 34.0 ± 1.0 g l⁻¹ salinity and dissolved oxygen was kept near saturation (7 mg l⁻¹). Thereafter, 20 European sea bass with an initial mean body weight of 34.4

g were distributed to each tank and the experimental diets randomly assigned to triplicate groups. The trial lasted 45 days and fish were fed by hand, twice daily, 6 days a week, until apparent visual satiation. The experiment was performed by accredited scientists (following FELASA category C recommendations) and was conducted according to the EU directive 2010/63/EU on the protection of animals for scientific purposes.

[0050] In an embodiment, sampling was carried out as follows. Fish in each tank were bulk-weighed at the beginning and at the end of the trial, after 1 day of feed deprivation. For that purpose, fish were slightly anaesthetized with 0.3 ml l⁻¹ ethylene glycol monophenyl ether (Sigma-Aldrich, Steinheim, Germany). On the sampling days (at day 15 after the beginning of the trial and at the end of the trial or day 45), fish were fed several times over the day to guarantee that gut was full at sampling time. At 4 h after the first meal, 3 fish per tank were randomly sacrificed with an overdose of ethylene glycol monophenyl ether, for collection of biological samples under aseptic conditions. To overcome inter-fish variation, the resulting material was pooled into one sample per tank to assess differences between dietary groups. Whole-gut (without pyloric caeca) were aseptically excised and squeezed to collect the digesta contents.

[0051] In an embodiment, the isolation of sporeforming bacteria was performed as follows. Each sample of digesta (1 g) obtained from fish fed the different dietary treatments was homogenized in 9 ml of buffered saline solution (0.9%). Serial dilutions were prepared in Bott & Wilson (B&W) salts and 100 µl aliquots spread on the surface of LB agar medium, after 20 min heat treatment at 65 °C, for sporeformers selection. Plates were incubated at 30 °C in aerobic conditions for up to 5 days. Following selection, sporeformers were isolated and characterized for morphology in DSM, to confirm spore production by phase-contrast microscopy. Colonies representing different morphologies were picked at random and purified by restreaking on agar plates of the same media, before storage at -80 °C in LB broth with 30% glycerol. Sporeformers isolates were routinely grown aerobically at 37 °C in LB or DSM. The laboratory strain *B. subtilis* 168 [14] was used as a control in most of the experiments described in the present disclosure.

[0052] In an embodiment, screening sporeforming bacteria for carbohydrates metabolism was carried out as follows. Each sporeformer isolate was cultured on solid M9 minimal medium [15] supplemented with 0.2% (w/v) of each of the following carbohydrates: D-glucose (G7528), D-fructose (F3510), D-xylose (X3877), L-arabinose (A3256), D-galactose (G0750), D-mannose (63580), all purchased from Sigma-Aldrich, Steinheim, Germany-Aldrich Co. LLC. The Xylooligosaccharides (XOS) and Galactooligosaccharides (GOS) are commercially available prebiotics from Qingdao FTZ United International Inc. (Qingdao, China) that were added at the same concentration (0.2%). Growth after 24 h at 37 °C was recorded by photographing colonies in a Gel Doc XR System (Bio-Rad) using the Image Lab software v.4.0.1 (Bio-Rad). Growth quantification was assessed by measuring the colony volume on fixed areas with local background

subtraction (adjusted volume = $[CNT \cdot mm^2]$ data counts/ mm^2) using the Quantity One software v.4.6.9 (Bio-Rad). Quantification of carbohydrates utilization in liquid M9 was performed after an overnight enrichment in liquid LB at 37 °C with agitation. Each isolate was diluted to an initial optical density (OD_{600} ; absorbance measured at 600 nm) of 0.1 in liquid M9 minimal medium alone or supplemented with 0.2% of the different carbohydrates previously tested. Bacterial growth was followed during 48 h and quantified by measuring the OD_{600} . In both solid and liquid medium assays, results presented were corrected by subtracting the colony volume/ OD_{600} measured in M9 alone.

[0053] In an embodiment, the taxonomic identification of PRO isolates was performed as follows. Identification was carried out for all the isolates with promising extracellular carbohydrolytic activities. Total genomic DNA extraction was performed from overnight LB cultures, using the EZNA bacterial DNA purification kit (Omega Bio-Tek, USA), according to the manufacturer's instructions and quantified with the Qubit 2.0 Fluorometer (Invitrogen, Oregon, USA). PCR amplification of the small-subunit rRNA (16S rRNA) was carried at an annealing temperature of 55 °C using primers 27F and 1492R. Each 20 µl reaction contained 1 x DreamTaq Buffer (Thermo Scientific, Vilnius, Lithuania), 0.2 mM of each dNTP (Thermo Scientific, Vilnius, Lithuania), 0.2 µM of each primer (STAB Vida, Lisboa, Portugal), 1 U of DreamTaq DNA Polymerase (Thermo Scientific, Vilnius, Lithuania) and 25 ng of DNA template. The Bioinformatics Resources Sequence Match package of the Ribosomal Database Project 11 (<http://rdp.cme.msu.edu>) and BLAST of the GenBank nonredundant (nr) nucleotide database (<http://www.ncbi.nlm.nih.gov>) were used to analyse the sequencing data.

[0054] In an embodiment, the screening of PRO isolates for NSPases was performed as follows: to tentatively obtain a set of primers specific for the genes encoding NSPs degrading enzymes (NSPases), an initial search was conducted at the Protein Knowledgebase - UniProtKB with terms "family:hydrolase AND annotation:(type:location AND secreted) AND taxonomy:"Bacteria". A file containing bacterial secreted glycosyl hydrolases (GH) was then created and the ones involved in the utilization of NSPs of interest were chosen for further analysis. Enzymes chosen included mannanases, mannosidases, arabinofuranosidases, arabinanases, glucosidases, glucanases, fructosidases (fructanases), fructafuranosidases, galactorunases, xylosidases, and xylanases. The protein sequence of each individual enzyme was used to search for similar proteins in the translated nucleotide database (tblastn) (<http://www.ncbi.nlm.nih.gov>) and to make nucleotide alignments between the sequences obtained with ClustalW algorithm using Geneious R7 v7.1.7 (Biomatters, Auckland, New Zealand). Regions of sequence conservation were chosen to design primer pairs (**Table 4**) with the Vector NTI 10 software (Invitrogen, Carlsbad, CA), with a calculated annealing temperature of approximately 55 °C and an amplicon size of 200 to 250 base pairs (bp). PCR amplification was done essentially as described for the 16S rRNA (previous section), adjusting the annealing temperature to 55 °C and the extension time to 30 s.

[0055] In an embodiment, biosafety issues in particular antibiotics susceptibility and hemolytic activity were also evaluated. Antimicrobial resistance was studied by testing susceptibility of sporeforming isolates to different classes of antibiotics, namely Macrolides (Erythromycin, EM), Aminoglycosides (Kanamycin, KM, Streptomycin, SM, and Gentamycin, GM), Tetracyclines (Tetracycline, TC), Glycopeptides (Vancomycin, VA) and Cloramphenicol (CL), following the recommendations of the EFSA Panel on Additives and Products or Substances used in Animal Feed [16]. Minimal inhibitory concentrations (MIC) were determined using Etest® (bioMérieux, Inc.). Hemolysis was determined on Columbia 5% sheep blood agar plates streaked with colonies from fresh LB plates, after incubation at 37 °C for 24, 48 and 72 h.

[0056] In an embodiment, antimicrobial activity screening assays were performed as follows. The antimicrobial activity of selected sporeforming isolates was assessed by a colony overlay assay using as targets different fish pathogens. Zones of growth inhibition around the producer strains spots after 24 h incubation at 25 °C (for *Photobacterium damsela*, *Vibrio harveyi*, *Tenacibaculum maritimum* and *Aeromonas bivalvium*) or 37 °C (for *Staphylococcus aureus*) were considered as positives and the corresponding growth-inhibition halos diameter measured (mm). A cell-free supernatant screening assay was performed by inoculating BHI or Marine Agar (for *T. maritimum*) plates with overnight cultures of indicator strains, assuring a uniform and complete coverage of the agar plate. After 15 min rest to allow plates to dry, 1 cm holes were done in the agar and consequently filled with 200 µl of cell-free supernatant of each producer strain, previously centrifuged and filtered through a 0.2 µm cellulose filter, from stationary phase LB cultures (grown overnight at 37 °C). Zones of growth inhibition around the producer strains supernatant holes obtained after 24 h incubation at 25 °C or 37 °C (as before) were considered as positive. All observations were recorded by photographing in a Gel Doc XR System (Bio-Rad) using the Image Lab Software (Bio-Rad).

[0057] In an embodiment, sporulation, germination and resistance to gut environment were also carried out as follows. The kinetics of spore formation and germination was quantified using adaptations of well-established methods [15, 17]. Sporulation occurred in DSM for 24 h at 37 °C in an orbital shaker at 200 rpm, and its efficiency was determined by plating serial dilutions made in B&W isotonic buffer (Bott and Wilson salts: 1.24% K₂HPO₄, 0.76% H₂PO₄, 0.1% trisodium citrate, 0.6% [NH₄]₂SO₄, pH 6.7) on LB agar, before and after a 20 min heat treatment at 80 °C to eliminate vegetative cells. Following 24 h incubation at 37 °C, visible colonies were counted, and sporulation efficiency calculated as the titre of colony forming units (CFU ml⁻¹) before and after the heat treatment.

[0058] Preparation of highly purified spores was done as follows: in brief, 48 h spores preparations (in liquid DSM) of each isolate were centrifuged for 10 min at 10000 g and 4 °C. Cell pellets were suspended in 50 mM Tris-HCl (pH 7.2) containing 50 µg ml⁻¹ of lysozyme, and incubated for 1 h at 37 °C. After a single wash with 1 volume of distilled water (10 min at 10000 g, 4 °C), cell pellets were suspended in 0.05% SDS, followed by three washes with distilled water and finally suspended in 1 volume of distilled water. Spores

purity and recovery yields were determined by plating serial dilutions on LB agar, before and after a 20 min heat treatment at 80 °C.

[0059] Spore germination in response to the addition of 100 mM L-alanine or to a mixture of 100 mM KCl, 56 mM glucose, 56 mM fructose and 33 mM L-asparagine (AGFK), was performed at 37 °C in 50 mM Tris-HCl, pH 7.5.

[0060] Potential resistance to gut transit was evaluated by determining the acid and bile tolerance of each selected isolate. For that purpose, 48 h DSM spores preparations were heat-treated for 20 min at 80 °C to eliminate vegetative cells and harvested by centrifugation. After a double wash with Phosphate-buffered saline (PBS), serial dilutions made in B&W salts were plated onto LB agar plates to determine the initial bacterial counts. Spores were then diluted in 1 volume of 0.85% NaCl, pH 2, containing 3 mg ml⁻¹ pepsin (Sigma-Aldrich, Steinheim, Germany), to mimic stomach conditions. Following 4 h incubation at 37 °C with agitation, serial dilutions made in B&W were again plated onto LB agar plates to determine bacterial counts, and, after a single wash with PBS, spores were resuspended in LB, pH 8 containing 1 mg ml⁻¹ pancreatin (Sigma-Aldrich, Steinheim, Germany) and 0.3% bile salts (Sigma-Aldrich, Steinheim, Germany). Bacterial incubation continued for 24 h at 37 °C with agitation to mimic passage through the gut. Finally, serial dilutions made in B&W were again plated onto LB agar plates to determine the final bacterial counts. All plates were incubated at 37 °C during 24 h prior to colonies count.

[0061] In an embodiment, shotgun genome sequencing was carried out at the Research and Testing Laboratory (Lubbock, TX, USA) using the PacBio RSII sequencer (Pacific Biosciences, CA, USA). A total of 78,219 and 96,855 reads (with a mean read length of 13,383 and 15,478 base pairs) were obtained for ABP1 and ABP2, respectively, using as reference the *Bacillus subtilis* subsp. *subtilis* str. 168 (AL009126.3) [14]. The raw sequences were assembled using Pacific Biosciences SMRT Analysis v2.3.0. The total size of the assembly was around 4,068 Mb (2 final contigs) for ABP1 and 4,308 Mb (3 final contigs) for ABP2. A BLAST analysis against the RefSeq_genome database (NCBI) revealed that the best match for ABP1 is the *Bacillus subtilis* subsp. *subtilis* str. BSP1 (CP003695.1; (11)) while for ABP2 a best match is *Bacillus* sp. LM 4-2 (CP011101.1; (12)). The BLAST version used was the 2.7.1.

[0062] Both assemblies were analysed by using the Rapid Annotation Subsystem Technology (RAST) server. The amino acid sequences of each gene identified in RAST were processed using BLASTP+ against the RefSeq_Protein (NCBI), RefSeq_RNA (NCBI) and All-tRNA [4] (<http://gtrnadb.ucsc.edu/>) databases and then passed along the DAVID web service to determine other crucial annotation data such as GO Terms, PFAMs, TIGRFAMS, EC numbers or KEGG Pathways.

[0063] In an embodiment, statistical analysis was conducted by one-way ANOVA using the SPSS 21 software package for Windows (IBM® SPSS® Statistics, New York, USA). Data were tested for normality and homogeneity of variances by the Shapiro-Wilk and Levene's test, respectively. When normality was not verified, data were transformed prior to ANOVA. Significant differences among groups were determined

by the Tukey's multiple range test. The probability level of 0.05 was used for rejection of the null hypothesis.

[0064] More than 200 bacterial isolates were obtained from the heat-treated gut contents of European sea bass fed each dietary situation (CTR, SBM, RSM and SFM). Following purification, 160 isolates representing different samples and colony morphologies (illustrated in **Fig. 1, Panels A to J**) were chosen for analysis. Spore production of each isolate, induced by nutrient exhaustion on Difco Sporulation medium, was confirmed by phase-contrast microscopy (**Fig. 1, Panel K**). All isolates were identified by partially sequencing the 16S rRNA gene revealing a predominance (60%) of *Bacillus* species among European sea bass gut contents (**Fig. 2A**). *Oceanobacillus* were also present, although to a lower extent (~10%), with the remaining isolates distributed between the genera *Lysinibacillus* and *Sporosarcina* (with 5% each), *Aneurinibacillus* and *Virgibacillus* (with less than 1% of the isolated population, each). Identification to the species level was in most cases inconclusive. Nevertheless, the great majority (> 60%) of the isolates belonging to the *Bacillus* genus fall in the *B. cereus* group (*B. cereus*, *B. anthracis*, *B. thuringiensis*, *B. mycoides*, *B. pseudomycoides*, *B. weihenstephanensis*, and *B. cytotoxicus*) or in the *B. subtilis* - *B. licheniformis* clade (*B. subtilis*, *B. vallismortis*, *B. mojavensis*, *B. atrophaeus*, *B. amyloliquefaciens*, *B. licheniformis*, *B. sonorensis*, and *B. tequilensis*) (**Fig. 2B**).

[0065] In an embodiment, the carbohydrolytic activity of gut sporeforms was evaluated. The entire collection of 160 isolates was screened for their carbohydrolytic potential by substrate specific culture-based methods, and different profiles of carbohydrate utilization could be assigned to different isolates, as illustrated in **Fig. 3**. The great majority of isolates grew well on glucose-supplemented medium, but not in the other carbohydrates tested. The quantification of each colony density or volume revealed the 43 isolates with higher and/or broader carbohydrolytic capacity (**Fig. 8**).

[0066] In an embodiment, the carbohydrate-active gut sporeforms were tested as PRO for aquaculture as follows. The selected 43 isolates were checked for minimal biosafety requirements to be considered as PRO, following the guidelines from the EFSA and the World Health Organization (WHO) [8, 17]. The majority (33) of the isolates exhibited some degree of hemolytic activity when cultivated on 5% sheep blood agar plates, with 14 isolates showing strong or β hemolysis (**Table 3**). Half of the isolates revealed to be resistant to at least 1 antimicrobial, and 10 isolates were resistant to 2 or more antimicrobials, defined as MR in **Table 3** and detailed in **Table 5**. These tests allowed selecting a strict group of 11 isolates as good candidates to become a PRO for European sea bass (**Table 3**, highlighted in bold lettering), as isolates showing strong hemolytic activity or any antimicrobial resistance to the different classes of antibiotics tested were not further studied.

[0067] **Table 3.** Characterization and identification of the 43 isolates with broader carbohydrate-activity

Isolate ^a	Diet ^b	Spores ^c	Catalase ^d	Hemolysis ^e	AbR ^f	16S rRNA sequence analysis	
						Closest known species ^g	% ID

<u>ABP3</u>	CTR	+	+	β	-	<i>B. thuringiensis; B. cereus</i>	100
ABP4	CTR	+	+	γ	-	<i>Bacillus</i> sp.	99.2
ABP5	CTR	+	+	γ	-	<i>B. subtilis</i>	98.2
<u>ABP6</u>	SFM	+	+	β	-	<i>B. cereus</i>	100
ABP7	SFM	+	+	α	-	<i>B. pumilus; B. safensis</i>	100
<u>ABP8</u>	SFM	+	+	α	MR	<i>B. licheniformis</i>	100
<u>ABP9</u>	SFM	+	+\-	β	-	<i>B. cereus</i>	100
<u>ABP10</u>	SFM	+	+	β	-	<i>B. simplex; B. macroides</i>	100
ABP1	SFM	+	+	α	-	<i>B. subtilis</i>	100
<u>ABP11</u>	SBM	+	+	β	R	<i>B. sp</i>	99.2
<u>ABP12</u>	SBM	+	+	α	R	<i>B. safensis</i>	99.8
<u>ABP13</u>	RSM	+	+	α	MR	<i>B. licheniformis</i>	100
<u>ABP14</u>	RSM	+	+	α	R	<i>B. pumilus</i>	99
<u>ABP15</u>	RSM	+	+	β	R	<i>B. cereus; B. subtilis</i>	99.6
<u>ABP16</u>	RSM	+	+	α	R	<i>B. safensis; B. pumilus</i>	100
<u>ABP17</u>	CTR	+	+	β	-	<i>B. subtilis; B. mojavensis</i>	99.2
<u>ABP18</u>	CTR	+	+	α	MR	<i>B. licheniformis; B. aerius</i>	100
<u>ABP19</u>	CTR	+	+	β	-	<i>B. subtilis</i>	99.6
ABP20	SBM	+	+	α	-	<i>B. subtilis; B. amyloliquefaciens</i>	100
<u>ABP21</u>	RSM	+	+	α	MR	<i>B. licheniformis</i>	100
<u>ABP22</u>	RSM	+	+	γ	MR	<i>B. licheniformis; B. aerius</i>	86.2
<u>ABP23</u>	RSM	+	+	α	MR	<i>B. licheniformis</i>	100
<u>ABP24</u>	RSM	+	+	α	MR	<i>B. licheniformis</i>	100
<u>ABP25</u>	RSM	+	+	α	R	<i>B. pumilus</i>	99.9
<u>ABP26</u>	RSM	+	+	β	-	<i>B. licheniformis</i>	100
ABP27	SFM	+	+	α	-	<i>B. subtilis; B. amyloliquefaciens</i>	100
<u>ABP28</u>	SFM	+	+	β	R	<i>B. cereus</i>	100
<u>ABP29</u>	SFM	+	+	α	MR	<i>B. licheniformis; B. aerius</i>	100
<u>ABP30</u>	SFM	+	+\-	β	R	<i>B. cereus</i>	100
<u>ABP31</u>	CTR	+	+	β	-	<i>B. cytotoxicus</i>	97.8
<u>ABP32</u>	SFM	+	+	γ	MR	<i>B. licheniformis</i>	100
<u>ABP33</u>	SFM	+	+	α	R	<i>B. safensis</i>	99.5
ABP34	SFM	+	+	α	-	<i>Bacillus</i> sp.	100
<u>ABP35</u>	SBM	+	+	γ	MR	<i>B. licheniformis</i>	100
ABP2	SBM	+	+	α	-	<i>B. subtilis</i>	100
ABP36	SBM	+	+	γ	-	<i>B. simplex; B. macroides</i>	100
<u>ABP37</u>	SBM	+	+	β	-	<i>B. subtilis</i>	76.1
ABP38	SFM	+	+	γ	-	<i>Bacillus</i> sp.	99.5
<u>ABP39</u>	SFM	+	+	γ	R	<i>Bacillus</i> sp.	100
ABP40	RSM	+	+	α	-	<i>Bacillus</i> sp.	98.7
<u>ABP41</u>	SFM	+	+	γ	R	<i>B. licheniformis</i>	100
<u>ABP42</u>	SBM	+	+	γ	R	<i>B. licheniformis</i>	100
<u>ABP43</u>	RSM	+	+	β	-	<i>B. thuringiensis; B. cereus</i>	100

^a In underlined lettering are the isolates showing strong hemolytic activity or any antimicrobial resistance, discarded from the rest of the disclosure and in bold the 11 isolates used in subsequent tests. ^b CTR, control fishmeal-based diet; SBM, soybean meal-based diet; RSM, rapeseed meal-based diet; SFM, sunflower meal-based diet. ^c Spores detected by phase-contrast microscopy of 24 h cultures in DSM agar. ^d Catalase activity tested by resuspending a colony in a 3% solution of hydrogen peroxide (Sigma). ^e Hemolysis determined on Columbia 5% sheep blood agar plates after incubation at 37 °C for 24, 48 and 72 h (shown is the final reading at 72 h incubation). β -hemolysis, the bacterial hemolytic enzymes completely break down the blood cells; α -hemolysis, the bacterial hemolytic enzymes only partially break down the blood cells; γ -hemolysis corresponds to essentially no hemolytic activity detected. ^f AbR-Antimicrobial resistance determined by the E-test method against several antibiotics (Table 5). R-resistance to one antimicrobial; MR-resistance to 2 or more antimicrobials; - no resistance phenotype detected. ^g Closest known species found using RDP based on partial sequences (600 to 800 nt) of the 16S rRNA gene.

[0068] The selected 11 isolates were then simultaneously cultured in M9 liquid medium to quantify bacteria growth after 24 h in liquid M9 supplemented with the different carbohydrates (Fig. 4A). The

results from 3 independent experiments (Fig. 4A) allowed to eliminate fish isolates ABP4 and ABP5 from the follow-up tests, after revealing the lowest capacity to metabolize the carbohydrates tested.

[0069] The presence of specific carbohydrases coding genes in these 11 isolates was investigated by using oligonucleotide primers specifically designed to target the genes coding for β -glucanase (*bgIS*), levanase or β -D-fructofuranosidase (*sacC*), mannan endo-1,4- β -mannosidase (*gmuG*), endo-1,5- α -L-arabinanase (*abnA*), and arabinoxylan arabinofuranohydrolase (*xynD*) (Table 4). Their broad carbohydrolitic phenotype could not be correlated with the presence of the target genes, since no PCR amplification was obtained for the most promising isolates (ABP38 and ABP40) while all target genes seem to be present in the worst fish isolates ABP4 and ABP5 (Fig. 4B).

[0070] **Table 4.** Oligonucleotide primers used in the present disclosure

Target enzyme ^a / gene ^b	Primer Name	Primer Sequence (5'-3')
β -glucanase (GH16 - EC 3.2.1.73) / <i>bgIS</i>	BgIS-339F	AGGGATCGTTTCATCGTTCT
	BgIS-553R	TAATAGAGTTTGGCTGCCAATC
Levanase (β -D-fructofuranosidase) (GH32 - EC 3.2.1.80) / <i>sacC</i>	SacC-106F	CCTCAATATCACTTCACACCGGAG
	SacC-336R	ATCTACAACGCTGCGCTTCCAGAAAA
Mannan endo-1,4- β -mannosidase (GH26-EC 3.2.1.78) / <i>gmuG</i>	GmuG-563F	TCAGGCCGCTGCATGAAATGAACG
	GmuG-786R	AATATCCACGTAAGACGCGCCCGG
Endo-1,5- α -L-arabinanase (GH43 - EC:3.2.1.99) / <i>abnA</i>	AbnA-311F	GGGCGCCGGACATCCAATACTATA
	AbnA-564R	AGTCAGCTTAATGCCGCTCCAAAA
Arabinoxylan arabinofuranohydrolase (GH43 - EC:3.2.1.55) / <i>xynD</i>	XynD-361F	AAATGGGCAGGTGCGTCATGGGC
	XynD-591R	GTCGTCATCTACAAATACTGCCGG

^a The enzyme Glycoside Hydrolase Family (GH) number and the EC number are providing in brackets

^b gene name in *B. subtilis* strain 168 genome, whose sequence was used to design the oligonucleotide primers

[0071] **Table 5.** Susceptibility of selected isolates to various antimicrobial agents

Isolate ^b	MIC ^a (μ g ml ⁻¹)						
	CL	TC	EM	KM	VA	GM	SM
ABP3	6	1.5	0.19	1.5	3	0.38	1,5-2
ABP4	4	0.094	0.094	0.75	0.75	0.125	4-6
ABP5	4	0.125	0.094	0.75	1	0.125	4
ABP6	4	0.75	0.125	3	2	0.75	0.75
ABP7	5	0.75	0.142	0.625	0.375	0.094	0.75
ABP8	> 256	4	> 256	3	8	0.75	24
ABP9	4	0.38	0.125	2	2	0.28	0.38
ABP10	1.5	0.047	0.032	0.25	0.094	0.094	0,75-1,0
ABP1	3.5	0.22	0.0945	0.625	0.625	0.1095	1.875
ABP11	4	0.75	0.125	3	8	0.75	1.5
ABP12	8	0.5	0.094	1	0.25	0.38	1.5
ABP13	> 256	4	> 256	2-3	4	0.75	16-24
ABP14	12	0.5	1	1.5	0.38	0.125	1.5
ABP15	4	0.75	0.125	2	4	0.38	2
ABP16	12	0.38	0.5	1.5	0.5	0.19	2,-3

ABP17	6	4	0.19	1	1	0.064	4
<u>ABP18</u>	> 256	4,-6	> 256	3	4	0.5	24
ABP19	6	3,-4	0.125	0.75	1	0.125	4
ABP20	3.5	1.75	0.1095	0.875	0.875	0.1095	2.5
<u>ABP21</u>	> 256	2	> 256	1,5-4 (?)	6	0.75	32
<u>ABP22</u>	14	0.315	> 256	1.75	2.75	0.565	3
<u>ABP23</u>	> 256	2	> 256	4	6	0.75	32
<u>ABP24</u>	> 256	2	> 256	12	4	0.5	19
ABP25	16	0.5	0.75	1.5	0.5	0.125	3
ABP26	6	1.5	0.125	0.75	1	0.125	2
ABP27	3	1.5	0.125	0.875	1.125	0.172	2.5
ABP28	6	0.5	0.19	2	4	0.38	0,75-2
<u>ABP29</u>	> 256	4	> 256	3	6	0.5	16
ABP30	6	0.75	0.125	2	6	0.38	1.5
ABP31	3	0.094	0.125	0.75	1.5	0.25	0.5
<u>ABP32</u>	12	0.25	0.5	2	3	0.5	8
ABP33	8	0.625	0.315	0.875	0.315	0.1095	0.625
ABP34	3	4.5	0.1095	0.315	1	0.079	1.75
<u>ABP35</u>	32	4,-6	> 256	2	2,-3	0.38	48
ABP2	3.5	6	0.1095	0.75	1.125	0.094	7
ABP36	5.5	20.625	2.032	0.3125	1	0.0585	4.25
ABP37	4	0.094	0.094	0.38	0.75	0.094	1
ABP38	4.5	0.1875	0.0705	0.875	0.22	0.094	2.5
ABP39	8	0.047	0.064	0.38	0.125	0.016	0.75
ABP40	2	0.625	0.1095	3	3	0.315	0.565
ABP41	3	0.22	0.25	1.5	4	0.845	2.5
ABP42	48	0.19	0.25	1.5	1.5	0.38	4
ABP43	4	0.5	0.125	4	3	0.38	1.5

^a MICs were determined by the Etest® method and in grey boxes are the MIC values above the reference breakpoint (EFSA-FEEDAP, 2012). CL, Chloramphenicol; TC, Tetracyclin, EM, Erythromycin; KM, Kanamycin; VA, Vancomycin; GM, Gentamycin; SM, Streptomycin.

