RESEARCH PAPER



# *In Silico* Structural Analysis, Classification, and Functional Annotation of an Uncharacterized Protein from an Aquatic Fungus *Lindgomyces ingoldianus*

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## Abstract

An uncharacterized protein from Lindgomyces ingoldianus was initially annotated to contain various domains with promising biotechnological applications. Thus, this study was conducted to determine the structural characteristics, classification, and potential function of this protein through in silico methods. Results revealed that this protein has a neutral charge and is unstable and non-polar. It is predicted to have a signal peptide, glycoside hydrolase family 114 (GH114) domain, low complexity region, and fungal type cellulose-binding domain (fCBD) or type 1 carbohydrate-binding module (CBM1) region. Structural characterization and phylogenetic analysis revealed that this protein is an endo- $\alpha$ -1,4-polygalactosaminidase enzyme. This protein was also predicted to contain 36 active sites and is extracellularly secreted. Molecular docking analysis showed that it could bind galactosaminogalactan (GAG), a key virulence factor for Aspergillus fumigatus chronic infections. The binding of this protein to GAG was much better than Ega3, which could be attributed to the presence of the fCBD region that is unique to this protein. It is hypothesized that the fCBD domain helps in carbohydrate recognition and holds them in place for maximum catalysis in the GH114 domain. Finally, this protein is found to be related to its orthologue from the plant pathogenic fungus Zopfia rhizophila.

## Introduction

Fungi represent one of the most diverse groups of organisms on earth. Organisms under Kingdom Fungi are eukaryotic and bear spores. They are achlorophyllous organisms, meaning they do not have chlorophyll and are thus, not capable of photosynthesis. Fungi generally reproduce both sexually and asexually. They could either occur as single-celled organisms as yeasts or multicellular organisms by forming filaments. Fungal cells contain cell walls that are made up of chitin or cellulose or both, together with many other complex organic molecules (Alexopoulos & Wims, 1979)

Fungi are recognized for their various roles as pathogens of plants and animals, as one of the key drivers in the decomposition of many organic and inorganic materials, and as a source of compounds with enormous biotechnological potentials (Newbound *et al.*, 2010). One group of fungi, the *Dothideomycetes*, is the largest class under this kingdom. This group comprises species with an incredible diversity of lifestyles that have evolved multiple times. The first large-scale wholegenome comparison of 101 Dothideomycetes species was reported by Haridas et al. (2020). Their study produced a high-confidence phylogeny leading to the reclassification of 25 organisms, provided a clearer picture of the relationships among the various families, and indicated that pathogenicity evolved multiple times within this class. They also identified gene family expansions contractions across and the Dothideomycetes phylogeny linked to ecological niches providing insights into genome evolution and adaptation across this group.

One species included in the study mentioned above is Lindgomyces ingoldianus strain ATCC 200398 (Shearer & Hyde) Hirayama et al. This species is a freshwater fungus isolated from submerged decorticated wood. Part of the whole-genome shotgun sequence of this species is an unplaced genomic scaffold BDR25scaffold\_49 (Accession No.: NW\_022985210). Unplaced genomic scaffolds are those sequences found in an assembly with unknown chromosome placement. This genomic scaffold was predicted to express an mRNA (Accession No.: XM\_033697727) which encodes an uncharacterized protein BDR25DRAFT 381691 (Accession No.: XP 033540912). This protein was initially annotated to contain glycoside hydrolase family 114 (GH114), UV excision repair protein Rad23, and fungal cellulose-binding domain (CBM1) regions.

GH114 has been shown to disrupt microbial biofilm produced by Aspergillus fumigatus (Bamford et al., 2019). Moreover, Rad23 plays a central role in proteasomal degradation of misfolded proteins and DNA repair (Dantuma et al., 2009), while CBM1 is found in many proteins that catalyze the recognition and degradation of carbohydrates (Gilkes et al., 1991). The predicted presence of these domains makes this uncharacterized protein an interesting subject for investigation. Thus, this study was undertaken to confirm the expression of the uncharacterized protein from the mRNA expressed by the unplaced genomic scaffold of L. ingoldianus, as well as determine its physicochemical characteristics, domain architecture, tertiary structure, classification, active site location, subcellular localization, cleavage site, and ligand interaction through in silico methods.

## **Materials and Methods**

#### **Confirmation of mRNA Translation**

The fasta sequence of the mRNA (Accession No.: XM\_033697727) expressed by unplaced genomic scaffold BDR25scaffold\_49 (Accession No.: NW\_022985210) from *L. ingoldianus* was submitted to Expasy's Translate Server (Galsteiger *et al.*, 2005). Output format was set at Compact: M, -, no spaces on both forward and reverse strands. The selected open reading frame (ORF) was then aligned with uncharacterized protein BDR25DRAFT\_381691 (Accession No.: XP\_033540912) using Clustal Omega from the EMBL-EBI server (McWilliam et al., 2013).

## Physicochemical Characterization

The physicochemical characteristics of the uncharacterized protein from *L. ingoldianus* were determined by submitting the amino acid sequence to Expasy's ProtParam Server (Galsteiger *et al.*, 2005). This server is a tool that allows the computation of various physical and chemical parameters for a given protein stored in Swiss-Prot or TrEMBL or for a user-entered protein sequence.

## **Domain Architecture Analysis**

To investigate the identification of the conserved domains found in the uncharacterized protein of L. ingoldianus, domain architecture analysis was performed using the Simple Molecular Architecture Research Tool (SMART) (Letunic et al., 2021). SMART allows the identification and annotation of genetically mobile domains and the analysis of domain architectures. More than 500 domain families found in extracellular, and chromatin-associated signaling. proteins are detectable. These domains are extensively annotated concerning phyletic distributions, functional class, tertiary structures, and functionally important residues. Each domain is found in a non-redundant protein database, and search parameters and taxonomic information are stored in a relational database system. User interfaces to this database allow searches for proteins containing specific combinations of domains in defined taxa.

#### **Structure Prediction**

The online tool I-TASSER (Yang & Zhang, 2015) was used for homology modeling of the uncharacterized protein from L. ingoldianus. I-TASSER or Iterative Threading ASSEmbly Refinement is a hierarchical approach to protein structure prediction and structurebased function annotation. It first identifies structural templates from the PDB by multiple threading method LOMETS, with full-length atomic models constructed by iterative template-based fragment assembly simulations. Function insights of the target are then derived by re-threading the 3D models through the protein function database BioLiP. The PDB files of the models generated by I-TASSER were then visualized using EzMol v2.1 Molecular Display Wizard (Reynolds et al., 2018).

#### **3D Structure Refinement and Quality Validation**

The top predicted structure (Model 1) of I-TASSER was refined using local Protein structure REFinement via Molecular Dynamics (*loc*PREFMD) tool (Feig, 2016). This tool refines the predicted 3D structure of the protein by improving its local stereochemistry at the same time preserving the overall fold presented. The method uses force field-based minimization and sampling via molecular dynamics simulations with a modified force field to bring bonds, angles, and torsion angles into an acceptable range for high-resolution protein structures.

Furthermore, an assessment of the predicted model quality was done by submitting the top model predicted by I-TASSER and the model refined by locPREFMD to Ramachandran Plot Server (Anderson et al., 2005) and ProSA-web server (Wiederstein & Sippl, 2007). The refined structure was finally validated using VERIFY3D (Eisenberg *et al.*, 1997).

## **Protein Classification**

To confirm the relationship of the uncharacterized protein from L. ingoldianus to other proteins with known functions, molecular phylogenetic analysis was done. Initial identification of the protein was done through homology analysis using BLASTp (Johnson et al., 2008) and homology modeling using I-TASSER (Yang & Zhang, 2015) as previously. FASTA sequences of representative proteins were retrieved from UniProt KB (2021) and were aligned using Clustal W. Phylogenetic tree was constructed through Maximum Parsimony analysis using all sites for gaps/missing data treatment, tree-bisection-reconnection (TBR) as MP search method, and with 1000 bootstrap replicates. The alignment and construction of the phylogenetic tree were done using MEGA 11 software (Tamura et al., 2021).

#### **Active Site Detection**

To determine the active site of the uncharacterized protein from *L. ingoldianus*, the refined predicted 3D structure was submitted to Computed Atlas of Surface Topography (CASTp) of Proteins (Dundas *et al.*, 2006) server. This tool provides an online resource for locating, identifying and quantifying concave surface areas on three-dimensional protein structures.

#### Subcellular Localization & Signal Peptide Analysis

To predict the subcellular localization of the uncharacterized protein from L. ingoldianus, its fasta sequence was submitted to the DeepLoc-1.0 server (Almagro Armenteros et al., 2017). This server predicts the subcellular localization of eukaryotic proteins using the Neural Networks algorithm trained on UniProt proteins with experimental subcellular localization evidence. It only uses the sequence information to perform the prediction. Furthermore, the amino acid sequence of the uncharacterized protein was submitted to the SignalP-6.0 server (Teufel et al., 2022) to determine the cleavage site and further analyze the secretion and translocation of the protein encoded by L. genomic ingoldianus unplaced scaffold BDR25scaffold\_45. This online server predicts the presence and type of signal peptides and the location of their cleavage sites in proteins from Archaea, Grampositive Bacteria, Gram-negative Bacteria, and Eukarya.

#### **Protein-Protein Interaction Analysis**

Protein-protein interactions were predicted using STRING v.11.5 software (Szklarczyk *et al.*, 2021). On the web server, "GH114" was used in the query, and a fungal species was selected among the matches displayed.

## Ligand/Substrate Interaction

HDOCK server (Yan *et al.*, 2020) was used to determine the interaction of the uncharacterized protein from *L. ingoldianus* to its probable ligand or substrate. This docking server is based on a hybrid algorithm of template-based modeling and *ab initio-free* docking. Model 1 of the predicted structure was compared against its closest structural homolog, indicated by I-TASSER. Before submission for docking, the target protein sequence was cleaved first at a site determined by SignalP-6.0. Also, the structure of the carbohydrate substrate was constructed first using the Carbohydrate Builder tool on the Glycam website (Grant *et al.*, 2016).

## **Protein Evolution Analysis**

Orthology analysis was conducted to determine the relationship between this uncharacterized protein from L. ingoldianus and those same proteins from other fungal species. This was done by homology analysis followed by molecular phylogenetic analysis. BLASTp (Johnson et al., 2008) was used to search for protein orthologues. Only those above 90% identity with the query sequence were retrieved. The retrieved sequences were then aligned using Clustal W. Phylogenetic tree was constructed through Maximum Parsimony analysis using all sites for gaps/missing data treatment, tree-bisection-reconnection (TBR) as MP search method, and with 1000 bootstrap replicates. The alignment and construction of the phylogenetic tree were done using MEGA 11 software (Tamura et al., 2021).

## **Results and Discussion**

#### **Translated mRNA**

Figure 1A shows several ORFs found in both forward and reverse strands of the translated mRNA expressed by unplaced genomic scaffold BDR25scaffold\_49 from *L. ingoldianus*. Among these ORFs, the longest one was from the 5'3' Frame 2 (Figure 1A pink box). All the amino acid residues of this ORF were aligned with the amino acid residues of the uncharacterized protein BDR25DRAFT\_381691 (Figure 1B). This confirms that the uncharacterized protein BDR25DRAFT\_381691 is encoded by the mRNA expressed by unplaced genomic scaffold BDR25scaffold\_49.

#### **Physicochemical Characteristics**

Δ

В

The physicochemical characteristics of the uncharacterized protein from *L. ingoldianus* are summarized in Table 1. This protein has 370 amino acid residues and a molecular weight of 40, 442.44 Da. The theoretical isoelectric point of 6.71 suggests that this protein is neutral. The equal presence of positively charged and negatively charged residues further supports this protein's neutrality. Moreover, the computation of the instability index at more than 40 classifies this protein as unstable. The aliphatic index of

the protein is 57, which regards it as a positive factor for increasing its thermostability. Lastly, the grand average of hydrophobicity (GRAVY) of this protein is -0.582. A negative GRAVY implies a non-polar characteristic of this protein.

#### **Domain Architecture**

The uncharacterized protein from *L. ingoldianus* was shown to contain a signal peptide, glycoside hydrolase family 114 (GH114) domain, low complexity region, and fungal type cellulose-binding domain (fCBD) also known as carbohydrate-binding module 1 (CBM1) (Figure 2). The signal peptide comprises the amino acid residues 1-17, the GH114 domain of the residues 27-259, the low complexity region of the residues 287-332,

