## RESEARCH



# Eggs-posed: revision of *Schistosoma mansoni* venom allergen-like proteins unveils new genes and offers new insights into egg-host interactions

Lukáš Konečný<sup>1,2\*</sup>, Lucie Jedličková<sup>1,3</sup>, Zaina Ibnahaten<sup>4</sup>, Adam Roberts<sup>4,6,7</sup>, Cecile Crosnier<sup>4,7</sup> and Jan Dvořák<sup>2,5</sup>

## Abstract

**Background** Venom allergen-like proteins (VALs) are abundant in the excretory-secretory products (ESPs) of numerous parasitic helminths and have been extensively studied for over 30 years because of their potential to interact with host systems. Despite substantial research, however, the precise functions of these proteins remain largely unresolved. Schistosomes, parasites of the circulatory system, are no exception, with 29 SmVAL genes identified in the genome of *Schistosoma mansoni* to date. The eggs of these parasites, as primary pathogenic agents, interact directly with host tissues and release excretory-secretory products that aid their egress from the host. Although SmVALs have been detected in the egg secretome in the past, direct evidence of their secretion and functional interaction with host molecules has never been demonstrated. These findings fuel the ongoing debate as to whether egg-expressed SmVALs interact with the mammalian host or are rather miracidial proteins synthesized within the egg during larval development.

**Results** Based on complete revision of the SmVAL family and an associated robust transcriptomic meta-analysis of gene expression across the life cycle, we show that many of SmVAL genes, including 6 newly identified genes, are expressed in the infective larvae-producing stages (eggs and sporocysts). Following localization of two "egg-specific" SmVAL9 and SmVAL29 did not prove active secretion of these molecules into surrounding tissues but were aligned with miracidial structures interfacing with the molluscan host, specifically the larval surface and penetration glands. Finally, we show the complete lack of interactions between candidate SmVAL proteins and an array of 755 human cell receptors via a state-of-the-art SAVEXIS screen.

**Conclusions** Overall, we conclude that these "egg" SmVALs are not involved in direct host–parasite interactions in the mammalian host and are rather proteins employed during intermediate host invasion. Our study revisits and updates the SmVAL gene family, highlighting the limitations of in silico protein function predictions while emphasizing the need for up-to-date datasets and tools together with experimental validation in host-parasite interactions. By uncovering the diversity, expression patterns, and interaction dynamics of SmVALs, we open new avenues for understanding host manipulation and reevaluating orthologous proteins in other helminths.

Keywords Schistosomiasis, Venom allergen-like, Egg, Miracidium, Transcriptome, SCP, CAP, SAVEXIS

\*Correspondence: Lukáš Konečný lukkas.konecny@gmail.com Full list of author information is available at the end of the article



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## Introduction

Schistosoma mansoni is a major causative agent of schistosomiasis, for which more than 250 million individuals required preventive treatment in 2021 [1]. These parasitic flatworms are distinctive among trematodes in terms of their gonochoristic lifestyle, where adults form pairs within the host's vascular system and constantly lay eggs directly into the bloodstream. Successful egg excretion relies on parasite-induced granuloma formation, which aids in transporting eggs across the vascular and intestinal walls into the external environment [2]. The interaction between S. mansoni eggs and host tissues is believed to be facilitated mainly by egg excretory-secretory products (ESPs), which reportedly originate from the syncytial outer subshell envelope of the egg [2, 3]. To date, nearly 200 proteins have been identified in the S. mansoni egg secretome [4-6]. Of these however, only IPSE-1/alpha-1 and omega-1 have been intensively studied, and their immunomodulatory functions have been revealed [7–10] whereas other identified proteins remain enigmatic.

A significant group of alleged egg-secreted molecules are venom allergen-like proteins (VALs) [5, 11, 12]. The VAL protein family is part of the sperm coating protein/ Tpx-1/Ag5/PR-1/Sc7 (SCP/TAPS) superfamily (SMART: SM00198, Pfam: PF00188). All VALs are defined by a CAP domain in their core, which stands for cysteine-rich secretory proteins, antigen 5 proteins, and pathogenesis-related 1 proteins. The CAP domain is a structurally conserved, cysteine-rich, approximately 15 kDa domain with a typical  $\alpha$ - $\beta$ - $\alpha$  sandwich fold and encompasses the SCP/TAPS domain within its structure. This strong conservation of the tertiary structure could indicate shared common biochemical activity for all SCP/TAPS proteins [12–14]. Despite the general diversity in ESPs of various stages of helminths, VAL proteins are ubiquitous in these products and are likely specifically associated with the parasitic lifestyle [15].

To date, 29 VALs with complete SCP/TAPS domains have been identified in S. mansoni (SmVAL). The SmVAL superfamily is divided into two groups. Group 1 SmVALs were described as having 3 conserved disulfide bonds, an extended first loop region, and, importantly, predicted signal peptides indicating their active secretion. Group 2 representatives (SmVAL6, 11, 13, 16, and 17) lack these features but have unique conserved histidine and tyrosine residues [14]. The gene expression of SmVALs seems to be stage- and tissue-specific [14, 16-19], with several of these genes from group 1 being exclusive to the egg and miracidia stages [14, 16, 20]. Moreover, group 1 SmVALs were identified among the most highly expressed genes in mature eggs from both liver and intestinal tissues [21]. Owing to the assumption that these proteins are actively secreted from the egg, many functions have been attributed to them in the past, including possible anticoagulant, immunomodulatory and tissue remodelling functions [12, 22]. However, the lack of direct evidence fuels an ongoing debate regarding whether SmVALs are truly secreted from the egg to the mammalian tissues or are rather miracidial proteins expressed by the egg and the developing miracidium stage *in ovo* [13, 23, 24].

In this work, we sought to resolve this debate by localizing the putative secretion of these proteins from the egg into the surrounding tissues of the infected host. This is preceded by a complete revision and de novo identification of all SmVAL genes according to the recent genome version and a reanalysis of their sequences, annotations and phylogenetic relationships, which in the past were only adopted from seminal studies. Furthermore, we employed a high-throughput state-of-the-art protein-protein interaction screen to investigate whether egg-specific SmVALs can directly interact extracellularly with host cell receptors. This approach aimed to further confirm or challenge their potential functions within the mammalian host.

## **Materials and methods**

### **Ethics statement**

Research involving experimental animals was performed in accordance with the animal welfare laws of Czechia and under the European regulations for transport, housing and care of laboratory animals (CZ Act No. 246/1992, EU Directive 2010/63/EU amended by Regulation 2019/1010/EU). Experiments were approved by the Animal Welfare Committees of University of Life Sciences and the Ministry of Education, Youth and Sports of Czechia (MSMT-29299/2020–3). All animals used in the study were maintained by a certified person (Certificate Number CZ 02847) in an accredited facility. Ketaminexylazine anaesthesia was employed to sacrifice the mice as indicated in "Parasite material" section.

## Parasite material

The life cycle of the *S. mansoni* Puerto Rican strain is maintained in our laboratories using *Biomphalaria glabrata* as an intermediate host snail and C57BL/6JRj (Janvier Labs) female mice as the definitive host. The mice were infected in a water bath with 150 cercariae per mouse for one hour. The mice were sacrificed 7 weeks post infection by an intraperitoneal injection of keta-mine (Narkamon 5%—1.2 ml/kg body weight) and xyla-zine (Rometar 2%—0.6 ml/kg body weight), with heparin to prevent blood clotting. The small intestines and livers were harvested and processed as described previously [21]. The infected hepatopancreases were dissected from the snails 6 weeks after infection with miracidia.

## SmVALgenes de novo identification and analysis

To identify all S. mansoni genes coding for SmVAL proteins, the SCP/TAPS Hidden-Markov Model (HMM) consensus domain profile was built with hmmbuild on the basis of seed alignment acquired from Pfam (PF00188). The protein sequences for all S. mansoni protein-coding genes were acquired from the WormBase ParaSite database (S. mansoni genome PRJEA36577 v9; database version WBPS19) [25, 26]. Sequences containing the SCP/TAPS domain were identified via hmmscan and were manually evaluated to determine whether they contained the complete domain. Only those sequences with identified domains > 100 amino acids and domainspecific features such as conserved cysteines and residues at specific positions identified previously were included in the subsequent analyses [14, 27]. The whole peptide sequences of proteins identified as SmVALs were retrieved via BioMart at the WormBase ParaSite server [25]. The prediction of signal peptides and transmembrane elements was performed via Phobius [28]. Additionally, SignalP 6.0 [29] was used for comparison and presence of signal peptides was assumed when the probability score was  $\geq 0.5$ . The amino acid positions bordering the peptide sequences identified as forming the CAP or SCP/TAPS domain (for phylogenetic analysis and domain alignment, respectively) served as input for esl-fetch, which was used to extract the respective domain sequences. The tools hmmbuild, hmmscan and esl-sfetch used for the genes and domain recognition are part of HMMER v3.4 software [30]. All relevant intermediate files are available at https://github.com/lukykony/ SmVAL identification).

## Alignment and phylogenetic analysis

To increase the reliability of the phylogenetic analysis, the CAP domain sequences were used, as they are the most conserved part of the SCP/TAPS proteins, providing a stable basis for evolutionary comparisons. The amino acid sequences of 36 complete CAP domains encoded by 35 identified SmVAL genes were aligned with MAFFT v7.520 using the L-INS-I strategy [31]. The resulting alignment in fasta format was trimmed with trimAl using default settings to remove poorly aligned regions that would later affect the accuracy of the phylogenetic analysis [32]. The best-fitting model WAG+R3 was chosen on the basis of ModelFinder analysis as a part of IQtree analysis [33]. The maximum likelihood analysis was performed via IQtree v2.3.5 with bootstrap values based on 1000 replicates. The resulting phylogenetic tree was visualized with FigTree v1.4.4 software [34]. For sequence analysis, the amino acid sequences predicted to form SCP/TAPS domains were extracted. 36 SCP/

TAPS-forming protein sequences were aligned with MAFFT v7.520 using the L-INS-I strategy, and the resulting multiple sequence alignment was manually inspected with Jalview 2 [35].

## Gene expression of SmVALs throughout the parasite life cycle

The RNA-Seq datasets of selected parasite stages, which are freely available in the NCBI Sequence Read Archive (SRA) or European Nucleotide Archive (ENA), were processed so that the expression of each gene was directly comparable between samples and within the sample. This was achieved by selecting public RNA-seq datasets prepared using the same methodology, specifically library preparation via PolyA selection and paired-end sequencing layout. Three datasets for each stage (mammalian liver eggs, miracidia, sporocysts, cercariae, schistosomula and intramammalian parasitic stages collected at 6, 13, 17, 21, 28 and 35 days post infection) from previously published studies were selected for comparative gene expression analysis [16, 36] (see Additional file 1: Table S1 for details on used datasets). The counts of aligned reads per run were acquired from the Worm-Base ParaSite database [25, 36]. The read counts in the database were produced as described by Wangwiwatsin et al. (2020) [36]. Briefly, the acquired reads were mapped to the S. mansoni genome via TopHat version 2.0.8 and counted with HTSeq-count version 0.7.1 (for HTSeq counts see Additional file 2: Table S2). Gene length corrected trimmed mean of M-values (GeTMM) normalization, which allows for accurate inter- and intrasample comparisons, was performed in EdgeR according to a published methodology [37]. The resulting normalized GeTMM gene counts for each stage were averaged, and expression values for individual genes encoding SmVALs were retrieved via respective gene identifiers (for GeTMM normalised counts see Additional file 3: Table S3). The gene expression across the parasite life cycle was visualized as a heatmap created via the pheatmap R package. For better resolution of SmVAL expression in S. mansoni eggs, the data from immature and mature eggs from liver and intestinal tissues from our recent work were also analysed (data from Supplementary Table 2 from Peterková et al. (2024) [21]. Because cDNA library preparation for these datasets differed from that for the other publicly available datasets mentioned above, these data were assessed and visualized separately.

## SmVAL genes amplification

To verify the sequences and in silico expression of the predicted novel SmVALs, genes from life stages where they are expected to be most highly expressed according to the gene expression meta-analysis were amplified via

conventional PCR. Total RNA was isolated from parasite eggs and sporocysts with TRIzol Reagent (Invitrogen) according to the manufacturer's instructions. The concentration of isolated RNA was measured on a NanoDrop (Thermo Fisher), and 1 µg of RNA per sample was treated with Turbo DNase (Ambion) to remove contaminating genomic DNA. cDNA was generated with a Super-Script IV RT kit (Invitrogen). The gene sequences of the SmVALs were retrieved from the WormBase ParaSite database, and specific primers were designed on the basis of CDSs (see Additional file 4: Document S1). PCR was performed with DreamTaq PCR Master Mix 2x (Thermo Scientific) according to the manufacturer's instructions. The resulting PCR amplicons were purified via the PCR Cleanup Kit (Geneaid) and cloned with the pGEM T Easy Vector system (Promega Corporation), and the correct gene sequences were confirmed via Sanger sequencing. SmVAL9 and SmVAL29, the two most highly expressed SmVALs throughout the life cyclxe, were chosen for further studies.

## Recombinant production of SmVAL9 and SmVAL29 in E. coli

For polyclonal antibody production, SmVAL9 and SmVAL29 were heterologously expressed in an E. coli expression system. The coding sequences without signal peptides and stop codons were amplified with PCR using PrimeSTAR Max DNA Polymerase (Takara Bio) and cloned into the pET22b(+) vector in frame with a 6×His tag via an In-Fusion cloning kit (Takara Bio) (for details on constructs see Additional file 5: Document S2). The recombinant proteins were expressed in E. coli BL21 (DE3) cells in LB medium at 37 °C for 6 h upon 0.5 mM IPTG induction and further purified from inclusion bodies. Briefly, the cells were resuspended in 20 ml (per 200 ml culture) of lysis buffer (50 mM NaH2PO4, 0.3 M NaCl, and 10 mM imidazol, pH 8.0) and left at -80 °C overnight. The samples were subjected to three freeze-thaw cycles in an ice bath (methanol and dry ice) with  $4 \times 15$  s of sonication after every cycle. The cell lysates were centrifuged at  $12,000 \times g$  for 30 min at 4 °C, and the supernatant was discarded. The inclusion bodies were further purified via consecutive sonication-assisted solubilization via incubation in 50 mM Tris base, 2 M urea, 150 mM NaCl, and 1 mM EDTA, pH 8.0, followed by incubation in 50 mM Tris base, 150 mM NaCl, 1 mM EDTA, and 0.1% Triton-X 100, pH 8.0 for 10 min, after which both solubilization steps were followed by  $4 \times 15$  s sonication and 30 min of centrifugation at  $12,000 \times g$ . Then, the pellets were repeatedly washed with two volumes of dH2O, followed by centrifugation until the supernatant became clear. The resulting inclusion bodies were dissolved in equilibration buffer (50 mM phosphate buffer with 300 mM NaCl and 10 mM imidazole, pH 8.0) and centrifuged at  $12,000 \times g$  for 30 min. The supernatant was loaded onto a 5 ml Ni–NTA column. The bound rSmVAL proteins were washed with 10 volumes of equilibration buffer with 20 mM imidazole and eluted with equilibration buffer with 250 mM imidazole. Fractions containing the purified proteins were pooled and used to prepare polyclonal mouse antisera.

## Polyclonal antibody production

Polyclonal antibodies against rSmVAL9 and rSmVAL29 were produced in NMRI mice by injecting 30 µg of purified proteins in TiterMax Gold adjuvant (Sigma–Aldrich) according to the manufacturer's instructions intraperitoneally three times at intervals of 14 days. The immunized mice were bled under deep ketamine/xylazine anaesthesia 5 days after the last injection, and the resulting antisera were collected via centrifugation. Control serum samples were collected from the mice prior to immunization. The specificity of the produced antibodies was confirmed by immunoblotting following established protocol [38].

## Immunolocalization of SmVALs in eggs and surrounding host tissues

For immunolocalization of the SmVALs in the parasite eggs and surrounding tissues, liver and small intestine samples were collected from female C57BL/6JRj mice (Janvier) at 7 weeks post infection. The organs were rinsed in PBS and then fixed in 4% neutral buffered formalin for 3 days. The fixed tissues were dehydrated through a graded ethanol series (50%, 70%, 90%, 96%, and 100% v/v ethanol), with each step lasting 20 min. Following dehydration, the tissues were cleared in xylene (VWR) twice for 15 min each. The cleared tissues were then embedded in Paraplast (Sigma-Aldrich). Sections (5 µm thick) were prepared via a Shandon Finesse® ME + microtome (Thermo Fisher Scientific) and mounted onto X-tra adhesive slides (Leica). The paraffinembedded sections were deparaffinized and rehydrated. Antigen retrieval was performed by boiling the sections in 0.05 M citrate buffer (pH 6.0) containing 0.05% Tween 20 in a microwave oven (500 W) for three cycles of 3 min each, followed by a 20-min cooling period. The sections were then blocked with buffer containing PBS, 2% BSA, 0.25% Triton X-100, and a goat anti-mouse polyclonal antibody (Abcam, ab6668) diluted 1:50 for 1 h. After blocking, the sections were washed three times in PBS-T (PBS with 0.25% Triton X-100) for 5 min each. The sections were then incubated overnight at 4 °C in a wet chamber with immunized mouse serum against SmVAL9 or SmVAL29 diluted 1:50 in an antibody mixture (PBS, 1% BSA, 0.25% Triton X-100). Preimmunized mouse serum was used as the negative control. Following primary antibody incubation, the sections were washed three times in PBS-T for 5 min each. The slides were then incubated with goat anti-mouse IgG (H+L) conjugated with Alexa Fluor<sup>®</sup> Plus 647 (Invitrogen, A48289) diluted 1:500 in PBS-T with 1% BSA for 1 h in the dark. The sections were subsequently washed three times in PBS-T for 5 min each and mounted with Fluoroshield containing DAPI (Sigma–Aldrich). The fluorescence signals were visualized via a Leica TCS SP8 confocal microscope. The background signal threshold was determined via slides probed with control serum.

## SAVEXIS protein–protein interaction screen

To identify whether egg/miracidium-specific SmVALs could directly interact with mammalian host tissues, a resource of 755 recombinant human surface receptors was used for protein-protein interaction screening. Recombinant monobiotinylated S. mansoni SmVALs and human receptor proteins were produced via transient transfection of HEK293-6E cells grown in Freestyle 293 media supplemented with 0.1% Kolliphor, 0.5  $\mu$ g/ mL G418 and 48 µg/mL D-biotin and cotransfected with a plasmid encoding the BirA biotin ligase as previously described [39]. Proteins were purified via His MultiTrap plates with a previously described purification platform and pneumatic press [40], followed by confirmation of expression via protein gel electrophoresis and western blotting with HRP-streptavidin (Jackson ImmunoResearch, 016-030-084, 0.2 µg/mL). Protein concentrations were measured via the Bradford assay. To create "preys" for SAVEXIS, SmVAL proteins were normalized to 17.5 nM and tetramerised with PierceHigh Sensitivity Streptavidin-HRP (Thermo Scientific, 21,130) as previously described. The human protein library was assembled from 755 proteins primarily expressed on the surface of leukocytes [41] with additional proteins from erythrocytes [42] and megakaryocytes [40] as proteins accessible to extracellular parasite antigens and arrayed on 384-well streptavidin-coated microtiter plates [41]. The preys were incubated with the baits for one hour and then washed in HBS-T with desthiobiotin; the hostparasite interactions were then revealed with a TMB/E chromogenic substrate. The plates were measured with a Tecan Spark plate reader at an absorbance of 650 nm as previously described [41].

## Results

## Revision of the SmVAL family revealed 6 novel SmVAL genes

The first objective of this study was to uncover a complete repertoire of genes encoding *S. mansoni* VAL proteins to characterize their sequence features on the basis of the latest databases and bioinformatics tools. The search using the SCP/TAPS HMM profile revealed 40 transcripts, 38 of which contained the complete CAP domain. The incomplete SCP/TAPS domains of the identified transcripts Smp\_345050.1 and Smp\_176170.1 are only 26 and 73 amino acids long, respectively, therefore they lack critical conserved sites and are not expressed at any stage of the parasite according to our analyses. In addition to the SmVAL1-28 genes already described by Chalmers et al. (2008) [14] and SmVAL29 identified by Wu et al. (2009) [24], our analysis revealed 6 previously undescribed members of this family. In addition to these newly identified genes, one previously undiscovered splice variant, SmVAL11.2, was detected, where the sixth exon not transcribed, thus the resulting protein product is 23 amino acids shorter than that in SmVAL11.1. The new genes were named on the basis of the numerical order of their Smp identifiers (Smp\_131370-SmVAL30, Smp 200460—SmVAL31, Smp 300080—SmVAL32, Smp 313710-SmVAL33, Smp\_317520-SmVAL34 and Smp\_ 347320-SmVAL35). These newly discovered genes, except for SmVAL32, were successfully amplified from the cDNA stages where these genes are the most expressed based on our gene expression analysis across the life cycle (SmVAL30, SmVAL34 and SmVAL35 from sporocysts and SmVAL31 and SmVAL33 from eggs). SmVAL32 is identical to SmVAL7; therefore, it was not possible to distinguish these genes via conventional PCR. However, for example, the successful amplification and resolution of the SmVAL34 and SmVAL35 genes, which share 93% identity, convinced us that SmVAL32, like the other newly discovered genes, is real and not just an artifact of the genome assembly. The updated SmVAL gene family and gene characteristics, including the new nomenclature, can be found in Table 1. A comparison of the current state of knowledge with previously published data is shown in Additional file 6: Table S4.

## Updated analyses of SmVAL proteins confirm two distinct groups with unique features, challenging historical views on signal peptides

Updated phylogenetic analysis of all CAP domains of the previously known and newly identified SmVALs via the maximum likelihood method strongly supported the previously published division of this family into two distinct phylogenetic branches (100% bootstrap value) and proposed division of these proteins into group 1 and group 2 [13, 14, 23] (Fig. 1). Accordingly, 5 newly identified SmVAL genes belong to group 1 (SmVAL30, SmVAL32, SmVAL33, SmVAL34 and SmVAL35), and one belongs to group 2 (SmVAL31). In line with previously published phylogenetic analyses [13, 14, 23], the second domain of SmVAL11 belongs to group 2 according to our phylogenetic analysis. Moreover, the division of two groups is

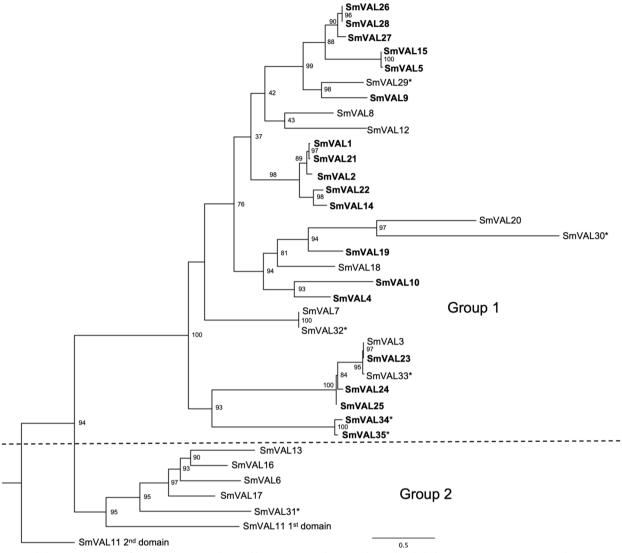
Name	Chromosome	Gene ID	Transcript ID	Gene start (bp)	Gene end (bp)	Gene length	Protein length	SP/TM (Phobius)	Group
Previously iden	tified SmVALs								
SmVAL1	6	Smp_193680	Smp_193680.1	12,437,483	12,439,150	1667	234	YES	1
SmVAL2	6	Smp_002630	Smp_002630.1	12,468,974	12,470,914	1940	229	YES	1
SmVAL3	6	Smp_316760	Smp_316760.1	17,278,025	17,279,298	1273	178	N/O	1
SmVAL4	6	Smp_002070	Smp_002070.1	4,187,554	4,193,626	6072	181	YES	1
SmVAL5	6	Smp_336880	Smp_336880.1	17,331,374	17,335,886	4512	184	YES	1
SmVAL6.1	1	Smp_124050	Smp_124050.1	11,722,354	11,790,303	67,949	429	N/O	2
SmVAL6.2	1	Smp_124050	Smp_124050.2	11,722,354	11,790,303	67,949	423	N/O	2
SmVAL6.3	1	Smp_124050	Smp_124050.3	11,722,354	11,790,303	67,949	414	N/O	2
SmVAL7	6	Smp_300070	Smp_300070.1	17,323,751	17,327,231	3480	193	TM	1
SmVAL8	6	Smp_123550	Smp_123550.1	12,477,072	12,480,198	3126	249	TM	1
SmVAL9	6	Smp_176180	Smp_176180.1	16,367,696	16,373,800	6104	182	YES	1
SmVAL10	6	Smp_002060	Smp_002060.1	4,171,241	4,183,900	12,659	170	YES	1
SmVAL11.1	2	Smp_012350	Smp_012350.1	25,764,239	25,784,550	20,311	400	N/O	2
SmVAL11.2	2	Smp_012350	Smp_012350.1	25,764,239	25,784,550	20,311	423	N/O	2
SmVAL12	6	Smp_123540	Smp_123540.1	12,487,474	12,491,566	4092	204	TM	1
SmVAL13	1	Smp_124060	Smp_124060.1	11,676,364	11,702,352	25,988	236	N/O	2
SmVAL14	1	Smp_078490	Smp_078490.1	2,040,271	2,042,090	1819	219	YES	1
SmVAL15	6	Smp_070250	Smp_070250.1	17,308,316	17,312,821	4505	248	YES	1
SmVAL16	1	Smp_124070	Smp_124070.1	11,644,064	11,669,918	25,854	169	N/O	2
SmVAL17	1	Smp_331830	Smp_331830.1	19,494,075	19,508,994	14,919	157	N/O	2
SmVAL18	6	Smp_001890	Smp_001890.1	3,518,374	3,526,057	7683	194	TM	1
SmVAL19	6	Smp_123090	Smp_123090.1	3,503,241	3,510,772	7531	186	YES	1
SmVAL20	6	Smp_127130	Smp_127130.1	22,505,531	22,514,880	9349	225	N/O	1
SmVAL21	6	Smp_159290	Smp_159290.1	12,417,430	12,419,089	1659	234	YES	1
SmVAL22	4	Smp_139450	Smp_139450.1	2,688,513	2,690,855	2342	219	YES	1
SmVAL23	6	Smp_160250	Smp_160250.1	17,281,855	17,283,130	1275	182	YES	1
SmVAL24	6	Smp_141550	Smp_141550.1	17,213,661	17,215,006	1345	195	YES	1
SmVAL25	6	Smp_141560	Smp_141560.1	17,239,323	17,240,623	1300	195	YES	1
SmVAL26	6	Smp_154260	Smp_154260.1	16,413,349	16,416,075	2726	182	YES	1
SmVAL27	6	Smp_154290	Smp_154290.1	16,593,216	16,595,909	2693	182	YES	1
SmVAL28	6	Smp_176160	Smp_176160.1	16,378,302	16,381,034	2732	182	YES	1
SmVAL29	6	Smp_120670	Smp_120670.1	16,391,667	16,396,592	4925	153	N/O	1
Newly identified	d SmVALs								
SmVAL30	6	Smp_131370	Smp_131370.1	21,769,518	21,776,061	6543	208	N/O	1
SmVAL31	1		Smp_200460.1	4,030,097	4,049,167	19,070	197	N/O	2
SmVAL32	6	Smp_300080	Smp_300080.1	17,338,761	17,341,822	3061	193	TM	1
SmVAL33	6	Smp_313710	Smp_313710.1	17,299,341	17,300,791	1450	178	N/O	1
SmVAL34	6		Smp_317520.1	17,237,013	17,238,811	1798	185	YES	1
SmVAL35	6		Smp_347320.1	17,210,799	17,213,179	2380	185	YES	1

## Table 1 Overview and characteristics of an updated SmVAL family

SP/TM – signal peptide/transmemembrane domain – YES marks signal peptide, N/O marks the lack of signal peptide, TM marks the presence of transmembrane domain

also supported by the pairwise identity matrix (see Additional file 7: Figure S1).