^b Highlighted in underlined lettering are the isolates showing resistance to 2 or more antimicrobials. All isolates showing any antimicrobial resistance were discarded.

[0072] In an embodiment, sporeforming isolates ABP7, ABP1, ABP20, ABP27, ABP34, ABP2, ABP36, ABP38, and ABP40, that simultaneously met the minimal safety requirements to be eligible as PRO and were the most efficient isolates in metabolizing the carbohydrates tested, were further characterized to determine their sporulation efficiency, an important characteristic for future industrial production and feed incorporation.

[0073] In an embodiment and by comparison with the well-studied standard strain *B. subtilis* 168 [14], isolates ABP36, ABP38, and ABP40 did not reach a minimum titer of 10^7 ml⁻¹ heat-resistant cells, after 24 h sporulation induction by nutrient exhaustion in DSM liquid medium (Fig. 5) and were discarded from the subsequent tests. Furthermore, ABP38, and ABP40 did not even reach that minimum level of total (viable) cells, revealing to be inadequate for future industrial applications. With the exception of ABP20, the remaining six isolates presented an efficiency of sporulation higher than 70%, which anticipates a high suitability for cost-effective spore production (Fig. 5).

[0074] In an embodiment, the potential to survive passage through the gastrointestinal tract, important for *in vivo* efficacy, was determined by exposure to sequential simulated stomach and gut conditions. Purified spores of isolates ABP7, ABP1, ABP20, ABP27, ABP34 and ABP2 were first subjected during 4 h to acidified NaCl containing pepsin, to mimic stomach conditions, followed by 24 h exposure to alkalized LB medium containing pancreatin and bile salts. While 4 h in simulated stomach conditions had nearly no effect on the isolates survival, the subsequent 24 h exposure to simulated gut conditions lead to a reduction in each bacterial population (**Fig. 6**). In particular, cell survival was dramatically decreased in isolates FI92 and FI157, similarly to what was observed to the standard strain *B. subtilis* 168 (**Fig. 6**). Isolates ABP1 and ABP2, which showed higher sporulation efficiency, and consequently higher cell number at time 0, were the best fit to survive in the gut.

[0075] In an embodiment, the remaining four isolates, namely ABP1, ABP20, ABP27, ABP2, were characterized for their antimicrobial activity against several fish pathogenic strains, namely *P. damsela*, *V. harveyi*, *T. maritimum*, *A. bivalvium*, and *S. aureus*. As illustrated in **Fig. 7A**, all isolates showed some extent of antimicrobial activity. Strain ABP1 was successful in inhibiting the growth of *S. aureus*, *T. maritimum* and to a lower extent *V. harveyi*. ABP20 was only active against *Ph. damsela*. ABP27 inhibited the growth of *S. aureus* and of *Ph. damsela* while ABP2 was active against *Ph. damsela*, *V. harveyi* and *T. maritimum*. The control *B. subtilis* 168 could also effectively inhibit the growth of *S. aureus*, *Ph. damsela* and *T. maritimum*, but this last inhibitory activity was lost when using its cell-free supernatant (**Fig. 7B**) as opposing to the killing activity observed with the cell-free supernatant of ABP2, clearly indicating that this strain produces an extracellular inhibition molecule(s) capable of inhibiting *T. maritimum* growth (**Fig. 7B**).

[0076] In an embodiment, and in an attempt to infer the germination capacity of these strains inside the animal gut, spores of the same four isolates, ABP1, ABP20, ABP27 and ABP2, were subject to different germinants, namely L-alanine and a mixture of KCl, glucose, fructose and L-asparagine (AGFK). For the conditions tested, isolates ABP20 and ABP27 were unable to germinate (**Fig. 9**), leading to the selection of isolates ABP1 and ABP2 as the best PRO strains.

[0077] In an embodiment, the 4,068,058 bp genome of ABP1 was found to consist on 4,304 open reading frames (ORFs) with 4,184 genes identified (30 rRNAs genes and 86 tRNA genes).

[0078] In an embodiment, isolate ABP2 contained a slightly bigger genome, with 4,308,180 bp. A total of 4,643 genes (from 4,759 ORFs) were identified, including 28 rRNAs genes and 82 tRNA genes.

[0079] In an embodiment, the G+C content of ABP1 and ABP2 genomes was estimated to be 43.9% and 43.4% respectively.

[0080] In an embodiment, an exhaustive comparative analysis against the reference *B. subtilis* str. 168 [14] using Geneious R7 v7.1.7 software (Biomatters, Auckland, New Zealand) revealed the absence of

more than 200 genes from ABP1 and ABP2 genomes. These are mostly associated with prophage like regions, namely Prophage3, SP β and the *Skin* element, or with mobile genetic elements such as the integrative and conjugative element ICEBs1. As previously described for other gut isolates including *B. subtilis* str. BSP1 [17], several negative regulators of sporulation (e.g. *rapE*, *rapK*) are also absent, resulting in a higher sporulation efficiency of these isolates when compared to the *B. subtilis* str. 168, with the advantage that this behaviour can have at the industrial and gut levels. Interestingly, both isolates lack the *sdpABCIR* operon of sporulation delaying proteins, which might result in even earlier trigger of sporulation.

[0081] In an embodiment, ABP1 and ABP2 genomes also accommodate new genes, some of which coding for NSPs-active hydrolases. For instance, additional genes that might be involved in xylose and mannose metabolism are found in ABP1, while ABP2 contains one myo-inositol catabolic operon, that might contribute to the cycling of inositol phosphates in the marine environment or to their bioavailability (from PF-diets) inside the fish-gut.

[0082] In an embodiment, by sequencing the 16S rRNA gene, all isolates could be assigned to a genus, being *Bacillus* the most prevalent (>60%). Affiliation to a species based on a single molecular marker (16S rRNA) was limited, as expected. This was the case for isolates belonging to the *B. cereus* group (*B. cereus*, *B. anthracis*, *B. thuringiensis*, *B. mycoides*, *B. pseudomycoides*, *B. weihenstephanensis*, and *B. cytotoxicus*) or to the *B. subtilis* - *B. licheniformis* clade (*B. subtilis*, *B. vallismortis*, *B. mojavensis*, *B. atrophaeus*, *B. amyloliquefaciens*, *B. licheniformis*, *B. sonorensis*, and *B. tequilensis*), whose 16S rRNA gene sequences obtained do not differ enough to distinguish them.

[0083] Although several *Bacillus* spp. are quite common in the gut of different animals, including the ones with high-fiber feeding habits, such as soil invertebrates or the giant panda [19], few studies have focused on their carbohydrateolytic potential. For example, predominant *B. subtilis* strains from the gut microbial community of the giant panda, seem to have the capacity to growth in a higher fiber environment [20], opening the possibility that also in fish, *Bacillus* spp. may have a decisive role in shaping their host digestive capacity towards the efficient utilization of PF-diets. In fact, two recent studies, although limited to cellulase and xylanase activities, reported the isolation of carbohydrate-active *Bacillus* spp. from the gut of different fish species. The 160 isolates tested in the present disclosure showed different, and in some cases potent, hydrolytic capacities when using as sole carbon source selected carbohydrates including xylose, galactose, arabinose, or mannose. This observation was further sustained by the presence of genes coding for specific extracellular CAZymes that can help fish in obtaining the otherwise unavailable energy trapped in PF. The absence of amplification for these specific genes in some isolates, despite showing broad carbohydrateolytic activities, is not surprising considering that some studies suggests that new or substantially different CAZymes involved the metabolism pathways are yet to be found in the Bacilli group of organisms. Furthermore, the lack of PCR amplification of these genes, observed with

some isolates, may also be caused by mismatches of the primer pairs, due to the difficulty to design gene-specific primers regarding genomic regions poorly conserved.

[0084] In an embodiment, PRO approval within EU for incorporation into animal feed, including aquafeeds, is subject to strict and exhaustive exigencies following EFSA guidelines on quality, safety, and efficacy of the candidate(s) bacterial strain(s) [21]. Besides the obligation of strain deposition in an internationally recognised culture collection, candidate PRO isolates must be tested for the presence of any acquired antibiotic resistance genes [11, 16, 22]. PRO, which are given to animals in massive amounts, should not contribute to the escalation of antimicrobial resistance by acting as vehicles of transferable genetic determinants. Unfortunately, these rules do not apply worldwide, and very recently antimicrobial resistant strains were found in PRO products used in Vietnamese shrimp culture or in Chinese human commercial products, with all the risks those findings pose to the aquaculture production sector and to public health [23]. Although EFSA guidelines only require the absence of acquired (transmittable) resistance genes, allowing the use of bacterial strains whose antibiotic resistance is chromosomally encoded, the option of eliminating all the strains showing any antimicrobial resistance to the different classes of antibiotics tested. Adding to that criterion, strains showing strong hemolytic activity, indicative of virulence potential in several pathogenic bacterial species, including sporeforming ones, were also not further tested. These tests allowed to select a group of 11 PRO candidates that qualify with the minimal biosafety issues to be approved by EFSA.

[0085] In an embodiment, to demonstrate efficacy, EFSA requires three *in vivo* studies showing statistically-significant effects on each target animal species [21]. To conduct such follow-up *in vivo* studies in European sea bass growth and digestibility trials, it was necessary, for practical reasons, to narrow the group of interesting and potential PRO candidates. These were subjected to a series of consecutive tests to analyze some desired characteristics on a future PRO product. First the sporulation yield, an important parameter in industrial and economical terms, was determined by comparison with the well-studied standard laboratory strain *B. subtilis* 168 [14]. Six isolates demonstrated high yield spore formation, which anticipates a good suitability for cost-effective spores' production in industrial scale. Additionally, higher sporulation levels might also act as a form of propagation inside the animal gut, maximizing these strains beneficial effect [10, 17]. Second, exposure of purified spores to sequential simulated gastric and gut conditions, revealed the four isolates best equipped to survive passage through the gastrointestinal tract, important to guarantee their *in vivo* efficacy. In particular, isolates ABP1 and ABP2, which also showed higher sporulation efficiency, seem to be the best suited to reach, at higher numbers, the gut where their PRO action can take place. To take advantage of these isolates as PRO, upon passage through the stomach and anterior gut, spores must germinate to originate new vegetative cells that can produce the enzymes / molecules thought to benefit their host. In nature, spore germination is believed to occur in response to specific nutrients. For example, *B. subtilis* spores are known to germinate in response to L-alanine, L-valine

and L-asparagine but not in response to their D-enantiomers. Taken this, and although the mechanisms of germination of spores of different Bacilli (independently of their specific species) are thought to be essentially the same, it cannot be ruled out that some of the isolates might respond efficiently to other germination molecules that might be abundant *in vivo* (inside the animal gut), explaining the germination failure of isolates ABP20 and ABP27 under the conditions assayed. Finally, and besides their carbohydrolytic potential, these PRO might also benefit the fish host by minimizing colonization with pathogenic species, known to be especially problematic in marine aquacultures. This is the case of *T. maritimum* whose growth was efficiently inhibited *in vitro*, when exposed to both cells and cell-free culture medium of isolate ABP2.

[0086] In an embodiment, sequencing ABP1 and ABP2 genomes allowed a comprehensive screening of their genomic potential to better meet the EFSA criteria for PRO. Both genomes accommodate new genes, some of which coding for NSPases (NSP-active hydrolases). For example, additional genes that might be involved in xylose (e.g. ABP10666, ABP10667), mannose (e.g. ABP10654, ABP10671) and sucrose (e.g. ABP10829, ABP10830) metabolism are found in ABP1, while ABP2 contains one myo-inositol catabolic operon (ABP24564 to ABP24567), that might contribute to the cycling of inositol phosphates in the marine environment or to their bioavailability (from PF-diets) inside the fish-gut.

[0087] In an embodiment, dissecting these genomes permitted to detail and further document their biotechnological value as PRO and / or as sources of carbohydrases or antimicrobial molecules. For instance, determining the number and type of CAZymes present in each genome provides deeper understanding on their carbohydrolytic potential also allows identification of genomic features responsible for adaptation to life within the gut that may support the role of *Bacillus* spp. as PRO [10, 12-13, 17-18]. The growing applications of spores in biomedicine and biotechnology (as oral vaccines, PRO or display systems) [12-13, 18], and the fact that there are approximately 30 PRO strains approved as feed additives in EU, but only one for aquaculture (Bactocell®, which is not a sporeformer formulation), underscore the importance of this disclosure.

SEQUENCES

[0088] This disclosure relates to 2 PRO strains, ABP1 and ABP2, which genome comprises at least one polynucleotide encoding a protein which is involved in PRO behavior, and which polynucleotide is substantially identical to a polynucleotide sequence according to ABP10666, ABP10667, ABP10654, ABP10671, ABP10829, ABP10830 for ABP1 and ABP24564 to ABP24567 for ABP2.

[0089] In an embodiment, the polynucleotides as listed in **Table 6** were isolated from *Bacillus subtilis* strain ABP1 or ABP2, and are absent or divergent in/from *B. subtilis* 168 [14], and at least in 5 out of 11 sequenced *Bacillus* isolates including:

Table 6

Gene Name	Lenght (aa)	SED ID NR / Protein	Gene Name	Lenght (aa)	SED ID NR / Protein	Gene Name	Lenght (aa)	SED ID NR / Protein
ABP10118	202	1	ABP10888	66	70	ABP23149	306	139
ABP10119	215	2	ABP10889	982	71	ABP23150	60	140
ABP10120	286	3	ABP10890	715	72	ABP23151	62	141
ABP10121	153	4	ABP10891	56	73	ABP23223	973	142
ABP10181	604	5	ABP10892	84	74	ABP23238	376	143
ABP10182	851	6	ABP10981	427	75	ABP23224	200	144
ABP10654	316	7	ABP10982	300	76	ABP23225	623	145
ABP10655	880	8	ABP10983	390	77	ABP23226	65	146
ABP10656	37	9	ABP10984	467	78	ABP23227	378	147
ABP10657	254	10	ABP10985	392	79	ABP23228	107	148
ABP10658	422	11	ABP10986	594	80	ABP23229	130	149
ABP10659	74	12	ABP10987	446	81	ABP23230	51	150
ABP10660	771	13	ABP10988	335	82	ABP23231	156	151
ABP10661	425	14	ABP10989	248	83	ABP23232	670	152
ABP10662	710	15	ABP11306	51	84	ABP23233	112	153
ABP10663	280	16	ABP11307	272	85	ABP23234	306	154
ABP10664	623	17	ABP11308	504	86	ABP23235	273	155
ABP10665	389	18	ABP11309	341	87	ABP23236	47	156
ABP10666	163	19	ABP11310	464	88	ABP23237	285	157
ABP10667	178	20	ABP11311	404	89	ABP23502	37	158
ABP10668	237	21	ABP11312	269	90	ABP24563	41	159
ABP10669	355	22	ABP11821	388	91	ABP24564	484	160
ABP10670	65	23	ABP11822	130	92	ABP24565	388	161
ABP10671	257	24	ABP11823	162	93	ABP24566	309	162
ABP10672	130	25	ABP11824	669	94	ABP24567	339	163
ABP10673	275	26	ABP11825	112	95	ABP24568	41	164
ABP10674	527	27	ABP11826	306	96	ABP24598	52	165
ABP10675	294	28	ABP11827	335	97	ABP24599	111	166
ABP10676	509	29	ABP11828	284	98	ABP24600	48	167
ABP10677	79	30	ABP11889	298	99	ABP24601	384	168
ABP10678	61	31	ABP11890	308	100	ABP24602	189	169
ABP10825	106	32	ABP11891	52	101	ABP24603	674	170
ABP10826	111	33	ABP12521	153	102	ABP24604	389	171
ABP10827	194	34	ABP12522	63	103	ABP24605	170	172
ABP10828	520	35	ABP12523	92	104	ABP24606	43	173
ABP10829	516	36	ABP12651	250	105	ABP20078	155	174
ABP10830	473	37	ABP12652	58	106	ABP20079	56	175
ABP10831	451	38	ABP12653	43	107	ABP20080	196	176
ABP10832	227	39	ABP13703	49	108	ABP20081	93	177
ABP10833	151	40	ABP13704	185	109	ABP20082	43	178

ABP10834	161	41	ABP13705	44	110	ABP20083	109	179
ABP10835	63	42	ABP13706	303	111	ABP20084	144	180
ABP10836	489	43	ABP13707	82	112	ABP20085	51	181
ABP10837	152	44	ABP13708	243	113	ABP20086	182	182
ABP10838	234	45	ABP13709	260	114	ABP20087	49	183
ABP10839	227	46	ABP13710	48	115	ABP20088	53	184
ABP10840	598	47	ABP13711	339	116	ABP20089	73	185
ABP10841	381	48	ABP13712	78	117	ABP20090	67	186
ABP10842	278	49	ABP13713	382	118	ABP20091	216	187
ABP10843	384	50	ABP13714	141	119	ABP20092	117	188
ABP10844	367	51	ABP13715	49	120	ABP20093	66	189
ABP10845	344	52	ABP13716	224	121	ABP20094	279	190
ABP10846	358	53	ABP13717	58	122	ABP20095	40	191
ABP10847	344	54	ABP13718	50	123	ABP20096	101	192
ABP10848	482	55	ABP13719	192	124	ABP20119	72	193
ABP10849	202	56	ABP13720	209	125	ABP20120	503	194
ABP10850	216	57	ABP13721	273	126	ABP20121	269	195
ABP10851	388	58	ABP22957	419	127	ABP20122	172	196
ABP10852	322	59	ABP22958	299	128	ABP20123	165	197
ABP10853	72	60	ABP22959	187	129	ABP20226	227	198
ABP10854	39	61	ABP22960	102	130	ABP20227	2296	199
ABP10855	437	62	ABP22961	573	131	ABP20228	253	200
ABP10856	563	63	ABP22962	84	132	ABP20229	880	201
ABP10857	240	64	ABP22963	58	133	ABP20230	285	202
ABP10858	332	65	ABP22964	222	134	ABP20231	744	203
ABP10859	421	66	ABP23145	87	135	ABP20232	355	204
ABP10860	418	67	ABP23146	273	136	ABP20233	83	205
ABP10886	52	68	ABP23147	52	137	ABP20234	379	206
ABP10887	1015	69	ABP23148	81	138	ABP20235	58	207

Sequence Listing

SEQ. ID No.	SEQ. Name	Amino acids sequence (one letter code)
SEQ. ID. NO. 1.	ABP10118	MNLTGESKNFDDYLLELNEVDYSNPIICALANELFNPLQTEIEKVKIAYEFVRDEISHTWDTQSKRVTCNASE VLSFKEGICYAKSNLLAALLRSEGIPTGFCYQRLMLFNTPDKGYCIHALNAVFFHSLNKKWIRLDSRGNKIGID AQFSLDKERLAFPIRQEFDEIDYPLIYVRPHPKTIAVLKEHKDAIEMYKYHLPERI
SEQ. ID. NO. 2.	ABP10119	MIWLVGLDWSIQWGTVFTVAGTLTAAFLGQVFSHRYSQKREEIKQKKEFQNLSPVVFILNYLELEREK QNIMFIKGLDETEFTERYQDDELYNPSIEFKEILEIVGLNLKYGSLIELIREYQETLSIAKRMEAFEGHCGTHLYF CGVFISDYINLSKDLGVYSQTMETSTEGSLLSRLETLPQLVLECLWNFYLGFFMQYLVLIKKINIL
SEQ. ID. NO. 3.	ABP10120	MELKNKIKRVAIYLRKSRNKEGEETEETLAKHRKRLDIAHKNNWQYEIQFQEVGSSMDEMPECQRMINKL TDGIFDAVLSVNLARVTRDDAETPKFMNLLRQDDILFVTDSEVYDLEVQEDWQALKFTGFVNNWEYENI KAQLRKGKKDSAKMGRWSNGKPNYGYIYNRLERKLEIDEEKAKAVKLAQMTIDGIGADNIAVKNLKLGY RTNKGKFFHGGQSIVRMIRSEIYKGWIVANRLKGRNKTNGKIRPQDQWIVVKDAVKPCIIDEDTWDKANKA GHLIK
SEQ. ID. NO. 4.	ABP10121	MYSYKLIDNEKVRKLEELIDEKREIHLKLTDNHLDKHLGITYDLLDVNDGSGYGFRTTPYIRRSIDLPGESI GIKLPSYFLIMINYLSRLEEQDCFPELELKITYNDNTNFKTWETKFIKVDQISKIEISSFYKLQTSLVYEFISKNNK
SEQ. ID. NO. 5.	ABP10181	MAVVTTIKHPMISGYVKGFDVKEYISRRKAKNEHNIFEMFINDLILSSYNNDPNASYEDMETGTAFGIDGV AIFINDKLVEGVEDVDYICNSTRKIEVKFLFTQTKTSEKFRSEVRDFLQGVNRRFFNFEFCEITELKNSWETAK YIYDLSTKFNPDALKMYTALAPKKISVKDEIDIDLHLKSEILTGLEVLKQRYIFEDENISLNFILKEIRELHQK ENNLTEIKFNLDKQVPYPKDGSTGIIKSAYFGLIKLEDLLDILSEAVDGERILRKGIFEDNIRDYLGANEKFDVNL DMKNGLTGTNAHLFGLLNGITIIADQVHIISTEASLVNYQIVNGCQTSNVIFESLKDIEKNYIPIRLIGTEDE DTKNAIKATNSQTALKPEQLLALRDEQKSLEEYRAKRNQNKFLLYERRTEQYRNEDIQKTKIINIPFQIKA TSAMFLDLPHEVSGQYKGVEQKTRGKLFTDSSLLNPYYVSGLTWYRVEAFIRNNEEGKKHRRARWHIMM VIKYLISDLKNPSKIIDKNAEKISEKVEKVMLNDAKSLEIENALSLIKEFIINEGILDISEDKFFERKETTGLIEM LKNRLKTL
SEQ. ID. NO. 6.	ABP10182	MEHSNKLNIYKSIQQMKEYSGKLLKVEFHIHTPASHDYRLLPGKLFKNMMLTEVFDVALNEGLYSKEFLERI QKEDFAIFEKQVIEDINRDFHVSFSNFKEILGYQLIAHSYKNNIHAAVISDHNTINGFKKLQAVLVDYYSRI KGNTQRKSIKFLGLIEISCDYYHLVGIFDEHKYTDLKNFVSKYIHSEEEGTYSCLDMVNRRITENGIPYIAHIN TSDFLGTNLYKRSFGFSGLKILGLTNIDSKERISNRIKKYQESSKGFDFCFIHEGDSHELNQLGKKNTWIKFNN LSFKSLKKAFFKNYQFCIYIDKPIYNDRFLKGIYIEPGEKGLGDKEQPEKPFIVDFSRDLNCIIGGRGVGKSTILSI LETAFTLEVTNINQLEYISRHNLIYVFNYKNMDYILNFIPQITESGSGNNYFLRKAFSETTETESGTRRLSQN WINLYRVSQVESSNGYKFQELNynetTTIIESVYKSYSINNIVELSNTRISEFIRDIVLNGERLNGSKIVLSKL NKLHKNNYRKYLRENIQSVLVNIKKREENVKMAIEEFNRLNNKLIQIVYSPKLDPTFYLKELELRYDPIFDRE KGKRVLNTYLTWDDIDEFVYEATKKFGYLEFLELILNKEHKQIENELSLNNFISGTITGEYENVSIKNNMVRVYN KIEERIFRNIKVNTSFKLFEIIDEFSLKFNINSKETIRTEKVVMDIDELSGQKVVAILTLIFNYGEHSVDSTPL VIDQPEDNLDNLYIQNLVKSRLKIKNKRQVIIATHSATIVTNADAEQVILESDNKRGWLSKKGYPDDEVVL KHIVSILEGGRESFIHKKETYMTVLDI

SEQ. ID. NO. 7.	ABP10654	MTQSPILFPTVPFKEKIWGGTALRDRFGYSIPSETTGECWAISAHKPGPSTVANGPYKGKTLIELWEEHREVF GGVEGDRFPLLTCLLDVKEDTSIKVHPDDYYAGENEELGKTECWYIIDCKENAEIYGHRTARSKTELVTMI NSGDWEGLLRRRIKIPGDFYYVPSGTLHALCKGALVLETQQNSDATYRVYDYDRDLSNGSPRELHFAKAVN AATVPHVDGYIDESTESRKGITIKTFVQGEYFSVYKWDINGEAEAMAQDESFLICSVIEGSGLLMYEDKTCLLK KGDHFIIPAQMPDFTIKGTCTLIVSHI
SEQ. ID. NO. 8.	ABP10655	MKKRLIAPMLLSAASLAFFAMSGSAQAAAYTDYSLYKVEPSNTFSTESQASQAVAKLEKDTGWDASYQAS GTTTTYQISASGIHSESEAKILSGLAKQTSITGTSSPVGSKQPYVTISSGAISGEKQANTILAKLKQETGVAGA VKAYGAAQPYMNMVMTSDIADETKVKALIQSLAKQTGIKSSYQPITHTVSVTTIQSGTIVGDSRAAQIKNAFQ KESGLQASLKETVKGQAYYFTTAAISGEANAKTLLQQLKQSTGITGSYKINQKTTVESYNVQSAYFKGLNT VKDAISQIKKNTGVSGSYQQVGKSTSYTNMKGITKQQLKIDTFFKKKKWHYTSVVKKTTTSAAYQITTA KILGEQQANKAAFFAQKKVKATKTTAGTTAENQYQLISEETSDQSKVTGKLNILKKNQLSASAKSVKKQIA DTFKITTESLLDQTKVNQALTFKSNHISAASQKTGQTAASSYQITTEAISQEEIDRVLTFFKQNKIAVTTSTK GQTAYTQYKIVTAQLSSKTALNNGLTLYKSQGLTPSYTTKSNLTLYKISVNEQFTGNDTAAASSKLKQLYGW ASSIVKVKNPQIMKTNYNLSLRDMVQKQMTVSPQTDGAAYVSLTYINTATSTVTADALNIRSTPEVSPTN VIGQFKKGDKVKIIGQTNGWAKINLWGRNASSDEVVQYVDPNNFSRDSKYFFQLKLSQTAGLNATEVN QKVLAKGILTGAFAFIDAANKYGINELYLISHALLETGNGTSDLANGLTYNKTVYNMYGIGAYDSNPNY YGAKYAYEQGWFTPEAAIIGGAKFIGSSYIHNTAYNQDTLYKMRWSATATHQYATDIGWAYKQVNRMY LYSLLDGYTLVFDVPEFK
SEQ. ID. NO. 9.	ABP10656	MYYLEIMIKMLKEIRKEPKKFDIIFVSSPPFLLLSG
SEQ. ID. NO. 10.	ABP10657	MKGVKVFHHPIIVESFRILEKLLYKKADHIVINSEGFLHYLNEHSPLVKEKVTFIPNSAREKELLISNDAKTALK IIVYGNIGLAQNVHIIRNLAELHEHQIEFLIVGYGVEKKELLYIREKNLMNVKIVNPMTRKECLELMSGCDI GIVTLKDSTVFETVLPGRIIDYITCGPIVGSAGYSKTIIEQEGVGLVTSNNSSEEMLANIMKIYNDPGLLKKM QKNCHKLIRENFMWETNIEKLINVEDTR
SEQ. ID. NO. 11.	ABP10658	MRKKVCMFVWNHFTNDARVLRCTALSDKYYDVLICHDPPNPDLDLIQKYNDHFTVYRVKRSPLLFYIQ FIYKLFKNKWSILFFLLIWICLLRMFPLLTIGFSLFAVIVLTKLKTMLVGRSIIIRMLKGYSKKYDIYHSNDLN TLPQGFCISKFRKKRKLIDSHVQTSRTGYDSPFYSKMEAYLIRKIDIMIVENHTRAAYNKELYGFYKVLH NYPFLEETKEQIDIHMLGLPKNEKILLYQGGIQVGRGLDKLIKAMPFINEGTLLFIGDGRIKKDLENMNVN MELQHRVRFLPKVPLSELPHYTRSAYLGFQVLNNVCFNHYSASSNKLFEYIMAGVPVIGCDFPEIKKVIQGE KVGLVVDSDHLSIAKGVNTLLENADLHFEHKNCDKAKRKYNWETESQLLSLYN
SEQ. ID. NO. 12.	ABP10659	MQIKKNQKNQELADKYNDLKIKYHKSLEVQEDLITLCQELIREKEYIEARYNNLKESKLGRITVWMWKRRR RNK