| -5'3' Frame 1  |
|--|
| RQHVVMASVGLVVC-YILRANHSLHSGAKMADHPYWHAGYVEESTSTHGCSSI-CRPFRQ-CHHHSFESSREDGNLLFQRRHGGGLEGRRERLPDK-PRKNTSRVAE-EMDTDG-LQS-RCYGEKNQDGFRQRVRCFGP<br>R-YRWLPKR-RLKPPESRRHQLHAIPAKERFVL-HEYWPQK-P-YSFDCGSDHRFRGERGVCS-GRMLCLQRVSQFEQTCVPYRISP-NEPCLRQ-QADCLHLSWNHGYEYCYEE-VLGWIDTLLRW-PGHPHKGRNPT<br>SEEYIKACIWPNYKPNHSIFNTRTTYHEIKTSKFDQDVHSEATNNHTSESGRWWLPAKALGSVRWTGLEGLYGLRIAVPVQGGIAAVLLPVSIKVGLI-GSSGFFV-CIFNIPGA-TITSRAFSH-                 |
| 5'3' Frame 2   |
| ANMLSWILWAWLFASTSFAQTTLFTRGQKWQIILTGTPDMSKSPLPPTDAPVFDVDLFDNDATTITALKAQGKTVICYFSAGTVEDWRDDAKDFPTNDQGKILPEWPNEKWIRTGSSKVRDVMARRIKMASDKGCDALDP<br>DNIDGYQNDNGLNLQKADAISFMQFLQKNASYYNMNIGLKNSLDILSTVAPIIDFAVNEECAARAECSAYNEFLNSNKPVFHIEYPFKMNPVSDNDKRTACTSAGTTGMSTVMKNKSLDGLTLYCDGSQADTPTKGGTRP<br>PKSTSRPVSGPTTNLTTPSSTPEPPTTKSKPPSSTKTSTQRPPTTTPANPGGGGCQQKHWDQCGGQDWKGCTVCASPYQCKGVSPPYYYQCL-KLA-FRAVLDSLCNVSSIYPVHRR-RQGLFPTE               |
| 5'3' Frame 3   |
| PTCCHGECGLGCLLVHPSRKPLSSLGGKNGRSSLLARRICRRVHFHPRMLQYLMSTFSTMMPPPSQL-KLKGRR-FAISAPARWRTGGTTRKTSRQMTKEKYFQSGRMRNGYGRVAPKLEMLWREESRWLPTKGAMLWTQ<br>II-MATKTITA-TSRKPTPSASCNSCKRTLRTIT-ILASKIALIFFRLWLRS-ISR-TRSVQLGQNALPTTSFSIRTNLCSISNIPLK-TLSQTMTSGLPAPQLEPRV-VLL-RISPWMD-HFTAMVARRTPPQRAEPDL<br>RRVHQGLYLAQLQT-PLHLQHQNHLPRNQNLQVRPRPLRGHQQPHQRIRAVVAASKSTGISAVDRTGRVVRFAHRRTSARGYRRTITSVYKSWPNLGQFWILCVMYLQYTRCIDDNVKGFFPL                  |
| 3'5' Frame 1   |
| LGGKKPLTLSS <mark>MHRVY-R</mark> YITQRIQNCPKLGQLL-TLVIVRRRYPLALVRCANRTTLPVLSTALIPVLLLAATTARIRWCGCWWPLSGRLGRTWRF-FRGRWFWC-RWSG-VCSWARYRP-CTLRRSGSALCGGVRLAT<br>IAVKCQSIQGLILHNSTHTRGSS-GAGSPLVIV-DRVHFRGIFDWEHRFVRIEKLVVGRAFCPSCTLLVHREIYDRSHSRKNIKAIFEANIHVIVRSVLLQELHEADGVGFLEV-AVIVLVAIYIIWVQSIAPFVGSHLD<br>SSRHNISNFGATRPYPFLIRPLWKYFSLVICREVFRVVPPVLHRAGAEIANYRLPLSFQSCDGGGIIVEKVDIKYWSIRGWKWTLRHIRRASKDDLPFLPPSEESGLREGCTSKQPSPQKP-QHVG |
| 3'5' Frame 2   |
| SVGKSP-RYRLCTGYIEDTLHKESRTALN-ANFYRHWYGGDTPLHWYGDAQTVQPFQSCPPH-SQCFCWQPPPGFAGVVVGGL-VDVLVELGGFDFVVGGSGVEDGVVRFVVGPDTGLDVLFGGRVPPFVGVSAWLP<br>SQ-SVNPSKDLFFITVLIPVVPAEVQAVRLSLSETGFILGGYSIWNTGLFELRNSL-AEHSALAAHSSFTAKSMIGATVERISRLFLRPIFML-YEAFFCRNCMKLMASAFWRFKPLSFW-PSILSGSKASHPLSEAILI<br>LLAITSLTLELPVRIHFSFGHSGSIFPWSFVGKSFASSLQSSTVPALK-QITVFP-AFKAVMVVASLSKRSTSNTGASVGGSGLFDISGVPVRMICHFCPRVKRVVCAKDVLANNQAHRSHDNMLA                  |
| 3'5' Frame 3   |
| QMEKALDVIVYAPGILKIHYTKNPELP-IRPTFIDTGNSTAAIPPCTGTAM <mark>RKPYNPSSPVHRTDPSAFAGSHHRPDSLVWLLVASEWTSWSNLEVLISW-V</mark> VLVLKMEWLGL-LGQIQALMYSSEVGFRELWGCPPGYH<br>RSKVSIHPRTYSS-QYSYPWFQLRCRQSACHCLRQGSF-GDIRYGTQVCSN-ETRCRQSILP-LHTPRSPRL-SEPQSKEYQGYF-GQYSCYSTKRSFAGIA-S-WRRLSGLSRYRFGSHLYYLGPKHRTLCRKPS-F<br>FSP-HL-LWSYPSVSISHSATLEVFFLGHLSGSLSRRPSSPPPCRR-NSKLPSSLELSKL-WWWHHCRKGRHQILEHPWVEVDSSTYPACQ-G-SAIFAPE-REWFARRWY-QTTKPTEAMTTCW   |
|  |

| VIRT-47012:5'3'   | MLSWLLWAWLFASTSFAQTTLFTRGQKWQIILTGTPDMSKSPLPPTDAPVFDVDLFDNDA | 60  |
|---|--|-----|
| XP_033540912.1  | MLSWLLWAWLFASTSFAQTTLFTRGQKWQIILTGTPDMSKSPLPPTDAPVFDVDLFDNDA | 60  |
|   | *******************  |     |
| VIRT-47012:5'3'   | TTITALKAQGKTVICYFSAGTVEDWRDDAKDFPTNDQGKILPEWPNEKWIRTGSSKVRDV | 120 |
| XP_033540912.1  | TTITALKAQGKTVICYFSAGTVEDWRDDAKDFPTNDQGKILPEWPNEKWIRTGSSKVRDV | 120 |
|   | ***********************                                      |     |
| VIRT-47012:5'3'   | MARRIKMASDKGCDALDPDNIDGYQNDNGLNLQKADAISFMQFLQKNASYYNMNIGLKNS | 180 |
| XP 033540912.1  | MARRIKMASDKGCDALDPDNIDGYQNDNGLNLQKADAISFMQFLQKNASYYNMNIGLKNS | 180 |
| _   | **********************                                       |     |
| VIRT-47012:5'3'   | LDILSTVAPIIDFAVNEECAARAECSAYNEFLNSNKPVFHIEYPPKMNPVSDNDKRTACT | 240 |
| XP 033540912.1  | LDILSTVAPIIDFAVNEECAARAECSAYNEFLNSNKPVFHIEYPPKMNPVSDNDKRTACT | 240 |
|   | *************************                                    |     |
| VIRT-47012:5'3'   | SAGTTGMSTVMKNKSLDGLTLYCDGSQADTPTKGGTRPPKSTSRPVSGPTTNLTTPSSTP | 300 |
| XP 033540912.1  | SAGTTGMSTVMKNKSLDGLTLYCDGSQADTPTKGGTRPPKSTSRPVSGPTTNLTTPSSTP | 300 |
|   | *********************  |     |
| VIRT-47012:5'3'   | EPPTTKSKPPSSTKTSTQRPPTTTPANPGGGGCQQKHWDQCGGQDWKGCTVCASPYQCKG | 360 |
| XP 033540912.1  | EPPTTKSKPPSSTKTSTQRPPTTTPANPGGGGCQQKHWDQCGGQDWKGCTVCASPYQCKG | 360 |
| 57  | *************************************                        |     |
| VIRT-47012:5'3'   | VSPPYYYQCL 370   |     |
| XP 033540912.1  | VSPPYYYQCL 370   |     |
| 1.00 - 121 - 121 - 121 - 121 - 121 - 121 - 121 - 121 - 121 - 121 - 121 - 121 - 121 - 121 - 121 - 121 - 121 - 12 | ****   |     |

**Figure 1**. Expasy's Translate tool shows the possible ORF encoded by the mRNA expressed by the unplaced genomic scaffold from *L. ingoldianus* in the pink box (A). Alignment of the ORF (VIRT-47012:5'3' to the uncharacterized protein (XP\_033540912.1) shows all of the residues to be identical.

and fCBD of the residues 336-370. This result is not consistent with the previous annotation done by Haridas *et al.* (2020). Their study reported that Rad23 domain was included as part of the predicted regions found in this protein. However, the SMART analysis done in this study does not have this domain as one of those confidently predicted domains, repeats, motifs, and features. This inconsistency is understandable because the previous study used the JGI annotation pipeline to predict the function of all the genes found in 101 Dothideomycete genomes that they studied compared to this study which is only specific to this particular uncharacterized protein.

Signal peptides (SPs) are short peptides located in the N-terminal of proteins, carrying information for protein secretion, and are common to all prokaryotes and eukaryotes (Owji *et al.*, 2018). The GH114 domain family is recognized as a glycosyl-hydrolase family, number 114. is found endo-α-1,4lt in polygalactosaminidase, a rare enzyme. It is proposed to be TIM-barrel, the most common structure amongst the catalytic domains of glycosyl-hydrolases (Naumov & Stepushchenko, 2011). Moreover, low-complexity regions (LCRs) are amino acid sequences that contain repeats of single amino acids or short amino acid motifs and are highly abundant in eukaryotic proteins (Toll-Riera et al., 2012). Finally, the fCBD or the CBM1 domain is fungi's small four-cysteine cellulose-binding domain. This domain is commonly found in carbohydrate degrading enzymes. These enzymes generally consist of a catalytic domain joined to a cellulose-binding domain (CBD) by a short linker sequence rich in proline and hydroxy-amino acids (Gilkes et al., 1991). In the case of this uncharacterized protein, the GH114 could serve as the catalytic domain that is joined to fCBD by a low complexity region (Figure 2)

| Table 1. Phy | ysicochemical | characteristics | of the u | uncharacterized | protein from | L. ingoldianus |
|--------------|---------------|-----------------|----------|-----------------|--------------|----------------|
|              | /             |                 |          |                 |              | 2              |

| Physicochemcial Characteristics                       | Values                                 |
|---|--|
| Number of amino acids                                 | 370                                    |
| Molecular weight                                      | 40442.44                               |
| Theoretical pl  | 6.71                                   |
| Amino acid composition (No.)                          |  |
| Ala (A)   | 26                                     |
| Arg (R)   | 11                                     |
| Asn (N)   | 20                                     |
| Asp (D)   | 28                                     |
| Cys (C)   | 12                                     |
| Gln (Q)   | 17                                     |
| Glu (E)   | 9                                      |
| Gly (G)   | 25                                     |
| His (H)   | 2                                      |
| lle (I)   | 14                                     |
| Leu (L)   | 23                                     |
| Lys (K)   | 26                                     |
| Met (M)   | 9                                      |
| Phe (F)   | 12                                     |
| Pro (P)   | 32                                     |
| Ser (S)   | 31                                     |
| Thr (T)   | 39                                     |
| Trp (W)   | 9                                      |
| Tyr (Y)   | 11                                     |
| Val (V)   | 14                                     |
| Total number of negatively charged residues (Asp+Glu) | 37                                     |
| Total number of positively charged residues (Arg+Lys) | 37                                     |
| Atomic composition                                    |  |
| Carbon (C)  | 1772                                   |
| Hydrogen (H)  | 2747                                   |
| Nitrogen (N)  | 479                                    |
| Oxygen (O)  | 563                                    |
| Sulfur (S)  | 21                                     |
| Formula   | $C_{1772}H_{2747}N_{479}O_{563}S_{21}$ |
| Total number of atoms                                 | 5582                                   |
| Extinction coefficients:                              |  |
| Assuming all pairs of Cys residues form cystines      | 66640                                  |
| Assuming all Cys residues are reduced                 | 65890                                  |
| Estimated half-life (hrs)                             | >20                                    |
| Instability index (II)                                | 48.71                                  |
| Alipathic index                                       | 57.00                                  |
| Grand average of hydrophobicity (GRAVY)               | -0.582                                 |

#### **Predicted Structure**

Figure 3 shows the backbone (Figure 3A) and surface (Figure 3B) views of the top final model (Model 1) for the predicted tertiary structure of the uncharacterized protein from L. ingoldianus. Model 1 has the highest C-score of -1.43, with an estimated TMscore of 0.54±0.15 and an estimated RMSD of 9.9±4.6Å. According to Yang and Zhang (2015), C-score is a confidence score for assessing the quality of predicted models by I-TASSER. It is calculated based on the significance of threading template alignments and the convergence parameters of the structure assembly simulations. C-score is typically in the range of [-5,2], where a C-score of higher value signifies a model with increased confidence and vice-versa. Moreover, TMscore and RMSD are known standards for measuring structural similarity between two structures which are usually used to measure the accuracy of structure modeling when the native structure is known.

The Top 5 predicted models are based on the templates used by I-TASSER for threading. The top 10 threading templates include hydrolases, transcription,

and toxin proteins. Of the ten templates, Ega3, an endo- $\alpha$ -1,4 polygalactosaminidase found in *A. fumigatus*, was ranked 1st, 3rd, 5<sup>th</sup>, 7<sup>th</sup>, and 9<sup>th</sup> (Table 2). Furthermore, the top 10 structural analogs of the uncharacterized protein in PDB were composed of endo- $\alpha$ -1,4galactosaminidase from *A. fumigatus*, endo-α-Nacetylgalactosaminidase from Bifidobacterium longum, Lacto-N-biosidase from Bifidobacterium bifidum, Nacetyl-β-D-glucosaminidase Streptococcus from qordonii, Endo- $\alpha$ -N-acetylgalactosaminidase from Streptococcus pneumoniae, N-acetyl- $\alpha$ -glucosaminicase from Homo sapiens, Trimethylamine dehydrogenase from Methylophilus methylotrophus, Chitibiose from *Flavobacterium johnsoniae*,  $\beta$ -galactosidase from Trichoderma reesei, and Histamine dehydrogenase from Pimelobacter simplex, respectively (Table 3). Of these ten structural analogs, only the 1<sup>st</sup> ranked endo- $\alpha$ -1,4galactosaminidase from A. fumigatus aligned perfectly with model 1 generated by I-TASSER (Figure 3C). The rest of the structural analogs have domains not present in the uncharacterized protein from *L. ingoldianus*.

These structural prediction and alignment results reveal that the uncharacterized protein encoded by the



**Figure 1**. Domain architecture of the uncharacterized protein from L. ingoldianus. This protein consists of a signal peptide (red bar), GH114 domain (black box), low complexity region (pink bar), and fCBD region (green triangle).



**Figure 2**. Top final model (Model 1) of the tertiary structure of the uncharacterized protein from L. ingoldianus predicted by I-TASSER shown in cartoon (A) and surface (B) views and in alignment with the top structural analog (C). The structural analog is colored purple in C while the model 1 structure from A-C shows the signal peptide (red), GH114 domain (yellow), low complexity region (pink, and fCBD region (green).

mRNA from the unplaced genomic scaffold of *L. ingoldianus* could probably be an endo- $\alpha$ -1,4-polygalactosaminidase with GH114 catalytic domain same as Ega3 from *A. fumigatus*. Ega3 is an active glycoside hydrolase that disrupts GAG-dependent *A. fumigatus* and Pel polysaccharide-dependent *Pseudomonas aeruginosa* biofilms at nanomolar concentrations (Bamford *et al.*, 2019).

## **Refined and Validated 3D Structure**

Figure 4 shows the top predicted model by I-TASSER that is refined by *loc*PREFMD. Although the refined model has not really reached the targeted values for various stereochemical parameters, this version has significantly enhanced values compared to the crude/submitted model (Table 4). In terms of the assessment of model quality, Ramachandran Plot analysis revealed that the refined model has increased observation values than the crude model. The crude model has highly preferred observations of 79.076%, preferred observations of 13.859%, and questionable observations of 7.065% (Figure 5A). After the refinement of the model, the values improved to 91.304%, 5.707%, and 2.989%, respectively (Figure 5B).