The division of SmVALs into two groups has historically been associated with the presence of signal peptides in group 1 and their absence in group 2. The prediction of signal peptides via the latest version of SignalP 6.0 indicated that the previously described Group 1 SmVAL3, SmVAL5, and SmVAL20 lack this feature together with the newly analysed Group 1 SmVAL29, SmVAL30 and SmVAL33. Further analysis with Phobius revealed that the



**Fig. 1** Phylogenetic analysis of *S. mansoni* venom allergen-like protein CAP domains. The updated phylogenetic tree supports an evolutionary split between two distinct branches of previously proposed group 1 and group 2 proteins. The relative branch lengths are indicated by the scale bar. Newly identified SmVALs within this study and SmVALs put in the phylogenetic analysis are marked with an asterisk. SmVALs containing signal peptides within the sequence according to Phobius analysis are in bold

signal peptides of Group 1 SmVAL7, SmVAL8, SmVAL12, SmVAL18 and SmVAL32 are in fact transmembrane domains. This finding contradicts previously published data; however, our updated multiple sequence alignment further supported the division of the SmVAL family into two distinct groups. All five newly identified group 1 SmVALs contain 6 disulfide bond-forming cysteines characteristic of this group. Additionally, SmVAL34 and SmVAL35, which are closely phylogenetically related, contain two extra cysteine residues at positions 21 and 66 within the SCP/TAPS domain, which might indicate specific folds of these two proteins and possibly distinct shared functions (Fig. 2). In addition to the previously described common deletion in the SCP/TAPS domain for all old and new members of group 1, the typical deletion for all the members of group 2 is also present.

Detailed analysis of individual identified gene features also revealed differences in the length of genomic sequences for most of the previously described SmVALs (Table 1). In addition, three of the 13 coding sequences verified by PCR and deposited in GenBank (SmVAL1-13) by Chalmers et al. (2008) [14] have different coding sequences according to WormBase ParaSite prediction. While the predicted CDS of SmVAL1 according to the