SEQ. ID. NO. 13.	ABP10660	MKQSKDIKTLSSKQLEKVRREKEILIGLKEKEVSITGFDDFFDTPMRILAEYNNKQTELEDAEKVYLSLFERTTN FSIPSNKEIYKLTGDRIIDPFITLSGSVKGQIYAFYKNNELYSTKIFEAPFDKISADVPENTTSYRFALRLEGKGY LQLNKLKIKQVFKEQIASKNIGVNRISITISKASKIQQFIDSIEAETQNYKNEKKELRIAAILDEFSECFKHDAEIL RLSNTDWDNEILEFNPHFVFVESCWQGNQGHWQYEVANLHKNKHRTALKKLT EYCKSKNIKT VFW DKE GYENFEFFKTAASYFDYVMTADENTVKKFKETSSINNVGILPFAAQPRIHNPINKNLHHLGGIAFAGSYNN KHESRKRDIIEIIPALDFGIDYDRYYNVPAKKVNNNTWPEEYQRHIVGSLNYSQMNVAYKNYNMFVNV NSVQNSKMHMFARRVFELLASKTMVISGSPSKGVQEYFGDLVPVACSKEETVNILKTFLYNPVYREMYEKKGH RLVLNSHTYKNRLQEICDHIGIDINLLEKPRISIISSTQRTEYMENLYNNARHQT YQNLELIILNKNSMDAEE WKQKFSSLFHPVTILQVDENVSLGHCLNKAVQRSTGEIIAKFDDDDYYAPHYLEDMLHSMEYSGADIVGKS AHYVYLEERELLILKT VGS GAERYSDFISGATLVFKKEVFVSLGGFSDKNRGEDSDFLKRAKENGNIISNDS WNFCLVRRANRNSHTWNITADDLLRNSTVHSMCKDYKKPITI
SEQ. ID. NO. 14.	ABP10661	MKVCVIGLGYIGLPTSVMFAKYGVDVIGVDVQPHVVDLSLNNGEAHLEEPGLQEFLDEALANGNFAQLVP EPADAFIIVPTPNINNDNMSCDLTYVLQAVDNIIPIYIRKGSTIIVESTIAPRSIEDYVQPLLEQNGFTIGEDIYL VHCPERVMPGNIFHELANNMRIVGGITPSCSEAGEKVYRTFVKSKIVKTDAKTAEMSKLMENTYRDVNIAL ANELTKICNDLHINALDVIEMANMHPRVNIHSPGPGVGGHCLAVDPYFIVAKAPETADLISRSRINSMPPI YIVEKVREIMEMVNGRTITIGGLAYKGDIDDLRESPALEILEMLKSEKKYEVRAIDPYVNHSENAQNLTEAL GGSDLFLILTDHSLFKTINDEDTNRMSNKVIFDTRNIVRNVPEDECEINLGSIHNFNLNAV LNV
SEQ. ID. NO. 15.	ABP10662	MRKYLCLFSFVILFLLTSFYGERVLAYTDTSTYKVTIKDEFTSEDKVKGISNKINNETGWDANYKLTGNTRRA FKIITGGFYGEDKVVDVLNDFEQNTGINGSYSENGNVQTIYQITGGFTGESKVKQVLDILQSQTGKGTYT STGEKQYYYRIVSGGFQSEQRIKEVLSKFENETSIKGSYEPIGNSKITYTVLSGGFSTEDNVKAAAETKSQTGI EASYEKIPDSESYRLVISNITESELTGIESFFGKKNWVYVKEVKNQSYRLISEPILDDQIIDKGLSFFESNKW WASKQKTDQLGENKFRTTEKISDETKLLKALNFFESNKWWAVSQTTIKGYRITSEVINSEAVLNKGLDFFK SKNLWATYSNLSKDTYIINLNEEFTGIENATSAVNKLSNVYGLNAEVVKIKDGPQIMNTNYNLTLSDMISKQ MNANPQTDSAAYVLSYINTSTSTVTADYLNVRSTPEVKSNDIIGQVQKSDKVTIISKEGNWAKINMGWR KASREEVYYINPENFSISSKYFQFLKLSQYAGLTATEVNNKILKGKIGLEGKGESFIKAAESNNINELYLIAHS LLETGNGSSELANGVMYNGKKVYNMYGIGAYDGDVTKGAQYAYNQGWFTPEAAILGGAKFIGSSYIHN ATYHQDTLYKMRWEPTVSHQYATDIGWAYKQVNRMYSLYTLDDNYTLYDIPKYK
SEQ. ID. NO. 16.	ABP10663	MEINQLRKETIKFIDLKEYKIRIEEPYLLCVTTEDGVPFEFLINIRLNQNKLLILSSGAYDNVCLKPPIFQRYTW MTEFNHSHVVYFNDPTLYINQKLSIGWQGKTNHFYLATITNVIRELAYKIKVNTKDIFFYGSSAGGFMSLILA SFLRANAIVNNPQTDVCTFYQSHVDRLFETLYPNEDKHEVIKQFRYRLNVCAFFQKLKQVPKIFYQNYACS FDVETQLIPFLNSIKSEKTLAHLTADKEIELHLYYDAELGHNPLNKQKTMEIHKAMFGS
SEQ. ID. NO. 17.	ABP10664	MRYKVKLARKIKNRLFRSKKKTQKENAAVIVHPADNRVFSLFDKTKRIEENQVQVPRKISEFSWNGSILKIA GYMYIKGLPLQKEDQVRKRLLLVNGVLF TAVSLRDPVPDKLSIDTSNVP GAYKWAGFSQQINFSKLMND KPLPQGEYKLFLEIAVDDQNVKHQEVHTVGNVSNFLSNDVYATKMEFHS AKKLMKFNLIVNYDEGEKTI NLSCNKLQEIDPSLLELDTGKEANRFLRKLNTSLFH FAYDVFRLLPIKSNKIVFASDSRLDMTGNFEFVYEELL KREENFDKFFLKSSIRDKSLSELMSMAYHFATSKII FIDDFYPIIYPLKIRKNADLVQLWHAVGAFKTFGYSR IGLPGGSPSPHSKNHRNYTKVIVSSENIRKHYAEGFGVDIENVIATGVPRTDFFDEAKKAFVKERLYTEYFPLK DKKVLFAPTFRGNGQQAHYHPEVLD FDRLYRELKDEYIFLKIHPFVRNDANIPYQSDFFYDFSSFREINE LLLVTDILITDYSSVCFEYALLNKPMIFFSYD VDDYIRKRDFFYDYDFIPGPLAKTSEQMISIIKEEKYNFEQIDS FVHYFFDDL DKGASERVVDQIVFPQEEEPSEDKVLKR

SEQ. ID. NO. 18.	ABP10665	MKTFLTRIVKGVFGTAYKLLSALLPVQHNKIVIASYREDHLSDNFKGVYEKLKQDPSLRITLLFRKMDKGLIGR VAYLLHLFSSLYHLATCRVLLDDYYFPLYVVPKRKETVAIQLWHACGAFKKFGYSIVNKPFGPSSDYLKIVPV HSNYDYAIVSAPAAVPHFAEAFQMEQKQILPLGIPRTDYFYHKEHIRTVLDEFHRVYELKHKKKLLYAPTFR GSGHHQEGDAIPLDLLQKSALSHKDYVILHLHPYMRKHAHTEEDDFVLDLTDYSYSLYDLMAISDGLITDY SSVIFEYSLLKRPMYFYCPDLEDYLEERDFYYPFESFVPGPISKDVPSPSLVHDIESDHEADTKRIEDFSQAFITHQ DGKSSGRVADFISSTLTSGAD
SEQ. ID. NO. 19.	ABP10666	MTLLKKKYPDSKVFIKGTYPYKLDHFSFVDAAYQINDIPEDVRIDHAFECVGGRGSESAIEQIIAHVHPEAC VALLGVSEYPVEIETRMVLEKGITLIGSSRSGREDFARTVDFLAQYPEVVDYLETLVGGRFPVRSIEEITNAFE ADLTSSWGKTVIEWEI
SEQ. ID. NO. 20.	ABP10667	MINQTYRLVSARQFEVYKDKVVHSDKVVVRPHTLSICAADQRYTGSRGKEAMDKKLPMALIHEGIGKV MFDPTGTFKVGTRVVMVNPPTVEEHVIAENYLSSRFRSSGYDGMQDYMFMADPRLVELPDSINPHV AAFTELITIAVHALSRFERMAHKKRDTFGVWGTEISDLS
SEQ. ID. NO. 21.	ABP10668	MIYAEILAGGKSRMGVNMMPKQFLPLNKRPIIHTIEKFLNDRFDKILIVSPKEWINHTKDILKKFIGQDDR LIVVEGSDRNEISMSGIRYIEKEFGIQDDDVITHDSVRPFLTHRIIDENIDAVLQYGAVDTVISAIDTIIASED QEFISDIPVRDNMYQGQTPQSFRISKLELYNKLSDQKAVLTDACKICSLAGEKVKLVRGVEFNIVKVTTPYD LKVANAILQERISQ
SEQ. ID. NO. 22.	ABP10669	MTLLVSFPDNARAILKEYQMGHYSFPIHVLLTQHAKSLETEFPELTVSVINEKHPLHIYKAVFSMLSSKAVIV DNYFVLTTVLTCPDIECIQVWHANGAFKRFGKLDINTQNRSRADVRRFRKVVYASFDRIVVGSEHMADIFK EFFDIKGDKFLRFGVPLTDAYYEVQENSNDLKNKYHLPADKKIILYAPTFRDHQFESFSLPFSEKQLQHDLKG EYLLAVKLHPVMKQSAELPGDSAWIKDVSDLPADLLKMSDLLISDYSSVPFEFALLDKPILFYTYDMEAYNR TRGLIRNYSEVIPGVPCCDSRALLDQLKVMNDLQSEFERFSREWNLYSRGNASKQLLSYINEKSI
SEQ. ID. NO. 23.	ABP10670	MTSRFDPKQQCADDDEQIVKKRKPQGFQSVISSKRLPRIVGRHSERFMHFITYHSSFAHYRWDR
SEQ. ID. NO. 24.	ABP10671	MQTKPINQLDFVDGELTSFVSHLETSFLDQNKGAFIVTANPEIGFEAMQNPRYEAVLSSADFILPDGIGVVL VSKLIGKPLQSRAGYDLFTSLLEKADQKKRVFFYGAAKHVIAQTIERIERDYPGIEIAGYSDGYVKNQREVA DKIAATNPDMVFVALGYPNQEFFIHKYRHLFPQAVSVGLGGSFDFVSGNVKRAPSFFIRFHLWMYRLITN PARWRRMLSIPKYVTAVLKHERTSAPQYTGQVKDQSRHL
SEQ. ID. NO. 25.	ABP10672	MKKVITYGTFDLFHYGHMKLLERARCLGDYLIVGLSTDDFNLQKQKSHHSYEHKRLILETIDFVNLVPEKS WEQKITDIKKYGVDTFVIGDDWKGKFDYLNKYCKVIYLPRTGISSTKIKKEISDLS
SEQ. ID. NO. 26.	ABP10673	MNALVRIVKEQVTSFPLILRLASYETKSQYQMNYLGVWQFLNPLIQMLAYWVFGMGIRNSKPVLTGAG EVPFIVWMLAGLIPWFFISPTILDGNSVFKRINMVAKMNFPISSLPSVVIASNLFSYFVMMGIYVIVLFASG VYPSMHWIQYIYILCMIAFMFSFSLFNSTISVLVRDYQFLLQAVTRLLFFLLPIFWNISEQLGKNHPNLLPVL KLNPIFYLIEGFRNSFLDGKWWFQDMKYTLFWLFTFLLLVGSILHMKFRDKFVDFL
SEQ. ID. NO. 27.	ABP10674	MKLKVSFRNVSKQYHLYKKQSDKIKGLFFPAKDNQFFAVRNVSDVYEGETIGFVGINGSGKSTMSNLLAKI IPPTSGEIEMNGQPSLIAAAGLNNQLTGRDNVRLKCLMMGLTNKEIDDMYDSIVEFAEIGDFINQPVKNY SSGMKSRLGFAISVHIDPDILIDEALSVDGQTFYQKCVDRINEFKKQKGTIFFVSHSIGQIEKMCDRVAVWM HYGELRMFDETKTVVKEYKAFIDWFNLSKKEKETYKKEQTEERKKEDPEAFARFRQKKKKPKSLANAVQIA ILSILTVFMAGTMFFNAPLRTIASFGAIPQNEVKNNHGNAGKSEERLTAVNKQGFIANEKAAAYKDQGLK QKADVTLPFGTEVTVAAGKQQAQIKFDGHSYYVKKSAVAANMKHAELHAAFTSYVSQNAASSYEFK FLGDSRTSIQSKLNGYTEGDTADGRKTLDFDYEKISYVLENDKATELIFHNISIPTPASLSLSDSDVLYDSSKKR FLVNTADQVFAVDNEEHTLTMLK

SEQ. ID. NO. 28.	ABP10675	MKLKKVRKAIIPAAGLGTRFLPATKAMPKEMPLIVDKPTIQYIIIEAVEAGIEDIIIVTGKSKRAIEDHFDYSPE LERNLEEKGKTELLEKVKKASNLAIDHYIRQKEPKGLGHAVWCARNFIGDEPFAVLLGDDIVQAETPGLRQL MDEYEKTLSSIGVQQVPEEETHRYGIIDPLTSEGRRYQVKNFVEKPPKGTAPSNLAILGRYVFTPEIFMYLEE QQVGAGGEIQLTDAIQLNEIQRVFAYDFEGKRYDVGEKLGFITTTLEFAMQDKELRDQLVPFMEGLLNKE EI
SEQ. ID. NO. 29.	ABP10676	MKTVFMVVYTIDVNGGMMTTAMLNRSKMLVHNGYKSDLVTFDYNPYENITSELRQIGKLDPDVNILNV NDYYRDLNTEGNVDPSYYEDEAKTEQEGYFIQDSEYDTKQYIRYFKQGSYVYKKWTEDEGYLSHIDFFNEN RQRIKREEFHKNKYKHREISFDPSNNKMNYEKYTPDGFYLRWYNSETEKQQQVFLFNRNSNKLVMFK NNAEFHTYWLNEIAAAENKPIFICDGPSSGKVRGMKKELAHRIYVMVINHFETPTYGSKVKQDHDIDL SNIDKLDALVLTNDQKKDIEKQFGEHGNIFIIPNSMPYTDLPDIKKDNKKVSMFVRYHKQKAIDEAIKAFV RVIKKVPDARLEIFGHGAEKSRLEQLIELNLQQNVFIKGYAKNVREEMGSSLITLLTSNYEAFGLSITESFMN GTPVISYDCNYGPRDVISDGDIGYIVPQKDQKALANQIIKLLNPD LAKEMGLKGREKVLTEYTNVVLNK WLQLFNVLEKK
SEQ. ID. NO. 30.	ABP10677	MYDFLNVPPDYSWIEHPIEEAGLTYIKVPEKPVYRYGKYVKYQRFSSSVNWLYQVILMTAQAKVQKRRV RKTRTQRI
SEQ. ID. NO. 31.	ABP10678	MFLTNTNGEGEYHYQYLINELSLIFEGIFGKISILSGGAWHFIQNNKASALSFVNHFLS
SEQ. ID. NO. 32.	ABP10825	MAWFLLVIAGIEEIIAAIAMKYIDGTRKKWPIIVMTVGFLSFYCLSQAMIVLPAGVAYAVWTGIGSIGVSA VGFIWFKERFQLSQVISLCLILAGVIGLRLTSSS
SEQ. ID. NO. 33.	ABP10826	MNWVLVFIAGLLEVWASSLKHADSLDWWIIFILIAVSFILLIRSYQKIPMAAAAYTVFVGIGTVGTYLTVGLG ESFSAAQMFFLALLLAGILGMKLFTEKESQSGGEQ
SEQ. ID. NO. 34.	ABP10827	MPKQTSKGYEKILQAAIEVISEKGLDKASIDIVKKAGTAQGTFFLYFSSKNALIPAIENLLTHTLDQIKGRHL GDEDFWTVLDILIDETFLITERHKDIIVLCYSGLAIDHSMKEKWETIYQPYSWLEKIINKAIANLEVTEEINSKW TARTIINLVENTAERFYIGFEQDENVEVYKKEIFSFLKRS LGTA
SEQ. ID. NO. 35.	ABP10828	MSKQGNFQKSMFLDLILIGMGAIFGSAWLFVAVSNVASKAGPSGAFSWILGGAIILLIGLVYAEALGAALPRT GGIIRYPVYSHGHLVGLYISFVTIVAYTSLISIEVTAVRQYVAYWFPGLTIKGSDSPTISGWILQFALLCLFFLLN YWSVKTFAKANFIISIFKYIVPITIIIVLIFHFQPENLSVQGFAPFGFTGIQAAISTGGVMFAYLGLHPIVSVAGE VQNPKRNIPIALIIICIVSTIYTVLQVTFIGAIPTELKHWGPAIGREFSLPFKDIAVMLGLGWLATLVILDAILS PGGNGNIFMNTTSRLVYAWARNGTLFGIFSKVNKDTGTPRASLWLSFALSIFWTLPPFSWNALVNVCSVA LILSYAIAPISSAALRVNAKDLNRPFYLKGMISIGPLSFIFTAFIVYWSGWKTVSWLLGSQVLMFLIYLCFSKYT PKEDVSLAQQQLKSAWWLIGFYIMMLIFS YIGSFGHGLGIISNPVDLILVAIGSLAIYYWAKYTGLPKAAIDYDK
SEQ. ID. NO. 36.	ABP10829	MNYIKAGKWLTVFLTFLGILLFIDLFPKEEHDQKTKSKQKPDYRAAYHFTTPDKWKNDPQKPIYFDGKYHYF YLYNRDYPKGNGTEWRHVAVSEDLVHWTDEGVAIPKYTNPDGDIWGTGSSVVDKENTAGFGKNALVAIVT QPSAKDKKQEQLWYSTDKGSKFKFYSGNPVMNPNGTDDFRDPKVIWDDQDNKWMVMMAEGSKIGFY ESDNLKDWHTYSGFFPEQAGMVECPDLYMMRASDGANKWVLGASANGKPGWKPNYAYWTGSGFDG KEFKADQTEAQWLDYGFWDYGGVTFEDSKSTDPLEKRYALAWMNNWDYANNTPTMKNGFNGTDSVI RELRLKEQDGTYSLSQPIEALEQLTVSTEEIEDQDVNGSKTSLITGDTYQLDLDLSWSELKNAGVRLRESED QKRHIDVGIFAEGGYSYVNRAATNQPKSNTYVESKAPYDVSKRKVHLKILVDKTTIEVFVGDGKTIFSNEV FPKPEDKGITLFSDDGTASFKNITVKHFD SIHK

SEQ. ID. NO. 37.	ABP10830	MNIKKFAKQATVLTFTTALLAGGATQAFAKETNQKPYKETYGISHITRHDMLQIPEQQKNEKYQVPEFDSS TIKNISSAKGLDVWDSWPLQNADGTVANYHGYHIVFALAGDPKNADDTSIYMFYQKVGETSIDSWKNAG RVFKDSKFDANDSILKDQQTQEWSGSATYTSKGIRLFYTDGSGKHGKQTLTTAQVNVASDSSSLNINGV EDYKSIFDGDGKTYQNVQQFIDEGNYSSGDNHTRLDPHYVEDKGHKYLVFEANTGTEDGYQGEESLFNKA YYGKSTSFFRQESQKLLQSDKKRTAELANGALGMIELNDDYTLKKVMKPLIASNTVTDEIERANVFKMNGK WYLFTDSRGSKMTIDGITSNDIYMLGYVSNSLTGPYKPLNKTGLVLKMDLPNDVTFYSHFAVPQAKGN NVVITSYMTNRGFYADKQSTFAPSFLNKGKTSVVKDSILEQQQLTVNK
SEQ. ID. NO. 38.	ABP10831	MKQNKRNQLTLFETLGEKHQFNGTVLAAEGGDILYHHSFGYAEMTEKRPLKTNLSFELASLSKPFTALGIIL LEEKILGYEDKVDRWLPFGPYQGVITIRHLLNHTSGLPDYMGWFFANWDPHKIAVNQDIVDMLMNEGL SGYFEPNEGWMYSNTGYVLLAVIEKASGMSYADFMKTSIFLPAGMNETRNVNRRLSPERIDHYAGYVY DVHSETYVLPDELEETNYVVYLDGIQGDGTVNSVTSDLFRFDQALYQDDFISKASKESAFSPVRLNNGETID YGFQWVWLNQSPKGRIVSHSGWPGYSTLMIRYIDHRKTLIYLSNKEEDTEYEQAIIKAAEHILFGQPYEVP ERPADKKKKAIDTAIYSRYVGSYLLQDGTAAQVTAENERLYLEIAGQLRLELFPSETRFFLRALSVEVEFTLG VDAAKSFILYEDGSEEEAVRTK
SEQ. ID. NO. 39.	ABP10832	MIGILAGMGPKSTSPFIDKVIDYCQKLYGASNDIDYPHMMIYSCPTPFYADRPIDHDEMKAIDGAVKLEK TGVDIALPCNTAHVYEEIQQALSVPMLHIVEETIKEIPLAKKAVVLGTEPTIQSAIYQKVLKNGNGQVEVIHK DHWQQAVNQLIAAIKQPNHMQHTQALWQTLYEISQHADIIISACTDLNAVLDHIQSEIPIIDSSACLAKEST VSTYLAYQS
SEQ. ID. NO. 40.	ABP10833	MKKPVLPKFASLEIKVDPITIGETSLGRRFPIRSGTITGEVKGRILPGGADSQMIRANGRTDLSARYVIETA DHELIYIENNGIRQVSEPFKQAAAGEIIEPEHVYFRTVPTFETGSEVYQWLHDLRFIGSAERTPDVYLLDIYE VQ
SEQ. ID. NO. 41.	ABP10834	MENFIGSHMIYTYENGWEYEIYKNDHTIDYRIHSGMVAGRWRDQEVNIVKLTGVYKVSWEPTGTDV SLNFMPEKRMHGIIFPKWVHEHEITVCYQNDHIDLMKESREKYETYPKYVVPFEAITFLKNEGVDNE EVISKAPYEGMTDDIRAGRL
SEQ. ID. NO. 42.	ABP10835	MGKTGYIGAAIIVAACIIILSAVVCLRDVTYVYQPMRWGTGIIFFAGIVMVPAYSARKRPGKEK
SEQ. ID. NO. 43.	ABP10836	MTHQIVTTQYGVKGTENGVHKWKGIPYAKPPLGQWRFKAPEPPEVWEDVLATAYGPICQPSDLLS LSYTELPRQSEDCLYVNVFAPDTPSQNLPMVMVWIHGGAFYLGAGSEPLYDGSKLAAQGEVIVVTNLNRLGP FGFLHLSSFDEAYSNDLGLLDQAAALKWVRENISAFGGDPDNVTVFGESAGGMSIAALLAMPAAKGLFQK AIMESGASRTMTKEQAASTSAAFLQVLGINEGQLDKLHTVSAEDLLKAADQLRIAEKENIFQLFFQPALDPK TLPEEPEKAIAGAASGIPLIGTTREDEGYLFFTPDSVDVHSQETLDAALEYLLGKPLAEKVADLYPRSLESQIH MMTDLLFWRPAYAYASAQSHYAPVWMYRFDWHPKPPYNKAFHALELPFVFGNLDGLERMAKAEITD EVKQLSHTIQSAWITFAKTGNPSTEAVNWPAYHEETRETLILDSEITIENDPESEKRQKLFPSKGE
SEQ. ID. NO. 44.	ABP10837	MIGRIIRLYRKRKGYSINQLAVESGVSKSYLSKIERGVHTNPVQFLKKVSATLEVELTELDAETMMYEKISG GEEWRVHLVQAVQAGMEKEELFTFTNRLKKEQPETASYRNRKLTESNIEEWKALMAEAREIGLSVHEVK SFLKTMGR
SEQ. ID. NO. 45.	ABP10838	MNENMSFKELYAIVRHRFVLILLITIGVTLMMGFVQFKVISPTYQASTQVLVHESDGEENSNDIQRNLQY SSTFQSIMKSTALMEEVKAELHLSASSLKGVITSSENESEIINVAVQDHPAKAAEIANLTVNKFEKEVD ERMNVQGVHILSEAKASESPMIKPARLRNMVMAFGAAVMGGITLAFHLFLDDTCKSARQLSERTGLPCL GSVPDVHKGRNRGIKHFE