Furthermore, ProSA-web analysis showed that the overall model quality of the refined model is higher compared to the crude model. The Z-Score of the crude model was equivalent to -5.56 (Figure 5C) and increased to -5.61 in the refined model (Figure 5D). Finally,

**Table 2**. Top 10 threading templates used by I-TASSER to predict the structure of the uncharacterized protein from L. ingoldianus.

| Rank | PDB Hit | Name  | Class         | Organism                                  | Ident | Ident | Coverage | Norm Z- |
|------|---------|---|---------------|---|-------|-------|----------|---------|
|      |         |   |               |   | 1     | 2     |          | score   |
| 1    | 6oj1A   | Ega3 (endo-α-1,4-<br>polygalactosaminidase)                 | Hydrolase     | Aspergillus fumigatus                     | 0.46  | 0.32  | 0.66     | 2.79    |
| 2    | 700eG   | GH30 (mutant E188A)<br>complexed with<br>aldotriuronic acid | Hydrolase     | Thermothelomyces thermophilus ATCC 42464  | 0.10  | 0.20  | 0.94     | 1.15    |
| 3    | 6oj1    | Ega3 (endo-α-1,4-<br>polygalactosaminidase)                 | Hydrolase     | Aspergillus fumigatus Af293               | 0.46  | 0.32  | 0.66     | 6.64    |
| 4    | 7ktrC   | SAGA coactivator complex<br>(TRRAP, core)                   | Transcription | Homo sapiens, unclassified<br>Rhodococcus | 0.09  | 0.18  | 0.93     | 1.08    |
| 5    | 6oj1    | Ega3 (endo-α-1,4-<br>polygalactosaminidase)                 | Hydrolase     | Aspergillus fumigatus Af293               | 0.46  | 0.32  | 0.66     | 4.37    |
| 6    | 7wabA   | prolyl endoprotease (PEP)                                   | Hydrolase     | Aspergillus niger                         | 0.10  | 0.23  | 0.93     | 1.05    |
| 7    | 6oj1A   | Ega3 (endo-α-1,4-<br>polygalactosaminidase)                 | Hydrolase     | Aspergillus fumigatus Af293               | 0.47  | 0.32  | 0.66     | 2.94    |
| 8    | 7qfpA   | Botulinum neurotoxin<br>serotype E                          | Toxin         | Clostridium botulinum                     | 0.05  | 0.22  | 0.97     | 1.05    |
| 9    | 6oj1    | Ega3 (endo-α-1,4-<br>polygalactosaminidase)                 | Hydrolase     | Aspergillus fumigatus Af293               | 0.47  | 0.32  | 0.66     | 6.96    |
| 10   | 7m10A   | RNA polymerase II pre-<br>initiation complex (PIC1)         | Transcription | Saccharomyces cerevisiae                  | 0.06  | 0.19  | 0.82     | 0.72    |

Table 3. Proteins structurally close to the uncharacterized protein from L. ingoldianus in the PDB as identified by TM-align.

| Rank | PDB   | Name                              | Class          | Organism                | TM-   | RMSD | IDEN  | Coverage |
|------|-------|-----------------------------------|----------------|-------------------------|-------|------|-------|----------|
|      | Hit   |                                   |                |                         | score |      |       |          |
| 1    | 6oj1A | endo-α-1,4-                       | Hydrolase      | Aspergillus fumigatus   | 0.663 | 0.41 | 0.459 | 0.665    |
|      |       | polygalactosaminidase (GH114)     |                |                         |       |      |       |          |
| 2    | 2zxqA | endo-a-N-                         | Hydrolase      | Bifidobacterium longum  | 0.617 | 4.90 | 0.072 | 0.819    |
|      |       | acetylgalactosaminidase (GH101)   |                |                         |       |      |       |          |
| 3    | 4h04A | Lacto-N-biosidase (GH20)          | Hydrolase      | Bifidobacterium bifidum | 0.610 | 4.97 | 0.078 | 0.824    |
|      |       |                                   |                | JCM 1254                |       |      |       |          |
| 4    | 2epoA | N-acetyl-β-D-glucosaminidase      | Hydrolase      | Streptococcus gordonii  | 0.610 | 4.82 | 0.043 | 0.803    |
|      |       | (GCNA) (GH20)                     |                |                         |       |      |       |          |
| 5    | 3ecqB | Endo-α-N-                         | Hydrolase      | Streptococcus           | 0.603 | 5.08 | 0.077 | 0.822    |
|      |       | acetylgalactosaminidase (GH101)   |                | pneumoniae R6           |       |      |       |          |
| 6    | 4xwhA | N-acetyl- $lpha$ -glucosaminidase | Hydrolase      | Homo sapiens            | 0.595 | 4.84 | 0.054 | 0.797    |
|      |       | (GH89)                            |                |                         |       |      |       |          |
| 7    | 2tmdA | Trimethylamine dehydrogenase      | Oxidoreductase | Methylophilus           | 0.591 | 5.13 | 0.063 | 0.805    |
|      |       |                                   |                | methylotrophus W3A1     |       |      |       |          |
| 8    | 6yhhA | Chitobiose (GH20)                 | Hydrolase      | Flavobacterium          | 0.590 | 4.46 | 0.038 | 0.754    |
|      |       |                                   |                | johnsoniae UW101        |       |      |       |          |
| 9    | 3og2A | $\beta$ -galactosidase (GH35)     | Hydrolase      | Trichoderma reesei      | 0.588 | 5.06 | 0.064 | 0.811    |
| 10   | 3k30A | Histamine dehydrogenase (HADH)    | Oxidoreductase | Pimelobacter simplex    | 0.588 | 5.13 | 0.068 | 0.800    |

VERIFY3D analysis for validating the quality of the refined model reported a "pass" result. The analysis revealed that 86.76% of the residues have averaged 3D-1D score >= 0.2 (Figure 5E). According to Eisenberg *et al.* (1997) if at least 80% of the amino acids have scored >= 0.2 in the 3D/1D profile, then the model passes the quality validation test.

#### **Protein Classification**

BLASTp analysis and I-TASSER prediction initially identify the uncharacterized protein as GH114 domaincontaining protein. Thus, molecular phylogenetic analysis of its sequence together with other glycoside hydrolases was done to confirm this identity. Phylogenetic analysis of the uncharacterized protein from *L. ingoldianus* confirms that this protein is an endo- $\alpha$ -1,4-polygalactosaminidase with a catalytic domain belonging to the glycoside hydrolase 114 family (GH114). The phylogenetic tree in Figure 6A shows that this uncharacterized protein was grouped with the two GH114 domain-containing endo- $\alpha$ -1,4polygalactosaminidase sequences from *A. fumigatus* with a 100% bootstrap support value.

The GH114 group shares the same ancestor with endo- $\alpha$ -N-acetylgalactosaminidase or the GH101 family. Also shown in the tree are resolved clades of GH35 domain-containing  $\beta$ -galactosidases, GH20 domain-containing Chitooligosaccharide deacetylases, GH89 domain-containing N-acetyl- $\alpha$ -glucosaminidase, GH35

A B

**Figure 4.** Cartoon (A) and surface (B) views of the top structural model (Model 1) refined by *loc*PREFMD. The structure shows the signal peptide (red), GH114 domain (yellow), low complexity region (pink, and fCBD region (green).

| Table 4. Comparison of the stereochemical parameters of the top | structural model predicted | ed by I-TASSER and its | refined version by |
|---|----------------------------|------------------------|--------------------|
| locPREFMD.  |                            |                        |                    |
| Daramators  | Submitted                  | Pofinad                | Goal               |

| Parameters                            | Submitted | Refined | Goal    |
|---------------------------------------|-----------|---------|---------|
| Total score                           | 2.924     | 1.869   | < 1.0   |
| Clash score                           | 3.948     | 0.537   | 0       |
| C-beta deviations                     | 25        | 4       | 0       |
| Sidechain rotamer outliers            | 15.990    | 5.330   | < 0.3 % |
| Phi-psi backbone outliers             | 11.410    | 2.990   | < 0.2 % |
| Phi-psi backbone favored region       | 71.470    | 86.410  | > 98 %  |
| 21-window residue average             | 0.000     | 0.000   | 1.0     |
| Phi-psi backbone favored region       | 64.300    | 79.100  | > 90 %  |
| Phi-psi backbone allowed region       | 28.900    | 17.700  |         |
| Phi-psi backbone general region       | 5.500     | 2.900   | < 1 %   |
| Phi-psi backbone disfavored region    | 1.300     | 0.300   | < 0.2 % |
| Phi-psi backbone un-allowed region    | 0.179     | 0.087   | < 0.2 % |
| Chi1-chi2 sidechain un-allowed region | 0.076     | 0.021   | < 0.2 % |
| G-factor dihedrals                    | -1.040    | -0.600  | > -0.5  |
| G-factor covalent bonds               | -0.240    | 0.020   | > -0.5  |
| G-factor overall interactions         | -0.680    | -0.330  | > -0.5  |
| Favorable main chain bond lengths     | 99.300    | 99.800  | 100 %   |
| Favorable main chain angles           | 88.000    | 92.300  | 100 %   |
| Sidechain ring planarity              | 84.000    | 94.100  | 100 %   |

domain-containing  $\alpha$ -galactosidases, and the outgroup seq Oxidoreductases (EC 1). The maximum parsimony tree resi has a length of 7716, consistency index (CI) of 0.905780, seco

0.749774. A closer look at the aligned sequences of the uncharacterized protein from *L. ingoldianus* and the two sequences from *A. fumigatus* showed several conserved sequences found within their GH114 domains (Figure 6B). The GH114 domain of the first Ega3

retention index (RI) of 0.827766, and composite index of

sequence (pdb|6OJ1|A) is from 41 up to 273 amino acid residues. On the other hand, the GH114 domain of the second Ega3 sequence ((pdb|6OJB|A) is from 58 up to 290 amino acid residues. Lastly, in terms of their domain architecture, only the uncharacterized protein from *L. ingoldianus* has an fCBD linked to the GH114 domain via a low complexity region compared to the other two (Figure 6C), which makes it a unique form of an endo- $\alpha$ -1,4-polygalactosaminidase enzyme.



**Figure 5.** Ramachandran Plot Server and ProSA-web server analysis for the quality assessment of the top predicted model by I-TASSER (A&C) and the refined model by locPREFMD (B&D), as well as the refined model's validation through VERIFY3D (E).

#### **Detected Active Sites**

CASTp analysis predicted 36 active sites within the refined model of the uncharacterized protein from *L. ingoldianus* (Figure 7). The top active sites of the modeled protein were identified between the area of 2335.104 and the volume of 1817.838.

#### Subcellular Localization and Signal Peptide Profile

Figure 8A shows that the uncharacterized protein from *L. ingoldianus* is an extracellular enzyme. It is synthesized inside the fungal cell and is secreted outside for its catalytic function. Analysis of the signal peptide sequence of the uncharacterized protein further revealed that it contains a Sec/SPI signal peptide. Sec/SPI is the "standard" secretory signal peptide transported by the Sec translocon and is cleaved by Signal Peptidase I (*Lep*). Moreover, the analysis revealed that this protein has the signal peptide cleavage site between amino acid residues 17 and 18 (Figure 8B).

The protein endo- $\alpha$ -1,4-polygalactosaminidase is a type of carbohydrate-active enzyme (CAZyme). CAZymes are secreted by filamentous fungi, especially those that could efficiently degrade lignocellulose (Gabriel et al., 2021). Production of various CAZymes is an inherent characteristic of the heterotrophic fungal lifestyle to efficiently degrade the available biomass in their habitat (Barrett et al., 2020). Their biomass substrates are often composed of different plant cell wall polysaccharides, primarily cellulose, hemicellulose, pectin, and lignin (Benoit et al., 2015). In the case of endo- $\alpha$ -1,4-polygalactosaminidase, a critical action of ability this enzyme is its to disrupt galactosaminogalactan (GAG). GAG is an integral component of the A. fumigatus biofilm matrix and a key



**Figure 6.** Molecular phylogenetic analysis of the uncharacterized protein from *L. ingoldianus* with other glycoside hydrolase proteins (A). Multiple sequence alignment of the uncharacterized protein to the two sequences of endo- $\alpha$ -1,4-polygalactosaminidase from A. fumigatus (B) and the comparison of their domain architectures (C).

virulence factor for causing chronic infections in patients with pre-existing lung conditions such as chronic obstructive pulmonary disease or cystic fibrosis (Bamford *et al.*, 2019).

#### **Protein-Protein Interaction**

STRING query resulted in a match for endo- $\alpha$ -1,4polygalactosaminidase protein interaction from Aspergillus niger. Figure 9 shows that endo- $\alpha$ -1,4polygalactosaminidase (An08g04330) interacts with the following proteins: Udp-glucose 4-epimerase (An02g11320) which belongs to the NAD-dependent epimerase/dehydratase family, cell surface spherulin 4like protein (Am02g11330 & An03g05560) which belongs to the Spherulation-specific family 4, plasma membrane ATPases (An01g05670, An02g12510, An16g05840), large subunit ribosomal protein lp2 (An16g04930) which belongs to the eukaryotic ribosomal protein P1/P2 family, endo-arabinase (An07g04930) which belongs to the Glycosyl hydrolases family 43, and glycosyl transferases group 1 family protein (An02g11400). All of these predicted functional partners are based on textmining.

Molecular docking analysis conducted to compare catalytic activities of the enzyme endo- $\alpha$ -1,4-polygalactosaminidase from *A. fumigatus* and *L. ingoldianus* revealed almost the same interactions with the substrate galactosaminogalactan (GAG). GAG is a heterogeneous linear  $\alpha$ -1,4–linked exopolysaccharide of galactose and GalNAc that is partially deacetylated after secretion.

Docking of GAG to Ega3 revealed only eight out of ten models showing substrate binding to the active sites of the protein. The other two models were bound to the N-terminal sequences of the enzyme (Figure 10A). On the other hand, all ten models showed GAG binding to the active sites of the endo- $\alpha$ -1,4-polygalactosaminidase from *L. ingoldianus* (Figure 10B). This optimized binding for the studied protein could be due to cleaving the signal peptide before subjecting it to docking analysis.

Comparing the structures of the enzymes with the bound substrates, the uncharacterized protein appears to be more globular than Ega3. Using MS and functional assays, Bamford *et al.* (2019) demonstrated that Ega3 is



Figure 7. The active sites in the uncharacterized protein predicted by CASTp. The active sites are shown in red spheres found in the cartoon view of the protein (A) and in the specific amino acid residues highlighted in gray (B).



Figure 8. Results of the subcellular localization (A) and signal peptide analysis (B) of the uncharacterized protein from L. ingoldianus.

an endo-acting  $\alpha$ -1,4-galactosaminidase whose activity depends on the conserved acidic residues, Asp-189 and Glu-247. X-ray crystallographic structural analysis of the apo Ega3 and an Ega3-galactosamine complex, at 1.76 and 2.09 Å resolutions, revealed a modified ( $\beta/\alpha$ )<sub>8</sub>-fold with a deep electronegative cleft, which upon ligand binding is capped to form a tunnel. However, the cleft on the uncharacterized protein is deeper and more pronounced than the cleft found on the Ega3 (Figure 7). This difference could be due to the enzyme's fCBD and low complexity regions from *L. ingoldianus* (Figure 3). Thus, it is hypothesized that the fCBD part found in this protein does not just function for recognizing galactosaminogalactan but also for holding it in place for maximum contact with the active site of the catalytic domain GH114.

Finally, the mode of action of the endo  $\alpha$ -1,4 polygalactosaminidase from *Pseudomonas* sp. 881 on galactosaminooligosaccharides (GOSs) was studied by Tamura *et al.* (1992). This enzyme could hydrolyze  $\alpha$ -1,4



Figure 9. Interactions of endo-2-1,4-polygalactosaminidase from A. niger with other proteins as predicted by STRING v.11.5.



**Figure 10.** Molecular docking analysis results of GAG and Ega3 (A) and GAG and the uncharacterized protein from L. ingoldianus (B). All docking models of the substrate GAG were overlayed (sticks) on the enzyme endo-D-1,4-polygalactosaminidase (brown; surface view).

polygalactosamine to GOSs in an endo-split manner. They also found that tetraose and longer GOSs were hydrolyzed to galactosaminobiose and galactosaminotriose as the final products and galactosaminomonomer (galactosamine) could not be produced as an enzymatic product.