Simula	SmVAL26															
Smith 2         Smith 2         I - AMN RELET IN KAR AV SHOLL (CLOP - LAY SET V KUNN L ENK ALLS DOD VOCHD TANDRE) PE F-Q-V GWAACA		Smn 154260	1 – AMRNELLT	HNEARO	AVENGOL	EGOP - LA	VSIKP	KWNV F	LERKAC		O <mark>C</mark> R V G	HDTNADR	OIPEE-	- 0 Y V	GO NWA GA	76
Smith 28																
Simula Simula Simula Simula Simula Simula CLEOP - LAK SLF RUMNEL ELK ANLADT Y FUE SALEXVECF. TWO SIMULACA         76           Simula Simula Simula Simula CLEOP - LAK SLF RUMNEL ELK ANLADT Y FUE SALEXVECF. TWO SIMULACA         77           Simula Simula Simula Simula CLEOP - LAK SLF RUMNEL ELK ANLADT Y FUE SALEXVECF. TWO SIMULACA         77           Simula Simula Simula Simula CLEOP - LAK SLF RUMNEL ELK ANLADT Y FUE SALEXVECF. TWO SIMULACA         77           Simula Sim																
SmitLag         SmitLag <t< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></t<>																
SIMUL2 30         I = MID DY F I AN UV DY AA VEST (I F GD = 6.48 HML EVNT E AF K MIL F SD GD L GD ED DE KEN IP EF EVV GOWALL         75           SIMUL2 30         J = 5.00 DY L LA OLY NEL TAY EL LO Y NEL TAY E			I - AIREKLLK		SVMHGQL	EGQP - TA	AKSIKP	LKWNME	LEKKAC	ZMLAD		PDSALER	KVPGF-	- 1 N V	Q NWAGA	/6
Smith J. Smith J. THE RG LITIN NUV BLAKTELIP RGP - FAY MIK LIK NUNE LEKK QUIS DRG S FEND EGRE FIGE LEGE FIGE NUT FFE - DNN GT W/GT - THE SUBJECT - STORE AND GT W/GT -			1 - ATREKLLK	LHNNARI	SVMHGRL	EGQP – TA	A K S I K P	LKWNME	LEKKAC	2 M L A D	T C Y F G	PDSALER	KVPGF-	- I N V	<mark>G</mark> Q NWA G A	76
SmvL1         SmvL13         SmvL14         SmvL14 </td <td></td> <td></td> <td>1 – – MR DY F I AM</td> <td>и<mark>н</mark> N V V <mark>R</mark>Q /</td> <td>AVKYGLII</td> <td>° GQ P – E A</td> <td>ARHMNL</td> <td>LKWNTE</td> <td>LAKKAC</td> <td>Q N F S D</td> <td>Q<mark>C</mark>Q L G</td> <td>HDKDEER</td> <td>KIPGF-</td> <td>- E Y V</td> <td><mark>G</mark>Q NWA L T </td> <td> 75</td>			1 – – MR DY F I AM	и <mark>н</mark> N V V <mark>R</mark> Q /	AVKYGLII	° GQ P – E A	ARHMNL	LKWNTE	LAKKAC	Q N F S D	Q <mark>C</mark> Q L G	HDKDEER	KIPGF-	- E Y V	<mark>G</mark> Q NWA L T	75
SmvL1         SmvL13         SmvL14         SmvL14 </td <td>SmVAL9</td> <td>Smp_176180</td> <td>1 - T I R EQ L L T M</td> <td>M<mark>H</mark>NVV<mark>R</mark>E</td> <td>LAKFGLII</td> <td>? R Q P – E A</td> <td>A V HM K L</td> <td>LKWNME</td> <td>LERKAC</td> <td>Q N L S D</td> <td>QCK SE</td> <td>HDELEQR</td> <td>RIPEF-</td> <td>-QNV</td> <td><mark>G</mark>Q T W V G T  − − − − − − −</td> <td> 76</td>	SmVAL9	Smp_176180	1 - T I R EQ L L T M	M <mark>H</mark> NVV <mark>R</mark> E	LAKFGLII	? R Q P – E A	A V HM K L	LKWNME	LERKAC	Q N L S D	QCK SE	HDELEQR	RIPEF-	-QNV	<mark>G</mark> Q T W V G T  − − − − − − −	76
SmmL1         SmmL2360         1         K DQUY LLK M KE IL KL KVY GUY DCUY LCUY COP - PAX WS F, KVMD DA RAQ DS LA NET LEMPLK WS - CUY F, KV KF F, KVW RAM KA KY LEW S, KVK KF KK	SmVAL8	Smp 123550	1 - AQ LRKLLQ	Y <mark>H</mark> NEL <mark>R</mark> RI	NLTACKL	EGQP-PA	A K N L P D	LKWDNE	LASKAK	<b>VDLAN</b>	ECYFH	HNDVDL-	- P E K W-	-QYI	GONIAGY	74
SmwL12         SmpL12         SmpL2         SmpL2         SmpL2 <td></td> <td></td> <td>1 - K D O D Y I I K A</td> <td></td> <td>YARSCNI</td> <td>GOP - OA</td> <td>A K R I I N</td> <td></td> <td>LAIKAT</td> <td>TELSK</td> <td>TONER</td> <td>ESNVTT-</td> <td>YKE-</td> <td>- K D V</td> <td>ONTACY</td> <td> 73</td>			1 - K D O D Y I I K A		YARSCNI	GOP - OA	A K R I I N		LAIKAT	TELSK	TONER	ESNVTT-	YKE-	- K D V	ONTACY	73
Smblas         3mp_152990         1 = N = K = L = L = K K V = OL V D C V D C V D C V = A Y = K V = K = K							K VMSP		LAROAC		K C I I P		NOF	SWV		73
Smp.02620         1         F.K.NS ELLEUMKY NOLLOCK VDGUP - AT WISP, KWNDD, ARQACELAINNY, TLRGUPNS													NQT-	- 5 W V		/ / 3
Smith, J. Smi			I - KNSKELLE	LHRKTRU	DLVDCKVI	JGQP - PA	AKTMSP	LKWNHD	LARQAC	2 S L A N	KULK	HDKKHS-	NQ F-	- 5 W V	QNIALH	/3
SmWLL1       Smp. 27490       1 = KNSR KLEAL MERKY MOLING KV NGOP - PAYMSK (KYNND LAQQAD SLASY MLEGGER) SMLSS SMK KTET TWY GON LAFE       74         SmWLL10       Smp. 22090       1 = GATLENAK TWY BULLICK VP TOP - PAYMSK (KYNND LAQQAD SLASY MLESS SMK KTET FLST FYGULING KYNND SMK KTEN SMK KTET FLST FYGULING KYND SMK KTEN SMK KYND LYND LLEHF FLST SMK ALSS SMK KTEN FEFT SS SMK ALSS SM			1 - KNSEELLE	L H R K Y <mark>R</mark> QI	DLVDCKVI	GQP = PA	4 K Y M S P	LKWNHD	LARQAC	2 S L A I	NCILQ	HDKRYS-	KQF-	- I W V	<mark>G</mark> QNTALH	73
Smn2123         Smn21233         I - HE GRT IP NIKIT DYR ILLIKCK VP RQP RPYS 50 GE SWD DE EEL RACRAGS VV IRS YK YE TE FEK YR GO TE MTADN         78           Smn2133         Smn21333         I COL FF G LI HIK LC DUNDS KE TOG S S LK HE K RDB TG ONY YD SY DDR YE FE F - S SY QN IA DS         76           Smn2133         Smn200260         I - K YK EY DL HK YY KK S I F COM FC QP - AK XMS K. QWK HI, A EA OL TA SY DS YD DN PT EF F - S YQ O'N A BH         76           Smn213         Smn200260         I - K YK EY DL HK YY KK S I F COM FC QP - AK XMS K. WWK LA LK AL GYY KK TH DS ND DN PT I DF - S I QUL ADY         76           Smn214         Smn_00270         I - EC QE AT MYF HK K K H CD VF RCO Y CO YA SA KM K. UK AL GYY KK S THARK G S XY C YO S S DN FY U CO F - S I QUL ADY         76           Smn214         Smn_00270         I - E C QE LI LQ YN HE K K YR ADY RD P - C AL SM K. TO YK KL AL AK AL GYY KK S THARK G S XY C YO S S I AP YN C S Y D S YD S YD R YE EF F I C - NY CW N S YN C S YN			1 – K N S R K L L V I	L <mark>H</mark> R R F <mark>R</mark> Q I	DLVDCKVI	N G Q P – P A	4 K Y M S K	LKWNYD	LAQQAC	2 S L A N	YCILR	Q G K P H S –	KKF-	- I L V	<mark>G</mark> Q NMA F A	73
Smn2123         Smn21233         I - HE GRT IP NIKIT DYR ILLIKCK VP RQP RPYS 50 GE SWD DE EEL RACRAGS VV IRS YK YE TE FEK YR GO TE MTADN         78           Smn2133         Smn21333         I COL FF G LI HIK LC DUNDS KE TOG S S LK HE K RDB TG ONY YD SY DDR YE FE F - S SY QN IA DS         76           Smn2133         Smn200260         I - K YK EY DL HK YY KK S I F COM FC QP - AK XMS K. QWK HI, A EA OL TA SY DS YD DN PT EF F - S YQ O'N A BH         76           Smn213         Smn200260         I - K YK EY DL HK YY KK S I F COM FC QP - AK XMS K. WWK LA LK AL GYY KK TH DS ND DN PT I DF - S I QUL ADY         76           Smn214         Smn_00270         I - EC QE AT MYF HK K K H CD VF RCO Y CO YA SA KM K. UK AL GYY KK S THARK G S XY C YO S S DN FY U CO F - S I QUL ADY         76           Smn214         Smn_00270         I - E C QE LI LQ YN HE K K YR ADY RD P - C AL SM K. TO YK KL AL AK AL GYY KK S THARK G S XY C YO S S I AP YN C S Y D S YD S YD R YE EF F I C - NY CW N S YN C S YN	SmVAL 14	Smp_078490	1 – KNSRKLLA	L <mark>H</mark> R K Y <mark>R</mark> Q I	DLVDCKVI	NGQP – PA	A E Y M S K	LKWNYD	LAQQAC	SLAS	YCILR	Q G K P R S –	KKF-	- T W V	GQ N I A F F	73
BrmWLID         Smp. J3320         IK EQL MF GLUMH KLCODIDS KC F EQ.S. SLUME FLUK PUT OVER YV SCHUND KLLME - SLOWN KLES SLOWN KLES SUBOWN KLES SU	SmVAL20	Smp 127130	1 – HEGRTLFNI	K H T D Y R R	LLLKCKVI	PEQPRPF	Y S E G E	LSWDDE	LEELAC	GRQAS	VONLS	SEYKKTE	IEKEYF	R GQ I	GINTADN	78
smmLla         SmmLla<	SmVAI 30	Smn 131370			DHDDSKG	E E O S - S I	кнкен	KRDNT		FRYVK	OCDP S	ΙΤΙΤΚΟΥ	I N -	- N T P	SANISDN	74
SmmLab         Smm_D02800         I - K E Y E E Y D LIN YY N N S IF C C M P K Q - P A XY M S L Q NN KH A E K A D LT A S Y L C I Y S D S P S D M F E E F - S Y A Q N I A D S					STLLCKVI		EDMEV				KODIN	EDLVNDK	LIEHE	ESI	ONVAES	77
smv1al         Smv2a0200         1 - 5 TK ELITIME NILL         FUEL VECK 1 - SU VECK 1 - DS CD L CK LY - DS CD L CK LY P E L C L CK LY VECK 1 - DS CD L CK LY P E L C L C LY LY LO LY LA CA CS SY K K RY P E L C L C - LY CK VE SS CD K SS LI													DEEEE	- L J I		
smvLat       Smv_Q02070       1 = EGRA 11 YN FK KV KVV NC 11 F CQP P A KN TT K KVW KNL LANKA KQ YD SN DP MD T I GD F = S1 GN LADY       76         SmvLat       Smv_Q02070       1 = TGN SE LLAL WAY RAIK KG VW D DP - QAUSULK TWSKL A EWA GEWA LGO YP RS NMT MK KG SKW TY WG S1 A FY       76         SmvLat       Smv_Q02070       1 = TGN SE LLAL WAY RAIK KG VK D DP - QAUSULK TWSKL A EWA GEWA LGO YP RS NMT MK KG SKW TY WG S1 A FY       76         SmvLat       Smv_Q02070       1 = EVQL I LGV WAY RAIK KG VK D DP - QAUSULK TWSKL A EWA GEWA LGO YP RS NMT MK KG SKW TY WG S1 A FY       76         SmvLat       Smv_Q02070       1 = EVQL I LGV WAY RAIK KG CGE I VP A EE LGP EWD ELAAA AQ SW SK KG RP YE EP I G - NVGKW - SVG RN SN 10       76         SmvLat       Smv_Q1250       1 = EVQL I LGV WAY RAIK KG CGE DI VP A EE LI QP EWD ELAAA AQ SW SK KG RP YE EP I G - NVGKW - SVG RN SN 10       76         SmvLat       Smv_Q1250       1 = GE A M R N KH KL (CE ED I VP A EE LI QP EWD ELAAA AQ SW SK KG RP YE EP I G - NVGKW - SVG RN SN 10       76         SmvLat       Smv_Q12500       1 = GE A R N KH KL (CE ED I VP A EE LI QP EWD ELAAA AQ SW SK KG RP YE EP I G - NVGKW - SVG RN SN 10       76         SmvLat       Smv_Q12400       1 = GE A R N KH KL (CE ED I VP A EE LI QP EWD EN AAA AQ SW SK KG RP YE EP I G - NVGKW - SVG RN SN 10       76         SmvLat       Smv_Q12400       1 = GE A R N KH KL (CE ED I VP A EE LI QP EWD EN AAA AQ SW SK KG RP YE EP I G - NVGKW - SVG RN SN 10       77         Sm			I - KEVKEVFQ		STRFCUM	KQP-PA	AKTMSK	LOWNKH	LAEKAC	2 L I A S	RUDIS	TUSPSUM	KFEEF-	- 3 3 V		/0
smvL12         Smp. 300070         1 - TQN S E LLA L NAY R NI KY GNY DD P - QAN SMLK TY SHL A E MA GEWA LOG VP RS NMTMK KS KW - TY WG SI A FV			I - SIKELIFN	FHNKIKEI	DVFKGVL	S G Q P = K P	аккмзк	LKWNKL	LAKLAK	CGHVQ	KULD	SGDLGKL	YVGKF-	- D S V	QIVAEH	/6
smw1a13         smm2 3088         1 - TO IN SELLAL MAAY KIN LEY ON YE ADD - QAM SMLK LY TWISH LA FAMAG WAR AUGUY PRESINT MAR CG SW - TVY GO S IAF V         76           Smw1a13         Smm2 107690         1 - E AQ LL LQU ME ENA AN ALLY CE KG CUY ALE LL LQU FELED LG AAAA GO WSK CM YF EE FI G-N VGK			1 – EGQRAIYN	F <mark>H</mark> K K V <mark>R</mark> K I	DVKNCRI	° G Q P – P A	A K N L T K	LKWNKL	LANKAK	< Q Q A K	R <mark>C</mark> K Y D	SNDPNDF	I I G D F -	- E S I	<mark>G</mark> Q N L A D Y	76
smw1a13         smm2 3088         1 - TO IN SELLAL MAAY KIN LEY ON YE ADD - QAM SMLK LY TWISH LA FAMAG WAR AUGUY PRESINT MAR CG SW - TVY GO S IAF V         76           Smw1a13         Smm2 107690         1 - E AQ LL LQU ME ENA AN ALLY CE KG CUY ALE LL LQU FELED LG AAAA GO WSK CM YF EE FI G-N VGK	SmVAL7	Smp_300070	1 – TQNSELLA	L <mark>H</mark> N A Y <mark>R</mark> R I	NIKYGNVI	3 DQ P – Q A	AM SM L K	LTWSHK	LAEMAC	Q EWA L	QCVPR	R S NMTMR	K G S K W -	- T Y V	GQ S I A F V −−−−−	76
SmWAL23         SmJ 16760         1 - EEAQ LI LQV HN EM AY RINL CC EK GIV YA EE LI QP LEWDDE LAAAAG SW SK RUY YE EP IG - NV CKW - NS VG NS VI Q         76           SmWAL23         SmJ 11710         1 - EEAQ LI LQV HN EM AY RINL CC K GIV YA EE LI QP LEWDDE LAAAAG SW SK RUY YE EP IG - NV CKW - NS VG NS VI Q         76           SmWAL23         SmJ 11710         1 - EAQ LI LQV HN EM AY RINL CC K GIV YA EE LI QP LEWDDE LAAAAG SW SK RUY YE EP IG - NV CKW - NS VG NS VI Q         76           SmWAL23         SmJ 11720         1 - FF TS TLLQH HWW YG TR KK DS FW ST S EKK LC PI IV DC LAAAA GS WS SK RUY YE EP IG - NV CKW - SS VG NS VI Q         76           SmWAL23         SmJ 17220         1 - FF TS TLLQH HWW YG TR KK DS FW ST S EKK LC PI IV DC LV TA AQV EK CE HI P S CLIQPT THEW - KS VG AVAQV         76           SmWAL33         SmJ 17220         1 - FF TS TLLQH HWW YG TR KK DS FW ST S EKK LC PI IV DC LV TA AQV EK CE HI P S CLIQPT THEW - SS VG AVAQV         76           SmWAL13         SmJ 124000         1 - FF TS TLLGH HWW YG TR KK DS FW ST S EKK LC PI IV DC N S NMAQWAWELL AGK SW SC N YK G - MK V C N LG S WS NC PM E         71           SmWAL13         SmJ 124000         1 - FF NE CL HE NR R L         1 LG CP E LO DE D HI S GWWAEN LAAA EK LW K V C N LG S WS NC PM E         71           SmWAL13         SmJ 124000         1 - FF NE CL HE NR R L	SmVAL32	Smp_300080	1 – TQNSELLA	L	NIKYGNVI	R DQ P – Q A	AM SM L K	LTWSHK	LAEMAC	EWAL	Q C V P R	R S NMTMR	KGSKW-	- T Y V	GQ S I A F V	76
smv1al23         smv2al23	SmVAL3	Smp 316760	1 - EEAOLILO	<b>HNEHRA</b>	YRNLCGEI	GIVPAE	ELLOP	LEWDDE	LAAAAC	SWSK	K ONPY	EEEPIG-	NVGKW-	- N S V	GRNSVIO	76
SmvLa13         Smv_141570         1 - E EVQL IL QV IN EH AYR NL CD KK DI VP A E IL QP E WDD E LAAA AQ SW SK K N. PY DE E PL G - W CKW - NS V R NS XI IQ			1 = EEAO(110)	HNEHRA'	YRNLCGEI	GIVPAE	FLLOP	EWDDE	LAAAAC	SWSK	KONPY	EEEPIG-	NVGKW-	- NSV	GRNSVIO	76
SmvLa2         Smv_14250         1 - Q E AQ LML RV N ON HAYR K L G C E DI V P A E I L QP E WDD K L AAA AQ SW SE K M P F DE E I G - NV G KW - D SV R N S A I H							ELLOP			SWSK		EEEPIC	NVCKW	NSV	PNSVIO	76
SmvLa2         Smv_14350         1 - Q EAQ LML R.V IN LH AYR K.L G C ED IV PA EE LQ PL KWDD E LAAANG SW SE KAN PE DE EP LG - NV G KW - DS V R NS ALQ			1 0 5 4 0 1 1 0 0							2 3 10 3 10			NVCKW-			70
SmvLa13         Smv_2J3220         1 - K FT RT LLQ H NWV Q TANKE DS RWST - SEK LGD F MOD CLYV TA QV A KE CL PLP S CLQ RT TERV. K S W GAVA QV			I - QEAQLMER	HNDHRA	TRKLCGE	DIVPAE	ELUP	LEWDDK	LAAAAC	2 S W S E	KUNPF	DEEPIG-	NVGKW-	- U S V	KNSATH	/6
SmvLa15         SmvLa15 <t< td=""><td></td><td></td><td>1 - Q E A Q L M L R V</td><td>V HNEHRA'</td><td>YRKLCGEI</td><td>EDIVPAE</td><td>ELQP</td><td>LKWDDE</td><td></td><td>2 S W S E</td><td>KIQNP F</td><td>DEEPIG-</td><td>NVGKW-</td><td>- D S V</td><td>GRNSAIQ</td><td> 76</td></t<>			1 - Q E A Q L M L R V	V HNEHRA'	YRKLCGEI	EDIVPAE	ELQP	LKWDDE		2 S W S E	KIQNP F	DEEPIG-	NVGKW-	- D S V	GRNSAIQ	76
SmvAL11         Smv_0.2350, 2nd         1 = E5 I H S V Y Q L HAQY NSQ HG S NP V LDQ L S NP V V DR L AR A WAQ WAD H LQ S HL SN S G Y V R G			1 – K F T R T L L Q I	H <mark>H</mark> NWV <mark>R</mark> Q	T R N K <mark>C</mark> D S I	R W S T – S E	EKKLGD	FIWDDG	LYVTAC	QQYAE	K C E N I	PSGLQDR	TTCRW-	- K S V	<mark>G</mark> Q N V AQ V	76
SmvAL11         Smv_0.2350, 2nd         1 = E5 I H S V Y Q L HAQY NSQ HG S NP V LDQ L S NP V V DR L AR A WAQ WAD H LQ S HL SN S G Y V R G	SmVAL35	Smp_347320	1 – K F T S T L L Q I	H <mark>H</mark> NWV <mark>R</mark> Q	T R N K <mark>C</mark> D S I	<u>RWST –</u> SE	EKKLED	FIWDDG	LYVTAC	QQYAE	KCENI	PSGLHDR	TTCRW-	- K S V	<mark>G</mark> Q N V AQ V <u> </u>	76
smvLail         smv_12400         1         -Q_LHNDALNE MNR LK			1 - E S I H S V V O	LHNOYR-		S C	HGSNP	LVLDQN	LSNMAC	DOWAD	HLLQQ	SHLSNSG	YVYRG-	- M K V	<mark>G</mark> E N L G S R W S N G P M I	71
SmvALd5         Smv_124900         1 = FF NDQ AIR E NN L R			1-OLNHDALN			A I	НССРР	KYDRR	LARFAC	AWAF	NIARI	кімкня-	1 C -	- DEY	G EN LA SAO ST GKAI	67
SmvALd5         Smv_124900         1 = FF NDQ AIR E NN L R							HCCPE	ISVDSK			HLASI	NCLOHS	ĸc	DDY		67
SmvAL17         Smp_231830         1 = EFNEECTINE INR LR													K G-			67
Smv2A131         Smp_20280-014         1         INFNETCLKENNRLK         ILHHCPKLKKLSPLMKKS AQMES AVERUMS AQUALDUCKEQUQL         ICLKCQMMALLIGQUYC         G7           SmvAL13         Smp_12320-144         1         DFREDCERALMERK         ILHHCPKLKKLSPLMCAQUMAEALLSEGGKKNS-PLSSR-ECKESISVRTSGTHV-D         71           SmvAL28         Smp_154260         77 TDIKTGFQLWLDEYKNYDFYTRTGR-MGQGGHYTDLVWGGYTDCPNFPKGLSIVCNYG'GGNYPG         147           SmvAL25         Smp_154290         77 STVEIGFQSWLDEYKNYDFYTRTGR-MGQGGHYTDLVWGGYTDCPNFPKGLSIVCNYG'GGNYPG         147           SmvAL25         Smp_154290         77 STVEIGFQSWLDEYKNYDFYRTGR-MGQGGHYTDLVWGGYTDCPNFPKGLSIVCNYG'GGNYPG         147           SmvAL35         Smp_150207         75 STVEIGFQSWLDEYKNYDFYRTGR-MGQGGHYTDLVWEDTTDLVGGYTCPNFPKGLSIVCNYG'GGCP-         146           SmvAL35         Smp_175007         76 FRLLIGFRMWNEYN DFFNRLGL-VGRS SHTTLIVWEN TDLGGYATCPHSFKLSIVCNYG'GGCGP-         146           SmvAL35         Smp_175007         76 FRLLIGFRMWNEYN DFFNRLGL-VGRS SHTTLIVWEN TDLGGYATCPHS			I - K FNDQATKI			SL	HGCPE		LMISAC	ZKWAE	NLAAA	EKLTHS-	NT-			67
SmvALL1       Smp_12320_1st       1 - D F R E D C F R A IN E K       LLH GV C A LIR HS LALL D T A Q DW A E A LLS E DG LIX N S - P LS S R - G E V C E S I S V R T S T G F I V C F G N Y P C       147         SmvAL26       Smp_176160       7 T D I K T G F Q L W D E Y K N V D F Y T T T R - M G G G HY T D L V W E D T T D V G G V T D Q N F P Y C L S I V C N Y G G G N Y P C       147         SmvAL25       Smp_176160       7 T D I K T G F Q L W D E Y K N V D F Y T T T R - M G Q G HY T D L V W E D T T D V G G V T D Q N F P Y C L S I V C N Y G G G C Y A C       147         SmvAL25       Smp_126207       7 T S T V E I G F Q R W L NE Y N D F Y T T T R - M G Q G HY T D L V W E N T T D I G G V A T C P H S P F K L S I V C N Y G G G C Y = 146         SmvAL25       Smp_12680       7 T S T V E I G F Q R W L NE Y N D F F N R L L - V G R G S HY T D I V W E N T T D I G G V A T C P H S P F K L S I V C N Y G G G C N = 146         SmvAL25       Smp_12680       7 T S T V E I G F Q R W L NE Y N N D F N R L L - V G R G S HY T D I V W E N T T D I G G V A T C P H S P F K L S I V C N Y G G G C N = 146         SmvAL2       Smp_12350       7 T Y U E A V K L W S E AM Y N H N N N T O S S A T G N Y P L V W E N T D I G G V A T C P H S P F K L S I V C N Y G G G C N = 147         SmvAL2       Smp_123540       7 A A N Q T A M D E W N E Q Y D F D S N T C N - S K S G NY L E I W N N H N N N C C L HY T D N A W K H T D I G C V A N P R Y C L S I V O N C G C N N N N N N N T N T C S S A T G N Y P L V C N V A N A M K K T D I G C V A N P R Y C L S I V O N C G C N N N N N N N N P C L L HY T M A W A K H T D I G C V A N			I - EFNEECIN	EHNKLK-		A L	HGCPA	LILNYE	LAKDAC	2 K Y A E	HLASV	NELEHC-	ID-	- 105	GENLAFFIIIAIAG	KKD 70
SmvAl26       Smp_15420       77 TD IKTG FQ LW LD EYKNY D FYTR TG R - MGOG GHY TD LYWE DT TD YG G YTD G PN F PYG LS IVG NY G FGGNY PG       147         SmvAl28       Smp_176160       77 TD IKTG FQ LW LD EYKNY D FYTR TG R - MGOG GHY TD LYWE DT TD YG G YTD G PN F PYG LS IVG NY G FGGNY PG       147         SmvAl25       Smp_176160       77 TD IKTG FQ LW LD EYKNY D FYTR TG R - MGOG GHY TD LYWE DT TD YG G YTD G PN F PYG LS IVG NY G FGGNY PG       147         SmvAl25       Smp_070250       77 STV EIG FQ NW LNEYKNY D FFNR LC L- YGR S HYT II YWE NT TD IG GYA TG PH S PYG LS IVG NY G FGGCG CP -       146         SmvAl25       Smp_176180       77 STV EIG FQ NW LNEYKNY D FFNR LC L- YGR S HYT II YWE NT TD IG GYA TG PH S PYG LS IVG NY G FGGCG CP -       146         SmvAl29       Smp_176180       77 STV EIG FQ NW NYN NT NT G I - NNOC THYT D LWE NT TD FG G YT EK NM - FFNR LG LY YGR S NYN NYN NYN I S - SAT GNYP D LYWE NT TD FG G YT EK NM TK LK IV IG NYG G GG CO F       147         SmvAl25       Smp_176180       77 YT E KAYK LW F FS KAWY N FYN NYN S S S G S - GYG GHYT D LYWE NT TD FG G YT EK NM TK LK IV IG NYG GG CG NY L       147         SmvAl25       Smp_123350       73 GT IE QA FD AW KD EY NYN NYN FYN O F NYN LW YN NYN NYG NYG NYG GG CG NY L       147         SmvAl21       Smp_13360       74 PT IK SG YD AW FN EHK LY NYN NNC PO CL HYT MAWAK TD LG GYA NG P RY GL SI VG NY GG CG CNN N       140         SmVAl22       Smp_13360       74 PT IK SG YD AW FN			1 - NFNEICLK	E <u>N</u> NR L <mark>R</mark> -·		- – – – – R L	_ ННСРК	LKLSHQ	LMK S AC	Q Y H S E	YLQKQ	RQLQQI-	GD-	- L V C	<mark>G</mark> Q NMA LI I GQQ NY (	67
smv228         smv_2128         smv_2126         77 TDIKTCFQ.WLDEYKNYDPTTRTCR-MGQCGHYTDLVWEDTTDVGCYTDGPNFPYGLSIVCNYG CGNYAG         147           smv2215         smv_21278         77 KDIKTCFQ.SULDEYKNYDPTTRTCR-MGQCGHYTDLVWEDTTDVGCYTCRGPNFPYGLSIVCNYG CGCNYAG         146           smv2125         smv_23268         77 STVEIGFQ.WLNEYKNYDPTNLTGI-VGC SHYTDJVWENTTDIGCQVATGPNSPFKLSIVCNYG GGCP	SmVAL11	Smp_012350_1st	1 – D F R E D C F R /	4 <mark>H</mark> N E K <mark>R – –</mark>		LL	HGVCA	RHSIA	I DKTAC	DWAE.	ALLSE	DGIKNS-	PISSR-	- C F V	C F S I S V R T S T C T H V	'D 71
smv228         smv_2128         smv_2126         77 TDIKTCFQ.WLDEYKNYDPTTRTCR-MGQCGHYTDLVWEDTTDVGCYTDGPNFPYGLSIVCNYG CGNYAG         147           smv2215         smv_21278         77 KDIKTCFQ.SULDEYKNYDPTTRTCR-MGQCGHYTDLVWEDTTDVGCYTCRGPNFPYGLSIVCNYG CGCNYAG         146           smv2125         smv_23268         77 STVEIGFQ.WLNEYKNYDPTNLTGI-VGC SHYTDJVWENTTDIGCQVATGPNSPFKLSIVCNYG GGCP														0111		
smvL227         smv_L279				_	_											
smvL227         smv_L279	SmVAL26	Smp 154260	77 T D I K T G F O L	VLDEYKN	Y D F Y T R T		_	_		ov t d	P N F		_			147
SmvAL15         Smv_20250         77 STV EIGEOR WLNEYKNYD FFNRL CL-VCR G SHYT DI VWENTTDIG CG VAT CP HSPFKLSI V GNY CFGGCP-         146           SmvAL29*         Smv_21680         77 STV EIGEOR WLNEYKNYD FFNRL CL-VCR G SHYT DI VWENTTDIG CG VAT CP HSPFKLSI V GNY CFGGCPC-         146           SmvAL29*         Smv_21670         76 PRLLIGEKMWEDESON WNNTNT GI-NNO CTHYTDIG CG VTECKNMPFKLSI V GNY CFGGNIE         147           SmvAL29*         Smv_21680         77 STV EIGEOR WLNEYKNYD FFNIGSON CG GNY EG         147           SmvAL2         Smv_21680         77 STV EIGEOR WLNEYKNYD FFNIGSON CG GNY EG         147           SmvAL2         Smv_212350         75 QT IEQAEDAWK DEYKO WNYSKS GSCVG GHYT DI VWENTTDIG CG V TOCP NFRTKLVI V CNY CP GGNYEG         147           SmvAL2         Smv_2123540         74 ANVQT AMDEWV NEYOY V DFDSNTON-SKS GNY LD I VWENTTDIG CG V TOCP NF						R - MGQ	GНҮТ <mark>Q</mark>	L V W E D <mark>T</mark>	тру <mark>сс</mark>			PY	GLSIV	NYG	P G G N Y P G	
SmvAL5       Smv_336880       77 STVDIG G Q R W LN EYK NW D F FNR LG L- V C R G SHY TD L V W ENT TD IG C V AT C P H S P F K L S I V C NY C P G G C C P -       146         SmvAL29       Smp_1267610       77 F T K L LI G FK MW P E SQ MY NY NT TO I - N C NQ G HY TD L V W ENT TD G C V T E C X NM R T K L V I V C NY G P G C N I E E       147         SmvAL12       Smp_123550       75 Q T I E Q A FD AW K D E Y KO Y NY Y S K S G S C V G G HY TD L V W ENT TD IG C V T C C R K S Y S F P Y G V F V C NY A P G A K FD -       146         SmvAL1       Smp_123560       74 A NV Q T A MD E W N E Y KO Y NY Y S K S G S Q C HY TD AWAK K T TD IG C V AN C P R Y G L S I V C NY G P G G NW N       140         SmvAL12       Smp_139360       74 P T I K S C V D AW F N E H K L I N Y N N N N P Q C L HY TD AWAK K T TD IG C V AN C P R Y G L S I V C NY G P G G NW N       140         SmvAL2       Smp_139360       74 P T I K S C V D AW F N E H K L I N Y N N N N P Q C L HY TD AWAK T TD IG C V AN C P R Y G L S I V C NY G P G G NW N       140         SmvAL2       Smp_13780       74 S T I K S V D AW F N E H K L I N Y S V N N P Q C L HY TD AWAK T TD IG C V AN C R Y C L S I V C NY G P G G NW I N       140         SmvAL3       Smp_127370       75 S N N K I F K W S X N N P F N E H K L N Y S V N N P C C L HY TD AWAK T T D IG C V AN C R Y C L S I V C NY G P G G NW I N       140         SmvAL3       Smp_127370       75 S N N K S I F K W S K Y D W N C I - V H V M W AK T T D IG C V AN C R Y C L S V W C Y G P G C	SmVAL28	Smp_176160	77 TDIKTGFQL	VLDEYKN <mark>'</mark>	Y D F Y T R T	R – MGQ <mark>C</mark> R – MGQC	GНҮТ <mark>Q</mark> GНҮТQ	L V W E D <mark>T</mark> L V W E D <b>T</b>	T D V <mark>G C C</mark> T D V <mark>G C C</mark>	ov t d <mark>c</mark>	P N F – –	PY PY	G L S I V <mark>O</mark> G L S I V	NYG NYG	P G G N Y P G P G G N Y P G	147
SmwL29*       Smp_120670       76 PR LL I G FK MW FD E SQ.W NY NT NT G I – NAQ CTHY DL I WENT TD FG CC V TE CX NM L PN LNU I CMY CF GCN I LC       146         SmwL4.8       Smp_127610       77 YT VE AV K LW FS EAMY NY NT NT G I – SATC GNY PD L VWQ NT THV GC I TNCT G S PG FP VG L SV CMY GF GCN Y EC       147         SmwL4.8       Smp_123550       75 GT I EQA FDAWK D EYKQ V NY SK SG S - CV G GMV FD L VWQ NT THV GC I TNCT G S PG FP VG L SV CMY GF GCNY EC       147         SmwL1.1       Smp_12350       74 A NY OT AMD EW YN PS NT NN CS SG GMY LD I VWQ NT THV GC U TD CR KS PG L FY OF VS V CMY AF A KA KA CAK FD-       146         SmwL1.1       Smp_13960       74 PT I K S CV DAW FN EHKL I NY NT NN CP QC L HY TD MAWAK TT D I G CV AN CP R Y G L SI V CNY CF G GNW NN       140         SmvL2.1       Smp_020260       74 PT I K S CV DAW FN EHKL I NY NT NN CP QC L HY TD MAWAK TT D I G CV AN CP R Y G L SI V CNY CF G GNW IN       140         SmvL2.2       Smp_020260       74 ST I K S AV DAW FN EHKL I NY SV NN CP QC L HY TD MAWAK TT D I G CV AN CP S Y G L SI V CNY CF G GNW IN       140         SmvL2.2       Smp_021307       75 SD VI NA VE SW FN EYQ U D FT NNK CE V E D CL HY TD MAWAK TT D I G CV AN CP S Y G L SI V CNY CF G GNW IN       140         SmvL2.0       Smp_123307       75 SD VI NA VE SW FN EYQ U D FT NNK CE V E D CL HY T MAWAK TT D I G CV AN CP S Y G L SI V C Y S M GO NW IN       140         SmwL2.0       Smp_123307       75 SD VI NA VE SW F	SmVAL28 SmVAL27	Smp_176160 Smp_154290	77 TDIKTGFQL	VLDEYKN <mark>.</mark> VLDEYKN	Y D F Y T R T O	R – MGQC R – MGQC R – MGQC	GHYT <mark>Q</mark> GHYTQ GHYTQ	L V W E D <mark>T</mark> L V W E D T L V W E D T	T D V <mark>G C C</mark> T D V <mark>G C C</mark> T D V <mark>G C</mark> C	о v т d <mark>c</mark> с v т к <mark>c</mark>	P N F – – P N F – –	P Y P Y P Y	G L S I V G L S I V G L S I V	NYG NYG NYG	P GGNY P G P GGNY P G P GGNY AG	147 147
Smw129       Smp_125260       77 YT YERAYK LW FSEAMY YN FNTN I S-SATCGNYD LWENT TU YOGGYTD CPNFRTKLVI V CNYG GGYN FG       147         SmvAL12       Smp_123540       74 ANVQTAMDEW VN EYQYD FD SNT (N - 5K SG GNYED LWWANT TH I GGYD GR KS PQ FPYG LSVV (NYG G GGNWN       146         SmvAL12       Smp_139680       74 PT I K SGVDAW FN EHK LYNYNTNN CP QG LHYT DMAWAK TT DI GGGVAN GP RY CL SI V CNYG F GGNWN       140         SmvAL2       Smp_139680       74 PT I K SGVDAW FN EHK LYNYNTNN CP QG LHYT DMAWAK TT DI GGGVAN GP RY CL SI V CNYG F GGNWN       140         SmvAL2       Smp_13920       74 PT I K SGVDAW FN EHK LYNYNTNN CP QG LHYT DMAWAK TT DI GGGVAN GP RY CL SI V CNYG F GGNWN       140         SmvAL2       Smp_13940       74 ST I N SAVDAW FN EHK LYNYNTNN CP QG LHYT DMAWAK TT DI GGGVAN GP RY CL SI V CNYG F GGNWI N       140         SmvAL30       Smp_12370       75 SDNK SI F KYW SAKN CP C G LHYT DMAWAK TT DI GGGVAN GP RY CL SI V CNYG F GGNWI N       140         SmvAL30       Smp_12370       75 SDNK SI F KYW SAKN CP C G LHYK RWWAK TT DI GGGVAN GP RY C LS VV CY VG GGNWI N       140         SmvAL30       Smp_12370       75 SDNK SI F KYW SAKN CP K GVHYK RWWAK TT DI GGGVAN GP RY C LS VV CY VG GGNWI N       141         SmVAL30       Smp_123007       75 T N K SV F KY WY ST FN CY N CY C G GNYK N       140         SmVAL30       Smp_101200       75 T T I E KAWASKY F E YHNY N T NY	SmVAL28 SmVAL27 SmVAL15	Smp_176160 Smp_154290 Smp_070250	77 TDIKTGFQL 77 KDIKTGFQS 77 STVEIGFQR	VLDEYKN VLDEYKN VLNEYKN	Y D F Y T R T O Y D F Y T R T O Y D F F N R L O	R – MGQC R – MGQC R – MGQC L – VGRC	GHYTQ GHYTQ GHYTQ SHYTQ	L V W E D T L V W E D T L V W E D T I V W E N T	T D V <mark>G C C</mark> T D V G C C T D V G C C T D I G C C	SVTD <mark>C</mark> SVTKC SVATC	P N F – – P N F – – P H S – –	PY PY PY PF	G L S I V G L S I V G L S I V G L S I V K L S I V	NYG NYG NYG NYG	P G G N Y P G P G G N Y P G P G G N Y A G P G G G C P –	147 147 146
SmvALB       Smp_12350       75 QT I EQAFDAW KD EY KQY NYYSKS G S GV G MYT DLVWQ KT THV C GG I TN GT C S Y S F PY G LS VV G NY C P G G KY F D 146       147         SmvAL1       Smp_13680       74 PT I K S GV DAW F N EHK LY NY NTNN C P Q L HYT D MAWAKT TD I C GV V G V A C P R Y G LS I V G NY C P G G NW N       140         SmvAL21       Smp_102680       74 PT I K S GV DAW F N EHK LY NY NTNN C P Q L HYT D MAWAKT TD I C GV A N G P R Y G LS I V G NY C P G G NW N       140         SmvAL21       Smp_02670       74 PT I K S GV DAW F N EHK LY NY NTNN C P Q L HYT D MAWAKT TD I C GV A N G P R Y G LS I V G NY C P G G NW N       140         SmvAL22       Smp_02670       74 PT I K S GV DAW F N EHK LY NY NTNN C P Q L HYT D MAWAKT TD I C GV A N G M Y G LS I V G NY C P G G NW N       140         SmVAL20       Smp_12370       75 S D N S N K W F N EHK LY NY SVN C P C V HY K D WV WAKT TD I C GV A N G NY G LS I V G NY C P G G NW N       140         SmVAL30       Smp_13370       75 S D N S I F K W S A Y D HY NY SVN C P C V HY K D WV WAKT TD I C GV A N G NY S S N I I L U Y S S A D N       141         SmVAL30       Smp_123090       78 D T I K A MA W F N E HK LY NY NY C P C V HY K D WV WAKT TD I C GV A N G N H T EV K S Q I I V C Y S S A D D H A V S W S A D HY NY Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y	SmVAL28 SmVAL27 SmVAL15 SmVAL5	Smp_176160 Smp_154290 Smp_070250 Smp_336880	77 TDIKTGFQL 77 KDIKTGFQS 77 STVEIGFQR 77 STVDIGFQR	VLDEYKN VLDEYKN VLNEYKN VLNEYKN	Y D F Y T R T Y D F Y T R T Y D F F N R L Y D F F N R L	R – MGQ C R – MGQ C R – MGQ C L – VGR C L – VGR C	GHYTQ GHYTQ GHYTQ SHYTQ SHYTQ	L VW E D <mark>T</mark> L VW E DT L VW E DT I VW E NT I VW E NT	T D V <mark>G C C</mark> T D V G C C T D V G C C T D I G C C T D I G C C	VTDC VTKC VATC VATC	P N F – – P N F – – P H S – – P H S – –	PY PY PY PF PF	G L S I V G L S I V G L S I V K L S I V K L S I V K L S I V	NYG NYG NYG NYG NYG	P GGNY P G P GGNY P G P GGNY AG P GGCCP – P GGCCP –	147 147 146 146
SmvAl12       Smp_132540       74 ANVQTAMDEWVNEYQY PDFDSNTCN-SKS COYLEU VWQK THLIG CVTDCRKSPQFPYGVFVCNVAP CAKPD-       146         SmvAL12       Smp_159290       74 PTIKS GVDAW FNEHKLY NYNTNNCPQLHYT DMAWAK TTDIG CGVANCPRYGLSIVCNYCG GGNWNN       140         SmvAL2       Smp_02630       74 PTIKS GVDAW FNEHKLY NYNTNNCPQLHYT DMAWAK TTDIG CGVANCPRYGLSIVCNYCG GGNWNN       140         SmvAL2       Smp_02630       74 PTIKS GVDAW FNEHKLY NYNTNNCPQLHYT DMAWAK TTDIG CGVANCPRY	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL29*	Smp_176160 Smp_154290 Smp_070250 Smp_336880 Smp_120670	77 T D I K T G F Q L 77 K D I K T G F Q S 77 S T V E I G F Q R 77 S T V D I G F Q R 76 P R L L I G F K M	VLDEYKN VLDEYKN VLNEYKN VLNEYKN VLNEYKN VFDESQN	Y D F Y T R T ( Y D F Y T R T ( Y D F F N R L ( Y D F F N R L ( Y N Y N T N T (	R – MGQC R – MGQC R – MGQC L – VGRC L – VGRC I – NNQC	GHYTQ GHYTQ GHYTQ SHYTQ SHYTQ THYTQ	L VWED <mark>T</mark> L VWEDT L VWEDT I VWENT I VWENT L I WENT	T D V <mark>G C C</mark> T D V G C C T D V G C C T D I G C C T D I G C C T D F G C C	VTDC VTKC VATC VATC VATC	P N F – – P N F – – P H S – – P H S – – K NM – –	PY PY PY PF PF PF	G L S I V G L S I V G L S I V K L S I V K L S I V N L N V I	NYG NYG NYG NYG NYG NYG	P GGNY P G P GGNY P G P GGNY A G P GGCC P - P GGCC P - P GGN I L G	147 147 146 146 146
SmvAl12       Smp_132540       74 ANVQTAMDEWVNEYQY PDFDSNTCN-SKS COYLEU VWQK THLIG CVTDCRKSPQFPYGVFVCNVAP CAKPD-       146         SmvAL12       Smp_159290       74 PTIKS GVDAW FNEHKLY NYNTNNCPQLHYT DMAWAK TTDIG CGVANCPRYGLSIVCNYCG GGNWNN       140         SmvAL2       Smp_02630       74 PTIKS GVDAW FNEHKLY NYNTNNCPQLHYT DMAWAK TTDIG CGVANCPRYGLSIVCNYCG GGNWNN       140         SmvAL2       Smp_02630       74 PTIKS GVDAW FNEHKLY NYNTNNCPQLHYT DMAWAK TTDIG CGVANCPRY	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL29*	Smp_176160 Smp_154290 Smp_070250 Smp_336880 Smp_120670	77 TDIKTGFQL 77 KDIKTGFQS 77 STVEIGFQR 77 STVDIGFQR 76 PRLLIGFKM 77 YTVERAVKL	V L D E Y K N V L D E Y K N V L N E Y K N V L N E Y K N V F D E S Q N V F S E A M Y	Y D F Y T R T Y D F Y T R T Y D F F N R L Y D F F N R L Y N Y N T N T Y N F N T N L	R – MGQC R – MGQC R – MGQC L – VGRC L – VGRC I – NNQC S – SATC	GHYTQ GHYTQ GHYTQ SHYTQ SHYTQ THYTQ GNYPQ	L VWEDT L VWEDT L VWEDT I VWENT I VWENT L I WENT L I WENT	T D V <mark>G C C</mark> T D V G C C T D V G C C T D I G C C T D I G C C T D F G C C T D V G C C	VTDC VTKC VATC VATC VTEC VTDC	P N F – – P N F – – P H S – – P H S – – K NM – – P N F – –	PY PY PY PF PF RT	G L S I V G L S I V G L S I V K L S I V K L S I V N L N V I K L V I V	NYG NYG NYG NYG NYG NYG NYG	P GGNY P G P GGNY P G P GGNY A G P GGGC P - P GGG C P - P GGN I L G P GGN I P E	147 147 146 146 146
SmvAL1       Smp_193680       74 PT IKS GVDAW FNEHK LY NY NNNQ P QC LHYT DMAWAK T DI GCQ VANCP RY GLSI V GNY CP GCNWNN       140         SmvAL2       Smp_002630       74 PT IKS GVDAW FNEHK LY NY NNNQ P QC LHYT DMAWAK T DI GCQ VANCP RY GLSI V GNY CP GCNWN       140         SmvAL2       Smp_002630       74 PT IKS GVDAW FNEHK LY NY SVNNQ P QC LHYT DMAWAK T DI GCQ VANCP RY GLSI V GNY CP GCNWN       140         SmvAL2       Smp_07840       74 ST IKS AVDAW FNEHK LY NY SVNNQ P QC LHYT DMAWAK T DI GCQ VANCP RY GLSI V GNY CP GCNWI N       140         SmVAL30       Smp_13737       75 RDNKS IF KW SAKY DHY N O I - VHKG WWAK T DI GCQ VANCP RY GLSI V GNY CP GCNWI N       140         SmVAL30       Smp_13137       75 RDNKS IF KW SAKY DHY N O I - VHKG SVK DL MYKM WAK T DI GCQ VANCP RY GLSI V GNY CP GCNWI N       141         SmVAL30       Smp_13130       75 RDNKS IF KW SAKY DHY N O I - VHKG SVK DL MYKM N RN IA CS IGN CK RQ	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL29* SmVAL9	Smp_176160 Smp_154290 Smp_070250 Smp_336880 Smp_120670 Smp_176180	77 T D I K T G F Q L 77 K D I K T G F Q S 77 S T V E I G F Q R 77 S T V D I G F Q R 76 P R L L I G F K M 77 Y T V E R A V K L 75 Q T I E Q A F D A	V L D E Y K N V L D E Y K N V L N E Y K N V L N E Y K N V F D E S Q N V F S E A M Y V K D E Y K Q	Y D F Y T R T ( Y D F Y T R T ( Y D F F N R L ( Y D F F N R L ( Y N Y N T N T ( Y N F N T N T ( Y N Y N Y S K S (	R – MGQ R – MGQ R – MGQ L – VGR L – VGR I – NNQ S – SAT S – GV	GHYTQ GHYTQ GHYTQ SHYTQ SHYTQ SHYTQ GNYPQ GHYTQ	L VW E DT L VW E DT I VW E NT I VW E NT I VW E NT L I WE NT L VW E NT L VW Q NT	T DV GCC T DV GCC T DV GCC T D I GCC T D I GCC T D F GCC T D F GCC T DV GCC	VTDC VTKC VATC VATC VTEC VTDC	P N F – – P N F – – P H S – – P H S – – K NM – – P N F – – T G S – –	PY PY PF PF 	G L S I V G L S I V G L S I V K L S I V K L S I V K L S I V G L S V V G L S V V	NYG NYG NYG NYG NYG NYG NYG	P GGNYPG P GGNYPG P GGNYAG P GGGCP – P GGCP – P GGNILG P GGNIPE P GGNYEG	147 147 146 146 146 147
SmvL121       Smp_159290       74 PT IKS GVDAW FNEHKLY NYNMNNC P OC LHYT DMAWAK T DI GC VANC PRY GLSIV CNY GP GGNWNN       140         SmVAL22       Smp_139450       74 PT IKS GVDAW FNEHKLY NYNNNC P OC LHYT DMAWAK T DI GC VANC PRY GLSIV CNY GP GGNWIN       140         SmVAL23       Smp_139450       74 ST IKS AVDAW FNEHKLY NYS NNC P OC LHYT DMAWAK T DI GC VANC PRY GLSIV CNY GP GGNWIN       140         SmVAL20       Smp_139450       74 ST IKS AVDAW FNEHKLY NYS VNNC P OC LHYT DMAWAK T DI GC VANC PRY GLSIV CNY GP GGNWIN       140         SmVAL30       Smp_121370       75 SDVINAVES FNEYQLY DFT NNK GEVP EDC LHYT RMAWAK T DI GC VANC RY GLSIV CYY GP GGNWIN       141         SmVAL30       Smp_131370       75 RDNK SI FK WS AKY DHY N GI - VHNC SYK RU HWAK T RI IAC SI GNC KRQ T KS SN II LCYY SS LANADN       141         SmVAL10       Smp_001800       77 PT I EK AVASW FI EYK NY SF DDNT CK DT CMQ YK MWK KE HI GC GV KC SNR KLW CNY SP AAEE       141         SmVAL30       Smp_002060       77 PT I E KAVASW FI EYK NY SF DDNT CK DT CMQ YK MW KK T DI GCA SNK C CNR FLVV CNY AP GAD       141         SmVAL31       Smp_002060       77 PT I E KAVASW FI EYK NY SF NDT C KAVK T CADYK DLVANT T DI GCA SNK C CNR	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL29* SmVAL9 SmVAL8	Smp_176160 Smp_154290 Smp_070250 Smp_336880 Smp_120670 Smp_176180 Smp_123550	77 T D I K T G F Q L 77 K D I K T G F Q S 77 S T V E I G F Q R 77 S T V D I G F Q R 76 P R L L I G F K M 77 Y T V E R A V K L 75 Q T I E Q A F D A	V L D E Y K N V L D E Y K N V L N E Y K N V L N E Y K N V F D E S Q N V F S E A M Y V K D E Y K Q	Y D F Y T R T ( Y D F Y T R T ( Y D F F N R L ( Y D F F N R L ( Y N Y N T N T ( Y N F N T N T ( Y N Y N Y S K S (	R – MGQ R – MGQ R – MGQ L – VGR L – VGR I – NNQ S – SAT S – GV	GHYTQ GHYTQ GHYTQ SHYTQ SHYTQ SHYTQ GNYPQ GHYTQ	L VW E DT L VW E DT I VW E NT I VW E NT I VW E NT L I WE NT L VW E NT L VW Q NT	T DV GCC T DV GCC T DV GCC T D I GCC T D I GCC T D F GCC T D F GCC T DV GCC	VTDC VTKC VATC VATC VTEC VTDC	P N F – – P N F – – P H S – – P H S – – K NM – – P N F – – T G S – –	PY PY PF PF 	G L S I V G L S I V G L S I V K L S I V K L S I V K L S I V G L S V V G L S V V	NYG NYG NYG NYG NYG NYG NYG	P GGNYPG P GGNYPG P GGNYAG P GGGCP – P GGCP – P GGNILG P GGNIPE P GGNYEG	147 147 146 146 146 147 147
SIMUAL22       SIMUAL22 <td< td=""><td>SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL29* SmVAL9 SmVAL8 SmVAL12</td><td>Smp_176160 Smp_154290 Smp_070250 Smp_120670 Smp_120670 Smp_176180 Smp_123550 Smp_123540</td><td>77 TDIKTGFQL 77 KDIKTGFQS 77 STVEIGFQR 77 STVDIGFQR 76 PRLLIGFKM 77 YTVERAVKL 75 QTIEQAFDA 74 ANVQTAMDE 74 DTIKGCVDA</td><td>V L D E Y K N V L D E Y K N V L N E Y K N V L N E Y K N V F D E S Q N V F S E A M Y V K D E Y K Q V N E Y Q Y</td><td>Y D F Y T R T ( Y D F Y T R T ( Y D F F N R L ( Y D F F N R L ( Y N Y N T N T ( Y N F N T N T ( Y N F N T N T ( Y N F N T N T ( Y D F D S N T (</td><td>R – M G Q Q R – M G Q Q L – V G R Q L – V G R Q I – N N Q Q S – S A T Q S – S A T Q N – S K S Q</td><td>GHYTQ GHYTQ GHYTQ SHYTQ SHYTQ THYTQ GNYPQ GNYPQ GNYLQ</td><td>L VW E D L VW E D L VW E D I VW E N I VW E N I VW E N L VW E N L VW E N L VW E N I VW Q K I VW Q K</td><td>T DV GCC T DV GCC T DV GCC T D I GCC T D I GCC T D F GCC T D F GCC T H I GCC T H I GCC</td><td>VTDC VTKC VATC VATC VTEC VTDC ITNC VTDC</td><td>P N F P N F P H S P H S K NM P N F T G S R K S</td><td> P Y  P Y  P F  P F  L P  R T  Y S F P Y  P Q F P Y</td><td>G L S I V G L S I V G L S I V K L S I V K L S I V K L S I V G L S V V G L S V V G L S V V G L S V V</td><td>NYG NYG NYG NYG NYG NYG NYG NYG</td><td>P GGNYP G P GGNYP G P GGNYA G P GGCCP - P GGCP - P GGNIL G P GGNIP E P GGNYE G P GGNYE G P GGNYE G P GGNYE G</td><td>147 147 146 146 146 147 147 147</td></td<>	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL29* SmVAL9 SmVAL8 SmVAL12	Smp_176160 Smp_154290 Smp_070250 Smp_120670 Smp_120670 Smp_176180 Smp_123550 Smp_123540	77 TDIKTGFQL 77 KDIKTGFQS 77 STVEIGFQR 77 STVDIGFQR 76 PRLLIGFKM 77 YTVERAVKL 75 QTIEQAFDA 74 ANVQTAMDE 74 DTIKGCVDA	V L D E Y K N V L D E Y K N V L N E Y K N V L N E Y K N V F D E S Q N V F S E A M Y V K D E Y K Q V N E Y Q Y	Y D F Y T R T ( Y D F Y T R T ( Y D F F N R L ( Y D F F N R L ( Y N Y N T N T ( Y N F N T N T ( Y N F N T N T ( Y N F N T N T ( Y D F D S N T (	R – M G Q Q R – M G Q Q L – V G R Q L – V G R Q I – N N Q Q S – S A T Q S – S A T Q N – S K S Q	GHYTQ GHYTQ GHYTQ SHYTQ SHYTQ THYTQ GNYPQ GNYPQ GNYLQ	L VW E D L VW E D L VW E D I VW E N I VW E N I VW E N L VW E N L VW E N L VW E N I VW Q K I VW Q K	T DV GCC T DV GCC T DV GCC T D I GCC T D I GCC T D F GCC T D F GCC T H I GCC T H I GCC	VTDC VTKC VATC VATC VTEC VTDC ITNC VTDC	P N F P N F P H S P H S K NM P N F T G S R K S	P Y P Y P F P F L P R T Y S F P Y P Q F P Y	G L S I V G L S I V G L S I V K L S I V K L S I V K L S I V G L S V V G L S V V G L S V V G L S V V	NYG NYG NYG NYG NYG NYG NYG NYG	P GGNYP G P GGNYP G P GGNYA G P GGCCP - P GGCP - P GGNIL G P GGNIP E P GGNYE G P GGNYE G P GGNYE G P GGNYE G	147 147 146 146 146 147 147 147