SEQ. ID. NO. 46.	ABP10839	MIFRKKKARRGLAQISVLHNKSVVAEQYRTIRTNIEFSSVQTNLRSILVTSSVPGEKGSFSAANLAAVFAQQ QEKKVLLVDADLRKPTINQTFQVDNVTGLTNVLVGNASLSETVQKTPIDNLYVLTSGPTPPNPAELLSSKA MGDLISEIYEQFSLVIFDSPPLLAVADAQILANQTDGSLVVLVSGKTKTDTVLKAKDALEQSNALLGALLNK KKMKKSEHYSY
SEQ. ID. NO. 47.	ABP10840	MIIALDTYLVLSNVIAGYQFLKDSYQFYDSGALLTAVSLLSYHVCAFLFNQYKQVWYTYGLGELIVLLKGIT LSAAVTGIIQYAVYHTMFFRLLTACWVLQLLSIGGTRILSRVLNESIRKKRCASSRALIIGAGSGGTLMVRQLL SKDEPDIIIPVAFIDDDQTKHKLEIMGLPVIGGKESIMPAVQKLKINFIIAIPSLRTHQLVLYKECVRTGVSIIKI MPHFDEMILLGTRTAGQIRDVKAEDLLGRKPVTLDTSEISNRIKGKTVLVTGAGGSIGSEICRQISAFQPKIIL LGHGENSIHSIYTELNGRFGKHIVFHEIADVQDRDKMFTLMKKYEPHVYHAAAHKHVPLMEHNPEEAV KNNIIGTKNVAEADMSGTETFVLISDDKAVNPANVMGATKRAEIMIIMNLGKVSRTKFAVAVRFGNVLGS RGSVPIFKKQIEKGGPVTVTHPAMTRYFMTIPEASRLVIQAGALAKGRQIFVLDMGEPVKIVDLAKNLIHLS GYTTEQVPIEFTGIRPGEKMYEELLNKNEVHAEQIFPKIHIGKAVDGDWPVLMRFIEDFHELSEADLRARLF AAINTSDKMTAASVH
SEQ. ID. NO. 48.	ABP10841	MTKKILFCATVDYHFAFHLPYFKWFKQRGWEVHVAANGQTKLPYVDEKFSPIRRSPFPDQNLAVYRQLK KVIDTYEYDIVHCHTPVGGVLARLAARQARRHGTVLYTAHGFHFCKGAPMKNWLLYYPVEKWLSAYTD CLITINEEDYKRAKGLQRPGGRTQKIHIGVNTFRFPVSPIEQQRLREKHGFREDDFILVYPAELNLNKNQK QLIEAAALLKEKIPSLRLVFAGEGAMEQTYQMLAEKLGASANVCYFGFCSDIHELILQADSVASSIREGLG MNVLEGMAAEKPAIATDNRGHREIIRDGENGFILIKIGDSAAFARRIEQLYHKPEICRKLQGEGRKTALRFSE ARTVEEMADIYSAYMDMDTKEKSV
SEQ. ID. NO. 49.	ABP10842	MNSGPKVSVIMGIYNCERTLAESIESILSQSYKNWELILCDDASTDGTLRIAKQYAAHYSRIKLIQNKTNR LAASLNHCLSHATGDYIARQDGDLSFPRRLEKQVAFLEKHRHYQVVGTMGLVFDEFGVRGTRILPSVPEP GIMAKGTPFCHGTIMMRASAYRTLKGYRSVRRTRRMEDIDLWLRFFEEGFRGYNLQEAQYKVEDSDAFK RRSFTYSIDNAILVYQACRRLKLPLSDYIYIAKPLIRAFMPAAVMNRYHKKRVMNQKEGLVKHE
SEQ. ID. NO. 50.	ABP10843	MNSSQKRVLHVLSGMNRGGAETMVMNLYRKMDKSKVQDFLTyrNDPCAYDEEILSLGGRLFYVPSIGQ SNPLTFVRNVRNAIKENGPFSAVHAHTDFQTGFIALAARLAGVPVRVCHSHNTSWKTGFNWKDRQLQLLVF RRLILANATALCACGEDAGRFLFGQSNMERERVHLLPNGIDLELFAPNGQAADEEKAARGIAADRLIIGHV ARFHEVKNHAFLLKLAHLKERGIRFQLVLGADGPLRGEIEEARQNNLSDVFLGTEERIHELMTDFDV VMPSLYEGLPVVLEAQASGLPCIISDSITEKVDAGLGLVTRLSLSEPIVSWAETIARAAAAGRPKREFIKETL AQLGYDAQQNVGALLNVYNISTEKDHR
SEQ. ID. NO. 51.	ABP10844	MIVYAVNMGIVFIWSWFAKMCGRDDSLATGYRPNKLLIWIPLASLVLSGLRYRVGTDFQTYTLLYELAG DYQNVWQIFGFGTAKTATDPGFTALLWLMNFITEDPQIMYFTVAVVTYSFIMKTLADYGRPFELSVFLFLG TFHYASFNIRQYQYMAAVLFWAIRYIISGNWKRYFLIVLVSSLFHSSALIMIPVYFIVRRKAWSPAIFGLSAL FLGMTFLYQKFISVFFVLENSSYSHYEKWLMTNTNGMNVIKI AVLPLFLAFICYKERLSLWPDIDIVVN LCLLGLFLGLLATKDVIFARFNIYFGLYQMLVPYFVRIFDEKSNALIYIAIVVCYFLYSYLLMPVDSSVLPYRTIF SR
SEQ. ID. NO. 52.	ABP10845	METPAVSLLVAVYNTETYIRTCLSLRNQTMNDIEIIVNDGSADASPDAEEYAKMDNRKFVIHQENQGLG AVRNKGIEAARGEFI AFIDSDDWIEPDYCEQMLRAAGDETDLVICNYAAEFEDTGKTMDSIAQTYQDQP KEHYIKALFEGKVRGFSWNKLYRRSMIDAHRLSFPLRGELEHVEDQFFSFRAHFFARSVSIVKTPLYHYRIHL SSIVQRYQKLFESGLALYEANAFLQENNKLEEYRKELDTFIVLHSSICMLNEWKTSGRRLFEKLRNVGVI CADPVFQESLSKTGTAPFDAKRSCLLLMAKYRMIPFVAMASAVYQRVIEYKMRNRG

SEQ. ID. NO. 53.	ABP10846	MSLQSLKINFAEWLLKVKYPSQYWLGAADQPIKAAAHQKKIILTLLPSHDNLGDHAIYASKAFLEQEYDP FDIVEVDMKDIYKSAKSLIRSRHPEDMVFIIGGGNMGDLYRYEEWTRRFIIKTFHDYRVVQLPATAHFSDTK KGRKELKRAQKIYNAHPGLLLMARDETTYQFMKQHFHEKTILKQPDMLVLYLDRSKPPAEREGVYMCLRED QESVLQEDQRNRVKAALFEFGEIKSFTTTIGRRVSRDTREQEALWSKLQSAEAVVTDRLHGMIFCALTG TPCVVIRSFHDHKVMMEGYQWLKDIPFMKILIEHPEPERVTAAVNELLTKETPRAGFPRDVYFKGLRDKISGEA Q
SEQ. ID. NO. 54.	ABP10847	MTPLVSIIPMYNVEPFIEECIDSLCQTLSDIEIILVNDGTPDRSGEIAEDYAKRDARIRVIHQANGGLSSAR NTGIKGARGTYIGFVDGDDYVSSAMFQRLTEEAQNQLDIVGCGFYKQSSDRRTYVPPQLEANRVLTKE MTEQLKHAHETRFIWWYVWRYLYRRELFERANLLFDEDIRFAEDSPFNLSAFCEAERVKMLDEGLYIYRENPN SLTEIPYKPADDEHLQKQYQAKIAFYNHYGLAGACKEDLVYICRHQLPMLLANACASQNSPKDIKKIRQI LSYDMVRQAVRHTPIQHEKLLRGERLVLALCKWRLTFLIKLFFEQRGTMKGSAKQA
SEQ. ID. NO. 55.	ABP10848	MTPFIVKTLGVEAFGFVHLTQNVINYFSIITVALSSVVVRRFFSVAHRGEREKANAYISNYLAASVLISLLLLP LAGSAFFIDRVMNVQPALLADVRLSILIGSVLFLITFLMAGFGAAPPFYANRLYITSSIQAVQMLIRVLSVLLFA CFAPKIWQIQLAALAGAVMASVLSFYFFKKLIPWFSFRMKDLSFRTSKELFQAGAWSSVNQIGVLLFLQIDL LTANMLGASASGYAAIIQFPLLRSLAGTVASLFAPIMTSYYSKGDMDGLMNYANKAVRLNGVLLALPA ALLGGLAGPFLTIWLGPSFSSIAPLFIHAGYLVVSLAFMPLFYIWTAFNQKQTPAIVTLLGAVNVVLAVTLS GPAHLGLYGITLAGAISLILKNAIFTPLYVSRITGYKKHVFFKGIIGPLSAAVFAWTVCKAIQFIVKIDSWPSLIA AGVTVSFFYAVFAFMLVCTKEERQLVLKRFRKTKGAVNL
SEQ. ID. NO. 56.	ABP10849	MILKRLFDLTAAIFLLCCTSVIILFTIAVRLKIGSPVFFKQVRPGLHGKPFITYKFRMTDERDGEENLLPDEV RLTKTGRIRKLSIDELPQLLNVLKGDLSLVGPRPLMDYLPYTEKQARRHEVKPGITGWAQINGRNAISW EKKFELDVWYVDNRSFILDILCLTVRKVLVSEGIQQTNHVTAERFTGSGDVSS
SEQ. ID. NO. 57.	ABP10850	MKNVAIVGDGGHGKVIRELINARSDTRLAAVLDDKFKTFEGGKEWYTGPPEAVTELRLRIPDVFLIAVGN NSVRKQLAERLGLRKDDFITLIHPSAIVSRSAVIGEGTVIMAGAIQADARIGAHCIINTGAVAHDNQISDYV HLSPRVTLSGAVSVQEGAHVGTGASAIQITIGAWSIVGAGSAVIRPIPDVTAAGAPARISSIQTNSNG
SEQ. ID. NO. 58.	ABP10851	MHKKIYLSPPHMSGREQHYISEAFRSNWIAPLGPLVNSFEEQLAERVGVKAAAAVSSGTAIIHLALRLLEV EGDSVFCQSFTFVATANPILEYKAVPVFIDSEPDWNNMSPTALERALEEAKRNGTLPKAVIAVNLYGQSAK MDEIVSLCDAYGVPVIEDAAESLGTVYKKGKQSGTFRGFGIFSNGNKIITSGGGMLVSNDEAAIEKARFLA SQAREPAVHYQHSQIGHNYRLSNILAGVGIAQLEVLDERVEKRRTIFTRYKNVLGHIAGVRFMPEYAAGVS NRWLTTLTLDNGLSPYDVVQCLAENIEARPLWKPLHTQQLFDPALFYSHEDTGSVCEDLFKRGICLPSSGN MTEDEQDRVIEVLLHLFQTAEVKKWTASIR
SEQ. ID. NO. 59.	ABP10852	MDSKHSMLKQKLSGLLDVIPKQSEIYADYPLYGNVGDLFIMKGTEAFFKEHGIRVRKRWNPDPNFPVGR KLDPNLIIVCQGGGNFGDLYPYQGFREKIVQTPNHNKIVLPQSIYFQNKDNLKRTAEIFSCHANLHIMTRE KASYATAQAYFSKNHIQLLPDMAHQLFPVIPTQQPSNQKLRFIRDHEANQALQEHTETESYDWRTVLSAS DRRTIAFLQTLNVLNKKAGNPLPIAYIWGKYSDYIVQKAIRFFSRYESVTSRLHGHSALLQKENTVIDNSY GKNANYFHTWMEGVPGTRLIQHASKKENLPAHM
SEQ. ID. NO. 60.	ABP10853	MSELSVPYFIENLKQHIEMNQSEDKIHAMNSYYSRVSVTLVQDQLTKNAVVLKRIQHLDEAYNKVKRGES K
SEQ. ID. NO. 61.	ABP10854	MLTPLSSLYMIEITPYTFMKKELPKKCLNFFPSLILLRI

SEQ. ID. NO. 62.	ABP10855	MMDMKLQQVQVLKPQLTQELRQAITLLGYHSAELAHEYIDELSENPLIERKETDTPPLSYHKTNNRMNA QEAGLQLSNPQKTLQDALKQQSLDMNLTNTEKKIFNYLIHSLDSNGYLEEDVEEAARRLSVSAKETEAFLAK LQSLPAGIGARSLQECILLQLRQLPNRNEQAEMLVSAHFDAFAQKWKWALS SVETGIPLHTIQDISDDIAAL HPRPGLLFARPEQDVYIEPDIFITVKNGHIAAELNTRSFPEIDLHPQYRTLSSGSCQDQTVSYLSAKYQEW RW LSRALRQRKQTITRIINELITRQKDFFLKGRSAMKPLTLREVADCLSLHESTVSRAIKGKTIQTTPYGLFEMK LFF SAKAEASGEGDASNYAVKMHLEDLINQEDKTKPLSDQKLVDLLYEQHG IQISRRTVAKYRDQMKIPSSAAR KRYK
SEQ. ID. NO. 63.	ABP10856	MQWTQAYTPIGGNLLSALAALVPIIFFFWALAIKRMKG YTAGLATLGIALIIAVLVYRMPAEKALMSATQG AVYGLLPIGWIIVTSVFLYKITVKTGQFDIIRSSVLSITDDRR LQALLIAFSFGAFLEGAAGFGAPVAISAALLVG LGFNPLYAAGICLIANTAPVAFGAIGIPITAVEGPTGIPAMEISQMVGRQLPFLSVFIPLYLIIMSGFRKALEV WPAILVSGVSFAVVQYLSSNFLGPELPDVLSALVSMAALAVFLKWWPKTTFRFAGEQESAAS IETARTNP AAPAYSGGQIFKAWSPFLLLTAMISVWVGIPSVKSALTGHYEGSAVFLKWLNNAVGEKLT FAPGVPFLNNQIV NADGTPIEAVYKLEVLGSAGTAILIAAVLSKFITAISWKDWGTVFKETVQELKLPILT IASVVGFAVYTNSSGM STTLGMTLALTGSMFTFFSPVLGWLGVFITGSDTSANLLFGNLQKVTALSVGMDPVL SVAANSSGGVTGK MISPOQSIACAAVGLAGKESDLFRFTIKHSLFLLLVCITFLQH HVSFWMIP
SEQ. ID. NO. 64.	ABP10857	MKYKQIKTKKIYEEVADALLD MIKNGELKPGDKLDSVQALAESFQVSRSAVREALSALKAMGLVEMKQGE GTYLKEFELNQISQPLSAALLMKKEDVKQLLEVRKLEIGVASLAAEK RTEADLERIQDALKEMGSIEADDEL GEKADF AFHLALADASQNELLKHL MNHVSSLLETMR ETRKIWLFSKKT SVQRLYEEHERIYNAVAAGNGV QAEAAMLAHLTNVEDVLSGYFEENVQ
SEQ. ID. NO. 65.	ABP10858	MATIKDIAQEAGFSISTVSRVLNNDESLSVPDE TREKIYEA AEKLNRYRKTVRPLVKHIAFLYWLTDKEELEDV YFKTMRLEVEKLAKAFNVDMTTYKIADGIESIPEHTEGFIAVGTFSDEELAF LRNLTENGVFIDSTPDPDHFD SVRPDLAQMTKKT VNILTEKGHSIGFIGGTYKNPNTNQDEMDIREQ TFRSYMREKAMLDERYIFCHRGFS VENGYRLMSAAIDILGDQLPTAFMIAADPIAVGCLQALNEKGIAIPNRVSIVSINNISFAKYVSP LTTFHIDI HELCKNAVQLLEQVQDKRRTVKTLYVGAELIVRKSMNEG
SEQ. ID. NO. 66.	ABP10859	MKMAKKCSVFMLCAAVSLAACGPKESSAKSSSKGSELV VVEDKEKSIGIKDAVA AFEKEHDVKVKVVE KPYAKQIEDLRMDGPGAGTGPDLVTMPGDQIGTAVTEGLL KELHVKKDVQSLYTDASI QSQMVDQKLYGL PKAVETTVLFYKNDLISEKELPKTLEEWYDYSKKTANGSKFGFLALFDQIYYAESVMSGYGGYIFGKAKDGSY NPSDIGINNENGA VKGAALIQFYKDGLFPAGIIEQGINVLES LFTEGKAAAII SGPWNVEAFSKAGINYITK LPKLENGKNMSSFIGVKSYNVSAFSKNEELAQELAVFLANEKNSKTRY EETKEVPAVKSLANDPAIMKSGAA RAVTEQSRFSEPTNP IPEMNEI WTPADSALQTVATGKADPKQALDQAAETAKGQIKAKHSGK
SEQ. ID. NO. 67.	ABP10860	MQHRQVALLLSIIPGLGQFYNKQWIKGIVFLFLGASFFAVFGDLLNMGFWGIFTLGTEVPRD NSVFLAEGI IAVIVTCFGLAVVVYNLRDAFQSGKQRDENKPLSSLKEQYQH IIESEGYPYVVGPSLFILIFAVIFPILFSFALAF TNYDLYHSPPAKLIDWVGFTFANIFTVDIWRSTFFDVLAWTVVWTLAASTLQVSLGIFLAIIVNQDLRFK RFFRTILIPWAVPGFVTILIFAGLFNDSFGAMNHDILAFFGIDPLPWMTDANWSRLALILMQGWLGFPIYF LVSTGVLSQIPDDLYEAATIDGASVFSKLRITLPMVFIAMAPIIIITQFTFN FNNFNIIYLFNGGGPAVTGSTA GGTDILVSWIYKLTMQSSQYSLAAALTILLSVFVISIALWQFRQT KSFKEEA
SEQ. ID. NO. 68.	ABP10886	MRKDKLVSTVFKNNAIEIYTIILKNPDTLVRIKEIQLFHTKKSLAASAAKL

SEQ. ID. NO. 69.	ABP10887	MFPEVNDKDELQKIFLNVSGKTIHSLIRDDTNIQNTNIIDIRVLDHKKSDFLVRNSEEFLHNPFHFFSPF LSCKIEEFIVKVRIEDAVDNEDEFVKKVIKHILDLMEKAFRVLVLEVNIARLEGKLEGGTTPERLNHFLAVSLN DESFLKSVMYKEYEVLTSLLCVTIDDYFTYVMEIKNTKREISSLSKFNNDNLGAINITTGLGDTHQKGKSVS TIYFKSGKKIYKPRDLTLEQGFQEVLYWLDGKNIPGILNFKRVQIHTVNDSGWMEHIDYKSCFNKNEANDF YTRSGNLLCLLYLLNAVDFFHHENLIAHGSFPVLVDLESFHFARLKVDQDKKSAFVTATELVDNSVQSISLLPT KISKRVGDKDISLDIGGLGAYKEQLSPHKSIVIENAGTDTIKLRKNTFIKQLNNPSIKTGSYLYSENYTGQIK DGFESLYSWVMLNKDEFWDKISQTFKETNSRFIFRPTYLYTQLLRISHPDFMRDITYRRKIILHRIGIDYIEY KDILNSEYKDLTGDVPPFRSSIEHEHLIDSRGGKIHNILEEPIKTVKQKIFNLKEDLKRQIDFIEMSYISNEKR LKEVTDIKFSKAANLNKIKSENWIDEATQIGEFIVENSVCINKKQKDRMWIGPSLEGIEEDIWNANVLGFD IYNGNSGIALFLGYLGEILNRQDFKQAAIETMRPIQKFISEIKEDHPYLIGAFQGISGYFYTLNKLNSLFEDSELR KTTLENISVLSKLGKFDKVDYDLIGGSLGSLAVMLSIIPNITEENNKEILKISHIHCDHILSVAKNFEEQISWPGK FSAAYSGFSGHNSGFIAYLYKFFKLTNDEQLLEVIQRALRFERRLYSEDHNNWYTENKDKLANGWCHGAP GILLSKLILKDNCFEIDEYIEKEISTAIDSSIHNGIGNNPTYCHGDLGVLSILNYASDLTNNINLNKRCLRTYQDLF ENVLAMKWRKRDVCTRSYSLMIGLSGIGYSMIKNYAPEIVPNFLWLE
SEQ. ID. NO. 70.	ABP10888	MKKDMVKNASGFIEDELISLANGENATGGGTPVTAIITALTGTTFVTLSAASCTPSACTNLCNK
SEQ. ID. NO. 71.	ABP10889	MDISYENNNFIRDAVINFSSPTNEVEKLRIKNKDYFGNFYTFFLDYQQRLFNTLENASKENNLKLNKQKIIS ALEAFSQELIQLCIRTIVDINDRKEKGLLEGKDSKLRKYNYNLIFKSEYVAEILNKYPVLTYLISSRISNKILYK EVLNLRKNRQDIYRELRIEFDEVSNIFYSSGDTHNGGKNVLIETNQKGIVYKPHSLSPDILFNSIVDYVNS DKILKKIYKIRTLNYKDYGYQEFIDYKECETSEKLNIFYFYRVGVSLSFHIGCDDLHHENLIAHGEYPPVIDLET IKNNSIYKPRNNNLIDNFHEDINYSVLGTMILLPLNLQTSIFDFDLGGISNDENQTSIWKSYIIDFEGTDEIQL TKKSVIMNSTQNRATYNGKAADPKNYIEILKGFTDCYNFVLENISGFHDLVKKVGSNLEVRQVLRATSIYA RFLEASTHPNYLSSFEERKKLFKKINIAEGVTDKFSKKNLYELESMLCNDVPYFSTMYNSDLICNKSTSIVNFF RESLLDVVLNKTKSISKASLKKQYYIRMSLTITIKDSWKKTNKHNNKYRPKLFGNNNNKYLECATEIGDLFL ETAIWNDRSKCTWVAPISENKVKLGPLNFDLYEGGGVILFLALLGKENGKKEYFDLALAGMRGIEELFL SDDKMDDRLSLFTGIGLSYIYHLYHTNDYKYEKFKYIKKINEMNISGDIALDIVGGVSSLIVFLNLKET KLDILNSVCKLGNTLYQCLENDKHNYLTGLSHGYSGFTWALCYLGHITKEEKYTTLGKELLKIENKFFDLHTS NWKDLRVGEGNSDPVYWCHGAGGIALSRAFLKDLLKNKENVVDKEIDKEVDRDLSSAICKLLSDGFKKTTD HSLCHGSFGNIDILLKLEFLNDIDLQEVAFKEAQNAINYIRDKGFIPLQDHFDLNTFMLGLGGVGYSLLRL HNPVNPSSLAMEVRSYNE
SEQ. ID. NO. 72.	ABP10890	MIVKKKKRIPVQKQQTECGLCCCAMLIRFYNSTNETLFELRSFLEAGRDGLTIKQLKNLLVHKGFKADIYKST IPGLKKINVPFIAYWNNNEHFIVVEKTKKNFYIIPANGRRKLTEEFRRKGFSSYILYAVPSENFTPNKRKDKN VWFGVLKNITNYKLLFSIIVFLSLISYLLTYVPILVQKLIDTSIEHNNLNSISNIVWITFLISILYGMFVLRGLKM ISLNIFLSKNLVVDFAHLLKLPKFFDLRSPGDLLFRLNSMNGFRELLSTQLISGLIDLGAUVFILAYMFFKSIP LTLITILIFAITIFMFLTRPAVAQAIDDEVAEQSKSQAIQIESIFIAAIKISGMENEIFSTWNNSFNDVIKRFKK RSILQINIVNTVTQVFQTIAPLVILILELLFFDNKFTMGVEIAYHLSVTFGLTTSFLGTYTQFILATSYLERVKD ITETECEKNFENAVNLKRGNVKLENVSFSYTKHSPKVLKNISLEIREGQKIAIVGSSGSGKSTLSKLIMGLYDP TEGQICFDSIPLEKLDKKQLYKQMGIVPQDITLFNSSILKNITLNNKNTSIEKVRKVAQAAQIDKEIESMPMKY NTPISEMGMNLSGGQRQIVLARALLNDPKILILDEATSSLDLVNETLISKYLSMGCTRVVIAHRLSTIMDS DFIIVLDKGEVVEIGKHEELIALEGVSNLYRSQMKR
SEQ. ID. NO. 73.	ABP10891	MKNYKGDGAVFLVIGFCLGLFMGVVFDILPYGLSLGILIGSLIDFYFYARYKNNKK

SEQ. ID. NO. 74.	ABP10892	MSMSRKETPDDNAFIESFHSSLSKSTLYLNSIERTSTIIVERNVKDYIYNNIPYSNETKQPITDKLSAIGCLKG VLIPVSKTG
SEQ. ID. NO. 75.	ABP10981	MIDVIRVSGGYGRKDVLDISFAVKPGEFLGILPNGSGKTTLLKMLSGSITPRSGEVLLECRSVGSYKTKEL ARKVAALPQKTEQAFSFTVEETVQFGRYAYQSGLFRQLTGEDHDIVKRVMKQTDILRFAKKSIHELSSGGEQ QRVVYAQALAQEPYRLLDEPTSFLLDSFQKSLDLIKQETVASKLAVIGVFHDVNIASLYCDRLLLKDGKAE VLDRPEAALCADRIERVYHTDITALDHPERANPQFTIKAKTIPEKAEPFLKERIEQYLPRGITFSADRPMPRL SSEEGFAWRRKLVFDSGNNSGWPHDLSTVEQEALFIQHDKLTACHIVSESNDLCIIGMKDAKGRFIMWV VVGCLHDGQFVKVISATAKAAAQHRVFCSDVLIATHSGRLPDQTILLTQIQDQTAACVKALKN
SEQ. ID. NO. 76.	ABP10982	MKVEGIIPAILTPITKEQDFHPGVAEKLNVHLIDSGVHGIFALGTNGEFHLFSQEEKLQIAETVVKAVNKRVP VFIGAGENSTEATISLSNQMADIGADVLSIITPYFVAPSQKELYQHFRITSENVALPVLLYNIPSRGTGVSLEPET VERLAALPNIIKIDSSGSFDNIKAYLERTKDQSFVLAGTDSLILDTLKAGGTGAVAATANVLPQTVVSIYES YKQGNIEESEQYQKQLDPLRATFSLGSLPAPLKKATELAGIDVGPPKHPIAELSGEGLQKVKKMLEGYGIETK LVKEQ
SEQ. ID. NO. 77.	ABP10983	MKTLYHFQTAARIEAGAHSLNFLGDHLDQTSQWGNQIRSVFILTQPSIVSLGYADQIKEVLAEKGISSEINTDI QPEPTQNIIEVFQFLSAGSHDAILGIGGGSVLDAKILSVLKTNNKPISELVGTNLVEKPGVPLVLIPTTSGT GSEVTPNAIVTFPEKELKIGMVSPYLLPSLVILDPVLTIGLPKAITAATGMDAFTHALESYISNKANPFSDMFAL LESMRLISSSIQEAYHHGDKLEAREKMLIGAMYGGMALTSAGTAAVHAMAYPLGGKYKMSHGVANSML LPHVTAFNADHVTDRLSDVAGVIGIEQKGSKASQAERVIQKIEEWTADLNIPQNLKAFGVSKEDVPTLAEA AADVKRLMDNNPKPMSVAEIEAVYLKLEEV
SEQ. ID. NO. 78.	ABP10984	MDVLSGSVITFILAVIVVYILFTTWLTMFRFSKSSAEFNNAAKTLPAlVVGILLMSEFIGTKSTIGTAESAYTHG LAASWSIVTVSIAFFIFSYFLVGKFKYKTQYTISGIISDKFGRSTKLTVSTIMIVALLNLGNYLSGSAISSILG LPLMTCAIITAVSTFYFTFGGMKGVAWVTLHSLVKYVGVLTILGVALYLTGWEPMTQQLEHFFTWG SIGWGTIGAWFIGNMGAIFATQFIIQAITSSKSEKAKRSTLYAALLCLPLAIAIGVIGVAARHLYPDIDAIYAF PVFMQQMNPVLSAIVATSLVASIFVGVSTVALATTTLIMDDFYVPKAKPTPEQRMKVTRYASIIIGFIPLLG ALAPELLTSLFFTRALRTSIAVVAAMGFYLPYFNSNRGATIGLVLSGMATTVWYLLDNPFIDNMYIAIIVPF VVLVLDRLISSPAKKESNVKEEF
SEQ. ID. NO. 79.	ABP10985	MKQSEVSLIDGRIRKNETDEARKDAFLPTDCPQNHAANLLELDNGDLLCVWFGGTQEGADIISIYMSRLA KGSSEWTQIEKLSDDPSRSEQNPVLFQEPSSGRLWLMYTAQMSGNQDTAIRYRTSDDRHTWSGIDTLFG EAGTFIRQPLVLDNGDWLLPVFYCITLADVKTGNRDISAVKISSDKGKTWEEVKVPSSMGCVMHNIEK LHDGTLALFRSRFADSIYASRSIDNGRTWSEPEPTLPNNNSSIQFTALQDGTALVYNHMKANETTERRA SLYDEIEDEDDTRTGVDTEARPAFWGAPRAPMTLALSHDGGVTWPVKRNIIEVGDGYAMTNNSKDKLNR EFSYPSIKQKGKDGDLHIAFTYYRQAIKYVRVPQMWASADQE
SEQ. ID. NO. 80.	ABP10986	MKIKVLGIAPYKGLGDLLELAKEEQDIQFQLEVGLRSGVAIAEQAVSQGIDIMMSRGGTASLIQKHVRIP VVDIPVSGYDLLRALTLIKDYQGKAADVGFENITQGVRTISELFGIEVDLYTIKEEMEVWDLRLDIQQGTQI VLGDVITDKAAKELGMSMLITSGRESVKEAFHTAKQMYRLFKEASEEQRMFRDMIDQEEKGMLVIDDN SRVRFVNKMVKKWMKEGLLEPIAPAAVNEWWDELAFVQSIREGKLSGYFQLETGEVVWHMKGSLFSL KGELLIAIEQSSSRDDRNHPVWSFAAPVHSLHPFSSFTQQSSSMRDTVQQAAQFSQTHKPILLYGEEGTG KSDLALAIHQMSPRRQHTFMTIHCSKVKETSLLKALPAVQNGTIFLRYVEHLPLEVQHDLALQWMKPDQQ IRWLASSSADLCEEMKAGRFDPDLYSCLQGLTLVPSLSERVEDMEDMSRLFIAEFNSVYGTQVVGLAPEV MDAFNRNRTFRENVRQFKRVLEELALTVKSGYITLAEAAPQLDRLSNEKKEESLKGYTEGTLEDIERRIQAVL QENMNQSKAAKRLNINRTTLWRKLKE