#### **Protein Evolution**

A total of 26 orthologous protein sequences were retrieved from NCBI after filtering only those accessions with above 90% identity in the BLASTp result. Molecular phylogenetic analysis of these sequences revealed that the endo  $\alpha$ -1,4 polygalactosaminidase from *L. ingoldianus* is more closely related to CBM1 from *Zopfia rhizophila* (pink box; Figure 11A) than its other orthologues with a 74% bootstrap support value. The most parsimonious tree has a length of 1887, consistency index of 0.602014, retention index of 0.533250, and a composite index of 0.321024. *Z. rhizophila* is a plant pathogenic fungus that causes root rot in Asparagus (Sadowski, 1989).

Furthermore, although the orthologue from Z. *rhizophila* is named CBM1 in NCBI, comparison of their domain architectures showed both proteins are endo  $\alpha$ -1,4 polygalactosaminidase (Figure11B). Moreover, a



**Figure 11.** (A) Phylogenetic tree showing the relationship of endo-12-1,4-polygalactosaminidase from *L. ingoldianus* with its orthologues, (B) comparison of the domain architectures of the proteins from *L. ingoldianus* and *Z. rhizophila*.

| KAH7407183.1   | MLPSTLLWACIYSSASIAAVFKVGQKFQIILDSIPNLTASPKVVPGDA   | 48   | KAH7407183.1   | CSSYSAFLAAGKPVFHIEYPPSVPNVQPADRAKGCQNNGMNGMSTVFKNMSLSGWVGY  | 264   |
|--|--|--|--|---|---|
| KAG4442154.1   | MLPSTVLWACICSTVSLGAVFKVGQKFQIILDSIPNLTASPKVVPGDA   | 48   | KAG4442154.1   | CSSYSAFLAAGKPVFHIEYPPSVPNVQPADRMKGCQNNGMSGMSTVFKNMSLSGWVGY  | 264   |
| XP_031872955.1   | MLCWFLAACACVGTSLGVEFAVGQKFQIVLSGIPNLD-TP-LVPADA  | 45   | XP_031872955.1   | CEQYDDFIKSGKPVFHIEYPAKAPQVTDAEKKTDCQSTGMVGFSTVLKTMSVDGWVGY  | 271   |
| KAH8595570.1   | MLLSSILACACATVASGATFALGQKFQIILNSIPDLSAGP-LTP-DA  | 45   | KAH8595570.1   | CDRYGPFINAGKPVFHIEYPATVPNVSAADRTGVCTKDGKEQMSTVLKYLLLDGWVQY  | 259   |
| KAF2649322.1   | MAQMCLNLLAWVLWVGFFVGISLGQATFTRGQKWQIILLGTPDMSKMP-LPPTDA  | 54   | KAF2649322.1   | CNAYDAFLASNKPVFQIEYPVPLAVNQTNGVYCKGPGTAGMSTVLKDITLDGETIY  | 266   |
| KAF2118428.1   | MESLTSKIWLWVLTAALFISALAQDDPETPTAFRKGQKWQIILLGTPDMTKMP-LPPTDA   | 59   | KAF2118428.1   | CSSYSAFLASGKPVFHIEYPPSLNSSLGNTTYCKGAGTDGMSTILKDLTLDGRTFY  | 273   |
| XP_033540912.1   | MLSWLLWAWLFASTSFAQTTLFTRGQKWQIILTGTPDMSKSP-LPPTDA  | 48   | XP_033540912.1   | CSAYNEFLNSNKPVFHIEYPPKMNPVSDNDKRTACTSAGTTGMSTVMKNKSLDGLTLY  | 262   |
| KAF2186921.1   | MLPWLLWVGLFAGTSLGQ-SMFTQGQKWQIILTGQPDMTKSP-LPPTDA  | 47   | KAF2186921.1   | CFAYNQFLASGKPVFHIEYPSKLNPVPDAEKRNFCNNNSTGVNGMSTVLKNLTLNGLTIY  | 263   |
| PSN69717.1   | MARHSDAQTP-VSFRRGQKFQIILLGTPDMSKWP-LAPLDA  | 39   | PSN69717.1   | CAAYGRFLAMNKPVFHIEYPTPLDVRQANSTSCLGPGTEGMSTILKELSLNGNTIY  | 251   |
| KAF2682800.1   | MFSWLLWLALIAVPCFAQNFTRGQKWQIILLGTPDMSKMP-LPPTDA  | 46   | KAF2682800.1   | CERYNNFLASGKPVFHVEYPNPLNPAAAKTDLCTGPGTSLMSNILKNLALDGPTVY  | 263   |
| XP_033688226.1   | MLPWLLWPALLARPSLGQ-QNFTRGQKFQIILLGTPDTSKMP-IAPTDA  | 47   | XP_033688226.1   | CDRYTTFLATNKPVFHIEYPAPLNTSAARSTLCTGPGTTGMSTVLKNLALDGPTVY  | 259   |
| KAF2437396.1   | MLASLFWAALFAVPSWAQ-SQFVKGQKWQIILTGVPDVSKSP-LPPTDA  | 47   | KAF2437396.1   | CDRYAAFLAAGKPVFHIEYPTPLNPAAANGVSCTGPGTAGLSTVLKNLALDGPAVY  | 259   |
| KAF2634922.1   | MLFRFLWAAFFAGLSLAQ-VVFERGQKWQIILTGTPDVSKMP-LPPIDA  | 47   | KAF2634922.1   | CERYNNFLATNKPVFHIEYPNPLNANQANTTLCTGPGSANMSTILKNSALDGPTVY  | 259   |
| EFQ94882.1   | MFLVLLWVALLIDCTLAQNATFRRGQKFQIILLGVPDVSKVP-LPPTDA  | 48   | EFQ94882.1   | CTAYTSFLASNKPVFNIEYPQPLNAASVQGPACRNPVVGGMSTVLKDLTLDGRSVY  | 260   |
| KAI1663782.1   | MFPVLLSLLWVALLTGRTLAQNATFTRGQKFQIILLGVPDVSKMP-LPPTDA   | 51   | KAI1663782.1   | CTAYTTFLASNKPVFNIEYPQPLNAASVQGSACRNPVVDGMSTVLKDLTLDGRTVY  | 263   |
| KAF1835456.1   | MLSWILWIGFVAISCLAQNATFTRGQKFQIILLGVPDMPKMP-LPPTDA  | 48   | KAF1835456.1   | CQTYDNFIALNKPVFHIEYPKPLDAQAAKGLSCTAPGVTGLSTILKSLHLDGITYY  | 260   |
| KAH6849362.1   | MLLWLVLLGCYFSLIWAQNASFTQGQKFQIVLLGIPDMSKIP-ISPIDA  | 48   | KAH6849362.1   | CQAYENFIALNKPVFHIEYPLPLNAQAMNGASCKGTGVAGLSTIMKDLQLNGMSYY  | 260   |
| XP 018387059.1   | MLLWLVLLGCYFSLIWAONASFTOGOKFOIVLLGIPDMSKIP-ISPIDA  | 48   | XP 018387059.1   | COAYENFIALNKPVFHIEYPLPLNAOAMNGASCKGTGVAGLSTIMKDLOLNGMSYY  | 268   |
| KAH8725337.1   | MDNSSWVRALALFLWLAFVLPSLCONTPFTRGOKFOTILLGVPDTSKMP-LSPTDA   | 55   | KAH8725337.1   | CRVYDOFLTLNKPVFHIEYPTPLNEAATRGNSCTGAGVNGTSTILKDVKLNGKTYY  | 267   |
| KAH7399679.1   | M-LTWLLWGGLFVKPSICONVTFTLGOKFOTILIGVPDMSKMP-LPPTDA   | 4.8  | KAH7399679.1   | COAYANFITLNKPVFHIEYPTPLNPOAVNGVSCKGPGMTGFSTILKDMKLNGITYY  | 260   |
| KAH7076357 1   | MAFARYT_LSTATLLLALUFDU_SSONUTPSRCOKFOTTLLCTDDVSKMP_LPPTDA  | 5.4  | KAH7076357.1   | CSVYSOFLALDKPVFHTEVPVPLNAOAAAGVSCKGPGVNGMSTTLKDLOLNGTTVY  | 266   |
| KAH7069368 1   | MTATRYI-LPTATLIALTID-V-SSONVTFTRCOKFOILLCIDDVSKMD-LDTDA  | 5.4  | KAH7069368.1   | CSVYNOFLALDKPVFHIEYPVPLNAOATSGVSCKGPGVNGMSTILKDLOLNGITYY  | 266   |
| 05144252 1   |  | 4.9  | OAT-44252.1  | CSAVANFIATGKPVFOIEVPTPLNAOAVNGVSCKGPGVAGLSTILKDLOLNGTAVV  | 260   |
| VAD1425211   |  | 40   | KAF2847813.1   | CSTYANFLASGEPUFOTEYPOPLNAOAVNGVSCKGPSVAGLSTILEDLTLNGTAVY  | 260   |
| NAF204/013.1   | MICCILIUS ADDRUGA U NCO ACCONCONDUCTI CONDUCTION   | 40   | KAF2750897.1   | CTAYNNFLASGKPUFHTEYPSPLNUGOAGTNFCNCPCTNCMSTVLKEMNLNGRTIV  | 259   |
| KAF2/5005/.1   | MESCERWEATFINAVACV-ASFINGVROTILEGIPDIANAP-EFFIDA   | 47   | KAF2266012.1   | CNAVDSFLASNKPUFHTEVPNPLNKSSVNTPSCNCPCTNCMSTVLKELHLNGVTTV  | 259   |
| KAF2200012.1   | MLCWLIWYGLLASISLAY-IAFRRGYRFYIILLGIPDMSRFF-LFFIDA<br>MYDNCMCMIILUII CUCUIUCCC-IAO-UMDMDCOYDOTIII CMDDMCYND-IADYDA  | 14 /<br>5 /  | KAH7123803.1   | CVAYNNFLAANKPUFHTEVPTPLDPSOANSLHCKAAGUECMSTTLKDMOLNGATTY  | 266   |
| KRH/125005.1   | * ***:**:* . *: * : * **   | 54   | 1000712500511  | * * *: .****::*** * * *.::* *   | 200   |
|  |  |  |  |   |   |
| KAH7407183.1   | AVFDIDLFDTDAATISGLQSQGKIVICYFSAGTYEPWRPDAGNFTQEDMGQSLAPEWPDE   | 108  | KAH7407183.1   | CDGSSATTITKPGGGTNPWAPGKPKPTTTAKTTARPTTTKPPSTSR  | 310   |
| KAG4442154.1   | AVFDIDLFDTDAATISGLQSQGKIVICYFSAGTYEPWRPDAGNFTDADMGQSLAPEWPDE   | 108  | KAG4442154.1   | CDGSSATTVTKPGGGTNPWAPGKPKTTTTVKTTARPTTTRPPSTSR  | 310   |
| XP_031872955.1   | PVYDIDLEGTSAETITAMKAMGKTVICYFSAGTVENWRPDANKFAAADMGSV-LKEWPNE   | 104  | XP_031872955.1   | CDGSSATTSTSPGGEPPKPPKSTTTAPITTPTP   | 302   |
| KAH8595570.1   | AVFDVDAIDTPATTIAGLKAAGRIVICYFSAGTYEAWRADAPNFOASDLGKT-LPEWPDE   | 104  | KAH8595570.1   | CDGSIAETHTTAGIPNPHYSSRPTTSKTTSTSKSTSK   | 296   |
| KAF2649322.1   | QVWDIDLFDNDASAMTTLKAAGKTVICYFSAGTWEDWRDDAKDFASADLGKV-LPLWPNE   | 113  | KAF2649322.1   | CDGSRVDTPTKGGTRPTPTTRPGTPHRTSTPPGRPTSTFR  | 306   |
| KAF2118428.1   | EVWDLDLFDNDASTFOTLKAAGKTVICYFSAGTWEDWRDDAKDFPSADLGKV-LPLWPNE   | 118  | KAF2118428.1   | CDGSQADTPTKGGTRPTPSRGPSPPRTTTRWSTPPTPPRTSSSRPIVTP   | 322   |
| XP 033540912.1   | PUEDUDI FONDATTITAL KAOCKTUTOVESACTUEDWEDDAKDEPTNDOCKT_LEWDNE  | 107  | XP 033540912.1   | CDGSQADTPTKGGTRPPKSTSRPVSGPTTNLTT-PSSTPE  | 301   |
| KAF2186921 1   | PVD1DLPDNDLATTTALKAOCKUVICVPSACTWPDWRDDAKDPP1NDQGKI-BPBwPNE  | 106  | KAF2186921.1   | CDGSOVDTPTKGGTGPGRPPRPTSRPTSMPTSRPTSRPTSMPP   | 306   |
| DSN69717 1   | DUNDIDLEDNDASTIDTIKOACKIUTOVICACTURDUNDDNUDDUDADAADUOVU IDPUND   | 9.8  | PSN69717.1   | CDGSVVDTPTKGGTGPPRPSNPPIPPRPSTPLK   | 2.8.4   |
| V3002/11/.1  | PUMPTOL DOUDDOUTEDT VA A CUMUTOVOCA CODEDONADO ANDO ANDO ANDO ANDO ANDO ANDO AND   | 105  | KAF2682800 1   | CDCSOVDTPTKCCTSPPRPTPSKSSTTRASSTTRSTTSSKTPCCCMPDT   | 310   |
| NAF2002000.1   | EVWDIDLFDNDFSTITREKAAGKTVICIFSAGTREDWRDDARDFFAADQGRV-EFEWPRE   | 105  | XP 033688226.1   | CDCSOVDTPTKCCTSPPRPSPSSSSPPNPPRPTSTPSSPTSTPPRPTSNPPR  | 310   |
| AF_033688226.1   | FYWDYDDFDTDRASSINALQARGKIVICYFSAGTVEDWRDDAKDFPAADVGKV-LPEWPDE  | 106  | KaF2437366 1   | CDCSOVDTPT#CCTCDDDPTPTTTDDDTTTCCTTTDTTTTTDD   | 200   |
| KAF243/396.1   | PVWDVDLFDSDTATIAALKATGKIVICYFSAGTVEDWRSDAKDFPTGDVGKV-LPEWPNE   | 106  | KAF2437390.1   |   | 202   |
| KAF2634922.1   | PVWDVDLFDSDTATVKSLKTTGKTVICYFSAGTVEDWRDDVKDFPIADVGKV-LPEWPNE   | 106  | FF004002 1   |   | 201   |
| EFQ94882.1   | PVWDVDLFDTPATTISALKAAGKIVICYFSAGTAEDWRDDYRDFAATDLGKV-LPEWPNE   | 107  | Erg94002.1   |   | 204   |
| KAI1663782.1   | PVWDVDLFDTPVTTISALKKAGKTVICYFSAGTAENWRDDYGGFAAADLGKV-LPEWSNE   | 110  | KA11003702.1   | CDGGGVVVDIFIVGGSSSFRFSRFFMFVFIRSSIRSIG-FSR  | 204   |
| KAF1835456.1   | PVWDIDLFDNSATTVATLKAPGKIVICYFSAGTAEDWREDYKDFAAADLGKV-LPEWPNE   | 107  | KAF1835458.1   | CDGSFVDTFTVNGTVPGRPSAPFKPSNPF   | 209   |
| KAH6849362.1   | PVWDIDLFDNPVTTIETLKAAGKIVICYFSAGTAEDWRDDYGSFAAADLGKV-LPEWPNE   | 107  | KAH6849362.1   | CDGSYVDTFTLGGTSPPRPSQPPRPPSPPRTSSSRTAPMPTRTSSSRPQ   | 309   |
| XP_018387059.1   | PVWDIDLFDNPVTTIETLKAAGKIVICYFSAGTAEDWRDDYGSFAAADLGKV-LPEWPNE   | 107  | XP_018387059.1   | CDGSYVDTFTLGGTSPFRPSQFPRPPSPPRTSSSRTAPMPTRTSSSRPQ   | 317   |
| KAH8725337.1   | PVWDIDLFDSPASTIKSFKAAGKIVICYFSAGTAEDWREDYRTFPAGDLGKV-LPEWPNE   | 114  | KAH8725337.1   | CDGSYVDTPTLGGTSPPRPTRSLRPTSS-PSPRPSSSRPASSSGLPPK  | 314   |
| KAH7399679.1   | PVWDIDLFDNPASAIKTLKAAGKIVICYFSAGTAEDWREDYKDFPNADKGKI-LPAWPNE   | 107  | KAH7399679.1   | CDGSYVDTPTVGGPLPPIPSPSPPIPSPSRTSSARPTSTPPKSSSASPR   | 309   |