SIMUAL22       SIMUAL22 <td< td=""><td>SmVAL28 SmVAL27 SmVAL5 SmVAL5 SmVAL29* SmVAL9 SmVAL9 SmVAL12 SmVAL12</td><td>Smp_176160 Smp_154290 Smp_070250 Smp_336880 Smp_120670 Smp_176180 Smp_123550 Smp_123540 Smp_133680</td><td>77 TDIKTGFQL 77 KDIKTGFQS 77 STVEIGFQR 77 STVDIGFQR 76 PRLLIGFKM 77 YTVERAVKL 75 QTIEQAFDA 74 ANVQTAMDE 74 DTIKGCVDA</td><td>V L D E Y K N V L D E Y K N V L N E Y K N V L N E Y K N V F D E S Q N V F S E A M Y V K D E Y K Q V N E Y Q Y</td><td>Y D F Y T R T ( Y D F Y T R T ( Y D F F N R L ( Y D F F N R L ( Y N Y N T N T ( Y N F N T N T ( Y N F N T N T ( Y N F N T N T ( Y D F D S N T (</td><td>R – M G Q Q R – M G Q Q L – V G R Q L – V G R Q I – N N Q Q S – S A T Q S – S A T Q N – S K S Q</td><td>GHYTQ GHYTQ GHYTQ SHYTQ SHYTQ THYTQ GNYPQ GNYPQ GNYLQ</td><td>L VW E D L VW E D L VW E D I VW E N I VW E N I VW E N L VW E N L VW E N L VW E N I VW Q K I VW Q K</td><td>T DV GCC T DV GCC T DV GCC T D I GCC T D I GCC T D F GCC T D F GCC T H I GCC T H I GCC</td><td>VTDC VTKC VATC VATC VTEC VTDC ITNC VTDC</td><td>P N F P N F P H S P H S K NM P N F T G S R K S</td><td> P Y  P Y  P F  P F  L P  R T  Y S F P Y  P Q F P Y</td><td>G L S I V G L S I V G L S I V K L S I V K L S I V K L S I V G L S V V G L S V V G L S V V G L S V V</td><td>NYG NYG NYG NYG NYG NYG NYG NYG</td><td>P GGNYP G P GGNYP G P GGNYA G P GGCCP - P GGCP - P GGNIL G P GGNIP E P GGNYE G P GGNYE G P GGNYE G P GGNYE G</td><td>147 147 146 146 146 147 147 147 146 140</td></td<>	SmVAL28 SmVAL27 SmVAL5 SmVAL5 SmVAL29* SmVAL9 SmVAL9 SmVAL12 SmVAL12	Smp_176160 Smp_154290 Smp_070250 Smp_336880 Smp_120670 Smp_176180 Smp_123550 Smp_123540 Smp_133680	77 TDIKTGFQL 77 KDIKTGFQS 77 STVEIGFQR 77 STVDIGFQR 76 PRLLIGFKM 77 YTVERAVKL 75 QTIEQAFDA 74 ANVQTAMDE 74 DTIKGCVDA	V L D E Y K N V L D E Y K N V L N E Y K N V L N E Y K N V F D E S Q N V F S E A M Y V K D E Y K Q V N E Y Q Y	Y D F Y T R T ( Y D F Y T R T ( Y D F F N R L ( Y D F F N R L ( Y N Y N T N T ( Y N F N T N T ( Y N F N T N T ( Y N F N T N T ( Y D F D S N T (	R – M G Q Q R – M G Q Q L – V G R Q L – V G R Q I – N N Q Q S – S A T Q S – S A T Q N – S K S Q	GHYTQ GHYTQ GHYTQ SHYTQ SHYTQ THYTQ GNYPQ GNYPQ GNYLQ	L VW E D L VW E D L VW E D I VW E N I VW E N I VW E N L VW E N L VW E N L VW E N I VW Q K I VW Q K	T DV GCC T DV GCC T DV GCC T D I GCC T D I GCC T D F GCC T D F GCC T H I GCC T H I GCC	VTDC VTKC VATC VATC VTEC VTDC ITNC VTDC	P N F P N F P H S P H S K NM P N F T G S R K S	P Y P Y P F P F L P R T Y S F P Y P Q F P Y	G L S I V G L S I V G L S I V K L S I V K L S I V K L S I V G L S V V G L S V V G L S V V G L S V V	NYG NYG NYG NYG NYG NYG NYG NYG	P GGNYP G P GGNYP G P GGNYA G P GGCCP - P GGCP - P GGNIL G P GGNIP E P GGNYE G P GGNYE G P GGNYE G P GGNYE G	147 147 146 146 146 147 147 147 146 140
SIMUAL22       SIMUAL22 <td< td=""><td>SmVAL28 SmVAL27 SmVAL5 SmVAL29* SmVAL9 SmVAL9 SmVAL8 SmVAL12 SmVAL1 SmVAL21</td><td>Smp_176160 Smp_154290 Smp_070250 Smp_136880 Smp_120670 Smp_176180 Smp_123550 Smp_123540 Smp_13540 Smp_193680 Smp_159290</td><td>77 TDIKTGFQL 77 KDIKTGFQS 77 STVEIGFQR 77 STVDIGFQR 76 PRLLIGFKM 77 YTVERAVKL 75 QTIEQAFDA 74 ANVQTAMDE 74 DTIKGCVDA</td><td>V L D E Y K N V L D E Y K N V L N E Y K N V L N E Y K N V F D E S Q N V F S E A M Y V K D E Y K Q V N E Y Q Y</td><td>Y D F Y T R T ( Y D F Y T R T ( Y D F F N R L ( Y D F F N R L ( Y N Y N T N T ( Y N F N T N T ( Y N F N T N T ( Y N F N T N T ( Y D F D S N T (</td><td>R – M G Q Q R – M G Q Q L – V G R Q L – V G R Q I – N N Q Q S – S A T Q S – S A T Q N – S K S Q</td><td>GHYTQ GHYTQ GHYTQ SHYTQ SHYTQ THYTQ GNYPQ GNYPQ GNYLQ</td><td>L VW E D L VW E D L VW E D I VW E N I VW E N I VW E N L VW E N L VW E N L VW E N I VW Q K I VW Q K</td><td>T DV GCC T DV GCC T DV GCC T D I GCC T D I GCC T D F GCC T D F GCC T H I GCC T H I GCC</td><td>VTDC VTKC VATC VATC VTEC VTDC ITNC VTDC</td><td>P N F P N F P H S P H S K NM P N F T G S R K S</td><td> P Y  P Y  P F  P F  L P  R T  Y S F P Y  P Q F P Y</td><td>G L S I V G L S I V G L S I V K L S I V K L S I V K L S I V G L S V V G L S V V G L S V V G L S V V</td><td>NYG NYG NYG NYG NYG NYG NYG NYG</td><td>P GGNYP G P GGNYP G P GGNYA G P GGCCP - P GGCP - P GGNIL G P GGNIP E P GGNYE G P GGNYE G P GGNYE G P GGNYE G</td><td>147 146 146 146 147 147 147 146 140 140</td></td<>	SmVAL28 SmVAL27 SmVAL5 SmVAL29* SmVAL9 SmVAL9 SmVAL8 SmVAL12 SmVAL1 SmVAL21	Smp_176160 Smp_154290 Smp_070250 Smp_136880 Smp_120670 Smp_176180 Smp_123550 Smp_123540 Smp_13540 Smp_193680 Smp_159290	77 TDIKTGFQL 77 KDIKTGFQS 77 STVEIGFQR 77 STVDIGFQR 76 PRLLIGFKM 77 YTVERAVKL 75 QTIEQAFDA 74 ANVQTAMDE 74 DTIKGCVDA	V L D E Y K N V L D E Y K N V L N E Y K N V L N E Y K N V F D E S Q N V F S E A M Y V K D E Y K Q V N E Y Q Y	Y D F Y T R T ( Y D F Y T R T ( Y D F F N R L ( Y D F F N R L ( Y N Y N T N T ( Y N F N T N T ( Y N F N T N T ( Y N F N T N T ( Y D F D S N T (	R – M G Q Q R – M G Q Q L – V G R Q L – V G R Q I – N N Q Q S – S A T Q S – S A T Q N – S K S Q	GHYTQ GHYTQ GHYTQ SHYTQ SHYTQ THYTQ GNYPQ GNYPQ GNYLQ	L VW E D L VW E D L VW E D I VW E N I VW E N I VW E N L VW E N L VW E N L VW E N I VW Q K I VW Q K	T DV GCC T DV GCC T DV GCC T D I GCC T D I GCC T D F GCC T D F GCC T H I GCC T H I GCC	VTDC VTKC VATC VATC VTEC VTDC ITNC VTDC	P N F P N F P H S P H S K NM P N F T G S R K S	P Y P Y P F P F L P R T Y S F P Y P Q F P Y	G L S I V G L S I V G L S I V K L S I V K L S I V K L S I V G L S V V G L S V V G L S V V G L S V V	NYG NYG NYG NYG NYG NYG NYG NYG	P GGNYP G P GGNYP G P GGNYA G P GGCCP - P GGCP - P GGNIL G P GGNIP E P GGNYE G P GGNYE G P GGNYE G P GGNYE G	147 146 146 146 147 147 147 146 140 140
Smv4L20       Smp_127130       79 S DV I NAVE SW FNEYQ LY DFTNNK G EVPEDC HYK R I YWDK Å EFLGC SV GHQ TTHTEVK SQ I I V CY Y SE MGDVKT       153         SmVAL30       Smp_123070       75 R DNK SI FK VW SAKY DHY N G I - V HNC S SY K G LMAY NT R NI AC SI G NG K RQ T NS SI I L CY Y SE LANADN       141         SmVAL30       Smp_123070       78 DNK SI FK VW SAKY DHY N G I - V HNC S SY K G LMAY NT R NI AC SI G LNK C K K R NS SI I L CY Y SE LANADN       141         SmVAL18       Smp_0123070       77 PT I E KAVASW F I EVK NY SF DDNT C K DT CMQY K DW K K E K HI GC G LNK C K K R F L VV CN Y SP A A E E       141         SmVAL18       Smp_002070       77 PT I E GAMK DW L EEY K NY NF E K NQ C NE GC NY K DW WW K G E E F EI GC Q Y E K G K N Y LI V C NY AP G A D       141         SmVAL23       Smp_002070       77 PT I E GAMK DW L EEY K NY NF E KNT C A DY K Q LAFADT TH I GC Q Y AM G F N L T G L DK V F V Q NY CP G G K Y A N       150         SmVAL33       Smp_30070       77 PK V RQ AA S W F EQHK NY NF E NT C E ANTT C A DY K Q LAFADT TH I GC Q Y AM G F N L	SmVAL28 SmVAL27 SmVAL5 SmVAL29* SmVAL9 SmVAL9 SmVAL8 SmVAL12 SmVAL12 SmVAL21	Smp_176160 Smp_176290 Smp_070250 Smp_336880 Smp_120670 Smp_176180 Smp_123550 Smp_123540 Smp_13680 Smp_13680 Smp_159290 Smp_002630	77 T D I K T G F Q L 77 K D I K T G F Q S 77 S T V D I G F Q R 76 P R L L I G F K M 77 Y T V E R A V K L 75 Q T I E Q A F D A 74 A N V Q T A M D E 74 P T I K S G V D A 74 P T I K S G V D A	V L D E Y K N V L D E Y K N V L N E Y K N V F D E S Q N V F D E S Q N V F D E Y K Q V K D E Y K Q V N E Y K Q V N E Y K L V F N E H K L V F N E H K L	Y D F Y T R T ( Y D F Y T R T ( Y D F F NR L ( Y N F NR NT N Y N F NT N I ( Y N Y S K S S Y N Y NT NN Y N Y NT NN Y N Y NT NN	R – M G Q C R – M G Q C L – V G R C L – V G R C S – S A T C S – G V C N – S K S C P – – Q C P – – Q C	GHYTQ GHYTQ GHYTQ SHYTQ SHYTQ GNYPQ GHYTQ GHYTQ LHYTQ LHYTQ	L VWED L VWEDT L VWENT I VWENT I VWENT L IWENT L VWENT L VWENT I VWQNT I VWQKT MAWAKT MAWAKT	T D V G G G T D V G G G T D I G G G T H V G G G T H I G G G T D I G G G	G V T D G V T K G V A T C G V A T C G V T D G V T D G V T D G V T D G V A N G V A N G V A N G V A N G V A N C	P N F – – P H S – – P H S – – K NM – – F N F – – T G S – – R K S – – P R Y – – P R Y – – P R Y – –		G L S I V G L S I V G L S I V K L S I V K L S I V K L S I V G L S I V	NYG NYG NYG NYG NYG NYG NYG NYG NYG NYG	P GGNYP G P GGNYP G P GGNY A G P GGCC P - P GGC C P - P GGN I L G P GGN I E P GGN F D - P GGNWNN P GGNWNN P GGNWNN P GGNWNN	147 146 146 146 147 147 147 146 140 140 140
SmVAL30         Smp_131370         75 RDNK SIFK VW SAK YDHY NG (I-VHNC S SYK QLMAYN RNIAC SIGNCK RQTNS SN IILCY YS SLANADN         141           SmVAL10         Smp_121370         78 DT K NAME NW FREYHNY NY ET DK GNGS G SNYR QLWAAK KH I GC LNK GK RQTK KI I VC NY SF SADDA-         144           SmVAL18         Smp_001890         77 TT I E KAVA SW F E YK NY SF DD NT GKDT GMQ YK MV KG E ET EI GC QVQK G SNR	SmVAL28 SmVAL27 SmVAL5 SmVAL5 SmVAL5 SmVAL9* SmVAL8 SmVAL12 SmVAL12 SmVAL12 SmVAL21 SmVAL22	Smp_176160 Smp_176120 Smp_070250 Smp_336880 Smp_120670 Smp_123550 Smp_123540 Smp_13680 Smp_13680 Smp_13680 Smp_02630 Smp_002630	77 TDIKTGFQL 77 KDIKTGFQS 77 STVDIGFQR 76 PRLIGFQR 77 PTVERAVKLI 75 QTIEQAFDA 74 ANVQTAMDE 74 PTIKSGVDA 74 PTIKSGVDA 74 STIKSAVDA	V L D E Y K N V L D E Y K N V L N E Y K N V F D E S Q N V F S E AMY V K D E Y K Q V N E Y Q Y V F N E H K L V F N E H K L V F N E H K L	Y D F Y T R T G Y D F Y T R T G Y D F F NR L G Y N Y NT NT N Y N Y NT N Y N Y NY S K S Y D F D S NT Y N Y NT NN Y N Y NT NN Y NY N NN NN Y N F S V NN	R – MGQC R – MGQC L – VGRC L – VGRC S – SATC S – GVC N – SKSC P – – QC P – – QC P – – QC P – – QC	GHYTQ GHYTQ SHYTQ SHYTQ SHYTQ GHYTQ GHYTQ GHYTQ CHYTQ LHYTQ LHYTQ LHYTQ	L VWED L VWEDT I VWENT I VWENT L IWENT L VWENT L VWENT I VWQKT MAWAKT MAWAKT MAWAKT	T D V G G G T D V G G G T D I G G G	G V T D C G V T K C G V A T C G V A T C G V T D C G V T D C G V T D C G V A N C G V A N C G V A N C	P N F P N F P H S K NM P N F T G S R K S P R Y P R Y P R Y S M Y		G L S I V G G L S I V G K L S I V G K L S I V G K L V I V G G L S I V G	N Y G N Y G	P GGNY P G P GGNY P G P GGNY P G P GGCC P - P GGCC P - P GGNI L G P GGNY EG P GGNY EG P GGNY EG P GGNWNN P GGNWNN P GGNWNN P GGNWNN P GGNWNN	147 146 146 146 147 147 146 140 140 140 140
SmVAL19 <i>Smp</i> _123090       78 DT I K NAME NW FREY H NY NY ET DK GN GS SNY R DWWAK K K H LGC L NK GK K R	SmVAL28 SmVAL27 SmVAL5 SmVAL5 SmVAL5 SmVAL9* SmVAL8 SmVAL12 SmVAL12 SmVAL12 SmVAL21 SmVAL22 SmVAL24 SmVAL24	Smp_176160 Smp_176290 Smp_070250 Smp_336880 Smp_126670 Smp_176180 Smp_123550 Smp_123540 Smp_13680 Smp_13680 Smp_139450 Smp_002630 Smp_002630 Smp_078490	77 TD I K TG FQ LL 77 KD I K TG FQ SI 77 ST VE I G FQ R 77 ST VE I G FQ R 76 PR LL I G FK M 77 YT V ER A VK LL 75 QT I EQ A FD A 74 A N VQ TA M DE I 74 PT I K S G VD A 74 PT I K S G VD A 74 PT I K S G VD A 74 ST I K S A VD A 74 ST I K S A VD A	V L D E Y K N V L D E Y K N V L N E Y K N V F D E SQ N V F D E SQ N V F S E AMY V K E Y K N V N E Y Q Y V N E Y Q Y V N E Y K L V F N E H K L V F N E H K L	Y D F Y T R T G Y D F Y T R T G Y D F F N R L G Y N Y N T N T G Y N F N T N T Y N F N T N T Y N Y N T N N Y N Y N T N N Y N F S V N N Y N Y S V N N	R – MGQC R – MGQC L – VGRC L – VGRC S – SATC S – GVC S – GVC P – – QC P – – QC	GHYTQ GHYTQ SHYTQ SHYTQ SHYTQ GNYPQ GNYPQ GHYTQ LHYTQ LHYTQ LHYTQ LHYTQ VHYKQ	L VW ED L VW ED I VW EN I VW EN I VW EN L I WEN L VW EN L VW EN I VWQ K MAWAK MAWAK MAWAK MAWAK MAWAK		V T D V T K V A T C V A T C V T D V T D V T D V A N V	P N F P N F P H S K N M P N F T G S R K S P R Y P R Y P R Y Q R Y		G L S I V 0 G L S I V 0 K L S I V 0 K L S I V 0 K L S I V 0 G L S I V 0	NYG NYG NYG NYG NYG NYG NYG NYG NYG NYG	P GGNYP G P GGNYP G P GGNY A G P GGCCP - P GGCCP - P GGNI L G P GGNI P E P GGNY E G P GGNWNN P GGNWNN P GGNWNN P GGNWI N	147 146 146 146 147 147 147 146 140 140 140 140
SmVAL19 <i>Smp</i> _123090       78 DT I K NAME NW FREY H NY NY ET DK GN GS SNY R DWWAK K K H LGC L NK GK K R	SmVAL28 SmVAL27 SmVAL5 SmVAL5 SmVAL9* SmVAL8 SmVAL8 SmVAL2 SmVAL12 SmVAL12 SmVAL21 SmVAL21 SmVAL24 SmVAL24	Smp_176160 Smp_176160 Smp_070250 Smp_336880 Smp_120670 Smp_120670 Smp_123550 Smp_123550 Smp_13680 Smp_13680 Smp_026630 Smp_078490 Smp_078490 Smp_078490	77 TD I K TG FQ L 77 KD I K TG FQ S 77 ST VE I G FQ R 77 ST VE I G FQ R 76 P R L I G FQ R 77 T V F R A V K L 75 Q T I E Q A F D A 74 A N VQ T A M D E 74 P T I K S G V D A 74 P T I K S G V D A 74 ST I K S A V D A 74 ST I K S A V D A 75 SD V I N A V E S	V L D E Y K N V L D E Y K N V L N E Y K N V F D E S Q N V F D E S Q N V F S E A M Y V K E Y K N V F N E H K L V F N E H K L	Y D F Y T R T G Y D F Y T R T G Y D F F N R L Y N Y N T N T N Y N F N T N T Y N Y N S K S Y N Y N T N N Y N Y N M N N Y N Y S V N N Y N F S V N N Y N Y S V N N Y D F T N K	R – MGQ R – MGQ L – VGR L – VGR S – SAT S – SAT S – GV P – – QC P – – QC	GHYTQ GHYTQ GHYTQ SHYTQ SHYTQ SHYTQ GHYTQ GHYTQ GHYTQ LHYTQ LHYTQ LHYTQ LHYTQ LHYTQ LHYK <u>R</u>	L VW E D T L VW E D T I VW E D T I VW E N T L VW E N T L VW E N T L VW E N T L VW Q N T I VW Q K T MAWAK T MAWAK T MAWAK T MVWAK T I VW D K A	T D V G G T D V G G T D V G G T D I G G E F I G G	SVTDC SVTKC SVATC SVTEC SVTEC SVTDC SVTDC SVANC SVANC SVANC SVANC SVANC SVANC SVANC	P N F P N F P H S P H S P H S P N F T G S T G S T G S T G S P R Y P R Y P R Y P R Y P R Y P R Y Q R Y Q R Y N T H		G L S I V G L S I V G L S I V K L S I V K L S I V K L S I V G L S I V S	NYG NYG NYG NYG NYG NYG NYG NYG NYG NYG	P GGNYP G P GGNYP G P GGNYAG P GGCCP - P GGCCP - P GGNILG P GGNYEG P GGNYEG P GGNWNN P GGNWNN P GGNWIN P GGNWIN P GGNWIN	147 146 146 146 147 147 146 140 140 140 140 140
SmVAL10       Smp_002060       77 T S I Q N I LD T W L E E K ND Y D LD K NT G E - N E G C N Y K D L VWA NT T D I G G A S N K G C N R Y M V V Q N Y A F G A D 140       141         SmVAL3       Smp_02070       77 P T I E G A K ND V E E Y K Q M Y N F E K ND Q N - G D G K N Y K D L V A M G D T H I G G Y A M G F N L T G LD K V F V Y G N Y G F G G K Y A N       150         SmVAL3       Smp_00000       77 P K V RQ A A S V W F E Q H K N Y N F E N NT G E A N K T G A D Y K D L A F A D T H I G G Y A M G F N L T G LD K V F V Y G N Y G P G K Y A N       150         SmVAL3       Smp_00000       77 P K V RQ A A S V W F E Q H K N Y N F E N NT G E A N K T G A D Y K D L A F A D T H I G G Y A M G F N L T G LD K V F V Y G N Y G P G K Y A N       150         SmVAL3       Smp_00000       77 S E LA G A V A Y W E E S N I Y K H NT D S G S T F E C N S Y K D I V Q A E T A Y V G G G F T R G R Q Y E Y P S N M L I A G Y S F K V K S       148         SmVAL33       Smp_116750       77 S E LA G A V A Y W E E S N Y Y H H N S D L G S S T F E C N S Y K D I V Q A E T A Y V G G G T R C R Q Y E Y P S N M L I A G Y S F K V K S       148         SmVAL34       Smp_1141550       77 S E LA G A V A Y W K E S N Y D H N S D L G E P S H H G N T Y K D I V Q A E T A Y Y G G G Y T R G E Y E Y P S N M L I A G Y S F K V K S       148         SmVAL34       Smp_1141507       77 S E L A G A V A Y W K E S N Y D H N S D L G E P S H H G N T Y K D I V Q A E A Y Y G G G Y T R G E Y E Y P S N M L I A G Y S F K V K S       148         SmVAL35	SmVAL28 SmVAL27 SmVAL5 SmVAL5 SmVAL9* SmVAL8 SmVAL8 SmVAL2 SmVAL12 SmVAL12 SmVAL21 SmVAL21 SmVAL24 SmVAL24	Smp_176160 Smp_176160 Smp_070250 Smp_336880 Smp_120670 Smp_120670 Smp_123550 Smp_123550 Smp_13680 Smp_13680 Smp_026630 Smp_078490 Smp_078490 Smp_078490	77 TD I KTGFQL 77 KDI KTGFQS 77 STVEI GFQR 77 STVEI GFQR 77 STVEI GFQR 77 STVEI GFQR 74 PT U EQAFDA 74 ANVQT AMDE 74 PT I KSGVDA 74 PT I KSGVDA 74 STI KSAVDA 74 STI KSAVDA 75 STDNKS I FKV	V L D E Y K N V L D E Y K N V L N E Y K N V F D E S Q N V F D E S Q N V F D E S Q N V F D E Y K Q V V N E Y Q Y V F N E H K L V S A K Y D H	Y D F Y T R T Y D F Y T R T Y D F F N R L Y N Y N T N T Y N Y N T N T Y N Y Y S K S Y D F D S N T Y N Y N T N N Y N Y N T N N Y N Y N T N N Y N F S V N N	R - M G Q C R - M G Q C R - M G Q C L - V G R C L - V G R C S - S A T C S - S A T C S - S A T C P Q C I - N K S P Q C P Q C P Q C I - V F E D C I - V H N C	GHYTQ GHYTQ GHYTQ SHYTQ SHYTQ GNYTQ GNYTQ GNYLQ GHYTQ LHYTQ LHYTQ LHYTQ LHYTQ LHYTQ LHYTQ LHYKQ LHYKR	L VWE DT L VWE DT I VWE NT I VWE NT I VWE NT L IWE NT L VWE NT L VWE NT VWQ KT MAWAKT MAWAKT MVWAKT I VWD KA L VWD KA	T D V G C T D V G C T D V G C T D I	SVTD SVTKC SVATC SVATC SVTC SVTD SVTD SVTD SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC	P N F P N F P H S P H S P H S P N F F N F F N F Y F N Y - F N	PY PY PF PF RT RT 	GLSIV GLSIV KLSIV KLSIV KLSIV GLSVV GLSVV GLSVV GLSIV GLSVV GLSIV GLSVV GLSIV GLSVV GLSIV	NYG NYG NYG NYG NYG NYG NYG NYG NYG NYG	P GGNYP G P GGNYP G P GGNYP G P GGCCP - P GGCCP - P GGNIP E P GGNIP E P GGNYEG P GGNWNN P GGNWNN P GGNWNN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN	147 146 146 146 147 147 146 140 140 140 140 140
SmVAL10       Smp_002060       77 T S I Q N I LD T W L E E K ND Y D LD K NT G E - N E G C N Y K D L VWA NT T D I G G A S N K G C N R Y M V V Q N Y A F G A D 140       141         SmVAL3       Smp_02070       77 P T I E G A K ND V E E Y K Q M Y N F E K ND Q N - G D G K N Y K D L V A M G D T H I G G Y A M G F N L T G LD K V F V Y G N Y G F G G K Y A N       150         SmVAL3       Smp_00000       77 P K V RQ A A S V W F E Q H K N Y N F E N NT G E A N K T G A D Y K D L A F A D T H I G G Y A M G F N L T G LD K V F V Y G N Y G P G K Y A N       150         SmVAL3       Smp_00000       77 P K V RQ A A S V W F E Q H K N Y N F E N NT G E A N K T G A D Y K D L A F A D T H I G G Y A M G F N L T G LD K V F V Y G N Y G P G K Y A N       150         SmVAL3       Smp_00000       77 S E LA G A V A Y W E E S N I Y K H NT D S G S T F E C N S Y K D I V Q A E T A Y V G G G F T R G R Q Y E Y P S N M L I A G Y S F K V K S       148         SmVAL33       Smp_116750       77 S E LA G A V A Y W E E S N Y Y H H N S D L G S S T F E C N S Y K D I V Q A E T A Y V G G G T R C R Q Y E Y P S N M L I A G Y S F K V K S       148         SmVAL34       Smp_1141550       77 S E LA G A V A Y W K E S N Y D H N S D L G E P S H H G N T Y K D I V Q A E T A Y Y G G G Y T R G E Y E Y P S N M L I A G Y S F K V K S       148         SmVAL34       Smp_1141507       77 S E L A G A V A Y W K E S N Y D H N S D L G E P S H H G N T Y K D I V Q A E A Y Y G G G Y T R G E Y E Y P S N M L I A G Y S F K V K S       148         SmVAL35	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL5 SmVAL29* SmVAL5 SmVAL29 SmVAL2 SmVAL12 SmVAL21 SmVAL21 SmVAL22 SmVAL24 SmVAL20 SmVAL30	5mp_176160 5mp_176290 5mp_070250 5mp_336880 5mp_12670 5mp_12670 5mp_12550 5mp_123540 5mp_13680 5mp_13680 5mp_139450 5mp_002630 5mp_078490 5mp_127130 5mp_127130	77 TD I KTGFQL 77 KDI KTGFQS 77 STVEI GFQR 77 STVEI GFQR 77 STVEI GFQR 77 STVEI GFQR 74 PT U EQAFDA 74 ANVQT AMDE 74 PT I KSGVDA 74 PT I KSGVDA 74 STI KSAVDA 74 STI KSAVDA 75 STDNKS I FKV	V L D E Y K N V L D E Y K N V L N E Y K N V F D E S Q N V F D E S Q N V F D E S Q N V F D E Y K Q V V N E Y Q Y V F N E H K L V S A K Y D H	Y D F Y T R T Y D F Y T R T Y D F F N R L Y N Y N T N T Y N Y N T N T Y N Y Y S K S Y D F D S N T Y N Y N T N N Y N Y N T N N Y N Y N T N N Y N F S V N N	R - M G Q C R - M G Q C R - M G Q C L - V G R C L - V G R C S - S A T C S - S A T C S - S A T C P Q C I - N K S P Q C P Q C P Q C I - V F E D C I - V H N C	GHYTQ GHYTQ GHYTQ SHYTQ SHYTQ GNYTQ GNYTQ GNYLQ GHYTQ LHYTQ LHYTQ LHYTQ LHYTQ LHYTQ LHYTQ LHYKQ LHYKR	L VWE DT L VWE DT I VWE NT I VWE NT I VWE NT L IWE NT L VWE NT L VWE NT VWQ KT MAWAKT MAWAKT MVWAKT I VWD KA L VWD KA	T D V G C T D V G C T D V G C T D I	SVTD SVTKC SVATC SVATC SVTC SVTD SVTD SVTD SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC	P N F P N F P H S P H S P H S P N F F N F F N F Y F N Y - F N	PY PY PF PF RT RT 	GLSIV GLSIV KLSIV KLSIV KLSIV GLSVV GLSVV GLSVV GLSIV GLSVV GLSIV GLSVV GLSIV GLSVV GLSIV	NYG NYG NYG NYG NYG NYG NYG NYG NYG NYG	P GGNYP G P GGNYP G P GGNYP G P GGCCP - P GGCCP - P GGNIP E P GGNIP E P GGNYEG P GGNWNN P GGNWNN P GGNWNN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN	147 146 146 146 147 147 147 140 140 140 140 153 141
SmvAl4       Smp_002070       77 PT IEGAMK DW LEEYK NY NFEK NQQ N - COCK NY K DW WWT TEEL GC Y EK GCK N Y LIV CNY AP GD S 140         SmvAL3       Smp_30080       77 PK VRQAA S W FEQHK NY NFENNT GEANKT GADY K DLAFAD THIGC Y AM GFNL T GLDK VFV CNY GP GG KY AN       150         SmVAL3       Smp_30080       77 PK VRQAA S W FEQHK NY NFENNT GEANKT GADY K DLAFAD THIGC Y AM GFNL T GLDK VFV CNY GP GG KY AN       150         SmVAL3       Smp_30080       77 PK VRQAA S W FEQHK NY NFENNT GEANKT GADY K DLAFAD THIGG Y AM GFNL T GLDK VFV CNY GP GG KY AN       150         SmVAL3       Smp_316760       77 SELAGAVAY WM EESNIY K MNT DS GST FECN SYK DLVQA ET AY VGC GFTR GRQY EYP S NMLIA CYY SFK VK S       148         SmVAL33       Smp_313710       77 SELAGAVAY WM EESNIY K MNT DS GST FECN SYK DLVQA ET AY VGC GFTR GRQY EYP S NMLIA CYY SFK VK S       148         SmVAL34       Smp_114550       77 SELAGAVAY WM EESNIY DHN SDL GEYS FH GN SYK DLVQA ET AY VGC GFTR GRQY EYP S NMLIA CYY SFK VK S       148         SmVAL34       Smp_114500       77 SELAGAVAY WM KESNY DHN SDL GEP SHHCN TYK DLVQA ET AY VGC GYTR GEEY EYP S NMLIA CYY SFK VK S       148         SmVAL34       Smp_31750       77 SELAGAVAY WM KESNY DHN SDL GEP SHHCN TYK DLVQA ET AY VGC GYTR GEEY EYP S NMLIA CYY SFK WM S       148         SmVAL34       Smp_31750       77 SS V ND A NV W DG SR FYN LK ND E CYN NH DG SMY KOL VD IN T T HIGCG VHL GR V KN E	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL29* SmVAL8 SmVAL8 SmVAL12 SmVAL11 SmVAL22 SmVAL22 SmVAL20 SmVAL20 SmVAL30 SmVAL30	Smp_176160 Smp_176160 Smp_070250 Smp_336880 Smp_120670 Smp_123550 Smp_123550 Smp_123550 Smp_123540 Smp_159290 Smp_078490 Smp_127130 Smp_127130 Smp_123090	77 TD I KTGFQL 77 KDI KTGFQS 77 STVEI GFQR 77 STVEI GFQR 77 STVEI GFQR 77 STVEI GFQR 74 PT U EQAFDA 74 ANVQT AMDE 74 PT I KSGVDA 74 PT I KSGVDA 74 STI KSAVDA 74 STI KSAVDA 75 STDNKS I FKV	V L D E Y K N V L D E Y K N V L N E Y K N V F D E S Q N V F D E S Q N V F D E S Q N V F D E Y K Q V V N E Y Q Y V F N E H K L V S A K Y D H	Y D F Y T R T Y D F Y T R T Y D F F N R L Y N Y N T N T Y N Y N T N T Y N Y Y S K S Y D F D S N T Y N Y N T N N Y N Y N T N N Y N Y N T N N Y N F S V N N	R - M G Q C R - M G Q C R - M G Q C L - V G R C L - V G R C S - S A T C S - S A T C S - S A T C P Q C I - N K S P Q C P Q C P Q C I - V F E D C I - V H N C	GHYTQ GHYTQ GHYTQ SHYTQ SHYTQ GNYTQ GNYTQ GNYLQ GHYTQ LHYTQ LHYTQ LHYTQ LHYTQ LHYTQ LHYTQ LHYKQ LHYKR	L VWE DT L VWE DT I VWE NT I VWE NT I VWE NT L IWE NT L VWE NT L VWE NT VWQ KT MAWAKT MAWAKT MVWAKT I VWD KA L VWD KA	T D V G C T D V G C T D V G C T D I	SVTD SVTKC SVATC SVATC SVTC SVTD SVTD SVTD SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC SVANC	P N F P N F P H S P H S P H S P N F F N F F N F Y F N Y - F N	PY PY PF PF RT RT 	GLSIV GLSIV KLSIV KLSIV KLSIV GLSVV GLSVV GLSVV GLSIV GLSVV GLSIV GLSVV GLSIV GLSVV GLSIV	NYG NYG NYG NYG NYG NYG NYG NYG NYG NYG	P GGNYP G P GGNYP G P GGNYP G P GGCCP - P GGCCP - P GGNIP E P GGNIP E P GGNYEG P GGNWNN P GGNWNN P GGNWNN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN	147 146 146 147 147 147 146 140 140 140 140 153 141 144
SmVAL7         Smp_30070         77 PKVRQAASVW FEQHKNYN FENNT CEANKTCADYK DLAFAD THIGC YAMCFNLTGLDKVFVVCNYCPG GGKYAN         150           SmVAL32         Smp_30080         77 PKVRQAASVW FEQHKNYN FENNT CEANKTCADYK DLAFAD THIGC YAMCFNLTGLDKVFVVCNYCPG GGKYAN         150           SmVAL32         Smp_316760         77 SELAGAVAYWMEESNIYKHNT DGSSTFECNSYKOIVQAETAYV GGGTRK RQYEYPSNMLIACYYS FKVKS         148           SmVAL33         Smp_160250         77 SELAGAVAYWMEESNIYKHNT DSGSSTFECNSYKOIVQAETAYV GGGTRK RQYEYPSNMLIACYYS FKVKS         148           SmVAL33         Smp_1160250         77 SELAGAVAYWMEESNIYKHNT DSGSSTFECNSYKOIVQAETAYV GGGTRR RQYEYPSNMLIACYYS FKVKS         148           SmVAL34         Smp_115050         77 SELAGAVAYWMEESNIYCHNSDLGESSTFECNSYKOIVQAETAYV GGGYTR GEEYEYPSNMLIACYYS FKVKS         148           SmVAL34         Smp_141550         77 SELAGAVAYWMESNYDHNSDLGESSTFECNSYKOIVQAETAYV GGYTR GEEYEYPSNMLIACYYS FKVMS         148           SmVAL34         Smp_317520         77 SELAGAVAYWMESNYDHNSDLGEPSHHCNTYKOIVEAOTAYV GGYTR GEEYEYPSNMLVACYYS FKVMS         148           SmVAL35         Smp_347320         77 SEVAAVWMEDSSNYDUDGSMYKOUVNINGLVAINTHIGGVHLCNKNTNKGKYUVVGNYA AAG         147           SmVAL35         Smp_347320         77 SSINDAINVWRDGSR FYNLKNDECXNNNKOUVNINTHIGGVHLCNKNTNKGKYUVVGNYA AAG         147           SmVAL35         Smp_247600         68 MTGARATRWYDEIHYNFNKKYK FNSEP	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL9* SmVAL9 SmVAL9 SmVAL9 SmVAL12 SmVAL12 SmVAL12 SmVAL12 SmVAL12 SmVAL10 SmVAL10 SmVAL10	Smp_176160 Smp_176290 Smp_070250 Smp_336880 Smp_12670 Smp_176180 Smp_123540 Smp_123540 Smp_139680 Smp_139290 Smp_02630 Smp_139450 Smp_139450 Smp_131450 Smp_131370 Smp_131370 Smp_131370 Smp_131370 Smp_123090 Smp_0390	77 TD I KTGFQL 77 KD I KTGFQS 77 STVEI GFQR 77 STVEI GFQR 77 STVEI GFQR 77 STVEI GFKM 77 YTVERAVKL 75 QT I EQAFDA 74 ANVQT AMDE 74 PT I KSGVDA 74 PT I KSGVDA 74 ST I KSGVDA 74 ST I KSGVDA 75 STDNS VEN 75 STDNS I FKV 78 DT I KNAMEN 78 DT I KNAMEN 77 PT I EKAVAS	V L D E Y K N V L D E Y K N V L N E Y K N V F S E AMY V F S E AMY V F S E AMY V F N E HK L V F N E Y L V F N E Y L V F N E Y K N	Y D F Y T R T Y D F Y T R T Y D F F NR L Y N F NT N I Y N F NT N I Y N F NT N Y N Y NT NN Y NY NT NN Y NY NT NN Y NY S V NN Y NY S V NN Y NY S V NN Y N ( Y S F D D NT	R - M G Q C R - M G Q C R - M G Q C R - M G Q C I - V G R C I - V G R C I - V G R C I - N N Q C S - G Y C P Q C P	GHYTQ GHYTQ GHYTQ SHYTQ SHYTQ GNYPQ GHYTQ GNYPQ GHYTQ LHYTQ LHYTQ LHYTQ LHYTQ LHYTQ SNYRQ SNYRQ MQYKQ	L VWE DT L VWE DT L VWE DT I VWE NT L I WE NT L IWE NT L VWE NT I VWE NT I VWE KT MAWAK T WWA KT I VWE KT I VWE KT	T D V G C T D V G C T D V G C T D I G C C C T D I G C C C C C C C C C C C C C C C C C C	S V T D C S V T K C S V A T C S V A T C S V T D C S V T D C S V T D C S V T D C S V A N C S V C H C S V C H C S V C H C S V C K C	P N F P N F P N F P H S P H S P N F P N F T G S T G S T G S T G S T G S T G S T G S T G S T G S T G S T G S T G S T G S T G S		G L S I V G L S I V G L S I V K L S I V K L S I V G L S V V G L S V V G L S I V C S I S I S I S I S I S I S I S I S I S	NYG NYG NYG NYG NYG NYG NYG NYG NYG NYG	P GGNYP G P GGNYP G P GGNYP G P GGCCP - P GGCCP - P GGNIP E P GGNYEG P GGNYEG P GGNWNN P GGNWNN P GGNWIN P GGNUN P G GNUN P G GN	147 147 146 146 146 147 147 146 140 140 140 140 140 140 144 141
SmvAL32         Smp_30080         77 PK VRQAAS VW FEQHKNYN PENNT CEANTK CADYK DLAFAD TH ICC QYAMC FNL FGLDKV FVV CNV CP CGKYAN         150           SmvAL33         Smp_316760         77 SELAGAVAY WEESNIYK HNDSC SSTFECNSYK DIVQAETAVV GCG FTRCRQY EYP SNMLIACYYS FKVK S         148           SmVAL33         Smp_316760         77 SELAGAVAY WEESNIYK HNDSC SSTFECNSYK DIVQAETAVV GCG FTRCRQY EYP SNMLIACYYS FKVK S         148           SmVAL33         Smp_313710         77 SELAGAVAY WEESNIYK HNDSC SSTFECNSYK DIVQAETAVV GCG FTRCRQY EYP SNMLIACYYS FKVK S         148           SmVAL33         Smp_313710         77 SELAGAVAY WEESNIY KHNTDSC SSTFECNSYK DIVQAETAVV GCG FTRCRQY EYP SNMLIACYYS FKVK S         148           SmVAL34         Smp_141560         77 SELAGAVAY WEESNIY DHNSDLC EP SHHONTYK DIVCACTAVY GCYTRCEEY EYP SNMLIACYYS FKVK S         148           SmVAL34         Smp_31750         77 SELAGAVAY WKESNYY DHNSDLC EP SHHONTYK DI VCACTAVY GCYTRCEEY EYP SNMLIACYYS FKVK S         148           SmVAL34         Smp_31750         77 SELAEAVAY WKESNYY DHNSDLC EP SHHONTYK DI VCACTAVY GCYTRCEEY EYP SNMLVACYY SFKVK S         148           SmVAL35         Smp_31750         77 SEV DA INVWR DGS RFYNLK NDEC VNLVDINT HI UCCY VHLCAK N EYP SNMLVACYY SFK WS S         148           SmVAL35         Smp_31720         77 SS VI DA INVWR DGS RFYNLK NDEC VNLVOINT HI UCCY VHLCAK N EYP SNMLVACYY SFK WS S         148           SmVAL35	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL9* SmVAL9* SmVAL29* SmVAL2 SmVAL12 SmVAL22 SmVAL22 SmVAL22 SmVAL24 SmVAL20 SmVAL14 SmVAL20 SmVAL19 SmVAL19 SmVAL19	Smp_176160           Smp_176160           Smp_070250           Smp_336880           Smp_120670           Smp_123550           Smp_13580           Smp_13580           Smp_132540           Smp_139680           Smp_139450           Smp_129450           Smp_127130           Smp_123090           Smp_123090           Smp_001890           Smp_012800	77 TD I K TG FOL 77 KD I K TG FOS 77 ST VE I G FOR 77 ST VE I G FOR 77 ST VE I G FOR 77 YT VE RAVK L 75 QT I E QAFDA 74 ANVQ TAMDE 74 PT I K SG VDA 74 PT I K SG VDA 74 ST I K SAVDA 74 ST I K SAVDA 75 ST K SK SV 75 ST K SK SI FK V 78 DT I K KAMEN 77 T SI QN I LDT	V L D E Y K N V L D E Y K N V L N E Y K N V F D E S Q N V F D E S Q N V K D E Y K Q V F N E H K L V F N E Y Q H V F N E Y H N V F R E Y H N V F R E Y H N V F I E Y K N	Y D F Y T R T Y D F Y T R T Y D F F NR L Y N F N T N I Y N F NT N I Y N Y N Y S K S Y D F D S NT Y N Y N T NN Y N Y N T NN Y N Y S V NN Y N F S V NN Y N F S V NN Y D F T N K Y D F T N K Y N Y E T D K Y N Y E T D K Y S U D L D K N T	R – MGQC R – MGQC R – MGQC R – MGQC L – VGRC L – VGRC S – SATC S – SATC S – SATC P – – QC P – – – QC P – – QC P – – – P – – QC P – – – QC P – – – P – – QC P – – – P – – – QC P – – – – QC P – – – – QC P – – – – – – – – – – – – – – – – – – –	GHYTQ GHYTQ GHYTQ SHYTQ SHYTQ GNYLQ GNYLQ LHYTQ LHYTQ LHYTQ LHYTQ LHYTQ LHYTQ LHYTQ LHYKQ SNYRQ SNYRQ GNYKQ GNYKQ	L VWE DT L VWE DT I VWE NT I VWE NT I VWE NT L VWE NT L VWE NT I VWE NT VWWA KT WVWA KT I VWE AK I VWE NT I VWE AK L WA NT	T D V G G T D V G G T D V G G T D I G G K H I G G K H I G G G	V T D V T K C V T K C V T T C V T T C V T D V T D V T D V T D V T D V T D V A NC V A NC V A NC V A NC V A NC S V A NC S	P N F P N F P H S P H S F N F F N F N F F N F N F F N F N F F N F N F N F F N F N F N F N F N F N F N F N F N F N		G L S I V G G L S I V G G L S I V G K L S I V G K L S I V G G L S I V G S N I I L G S G S N I L	Y G NY G NY G NY G NY G NY G NY G NY G N	P GGNYP G P GGNYP G P GGNYP G P GGCCP - P GGCCP - P GGCNIP E P GGNYEG P GGNYEG P GGNWNN P GGNWNN P GGNWNN P GGNWIN P GGNUN P G P GGNUN P G P G P G P G P G P G P G P G P G P G	147 146 146 146 147 147 147 147 140 140 140 140 140 153 141 144 141
SmvAl3         Smp_316760         77 SELAGAVAY WMEESNIY KHNTDS GSTFEGNSYK DIVQAE AYV GCG FTR GRQYEYP SNMLIA GYY SEKVK S         148           SmvAl33         Smp_160250         77 SELAGAVAY WMEESNIY KHNTDS GSTFEGNSYK DIVQAE AYV GCG FTR GRQYEYP SNMLIA GYY SEKVK S         148           SmVAL33         Smp_13710         77 SELAGAVAY WMEESNIY KHNTDS GSTFEGNSYK DIVQAE AYV GCG FTR GRQYEYP SNMLIA GYY SEKVK S         148           SmVAL24         Smp_131710         77 SELAGAVAY WMEESNIY KHNTDS GSTFEGNSYK DIVQAE AYV GCG FTR GRQYEYP SNMLIA GYY SEKVK S         148           SmVAL24         Smp_141550         77 SELAGAVAY WMEESNIY DHNSDL GEP SHHGNTYK DIVQAE AYV GCG YTR GEEYEYP SNMLIA GYY SEKVM S         148           SmVAL34         Smp_141500         77 SELAGAVAY WMKESNY DHNSDL GEP SHHGNTYK DIVQAE AYV GCG YTR GEEYEYP SNMLIA GYY SEKVM S         148           SmVAL34         Smp_317520         77 SELAGAVAY WMKESNY DHNSDL GEP SHHGNTYK DIVQAE AYV GCG YTR GEEYEYP SNMLIA GYY SEKVM S         148           SmVAL35         Smp_317520         77 SS YND A NVWR DG SR FYN LKNDE GV NN DG SMYK DIVD IN TH I GCG YHL GAKN TNK GKY I VY GNY AP AAG         147           SmVAL35         Smp_23720         77 SS INDA I NVWR DG SR FYN LKNDE GK ANY DG SMYK DIVD IN TH I GCG YHL GAKN TNK GKYM V GNY AP AAG         147           SmVAL35         Smp_2124060         68 MTGARATR NWY DEI HY HN FNK SK CO SG FTR CI W SS SER I GW GI AL O SYK SEED LHKD SKM I L V C L YH P G KY SE	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL9* SmVAL9 SmVAL9 SmVAL2 SmVAL12 SmVAL12 SmVAL12 SmVAL21 SmVAL20 SmVAL20 SmVAL20 SmVAL19 SmVAL19 SmVAL10 SmVAL10	Smp_176160 Smp_176160 Smp_070250 Smp_336880 Smp_120670 Smp_123550 Smp_123550 Smp_123550 Smp_13540 Smp_13680 Smp_078490 Smp_078490 Smp_127130 Smp_123130 Smp_123130 Smp_01890 Smp_002060 Smp_002070	77 TD I K TG FQL 77 KD I K TG FQS 77 ST VE I GFQR 77 ST VE I GFQR 77 ST VE I GFQR 77 YT VE RAVKL 75 QT I EQAFDA 74 ANVQT AMDE 74 ANVQT AMDE 74 PT I K SGVDA 74 PT I K SGVDA 74 ST I K SAVDA 75 SD I NAVES 75 RDNK SI FKV 75 DT I KAMEN 77 TI EKAVAS 77 TI EKAVAS	V L D E Y K N V L D E Y K N V L N E Y K N V L N E Y K N V F S L S N V F S L S N V F S L S N V F N E H K L V F N E Y K N V F I E Y K N V L E E Y K N V V L E E Y K N V	Y D F Y T R T Y D F F N R L Y D F F N R L Y N F N T N I Y N F N T N I Y N Y N T N N Y N Y S V N Y N Y S V N Y N Y S T N K Y N Y S S N S N K Y N Y S S N S N S N S N S N S N S N S N	R - M G Q C R - M G Q C R - M G Q C R - M G Q C I - V G R C I - V G R C I - N N Q C S - G V C N - S K S C P Q C P Q C P Q C P Q C I - V H N C I - V H N C K - C T C K - C T C E - P C C K - C T C K - C T C K - C T C C - C C C C C - C C C C C - C C C C C - C C C C C - C C C C C C - C C C C C C - C C C C C C C - C C C C C C C C C - C C C C C C C C C C C - C C C C C C C C C C C C C C C C C C	GHYTQ GHYTQ SHYTQ SHYTQ SHYTQ GNYPQ GNYPQ GNYPQ LHYTQ LHYTQ LHYTQ LHYTQ LHYKR SSNYRQ SSNYRQ SNYRQ GNYKQ GNYKQ	L VWE DT L VWE DT L VWE DT I VWE NT L I WE NT L I WE NT L I WE NT L VWE NT I VWE NT I VWE NT NAWAK T MAWAK T MAWAK T MVWAK T I VWDKA LMAY NT MVWAK I VWDKA LMAY NT MVWAK MVWAK	T D V G G T D V G G T D V G G T D I G G G T D I G G T D I G G G G G G G G G G G G G G G G G G	V T D         V           V T K C         V T K C           V T K C         V T C           V T C         V T C           V T D         V T C           V T D         V T C           V T D         V T D           V T D         V T D           V T D         V T D           V T D         V T D           V T D         V T D           V A NC         V A NC           S V A NC<	P N F P N F P N F P H S K N M P H S K N M P N Y P R Y P R Y P R Y S M Y S M Y S M Y S M Y S M Y S M Y K K K R S M Y K K K R S M Y K K K R S M Y K K K R S M Y K K K R S M Y K K K R S M Y K K K R S M Y K K K R S M Y K K K R S M Y K K K R S M Y		G L S I V G G L S I V G G L S I V G K L S I V G K L S I V G K L V I V G G L S I V G C S I V G S I V G S I V G C S I V G S I V G S I V G S I V G	Y G G N Y G G N Y G G N Y G G N Y Y G G N Y Y G G N Y Y G N Y Y Y S N Y Y Y Y Y Y X Y Y Y Y X X N Y Y Y Y X X Y Y Y Y X X X Y Y Y Y X X X Y Y Y X X X Y Y Y X X X X X X Y Y Y X	P GGNYP G P GGNYP G P GGNYAG P GGCP – P GGCCP – P GGCN I L P GGNYEG P GGNYEG P GGNWNN P GGNWNN P GGNWIN P GGNUN P G G GNUN P G G GNUN P G G G G G G G G G G G G G G G G G G G	147 146 146 147 147 147 147 147 140 140 140 140 140 140 141 141 141 141