SEQ. ID. NO. 81.	ABP10987	MTNIRCKKGANISRKILIVADDLTGANDTGVQFVKAGMSAAVLFDRSGANPGDIKEDVMILDTDRGVSP SEAYKEVSSASHPFARLESHLFLKKIDSTLRGNIGIEIKALMDLGRFDVAVIAPAFPDARRITVDGMHYVNGL PVHETEAADVDPKTPVAESRIADLLFGQTNIQPKTIGTKQLHKPDEQIQDLRAWKTQGHWFVCDATNE DLRRIVQVFMNSGQSVLWVGAAGLAGALAQHVRKRALQTGRNEPVMIVSGSASNTTNRQLAYVREQR DLLDVRINPLNLNGCEAWEHKRAIDQVVVHQKDVLLYTDAPETVQRHAFGRKQGLDRQAVGEKLSL FLGAVTSEIVKLTGLKRLVLTGGDTARAICNELGADGIQLLGEIAGIPLGKLLNADIYAVTKAGAYGQTDVSL RAVEVLRNVEEEDRWQNSLR
SEQ. ID. NO. 82.	ABP10988	MAKPIIALTMGDAAGVGPEIIKAFEQTNLHENGTLFVIGDYSILNRAKTFIGSDVDIVKINEPEEAADVCPG VIPCLDLQLLTDEL RVGEVSAEAGNAAFRYLEKAIALANENQIDGICTAPLNKEALHKAGHMYPGHTEILAE TQTKDYAMMLAAPNLKVHVHTHVGLLDAIHLIDAKRVYTTIQLAHDTLIRAGIPQPKIAVCGINPHAGEN GLFGHGEEEEKIVPAVERAQSEGIQAFGLPADTLFFRAVRGDFDMVVMYHDQGHGPIKVLGLEAGVNI TVGLPIIRTSVDHGTAFDIAGTGKADPASLEEAVRQAIMLSGTRNRHA
SEQ. ID. NO. 83.	ABP10989	MEFYKKTAITGASRGIGRAIAETLADKGANVINGTNEELLKSMCTELNTERKCASYVAGDASLPETASLLI AEAKQQFGQIDILVNNAGINLRKTTVDTSLEEWRVIDLNLTGIFLMCQAVIPEMTAQGGGKIVNMSSTTS KTPHHNASPAYGASKAGINYLTMHLAKELAAHRIHVNAVCPGPIETDMSKQWSEEYRAAVVERIPLKMIG SPEHVANIVAFLASDKSDFMTGETININGGTYMN
SEQ. ID. NO. 84.	ABP11306	MSPPNEAPIPLDCGSLVTFQFSSISGMNWFVCQTHSLMELAFYYLRDRIP
SEQ. ID. NO. 85.	ABP11307	MKKLIENTENPRTTQSIKKDLEGLGNKGMTVLVHSSLSSIGWVNGGAIAVIQALMDIVTEEGNIVMPSQS VDLSDPSEWHYPSVPEKWWDTIRESMPAYNAQYPTTGMGKIVEVFRSYPEVKRSCHPNYSFIAWGKDK NKILNKQSLNFGLEQSPGLNLYMDNSYVLLGTDFDSNTCFHLAEYRIPFQKVVIKGAUVLINGKTVWKY KDLEFREDLFEEIGKSFEIESDMKSGKVGSAKCRFLSLKEAVDFAEKWFIEYDCKMNSRG
SEQ. ID. NO. 86.	ABP11308	MSNYRDYILKGKDVAVFEIDTDPISLDPACDDYIGQISQAMFEPLFIRDIETEQWVCGAAENFEVSSDGLT YIFNLKDRFWSDGISVVAQDFVFAFQRLFHPKINSPIGQILSFIKNGEELNGVLPVTELGEALGPRKLKISL TECLPFLPSILGSPNTSPFPYRTEQVSWTDERLNTNGAYVLKEYKSGQFVRLERNPFYPNSSSNHVKDVLV INRELDYSLQNYEKGNDVTCNTYFPFEEIKRFKQRDDFYMFPSGILFQLFGNRNDLFKKKQARQALYIVN KSQIAQTLHGGIIPWDHFASIGVSEKLFDDQSNYCYHPEKAVKLWKQEERENQALSILYADFFPNGEICHSI KSEMEKHLGITLTLEGCSFEDFVIRHEQREYDLCLALLSPLYNDPFNYFYFLSELSEDEDEFIDILQKALGDE KENHCTYYKKANDYLLEKLPSIPLFNGQSIFLKNPFLKGYKIFKDGSSISQNLWSWGTEEKPL
SEQ. ID. NO. 87.	ABP11309	MYKLADRIQIVSLHNGRIFLIDDEITELEGSPQHTEKALKLLEKGCMEELNRIMPLEDTQKLEFLKEEELLRE NWEENEYLDTIVEKQLYYLDDFSIDSNLQSNLKSAAVILGVGGVSVLIQLHIGAGIENFILDNDVNNIHN LNRQFLYTQEDFGPKPKVAAENFMRKVNPSVKVTSYQTTIDSISLDFLASHSIDIFINAADYPKHLDKIVDE YCFERKIPWVGSGVGRHQGFVGPLFVPGTKCLNCFIAEEEEKMEKEIKIIRERSNSIIQASFAPTNTIVSAFL AMDVIHFLAQINQIHSYLTRCQIDFTTLKLNRFIDEPKLCNCGGE
SEQ. ID. NO. 88.	ABP11310	MLSKNYSFSLSHLSKSDNHQVRVQEIGVTDQLNNRILFKNITFLMHDVYITGFSGSGKSTLVNLIKDF PDAVIPTPPAKQDPIIDLLDELQESMKILGWVGLGEAYLYLTPYSALSEGQKTRFLAMALSRNPSIIIVDEF LSNLDRIKVVAYSFQKICRKQEIHLIVASAHNDLIEALAPDILDLNGLTHRITNRPIEKPFVDPISGVQVES GTIKDYEELKRFHYFGDEDLFVDNEFETEIFTIRLKEKIGVSMKSPYKDWEEIDYFKDINDRIRCLVRLIH PSFRTIGLSKLLMRPKFLDVPIETRSALGLYMPIYLSGGYSRTELPDNKLSPLRQKLWNNLSFMGLSDVHLL RDDIYCENFVQNLSGKQKEALRYLALNVYVEMMVNNYIFRSISKMIPLPKEMDELKEMFLDVSEIPVTV LLQETSLFKMQGFVVQHKQ

SEQ. ID. NO. 89.	ABP11311	MPLFSTNKNVSFIYLTSCFNGFFFERGIWMLFLIEKGFSLFQIGLLQAFVNGTMFLFEIPGGMLADRYGRKV SLLIGRFMIMSYLLIIMIADSFESLALSFCLLGLGMTFISGSEESLLVDSVKEQTGENNFSRFLGRYMAITVALS LAMMIGGFLKEISWSLVFAVSFIFQMVAFFGCFFLKETKYKKGSRQESFTLIFKDTFNFLKTNNTSRTLIFGIA LFTGIGSIFYMFAQELFNQLGIKVYLISIFFGLESFLAAILADRAYILEKKFSSRGVMMVCVYLCGISFLLIYINFN WLILSFFIISAFYNLFTTISYSVINQDIPSKQRATLLSIISFISSLVMFISIPIFGYLSDKFGTAYLLSFTGVISMVLVA LSILSFYKNRKDSVEKHLLKVQEK
SEQ. ID. NO. 90.	ABP11312	MEKKLSHHPIDRRVDLTDEFMKEYGLPGKPVIIISNAINNWEAKKLWTLDFFREKYGHIIPFESGKRYELY ETTLGEYIDYILKEEQEDGIFNLADWEFSRDCPELREHYQVPNYFQSWLEDAPISLLPALRWIYINQKNTGSG LHIDYGHASWNAVISGKKKWILLNQNESENIYNGAVDAFNPDFFKFLYTHSQTFYGEQSEG DIMYIPSG WWHQVHNEELTIAVTENFINETNYKNCLWPLVSNIVEYQLEISKTEPKVQKV
SEQ. ID. NO. 91.	ABP11821	MGGGLYGHRNIEDERLKEWIKTWAENYIHFCCNYGVGMNAEFNDSLAKQVELVIQESSITVSKDRYLF DEVMMKYMTPEMFYCYFRYDSSTAYCGNYEVLIEFADELTKKKLIKGYDYVQTGGITLKNGEVIGHIGQMS DLFWQTFYDQYIVEDYGAIEHARNNGKDITLQIWNKVFENTEQFYKFIEQLFECNVNLGFGFKMSRFEN ESKLKGHTSNTKLCLSNIELEETPLRYFNANYTKIPRHKYLAYYQVIEFFTRAVRKARFPQPNELLIVKYIATN SITELEVVTWLDIISRGKHYPSEKYPALFPLEATEIVESVAKRIYLIRCSLVHSKEAPNDVNFIPNLNDEIID KEISLIKYVAEKVLYKWSNAPE
SEQ. ID. NO. 92.	ABP11822	MLESTYLQITDVIGKIIPADWSKIVLYAEILDGSREYFFFTPENDEYIYSHDIPEQFQVSKKIYTELLIDLQEL FKQLHNEFKENNPEAWTNLTNLNESNGTFSIDYNYDDVLSSELDDLQRRDVWKC
SEQ. ID. NO. 93.	ABP11823	MENELNALYRSIAETVNEMIEPEPWEKFLFYAQVSETGGGYFFYNSQNEPNHFYSLEIPFEFDIDENEFDQ YEMELFKLSEKMRDVFKDHDQELFYSFTLSLERSGKLTVNFDYTDWFKTDYSFSDQLIWKFKYLGEETPKDP SLQKLIKYLEEYPENPI
SEQ. ID. NO. 94.	ABP11824	MKVFEAKTLLSEATDRAKEYKELRTQMVNLRKALKSVADLSDSEFSGKGASNIKAFYHDHVGVTQDWIDYI DMKIAFFNSIAGAAEDKALSDAYIEESFLEHELANANKSKSIMSEQKKAMKDILNDIDDLPLDLFSTETFKD ELADANDKRKKTLEKLDALDEDLKTEYALSEPNEQFIKSDQKLQEQATGKGKNATPIHYNAYRESDIHKK KGDIESTRTEAYLIKKEEAKEREIEKLERLKNYDYADADEFYEMAKTIGYENLTAEQQRFTQIENTRELEAG FKGVAVGLYDSGKDAVVGWDMVTDPPGGTVEAITGAMAHPIKTYEASAAIEESYQKDMVNGDITYSRAR WVSYAVGTVVTSIVGTGKVGAVSKTGTAAKVTTKVKTAASKSATAQKAITVSKQTVDHQKQVNTGIEVSK KHVKTCLNQIGDLTLADILPYHPRHDLVPAGVPYNAVNGVTLKEGLQKFQAKVILPKPYGTSSSRGRTAPHV PPVTVKYGEHYAKWSRKKVLKPNVEYKTKEGYTYNTDNYGRITKVEADLQGEAKRNQYQSNAGKPD RLPDDGGHIGSQFRGSGELDNLVAQNSQINRSGGEWYKMETEWAAALKEEPPRKVSVRIRPKYLGDSL RPDSFEVIYRIEGKGLFKKFIKNQAGG
SEQ. ID. NO. 95.	ABP11825	MDKDFLIKIKDIQKGTDLTNACGNWDMKLSRAKECKRAIVVRSGVILNVYKIVDAWESDEPAKITKTNN RVRFQLAECRDYSYLIGGTLKTKTQNPVSSLSLETLMELVK
SEQ. ID. NO. 96.	ABP11826	MYLYKVNQNIQEDIREKPFKKEIKIQDLCEANLQQLGLGVKSEFRISNFRIDTLAFDAETKSFVIEYKN TKNFSVVDQGYAYLAAMLNHHKADFILEYNENHDLPLKRDDVDWSQSKVIFISPVFTVYQKQSIHFKDLPIEL WEVKRYENDLIQLNQMKADGVSESIKTSIQQSETIQEVSKEIKVFSEEDHLADKPFDIIELYQQLKEFIFNLDD HISIKPTKLYIAFTSNKRNFTDILLKSGKLKLVNMKKGELHDPEERMVDVSETGHWGNGDYEIFIKDEENIE YIMGLIKQSYEKNK

SEQ. ID. NO. 97.	ABP11827	MKKRFILLGLFASVFM LAVYISFQNK NTHPVQSPVIHPEEDRIFFIYSNLFIKESVLLSTSTGERFNRRTFKVAD VPYIQMKS YKSTDLVLLAEHEPFYTYLEKDAI KEHPLSDPFAFWHEGKDVSVKAYNVDTTGNEIRINDKKMK KEYTTLPSLV TMGASDENYIIQSM AIYVIDRKTEEMIETLSLASYADQFADSKEFIVASSEH LTVIEKGTW KATYIAYPEDLEYADTVYYDKESGSFYVYEDKKGEANLLEYGKEFSFHTYSLNFPYMEAKFKGNLLYIVAQE EHKKGIGGYVGVFDIHSKMLYQFDLP EEQVKVQDFVVD
SEQ. ID. NO. 98.	ABP11828	MGGSYLSDLCSMYQKDKFFTGFVPDELLTYACELFPLSEKETVTALLNCSMG NKA KS FVMFTSKGLYWKRF GEQEGCVTW EAFTDIQSIKSTDDY EIWFE GEEVFDVGFSSYPADLLAELLRMIQQFLSENGSDLLTEAWRD HVSVSASELKEISTLFQNSHDKMFG LTNGLLVGNEISEKREVRLRKLHIPKDQEMISFWSTFPVKQTDGITL TDKGIYFSDPFLRLFYPWHVFKETPVMLKDQELIVGKENVIQ LLENLMPAEDVF AFIEQVKRRISAVTS
SEQ. ID. NO. 99.	ABP11889	MLRKKGQETKDYKTQQVESWGLRLIGKNEKIEKSNISIAILD SGIDSNHEDLKG VVKKEYNALEPSKGVIED KFGHGTAVAGIASNDNKIGTLGIAPYADIYSVKVLDDKGRGSVESIVKGIEWSIDNNVDIVNISVGLKKSQDQ KLKRVIDEANEKGVIVVAAAGNNYGLNADYPARYQNVISVGAINKKMKRAKYSARGKIDFVAPGEDILTTS PKDNYINVSGTSMATPFVSGVIANIIMQEPVKYSKTKSRFTSIYKTLKYSTPYLSEKSDMKSLGNGLISLKKKE TNNEKIN
SEQ. ID. NO. 100.	ABP11890	MKKSIFIAISLIFAIIVSIIPEKNVASAGAETPVEITNEDLQRALVENGDIVDPDSVEIVKNNEDTIKAEVDVQT DDFGIDQDL DGSDESLEDELD ESSSETVTA EVDKEDATAIVTSVEKDEDEGKDIEKKYEVDIEEADGDDIVA TFKDLD TNQVYDVNTKEAQA SFAFLVPIAVVVG GALVEHLVAASLAIVAGVTVATKVRSKLKKKKKKYYY YAATLNKNKTNMYIGPALS KKAQAVSRLRKG DVWSVSKSAKNVAQTAGGGRKPVGPEIHNKKGDKIKKG TYYYHYHTYNRKG GHSFY
SEQ. ID. NO. 101.	ABP11891	MWESIQNGKRVNKIFESKDGNYISNFTVQGNVEKIEKELVFIRGILEKEKNN
SEQ. ID. NO. 102.	ABP12521	MKLIYPYGADKIYLG NPNVELFRDQDTGDYIIPKNATDIPPELNGEGMWRP MFNEEKQ TWIETADQAYKKS LLEDVPSES NPTNDQLSALGKQLTEEK LARIQADQAQKALGMQLTEEV IARKEAEALSQSLGKQIAALKDL LNLKGGMTSES
SEQ. ID. NO. 103.	ABP12522	MSLNFWVYALFYKWATTS MVREAMMFHDCSVDDLKEGVSEKYVTLAQFKEITDQTYEETMKAN
SEQ. ID. NO. 104.	ABP12523	MSELSEVPDMNLLEKEITEIKTEQKTLEQ RVSVLERSSDRQDQQIMTLNEKLNKIEENTTWIKRTITGAITAV STGIIGGAIAIMYSLQH
SEQ. ID. NO. 105.	ABP12651	MKLEQQEINILHSDSGPYGIAISPEGKVWFTQHKANKISCLDRTGQIQEYIVPTPDAGVMCLTVSSEGDIWF TENRANKIGKLTAKRQFIEYPLPHQHSAPYGITEGPDGDIWFTEMNGNRIGKLTSEGIHEYELPNEG SYPS FITLGS D HSLWFTENQ NNAIGKITESGELTEFPIPTPAAGPVGITKGHDDALWFVEIVGNKIGKITVSGDITEY DIPTPNARPHAIAAGVKS DLWFT EWGGIKSEG
SEQ. ID. NO. 106.	ABP12652	MVYRMGGNKIGRLTSDQTIEEY TINTPHAEPHGIGCDNDGTVWFAL ECNKIGKLKLT K
SEQ. ID. NO. 107.	ABP12653	MKVKEKRIVVNKFPSQPDEEDCRNL TLLGWGSGGFFLHTFR
SEQ. ID. NO. 108.	ABP13703	MKQKRRIIQKDRRKLKYFNAKFTA EERAMESLFCEKTSQSSSNVLLND
SEQ. ID. NO. 109.	ABP13704	MKTKSEPKVILEPAKESDLPEFQKKLQEAFAIAVIETFGDCEDGPIPSDNDVQESFNAPGAVVYHILQDGKN VGGAVVRINSQTNHNSLDLFVVSPEYHSQGIGLSAWKAIEAQYPDTVLWETVTPYFEKRNINFYVNKCGFH IVEFYNEHHS DPHIHRNGRVDDKPLPDNDFFRFVKIMKKKD
SEQ. ID. NO. 110.	ABP13705	MPLTLIWRNFEFSEKFLGTYADNV LKVLQEAQEELEDEFKIIVE

SEQ. ID. NO. 111.	ABP13706	MSLEEQLQSKEELTKLVSTFAAKEGTNETSISGLEFIRSAKPLMPVHTMHPEALCIVLQGRKVISIIGEDFFY GKGEYLVVAVDLPVIGEILKASEREPLYCLRLNFMNMQIAEVSKYQQHSTNHNAAGRIFVDQTDGVILDA LIRLVKLLHTPEDTEILAPLIKEILYRIMQGGKHGHTVKSLSVAKGSKLSEVAAALDYLRNHFSQEIKIDALAKKV NLSPSALYHHFKQVTMMTPIQYQRALRLHEARRLIFGKDMRVADAAAFQVGYESPSYFNREYRKMFGKPP GKDRKENLNLYYV
SEQ. ID. NO. 112.	ABP13707	MEKNNHSYGGWVTCKDRYIRHELLSNGRYVEARGNVECAVTGNYQITGDRIEYQDDAGFTADGDFINGIL YHAGMVLHRDRS
SEQ. ID. NO. 113.	ABP13708	MSIKNKVVLVTGGSSGIGAATVDLLAENGATVIAAARRTDRLTLVTTLQKGYHADYKQLDVTDFGQMQ QTVQEVTDAYGKIDVIVNAGVMPLSKLDSLKIAEWNRMIDVNIRGVLHGIGAVLPVMKEQNSGHIVNIA SIGAYEVTPTAAVYCATKYAVRAITEGLRQEATHNIRTTLIAPGVTESELADHITDKQASEAMIEYRRQALPA SAIAHAILYAISQPIEIDVSELIVRPTLSL
SEQ. ID. NO. 114.	ABP13709	MRRIDFGLTFLICTLIMLFNEIWKLLGNRPEAFKYGSIIYQVIAVFSSITNVAIGVAGAISFYIAQLIDKKKNRE LYTDLRKHLFMFYNLKLLTRLDQFREVNRRERRVADFYDIFDIPVFYDNFKKINSKEEVTRFKKNLYDYFA TQSEQQIKVFTEAFEKDIKKLKEKSNIIRFFKESKDLDITVCIYDDDFSMISSIYLSNFEDTQNKSNYIEELVKDY YDFLNATVILYEEEFLESMDKNRWVFIKMLD
SEQ. ID. NO. 115.	ABP13710	MENAEIYELVKEMSKTVKEIDETTKRIENTTKRIAKGYELITEELAE
SEQ. ID. NO. 116.	ABP13711	MTYRVGSMFAGIGGTCLGFIQAGAEIVWANEIDANACITYRNYFGDTYLQEGDITQIDKSTIPELDILIGGFP CQAFSIAGYRKGFEDDRGNVFFQILEVLEAQRNVYGRLPQAIMLENVKNLFTHDKGNTFRVIKEALEAYGY TVKAEVLNSMEYGNVPQNRERIYVGFQDENQAEMFRPEPIPLTNQLNDVVDTRTRYDERYYYDETSQY YEMLRAMVSTDTTYQLRRIYVRENRSNVCPTLTANMGTGGHNVPLVLDYENNIRKLTPEECLLQGFP DYHYPEGMANSHKYKQAGNSVTPVIRRIATNIINVNLGETNANDEQEHQYAITQ
SEQ. ID. NO. 117.	ABP13712	MIPFLGNRIQNAREARGLKPSQVADKVKVTRSTYSLYSENRTSPLETFIRIAETLNVADYLLGLKEEMTSL NEEN
SEQ. ID. NO. 118.	ABP13713	MFFTNQPASNRRTTYKQMLSSTGSLSNLFSSES DSPYLVSRNVENAFCEALGAENLGRSDCSADASKDRVIGIG IKTFLHGNHGHTLQKVAEFNRDSDLYRGKSPKELINIVATLRNERIEFTKRTYGIDTMIYHCVTRKPGKILIFE MDLVQISSITNIKVSNNRNTITFEDGLHEYSFNVTKSTLYKRFITDEPIEIDVEILENIPYQELAKLFGFEIPIQ VPEVSSPIENFEYVILPLFSDRGNKRVHPEKSGLNQWNAAGRPRNANEIYIPIMWIHRKFEFFPARDKPF QLRLPDKSLLSAKVCQDNSKALMSNPNSALGEWLLRQVMNLGERELTYEMLERLSIDSVIVYKHSEQHYSI DFREIGSYDEFENENN
SEQ. ID. NO. 119.	ABP13714	MTDTFSKEQRRKNMQAIKRSKLEDKVTKELVNWRGIRFRKNVKGFGKPDIAIKKHKIVIFIDSCFWHACEK HGNKPKSNTEYWEKKLQRNKERDREVNKYEEKGWNIKRIWEHELKEDFDETINRIAFIEAVKHEQRK
SEQ. ID. NO. 120.	ABP13715	MLKIKKLDMPFFNRMICFVDVKNPDEADKKALAKDILENNKDQYQGYD
SEQ. ID. NO. 121.	ABP13716	MKFIELDPALQIKVRQLEANAEEHQDKSHPDVRLWLELQKEDSICGALSEKDGSKYKCLRAPVEERNRCS LHGGKTLKGEQMTPAQKLNMMKNLRPRVVEHCWYAEESNFLASLSEIKYMSFLEKSVKDQYHVNDGL EELLLEDILQSAIHMVMNRGVFEKGSRTARPLQEVLTIKELGWTCKEKGGKVQFVSVRNDFMASIFG NNTEEEEEDKKLN
SEQ. ID. NO. 122.	ABP13717	MSLKEKLAELNKRAGKLEGLSKKASKASSEADRLKKKRQEREYYDAYEKKFPIDKNF
SEQ. ID. NO. 123.	ABP13718	MKKDWFSQRLELINKEQKLNNEEFNLWKLQKITKRMKEVTKKLDELETERV