| KAH7076357.1   | PVWDIDLFDNPASTMKALKAAGKIVTCYFSAGTAEDWRADYKDFAAADIGKV-LPEWPNE   | 113  | KAH7076357.1   | CDGSYVDTPTLGGTSPPRPSQPPKPSTSKPIPTPRPSSSRPGSSPTSI  | 314   |
| KAH7069368.1   | PVWDIDLFDNPASAMKALKAAGKIVICYFSAGTAEDWRTDYKDFAAADMGKV-LPEWPNE   | 113  | KAH7069368.1   | CDGSYVDTPTLGGTSPPRPSPPPKPSTSKPIPTPRSSSSRPGSSI   | 311   |
| OAL44252.1   | PVWDIDLFDNPASTIKGLKASGKIVICYFSAGTAEDWREDYREFPSSDTGKV-LPEWPNE   | 107  | OAL44252.1   | CDGSYVNTPTLGGASPPRPSPTPTPPRPSSTPRPSSTPR   | 299   |
| KAF2847813.1   | PVWDIDLFDSPASTITSLKTSGKNVICYFSAGTGEDWRDDYKDFSSADLGKV-LPQWPNE   | 107  | KAF2847813.1   | CDGSYVNTPTVGGTSPPRPSLPPKPSTTRPIPTPPRSSSIPLKPSTSTPR  | 310   |
| KAF2750897.1   | EVWDIDLFDTEAATIQTLKNAGKIVICYFSAGTVEDWREDARDFPSSDLGKV-LPEWPNE   | 106  | KAF2750897.1   | CDRSEVNTPTRTGVTPPRPSFSPLPSTTRQ-PIPTTSVPR  | 298   |
| KAF2266012.1   | PVWDIDLFDNEASTIQTLKQAGKIVICYFSAGTWEDWREDAKDFPQGDLGKV-LPEWPNE   | 106  | KAF2266012.1   | CDGSEVDTPTKGGTSPPRPSWSLPPVPPRSSSR-PIISTRTSTVMP  | 304   |
| KAH7123803.1   | PVWDIDLFDNEVSTIQTLKAAGKIVICYFSAGTWEDWRDDAKDFPAGDLGKV-LPEWPNE   | 113  | KAH7123803.1   | CDGSRVDTPTKGGKSPPRPSNPPRPTSRPP-ITPPRSSTQRSTTIPRTSTTLR   | 318   |
|  | *1*1* *1 *1 * ******* * ** * *   |  |  | ** * *  |   |
|  |  |  |  |   |   |
| *********  |  | 140  | KAH7407183.1   | TS  | 348   |
| KAH7407183.1   | YWLRVNNSNVKKIMTNRIQLAAAKGCDGVDPDNTDGYQNP   | 148  | KAH7407183.1<br>KAG4442154.1   | TSTRS-TTSVRTTSSAAPGGSNGCKSKHWDQCGGNDWKG   | 348   |
| KAH7407183.1<br>KAG4442154.1   | YWLRVNNSNVKKIMTNRIQLAAARGCDGVDPDNTDGYQNP<br>YWLRVNNSNVRRVMSNRIQLAASKGCDGVDPDNTDGYQNP   | 148<br>148   | KAH7407183.1<br>KAG4442154.1<br>XP 031872955 1   | TSTRS-TTSVRTTSSAAPGGSNGCKSKHWDQCGGNDWKG<br>PPTTSRTSTRT-SSTVRTTSSAAPAGGPSGCKSKHWDQCGGNDWKG<br>RTTSKPT  | 348<br>355<br>350   |
| KAH7407183.1<br>KAG4442154.1<br>XP_031872955.1   | YWLRVINSNVKKIMTNRIQLAAAKGCGGVDPDNT   | 148<br>148<br>155  | KAH7407183.1<br>KAG4442154.1<br>XP_031872955.1<br>KAH8595570.1   | TSTRS-TTSVRTTSSAAPGGSNGCKSKHWDQCGGNDNKG<br>PPTTSRTSTRT-SSTVRTTSSAAPAGGPSGCRSNHWDQCGGNDNKG<br>-RTSSPTPT-KTTSSTTSRTPTTAPGGGSPGCCTQHHDQCCGNDNKG<br>PTTTVUTT  | 348<br>355<br>350<br>344  |
| KAH7407183.1<br>KAG4442154.1<br>XP_031872955.1<br>KAH8595570.1   | YWLJAVINSNVKI LITNR I QLAAAR GCDGVDPDNT         DGY         QNP           YWLJAVINSNVKI KITOR I QLAASK GCDGVDPDNT         DGY         QNP           HMLKLSSDNVRS I MIKTER I QMAATK GCDG LDPDNT         DGY         QNP           HMLKLSSDNVRS I MIKTER I QMAATK GCDG LDPDNT         DGY         QNP           NMAR I GGSTWINS I MIKTER I QMAATK GCDG LDPDNT         DGN         QNP  | 148<br>148<br>155<br>143   | KAH7407183.1<br>KAG4442154.1<br>XP_031872955.1<br>KAH8595570.1<br>KAP5648322_1   | TSTRS-TTSVRTTSSA  | 348<br>355<br>350<br>344<br>355   |
| KAH7407183.1<br>KAG4442154.1<br>XP_031872955.1<br>KAH8595570.1<br>KAF2649322.1   | YHLRVINSIVKETHTNR I QLAAAR GCDGVDPDNT         DGY         QNP           YWLRVINSIVKETMSNR I QLAASK GCDGVDPDNT         DGY         QNP           NWLRVISSIVKETMGNAAT (GOALDPDNTYNBLIDE)         QN-         QN-           NWAR I GSTWYNS HTWR I THAGAG (GOALDPDNTYNBLIDE)         QN-         QN-           NWLRVSSTWYND I MARRI KLAAD XGCDALDPDNT         DGY-         QN-   | 148<br>148<br>155<br>143<br>152  | KAH7407183.1<br>KAG4442154.1<br>XP_031872955.1<br>KAR8595570.1<br>KAF2649322.1<br>KAF2649322.1   | TSTRS-TTSVRTTSSAAPGGSNGCKSKRWDQCGGNDWKG<br>PPTTSRTSPT-KTTSSTVRTTSSAPAGGPSGCPSHHWDQCGGNDWKG<br>-TRTSRPTPT-KTTSSTTRHTTTAPGGGSTGGCTQHHWDCGGNDWKG<br>PTTTVRT  | 348<br>355<br>350<br>344<br>355<br>370  |
| KAH7407183.1<br>KAG4442154.1<br>XP_031872955.1<br>KAH8595570.1<br>KAF2649322.1<br>KAF2118428.1   | YWLEVNESTVELTUTER I QLAAAFGCDGVDPDNT         DGY         ONP           YWLEVNESTVELTUTER I QLAASFGCDGVDPDNT         DGY         ONP           HILLIESDWIKENSTVERTER I QUAASFGCDA DEPENTVERNELT.LINNELDGY         ON           HIRLIESDWIKENSTVERTER I QUAASFGCDA DEPENTVERNELT.LINNELDGY         ON           HIRLIESSWIKENSTVERTER I QUAASFGCDA DEPENTVERNELT.LINNELDGY         ON           HIRLIESSWIKENSTVERTER I QUAASFGCDA DEPENTVERNELT.LINNELDGY         ON           HIRLIESSWIKENSTVERTER I QUAASFGCDA DEPENTVERNELT.         DGY         ON           HIRLIESSWIKENSTVERTER I QUAASFGCDA DEPENT         DGY         ON           HIRLIEGGARVINE DISSRIELIAADIS GCDA DEPENT         DGY         ON   | 148<br>148<br>155<br>143<br>152<br>157   | KAH7407183.1<br>KAG4442154.1<br>XP_031872955.1<br>KAH8595570.1<br>KAF2649322.1<br>KAF2118428.1<br>YP_03540912_1  | TSTRS-TTSVRTTSSAPAGGSNGCKSHEMDQCGGNDWKG           PPTTSRTSTR-TSSTVRTTT-SAAPAGGPSGCTSREMDQCGGNDWKG           -TTTSRTP  | 348<br>355<br>350<br>344<br>355<br>370  |
| KAH7407183.1<br>KAG4442154.1<br>XP_031872955.1<br>KAH8595570.1<br>KAF2649322.1<br>KAF2118428.1<br>XP_033540912.1   | YWLRVINSIVKETHTNR I QLAAAR GCDGVDPDNT         DGY  | 148<br>148<br>155<br>143<br>152<br>157<br>146  | KAH7407183.1<br>KAG4442154.1<br>XP_031872955.1<br>KAH8595570.1<br>KAF2649322.1<br>KAF2118428.1<br>XP_033540912.1<br>KAF2118421.1   | TSTRS-TTSVRTTSSAAPGGSNGCKSKEMDQCGGNDWKG PPTTSRTSTRT-SSTVRTTSSAPAGEPSGCTSKEMDQCGGNDWKG -RTTSKPTPT-KTTSSTTRKPT  | 348<br>355<br>350<br>344<br>355<br>370<br>301<br>348  |
| KAH7407183.1<br>KAG4442154.1<br>XP_031872955.1<br>KAHE595570.1<br>KAF2649322.1<br>KAF2118428.1<br>XP_033540912.1<br>KAF21186921.1  | VWLRVINSWYRLTHTNR I QLAAAR GCDGUDPDNT DGY OOP<br>VWLRVINSWYRLING I QLAASR GCDGUDPDNT DCY OOP<br>NRULLISSDWYRLSWERT RUAAR KICOCOUPDNT<br>I KARL GESTWYRLSWERT RUAAR KICOLD DE DNT VINSKILL I NNHLDGY ON<br>I KARL GESTWYRLSWERT I LAASD (GCDALDE DNT DGY ON<br>NHLRYGSTWYN DI KISREI LLASD KGCDALDE DNT DGY ON<br>NWLRGSS I VID VARAR LLAADR GCDALDE DNT DGY ON<br>OC ON   | 148<br>148<br>155<br>143<br>152<br>157<br>146<br>145   | KAH7407183.1<br>KAG4442154.1<br>XP_031872955.1<br>KAH8595570.1<br>KAF2649322.1<br>KAF218428.1<br>XP_033540912.1<br>KAF2186921.1<br>PSMR4016.1  | TS  | 348<br>355<br>350<br>344<br>355<br>370<br>301<br>348  |
| KAH7407183.1<br>KAG4442154.1<br>XP_031872955.1<br>KAB8595570.1<br>KAF2649322.1<br>KAF2118428.1<br>XP_033540912.1<br>KAF2186921.1<br>FSN69717.1   | YWLRVINSNVKITHTNR I QLAAAR GCDGVDPDNT         DGY         QNP           YWLRVINSNVKITHTNR I QLAAS KGCDGVDPDNT         DGY         QNP           RWLRLSSDVNS I MERTER I QNAATK GCDG LD DPDNT         DGY         QN-           RWLRLSSDVNS I MERTER I QNAATK GCD LD DPDNT         DGN         QN-           RWLRUSST VENS I MERTER I QNAATK GCD LD DPDNT         DGN         QN-           RWLRUSST VEND I MARKER I LAADR (GCD LD DPDNT         DGY         QN-           RWLRUSST VEND I MARKER I LAADR (GCD LD DPDNT         DGY         QN-           RWLRUSSK VEND VARKER I LAADR (GCD LD DPDNT         DGY         QN-           RWLRUSSK VEND VARKER I LAADR (GCD LD DPDNT         DGY         QN-           RWLRUSSK VEND VARKER I LAADR (GCD LD DPDNT         DGY         QN-           RWLRUSSK VEND VARKER LAADR (GCD LD DPDNT         DGY         QN-           RWLRUSSK VEND VARKER LAADR (GCD LD DPDNT         DGY         QN-           RWLRUSSK VEND VARKER LAADR (GCD LD DPDNT         DGY         QN-           RWLRUSSK VEND VARKER LAADR (GCD LD DPDNT         DGY         QN-   | 148<br>148<br>155<br>143<br>152<br>157<br>146<br>145<br>137  | KAH7407183.1<br>KAG4442154.1<br>XP_031872955.1<br>KAF2649322.1<br>KAF2649322.1<br>XP_03540912.1<br>KAF2186921.1<br>FSN59717.1  | TSTRS-TTSVRTTSSAAPGGSNGCKSKENDQCGGNDWKG PPTTSRTSTRT-SSTVRTTSSAPAGEPSGCTSKENDQCGGNDWKG PTTVRT  | 348<br>355<br>350<br>344<br>355<br>370<br>301<br>348<br>334   |
| KAH7407183.1<br>KAG4442154.1<br>XP_031872955.1<br>KAB2595570.1<br>KAP2649322.1<br>KAP2118428.1<br>XP_033540912.1<br>KAP2186921.1<br>PSN69717.1<br>KAP2682800.1   | YWLRVINSWYRLINTNEI (LAAARGCDCUDPDNT  | 148<br>148<br>155<br>143<br>152<br>157<br>146<br>145<br>137<br>149   | KAH7407183.1<br>KAG4442154.1<br>XP_031872955.1<br>KAB259570.1<br>KAP218570.1<br>KAP218428.1<br>XP_033540912.1<br>KAP2186921.1<br>FSN59717.1<br>KAP2682800.1  | TSTRS-TTSVRTTSSAAPGGSNGCKSKRWDQCGGNDNKG PPTTSKTSPTG-STVRTTSSAPAGGSSPGCTS/HHDQCGGNDNKG -RTTSKPTPT-KTTSSTTRKPTTAGGGGSPGGGGGCGCCMNKG PTTTVRT   | 348<br>355<br>350<br>344<br>355<br>370<br>301<br>348<br>334<br>334<br>352   |
| KAH7407183.1<br>KAG4442154.1<br>XP_031872955.1<br>KAF2649322.1<br>KAF2118428.1<br>XP_033540912.1<br>KAF2186921.1<br>PSN69717.1<br>KAF268200.1<br>XP_033688226.1  | YWLEVNINSIVICI IMTRI I CLAAAR GCDGVDPDNT DCY OOP<br>YWLEVNINSIVICI IMTRI I CLAAAR GCDGVDPDNT DCY OOP<br>WELLISSENVICE STUTTEI CLAAAR GCDA DPDNTTNIENLTL INHELDGY ON<br>MARTI GGTWYRS I MTRIE I CLAAAR GCDA LDPDNT CGO<br>WIELINSSET VICE I CLAAR GCDA LDPDNT DCY ON<br>MIKET GGSTWYRS I MTRIE I MAAG NGCDA LDPDNT DCY ON<br>MIKET GGSTWYRD I MARRIE TRAADR GCDA LDPDNT DCY ON<br>MIKET GGSTWYRD MARRIE TRAADR GCDA LDPDNT VLYTW SGWYN DGY ON<br>MIKET GGSTWYRD MARRIE TRAADR GCDA LDPDNT VLYTW SGWYN DGY ON G   | 148<br>143<br>155<br>143<br>152<br>157<br>146<br>145<br>137<br>149<br>145  | KAH7407183.1<br>KAG4442154.1<br>XP 031872955.1<br>KAF2649322.1<br>KAF218428.1<br>XP 033540912.1<br>KAF2186921.1<br>FSN65917.1<br>KAF2682800.1<br>XP 03368226.1   | TSTRS-TTSVRTTSSAPAGGSNGCKSKHWDQCGGNDWKG PPTTSRTSTRSTSTTSSAPAGGPSGCTSKHWDQCGGNDWKG PTTVRT  | 348<br>355<br>350<br>344<br>355<br>370<br>301<br>348<br>334<br>352<br>362   |