SmvAL23         Smp_1160250         77 SELAGAVAY WMEESNIY K HNTDS GSTFFEQNSYK DI VQAE AY VGC GFTR GRQYEYP SNMLIA GYY SP KVK S         148           SmVAL23         Smp_113750         77 SELAGAVAY WMEESNIY CHNSDLG SSTFEGNSYK DI VQAE AY VGC GYTR GRQYEYP SNMLIA GYY SP KVK S         148           SmVAL24         Smp_114150         77 SELAGAVAY WMEESNIY CHNSDLG SSTFEGNSYK DI VQAE AY VGC GYTR GRYEYP SNMLIA GYY SP KVK S         148           SmVAL24         Smp_114150         77 SELAGAVAY WMEESNIY CHNSDLG PS HHCNTYK DI VQAE AY VGC GYTR GRYEYP SNMLIA GYY SP KVM S         148           SmVAL25         Smp_114150         77 SELAGAVAY WMKESNY DHNSDL GPS HHCNTYK DI VQAE AY VGC GYTR GRYEYP SNMLIA GYY SP KVM S         148           SmVAL35         Smp_114150         77 SELAGAVAY WMKESNY DHNSDL GPS HHCNTYK DI VQAE AY VGC GYTR GRYEYP SNMLIA GYY SP KVM S         148           SmVAL34         Smp_114150         77 SELAGAVAY WMKESNY DHNSDL GPS HHCNTYK DI VQAE AY VGC GYTR GRYEYP SNMLIA GYY SP KVM S         148           SmVAL35         Smp_34730         77 SSINDA IN VWR DGSR FY SIK NDEGV VNHOCNY KU VDAE AY VGC GYTR GE CY EYP SNMLIA GYI VAGY AP AAG         147           SmVAL33         Smp_124060         68 MTGARATR NWY DEI HY HNFNKQ FQ S QSCH FTD IV WKS ST RIG GY ALO SYK SEGDLHKDS KMI IV CU YH P GOV IS         149           SmVAL16         Smp_124070         68 ING GRATR NWY DEI HY HNFNKQ FQ S QSCH FTD IV WKS TR AGF G SAL SK DG HWY FU G XY FP AGNIG<	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL5 SmVAL9* SmVAL9* SmVAL20* SmVAL20* SmVAL12 SmVAL12 SmVAL21 SmVAL21 SmVAL20 SmVAL14 SmVAL20 SmVAL19 SmVAL10 SmVAL10	Smp_176160           Smp_176160           Smp_070250           Smp_370250           Smp_120670           Smp_123550           Smp_123540           Smp_13540           Smp_13680           Smp_139680           Smp_13940           Smp_139450           Smp_127130           Smp_127130           Smp_113400           Smp_127130           Smp_12300070	77 TD I KTGFQL 77 KD I KTGFQS 77 STVEI GFQR 77 STVEI GFQR 77 STVEI GFQR 77 STVEI GFQR 74 PT I GFQR 74 ANVQT AMDE 74 ANVQT AMDE 74 PT I KSGVDA 74 PT I KSGVDA 74 ST I KSAVDA 74 ST I KSAVDA 75 RDNKS I FKV 78 DT I KNAMEN 77 PT I EKAVAS 77 TS I QN I LDT 77 PT I EGAMKD	V L D E Y K N V L D E Y K N V L N E Y K N V F D E SQN N F F S E A M Y K D E Y K Q V V N E Y Q V V N E Y Q V V N E Y Q V F N E H K L V F N E Y K N V F E Q H K N V L E E K N D V L E E K N D	Y D F Y R T T Y D F F Y R T T Y D F F N R L Y D F F N R L Y N Y N T N T Y N Y S S S Y D F D S N T Y N Y T N N Y N T T N Y D F T N K Y N T T N Y D F T N K Y S F D D T T Y S F D D T Y S F D D T T	R - MGQC R - MGQQC R - MGQQC L - VGRC L - VGRC S - GVC S - GVC P QC P QC P QC P QC I - VHNC I - VHNC C - D - C C - C - C - C - C - C C - C - C - C - C - C - C - C - C - C -	GHYTQ GHYTQ SHYTQ SHYTQ GNYTQ GNYTQ GNYTQ GNYLQ GHYTQ GHYTQ LHYTQ LHYTQ LHYTQ LHYTQ SSYKQ SNYRQ SNYRQ SNYKQ GNYKQ ADYKQ	L VWE DT L VWE DT I VWE NT I VWE NT L IWE NT L WE NT L VWE NT L VWE NT VWWAK MAWAK M	T D V G G G T D V G G G G G T D V G G G G G G G G G G G G G G G G G G	S V T D C V T K C S V T K C S V T C C V T C S V T C S V T D C V T T T T T T T T T T T T T T T T T T	P N F P N F P H S K N M F N S K N K S T R K S P R Y P R Y P R Y P R Y P R Y S N Y K K K R S N R K K K R S N R F K S N R S N R F K S N R F K S N R S N R F K S N R F K S N R F K S S N R		G L S I V G G L S I V G G L S I V G K L S I V G N L N V I G G L S I V G L S I V G G L S I V G L S I V G G L S I V G L S I V G G L S I V G L S I V G G L S I V G L S I V G G L S I V G L S I V G L S I V G L S I V G G L S I V G	G G G G G G G G G G G G G G G G G G G	P GGNYP G P GGNYP G P GGNYP G P GGCCP - P GGCCP - P GGC I - P GGNIP E P GGNYEG P GGNYEG P GGNWNN P GGNWNN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNUN P GGNUN P AAEE - P AAEE - P GAES P GGKYAN	147 146 146 146 147 147 147 146 140 140 140 153 141 144 141 141 141 141
SmvAL23         Smp_1160250         77 SELAGAVAY WMEESNIY K HNTDS GSTFFEQNSYK DI VQAE AY VGC GFTR GRQYEYP SNMLIA GYY SP KVK S         148           SmVAL23         Smp_113750         77 SELAGAVAY WMEESNIY CHNSDLG SSTFEGNSYK DI VQAE AY VGC GYTR GRQYEYP SNMLIA GYY SP KVK S         148           SmVAL24         Smp_114150         77 SELAGAVAY WMEESNIY CHNSDLG SSTFEGNSYK DI VQAE AY VGC GYTR GRYEYP SNMLIA GYY SP KVK S         148           SmVAL24         Smp_114150         77 SELAGAVAY WMEESNIY CHNSDLG PS HHCNTYK DI VQAE AY VGC GYTR GRYEYP SNMLIA GYY SP KVM S         148           SmVAL25         Smp_114150         77 SELAGAVAY WMKESNY DHNSDL GPS HHCNTYK DI VQAE AY VGC GYTR GRYEYP SNMLIA GYY SP KVM S         148           SmVAL35         Smp_114150         77 SELAGAVAY WMKESNY DHNSDL GPS HHCNTYK DI VQAE AY VGC GYTR GRYEYP SNMLIA GYY SP KVM S         148           SmVAL34         Smp_114150         77 SELAGAVAY WMKESNY DHNSDL GPS HHCNTYK DI VQAE AY VGC GYTR GRYEYP SNMLIA GYY SP KVM S         148           SmVAL35         Smp_34730         77 SSINDA IN VWR DGSR FY SIK NDEGV VNHOCNY KU VDAE AY VGC GYTR GE CY EYP SNMLIA GYI VAGY AP AAG         147           SmVAL33         Smp_124060         68 MTGARATR NWY DEI HY HNFNKQ FQ S QSCH FTD IV WKS ST RIG GY ALO SYK SEGDLHKDS KMI IV CU YH P GOV IS         149           SmVAL16         Smp_124070         68 ING GRATR NWY DEI HY HNFNKQ FQ S QSCH FTD IV WKS TR AGF G SAL SK DG HWY FU G XY FP AGNIG<	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL5 SmVAL9* SmVAL9* SmVAL20* SmVAL20* SmVAL12 SmVAL12 SmVAL21 SmVAL21 SmVAL20 SmVAL14 SmVAL20 SmVAL19 SmVAL10 SmVAL10	Smp_176160           Smp_176160           Smp_070250           Smp_370250           Smp_120670           Smp_123550           Smp_123550           Smp_133680           Smp_1393680           Smp_1393680           Smp_139450           Smp_139450           Smp_127130           Smp_131370           Smp_001890           Smp_002600           Smp_002000           Smp_002000           Smp_002000           Smp_000080	77 TD I K TG FQ L 77 KD I K TG FQ S 77 ST VE I G FQ R 77 ST VE I G FQ R 77 ST VE I G FK R 77 YT VE RAVK L 75 QT I EQAFDA 74 ANVQT AMDE 74 PT I K SG VDA 74 PT I K SG VDA 74 ST I K SAVDA 75 ST I K SAVDA 75 ST I K SAVDA 75 ST K SAVDA 75 ST I K SAVDA 75 ST K SAVDA 75 ST I K SAVDA 75 TI K SAVDA 75 TI K SAVDA 77 T S I QNI LDT 77 PT I EGAMKD 77 PK V RQAA SV 77 F K V RQAA SV	V L D E Y K N V L D E Y K N V L N E Y K N V N E Y K N V F D E S Q N V F S E AMY V K D E Y K Q V K V E Y K Q V F N E H K L V F N E Y K N V E E Y K N V L E E K N D V L E E K N K F F E Q H K N V F E Q H K N	Y D F Y T R T Y Y D F Y T R T Y Y D F F N R L Y D F F N R L Y N T N T N T Y N T N T N T Y N Y N T N N Y N Y N	R - MGQC R - MGQC R - MGQC L - VGRC L - VGRC I - NNQC S - SATC P QC P QC P QC P QC I - VNQC C - V - QC P QC P QC C - V - QC	GHYTQ GHYTQ SHYTQ SHYTQ GHYTQ GNYPQ GHYTQ GNYPQ LHYTQ LHYTQ LHYTQ UHYKQ SSYKQ SNYRQ SSYKQ SNYRQ SNYRQ SNYRQ ADYKQ ADYKQ	L VWE DT L VWE DT I VWENT I VWENT L I WENT L I WENT L VWENT L VWENT VWWAK MAWAKT MAWAKT MVWAKT I VWDKA L WAYAKT MVWAKT MVWAKT MVWAKT MVKGEE L VWANT LAFADT LAFADT	T D V G G C T D V G G C T D V G G C T D I G C C C C C C C C C C C C C C C C C C	J         J	P N F P N F P N F P N F S P P H S F N F S S F S S S S S S S S S S S S		G L S I V G G L S I V G G L S I V G K L S I V G K L S I V G K L S I V G G L S I V G S I I I L G S I V G S I V G S I I I L G S I S I V G S I S I S I S I S I S I S I S I S I S I	G G G G G G G G G G G G G G G G G G G	P GGNYP G P GGNYP G P GGNYP G P GGCP – P GGCCP – P GGNILG P GGNIPE P GGNYEG P GGNWNN P GGNWNN P GGNWNN P GGNWIN P GGNYAN P AA DE – – P GGYAN P GGKYAN	147 146 146 147 147 147 147 147 140 140 140 140 140 140 141 141 141 141
SmvAL33         Smp_31370         77         SE LAGAVAY WMEESNIY CHARDONG SETER (SUSY KOLVQAE AYVGC GFTR (SUSYEYPSNMLIACYYSEKVKS	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL9 SmVAL9 SmVAL2 SmVAL12 SmVAL2 SmVAL2 SmVAL22 SmVAL22 SmVAL23 SmVAL24 SmVAL20 SmVAL34 SmVAL30 SmVAL43 SmVAL43 SmVAL43	Smp_176160           Smp_176160           Smp_070250           Smp_370250           Smp_120670           Smp_123550           Smp_123550           Smp_133680           Smp_1393680           Smp_1393680           Smp_139450           Smp_139450           Smp_127130           Smp_131370           Smp_001890           Smp_002600           Smp_002000           Smp_002000           Smp_002000           Smp_000080	77 TD I K TG FQ L 77 KD I K TG FQ S 77 ST VE I G FQ R 77 ST VE I G FQ R 77 ST VE I G FK R 77 YT VE RAVK L 75 QT I EQAFDA 74 ANVQT AMDE 74 PT I K SG VDA 74 PT I K SG VDA 74 ST I K SAVDA 75 ST I K SAVDA 75 ST I K SAVDA 75 ST K SAVDA 75 ST I K SAVDA 75 ST K SAVDA 75 ST I K SAVDA 75 TI K SAVDA 75 TI K SAVDA 77 T S I QNI LDT 77 PT I EGAMKD 77 PK V RQAA SV 77 F K V RQAA SV	V L D E Y K N V L D E Y K N V L N E Y K N V N E Y K N V F D E S Q N V F S E AMY V K D E Y K Q V K V E Y K Q V F N E H K L V F N E Y K N V E E Y K N V L E E K N D V L E E K N K F F E Q H K N V F E Q H K N	Y D F Y T R T Y Y D F Y T R T Y Y D F F N R L Y D F F N R L Y N T N T N T Y N T N T N T Y N Y N T N N Y N Y N	R - MGQC R - MGQC R - MGQC L - VGRC L - VGRC I - NNQC S - SATC P QC P QC P QC P QC I - VNQC C - V - QC P QC P QC C - V - QC	GHYTQ GHYTQ SHYTQ SHYTQ GHYTQ GNYPQ GHYTQ GNYPQ LHYTQ LHYTQ LHYTQ UHYKQ SSYKQ SNYRQ SSYKQ SNYRQ SNYRQ SNYRQ ADYKQ ADYKQ	L VWE DT L VWE DT I VWENT I VWENT L I WENT L I WENT L VWENT L VWENT VWWAK MAWAKT MAWAKT MVWAKT I VWDKA L WAYAKT MVWAKT MVWAKT MVWAKT MVKGEE L VWANT LAFADT LAFADT	T D V G G C T D V G G C T D V G G C T D I G C C C C C C C C C C C C C C C C C C	J         J	P N F P N F P N F P N F S P P H S F N F S S F S S S S S S S S S S S S		G L S I V G G L S I V G G L S I V G K L S I V G K L S I V G K L S I V G G L S I V G S I I I L G S I V G S I V G S I I I L G S I S I V G S I S I S I S I S I S I S I S I S I S I	G G G G G G G G G G G G G G G G G G G	P GGNYP G P GGNYP G P GGNYP G P GGCP – P GGCCP – P GGNILG P GGNIPE P GGNYEG P GGNWNN P GGNWNN P GGNWNN P GGNWIN P GGNYAN P AA DE – – P GGYAN P GGKYAN	147 146 146 147 147 147 147 147 140 140 140 140 140 140 141 141 141 141
SmvAL24         Smp_141550         77 SELAEAVAYWMKESNYYDHNSDLGEPSHHGNTYKDIVEAQTAYVGGGYTRGEEYEYPSNMLIAGYYSEKVMS         148           SmVAL24         Smp_141560         77 SELAEAVAYWMKESNYYDHNSDLGEPSHHGNTYKDIVEAQTAYVGGGYTRGEEYEYPSNMLIAGYYSEKVMS         148           SmVAL24         Smp_141570         77 SELAEAVAYWMKESNYYDHNSDLGEPSHHGNTYKDIVEAQTAYVGGGYTRGEEYEYPSNMLIAGYYSEKVMS         148           SmVAL34         Smp_317520         77 SEVAEAVAYWMKESNYYDHNSDLGEPSHHGNTYKDIVEAQTAYVGGGYTRGEEYTNKGKYIVVGNYAPAAG         147           SmVAL35         Smp_347320         77 SSINDAINVWRDGSRFYNLKNDEGXVNHDGSMYKDLVNINTHIGGGYHLGNKNTNKGKYIVVGNYAPAAG         147           SmVAL35         Smp_347320         77 SSINDAINVWRDGSRFYNLKNDEGXNYNGUNNINTHIGGGYHLGNKNTNKGKYIVVGNYAPAAG         147           SmVAL35         Smp_124060         68 MTGARATRWYDEIHYNFNKQFQS QSCHFTDIVWSSERIEVGIALOSYK SEEDLHKDSKMILVCLYHP GON'IS         149           SmVAL16         Smp_124060         68 NTGARATRWYDEIHYNFNKQFQSQSCHFTDIVWKNS KAGFGIAHSYNGGALARSKNILVGRYEP GONIG         135           SmVAL16         Smp_124050         68 ITGEEVSQTWYSEIDYDFOSYNFNENFTOI VWKSTIKAGFGIAHSYNGGALARSKNILVGRYEP GONIG         135           SmVAL16         Smp_124050         68 ITGEEVSQTWYSEIDYDFOSYNFNENFTOINWKNETTRAGFGLAFSQDQKKYVVGRYER GONIG         135           SmVAL16         Smp_124050         68 ITGEEVSQTWYSEIDYDFOSYNFNENFTON WKSTIKAGFGLAFSQDQKKYVVGRYER G	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL5 SmVAL29* SmVAL2 SmVAL12 SmVAL12 SmVAL21 SmVAL21 SmVAL21 SmVAL21 SmVAL20 SmVAL23 SmVAL20 SmVAL3 SmVAL10 SmVAL13 SmVAL23 SmVAL23 SmVAL23 SmVAL23	Smp_176160 Smp_176160 Smp_070250 Smp_070250 Smp_126670 Smp_176180 Smp_123540 Smp_123540 Smp_13860 Smp_139280 Smp_002630 Smp_078490 Smp_078490 Smp_078490 Smp_078490 Smp_127130 Smp_01890 Smp_002060 Smp_002060 Smp_002070 Smp_300070 Smp_300080 Smp_300080 Smp_300080 Smp_300080 Smp_300080 Smp_300080 Smp_300080 Smp_300080 Smp_300080 Smp_300080 Smp_300080 Smp_300080 Smp_300080 Smp_300080 Smp_300080 Smp_300080 Smp_300080 Smp_3008650	77 TD I KTGFQL 77 KD I KTGFQS 77 STVEI GFQR 77 STVEI GFQR 77 STVEI GFQR 77 STVEI GFQR 77 YTVERAVKL 75 QT I EQAFDA 74 ANVQT AMDE 74 PT I K SGVDA 74 PT I K SGVDA 74 PT I K SGVDA 74 ST I K SAVDA 74 ST I K SAVDA 75 ST NKS I FKV 78 DT I KNAMEN 77 PT I EKAVAS 77 PT I EGAMKD 77 PK VRQAASV 77 SELAGAVAY	V L DE Y K N V L DE Y K N V L DE Y K N V L NE Y K N V F DE S Q N V K DE S Q N V K DE S Q N V K DE Y K N V	Y D F Y T T T Y Y D F Y T T T Y Y D F Y N T T T Y Y D F Y N T T T T Y Y N F N T T T T Y N F N T T T Y Y N Y S S Y Y D F D S N T Y N Y S S Y N N Y N T S Y N N Y N Y S S Y N N Y N T S Y N N Y N T S Y N N N Y N T S Y N N Y N T S Y N N N Y Y N T S Y N Y N Y Y N T S Y N Y N Y Y N T S Y N Y N Y N Y N Y N Y N Y N Y N Y N Y	R - MGQC R - MGQC R - MGQC L - VGRC L - VGRC I - NNQC S - SATC P QC P QC P QC P QC P QC I - VHNC C - P QC C	GHY TO GHY TO GHY TO SHY TO SHY TO SHY TO SHY TO GNY TO GNY TO GNY TO GNY TO GNY TO GHY TO LHY TO LHY TO LHY TO LHY TO SNY RO SNY RO SN	LVWEDT LVWEDT IVWENT LVWENT LVWENT LVWENT LVWENT LVWENT LVWQNT VWQNT VWAWAK IVWAK LMAYNT VVWAK LWAYNT VVWAK LWAYNT LAFADT LAFADT LAFADT		V T D         C           V T T C         V A T C           V A T C         V A T C           V T E C         V T E C           V T T C         V T E C           V T T C         V T E C           V T T C         V T E C           V T T C         V T E C           V T D C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A M C           V A M C         V A M C           V A M C         V A M C           V A M C         V A M C	P N F P N F P N F P N S P H S		GLSIVG GLSIVG GLSIVG KLSIVG KLSIVG GLSVG GLSVG GLSVG GLSVG GLSVG GLSVG GLSVG GLSVG GLSVG KLVVG KVFVG KVFVG	NY G	P GGNYP G P GGNYP G P GGNYP G P GGCCP - P GGCCP - P GGCNIP E P GGNIP E P GGNYEG P GGNWNN P GGNWNN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P AGEE - P AAEE - P GADD - P GGSYAN P GGKYAN P GGKYAN P GCKYAN	147 146 146 147 147 146 140 140 140 140 140 140 153 141 144 141 141 150 150 150
SmvAl25         Smp_141560         77         SELAEAVAY WMKESNYYDHNSDLGEYSHNEMUTYKDI VQAE AYYGG YTRGE EYEYPSNMLVAGYYSEKMMS         148           SmVAl34         Smp_317520         77         SEVADA INVWRDGSRFYNLKNDEG VNHDG SMYKQLVDI NT HI GG VHLGNKNTNKGKYIVVGNYAPAAG         147           SmVAL35         Smp_347320         77         SEINDA INVWRDGSRFYSLKNDEG VNHDG SMYKQLVDI NT HI GG VHLGNKNTNKGKYIVVGNYAPAAG         147           SmVAL11         Smp_012350_2nd         72         SLNDA INVWRDGSRFYSLKNDEG VNHDG SMYKQLVNINT HI GG VHLGNKNTNKGKYMVG VAPAAG         147           SmVAL11         Smp_012350_2nd         72         LNCKD I EHW YQESGKYKFNSEPDS-I QG IGNFT QI VWSSSERI GV CIAIOSYKSGEDLHKDSKMI LVCLYHP PGNVIS         149           SmVAL13         Smp_124060         68         NGREAATRNWYDEI HY HN FNKQFQS QG GFHT QI VWSST IKAGFG GA SLSKDG	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL29* SmVAL9* SmVAL2 SmVAL2 SmVAL12 SmVAL2 SmVAL22 SmVAL22 SmVAL22 SmVAL23 SmVAL30 SmVAL30 SmVAL32 SmVAL3 SmVAL3 SmVAL3	Smp_176160 Smp_176160 Smp_070250 Smp_336880 Smp_120670 Smp_126180 Smp_123550 Smp_123540 Smp_138680 Smp_02630 Smp_02630 Smp_026430 Smp_026430 Smp_026430 Smp_139450 Smp_026430 Smp_127130 Smp_127130 Smp_127130 Smp_01890 Smp_01890 Smp_002060 Smp_002060 Smp_002060 Smp_002060 Smp_002060 Smp_300080 Smp_316760 Smp_16250	77 TD I K TG FOL 77 KD I K TG FOL 77 ST VE I G FOR 77 ST VE I G FOR 77 ST VE I G FOR 77 ST VE I G FOR 74 PT I G FOR 74 ANVQ TAMDE 74 PT I K S G VDA 74 PT I K S G VDA 74 ST I K S A VDA 74 ST I K S A VDA 75 ST K S K S I F K V 78 DT I K A VA S 77 S I G N S I F K V 78 DT I E CAMK D 77 F V I E CAMK D 77 F V I E CAMK O 77 F V I CAMA S V 77 F K V RQAA S V 77 S E LAGAVA Y 75 S LAGAVA Y	V D E V K N V L D E V K N V L D E V K N V L N E V K N V F D E S Q N V V F S E A MY V K E V K Q V K E V K Q V K E V K Q V F N E H K L V F N E V K N V E E V K N V L E E K N N V E E Q H K N V F E Q H K N V M E E S N I V M E E S N I	Y D F Y T T T Y Y D F Y T T T Y Y D F Y N T T N T Y D F Y N T T N T Y Y N T T N T Y Y N Y S Y N Y Y N Y S Y N Y Y N Y S Y N N Y Y N Y T N N Y Y N Y S Y N Y Y Y N Y S Y N Y Y Y Y Y Y Y Y Y Y Y Y Y Y	R - MGQC R - MGQC R - MGQC L - VGRC L - VGRC S - SATC S QC P QC P QC P QC P QC C - P C - QC C - P C - QC C - QC P QC C - QC C	GHYTQ GHYTQ GHYTQ SHYTQ SHYTQ SHYTQ GNYPQ GHYTQ GNYLQ LHYTQ LHYTQ LHYTQ LHYTQ UHYTQ UHYKQ SNYRQ GNYKQ ADYKQ ADYKQ NSYKQ	LVWEDT LVWEDT LVWENT LVWENT LVWENT LVWENT LVWENT LVWENT LVWENT MAWAKT MAWAKT MAWAKT MAWAKT MVWAKT LVWAKT LVWAKT LWAYAT	T D V G G C T D I G C C C T D I G C C C T D I G C C C C C C C C C C C C C C C C C C	V T D         C           V T K C         V A T C           V A T C         V A T C           V T C         V T C           V T D         V T D           V T D         V T D           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A M C           V A M C         V A M C           V A M C         V A M C           V A M C         V A M C           V A M C         V A M C           V A M C         V A M C           V A M C         V A M C	P N F P P N F S P P N F S P P N F S P F N F S F S R T S S		GLSIVG GLSIVG KLSIVG KLSIVG KLSIVG GLSVVG GLSVVG GLSVVG GLSVVG GLSVVG GLSVVG GLSVVG GLSVVG GLSVVG GLSVVG GLSVVG GLSVVG KVFVVG KVFVVG KVFVVG	C NY G C NY A C NY A C NY A C NY A C NY G C NY A C	P GGNYP G GGNYP G P GGNYP G P GGCP - P GGCCP - P GGC I L G P GGN I L G P GGNY E G P GGNY E G P GGNWNN P GGNWNN P GGNWNN P GGNWNN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNYAN P GADD P GDS P GGSYAN P GGKYAN P GGKYAN P GGKYAN P KVKS	147 146 146 147 147 147 147 140 140 140 140 140 153 141 141 141 141 141 141 140 150 150
SmvAL34         Smp_317520         77 SSVYDAINVWRDGSRFYNLKNDEC VNNDCSMYKQLVDINT THIGC VHLQNKNTNKGKYIVVC NYAPAAG         147           SmvAL35         Smp_347320         77 SSINDAINVWRDGSRFYNLKNDEC VNDCSMYKQLVDINT THIGC VHLQNKNTNKGKYIVVC NYAPAAG         147           SmVAL31         Smp_012350_2nd         72 LNCKDLIEHWYQESCKYK FNSEPDS-IQGICNTTQIVWSSSERIGVCIAIQSYKSGEDLHKDSKMILVCLYHP PGNVIS         149           SmVAL31         Smp_124060         68 MTGARATRNYDEIHYHNFNKQFQSQSCHTTQIVWKNSSERIGVCIAIQSYKSGEDLHKDSKMILVCLYHP PGNVIS         149           SmVAL31         Smp_124060         68 MTGARATRNYDEIHYHNFNKQFQSQSCHTTQIVWKNSKAEFGIQHSVDGHHVFIVGRYEP PGNVIG         135           SmVAL45         Smp_124050         68 ITGREATRNYDEIHYHNFNKQFQSQSCHTTQIVWKNSKAEFGIQHSVDGHKVTVVGRYEP PGNVIG         135           SmVAL6         Smp_124050         68 ITGREAVYDEIHYHDFTQSYHPNSRHFTQVIWKSTIKAGFGLAFSQDQTKAYVVGRYEP PGNVIG         135           SmVAL6         Smp_124050         68 ITGEEVSQTWYSEIDYHDFTQSYHPNSRHFTQVIWKSTIKAGFGLAFSQDQTKAYVVGRYEP QNKCG         134           SmVAL17         Smp_331830         71 FTGADATKTWYQEIEDYDFKRENQFPCGHTTQVIWKSTITAGFGLAFSQDQHSIYVVGRYDP PGNFSD         135           SmVAL15         Smp_20460         68 VACLNAIQAWYKQEIEDYDFKEPCHTQFTQHYTDWENGKKKKVGFGFTKSDVGHSIYVVGRYDPROFFD         135           SmVAL17         Smp_20460         68 VACLNAIQAWYKQEIEDYDYDENCDUCESKCYFTQMIWKSTIKKKK	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL29* SmVAL29* SmVAL2 SmVAL12 SmVAL21 SmVAL21 SmVAL21 SmVAL21 SmVAL20 SmVAL20 SmVAL30 SmVAL30 SmVAL33 SmVAL33 SmVAL33	Smp_176160 Smp_176160 Smp_070250 Smp_070250 Smp_126070 Smp_176180 Smp_176180 Smp_123540 Smp_13860 Smp_13860 Smp_139290 Smp_02630 Smp_13450 Smp_13450 Smp_13450 Smp_131370 Smp_131370 Smp_131370 Smp_078490 Smp_002060 Smp_002060 Smp_002070 Smp_002070 Smp_300070 Smp_316760 Smp_160250 Smp_160250	77 TD I KTGFQL 77 KD I KTGFQS 77 STVEI GFQR 77 STVEI GFQR 77 STVEI GFQR 77 STVEI GFQR 77 STVEI GFKM 77 YTVERAVKL 75 QT I EQAFDA 74 ANVQTAMDE 74 PT I KSGVDA 74 PT I KSGVDA 74 ST I KSGVDA 74 ST I KSGVDA 74 ST I KSGVDA 75 SDNKSI FKV 78 DT I KNAMEN 79 SDVI NAVES 77 SELAGAVAY 77 SELAGAVAY	V L DE Y K N V F DE SQMY V F S E SAMY V F N E S K V V F N E H K L V E E Y K N V L E E Y K N V L E E Y K N V K Y K Y K N V K Y K Y K N V K Y K Y K Y K Y K Y K Y K Y K Y K Y K	Y D F Y T T T Y Y D F T T T T Y Y N Y T T Y Y N Y T Y S Y Y D T T Y S Y T T T Y Y N Y S Y S Y Y D T T N K Y N Y S Y S T T T Y Y D T T N K Y N F S Y N N Y N F S Y N N Y N F S Y N N Y N F S Y N T T Y Y S T D T T Y Y S T D T T Y Y S T D T T Y Y S T S T T T Y Y S T S T T T T T T T T T T T T T T T T	R - MGQC R - MGQC R - MGQC L - VGRC L - VGRC S - S A TC S - S A TC P QC P QC P QC P QC P QC P QC P QC P QC P QC C - V + NC C -	GHY TO GHY TO GHY TO GHY TO SHY TO SHY TO SHY TO SHY TO GHY TO GHY TO GHY TO GHY TO LHY TO LHY TO LHY TO LHY TO LHY TO CHY TO SNY RO GNY KO GNY KO GNY KO GNY KO ADY KO ADY KO NSY KO NSY KO	LVWEDT LVWEDT IVWENT IVWENT LIWENT LIWENT LVWENT LVWENT VWWAKT MAWAKT MAWAKT MVWAKT IVWCKE LVWANT VWWAKT LAFADT LAFADT LAFADT IVQAET IVQAET	T D V G G C T D V G G C T D V G G C T D I G C C T T D I G C C C C C C C C C C C C C C C C C C	V T D         C           V T K C         V A T C           V A T C         V A T C           V T D C         V T D           V T D         V T D           V T D         V T D           V T D         V T D           V T D         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A M C         V A N C           V A M C         V A M C           V A M C         V A M C           V A M C         V A M C           V A M C         V A M C <td>P P F P P P H S P P P H S P P P K N F</td> <td></td> <td>GLSIVG GLSIVG KLSIVG KLSIVG KLSIVG GLSVG GLSIVG GLSIVG GLSIVG GLSIVG GLSIVG GLSVVG KUNVG - FLVVG - YLVVG KVFVVG KVFVVG KVFVVG NMLIAG NMLIAG</td> <td>NY G C NY G C NY</td> <td>P GGNYP G P GGNYP G P GGNYP G P GGCP - P GGGCP - P GGC I L G P GGN I L G P GGNY EG P GGNWNN P GGNWNN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNYAN P SADDK - P SADDK - P SADCK - P GAYAN P GGYAN P KYKS</td> <td>147 146 146 146 147 147 147 140 140 140 140 140 140 153 141 144 141 141 141 144 141 144 148 150 150</td>	P P F P P P H S P P P H S P P P K N F		GLSIVG GLSIVG KLSIVG KLSIVG KLSIVG GLSVG GLSIVG GLSIVG GLSIVG GLSIVG GLSIVG GLSVVG KUNVG - FLVVG - YLVVG KVFVVG KVFVVG KVFVVG NMLIAG NMLIAG	NY G C NY	P GGNYP G P GGNYP G P GGNYP G P GGCP - P GGGCP - P GGC I L G P GGN I L G P GGNY EG P GGNWNN P GGNWNN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNYAN P SADDK - P SADDK - P SADCK - P GAYAN P GGYAN P KYKS	147 146 146 146 147 147 147 140 140 140 140 140 140 153 141 144 141 141 141 144 141 144 148 150 150
Smv2L35         Smp_347320         77 S S I NDA I NVWR DG SR FY S L K NDE G KANY DG SMYKQ L VN I N T TH I G G VH LQ NK N T NK G K YM V G NY AP A A G 147         147           Smv2L11         Smp_012350_2nd         72 L NCK D L I F HWY QE SC K Y K F NS EP D S - I Q G I C NF T Q I I WS SS ER I G V G I A I Q SY K SG ED L HK D SKM I L V L V H P G NV I S         147           Smv2L11         Smp_124060         68 MT GAR A T R NWY DE I HY H N F NKQ F Q S Q S G H FT Q I I WK N SK AG F G I G H S V D G	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL5 SmVAL9* SmVAL9* SmVAL20* SmVAL2 SmVAL12 SmVAL21 SmVAL22 SmVAL22 SmVAL23 SmVAL30 SmVAL19 SmVAL19 SmVAL19 SmVAL13 SmVAL13 SmVAL23 SmVAL23 SmVAL23	Smp_176160           Smp_176160           Smp_070250           Smp_370250           Smp_120670           Smp_123550           Smp_123540           Smp_13540           Smp_13540           Smp_13540           Smp_13540           Smp_13450           Smp_13450           Smp_127130           Smp_127130           Smp_121309           Smp_002600           Smp_002070           Smp_300080           Smp_313700           Smp_166250           Smp_131370           Smp_313710	77 TD I KTGFQL 77 KD I KTGFQS 77 STVEI GFQR 77 STVEI GFQR 77 STVEI GFQR 77 STVEI GFQR 74 PT I GFQR 74 ANVQT AMDE 74 ANVQT AMDE 74 PT I KSGVDA 74 PT I KSGVDA 74 ST I KSGVDA 74 ST I KSGVDA 75 STDNKS I FKV 78 DT K NAMEN 77 TS I QN I LDT 77 PT I EGAMKD 77 FVRQAASV 77 SELAGAVAY 77 SELAGAVAY 77 SELAGAVAY 77 SELAGAVAY	V D E V K N V L D E V K N V L D E V K N V L N E V K N V F D E S Q N V K D E V K N V K E V K Q V F N E H K L V F N E V K N V L E E V K N V L E E V K N V E E Q H K N V E E Q H K N V M E E S N I V M E E S N I	Y D F Y T T T Y Y D F Y T T T Y Y D F Y N T T N Y Y N T T N T Y Y N T T N T Y Y N Y S Y S Y Y N Y S Y S Y Y N Y S Y N N Y Y N Y S T D N T Y Y N Y S T D N T Y Y N F S N T N Y Y N F S N T N Y Y N F S N T T N T S N T N Y Y N T S N T N T S N T N Y Y N T S N T N T S N T N T S N T N T S N T N T	R - MGQC R - MGQC R - MGQC L - VGRC J - VGRC S - SATC S - GVC P QC P QC P QC P QC P QC C - P QC C - P QC C -	GHY TO GHY TO GHY TO SHY TO SHY TO SHY TO SHY TO GHY TO GHY TO GNY LO GHY TO LHY TO LHY TO LHY TO LHY TO LHY TO CHY TO SSY KO SNY KO ADY KO ADY KO NSY KO NSY KO	L VWE DT L VWE DT I VWENT I VWENT L VWENT L VWENT L VWENT L VWENT WAWAKT WAWAKT WAWAKT VAWAKT VWAKE L VWANT L LAPADT L AFADT I VQAET I VQAET I VQAET	T D V G G C T D V G G C T D V G G C T D I G C C C T D I G C C C C C C C C C C C C C C C C C C	V T D         C           V T C         V A T C           V A T C         V A T C           V T D         V T D           V T D         V T D           V T D         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A M C         V A M C           V A M C         V A M C           V A M C         V A M C           V T R C         V T R C	P N F P P N F S P P N F S P P N F S P P N F S F S S F S S S		GLSIV GLSIV GLSIV KLSIV KLSIV GLSV GLSIV GLSIV GLSIV GLSIV GLSIV GLSIV GLSIV GLSIV GLSIV CQIV CV CV CV CV CV CV CV CV CV CV CV CV CV	C NY G C NY A A A A A A A A A A A A A A A A A A	P GGNYP G P GGNYP G P GGNYP G P GGCP - P GGCCP - P GGC I - P GGNIP E P GGNYEG P GGNYEG P GGNWNN P GGNWNN P GGNWNN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNYAN P GGNYAN P GGYYAN P GGKYAN P GGKYAN P GGKYAN P GGKYAN P GGKYAN P GGKYAN P GGKYAN P GGKYAN P GGKYAN P GGKYAN	147 146 146 146 147 147 147 140 140 140 140 140 140 140 141 141 141
SmvAL11         Smp_012350_2nd         72         LNCKDLIEHWYQESGKY         KNSEPDS-IQGICNFTQIVWSSSERIGV         IAIOSYKSGEDLHKDSKMILVCLY         HP GOVIS         149           SmvAL13         Smp_0124060         68         MTGARATRNWYDEIHYHNFNKQFQSQSGHFTQLIWKNTSKAGFGIQHSVDGHVFIVGRYEPPGNVNG         135           SmVAL16         Smp_0124070         68         LNGREATRNWYDEIHYHDFNKQFQPCTGHFTQVIWKSTIKAGFGSALSKDGKKVYVVGRYKPAGNID         135           SmVAL6         Smp_0124050         68         LTGEDVSQTWYSEIDYHDFTQSYHPNSHFTQMIWKSTIKAGFGCALSKDGKKVYVVGRYLPAGNK-G         134           SmVAL17         Smp_031830         71         FTGADATKTWYQEIEDYDFKRENQFPCGHFTQVVWKSTITAGFGCAWSKDRHSIYVVGRYLPAGNK-G         138           SmVAL13         Smp_020460         68         VACLNAIQAWYKQSENYDYNDGKSKGYFTQVWKSTITAGFGFCKSDVGNTIFVVGRYDPPGNFSD         138	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL9 SmVAL9 SmVAL2 SmVAL2 SmVAL2 SmVAL2 SmVAL2 SmVAL2 SmVAL2 SmVAL2 SmVAL2 SmVAL2 SmVAL3 SmVAL3 SmVAL3 SmVAL3 SmVAL3 SmVAL3 SmVAL23 SmVAL23 SmVAL23	Smp_176160           Smp_176160           Smp_070250           Smp_370250           Smp_120670           Smp_123580           Smp_123550           Smp_133680           Smp_133680           Smp_133680           Smp_133680           Smp_139450           Smp_1231300           Smp_127130           Smp_018309           Smp_002060           Smp_002070           Smp_300070           Smp_316760           Smp_131370           Smp_131370           Smp_002050           Smp_316760           Smp_1313710           Smp_1313710           Smp_131560	77 TD I K TG FOL 77 KD I K TG FOL 77 ST VE I G FQ R 77 ST VE I G FQ R 77 ST VE I G FQ R 77 ST VE I G FQ R 74 PT I G FKM 74 N VQ TA MOLE 74 PT I K SG VDA 74 PT I K SG VDA 74 ST I K SG VDA 74 ST I K SG VDA 75 ST I K SG VDA 77 ST I G K SG VDA 77 ST I G K SG VDA 77 ST I G K SG VDA 77 SE LAG AV AY 77 SE LAG AV AY 77 SE LAG AV AY 77 SE LAG AV AY 75 SE LAG AV AY	V L DEYKN V L DEYKN V L DEYKN V N EYKN V FOESQN V FSEAMY V FOESQN V FOESQN V FOESQN V FOESQN V FOESQN V FOESKI V FOEKKI V FNEHKL V FNEHKL V FNEHKL V FNEHKL V EEKVD V L EEKVD V L EEKVN V L EEKVN V L EEKVN V V EEKVN V EEKVN V EEKVN V EEKVN V V V V V V V V V V V V V V V V V V V	Y D F Y R T Y Y D F Y R T Y Y D F F N R L Y D F F N R L Y N T N T N T Y N T N T N T Y N Y N T N N Y N Y N	R - MGQC R - MGQC R - MGQC L - VGRC L - VGRC I - NQC S - SATC P QC P QC P QC P QC P QC I - VHNC N - SKSC Q AC E - VEC C - QC C - QC	GHYT GHYT GHYT GHYT SHYT SHYT GHYT GHYT GHYT GHYT LHYT LHYT LHYT LHYT CHYT SSNYR GNYK GNYK GNYK GNYK GNYK GNYK CNYK CNYK CNYK CNYK CNYK CNYK CNYK C	LVWEDT LVWEDT LVWENT LVWENT LUWENT LUWENT LUWENT LVWQKT VWWKT VWWAKT VWWAKT VWWAKT VWWAKT VWWAKT LUWQNT LUWANT LLAFADT LAFADT LAFADT LVQAET IVQAET IVQAET IVQAET IVQAET		V T D         C           V T K C         V A T C           V A T C         V A T C           V T D         C           V T D         C           V T D         C           V T D         C           V T D         C           V T D         C           V T D         C           V T D         C           V A N C	P P P S S		GLSIVG GLSIVG KLSIVG KLSIVG KLSIVG GLSVVG GLSIVG GLSIVG GLSIVG GLSIVG GLSVVG GLSIVG GLSVVG KVFVVFVVG KVFVVFVVG KVFVVFVVG KVFVVFVVFVVFVVFVVFVVFVVFVVFVVFVVFVVFVVFV	C NY G C	P GGNYP G P GGNYP G P GGNYP G P GGNYAG P GGCP - P GGCP - P GGNILG P GGNYEG P GGNYEG P GGNWNN P GGNWNN P GGNWNN P GGNWNN P GGNWIN P GGNYIN P GGNYIN P GGNYIN P GGNYAN P AAEE - P GGYAN P AAEE - P GGYAN P GACYAN P GGYAN P GGYAN P GGYAN P GGYAN P GGYAN P KVKS P KVKS P KVKS P KVKS P KVMS	147 146 146 146 147 147 147 140 140 140 140 140 153 141 144 141 141 141 144 148 148 148 148
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MGQC R - MGQC R - MGQC L - VGRC L - VGRC S - SATC S - GVC P QC P	GHY TY GHY TY GHY TY SHY TY SHY TY SHY TY GHY TY GHY TY GHY TY GHY TY GHY TY LHY TY UHY KR SNY KQ ADY KQ ADY KQ NSY KQ NSY KQ NSY KQ NSY KQ NY KQ SNY KQ NY KQ SNY XQ SNY	L VWE DT L VWE DT I VWENT I VWENT L VWENT L VWENT L VWENT L VWENT I VWENT I VWENT I VWENT I VWENT I VWES L VWENT I VWES L VWENT L LAFADT I VQAET I VQAET I VQAET I VQAET I VQAET		V T D         C           V T K C         V T K C           V T K C         V T C           V T C         V T C           V T D         V T D           V T D         V T D           V T D         V T D           V T D         V T D           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V A N C         V A N C           V T N C         V T N C	P P F P P F N F P P F N F P P F N F		GLSTV       GLSTV       GLSTV       GLSTV       KLSTV       KLSTV       GLSTV       GLSTV <t< td=""><td>NY G CNY G C</td><td>P GGNYPG           P GGNYPG           P GGNYPG           P GGCCP-           P GGCCP-           P GGCNPEG           P GGNIPE           P GGNYEG           P GGNYEG           P GGNYEG           P GGNYEG           P GGNYEG           P GGNYEG           P GGNYEN           P GGNYNN           P GGNYIN           P GGNYIN           P GGNYIN           P GGNYIN           P GGNYIN           P GGNYIN           P GGNYAADN           P GGNYAAN           P GASS           P GGRYAN           P GCKYAN           P GCKYAN           P KVKS           P KVKS           P KVS           P KWS           P KWS</td><td>147 146 146 146 147 147 147 140 140 140 140 140 140 140 140 140 140 141 148</td></t<>	NY G CNY G C	P GGNYPG           P GGNYPG           P GGNYPG           P GGCCP-           P GGCCP-           P GGCNPEG           P GGNIPE           P GGNYEG           P GGNYEG           P GGNYEG           P GGNYEG           P GGNYEG           P GGNYEG           P GGNYEN           P GGNYNN           P GGNYIN           P GGNYIN           P GGNYIN           P GGNYIN           P GGNYIN           P GGNYIN           P GGNYAADN           P GGNYAAN           P GASS           P GGRYAN           P GCKYAN           P GCKYAN           P KVKS           P KVKS           P KVS           P KWS	147 146 146 146 147 147 147 140 140 140 140 140 140 140 140 140 140 141 148
SmvAL13       Smp_124060       68 MTGARATRNWYDEI HYHNFNKQFQSQSCHFTQLIWKNSKAGFCIQHSVDGHVFIVGRYEP GOVNG       135         SmvAL16       Smp_124070       68 LNGRATRNWYDEI HUHPKNQNQPCTGHFTQVIWKSTIKAGFGSALSKDGKKVVVGRYKPAGNID       135         SmVAL16       Smp_124050       68 ITGEEVSQTWYSEIDYHDFTQSYHPNSRHFTQVIWKSTIKAGFGLAFSQDQKKVVVGRYLPVGNK-G       134         SmVAL17       Smp_331830       71 FTGADATKTWYQEIEDYDFTQSYHPSRHFTQMIWKSTIKAGFGLAFSQDQHKVVVGRYLPVGNK-G       134         SmVAL17       Smp_20460       68 VAGLNAIQAWYKQEIEDYDFTQSYHPSRHFTQMIWKSTIKAGFGLAFSQDQHKVVVGRYDPPGNFSD       135         SmVAL15       Smp_20460       68 VAGLNAIQAWYKQETUDYDFTQSYHPSRHFTQMIWKKSTIKAGFGLAFSQDQHKVVVGRYDPFGNFSD       135	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL29* SmVAL2 SmVAL12 SmVAL12 SmVAL12 SmVAL21 SmVAL21 SmVAL21 SmVAL21 SmVAL21 SmVAL23 SmVAL24 SmVAL3 SmVAL3 SmVAL24 SmVAL24 SmVAL24 SmVAL24	Smp_176160           Smp_176160           Smp_070250           Smp_120670           Smp_170870           Smp_123540           Smp_123540           Smp_123540           Smp_13680           Smp_13680           Smp_13450           Smp_02630           Smp_078490           Smp_13370           Smp_13300           Smp_002600           Smp_002070           Smp_300080           Smp_160250           Smp_160250           Smp_1141550           Smp_141550	77 TD I K TG FOL 77 KD I K TG FOS 77 ST VE I G FQR 77 YT VE RAVKL 75 QT I EQAFDA 74 ANVQT AMDE 74 PT I K S G VDA 74 PT I K S G VDA 74 PT I K S G VDA 74 ST I K S A VDA 75 SVDA I S K VDA 75 SVDA I S K VDA 77 SI GNA SV 77 S I GNA SV 77 S K CAASV 77 S LAGAASV 77 SELAGAVAY 77 SELAGAVAY	V D E V K N V L D E V K N V L D E V K N V L D E V K N V F D E S Q N V V F D E S Q N V V F S E A M Y V F D E V K Q V K E V K V V F N E H K L V F N E V K N V E E Q H K N V L E E K N M V L E E K N M V E E Q H K N V M E E S N I V M K E S N I V K R D G S R F V R D G S R F	Y D F Y T T T Y Y D F Y T T T Y Y D F Y N T T N T Y D F Y N T T N T Y Y N T T N T Y Y N Y T Y T T N T Y Y N Y S Y N Y Y N Y S Y N N Y Y N Y T T N N Y Y N T N N N Y Y N N N N N Y Y N N N N N Y Y N N N N	R - MGQC R - MGQC R - MGQC L - VGRC J - VGRC S - SATC S - CVC P QC P QC P QC P QC P QC P QC C - VC C - V	GHY TY GHY TY GHY TY GHY TY SHY TY SHY TY GHY TQ GHY TQ GHY TQ GHY TQ GHY TQ LHY TY LHY TY LHY TY LHY TY LHY TY SNY RQ SNY RQ ADY KQ ADY KQ NSY KQ NSY KQ NSY KQ NSY KQ SMY KQ SMY KQ SMY KQ SMY KQ	LVWEDT LVWEDT LVWENT LVWENT LVWENT LVWENT LVWENT LVWENT LVWENT MAWAKT MAWAKT MAWAKT MAWAKT MVWAKT LVWANT LWAYNT LAFADT LAFADT LAFADT LAFADT LVQAET IVQAET IVQAET IVQAET LVVINT		V T K C           V T K C           V A T C           V A T C           V T E C           V T E C           V T T C           V T T C           V T T C           V T T C           V T T C           V T N C C           V A N C           V T R C           V T R C           V T R C           V T R C           V T R C           V T R C           V T R C           V T R C           <	P P F S		GLSIVG GLSIVG KLSIVG KLSIVG GLSIVG GLSIVG GLSIVG GLSIVG GLSIVG GLSIVG GLSIVG GLSIVG GLSIVG GLSIVG GLSIVG KLMIVG KVFVVFV KVFVVFV KVFVVFV KVFVVFVFVFV KVFVVFV KVFVVFV KVFVVFVFVFV KVFVVFVF	NY G C NY	P GGNYP G GGNYP G P GGNYP G P GGNYA G P GGCP - P GGCCP - P GGCNI LG P GGNYE G P GGNYE G P GGNWNN P GGNWNN P GGNWNN P GGNWNN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNYAN P GGNYA P GGNYA	147 146 146 146 147 147 147 140 140 140 140 140 140 153 141 141 141 141 141 144 148 148 148 148
SmvAL16       Smp_124070       68       LNGREATRNWYDEIIQHDFNGQNQPGTGHFTQVIWKSTIKAGFGSALSKDGKKVYVVGRYKPAGNIID       135         SmvAL6       Smp_124050       68       ITGEEVSQTWYSEIDYHDF-TSRHFTQMIWKSTIRAGFGLAFSQDQTKAYVVGRYLPVGNK-G       134         SmvAL17       Smp_331830       71       FTGADATKTWYQEIEDYHDFTSQFFFTQVIWKSTITAGFGRAWSKDRHSIYVVGRYDPPGNFSD       138         SmVAL13       Smp_200460       68       VACLNAIQAWYKQSENYDYNEDNQESKGYFTQMIWKKKKKKVGFGFKSDVGHSIYVVGRYDPPGNFSD       138	SmVAL28 SmVAL27 SmVAL15 SmVAL5 SmVAL29* SmVAL9* SmVAL2 SmVAL2 SmVAL12 SmVAL22 SmVAL12 SmVAL22 SmVAL14 SmVAL20 SmVAL19 SmVAL19 SmVAL30 SmVAL30 SmVAL3 SmVAL34 SmVAL24 SmVAL24 SmVAL25 SmVAL34 SmVAL35	<pre>Smp_176160 Smp_176160 Smp_070250 Smp_336880 Smp_12670 Smp_123550 Smp_123540 Smp_123540 Smp_13680 Smp_02630 Smp_02630 Smp_026490 Smp_026490 Smp_1231370 Smp_123090 Smp_001890 Smp_002060 Smp_002060 Smp_002060 Smp_300080 Smp_316760 Smp_316760 Smp_131720 Smp_141550 Smp_141550 Smp_141550 Smp_141550 Smp_141550</pre>	77 TD I K TG FOL 77 KD I K TG FOS 77 ST VE I G FQR 77 YT VE RAVKL 75 QT I EQAFDA 74 ANVQT AMDE 74 PT I K S G VDA 74 PT I K S G VDA 74 PT I K S G VDA 74 ST I K S A VDA 75 SVDA I S K VDA 75 SVDA I S K VDA 77 SI GNA SV 77 S I GNA SV 77 S K CAASV 77 S LAGAASV 77 SELAGAVAY 77 SELAGAVAY	V D E V K N V L D E V K N V L D E V K N V L D E V K N V F D E S Q N V V F D E S Q N V V F S E A M Y V F D E V K Q V K E V K V V F N E H K L V F N E V K N V E E Q H K N V L E E K N M V L E E K N M V E E Q H K N V M E E S N I V M K E S N I V K R D G S R F V R D G S R F	Y D F Y T T T Y Y D F Y T T T Y Y D F Y N T T N T Y D F Y N T T N T Y Y N T T N T Y Y N Y T Y T T N T Y Y N Y S Y N Y Y N Y S Y N N Y Y N Y T T N N Y Y N T N N N Y Y N N N N N Y Y N N N N N Y Y N N N N	R - MGQC R - MGQC R - MGQC L - VGRC J - VGRC S - SATC S - CVC P QC P QC P QC P QC P QC P QC C - VC C - V	GHY TY GHY TY GHY TY GHY TY SHY TY SHY TY GHY TQ GHY TQ GHY TQ GHY TQ GHY TQ LHY TY LHY TY LHY TY LHY TY LHY TY SNY RQ SNY RQ ADY KQ ADY KQ NSY KQ NSY KQ NSY KQ NSY KQ SMY KQ SMY KQ SMY KQ SMY KQ	LVWEDT LVWEDT LVWENT LVWENT LVWENT LVWENT LVWENT LVWENT LVWENT MAWAKT MAWAKT MAWAKT MAWAKT MVWAKT LVWANT LWAYNT LAFADT LAFADT LAFADT LAFADT LVQAET IVQAET IVQAET IVQAET LVVINT		V T K C           V T K C           V A T C           V A T C           V T E C           V T E C           V T T C           V T T C           V T T C           V T T C           V T T C           V T N C C           V A N C           V T R C           V T R C           V T R C           V T R C           V T R C           V T R C           V T R C           V T R C           <	P P F S		GLSIVG GLSIVG KLSIVG KLSIVG GLSIVG GLSIVG GLSIVG GLSIVG GLSIVG GLSIVG GLSIVG GLSIVG GLSIVG GLSIVG GLSIVG KLMIVG KVFVVFV KVFVVFV KVFVVFV KVFVVFVFVFV KVFVVFV KVFVVFV KVFVVFVFVFV KVFVVFVF	NY G C NY	P GGNYP G GGNYP G P GGNYP G P GGNYA G P GGCP - P GGCCP - P GGCNI LG P GGNYE G P GGNYE G P GGNWNN P GGNWNN P GGNWNN P GGNWNN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNWIN P GGNYAN P GGNYA P GGNYA	147 146 146 146 147 147 147 140 140 140 140 140 140 153 141 141 141 141 141 144 148 148 148 148
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Fig. 2 Multiple sequence alignment of 36 *S. mansoni* SCP/TAPS domains. Newly identified SmVALs within this study are in bold. The asterisk at SmVAL29 signifies that although identified before this study, it has been first time analysed. The black bar below the sequence alignment indicates CAP domain location. Highly conserved residues (≥ 90% identity threshold) are highlighted based on physicochemical properties (aliphatic/hydrophobic—pink, aromatic—orange, positive—blue, negative—red, hydrophilic—green, conformationally special—magenta). Conserved cysteine residues are highlighted in yellow. Distinct deletion regions typical for previously proposed group 1 and group 2 SmVALs are boxed. The alignment was processed in Jalview [35]