SEQ. ID. NO. 124.	ABP13719	MGLFNKKSEMVKFEEELNVVQGSIREVEAELRDFDTSKKGIELELKLGDSSLTKRLKKVSEKVAETEKCLAE LRQREGEINAERKTAYLNELADKDLASIDKGRRTAVIKYELQALMRVVDERDGRWGYSPENLLKEYGIEIG HIPAEHLRREEFDSFWKTRKNDAEKRIQNECQEAIELKKYLGGFDK
SEQ. ID. NO. 125.	ABP13720	MESKVNMLRILEFYMGETGNFKKLVVIQEIYRNNPSKMKGCESFLKDNKFVAKGFFAETIMVRNSFHSY NSELPKELKEHHFKKMEKRDQDSHYVPSETTVLYLSGYVFAEFKFHKIANDKKIGDKVYLPKLDKQKPDNS EFCKLLVLEEYRDGTFELPELPKRAEMFTCWVRLELAPDSKNDSGVKVVSEREFNKARMGEIKGNIA
SEQ. ID. NO. 126.	ABP13721	MSEDVKKYFTTGEFSKLCRVKKQTLFHYDEIGLFSPEIKKENG YRYSYHQFEIFQVISLFKELGVPLKEIKCLIK GKTPDKILHVLKEKSIEIDKKINELKQLQTLQTKVLTLEQALETDFSSISFEYLNEETFMLSRKTLNLPKRYVA AISELIHEVQQYELDEGYPIGGIFAREQILEKDFYNYSYFYIKVKDGAENINYHVRPKGLYAVGYEIGGKTEEA YRRIIEFIERNQMIGENAYEYMLDEMVDGYENTYAKILLQVKEV
SEQ. ID. NO. 127.	ABP22957	MREKKLGPVLLSGLIVGPILGSGIILLPPIYGKTGDYAILAWFIMMIISFLFASLFGKLSVLPNESGVAHTVEL AFGQHIKQLTSVFFIIAGSVGPVAVLMTASQYLKALFKSNGWSLETYGIILMMICLFLVLSNISSVGKVSFMT STVSTVLLSGGISSIPFMRDKAFIKTPFHLDDFGYSILLFWALVGWEIIGNYSLDVKNRKRTPQAISSSVVI TTVCIVVAAAYQWIDLHHTHTLTIILPLLGTFSASPTMAFITILCMSTYLLVTGGVSRLIASENKKITLISYRSK TNIPIGAISILTVHAIVFILLFINIINVEQIVGMANAFFISNAICGILSAYKLLPGKFSKLSLMLIISFLIISFSSIWI LLMIALITTFYLIRHFIWIRQLKKSATNSQDKLRF
SEQ. ID. NO. 128.	ABP22958	MEIRHLKTFITIVEKGGFTKAAEYLYGAQSTITSHIKDIEQEIGGPLFNRFGKKMLLTEVGEYLLPYANEMIRIS EKVKQIQSNDEPMMGNLVIGAPESLTVYRPLPIIHEFKKLPKVKITLKSSTCWELKDDLRNGKVDLAFLEYEQ EEADLYIEKLITEPMILVFPKQHKLQNTPFDDFYSSDEVILYTEHGCSYRTYFEEMKHQGLVSENTFEFWS VEAIKQCVCMGLGISLLPLITVQKELKENKLSGLIMDETRIITQVAYHKKRWNSLAMAEFINIVKKHAELWK RTQTL
SEQ. ID. NO. 129.	ABP22959	MNPLLLDVPLQLETERLILRAPHQTDGDKIVNQAIRDSFSELKAWLPFAQELPTVEETEINLRNAHINFLKRE SFRFLIFDKDSNDFIGITSLQRIDWNIPKCEIGYVWNTKYSNGGYMTEAVKKLANFGLHNIKFRRIEIRCDST NLKSRAIPEKLG FVFEGTLRNDLSADGSKLTDTCFYSIVK
SEQ. ID. NO. 130.	ABP22960	MVDQLWAYFLNLIEEAETGKSETYFPDQPLLLKMSISNDMLLFEIDQKQKVLPLKLDFFESLLKNAKSFFE TMNFVLEGNCDEYELNKKIDELQTKIKCM
SEQ. ID. NO. 131.	ABP22961	MKVFEAKSLLSEAENRAKDYKELKNQMIKLRKAFKAVADLDDSEFSGKGANNIAFYHDHVGVTDDQWIDL IEMKIAFLTSISGVLEDASLSDAYIEESFLEHETNAYKKSIMSEKQKAMKDILNDIDDLTDLFSTETFKDE LSSAENKRKKTVDKIGDV DENLKT EYAITEPNEQFIKADFQKLQESTGKGKNATPLHYNAYRESDIHKKK GDIEKQSEAYLKIKKEEANKCEIKDLKKQLVKVTDPEYLKIAKKIGYENLEPEQQVYFRQLEELQQKAEIGKG IAMGMYEAGKDTVMGLYQLARHPISLSGTVNAAALHPIDTYKIIAKDIEDTFQREMGDSDSHRAKWWVSYV GSTVVLAIVGPKGIDKVS KVAAGSKVAALKTLEVSKTGIKKGIEYVKIPSVFEQQFAMAGGSGTFPFNVLD GENYKNSALEIFKNSSTVQGLKKAKPHEVVNELKTFQSRKYTFGGQSFLIDKRGMKHILERHHPNLWDGSI KSQQSFLNKEMTVNDVADAIESIMKQNRRELTKKGTFSYQIRGSYEGQQYVVGFGKGRVGGQFYPEK
SEQ. ID. NO. 132.	ABP22962	MVQEVMMVMKKDFGDSISNKVVEYRVLARLSQQELAKKVGVSQKQTFVMEKGNVPTLLAFRIAEFFKVD VNEIFTYEKGNDQK
SEQ. ID. NO. 133.	ABP22963	MNNKKNIFDIVMYIIFGVLSLFLVAKTDYGTGVLVFAVILYLAIVYKIKQVFSNSDS

SEQ. ID. NO. 134.	ABP22964	MRKKRVITCVMAASLTGSLLPAGYASAKEDSKTPSYEELALHYMKSEKISSNGKLVEIEYVSGNETHKV QMNGNNHTVKVDGIEQKGLNFEYDENVAKRTNYENNLLKSNEFTTQAAKPKKGYHYVGTLSGHTKAAK NALSVTMSLVGIVPGLGWGSKAATILFSYWAKEQIPDAYKYDLYEKGAMTDSWYQYATVQFLKIKLIKRRK WANLGQVLLQK
SEQ. ID. NO. 135.	ABP23145	MKNFDKGTVVRTVLLIALINQTMFMFGKSPLDITDVQVNLADALYTAGSLIFTIGTTLAAWFKNNYVTA KGHKQKAILKQNNLT
SEQ. ID. NO. 136.	ABP23146	MTIAVKKNLVSEAKYALKCPNPMTAEYITIHTNTYNDASAANEVSYMIGNTSSTSFFHFAVDDKEVRQGIPTD RNAWHTGDTNGPGNRKSIGVEICYSKSGGAKYAAEKLAIKFVAQLLKERGWGIDRVRRKHQDWSGKYC PHRILSEGRWNEVKAIDAELKALGGKSSSKTTSSKAVKKPSSSKKSSFNLP SGIFVKVSPLMHSAAVEQI QTALAALHFYPDKAKNFGIDSYYGPKTADAVRRFQLMNGLKADGIYPATKAKLEALLK
SEQ. ID. NO. 137.	ABP23147	MKRKQTFIFSMILLSVASIGLRSFWTNPFTTGVMIFVLALTIYAIKDLRRR
SEQ. ID. NO. 138.	ABP23148	MEYHLKSRQEVEDFIRHEVLTTKEAAELLGVNRQRVSQLISSGKLNPIKKLSGISLFLRTDLEEKKELEAGRK KYRPYDE
SEQ. ID. NO. 139.	ABP23149	MDEGTYNIDIVGFHGTSLESAQKIITEQNFTSGDIRNDHWLGQGAYFFREDPEQAKIWAKNKIKGSETAVI KTIVSLDNNFLNLDTRSGLNYNRYIKTEVKKILEEKAEIELTDDHSKIHIYRCFFCNELPTNIKAIQRTFF VQSTLNEDETFKKMDVVFVQGVQVCIRDLSVIDFTKTGINNVINMHTFRRRKKTKQKENYRKDVMKMRRE FNNPELIKDAENLGIKITLNSSEPGVFANVNGERYRINIDDLFSECDDDLHYHEDFKLDDFSITRDSNQHKVEI IKEEKNFYKNELVEAA
SEQ. ID. NO. 140.	ABP23150	MKSFFQFDDYNIIDVNYKFNNNFEGDEAVLSPIFDLEFEDETKDEADLILGIELGIRI
SEQ. ID. NO. 141.	ABP23151	MTDFERKVYQIIVNMHLYGKNPTLDDLKRKTGKSKEDIRTAVKSLLMEGELKWDKQKKWII
SEQ. ID. NO. 142.	ABP23223	MTDSWQNGFIEKINRNGNNGGLRKPQYGALS AIRAHWTISSKPATIVLPTGTGKTETMLATILSEQIESVLII VPSNLLRDQTFEAKSFGILPDLKMVGKNILYPNTVLYKTRIKDETEVWEWFSEANVIVSTVNAVNGLSTSIL NKLVEKVDVLMIDEAHHIAAGGWSSSLREKFLNKRILQFTATPFRADGKKIDGDIYNYSLSLAQKDGYFKPID FYPIEEFNELGDIQIAEKAVELLNKDLEDKYM HQLLVRANSKKRAEELNYKIYSYKFNPNVLISGQSKKNKE NLKKLREGIAKIVVCVDMFGE GIDIPNLKIAAIHDKYKSLPITLQFIGRFARSKSGIGNARIVTNIANDDLKDAL QSLYSQDADWNQLLSMHSSDAIQTEISHRKFINQFYSNDNINIDISQIKMRISTRVLYLGGVHVHNRKGWR SVLNVDKTEFFINEESSVMILIESIESQVDWSDQKDISKYNVDVFIIYVDKKNLFINETNASKGNQLIKYMF EANQISGERVFRVL DGINQLMIGTLGLKEQPSGRISFRMFAGTNIKDGINQVARASTTKSNLFATGYKDNN KISIGCSYKGVVWMRWVDSVVFWRKWCQKIGSQILDSSINTDYILENSLQSEEITEYPRGIPYKIQMPVEFE LSNSELKAFYIPNEDKEIPFYLCEFNPRLDGKQLLFELWINERKYTSQTLKERGFVINRILGDKIKIKSRNM ITVEEYLQDNL PQVTFNEDGSLSIVEGNLVVNNKPLAEVLFPKEKLHIVDWKKLVKDITIESQGLTKLNNSIQ YASIKNIVPVDLIIFDDDNSGEIADIVCISTNEEHRKITVQLYHCKYSHGTNP GARLLDLLEVCGQAERSITW NDSMVELLKRMRFRENKRINENKTSRFEKGNLSDLKTIENTQIRSGFETEMKISIVQPGVSISNISQQMNQLL LATDTYLKETYGIDLNCYFSK
SEQ. ID. NO. 143.	ABP23238	MSQAIPSSRVGVKIN EWYKMIRQFSVPDAEILKAEVEQDIQQMEEDQDLLIYYSMLCFRHLMLDYLEPG KTYGNRPVTTELLETIETPQKLTGLLKYYSLFFRGM YEFQKEYVEAIGYYRAEKELPFVSDDIEKAEHFHK VAEAYYHMKQTHVSMYHILQALDIYQNHPLYSIRTIQSLFVIAGNYDDFKHYDKALPHLEAALELAMDION DRFIAISLLNIANSYDRSGDDQMAVEHFQKAAKVSREKVPDLLPKVLFGLCWTLCAGQTQKAFQFIEEGL DHITARSHKFYKELFLQAVYKETVDERKIHDLLSYFEKKNLHAYIEACARSAAAVFESSCHFEEQAAAFYRKV LKAQEDILKGECLYAY

SEQ. ID. NO. 144.	ABP23224	MSKIPPEKYEACITYHLVNYFEFTLEKKIYPFSISQIEEKEGYDFGYKMSEKFFIYKRPYKVPKDTYHWKI EIEQLKTINRKANNINTYYALPSFGDSMGWYEALDNTFFVNSRSLEYQIKQINRGRNIKTTFISPEKILLDKFY RISCNIVGDLHSVAVSQKNINSKIGNITNYIKGLNEDVKSSTWLYILEED
SEQ. ID. NO. 145.	ABP23225	MKYENVEVLGSYSVREGGSINFSMGKNLELGEINTYIHELHFMHLTNYSSLGFLLLFEKECNLSLEYQDEL HYNQIKELSTIIFNRTVDVQEVYANNQELLWLENNINSEFKEKSFKLKPKKYQEYCNKLNITNDMRLNNEEK RYWIDRVCFYALNIQIFSDKFIEALKSRQKLSEYLSRNHPNKRLEALVKYSKNEKFDGVVEIRIQDILSKIKKIN IIKYFNEILSQLEPNATNFKIGDYLCENDIKKFIELNQKRMDERVKLDFYNDLVIKVDDISNHLNFGIFAIKNY ESTINKENFYITEALINLTPSYISEEVSDFLNNPKIKVIGIPSQEFDIAMKMPNIEVKDTPIVVLDSYNTAKKI LKVLLNGELYVGDLYEQTVKNFSTILFFRTERTEPKIYIFPTLKKMSIRLVKELGIEDILVYSKDTFRKKILSIFNCE VEMLKFIKWIFSFMKSSCIFTSGDPATKMSFNLTRSLFDDVMKIKIPNYYIHWAAALPTKKTIGEPFYSLMEF ENGENIGSFKATNQNTIIFLNKNDAVNRYRKKIFTTDSMAHKLEVVGIDRHYWNIIEKYILETGINICICTDVN NNIGKIMKLKEVDNIITQFSKV
SEQ. ID. NO. 146.	ABP23226	MKFKLTLCALVIALIGVSFISSSLGNEVNVASRNMTSKAANDSTNSLADKAIFDKEMTIAENGTLG
SEQ. ID. NO. 147.	ABP23227	MRS LGTISSPHVGMKINEWNRHIQKFNVTDAEMLKAEIERDIDIMEEDQDLLIYYQLIAFRHQLMIDYVIPT EGNQMELSEYLRKIEGSNRKMEKLVEYYYYFFQGMYEFEKGNFLSAITFYQKAENTIPYISDEIERAEFYFKM AEVFYHMKQTHVSMHYSSQAYNIYKTHDLYSVRRRIQCHFVIAGNYDDLESHEKALPHLEQALKGARLLESK NKRIYQQALFNIGNCYLKMGEITKAAYMEKSIFQFKKSNFNNLTQAYHDLALIYFLQHKQEAMDCFRK GVRFACKFDDDLFKIMFEGLQTLFIKKGEASILLNVFNKLETSQGYPYMEELALLAAKFYTEIGQMDDSVICF KKMVHARKQIQRGDCLYEI
SEQ. ID. NO. 148.	ABP23228	MTVREELIKRNPTIMKNILKRYEEAKEFIQHSTKEQFEEDLSRVKNKLDLTRYLESANDYMNPMMLREMY KTEKLLKEYDETASVVITAIQSSKVEIVLPSQNQI
SEQ. ID. NO. 149.	ABP23229	MDLFEECIEALKDPKEILSDELTEQYFETLNNKFPITSWARIDWDKVPQKESIETYDDLNNWLKFQGI VDTTI NLLWNPSPDVPVVRTLENALVLDLAVGSDTFMYS DHGFVIEFFHDGEVTIGRSE
SEQ. ID. NO. 150.	ABP23230	MAQLFTAGLFLFQIGLAIMETEKGLLYKKSAAEQFNLLLLNEIRLTYTLKF
SEQ. ID. NO. 151.	ABP23231	METEKMGQLYQQIAEQLNEMIPSEWTKIVLYAEILDDSEVYFFFNTPQSEYIYSHDIPKQFDVSKKIYVSL LIELQELFEELREEFKANNQDWTNLTCLKLENTGKFSIDYDYTDVIASDLNGTQRQVWWEYKNGILPEDKE DKDFVINYFSL
SEQ. ID. NO. 152.	ABP23232	MVMKVFEAKTLLSEATDRAKEYKELRTQMVNLRKALKGVADLSDSEFSGKGASNIKAFYHDHVGADQW IDYIDMKIAFFNSIAGAAEDKGLSDAYIEESFLEHELANANKKSKSIMSEQKKAMKDILNDIDILPLDLFSTET FKDELADANDKRKKTKLEKLDALDEDLKT EYALSEPNEQFIKSDFQKLQEATGKGKNATPIHYNAKAYRES DI HKKKGDIKRTEAYLKIKKEEAKEREIEKLERLKNYDYADADEFYEMAKTIGYENLTAEQQR YFTQIENTREL EAGFKGVAVGLYDSGKDAVVGLWDMVTDPGGTVEAITGAMAHPIKTYEASAAIEESYQKDMVNGDTYS RARWVS YAVGT VVTSIVGTGKVGAVSKTGTAAKVTTKVKTAAKSATAQKAITVSKQTVDHIKQKVNTGIE VSKKHVKTCLNQIGDLTLADILPYHPRHDLVPAGVPYNAVNGVTLKEGLQKFAKIVLPKPYGTSSSGRRTPA PHVPPVTVKYGEHFARWSRKKVLKPNIIYKTKEGYTYTTDNYGRITSVKADLQLGEAKRNQYAQTNAGKPQ DRKPDDDGHHLIATQFKGSGQFDNIVPMNSQINRS GGKWKYEMEQEWAKALKEEPPKRVNVNIESIYKGD SLRPTKFIIETIGNKTKFVTIKNQAGG
SEQ. ID. NO. 153.	ABP23233	MDKDFLIKIKDIQKGDTLTNRACGNWDMKLSRAKECKRAIVVRSGVILNVYKIVDAWESDEPAKITKTNN RVRFQLAECRDYSYLIGGTLKTKTQNPVSSLSLETLMELVK

SEQ. ID. NO. 154.	ABP23234	MYLYKVNQNNQJEDIREKPFKEKEIQDLCEANLQQMLGLGVKSEFRISNFRIDTLAFDAETKSFVIEYKN TKNFSVVDQGYAYLAAMLNHHKADFILEYNENHDLPLKRDDVDWSQSKVIFISPVFTVYQKQSIHFKDLPIEL WEIKRYENDLIQLNQMKADGVSESIKTISRQSETIQEVSKEIKVFSEEDHLADKPFDIIELYQQLKEFINLDD HISIKPTKLYIAFTSSKRNFVDILLKSGLKVWVNMKKGELHDPEEKMRDVSETGHWGNGDYEIFIKDDEHI EYIMGLIKQSYEKNK
SEQ. ID. NO. 155.	ABP23235	MKKRFILLGLFASVFM LAVYISFQNKNTHPVQSPVIHPEEDRIFFIYSNPFIKESTLLSTSTGERFNRRTFKVAD VPFIQTKSYKSTDIVLLAEHEPFYTLKKDVIKEHPLSDPFAFWYEGKDVSVKAYNVDTTGNEIRINDKKMKK EYTLTLP SLVTMGASDENYIIQSMSIYVIDRKT EEMIETLSASYADQFADSKEFIVASSEHELTVIEKETWK ATYIAYPEDLEYADTVYYDKESGSFYVTYEDKEGEANLLEYGKEFFIHIV
SEQ. ID. NO. 156.	ABP23236	MYIVAQEEHKQGIGGYGVFDIHSKKMLYQFDLP EEQVKVQDFVVVD
SEQ. ID. NO. 157.	ABP23237	MGGLYLSDLCSMYQKDKFFTGFVPEELLTYAYELFPSSEKETVTALLNCSMGSKAKSFVMFTSKGLYWKRF GEQEGCVTW EAFDTIQSIKSTDDYEIWF DGVEVFDVGFSSYPADLLAELLRIIQQSLSENGDLLTEPRIDHV SVSASELREISILFQNKHDKMFGLTNGLLVGNEISEKREVRRLRKLHIPKDQEMISFWSTFPVKQTDGITLTD KGIYFSDPFLRLFPWHVFKETPVMLKDQELIVGKKNVIIQLEENLMPAKDVFAFLEQVKRRISAVTSS
SEQ. ID. NO. 158.	ABP23502	MFVLLLYPKQSLLIHYSSKA EKGRTLFI LFLASTLNI
SEQ. ID. NO. 159.	ABP24563	MFNGKHLKVKACFKSNAFLIIKESVYIFISPLPDDAFRTP
SEQ. ID. NO. 160.	ABP24564	MDQREKMDTAGGNTSCKHKKFFRKITIISTFGGLLFGYDTGVINGALPFMAQRDQLDLTPFTEGLITSSLLF GAAFGLSLAGGRLADRIGRRKITLNLAF LFIATIGCSFAPNTSVMIIICRSLLGLAVGAASVTVPAFLAEMSPA E QRGKTITQNDLMIILGQLLAFTCN AVIGTSMGEYAHVWRFMLILATLPAIFLWFGMLIVPESPRWLASKGK VGEAFRVLKHVREENCAKAE LTEIKASINRETEINRATLKDLSVPWIRRLVGLGIGIAVVQQITGVNSIMFYG TQILQKAGFARDAALVANIGNGVISVIAC TFGIWIWGVKVGRRPLLTGLAGTTASILLIAICITLQGTVPVLPFIV IGLTITFLAFQQSAVSVVTWLMISEIFLRLRGLGMGISVFFLWMMNFI GLTFFVLLDQLGMSSTFFVFVV LGASAILYVKKYL PETKGR TLELENDFRSNQGV RKASSGKGEINM
SEQ. ID. NO. 161.	ABP24565	MINGEKKVDRPIRWAMVGGGRGSQIGYIHRSAALRDH HFQLVAGAFDINPERGKDFGMNLHVTPERCYL DFQQMFEEEA KREDGIEAVSIATPNGTHYEICKAALNVGLHV VCEKPLCFTFEEAKEL ENLAKKKNRVVGIT YGYSGHQMI EQARQMIANGELGDIRIINMQFAHG FHS DPVEMNPNSTKWRVDPKFAGPSYVLGDLGTH PLFLSEIMIP ELKINKLLCTRQSFVKS RAPLEDNAYTIMEYDNGAVGTWSSCVNAGSMH GQKIRVIGSKAS IEWWDEQPNQLRFEIQGKPVQILERMGYLYPEALQDDRIGGGHPEGLFEAWSNLYSRFAVAMEAADR GKELEHMWYPGIEAGVGGVRWVENCVRSADKGAVWVDYQ
SEQ. ID. NO. 162.	ABP24566	MSIHAGAPCCWGVDDPKNPYLP PWERVLQEASQAGYKGIELGPYGYIPMDIERVQAELLKNNLSIIAGTIF DDLVS ESHLGNLLEQVDEICSLITLKPFSFQDKEERFRFSPPYLVLDWGH DERDYKAGRPDQAKRLSKKEW NRMMSHIRTIAERAWKQYGVRAVIHPHAGGYIEFEDEIQQLKDIPYDIAGLCLDTGHL YYSKMDPEQWL RDYADRVDIYHFKDIDEHVYQQVMGEHIRFFDACAGVMCPIGQGIIDYEA IYKLLKDIHYHGYITIEQERD PRNSDTSRLDVSQS LAYLKNVGY
SEQ. ID. NO. 163.	ABP24567	MEKEVFSKMKT TIYDVAEKAGVSISTVSKVINHQPVGMKSKQKVL DAMQELNYKPSVLASALTGKRTSTIG FLLPDIANPLIAEMARRVEDRAHEYG FNVVICSTDFKSEKEERYVSLLRQKRV DGFILAGGFRNKQVIHELIS DNIPVILLSESQPYSSLTTVTVDN FLGGYELTAYLISLGHSRIA VIAEDNASSRERIRGYSQALQESDLDIHEDLI VVTDS TAESAQSLASSLLQSSNPPTAMICCN DILAIGALLAAREEHVLVPEELSITGFDNTLISKSSDPLTTVE VPVQSMCSQAVDLLIDEIEGKASEKQKILVLPKLIVRKSTSRFH
SEQ. ID. NO. 164.	ABP24568	MSLVKNGDSIKVVVFQKNEQIEEVELNSAQLSALLHSKQV

SEQ. ID. NO. 165.	ABP24598	MDINDASEHLIQLKQDLIDRSKIEMINKLRWAFSLKHLNFEIQTfNYGFV
SEQ. ID. NO. 166.	ABP24599	MKKRLIGFLVLPALIMSGIILIEANKKAPVEVLESAWDEFLFSFQIGKTDPSITIGMDHTKSEAKLREYLEH NLSREAKEYKIYIFKDDIDKLEKEHREYLNKANNPNK
SEQ. ID. NO. 167.	ABP24600	MRFTAGGNLSTMDSQVLDVIKKAYNLGMVKNKDNMLLRNEAINAYRNSI
SEQ. ID. NO. 168.	ABP24601	MLPEYRKKTPEEILEEIERLKRGRKLVYIGSAPGVGKTYRMLQEAHELKAEGLDVVIGLIETHNRKETEDLIGD LEIVPKKNIDYKGRLLLEEMDEAIKRAPDLVLIDELAHTNVPFSQRNKRYMDVEEILKSGINVL SAVNIQHLE SLHDIVQQITGVQVRERIPDSFLHMAHEIILVDVTPEILRKRLSEGKIYHPSKIEQALNNFFTASNLGALRELSL REVANDVDERVEKANEKNGKNKPSGINEKIMVCVQHGSNAERLIRRGWRIRNRLKTEILHVTNEVSMK RSTENRKKIQDWKRLAIQFNARFIEQIKKRHIAKAITDVAKEHDVTQIILGQSARSRWEEIRKGSIVNMIMR YTTGVDIHIVSDQQPRRK
SEQ. ID. NO. 169.	ABP24602	MLKIIRLALLMIIICGILYPLLMTGLAQAIFPDQANGSILKNKDGQIVGSELIGQQFTKSNYFQGRISSIKYNAV GSGSNNGPTNQEMLERTKSFIRVLEEGNPDLKTKELPIDLITNSGSGLDPDISVKAQFQVNRVSNATGVS ESTLNKLIDNTIDGRSLGIFGEPRVNVKLKLNKMKVQEISKGN
SEQ. ID. NO. 170.	ABP24603	MNKSNSESEMIKEAITQSFIKLNPLSMMKNPVMFVVEVGTFVLMLMIMPFAHSEEGYVYNLIVFLILLFTI LFANFAEALAEGRGKAQADSLKTKKDTVARRINKNGTVTDISSADLKKGDIVLVETGDFIPGDGEIIEGLASI DESAITGESAPVIKEAGGDFSSVTGGTKVVSISIKVRITADPGESFLDKMISLVEGAKRQKTPNEIALTILLVTL TIIFLLVVVTLPIANYGVGHIELSTLIALLVCLIPTTIGALLSAIGIAGMDRVTQFNVLAMSGKAVEVAGDINTII LDKTGTITFGNRLAAEFIPVSSTTQEELMQAAVITSLFDETPEGRSVLELAKNNGASWEASAYESAIEIPFTAE ERMSGLIKDGHHYRKGAVDSIKAFVQEMGGPLPLDLQSKSEEVARQGGTPLAVSYNNRILGLIYKDTVKP GMRERFDELKRMGIKTIMCTGDNPLTASTIAKEAGVDDFIAEAKPEDKIRVIREEQEKGLVAMTGDGTN DAPALAQADVGLAMNSGTIAAKEAANMVDLSDPTKIIIEVVAIGKQLLMTRGSLTTFSIANDIAKYFAIIPA MFTVAIPGMQVLNIMRLHSPPTAILSALIFNAIIIPLLIPLAMKGVKYVPMASAKLLSRNLIYGLGGIVVPFIGI KLIDILVSVFMS
SEQ. ID. NO. 171.	ABP24604	MKGHTRLLIPMSIILTILVSLKVPQTLSPSIEVTTLEGVKQVISIGPVASLESIKHLGTNGGGFFGANSAPFE NPSPLTNVIEILSMWCIPASLTYYGRFAKKQKQGWVIFGAMFILFIAFLSLIYVSESHGNPALTALGLDPSQ GSMGKEVRFGIAQSALFSSVTTAATTGTVNNMHDTLPLGQITPLSLMMLNTVFGGDDGVGLVNMLMY AIGVFICGLMVGRTPFLGRKIEPKEMKLITVALLAHPLIILAPTALAFADIGKGSISNPGFHGVSQVLYEFA SSAANNNGSGFEGLDNTPFWNISTGLVMLVGRYISIIALLAVAGSLVQKQVPETIGTFKTDNLLFIGILVGV VLIVGALTFFPVIALGPAAEYLSIR
SEQ. ID. NO. 172.	ABP24605	MGILQIIVVIMLMLFMKPLGTYYHVFSNEPNKTDKIFNPIEKIYKICGMKNRLSMTWKQYAGSLLTNMV FIAVGYVILRFQYILPLNPNGIENMNSMLSFNTIISFMTNTNLQHYSGETGLSYFSQMAVIMMMMFSA TGIAAAIAFIRGITSKGTIGNFLKIL
SEQ. ID. NO. 173.	ABP24606	MNNNLGGITLDDVCMLAVIAVIFAVFWAFVKWCDFITGGGEKQ
SEQ. ID. NO. 174.	ABP20078	MPKQQTAEKPPFFHNKTVLVTGGTSGISQIVKRLLMLTPKQVIVFSKDDSKQYVMSQKYAEDKRLLFVLG DVRDHRVNVQVMKGVDIVFHAAALKQVPTCEDHPFEAIQTNLIGGQNVVEAALSHRVQHVINISTKAV FKDIDYKLIKKGGLF
SEQ. ID. NO. 175.	ABP20079	MPYEEYEELKKKTIKVIQRKNYSIRIIDQKFENDNLDQLYKEVARLLFERALKSSE
SEQ. ID. NO. 176.	ABP20080	MGANNQGVFEANIEKSAADQKLFYRIKDVNPMFLKRGAAVSKNKYDCFLHFNGYLPFELKSTKDKSIA FREKIIPQQIKYKLEATQYPNIIPGFLFQFREPENKVYFVHIDEFLKYKNIAEKQLKHTYKNKVNKASIPAI EIGTEVRWMKKKVNYTYLNLKLCVELIKKEQSRDKPLHTYNTVPKTGVR