| KAH7407183.1<br>KAG442154.1<br>XP_031872955.1<br>KAH8595570.1<br>KAF2118428.1<br>XP_033540912.1<br>KAF2118428.1<br>XP_033540912.1<br>KAF2186921.1<br>FSN89717.1<br>KAF2682800.1<br>XP_03368226.1<br>KAF2437396.1   | YWLRVINSWYRLINTNEIQLAAARGCDGVDPDNT         DGY         ONP           YWLRVINSWYRLINTNEIQLAASRGCDGVDPDNT         DGY         ONP           YWLRVINSWYRLINTNEIQLAASRGCDGVDPDNT         DGY         ONP           YWLRVINSWYRLINTNEIQLAASRGCDGVDPDNT         DGY         ONP           YWLRVINSWYRLINTNEIQLAASRGCDAUPDNT         DGY         ONP           YWLRVINSWYRLINTNEIQLAASRGCDAUPDNT         DGY         ONP           YWLRVINSWYRLINTNEIGLAASRGCDAUPDNT         DGY         ONP           YWLRVINSWYRLINTAGDVGCDAUPDNT         DGY         ONP           YWLRVINSWYRLINTAGDVGCDAUPDNT         DGY         ONP           YWLRVINSWYRLIASRUGCDAUPDNT         DGY         ONP           YWLRVINGSANTRIASRASENGCOAUPDNT         DGY         ONP           YWLRVINGSANTRIASTAGNAGCOAUPDNT         DGY         ONP           YWLRVINGSANTRIASTAGNAGCOAUPDNT         DGY         ONP           YWLRVINGSANTRIASTAGNAGCOAUPDNT         DGY         ONP           YWLRVINGSANTRIASTAGNAGCOAUPDNT  | 148<br>148<br>155<br>143<br>152<br>157<br>146<br>145<br>137<br>149<br>145<br>145   | KAH7407183.1<br>KAG4442154.1<br>XP_02187255.1<br>KAB259570.1<br>KAP2142821<br>XP_033540912.1<br>KAP2186921.1<br>PSN69717.1<br>KAP2682800.1<br>XP_03368226.1<br>KAP2437396.1<br>KAP2437396.1  | TSTRS-TTSVRTTSSAAPGGSNGCKSKRWDQCGGNDWKG PPTTSKTSTR-SSTVRTTSSAPAGEPSGCTSKRWDQCGGNDWKG -RTTSKPTPT-KTTSSTRKPTTTAFGGSGCGGGGGGGGCGCMSKRWDQCGGNDWKG PTTTVIR   | 348<br>355<br>350<br>344<br>355<br>370<br>301<br>348<br>334<br>352<br>362<br>339  |
| KAH7407183.1<br>KAG4442154.1<br>XH_031872955.1<br>KAH8595570.1<br>KAF2118428.1<br>XMF2118428.1<br>XMF2186291.1<br>PSN69717.1<br>KAF226200.1<br>XF_033688226.1<br>KAF2437396.1<br>KAF26422.1  | YWLRVINSNYKLINTNR I QLAAAR GCDGVDPDNT         DGY         ONP           YWLRVINSNYKLINTNR I QLAASR GCDGVDPDNT         DGY         ONP           WHLRUSSNYKLINTNR I I MASOR GCDALDPDNT         DGY         ONP           WILLINSNYKLINTNR I I MASOR GCDALDPDNT         DGN         ON           WILLINSNYKLINTNR I I MASOR GCDALDPDNT         DGN         ON           WILLINGSNYKLINTNR I I MASOR GCDALDPDNT         DGY         ON           WILLINGSNYKLINTNR I I MASOR GCDALDPDNT         DGY         ON           WILLINGSNYKLINTSKI I MASOR GCDALDPDNT         DGY         ON           WILLINGSNYKLINTAKSKER GCDALDPDNT         DGY         ON           WILLINGSKER KLARDSKER GCDALDPDNT         DGY         ON  | 148<br>148<br>155<br>143<br>152<br>157<br>146<br>145<br>137<br>149<br>145<br>145<br>145  | RAH7407183.1<br>RAG442154.1<br>XP 01187955.1<br>RAF2182645322.1<br>RAF218428.1<br>XP 033540912.1<br>PSN69717.1<br>RAF2218428.1<br>XP 033540912.1<br>PSN69717.1<br>RAF256280.1<br>XP 03368226.1<br>RAF2534922.1<br>RAF2534922.1   | TSTRS-TTSVRTTSSAPAGGSNGCKSKHWDQCGGNDWKG PPTTSRTSTRS-TSTVRTTSSAPAGGSSGCTSKHWDQCGGNDWKG PTTYRT  | 348<br>355<br>350<br>344<br>355<br>370<br>301<br>348<br>334<br>352<br>362<br>339<br>337   |
| KAH7407183.1<br>KAG442154.1<br>XF_03187295.1<br>KAH2595570.1<br>KAF264922.1<br>KAF218428.1<br>XF_033404912.1<br>KAF2186921.1<br>FSH59717.1<br>KAF2662800.1<br>XF_2437396.1<br>KAF2634922.1<br>EF0964882.1  | VWLRVINSWYRTHTNR I QLAAARGCDCVDPDNT DCY (WRRVINSWYRTHTNR I QLAARGCDCVDPDNT DCY (WRRVINSWYRTHSWR I QLAARGCDCVDPDNT DCY (WRRVINSWYRTHSWR I RURAFGCA DLADWINSWYRTHSWR I RURAFGCA DLADWINSWYRTHSWR I RURAFGCA DLADWINSWYRTHSWR I RURAFGCA DLADWIN DCY (WRRVINSWYRTH RURAFGCA DLADWIN DCY (WRRVINSWYRTHAR RURAFF RURAFFGCA DLADWIN DCY (WRRVINSWYRTHAR RURAFF RURAFF RURAFFGCA DLADWIN DCY (WRRVINSWYRTHAR RURAFF RURAFF RURAFF RURAFFF  | 148<br>148<br>155<br>143<br>152<br>157<br>146<br>145<br>137<br>149<br>145<br>145<br>145<br>145   | KAH7407183.1<br>KAG442154.1<br>XP_031872955.1<br>KAR2595570.1<br>KAP21428.1<br>XP_033540912.1<br>KAP2186921.1<br>PSN6917.1<br>KAP2462800.1<br>XP_03368226.1<br>KAP2437396.1<br>KAP2437396.1<br>KAP2437396.1  | TSTRS-TTSVRTTSSAAPGGSNGCKSHENDQCGGNDWG PPTTSRTS   | 348<br>355<br>350<br>344<br>355<br>370<br>301<br>348<br>334<br>352<br>362<br>339<br>337<br>349<br>337<br>349  |
| KAH7407183.1<br>KAG4442154.1<br>XH_03182955.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF218428.1<br>XP_033560912.1<br>FSN69717.1<br>KAF268220.1<br>XF263200.1<br>XF263200.1<br>KAF263736.1<br>KAF263786.1<br>KAF263786.1   | YWLEVNINSWYRTHYNR I QLAAAR GCDGUDPDIT         DGY         ONP           YWLEWNINSWYRTH NGLAAR GCDAUPDNT         DGY         ONP           WRLINGSWYRTH NGLAAR GCDALDPDNTYNENLTLINNELDCY         ONP           WRLINGSWYRTH NGLAAR GCDALDPDNTYNENLTLINNELDCY         ON           WRLINGSWYRTH NGLAAR GCDALDPDNT         DGY         ON           WRLINGSWYRTH NGLAAR GCDALDPDNT         DGY         ON           WRLINGSWYND INSRIFT NAADN GCDALDPDNT         DGY         ON           WRLINGSSWYND INSRIFT NAADN GCDALPDNT         DGY         ON           WRLINGSSWYND INSRIFT NAADN GCDALPDNT         DGY         ON           WRLINGSSWYND INSRIFT NAADN GCDALPDNT         DGY         ON           WRLINGSGY I DI MARKIT NAADN GCDALDPDNT         DGY         ON  | 148<br>148<br>155<br>143<br>152<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>149   | RAH7407183.1<br>RAH7407183.1<br>RAP214442154.1<br>XP_011872955.1<br>RAF2148595570.1<br>RAF214828.1<br>XP_033540912.1<br>RAF214828.1<br>RAF2148291.1<br>PSM69717.1<br>RAF2482820.1<br>XP_03368226.1<br>RAF243922.1<br>RAF2434922.1<br>RAF2434922.1<br>RAF2434922.1  | TSTRS-TTSVRTTSSAPAGGSNGCKSHENDQCGGNDWKG PPTTSRTSTRSSTTRFTTTPAGGGSGCGCGNDWKG PTTYURT   | 348<br>355<br>350<br>344<br>355<br>370<br>301<br>348<br>334<br>352<br>362<br>339<br>337<br>349<br>357   |
| KAH7407183.1<br>KAG442154.1<br>KAB595570.1<br>KAF2649225.1<br>KAF264922.1<br>KAF264922.1<br>KAF218428.1<br>KAF264922.1<br>KAF264920.1<br>KAF2649226.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF1653782.1<br>KAF1653763.1  | YWLEVNINSWYELHTNEIGLAAARGCDCVDPDNT         DOY         ONP           YWLEVNINSWYELHTNEIGLAARGCDCVDPDNT         DOY         ONP           WIRLIGSDWINSWYENIETLAARGCDCVDPDNT         DOY         ONP           WIRLIGSDWINSWYENIETLAGDARGCDALDPDNT         DOX         ON           WIRLIGSDWINSUTTRIAGARGCDALDPDNT         DOX         ON           WIRLINGSDWINSUTTRIAGARGCDALDPDNT         DOX         ON           WIRLINGSDWINSUTTARGRAFTLAGDIGCDALDPDNT         DOX         ON           WIRLINGSDWINSUTTARGRAFTLAGDIGCDALDPDNT         DOX         ON           WIRLINGSTWINSUTTARGRAFTLAGDIGCDALDPDNT         DOX         ON           WIRLINGSTWINSUTTARGRAFTLAGDIGCDALDPDNT         DOY         ON           WIRLINGSTWINSUTTARGRAFTLAGDIGCDALDPDNT         DOY         ON           WIRLINGSTWINSUTTARGRAFTLAGDIGCDALDPDNT         DOY         ON           WIRLINGSTWINSUTARGRAFTLAGDIGCDALDPDNT         DOY         ON           WIRLINGSTWINSUTARGRAFTLAGDIGCDALDPDNT         DOY         ON         ON           WIRTGSTWINGSTELARARTAGRIGCDALDPDNT         DOY         ON         ON         ON           WIRTGSTWINGSTELARARTAGRIGCDALDPDNT         DOY         ON         ON         ON         ON         ON           WIRTGSGGUININARRIETLAGRIGCDALDPDNT         DOY   | 148<br>148<br>155<br>143<br>152<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>149<br>146  | KAH7407183.1<br>KAG442154.1<br>XP 031872955.1<br>KAR2595570.1<br>KAP214282.1<br>XP 033540912.1<br>XP 033540912.1<br>PSN69717.1<br>RAP22462800.1<br>XP 03368226.1<br>KAP2437396.1<br>KAP2437396.1<br>EF094882.1<br>EF094882.1<br>KAP1643782.1<br>KAP164372.1  | TSTRS-TTSVRTTSAPAGGSNGCKSKENDQCGGNDWG PPTTSRTS  | 348<br>355<br>350<br>344<br>355<br>370<br>301<br>348<br>334<br>352<br>362<br>339<br>337<br>349<br>357<br>349  |
| KAH7407183.1<br>KAG442154.1<br>XH_03182955.1<br>KAH75418225.1<br>KAF2649221.1<br>KAF2118428.1<br>XM_213540912.1<br>KAF218220.1<br>XHF2612821.1<br>FDNS9717.1<br>KAF262200.1<br>XH_203368226.1<br>KAF263786.1<br>KAF263786.1<br>KAF1835456.1<br>KAF1835456.1  | YWLEVNINSWYREINTINE I GLAAAR GCDGUDPDNT DCY (WLEVNINSWYREINTINE I GLAAAR GCDGUDPDNT DCY (OP<br>YWLEWNINSWYREINE I GLAAAR GCDGUDPDNT DCY (OP<br>IWALFGSTEINE I WERTE I GLAAAR GCDA DDPNTVINENLEL INNELDGY (OP<br>IWALFGSTEN DE IMAREELI LAADR GCDA I DPNNT DGY (OP<br>IWALFGSTEN DE IMAREELI LAADR GCDA I DPNNT DGY (OP<br>IWALFGSTEN DE IMAREELI LAADR GCDA I DPNNT DGY (OP<br>IWALFGSTEN DE IMAREELI HAADR GCDA I DPNNT DGY (OP<br>IWALFGSTEN DAAREELI HAADR GCDA I DPNNT DGY (OP<br>IWALFGSTEN DHARREELI HAADR GCDA I DPNNT DGY (OP<br>IWALFGSGEN I NAARREELI HAADR GCDA I DPNNT DGY (OP INT<br>I WALFGSGEN I NAARREELI HAADR GCDA DDDNT DGY (OP<br>I WALFGSGEN I NAARREELI HAADR GCDA DDDNT DGY (OP<br>I WALFGSGEN I NAARREELI HAADR GCDA DDDNT DGY (OP<br>I WALFGSGEN I NAARREELI HAADR GCDA DDDNT (OP INT DGY (OP INT<br>I WALFGSGEN I NAARREELI MAADR GCDA I DDNT (OP INT I DDY (OP INT I DNT) I WALFGSGEN I NAARREELI WAADR I GCDA I DDNT (OP INT I DDY (OP INT I DDY (OP INT I DNT) I MAARREELI WAADR I GCDA I DDNT (OP INT I DNT) (OP INT I DNT) I WAARREELI WAADR I GCDA I DDNT (OP INT I DNT) (OP INT I DNT) (OP INT I DNT) (OP INT I MARKEELI WAADR I GCDA DDNT (OP INT I DNT) (OP INT I MARKEELI WAADR I GCDA DDNT (OP INT I DNT) (OP INT I MARKEELI WAADR I GCDA DDNT (OP INT I DNT) (OP INT I MARKEELI WAADR I GCDA DDNT (OP INT I DNT) (OP INT I MARKEELI WAADR I GCDA DDNT (OP   | 148<br>148<br>155<br>143<br>152<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>149<br>146<br>146   | RAH7407183.1<br>RAH7407183.1<br>RAP24442154.1<br>XP 011872955.1<br>RAP2449322.1<br>RAP214428.1<br>RAP214828.1<br>RAP214828.1<br>RAP21482810.1<br>RAP24521.1<br>PSM65717.1<br>RAP2452810.1<br>RAP24531736.1<br>RAP2431736.1<br>RAP2431936.1<br>RAP2431936.1<br>RAP2431956.1<br>RAP1435456.1<br>RAP1435456.1   | TSTRS-TTSVRTTSSAPAGGSNGCKSHENDQCGGNDWKG PPTTSRTSTRSTSTTRHTTTRAFGGSGCGGGGGCGNDWKG PTTTVRT  | 348<br>355<br>350<br>344<br>355<br>370<br>301<br>348<br>334<br>334<br>334<br>334<br>334<br>337<br>339<br>337<br>349<br>357<br>335<br>354  |