latest genome annotation differs by only 9 nucleotides from the original characterization, the SmVAL3 and SmVAL5 CDSs are now shorter at the 5' end by 105 bp and 66 bp, respectively. The complete comparison of previously published characterizations of individual genes with the current analysis we present in this work, including the changes in nomenclature, can be found in Additional file 6: Table S4.

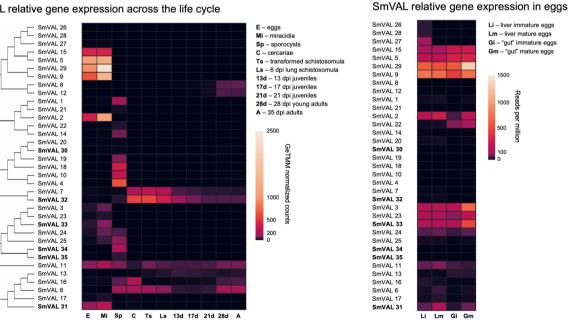
## Life cycle expression patterns of SmVAL genes highlight dominance in early larval stages and stage-specific profiles for SmVAL9 and SmVAL29

After SmVAL family members were identified according to the recent genome version, it was important to determine gene expression across the life cycle to identify which of these genes are specific for the egg stage. This was accomplished via comparative bioinformatic analysis of publicly available gene expression datasets for each stage. In selecting the datasets, emphasis was placed on covering the widest possible range of life stages while maintaining the comparability of these datasets with respect to the methodology of their preparation and appropriate data standardization. For this purpose, GeTMM normalization was used, as it allows not only a direct comparison of relative gene expression between stages but also of individual genes within a stage. According to our analysis, SmVALs are relatively highly expressed at the miracidia stage, accounting for more than 41% of all SmVAL transcripts cumulatively across the life cycle. The second most active stage in terms of expression was the egg stage, with just under 21% of the transcripts being expressed, and the third stage was the sporocyst stage, with just over 12% of the total relative SmVAL expression. For the remaining life stages analysed, the relative expression of SmVAL genes was very low, ranging from as low as 1.31% in 21 dpi juveniles to 5.84% in cercariae (see Additional file 8: Table S5).