SEQ. ID. NO. 177.	ABP20081	MYVLKSLLEKVVYVKKQWKPVD SRLNLMHEYSV SIEDLVERTGLPKQRINDYVSGFKSNM NIGTAMTFAD AIGCSIEELYVWNFKERRQLIK
SEQ. ID. NO. 178.	ABP20082	MKTVKEAIDEKDLQRAHRNLINLADNNEELMQEIRWIKGTTL
SEQ. ID. NO. 179.	ABP20083	MNLKNIDENRYKKTYSVQPNDIFFVVRKNGNQTPYLIYKDKNKM LKLN LQSGASNYCADTIDSLVGIIKE NQESPANKVNPIKEYFFAKSHETSIRVHNTFNYPNIK
SEQ. ID. NO. 180.	ABP20084	MKTIKLYELVSEGKKPIKFNDNVYEWIEESVDTMMMGKIIGASIEYEDSVRFLIDLNPFEAYNRSVARHWD RDDEGNCVLTWFDTSFY PKNGIEAIYLPINGRTEIAFDTEEDSLLNEYAKVPQEISYVEWLENEVKQLISK
SEQ. ID. NO. 181.	ABP20085	MIVTAWILLIMFGLFALS DNLNTEDETKHIKFFMLMKFFSVFIAAIAAGVI
SEQ. ID. NO. 182.	ABP20086	MKNTEFKKTSFLEEYKRGDEMRRDFIIEGYTAIEEIIKEVNQRGSLNEADIYGT PKPQLSFSDVELGYMLT SMM EYATNHVGNPVD EEC EFENKLAYFEYKDEIVQIFEVYGGQTESWFSKPSDDTIDKLNNTAYGVYLIQF DDFINYTKNKDSESEKLSPSSTILNDITGGYTVGRGSK
SEQ. ID. NO. 183.	ABP20087	MLELDEYILKSEMDFADPEEIRSCIISFVSSLQQYIDLCKEELNEEYRV
SEQ. ID. NO. 184.	ABP20088	MVELAKEENMLFFDHYPT EYGGWQTGNRDVWGIWQGRYLLKKVSDGCCEYVSR
SEQ. ID. NO. 185.	ABP20089	MYGEDVEVTL DGNIKVKVFVCLPTTCKEEKEKRALLTKNLIDKRLKNEDLK YLDVQSDFVLIPKMIENG EF
SEQ. ID. NO. 186.	ABP20090	MRVSSEALKIVIVQH LERDNDLMSEGKIIVLPCRDEKTAKEFEDFYRKKFPSTQLMSIEIVDSNIYG
SEQ. ID. NO. 187.	ABP20091	METKKYVRIIRNASKYGD MTGQIFPLFGTWEDSYKIDGSDGVVYVRK KDVEVIVTENRRPKVDERVLITEVL LSSGHYKIGDIYTVLSVVDIYGTITVKEHSNCVISREYEVIVDEVKKEEADGMENVNQTVINNANTVFEKKDD KYFGYKS RFGDIVIGGAYS YRFV VQYAKTNQD VV VPGDENTVTTPVCTTLEERLWQPEKAVKSSPRNLHY
SEQ. ID. NO. 188.	ABP20092	MEVGDKIHNTNEQITALEKKYQIETTLEKQRDLLKLETQQNKEKLELLFELSEVLTQLQDEEWVSCMIALR IIRRNKRKYLNLFELVNEKAYINKDKFKVLHDEFFDLKQQLNEI
SEQ. ID. NO. 189.	ABP20093	MIYKTFLPYADKVYLTIVDSAQREADSYFPM LDDRWKLTDRHNKADEKNKYNYSFITFENNYRQK
SEQ. ID. NO. 190.	ABP20094	MTQFDKQYNSIIKDIINNGISNEEFVVRTKWDS DGT PAHTLSVMSKQMRFDNSEVPILT TTKKVAWKTAIKE LLWIWQLKSNDVNDLNKMGVHIWDQWKQEDGTIGHAYGFQLGKKNRNLNGEKVDQVDYLLHQLKNN PSSRRHITMLWNPDELDAMALTPCVYETQWYVKHGKLHLEVRARSNDMALGNP FNVFQYNVLQRMIA QVTGYELGEYIFNIGDCHVYTRHIDNLKIQMEREQFEAPELWINPEVKDFYDFTIDDFKLINYKHGDKLFFEV AV
SEQ. ID. NO. 191.	ABP20095	MFKVL DVL DGEKTKQNTYIYWLFVCGN FLVVFYLADVFL
SEQ. ID. NO. 192.	ABP20096	MLKDKNKITKSIEKINKLEEG LALFEEGD EEYLSVLVKIQGLYDEIADTALECFKEMTTKIRKTGQKRIGKIDQ LPYTIKENIADQVNELKGSFLDESKY
SEQ. ID. NO. 193.	ABP20119	MDSYPESLKKETEIEKERVNRNGNIKEDRIEIAETTVEFLKSEK RHYKFSEVAAAMADNLSEFFKSYLKGE
SEQ. ID. NO. 194.	ABP20120	MKKLRVMSLFSGIGAFEALRNIGVEYELVGFSEIDKYAIKSYCAIHNVDEQLNYGDVSKIDKKKLPEFDLLV GGSPCQSFSVAGYRKGFEDTRGTLFFQYIDTLKEKQPRYFV FENVKGLINHDKGNTLNIMAESFSEVGYRID LELLNSKFFNVPQNRERIYIIGVREDLIENDEWVVEKGRNDVLSKGKKRLKELNIKSFNFKWSAQDIVGRRLR EILEEYVDEKYLLSEEKSKLIEQIEKPEKDVVFGGINVGKRWLNNGKTYSRNFQGNRVYDSNGIATTLT SQSVGGLGGQTSLYKVEDPIMIGHIDLKGHDAIKRVYSPDGVSPTLTMMGGGHREP KIAVEYVGNINPSGK GMNDQVYNSNGLSPTLTNNKGEGVKISVPNPEIRPVLTPEREEKRQNGRRFKEDDEPAFTVNTIDRHGVAI GEYPKYRIRKLTPLCEWRLQAFDEEDFEKALSVGISNSQLYKQAGNSITVTVLESIFKELIHTYVNEESE

SEQ. ID. NO. 195.	ABP20121	MDINGKDLNKHIDCVQFMRENMGDCSIDLTVTSPPYDDLRLKYNGYSFNFEATARELYRVTKDGGVVV WVIGDKTHNGSESGTSFKQALYFKEIGFNLHDTMIYEKDSISFPDKNRYQIFEYMFVFSKGKPKTINLISDR KNKWYNGKKHIKGHYRKMDGEKVRHNKQNLLEFGVRFNIWRIPNGHQKSTLDKVAFEHPAIFPERLAE DHILSWSNEGDIVLDPFMGSGTTAKMAALNNRKYIGTEISKEYCDIANERLRNYIGTI
SEQ. ID. NO. 196.	ABP20122	MKKVIAIDMDQVLADLLSDWVAYINTHDDPFLKEEEILCWDIKKYTNTNNNVYRHLDYDLFRNLDVIEGSQ RVVKELMKKYEYVYVTTATNHPESLKAKLEWLTEHFSFIPHSNVVLCGNKSIKADIMIDDGIHNLESFEGM KILFDAPHNRNDNRFIRVMNWEEIERKLL
SEQ. ID. NO. 197.	ABP20123	MALIILEGPDCCFKSTVAAKLSKAMKYPIIKGSSFELATSGNQKLFEHFNRLADEDSVIIDRFVYSNLVYAKKF KDYSILTEQQLRIIEDKIKLKAKVYLHADPSVIKERLSIRGDEYIEGKDIDSILELYREVMSNAGLHTYSWDTG QWSSDEIAKDTIFLVE
SEQ. ID. NO. 198.	ABP20226	MGYKLMAYGGYFLCLFFLLMDGWGRMGICLIAGLALLALEPYKIKAQKNIDKLKENAETLKHYESGFNPD NFFNTYKTKIAFKESDSLVKIYQLNRNEHIEEYTIFFSNIESEITLDNQIISKVSKSGIVAGGLLAGGIGAALGGL SASSIQNEMVKSVTLKITVEDLGKPIHYIDFLPTQEVEGYNTQGYKKDSNIIQQALKNAEYWHGVMDVIAKK ASKVAQ

SEQ. ID. NO. 199.	ABP20227	MSQNLKIILTPQADTSSKTVEQLNQJQSLEKLNLSKLNTNIDSTTLKALQEFSSAVDAYQKNLKSYNQTVR ETSTVIKNADGSVEKLTQQYKKNGEILQRETKIINNRRNTALKQETQEVNKLQATEKLGQVQKKTQVRNLQ GQPTKIVQKNRQGFDDIVYTTDPKTNSTSSKTTTNYDQQRRAIEQLKQDLEKLRQQGIVTDDTTISSLGRKIN TAQSAQQIEALQNRIRMLDDKSAAVAKNNELKKTIELYQRQAQVNVQNLNTRYGSSMGSSNRQAVQDY LNAVNSLNVSTGSNNIRSQISLNMQFRELASSAQAAANQASSFGAELTQTFKSMSTYLISGSLFYGAISGL KEMVVSQAVEIDTLMTNIRRMNPDYKYNELQESIDLGDLSNKITDILQMTGDFGRMGFDESELSTLTK TAQVLQNVSDLTDPDDVTNTLTAAMLNFNIAANDSISIADKLNEVDNNYAVTTLDLANSIRKAGSTASTFGV ELNDLIGYTTAIASTTRESGNIVGNSLKTIFARIGNNQSSIKALDEIGISVKTASGEAKSASDLISEVAGKWDTL TDAQKQNTSIGVAGIYQLSRFNAMMNNFSIAQNAAKTAANSTGSWSEQQKYADSLQARVNKLQNNFT EFAIAASDAFISDGLIEFTQAAGSLLNASTGVIKSVGFLPPLAAVSTATLLLSKNTRTLATTLLIGTRAMGQET LATAGLEAGMTRAASRVLKTALRGLLVSTLVGGAFALGWALESLISSFAEAKKAKDDFEQSQQTNVEA ITTNKDSTDKLIQQYKELQKVESRSLTSDEEQEYLQVTQQLAQTFPSLVKGYDSQGNAILKTNKELEKAIEN TKEYLALKKQETRDSAKKTFEDASKEIKSKDELKQYKQIADYNDKGRPKWDLIADDDYKVAADKAKQS MLKAQSDIESGNAKVKDSVLSIANAYSSIDISNTLKASISDVVNKLNLKDNLDPEELEKFSSSLGKLQEKMQK ALDSGDEKAFDNAKKDIQSLETTYKSDSSIDVFKMSFDKAQKNIKDGDKSLSSVKSEVGDLGETLAEAGNE AEDFGKKLKEALDANSVDDIKAAIKEMSDAMQFDSVQDALNGDIFNNTKDQVAPLNDLLEKMAEGKSISA NEANTLIQDKELAKAISIENGVVKINRDEVIKQRKVKLDAYNDMVYTSNKLKTEVNNAIKTLNADTLRID SLRKLKRLKLDMSAELESDLEVKSINNVADAKKELKLEEKMLQPGGYSNSQIEAMQSVKSALESYISASEE AASTQEMNKQALVEAGTSLENWTDQKEKANEETKTSMYVVDKYKEALEKVNAEIDKYNKQVNDYPKYS QKYRDAIKKEIKALQKKKLMQEQAALLKQDKISGNIAQYGIVTTTSSPGGTSTSTGGSYSGKYSSYNSAAS KYNVDPALIAAVIQQESGFNAKARSGVGAMGLMLPATAKSLGVNNAYDPYQNVMMGGTKYLAQQLE KFGGNVEKALAAYNAGPGNVIKYGGIPPFKETQNYVKKIMANYSKSLSSATSSIASYYTNNSAFRVSSKYGQ QESGLRSSPHKGTDFAAKAGTAIKSLQSGKVQIAGYSKTAGNWWVIKQDDGTVAKYMHMLNTPSVKGTGQ SVKAGQTIGKVGSTGNSTGNHLHLQIEQNGKTIDPEKYMKGIGTSISDASQAEERQQGIAQAKSDLLSLQ GDIDSVNDQIQELQYELVQSKLDEFDKRIGDFDIRIAKDESMANRYTSDSKEFRKYTSQKKAQAEQAKIQQ QKVNWIQKEIKTNKALNSAQRAQLQEELKQAKLDLISVQDQVRELQKQLVQSKVDETLSIEKSSSKTQGKI KDVDNKISMTEEDDKVKYYSKQIKLIQQQKQKAKYIKQLEEQQKAAKGFPDIEQITEEIEENWKDKQKDF NLELYNTKSIKDIYKSLADEVVSIYKEMYKMRDIEAHQKATQDKIDEIDKEDEEAKYQKELKEKNQAIQ ETKDKISKLSMDDSSEAKSQVKDLEKQLQEQQEALDEYIKDRSNTKRKEALQDQLDKDEESINNKYDDLNV DERAFKKLEDKLMGKITDIKQLNEFTKFINENMKSIGSISNNLIDKLDAASALNTVTTGNTTGKKVSSF ASGGYTGTGLGAGKLAFLHDKELILNKTDTENMLEAVKQVRQTSTDNSVKTTSKWGQPGKISDVLSKSISL VTPAMNAAVASQTSCLKGLIPTLKNFSTPTVTPSTPQGNTSNNQNSFTINVTEASNAKETASLVYKQLANG LKNTGLNFNIT
SEQ. ID. NO. 200.	ABP20228	MIRQSQYFLDNEKSIDYGVENVNTESGLVEESFLGSRSVNETYVKGRSEPYTEGVKREKQFPLNFYVGEN YDEKKIRAIKRWLDVDDYKPLAFSENLDIVVYAMPVDTSDLVHNAARHGYVRLTMKCNSPYASRNTSTHS FDISSGMKTIELHNKGDVAIYPTVEILKIGDGDVKIENLSDYTDPFIFSNLKDREIVKVNGDKIEIESSLYGNERY DDFNDNYIRLDYGKNRLKVTGKCKLRLTFRFKYR

SEQ. ID. NO. 201.	ABP20229	MITIRKDEIKNIRLSLAKPDKTKIANIDEVLNPTVTNLNHGSSVHELSEFSIPLKATYDGVIKRNHVVDLLKPWYL IKTEFYGLAIWFIITKRTKSFSSEMDTVQVECRSLQHELRSISVLKYEETSKNLQEVVTDCLKNTSWTVGYIDT LFNVKRRQFDVSSTNKLDFLYSICEKFDAVPVFDTVKETVSFYKESDISKYKGLKNPRQYMISMDSDDDAD ELVTRLYATGKDGISINSVNPTGQSYIDDFSYFLFPFQRDEQRNVISHSAYMPDELCHAILDYNDLVNSEGN AFNKLLTQKNEAETGLTELNNELYTLDEVLQKLLDRIEVAKKAGDDTSQKLAQLAVKQKAVALKKNQIATIE STISQISASISKLKEKLSFENNFSENQKLLSRFISTTEWSNDSIYDENELYDDANEELSRNTPPVNVTLDIVN FFNCISEKHNVDRFSLGDIVRVQQSDLNTDIKAILSAITIDFEQSNISVTVTNGKRVQSDFEKVIKTVYRTNKI STELNKRKIEWDKVTENFNIRNDRISVQPAPPVIASDGTATHKVNDRNGSVDITIQWNYVDSNEDKYNDIG FEVYLHGSDDNEEYTFGSVQASENLQNVKYDRRTATFTGLPSNMYTIGVQAYRRVDADIDINQILLSDIVK SNHPSENPLYPTPSIEVKGSLSGKVNGLYTISTESKPEEPETGTIWDPKTNKQELFNGEEWIVSSAGSADSL NGFTASLTTPSPNIPVRDQSGVISGSDGNAEMLGGRAASDYALTENIPVPPKFAKGVYTGDTLSKQIPLA FTPDLVKITPISPEDSQLVIESQLGGYAYQVTSTGLSLIGGDLGYALGNNLFTGSDSNCRGNKLVNKKYIWE AYQQN
SEQ. ID. NO. 202.	ABP20230	MGSLPTKLEVIKLADFAELYNDPILSKKRIGSVEDPYLTYSETLTVYNGRALLTEIPNREFRVEIGDKKEWR EIEDGELEDNYFKVDYLMGVVFFNASNEGKSLTFNYSGEGASFFPASRIWIKRQGNMVIETLQGLIDDAED TIIRMNERIAECERVTKRCIEITNWCQRATSDYEYVVENTRKYIPLMVYTYQDLMDTYPNPQIGWVVITRDT GIEYRWDFDWINISISDQFDGYNVVSSEIYPYNIRTVWLRTNSPPSKKRVKPSKDAPDGSMMVWIRKG
SEQ. ID. NO. 203.	ABP20231	MSDNLIPVNTMGYYDEETKQWVPIDAVALKSENYRFTADDISQKFNKIGDIDAIGATGNTLSEKIINEFNRY GINISWLGAKGDGTTDDSSVFSSISTYQDKVFDLAGKTYVNSFPNKNKYLNKYFIIDGNKYFGSVSSSQ TGNSNIIIGNNAAKNFRPGDQYKGIAGHNIIAIGENALSNASEYTKNTTAIGAGALFNNKYGVYNLAIGLQS QYYVTGVQGDFAKGTNRNTSVGDNSMRFNKDGYSNVAMGRNALQTNEKSLWNLTALGAAAMSGYAPLN LDSKTIINNSPQTAGYQVAVGTNSLYWSNGIGNVGVGNAGREIKNSQRNVAMGYAMSQLDSDVSFE GKQRRFPSIQAGYTWIGQDITLTHIGHTFIVGQNLALDGGGEKFTTVKSITVDTFTVSTTQIAQNEISGMA QVSEYTTTGTVYVWKDNNIQVSMGNHFPQNGYKVLMSVGGREAIYFTVANSTSSGFTVSTDIIGDESGAV KITEYSDTPMAVNYDNTAIGVKAAMKMKGSFNATIGGLSLENNKGDYNTALGYMALKNNNTTGNQNT ALGYGALRFTTGGDEMMDISNSTGVGFNSRVSGSNQIQLGDGNSTPYSFNALQNRSDLRDKADIRDTVLG LDFINKVRPVDYKWDIRDEYVEIKEDGTVITHERDGSKKKNRYHHGVIAQEIQKVIEAEGIDFGGFQHHELS GGEDVMSIGYTEFIAPLIKAVQELSAKVEEQAKEIAALKKA
SEQ. ID. NO. 204.	ABP20232	MTIQARQMLVSPGKYPKIGRYAMTAEYITFHNTANDASANNEISYMRNNNETVSYHFAVDDKEVVQGLP TNRSFAHCGDGEYGTGNRKSIGVEVCYSKSGGERYKAEALAIKFAIQLKERGWGVERVKKHQEWGSKY CPHRVLDEGRWNEVKAIAAELKSLGGKSTPTKTSTKPTTSSPSSSSAASGLSKVDGLRFYKSPSWEDK NVVGTVNKGIGFPTVVEKVKVGSAYQYKVKNSKGATYYITASDKYVDVTGSKASSPTPKTTSTSSSSSIKS VGKIKIVGVSSAAIVMDKPDRNSSKNIGTVKLGSTVISGSVKGKNNKSGYWEVIYNGKRGYISGQFGSKI
SEQ. ID. NO. 205.	ABP20233	MTKINWKVRLKKKTLVLAIFSATLLFVQAIASAFGYDLTVFGDNLTEKFNALLTFLTAMGIIVDPTTQGISDSE QAMDYDSR
SEQ. ID. NO. 206.	ABP20234	MLEQMISSKVGKINNEWYKYIRLFSVPDSEILKAEVEEIRHMKEDQDLFLYSLMCFRHQLMLDYLEPKT LNEERPKVSDLLEKIESSQTDLKGILEYYNFFRGMYEFEQYELNAISFYKQAEKLSLVADEIERAEFHYKVA EIIYHMKQTHMSMHIVQAIDSYKAHENYTVRVIQCSFVIGLNYLMDYPEKAIPHFKDALDKAREIDMS RLIGSSLYNLGLCSFAEEAYEKASEYFKEGIRVYQDNGYEHSNRILDILLMLTKTTFKMRNHSEGISWCAHGL SLSKNLNDEIMAKMFEFIHALYVDNDNEKLSILNYLELKSMLSDVEDLASDAKYYNEKEDHKVAVAYYEK VLYARKQIQRGDCLYET

SEQ. ID. NO. 207.	ABP20235	MKLKHASVFILAIVLIGFVSTYLTNTQKDVQEARRGHTASIGFTDGHSEIASRGHTS
-------------------	----------	---

[0090] The term "comprising" whenever used in this document is intended to indicate the presence of stated features, integers, steps, components, but not to preclude the presence or addition of one or more other features, integers, steps, components or groups thereof.

[0091] The disclosure should not be seen in any way restricted to the embodiments described and a person with ordinary skill in the art will foresee many possibilities to modifications thereof.

[0092] The above described embodiments are combinable.

[0093] The following claims further set out particular embodiments of the disclosure.

References

1. Fetissov SO. Role of the gut microbiota in host appetite control: bacterial growth to animal feeding behaviour. *Nat Rev Endocrinol*. 2016. doi: 10.1038/nrendo.2016.150. PubMed PMID: 27616451.
2. Bäuml AJ, Sperandio V. Interactions between the microbiota and pathogenic bacteria in the gut. *Nature*. 2016;535. doi: 10.1038/nature18849.
3. Ganguly S, Prasad, A. Microflora in fish digestive tract plays significant role in digestion and metabolism. *Reviews in Fish Biology and Fisheries*. 2012;22:11-6.
4. Ray AK, Ghosh, K., Ringo, E. Enzyme-producing bacteria isolated from fish gut: a review. *Aquaculture Nutrition*. 2012;18:465-92. doi: 10.1111/j.1365-2095.2012.00943.x.
5. FAO. The state of world fisheries and aquaculture: Opportunities and challenges. Food and agriculture Organization of the United Nations. . Rome, Italy. 2014. 243 p.
6. Krogdahl A, Penn, M., Thorsen, J., Refstie, S., Bakke, A.M. Important antinutrients in plant feedstuffs for aquaculture: an update on recent findings regarding responses in salmonids. *Aquaculture Research*. 2010;41:333-44.
7. Sinha AK, Kumar, V., Makkar, H.P.S., De Boeck, G., Becker, K. Non-starch polysaccharides and their role in fish nutrition – A review. *Food Chemistry*. 2011;127:1409-26.
8. Joint FAO/WHO Working Group Report on Guidelines for the Evaluation of Probiotics in Food, (2002).
9. Setlow P. Spore Resistance Properties. *Microbiol Spectr*. 2014;2(5). doi: 10.1128/microbiolspec.TBS-0003-2012. PubMed PMID: 26104355.
10. Tam NK, Uyen NQ, Hong HA, Duc le H, Hoa TT, Serra CR, et al. The intestinal life cycle of *Bacillus subtilis* and close relatives. *J Bacteriol*. 2006;188(7):2692-700. doi: 10.1128/JB.188.7.2692-2700.2006. PubMed PMID: 16547057; PubMed Central PMCID: PMC1428398.
11. EFSA-BIOHAZ. Scientific Opinion on the update of the list of QPS-recommended biological agents intentionally added to food and feed as notified to EFSA, European Food Safety Authority Panel on Biological Hazards (EFSA-BIOHAZ). *EFSA Journal* 2017;15(3):4664. doi: 10.2903/j.efsa.2017.4664
12. Cutting SM. *Bacillus* probiotics. *Food Microbiol*. 2011;28(2):214-20. doi: 10.1016/j.fm.2010.03.007. PubMed PMID: 21315976.
13. Bader J, Albin A, Stahl U. Spore-forming bacteria and their utilisation as probiotics. *Benef Microbes*. 2012;3(1):67-75. doi: 10.3920/BM2011.0039. PubMed PMID: 22348911.
14. Kunst F, Ogasawara N, Moszer I, Albertini AM, Alloni G, Azevedo V, et al. The complete genome sequence of the gram-positive bacterium *Bacillus subtilis*. *Nature*. 1997;390(6657):249-56. doi: 10.1038/36786. PubMed PMID: 9384377.

15. Harwood CR, Cutting SM. Chemically defined growth media and supplements. In: Harwood CR, Cutting SM, editors. *Molecular biological methods for Bacillus*. Chichester, UK: John Wiley & Sons Ltd; 1990. p. 548.
16. EFSA-FEEDAP. Guidance on the assessment of bacterial susceptibility to antimicrobials of human and veterinary importance, European Food Safety Authority Panel on Additives and Products or Substances used in Animal Feed (EFSA-FEEDAP). *EFSA Journal*. 2012;10(6):2740.
17. Serra CR, Earl AM, Barbosa TM, Kolter R, Henriques AO. Sporulation during growth in a gut isolate of *Bacillus subtilis*. *J Bacteriol*. 2014;196(23):4184-96. doi: 10.1128/JB.01993-14. PubMed PMID: 25225273; PubMed Central PMCID: PMC4248874.
18. Casula G, Cutting SM. *Bacillus* probiotics: spore germination in the gastrointestinal tract. *Appl Environ Microbiol*. 2002;68(5):2344-52. PubMed PMID: 11976107; PubMed Central PMCID: PMC127533.
19. Xue Z, Zhang W, Wang L, Hou R, Zhang M, Fei L, et al. The bamboo-eating giant panda harbors a carnivore-like gut microbiota, with excessive seasonal variations. *MBio*. 2015;6(3):e00022-15. doi: 10.1128/mBio.00022-15. PubMed PMID: 25991678; PubMed Central PMCID: PMC4442137.
20. Zhou Z, Zhou X, Li J, Zhong Z, Li W, Liu X, et al. Transcriptional regulation and adaptation to a high-fiber environment in *Bacillus subtilis* HH2 isolated from feces of the giant panda. *PLoS One*. 2015;10(2):e0116935. doi: 10.1371/journal.pone.0116935. PubMed PMID: 25658435; PubMed Central PMCID: PMC4319723.
21. EFSA-FEEDAP. Guidance for the preparation of dossiers for technological additives, European Food Safety Authority Panel on Additives and Products or Substances used in Animal Feed (EFSA-FEEDAP). *EFSA Journal*. 2012;10(1).
22. EFSA-FEEDAP. Guidance on the assessment of the toxigenic potential of *Bacillus* species used in animal nutrition, European Food Safety Authority Panel on Additives and Products or Substances used in Animal Feed (EFSA-FEEDAP). *EFSA Journal* 2014;12(5).
23. Cabello FC, Godfrey HP, Buschmann AH, Dolz HJ. Aquaculture as yet another environmental gateway to the development and globalisation of antimicrobial resistance. *Lancet Infect Dis*. 2016. doi: 10.1016/S1473-3099(16)00100-6. PubMed PMID: 27083976.