| KAH7407183.1<br>KAG442154.1<br>XF_031872955.1<br>KAH2595570.1<br>KAF264922.1<br>KAF218422.1<br>KAF218422.1<br>KAF2184922.1<br>KAF2407396.1<br>KAF2407396.1<br>KAF2407396.1<br>KAF2407396.1<br>KAF2407396.1<br>KAF2407396.1<br>KAF240755.1<br>KAF1853545.1<br>KAF1853545.1<br>KAF1853555.1  | YHLEVINSINVELTHYN I QLAAAR GCDCUDPDNT DCY OUP<br>YHLEVINSINVERTHEN I QLAAAR GCDCUDPDNT DCY ONP<br>HHLLISSENVERTHYN I QLAAAR GCDAUDPNT CONTRILLINHLLDGY ONP<br>HHLLISSENVERTHYN I ANNE GCDALDDNT DCY ONP<br>HHLLISSENVERTHYN I ANNE GCDAUDDNT DCY ONP<br>HHLLISSENVERTHYN I GANLARD GCDAUDDNT DCY ONP<br>HHLISSEN HHLISSEN I LAADR GCDAUDDNT DCY ONP<br>HHLISSEN HURSEN HLAADR GCDAUDDNT DCY ONP<br>HHLISSEN HLAADR HLAADR GCDAUDDNT DCY ONP  | 148<br>148<br>155<br>143<br>152<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>146<br>146<br>154  | RAH7407183.1<br>KA0442154.1<br>XP 031872955.1<br>RAB2595570.1<br>RAP214282.1<br>XP 033540912.1<br>RAP214282.1<br>XP 033540912.1<br>RAP245921.1<br>PSNM59717.1<br>RAP26282800.1<br>XP 033548226.1<br>RAP2634922.1<br>EF094882.1<br>RAP2634922.1<br>RAP163726.1<br>RAP1635456.1<br>XP 018387059.1  | TSTRS-TTSVRTTSAPAGGSNGCKSKENDQCGCNDWKG PPTTSRTS   | 348<br>355<br>350<br>344<br>355<br>370<br>301<br>348<br>334<br>352<br>339<br>337<br>349<br>357<br>349<br>357<br>354<br>362  |
| KAH7407183.1<br>KAG442154.1<br>XL_03187295.1<br>KAH254925.1<br>KAF218428.1<br>XP_033540912.1<br>KAF218428.1<br>XF2186221.1<br>PSN69717.1<br>KAF26200.1<br>XL_033688226.1<br>KAF2634922.1<br>EF004882.1<br>KAF2634922.1<br>KAF1835456.1<br>KAF85456.1<br>KAH684956.1<br>XD=018387059.1<br>XD=018387059.1  | YWLRVINSIWYR INTNEI QLAAAR GCDGUDPDNT DCY (WRRVINSIWYR INTNEI QLAABR GCDGUDPDNT DCY (WRRVINSIWYR INT QLAABR GCDGUDPDNT DCY (WRRVINSIWYR INTRE QLAAR FICCOLD DPNNTWINILTLINHELDCY (WRRVINSIW INTRE GARTING DAWN GCDALDPNT DCY (WRRVINSIW INTRE GARTING DAWN GCDALDPNT DCY (WRRVINSIW WRRVINSIW INTRE GARTING DAWN GCDALDPNT DCY (WRRVINSIW WRRVINSIW INTRE GARTING DAWN GCDALDPNT DCY (WRRVINSIW WRRVINSIW WRRVINSIW INTRE GARTING DAWN GCDALDPNT DCY (WRRVINSIW WRRVINSIW WRRVINSI   | 148<br>148<br>155<br>143<br>152<br>157<br>146<br>145<br>145<br>145<br>145<br>146<br>146<br>154<br>153  | RAH7407183.1<br>RAH7407183.1<br>RAPC4442154.1<br>XP.011872955.1<br>RAP2649322.1<br>RAP2118428.1<br>XP.0133540912.1<br>RAP2168521.1<br>PSN69717.1<br>RAP2682800.1<br>XP.033688226.1<br>RAP2631936.1<br>RAP2631936.1<br>RAP2634922.1<br>RAT1663756.1<br>RAP163356.1<br>RAP1649356.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP163556.1<br>RAP165556.1<br>RAP165556.1<br>RAP165556.1<br>RAP165556.1<br>RAP165556.1<br>RAP165556.1<br>RAP165556.1<br>RAP165556.1<br>RAP165556.1<br>RAP1655556.1<br>RAP1655556.1<br>RAP1655556.1<br>RAP16555555555555555555555555555555555555   | TSTRS-TTSVRTTSAPAGGSNGCKSHENDQCGGNDWKG PPTTSRTG   | 348<br>355<br>350<br>344<br>355<br>370<br>301<br>348<br>344<br>352<br>362<br>339<br>337<br>349<br>357<br>335<br>354<br>354<br>355   |
| KAH7407183.1<br>KAG442154.1<br>XH_03187255.1<br>KAH8595570.1<br>KAF218428.1<br>XF_033540912.1<br>KAF218428.1<br>XF_033540912.1<br>FNNF05717.1<br>KAF263200.1<br>XF_033688226.1<br>KAF263200.1<br>XF_033688226.1<br>KAF263782.1<br>KAF263782.1<br>KAF263782.1<br>KAF263782.1<br>KAF263782.1<br>KAF263782.1<br>KAF263782.1<br>KAF263782.1<br>KAF263782.1<br>KAF263782.1<br>KAF263782.1<br>KAF263782.1<br>KAF2637852.1<br>KAF263765.1   | YHLRVINSINVELITYNE I GLAAAR GCDGVDPDIT DCY ON P<br>YHLRVINSINVERIYGEN I GLAAAR GCDGVDPDIT DCY ON P<br>HHLLISSINVERIYGEN GCAALDPDIT DCY ON P<br>HHLLISSINVERIYGEN HATRIELIAAD GCAALDPDIT DCY ON H<br>HHLISSINVESINVERIYGEN GCAALDPDIT DCY ON H<br>HHLIGSSINVESINVERIYGEN GCAALDPDIT DCY ON H<br>HHLIGSSINVESINVERIYGEN GCAALDPDIT DCY ON H<br>HHLIGSSINVED HARRELIYAAD GCAALDPDIT DCY ON H<br>HHLIGSSIN H HARRELIYAAD GCAALD   | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>146<br>149<br>146<br>154<br>153<br>146  | RAH7407183.1<br>RAH7407183.1<br>RAH8595570.1<br>RAH8595570.1<br>RAF214282.1<br>RAF214282.1<br>RAF214282.1<br>RAF2142821.1<br>FM69717.1<br>RAF262820.1<br>XP_03368226.1<br>RAF264222.1<br>EF094882.1<br>RAF264322.1<br>RAF1661782.1<br>RAF1643722.1<br>RAF1643722.1<br>RAF1643723.1<br>RAF163737.1<br>RAF163737.1<br>RAF163737.1<br>RAH7396679.1  | TSTRS-TTSVRTTSAPAGGSNGCKSKHWDQCGGNDWG PPTTSRTSTRS-STVRTTSAAPAGGSSGCTSKHWDQCGGNDWG PTTVRT  | 348<br>355<br>350<br>344<br>352<br>301<br>348<br>334<br>352<br>362<br>339<br>337<br>349<br>357<br>354<br>355<br>354<br>362<br>359<br>343  |
| KAH7407183.1<br>KAG442154.1<br>XF_031872955.1<br>KAH2595570.1<br>KAF2649221.1<br>KAF218422.1<br>KAF2186921.1<br>XF_031540912.1<br>KAF268200.1<br>XF_033688226.1<br>KAF2634922.1<br>EF205482.1<br>KAF183556.1<br>KAF183556.1<br>KAF183556.1<br>XF_01310759.1<br>KAH707557.1   | YWLRVINSWYRTRYN YN CLAAR GCOLUDDNT DCY (MP<br>YWLRVINSWYRTWISN CLAAR GCOLUDDNT DCY (MP<br>YWLRUNSWYRTWISN CLAAR GCALDDNT COLUDNT<br>NRHLGSTWYRTRYN CHARAFLLARD GCOLDDNT<br>DCY (MP<br>NRHLFSSTWYRTRYN CHARAFLLARD GCOLDDNT DCY (MP<br>NRHFGSALVD LMARFLLARD GCOLDDNT DCY (MP<br>NRHFGSALVD LMARFLLARD GCOLDDNT DCY (MP<br>NRHFGSALVD LMARFLLARD GCOLDDNT DCY (MP<br>NRHFGSALVD LMARFLLARD GCOLDDNT COLUDNT (MP<br>NRHFGSALVD LMARFLLARD GCOLDDNT (MP<br>NRHFGSALVD MARFLLARD GCOLDDNT (MP<br>NRHFGSALVD (MR<br>NRHFGSALVD MARFLLARD (GCOLDDNT (MP)<br>NRHFGSALVD (MR<br>NRHFGSALVD (   | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>154<br>153<br>146<br>153  | KAH7407183.1<br>KA0442154.1<br>XP 011872955.1<br>KA18595570.1<br>KA7246322.1<br>KA72118428.1<br>XF 013540912.1<br>KA72184921.1<br>KA7248200.1<br>XF 013540912.1<br>KA724234922.1<br>EP094882.1<br>KA171663782.1<br>KA71663759.1<br>KA71663759.1<br>KA718759.1<br>KA1719679.1<br>KA1705197.1<br>KA17076197.1<br>KA17076197.1  | TSTRS-TTSVRTTSSAPAGGSNGCKSHENDQCGGNDWKG PPTTSITSTRS-TSTVRTTSSAPAGGPSGCTSHENDQCGGNDWKG PTTYIRT   | 348<br>355<br>350<br>341<br>345<br>334<br>352<br>362<br>337<br>349<br>357<br>354<br>362<br>354<br>362<br>354<br>362<br>354<br>362<br>354<br>362<br>354  |
| KAH7407183.1<br>KAG442154.1<br>XH_03182955.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF218428.1<br>XP_033560912.1<br>KAF218621.1<br>PSN69717.1<br>KAF263200.1<br>XH7263200.1<br>XH7263786.1<br>KAF2634922.1<br>EF094882.1<br>KAF263786.1<br>KAF649562.1<br>KAF649562.1<br>KAF649562.1<br>XH6649562.1<br>KAF63785.1<br>KAH705657.1<br>KAH705657.1<br>KAH705657.1<br>KAH705657.1   | YWLRVINSINVELITINE I GLAAAF GCDGVDPDIT DCY QP<br>YWLRVINSINVERING I GLAASF GCDGVDPDIT DCY QP<br>WHLRVISSINVERITE I GUAAFF GCDA DE PNITVIENIUT LINHELDGY<br>WHLRVISSINVERITE I GUAAFF GCDA DE PNITVIENIUT LINHELDGY<br>WHLRVISSINVERITE I GUAAFF GCDA DE PNITVIENIUT LINHELDGY<br>WHLRVISSINVERITE I GUAAFF GCDA DE PNIT<br>DGY QP<br>WHLRVISSINVED I MARFEI HAADN GCDA DE PNIT<br>DGY QP<br>WHLRVISSINVED I MARFEI HAADN GCDALE PNIT<br>DGY QP<br>WHLRVISSINVED I MARFEI HAADN GCDALE PNIT<br>DGY QP<br>WHLRVISSINVED HARFEI HAADN GCDALE PNIT<br>DGY QP<br>WHLRVISSIN HARFEI HAADN GCDALE PNIT<br>DGY QP   | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>154<br>153<br>146<br>153<br>146<br>152<br>152  | RAH7407183.1<br>RAA442154.1<br>XP 01187955.1<br>RAF2184595570.1<br>RAF218428.1<br>XP 033540912.1<br>RAF218428.1<br>XP 033540912.1<br>PSN69717.1<br>RAF268220.1<br>XP 03368226.1<br>RAF26320.1<br>RAF2631936.1<br>RAF2631936.1<br>RAF2631936.1<br>RAF2631936.1<br>RAF2631936.1<br>RAF2631936.1<br>RAF2631936.1<br>RAF2631936.1<br>RAF2631936.1<br>RAF263757.1<br>RAH707637.1<br>RAH707637.1<br>RAH707637.1  | TS         TRS-TTSVRTTSAPAGENGCKSHENDQCCGNDWKG           PPTTSRTSFK-TSSTTRFFT-TSAPAGENGCKSKENDQCCGNDWKG           PTTSSRTS         PFTSSTRFFT-TSSAPAGENGCKSKENDQCCGNDWKG           PTTTSRTS         PFTTSTSTSTRFFT-TSFAPAGEGGSCCKSKENDQCCGNDWKG           PTTTIRFSATTSSTRFFT-TSTSAPAGEGGSCCKSKENDQCCGNDWKG           PTTTIRFSATTSSTRFFT-TFNCGGGGGGGCCKSKENDQCCGNDWKG           PTTTIRFSATTSSTRFFT-TFNGGGGGGGGCCKSKENDQCCGNDWKG           PTTTIRFSATTSTSTTSTTSTTSTTFFT-TFNGGGGGGGGCCKSKENDQCCGNDWKG           PTTTLRP         TSSFTTSTSTTSTTSTTSTTFFT-TFNGGGGGGGGCCKSKENDQCCGONWKG           PTTTLRP         TSSTTTSTTSTTSTTSTTFFT-TFNGGGCCKSKENDQCCGNDWKG           PTTTLRPS         TTSSTTTRFTS-TFCNGGCCGCKSKENDQCCGONWKG           STTTKSTTKTSTTSTTSTTRFTS-TFCGGCCCKSKENDQCCGONWKG         SVTTYSSTVTSQTATSTQRTTGTSGGCCKSKENDQCCGONWKG           STTTSSTTKSTSTSTSTTSTTSTTRFTS-TFGGCCCKSKENDQCCGONWKG         SVTTYSSTVTSQTATSTSTTRFTS-TFGGCCCKSKENDQCCGONWKG           STTTSST  | 348<br>355<br>350<br>344<br>355<br>370<br>301<br>348<br>344<br>352<br>339<br>337<br>349<br>357<br>357<br>355<br>354<br>362<br>359<br>3456<br>353  |