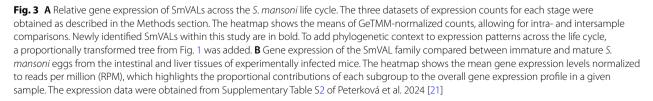
As Chalmers et al. (2008) [14] and Farias et al. (2019) [23] revealed through qPCR analysis in their seminal work, our meta-analysis of publicly available RNA-Seq data pointed to both universal and development-specific expression patterns of various SmVALs across different life cycle stages (Fig. 3A). First, of a total of 35 genes, SmVAL20, SmVAL26, SmVAL27, SmVAL28 and SmVAL30 do not seem to be transcribed at any life stage (<10 GeTMM normalized counts). In contrast, SmVAL11, the only member of the SmVAL family that contains two SCP/TAPS domains, appears to be consistently expressed regardless of developmental stage. A similar trend was observed for SmVAL6 and SmVAL7. In addition, the newly identified SmVAL32 gene was also relatively universally expressed, except at the egg and miracidium stages. In terms of developmentally specific expression, the sporocyst is a stage where the most stage-specific SmVALs are expressed. While SmVAL14, SmVAL19, SmVAL21, SmVAL22 and SmVAL35 are expressed relatively weakly, SmVAL1 and SmVAL34 expression is notable (between 100 and 200 GeTMM normalized counts); SmVAL4, SmVAL10, and SmVaL18 are among the most expressed SmVAL genes across the life cycle (>250 GeTMM normalized counts). Another developmentally specific expression pattern was observed for SmVAL8 and SmVAL12, which formed