C L A I M S

1. A bacterial strain selected from ABP1 with a deposit under the accession number CECT 9675, of 08.06.2018, at Colección Española de Cultivos Tipo, and/or from ABP2 with a deposit under the accession number CECT 9676, of 08.06.2018, at Colección Española de Cultivos Tipo.
2. Composition for aquatic animal feed comprising a bacterial strain according to the previous claim.
3. Composition according to the previous claim comprising 1×10^5 - 1×10^{12} of colony forming units of the bacterial strain per gram of the composition.
4. Composition according to any of the previous claims 2-3 comprising 1×10^7 - 1×10^{10} colony forming units of the bacterial strain per gram of the composition, more preferably 2×10^9 colony forming units of the bacterial strain, per gram of the composition.
5. Composition according to any of the previous claims 2-4, further comprising a preservative.
6. Composition according to any of the previous claims wherein 2-5, wherein said composition is in a granulate form, a powdered form or a pellet.
7. Composition according to the previous claim, wherein the granulate form is coated, in particular wherein the coating comprises a salt and/or wax and/or a flour.
8. Method for feeding an aquatic animal present in an aquaculture comprising the step of feeding the aquatic animal with a composition according to any of the previous claims 2-7.
9. Method according to the previous claim, wherein the step of feeding the aquatic animal is carried out during the life span of the aquatic animal.
10. Method according to any of the previous claims 8-9, wherein the aquatic animal is selected from the following list: a shellfish, fish, amberjack, arapaima, barb, bass, bluefish, bocachico, bream, bullhead, cachama, carp, catfish, catla, chanos, char, cichlid, cobia, cod, crappie, dorada, drum, eel, goby,

goldfish, gourami, grouper, guapote, halibut, java, labeo, lai, loach, mackerel, milkfish, mojarra, mudfish, mullet, paco, pearlspot, pejerrey, perch, pike, pompano, roach, salmon, Atlantic salmon, sampa, sauger, sea bass, European sea bass, seabream, gilthead seabream, white seabream, shiner, sleeper, snakehead, snapper, snook, sole, spinefoot, sturgeon, sunfish, sweetfish, tench, terror, tilapia, trout, tuna, turbot, vendace, walleye, halibut, whitefish or shrimp.

11. Use of a bacterial strain selected from ABP1 with a deposit under the accession number CECT 9675, of 08.06.2018, at Colección Espanola de Cultivos Tipo, and/or from ABP2 with a deposit under the accession number CECT 9676, of 08.06.2018, at Colección Espanola de Cultivos Tipo, as a probiotic.
12. Use of a bacterial strain selected from ABP1 with a deposit under the accession number CECT 9675, of 08.06.2018, at Colección Espanola de Cultivos Tipo, and/or from ABP2 with a deposit under the accession number CECT 9676, of 08.06.2018, at Colección Espanola de Cultivos Tipo, as a supplement to feedstuff.
13. Use according to the previous claim, as a supplement to feedstuff for fish or shellfish.
14. Isolated polynucleotide from ABP1 with a deposit under the accession number CECT 9675, of 08.06.2018, at Colección Espanola de Cultivos Tipo, wherein the isolated polynucleotide is selected from the following list: SEQ. ID. No. 19 (ABP10666), SEQ. ID. No. 20 (ABP10667), SEQ. ID. No. 7 (ABP10654), SEQ. ID. No. 24 (ABP10671), SEQ. ID. No. 36 (ABP10829), SEQ. ID. No. 37 (ABP10830), or combinations thereof, wherein the isolated polynucleotide encodes for a polypeptide that hydrolyses a non-starch polysaccharide, preferably non-starch polysaccharides present in plant feedstuffs.
15. Isolated polynucleotide from ABP2 with a deposit under the accession number CECT 9676, of 08.06.2018, at Colección Espanola de Cultivos Tipo, wherein the isolated polynucleotide is selected from the following list: SEQ. ID. No. 160 (ABP24564), SEQ. ID. No. 161 (ABP24565), SEQ. ID. No. 162 (ABP24566), SEQ. ID. No. 163 (ABP24567), or combinations thereof, wherein the isolated polynucleotide encodes for a polypeptide that hydrolyses a non-starch polysaccharide, preferably non-starch polysaccharides present in plant feedstuffs.
16. Isolated polynucleotide according to any of the previous claims 14-15, wherein the non-starch polysaccharide is mannan, glucan, xylan, arabinan, and/or galactan.

17. Isolated polypeptide from ABP1 with a deposit under the accession number CECT 9675, of 08.06.2018, at Colección Española de Cultivos Tipo, wherein the isolated polypeptide is selected from the following list: SEQ. ID. No. 19 (ABP10666), SEQ. ID. No. 20 (ABP10667), SEQ. ID. No. 7 (ABP10654), SEQ. ID. No. 24 (ABP10671), SEQ. ID. No. 36 (ABP10829), SEQ. ID. No. 37 (ABP10830), or combinations thereof, wherein the isolated polypeptide hydrolyses a non-starch polysaccharide, preferably non-starch polysaccharide present in plant feedstuffs.
18. Isolated polypeptide from ABP2 with a deposit under the accession number CECT 9676, of 08.06.2018, at Colección Española de Cultivos Tipo, wherein the isolated polypeptide is selected from the following list: SEQ. ID. No. 160 (ABP24564), SEQ. ID. No. 161 (ABP24565), SEQ. ID. No. 162 (ABP24566), SEQ. ID. No. 163 (ABP24567), or combinations thereof, wherein the isolated polypeptide hydrolyses a non-starch polysaccharide, preferably non-starch polysaccharide present in plant feedstuffs.
19. Isolated polypeptide according to any of the previous claims 17-18, wherein the non-starch polysaccharide is mannan, glucan, xylan, arabinan, and/or galactan.

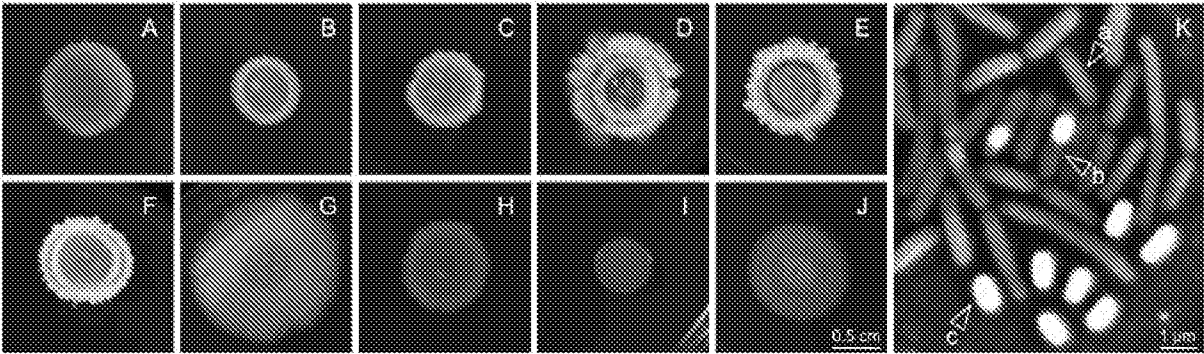


Fig. 1

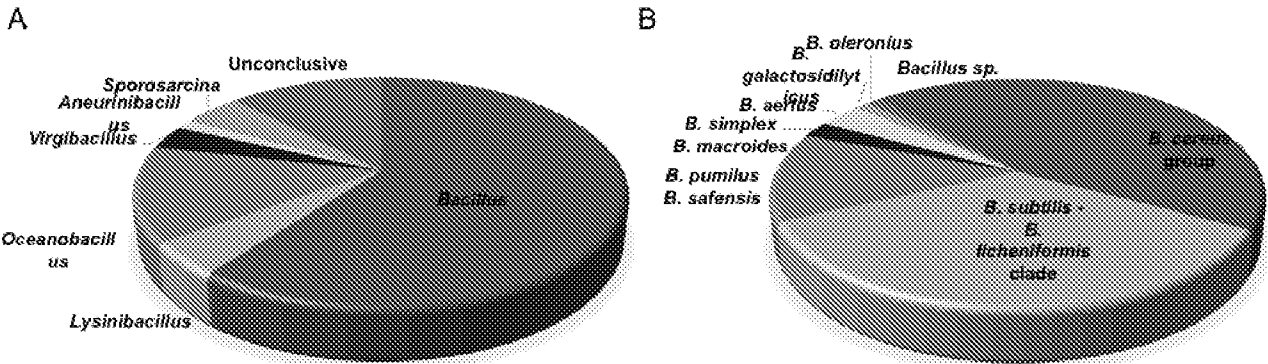


Fig. 2

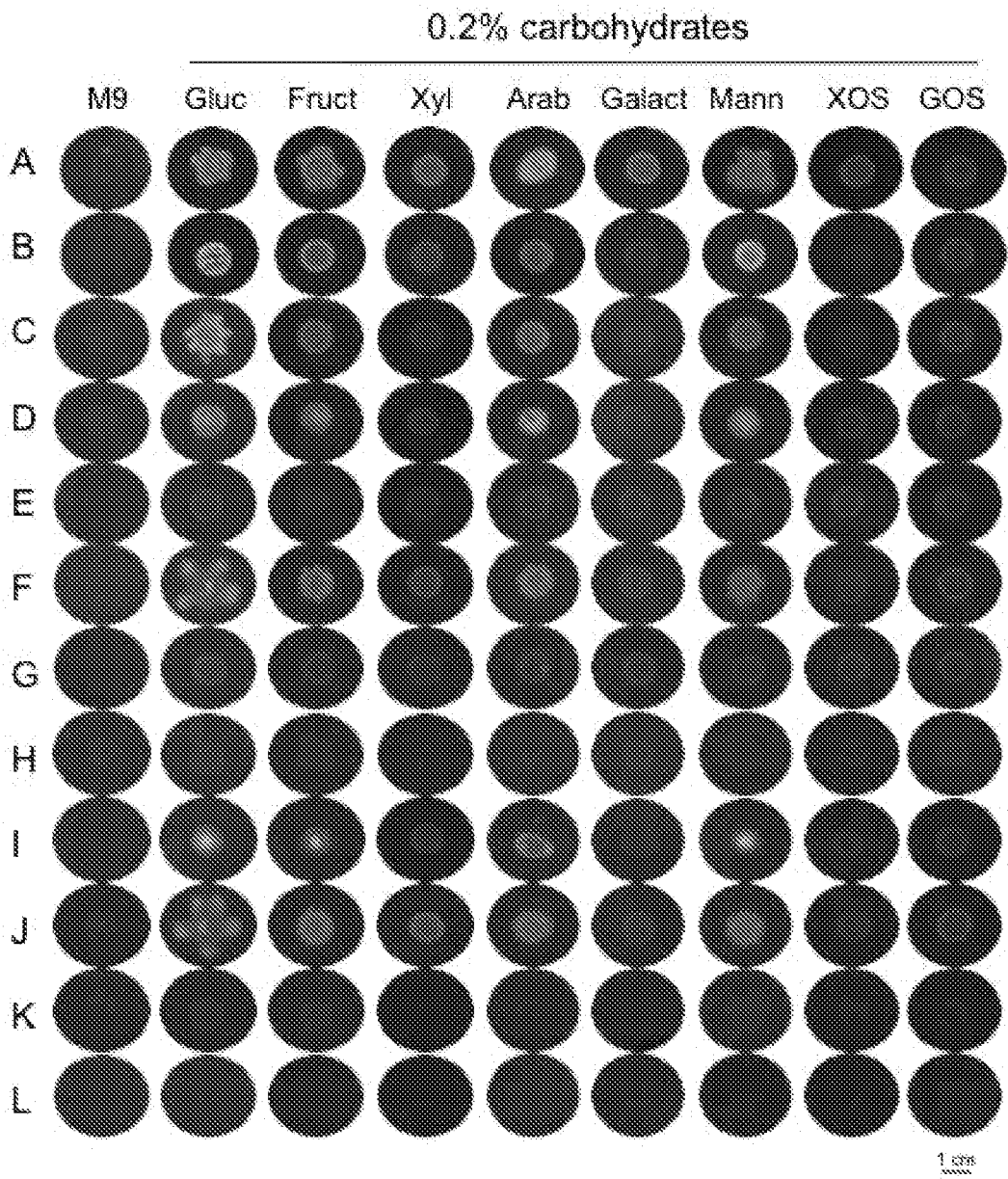


Fig. 3

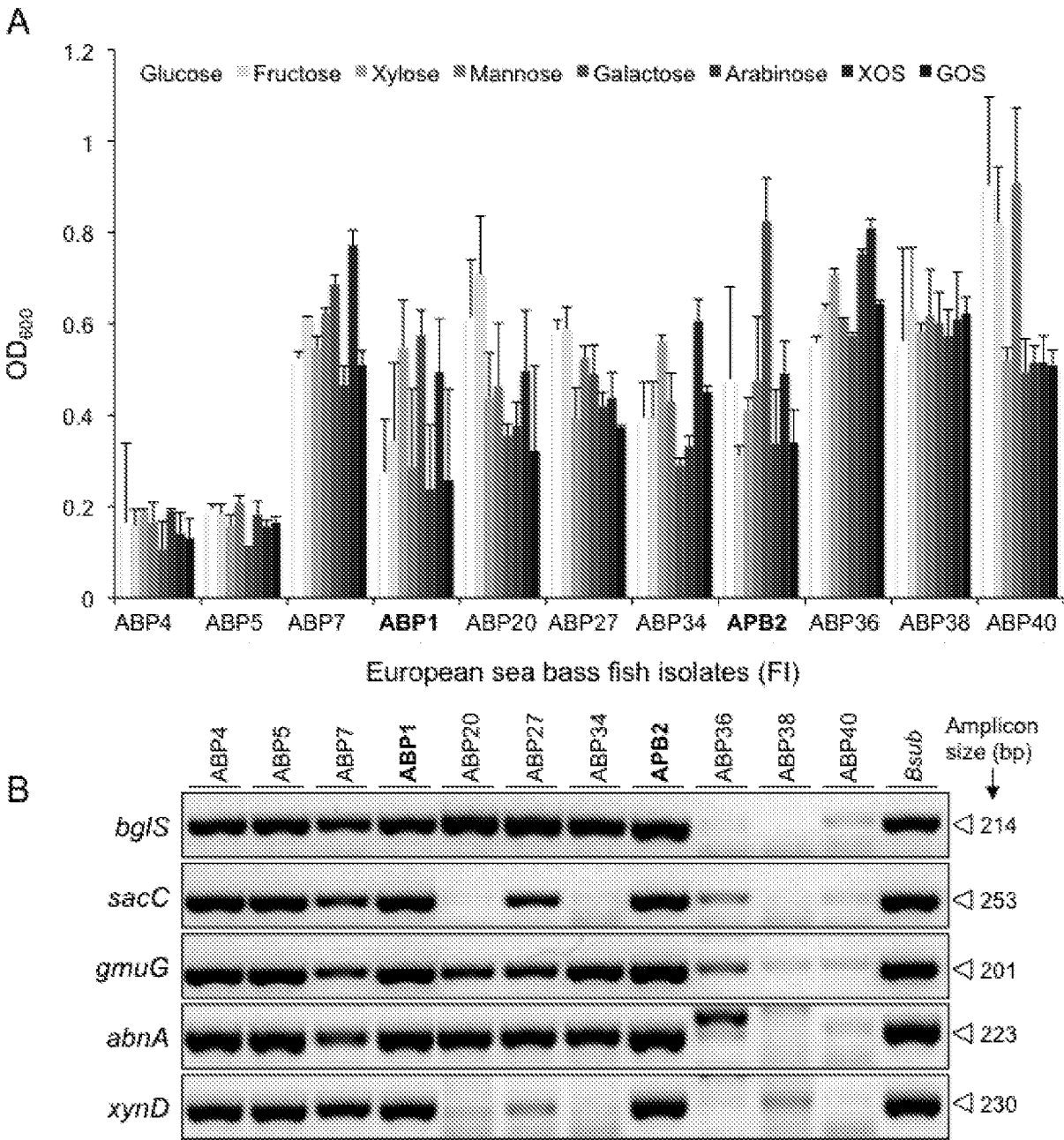


Fig. 4

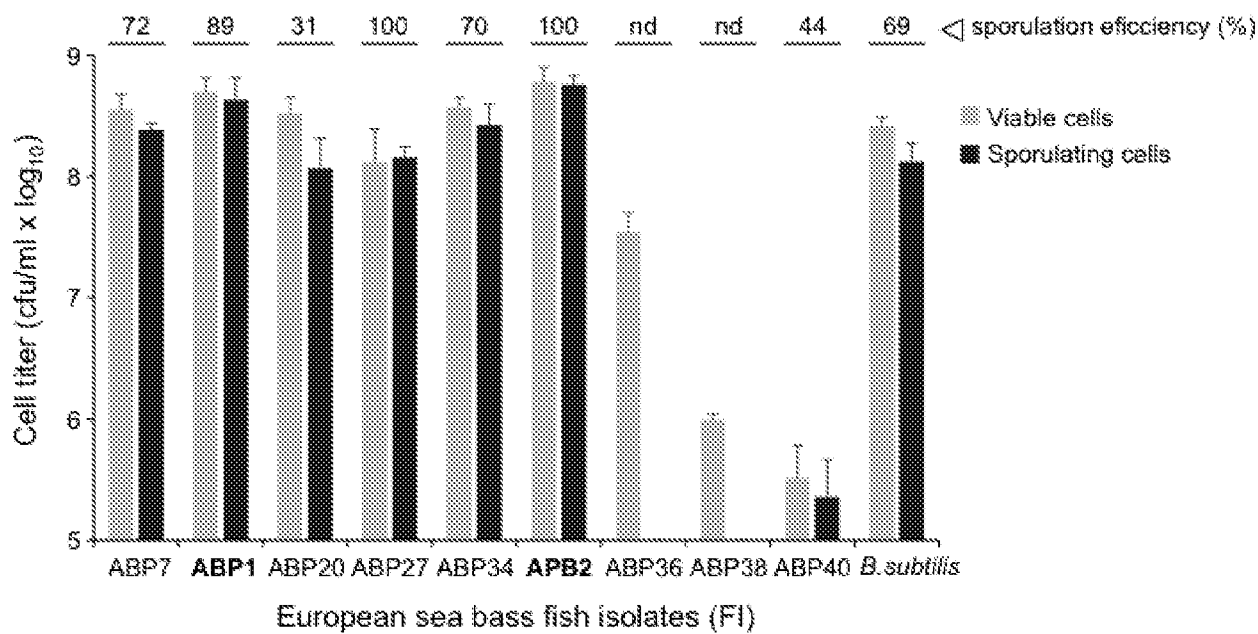


Fig. 5

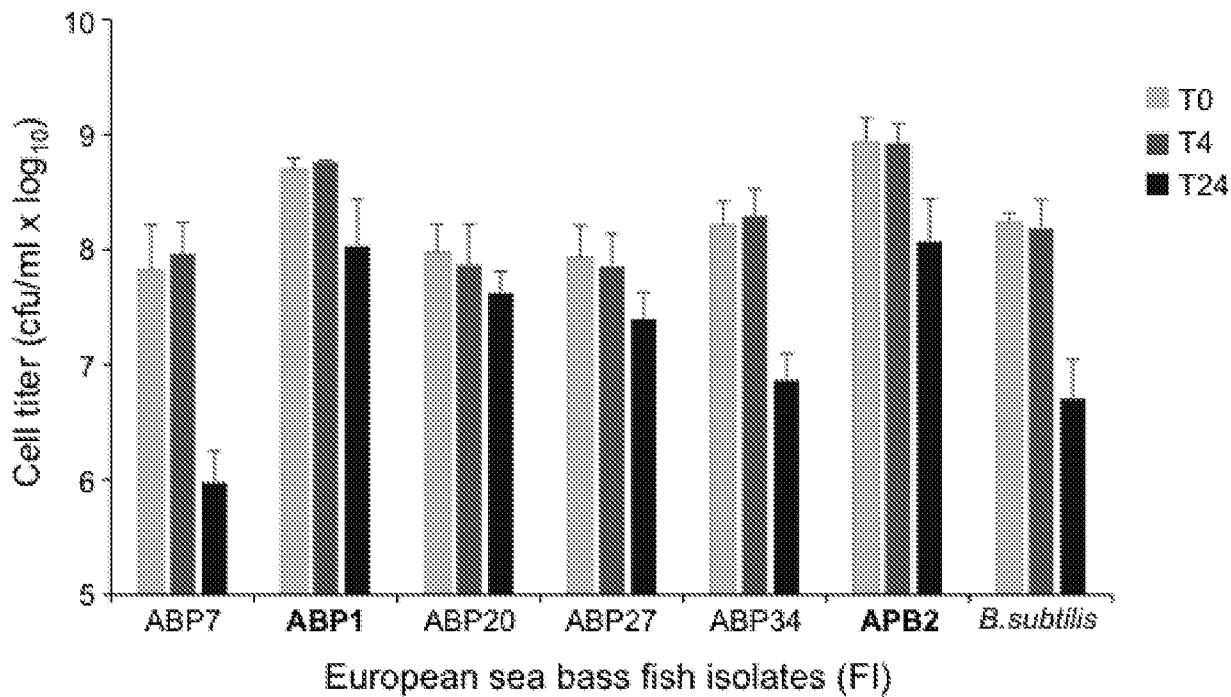


Fig. 6

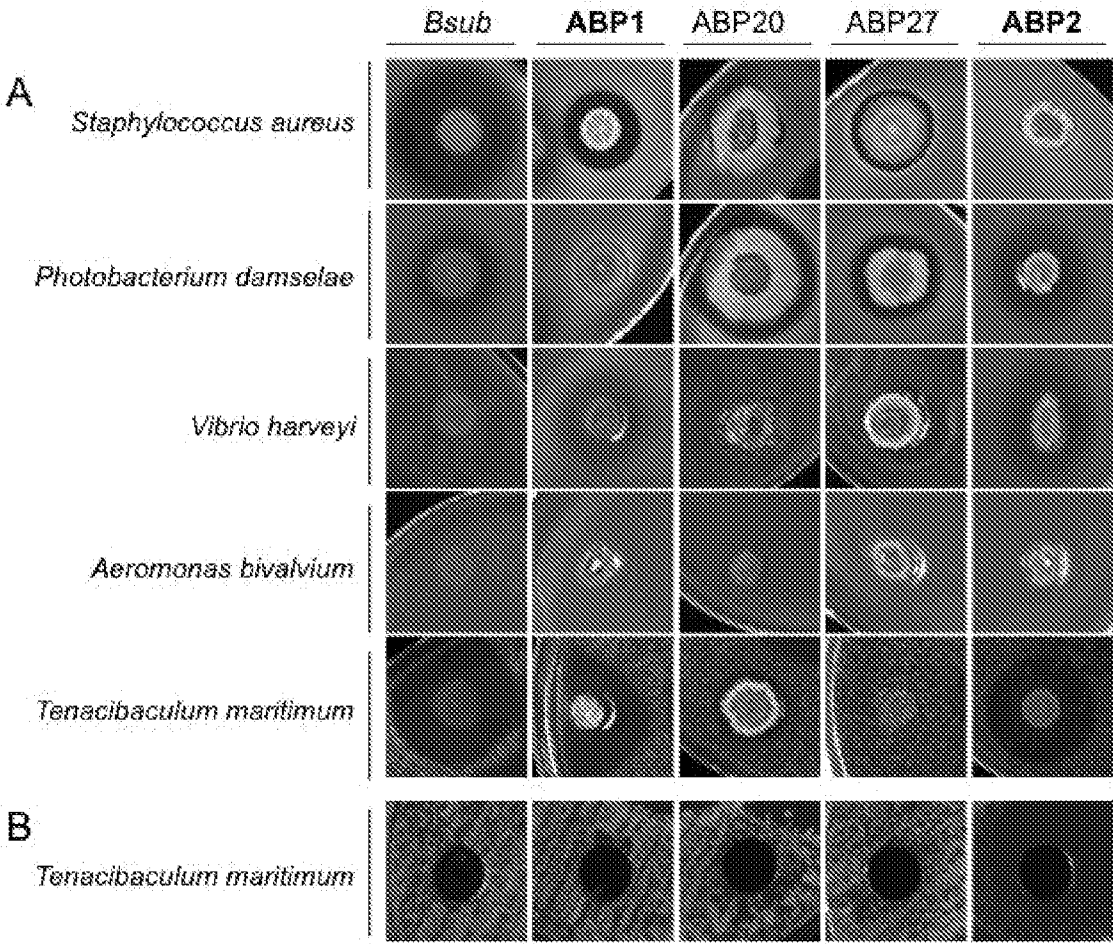


Fig. 7

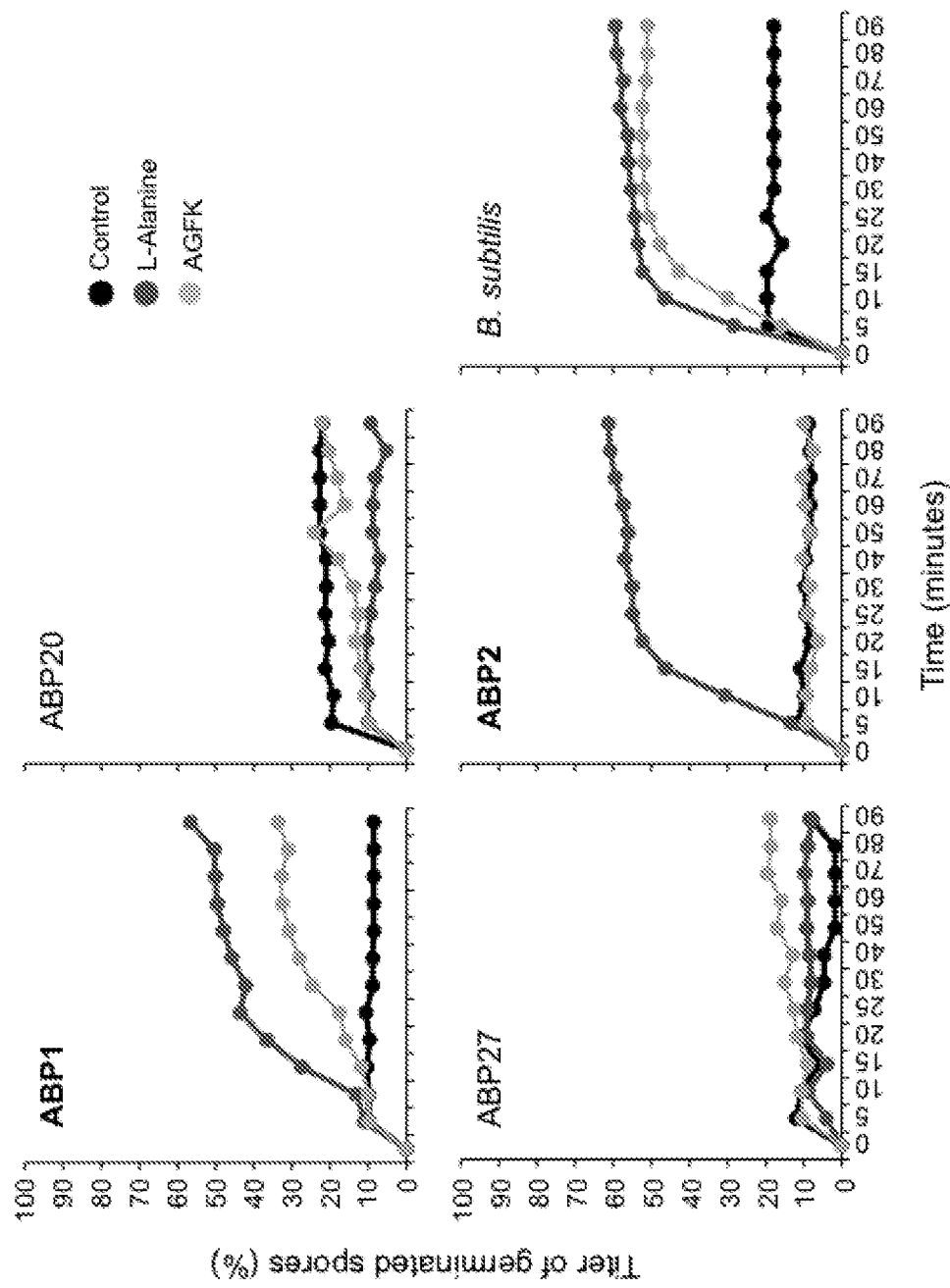


Fig. 8