## Α

SmVAL relative gene expression across the life cycle



Β



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Fig. 4 Pairwise sequence alignment of SmVAL29 and SmVAL9. Identical residues are highlighted in green, and the predicted signal peptide between positions 24 and 25 according to Phobius analysis is indicated by a red box. Conserved cysteine residues are highlighted in yellow

a common branch according to our updated phylogenetic analysis. These two genes are the only SmVALs exclusively expressed in juvenile and adult worms in the definitive host. The expression of SmVAL8 and SmVAL12 is first detectable in the third week after host infection, and their levels increase markedly in the fourth week in freshly paired adults, reaching a maximum at the fifth week after infection in egg-laying adults. The most striking trend in our analysis was the observed combination of the abundance and intensity of SmVAL expression in the eggs and miracidia. A total of 9 different SmVALs were specifically expressed at these stages. While this stage-specific expression has been previously described for SmVAL2, SmVAL3, SmVAL5 and SmVAL9, our complete comparative analysis of all 35 SmVAL genes revealed that SmVAL15, SmVAL23, SmVAL29, SmVAL31 and SmVAL33 also follow this pattern. Furthermore, SmVAL2, SmVAL5, SmVAL9 and SmVAL29 presented the highest expression compared with the other genes in the whole family. The most highly transcribed gene from this family is SmVAL29, with 2344 GeTMM normalized counts in miracidia, almost twice as high as the second most highly expressed SmVAL of all, SmVAL9, and many fold greater than most of these genes throughout the life cycle. Together with SmVAL5, these two genes were also the most transcriptionally active at the intramammalian egg stage (Fig. 3B).

Since our recent study revealed that *S. mansoni* egg gene expression is critically dependent on the developmental stage of the egg and, more importantly, the tissue of origin [21], we also analysed SmVAL gene expression within these datasets (further referred to as "organ datasets"). These data could not be directly compared with the rest of the datasets used because of different library preparations and were therefore analysed separately. When examining the overall pattern of expression in different groups of eggs, it is clear that the expression patterns of the most highly expressed genes correspond to the meta-analysis where mixed liver eggs were used. These genes are primarily SmVAL2, SmVAL5, SmVAL9, SmVAL15 and SmVAL29.

However, some genes have remained undetected due to the limited resolution of life cycle expression analyses. While no expression of SmVAL26 or SmVAL28 was detected in the GeTMM-normalized datasets, low expression in immature liver eggs was detected within the organ egg datasets. SmVAL27 was also clearly detected in liver immature eggs, although it was present in very low numbers in the life cycle expression meta-analysis (see Additional file: 2 Table S2) and this signal was lost due to data normalization. Another example is SmVAL22, which is expressed only in intestinal eggs; therefore, its expression was not detected in the life-cycle analysis because the source study for the egg dataset used only liver eggs [16]. This is likely the reason why the expression levels of SmVAL3 and SmVAL33, which are prominent in intestinal eggs within organ datasets, are only weakly evident in the life cycle analysis. In the organ datasets, SmVAL9 and SmVAL29 were also the most highly expressed SmVALs, which were steadily expressed from immature to mature eggs in both liver and intestine of the host. Compared with that of SmVAL9, the gene expression of SmVAL29 in intestinal eggs increased even more markedly at maturity (Fig. 3B).

The first secretomic study identified SmVAL9, which has a signal peptide, in egg secretions and this protein has also previously been hypothesized to assist in extracellular matrix (ECM) remodelling during the migration of eggs through tissues [5, 22]. On the other hand, the closely related SmVAL29 protein lacks a signal peptide (Fig. 4), has not been detected in egg secretions, and its function is unknown. Both SmVALs are the most dominantly expressed in eggs and miracidia, and for these reasons, these two proteins were selected for further studies.

## The most transcribed SmVAL9 and SmVAL29 are localized to miracidial glands and surface with no detected secretion from eggs

For the immunolocalization of the most highly expressed SmVAL9 and SmVAL29 in eggs and miracidia, antisera were raised against proteins produced recombinantly in the bacterial system. Primarily mature eggs were selected for immunolocalization, as these are the eggs that should be the most active in terms of secretion [3, 43]. Our experiments revealed that the tissue localization of both proteins in eggs and miracidia is identical. Neither SmVAL9 nor SmVAL29 were observed to be secreted into the surrounding liver or intestinal tissues, nor did the signal correspond to the egg subshell envelope, where the egg-secreted proteins are believed to be synthesized [3]. In contrast, on the basis of the atlas of *S. mansoni* organs [44], the observed localizations corresponded

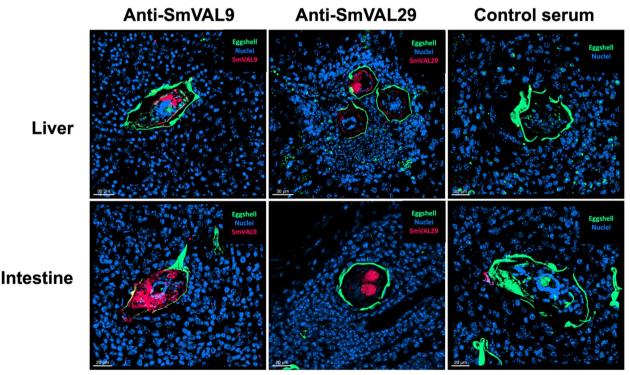
with the lateral (penetration) glands of the miracidium, in both intestinal and liver sections. These effects were noticeably observed in both transverse and longitudinal sections through the egg/miracidium. Moreover, anti-SmVAL9 and anti-SmVAL29 immunoreactivity was also clearly associated with the surface of developed miracidia larvae (Fig. 5), again in sections from both intestine and liver tissues. No significant signal was observed in the samples treated with the control sera (Fig. 5).

## SmVAL9 and SmVAL29 do not interact with the array of human cell receptors

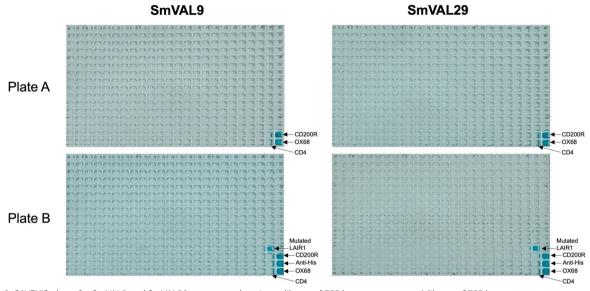
Because our immunolocalization experiments did not indicate that SmVAL9 and SmVAL29 are secreted from the egg, we decided to support these findings by screening for potential protein interactions between the parasite and its mammalian host. The *S. mansoni* SmVAL proteins SmVAL9 and SmVAL29 were produced recombinantly in HEK293-6E cells and tested with SAVEXIS against a library of 755 human cell surface receptors. In these assays, no significant interactions were observed between the parasite proteins and human receptors, as shown by the lack of blue signals in any of the wells aside from the positive controls and a mutated LAIR1 receptor (containing T67L, N69S, and A77T mutations; well M23 of plate B), which was proven to bind indiscriminately to many different proteins in the SAVEXIS screens and was therefore excluded from the final results (Fig. 6). These observations support our findings that these proteins are not secreted into the vicinity of the egg and are more likely function in the miracidium stage. For readings for each well see Additional file: 9 Table S6.

## Discussion

Our comprehensive study of VAL in *S. mansoni* proteins challenges existing assumptions about the roles of SmVALs previously attributed to the egg stage, particularly in relation to mammalian host interactions. Initial hypotheses about numerous egg SmVALs were largely based on their detection in the early secretome [5] leading to assumptions that these proteins might contribute to mammalian host immunomodulation and tissue remodelling and aid in egg migration [12–14, 21–23]. However, our findings challenge this view, highlighting the complexity of the SmVAL family and raising new questions about their precise roles in host invasion and tissue interactions.



**Fig. 5** Immunolocalization SmVAL9 and SmVAL29 in the sections of *S. mansoni* infected mouse liver and intestine. Confocal close-ups illustrate mature eggs with developed miracidia. The red signal represents anti-SmVAL serum-specific sites, the green signal indicates eggshell autofluorescence, and the blue signal indicates the DAPI-labelled cell nuclei. Both SmVAL proteins are localized in the miracidia penetration glands and the surface of the developed larvae. There was no specific protein signal in the control serum obtained from an non-immunized mouse



**Fig. 6** SAVEXIS plates for SmVAL9 and SmVAL29 preys tested against a library of 755 human receptors. A library of 755 human receptors was arrayed across two 384-well plates (plates A and B). Controls are located in the bottom right corner of each plate. OX68 (well P24 on plates A and B) and anti-His (well O24 on plate B) are two biotinylated antibodies used as baits and target the Cd4 tag and 6 × His tag of the recombinant proteins, respectively. They act as positive controls by capturing prey through the relevant tags. CD4 (well P23 on plates A and B) corresponds to the biotinylated rat Cd4 (d3 + 4) tag used as bait. It acts as a negative control, and any signal observed in this well is considered background noise from the prey. CD200R (well O24 in plate A and N24 in plate B) is a positive control interaction between rat Cd200, which is used as bait, and rat Cd200R, which is used as prey. A mutated human LAIR1 ectodomain (well M23 in plate B) was included as bait in the SAVEXIS assay and proved to be very promiscuous, binding to > 75% of all preys tested in the assay

Since the last SmVAL family revision, the S. mansoni genome assembly has advanced significantly [26], as has the capacity and accuracy of bioinformatic tools [25]. Using an updated genomic dataset, we identified six previously undescribed SmVAL genes, notably expanding the known family diversity. Consequent sequence analysis of the revised family challenges the classification of SmVALs on the basis of signal peptide presence, which was previously used to divide SmVALs into secretory (Group 1) and nonsecretory (Group 2) categories, reflecting their phylogenetic relationships [12–14, 23]. Using the most advanced version of SignalP (v6.0), we found that previous assumptions about group features based on SignalP 3.0 may have been flawed by an early version of the tool. Consequent analysis with the Phobius tool, which enables the differentiation of signal peptides and transmembrane elements, revealed that in several SmVAL group 1 proteins these elements were likely confused, leading to incorrect conclusions. Even though predictive tools are not always completely accurate and extra care must be taken when interpreting in silico data (reviewed in [21]), we believe that our combined approach yields more accurate insights. Together, our revision suggests that earlier assumptions about these proteins and their potential secretion and functional roles of these proteins may require substantial reconsideration while highlighting the importance of regular re-evaluation as genomic datasets and prediction tools improve.

Following SmVAL family revision and sourcing high-quality data for eggs and miracidia from existing databases, along with the application of an innovative normalization method [37], we created a new gene expression atlas for both the updated SmVAL family and all S. mansoni genes. Although the expression profiles of SmVALs throughout the life cycle have been investigated relatively recently via RT-PCR [23], the expression in the egg stage was omitted, as were expression profiles of newly identified genes presented in this study. Additionally, RT-PCR may not be reliable for comparing gene expression across schistosome stages because of the lack of stable reference genes [45]. In contrast, RNA-Seq-based approaches have proven invaluable, but highquality egg and miracidia RNA-Seq data have long been lacking in current gene expression atlases [16, 46]. In addition to supporting previous hypotheses that SmVALs likely play distinct roles throughout schistosome development, the pronounced expression of distinct SmVALs in eggs and sporocysts (stages that produce invasive

larvae) indicates that these proteins likely play a role in host invasion.

That SmVALs are likely to be employed during host invasion rather than host exit is also supported by our localization experiments. SmVAL9 and SmVAL29, the most highly expressed SmVALs in eggs, are concentrated within miracidial penetration glands and the larval surface which are critical for the establishment of infection in the molluscan intermediate host. Preceding studies have suggested that SmVAL proteins expressed in eggs are actively secreted into mammalian host tissues on the basis of their detection in excretory-secretory products (ESPs). However, while SmVAL2, SmVAL3, SmVAL5 and SmVAL9 were identified in the first proteomic study of egg ESPs [5], they were not identified in later egg secretomic studies [4, 6]. In contrast, SmVAL2, SmVAL3 and SmVAL9 were detected during miracidium-to-sporocyst transformation, indicating their role in molluscan invasion [24]. Additionally, SmVAL9 was previously localized within the miracidium, and its proposed role in snail invasion this protein has been attributed a possible role in mammalian tissue remodelling and egg translocation [22]. However, this protein was only localized in the parenchyma of the miracidium, and no evidence was provided regarding its localization in the egg or its secretions [22]. Although SmVAL9-specific igGs were detected in the mice at 14 weeks post infection, thus indicating protein release from the eggs, it is likely a consequence of the late, chronic phase of infection, in which the death and disintegration of eggs trapped in the host tissues take place [2, 22, 47]. The only SmVAL that has been detected in egg secretions without the use of highthroughput omics methods is SmVAL26, but this protein appears to be a component of hatch fluid and is not truly secreted from intact eggs [4, 6, 11]. In line with the provided background, we found no evidence of SmVAL9 or SmVAL29 secretion from eggs into mammalian tissues, further supporting its miracidial origin.

Another support for our conclusions is the conspicuous similarity to the analogous situation in cercariae, which are invasive larvae that infect mammals. We found that SmVAL4, SmVAL10 and SmVAL18 were the most highly expressed SmVALs in sporocysts. These proteins have also been repeatedly identified in cercarial secretomes and localize to penetration glands of cercariae, likely supporting tissue invasion when schistosomes encounter the mammalian host [48–50]. Egg expression may therefore reflect the protein weaponry of miracidia in the same way that sporocysts reflect the protein weaponry of cercariae, as has been shown several times in the past [51–53]. These similarities further suggest that SmVALs may

function as multipurpose proteins essential for the invasion of both molluscan and mammalian hosts rather than facilitating tissue remodelling for egg migration in mammalian tissues.

Finally, the lack of binding to the 755 tested human cell receptors in our SAVEXIS screen further suggests that egg SmVALs may not engage directly in proteinmediated interactions with mammalian cells. Despite the previously reported ability of SmVAL9 to influence the expression of ECM remodelling-related molecules in murine macrophages [22], our screen did not identify any human receptors able to interact with the protein. This finding suggests that the previously observed interaction is either mediated by a cellular receptor that was not present in our high-throughput assay or that the ECM remodelling effects observed in earlier studies may be due to a nonspecific response to artificial protein treatment rather than a true biological interaction. Alternatively, interactions of different natures may take place, such as signalling lipid binding at the cell surface, a likely scenario given the lipid-binding properties of the CAP domain [54-57]. Nevertheless, the absence of specific interactions with mammalian host receptors aligns with the localization experiments, further supporting the conclusion that these proteins function in the miracidia rather than the egg.

## Conclusions

Our findings suggest that egg-expressed SmVALs are unlikely to directly mediate interactions with mammalian host tissues, as previously proposed. Rather, these molecules appear to be adapted primarily for the invasion of molluscan hosts. Notably, the identification of new SmVAL genes and their distinct expression profiles throughout the S. mansoni life cycle further supports the idea that SmVALs function at critical stages of invasion by miracidia and cercariae. While we cannot entirely dismiss a role for egg-expressed SmVALs in host-parasite interactions owing to their release upon egg damage, we believe that SmVAL molecules involved in host manipulation are more effectively studied at the life stages where the secretion of these proteins is undeniable. In future work, we therefore plan to apply a high-throughput SAVEXIS screen to cercarial SmVALs to definitively prove or disprove the ability of these proteins to bind to mammalian host cell receptors. In addition, techniques such as laser microdissection and improved proteomics could be implemented to further elucidate the localization and dynamics of SmVAL secretion across life stages, allowing a more precise understanding of these enigmatic proteins.

## **Supplementary Information**

The online version contains supplementary material available at https://doi.org/10.1186/s12864-025-11369-4.

Additional file 1: Table S1. Datasets for gene expression meta-analysis. Accession numbers of publicly available RNA-Seq datasets used for the meta-analysis of gene expression of SmVALs across the *S. mansoni* lifecycle.

Additional file 2: Table S2. HTSeq counts for gene expression meta-analysis. HTSeq counts for all the compared life stages and replicates retrieved from Wormbase ParaSite to which the GeTMM normalisation was applied.

Additional file 3: Table S3. GeTMM counts for gene expression metaanalysis. GeTMM normalised counts for all *S. mansoni* genes used for direct intra- and intersamples comparisons of gene expression throughout the life-cycle.

Additional file 4: Document S1. Novel SmVAL primers and sequencing data. The sequences of primers used to amplify novel SmVAL30-35 genes and sequencing data of amplicons.

Additional file 5. Document S2. Primers and cloning for *E. coli* expression. The primers for SmVAL9 and SmVAL29 gene constructs for In-fusion cloning and subsequent *E. coli* protein expression.

Additional file 6: Table S4. Revision of the SmVAL family. The complete revision of SmVAL family including newly identified SmVALs and comparison of current analysis with previously published data on the family regarding gene details, signal peptide predictions and nomenclature.

Additional file 7: Figure S1. S. mansoni SCP/TAPS domains distance matrix. The similarity distance matrix of identified S. mansoni SCP/TAPS domains.

Additional file 8: Table S5. Relative SmVAL expression across the life cycle. Relative expression of all the members of SmVAL family throughout the lifecycle.

Additional file 9: Table S6. SmVAL SAVEXIS results. Complete readout of the SmVAL9 and SmVAL29 plates used for SAVEXIS protein interaction screen.

### Acknowledgements

Microscopy was performed in the Vinicna Microscopy Core Facility cofinanced by the Czech-Biolmaging large RI project LM2023050. Computational resources were supplied by the project "e-Infrastruktura CZ" (e-INFRA LM2018140) provided within the program "Projects of Large Research, Development and Innovations Infrastructures". We would like to acknowledge Gavin Wright for providing access to the library of human receptors, Kristýna Peterková for her help with the study design and brainstorming and Tomáš Macháček for reading and commenting on the manuscript.

#### Authors' contributions

LK has performed the bioinformatic analyses, cloning and PCR verification, E. coli protein expression and animal immunization, data interpretation and visualisation and composed the manuscript. LJ performed the histological processing and immunolocalization experiments. ZI, AR and CC performed the HEK protein expression followed by SAVEXIS protein–protein interaction screen. JD supervised the project and reviewed the manuscript. All authors read and approved the final manuscript.

#### Funding

This study was supported by the Czech Science Foundation 23-06638S (https://gacr.cz/en) (to JD), Schistosomiasis Research Grant FR4003935 by ARES Trading S.A., A., an affiliate of Merck KGaA, Darmstadt, Germany (https:// www.merckgroup.com/en) (to JD), the Grant Agency of Charles University project 198722 (https://cuni.cz/UKEN-753.html) (to LK), and Charles University institutional funding (https://cuni.cz/UKEN-1889.html): Cooperatio Biology, UNCE24/SCI/011 (LJ), SVV 260678/2023 (to LK) and an MRC Career Development Award MR/W016397/1 (to CC)—this UK funded award is carried out in the frame of the Global Health EDCTP3 Joint Undertaking". Microscopy was performed in the Vinicna Microscopy Core Facility co-financed by the Czech-Biolmaging large RI project LM2023050 funded by MEYS CR. Computational resources were supplied by the project "e-Infrastruktura CZ" (e-INFRA LM2018140 funded by MEYS CR) provided within the program "Projects of Large Research, Development and Innovations Infrastructures". The funders had no role in the study design, data collection and analysis, decision to publish, or preparation of the manuscript.

### Data availability

Nucleotide sequence data reported in this paper are available in GenBank<sup>™</sup> under the accession numbers PQ565842 for SmVAL29, PQ565715 for SmVAL30, PQ565716 for SmVAL31, PQ565730 for SmVAL33, PQ565731 for SmVAL34, and PQ565841 for SmVAL35. All relevant intermediate files regarding SmVAL gene identification are available at https://github.com/lukykony/ SmVAL\_identification. All data generated or analysed during this study are included in this published article and its supplementary information files. Any intermediate datasets in the analyses performed and relevant data not directly present in the manuscript can be obtained from the corresponding author upon reasonable request.

### Declarations

### Ethics approval and consent to participate

Research involving experimental animals was performed in accordance with the animal welfare laws of Czechia and under the European regulations for transport, housing and care of laboratory animals (CZ Act No. 246/1992, EU Directive 2010/63/EU amended by Regulation 2019/1010/EU). Experiments were approved by the Animal Welfare Committees of University of Life Sciences and the Ministry of Education, Youth and Sports of Czechia (MSMT-29299/2020–3). All animals used in the study were maintained by a certified person (Certificate Number CZ 02847) in an accredited facility. Ketamine-xylazine anaesthesia was employed to sacrifice the mice as indicated in "Parasite material" section.

## **Consent for publication**

Not applicable.

## **Competing interests**

The authors declare no competing interests.

#### Author details

<sup>1</sup>Department of Parasitology, Faculty of Science, Charles University, Prague, Czechia. <sup>2</sup>Department of Ecology, Center of Infectious Animal Diseases, Faculty of Environmental Sciences, Czech University of Life Sciences, Prague, Czechia. <sup>3</sup>Department of Zoology and Fisheries, Center of Infectious Animal Diseases, Faculty of Agrobiology, Food and Natural Resources, Czech University of Life Sciences, Prague, Czechia. <sup>4</sup>Department of Biology, University of York, York, UK. <sup>5</sup>Institute of Organic Chemistry and Biochemistry, Czech Academy of Sciences, Prague, Czechia. <sup>6</sup>Hull York Medical School, University of York, York, UK. <sup>7</sup>York Biomedical Research Institute, University of York, York, UK.

#### Received: 4 December 2024 Accepted: 14 February 2025 Published online: 24 February 2025

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