| KAH7407183.1<br>KAG442154.1<br>XF_031872955.1<br>KAH2595570.1<br>KAF2649221.1<br>KAF218428.1<br>XF_031540912.1<br>KAF2186921.1<br>KAF2616921.1<br>XF_033688226.1<br>XAF243736.1<br>KAF2634922.1<br>EF2034882.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF183759.1<br>KAF183759.1<br>KAF183759.1<br>KAF183759.1<br>KAF1709536.1<br>OAL44252.1   | YWLEVNINSWYELHTNEI (LAAARGCDCVDPDNT DCY (WLEVNINSWYELHTNEI (LAARGCDCVDPDNT DCY (WP<br>YWLEVNISSWYELHTNEI (DAARGCDALDPDNT)<br>FINLISSBWYELHTEN (DAARGCDALDPDNT)<br>DCW (WLEVSETWEN)<br>FINLISSBWYELHTARSBWEGDALDPDNT DCY (WP<br>WHLEVSETWENDERSETLASDWGCDALDPDNT DCY (WP<br>WHLEVSETSTEINTARSWGCDALDPDNT DCY (WP<br>WHLEVSETSTEINTARSWGCDALDPDNT DCY (WP<br>WHLEVSETSTEINTARSETLASDWGCDALDPDNT DCY (WP<br>WHLEVSESSTEINTARSETLASDWGCDALDPDNT DCY (WP  | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>154<br>153<br>146<br>154<br>152<br>152<br>152<br>146  | RAH7407183.1<br>KA0442154.1<br>XP 031872955.1<br>RAH8295570.1<br>RAP214282.1<br>XP 033540912.1<br>RAP214282.1<br>PSN09917.7.1<br>RAP2682800.1<br>XP 0315469216.1<br>PSN09917.7.1<br>RAP2632802.1<br>RAP2631922.1<br>RAP2631922.1<br>RAP163725.1<br>RAT1663752.1<br>RAT163752.1<br>RAT163759.1<br>RAH7075357.1<br>RAH77075357.1<br>RAH7075356.1<br>ORL44252.1<br>VA17076356.1<br>ORL44252.1<br>VA17076356.1<br>ORL44252.1<br>VA17076356.1<br>ORL44252.1   | TSTRS-TTSVRTTSAPAGESNGCKSHENDQCGGNDWKG PPTTSIT5   | 348<br>355<br>350<br>341<br>355<br>370<br>301<br>348<br>334<br>352<br>369<br>357<br>355<br>354<br>362<br>359<br>343<br>356<br>353<br>346<br>353<br>354<br>353<br>346  |
| KAH7407183.1<br>KAG442154.1<br>XH_03182955.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF218428.1<br>XP_033560912.1<br>KAF218621.1<br>PSN69717.1<br>KAF263200.1<br>XH_25200.1<br>XH_25200.1<br>KAF2634922.1<br>EF094882.1<br>KAF2634922.1<br>EF094882.1<br>KAF263786.1<br>KAF263786.1<br>KAF647950.1<br>XH056377.1<br>KAH73996719.1<br>KAH7076357.1<br>KAH7076357.1<br>KAH7076356.1<br>OLA44252.1<br>CAF2647813.1  | YHLRVINSINVELITINI I QLAAA/GCDCVDPDT DCY QP<br>YHLRVINSINVELITINI I QLAAA/GCDCVDPDT DCY QP<br>YHLRVINSINVERVESIN (20LAAS/GCDCVDPDT)<br>DCY QP<br>HARLIGSTWISSINTTI QUAAS/GCDAIDPDNT DCY QP<br>HARLIGSTWISSINTTI AASOLGCAIDPDNT DCY QP<br>HARLIGSTWISSINTI HARSINGCAIDPDNT DCY QP<br>HINRIGGSINTUSSINTI HARSINGCAIDPDNT DCY QP<br>HINRIGGSISTI HARSINTAD/GCAIDPDNT DCY QP<br>HINRIGGSISTI HARSINTAD/GCAIDPDNT DCY QP<br>HINRIGGSISTI HARSINTI HARSINGCAIDPDNT DCY QP<br>HINRIGGSISTI HARSINTAD/GCAIDPDNT DCY QP<br>HINRIGGSISTI HARSINTAD/GCAIDPDNT DCY QP<br>HINRIGGSISTI HARSINTAD/GCAIDPDNT DCY QP<br>HINRIGGSISTI HARSINTAD/GCAIDPDNT DCY QP<br>HINRIGGSISTI HARSINTAD/HINGCOIDPDNT DCY QP<br>HINRIGGSISTI HARSINTAD/HINGCOIDPDNT DCY QP<br>HINRIGSSISTI HARSINTAD/HINGCOIDPDNT DCY QP<br>HINRIGSSI HINGSSISTI HARSINTAD/HINGCOIDPDNT DCY QP<br>HINRIGSSIGNI HARSINTAD/HINGCOIDPDNT DCY QP<br>HINRIGSSIGNI HARSINTAD/HINGCOIDPDNT DCY QP  | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>145<br>146<br>154<br>153<br>146<br>154<br>153<br>146<br>152<br>152<br>146   | RAH7407183.1<br>RAA442154.1<br>XP 01187955.1<br>RAF2184595570.1<br>RAF218428.1<br>XP 033540912.1<br>RAF218428.1<br>XP 033540912.1<br>PSN69717.1<br>RAF268220.1<br>XP 03368226.1<br>RAF2631936.1<br>RAF2631936.1<br>RAF2631936.1<br>RAF2631936.1<br>RAF2631936.1<br>RAF2631936.1<br>RAF263757.1<br>RAH7395679.1<br>RAH7395679.1<br>RAH7395679.1<br>RAH7395679.1<br>RAH73957.1<br>RAH73957.1<br>RAH74878.1.1   | TS         TRS-TTSVRTTSAPAGENGCKSHENDQCGCNDNKG           PPTTSRTSFK-TSSTRTKPTREGGSGCGCGCNDNKG           PTTSSTRS         PFTTSSTRSTKPT-TSAPAGESGCSCGCGNDNKG           PTTTSRTS         PFTTSSTRTKPT-TSAPAGESGCSCGCGNDNKG           PTTTSRTS         PFTTSTSTSTRTKPT-TSTSAPAGEGGSGCGCGCGCNDNKG           PTTTIR         PFTTSTSTSTRTKPT-TSTSGCGGGGGGCCKSHNDQCGNDNKG           PTTTIR         PSSTPASPSSADPTS-TFCN-GGGGGGGCCKSHNDQCGQDNNKG           PTTTIR         PSSTPASPSSADPTS-TFCN-GGCGCCCCNHNDQCGQDNKG           PTTTIR         PSSTPASPSSADPTS-TFCN-GGCGCCCKSHNDQCGQDNKG           PTTSTSTINPTSTSTTSTTTSTTTRTP-TGC-GGCCCSHNDQCCQDNKG         PTTSTTTRSTTTPTSTTTRTPT-TFCN-GGCGCCSHNDQCCQDNKG           PTTSTSTRTSTSTSTTRTSTTRTS-TFC-GGCCCSHNDQCCQDNKG         PTTSTSTTRTSTTRTSTTRTS-TFC-GGCCCSHNDQCCQDNKG           PTTSSTTRTSSTTRTSTSTTRTSTTRTS-TFC-GGCCCSHNDQCCQDNKG         PTTSSTTTRTSTSTTRTSTTRTSTTRTSTTRTSTTRTS-TFC-GGCCCSHNDQCCQDNKG           PTTSSTTSTSTTRTSTTRTSTTRTSTTRTS-TFC-GGCCCSHNDQCCQDNKG         PTTSSTTRTSTTRTSTTRTSTTRTS-TFC-GGCCCSHNDQCCQDNKG           PSTTTSTSTMMED-STRTSSTQRTS-T-S-GGGCCCSHNDQCCQDNKG         PTTSSTTASS-QRTFS-T-S-GGGCCSHNDQCGQDNKG           PSTTTAPT         PTSSRTSTTRTSTTRTSTTRTSTTRTS-TFC-GGCCCSHNDQCCGDNKG           PSTTTSTST         PTSSRTSTTRDPTSTSSDQPTS-T-S-GGGCCCSHNDQCGGDNKG           PSTTTSTST         PTSSRTSTTRPPTS-T-S-GGGCCCSHNDQCGGDNKG           PSTTTSTST         PTSSRTSTPPTS-T-S-GGGCCCSHND  | 348<br>355<br>350<br>344<br>355<br>370<br>301<br>348<br>349<br>357<br>354<br>362<br>359<br>354<br>362<br>359<br>354<br>362<br>359<br>354<br>362<br>359<br>354<br>356<br>356<br>353<br>356<br>358  |
| KAH7407183.1<br>KAG442154.1<br>XF_031872955.1<br>KAH2595570.1<br>KAF2649221.1<br>KAF218428.1<br>XF_031540912.1<br>KAF2186921.1<br>KAF2618620.1<br>XT_033688226.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF183759.1<br>KAH705956.1<br>KAH7065368.1<br>0AL44252.1<br>KAF25.1<br>KAF25.1<br>KAF25.1<br>KAH70697.0<br>KAF25.1<br>KAH70697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH707697.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH70767.0<br>KAH   | YWLEVNINSWYELHTNEI QLAAARGCDGVDPDIT     DOY     ONP       YWLEVNINSWYELHTNEI QLAASRGCDGVDPDIT     DOY     ONP       YWLEVNINSWYELHTNEI QLAASRGCDGVDPDIT     DOY     ONP       INKLISSBWYELHTNEI QLAASRGCDALDPDIT     DOY     ON       INKLISSBWYELHTNEI QLAASRGCDALDPDIT     DOY     ON       INKLISSBWYELHTNEINAELIARGOLODALDPDIT     DOY     ON       INKLISSBWYELHTARSBYEGDALDPDIT     DOY     ON       INKLISSBWYEN     DARABELTARSBYEGDALDPDIT     DOY     ON       INKLISSBWYEN     DARABELTARSBYEGDALDPDIT     DOY     ON       INKLISSBWYEN     DARABELTARSBYEGDALDPDIT     DOY     ON       INKLISSBWYEN     DOY     ON     ON       INKLISSBWYEN     DOY </td <td>148<br/>148<br/>155<br/>143<br/>157<br/>146<br/>145<br/>145<br/>145<br/>145<br/>145<br/>146<br/>146<br/>154<br/>153<br/>146<br/>154<br/>153<br/>146<br/>154<br/>152<br/>152<br/>152<br/>146<br/>146</td> <td>RAH7407183.1<br/>KAG442154.1<br/>XP 011872955.1<br/>RAH8295570.1<br/>RAF214282.1<br/>XP 033540912.1<br/>RAF21428.1<br/>XP 033540912.1<br/>RAF218428.1<br/>KAF261428.1<br/>RAF261428.1<br/>RAF2634280.1<br/>XP 03368226.1<br/>RAF2634280.1<br/>RAF263422.1<br/>EF094882.1<br/>RAF1637542.1<br/>RAF1637545.1<br/>RAF163759.1<br/>RAF163759.1<br/>RAF163759.1<br/>RAF163759.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF17075357.1<br/>RAF170757.1<br/>RAF170757.1<br/>RAF170757.1<br/>RAF170757.1</td> <td>TSTRS-TTSVRTTSAPAGESNGCKSHENDQCGGNDWKG PPTTSIT5</td> <td>348<br/>355<br/>350<br/>344<br/>355<br/>370<br/>301<br/>348<br/>334<br/>352<br/>362<br/>337<br/>349<br/>357<br/>354<br/>362<br/>359<br/>343<br/>359<br/>343<br/>359<br/>343<br/>356<br/>353<br/>354<br/>858<br/>358<br/>346</td>   | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>154<br>153<br>146<br>154<br>153<br>146<br>154<br>152<br>152<br>152<br>146<br>146  | RAH7407183.1<br>KAG442154.1<br>XP 011872955.1<br>RAH8295570.1<br>RAF214282.1<br>XP 033540912.1<br>RAF21428.1<br>XP 033540912.1<br>RAF218428.1<br>KAF261428.1<br>RAF261428.1<br>RAF2634280.1<br>XP 03368226.1<br>RAF2634280.1<br>RAF263422.1<br>EF094882.1<br>RAF1637542.1<br>RAF1637545.1<br>RAF163759.1<br>RAF163759.1<br>RAF163759.1<br>RAF163759.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF17075357.1<br>RAF170757.1<br>RAF170757.1<br>RAF170757.1<br>RAF170757.1   | TSTRS-TTSVRTTSAPAGESNGCKSHENDQCGGNDWKG PPTTSIT5   | 348<br>355<br>350<br>344<br>355<br>370<br>301<br>348<br>334<br>352<br>362<br>337<br>349<br>357<br>354<br>362<br>359<br>343<br>359<br>343<br>359<br>343<br>356<br>353<br>354<br>858<br>358<br>346  |
| KAH7407183.1<br>KAG442154.1<br>XH_031872955.1<br>KAH754959570.1<br>KAF2649221.1<br>KAF218428.1<br>XM_213540912.1<br>KAF218428.1<br>XM_2126521.1<br>PSN59717.1<br>KAF2621922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF26375.1<br>KAH705536.1<br>KAH705537.1<br>KAH705936.1<br>KAF2750897.1<br>KAF2750897.1<br>KAF2750897.1<br>KAF25081.1<br>KAF25081.1<br>KAF2621.1  | YHLRVINSIWKILITNIR I QLAAAR GCDGVDPDIT DCY QP<br>YHLRVINSIWKILITNIR I QLAAAR GCDGVDPDIT DCY QP<br>YHLRVINSIWKIRVISIN I QLAABR GCDA UPPNIT<br>HILLIGSTWUS I HITTINI (AAAR GCDA DPDIT)<br>DGY QP<br>INHLIGGSTWIS I HITTINI I AAAR GCDA DPDIT<br>DGY QN<br>INHLIGGSTWIS I HITTINIA I LAADR GCDA DPDIT<br>DGY QN<br>INHLIGGSTWIS I HITTINIA I LAADR GCDA DPDIT<br>DGY QN<br>INHLIGGSTWIS I HARRI I LAADR GCDA DPDIT<br>DGY QN<br>INHLIGGST I LAARRI I LAADR GCDA DPDIT<br>DGY QN<br>INHLIGGST I LAARRI I LAADR GCDA DPDIT<br>DGY QN<br>INHLIGGST I LAARRI I LAADR GCDA DPDIT<br>DGY QN<br>I NILIGGST I LAARR I LAADR GCDA DPDIT<br>DGY QN<br>I NILIGGST I   | 148<br>148<br>155<br>143<br>152<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>154<br>154<br>153<br>146<br>154<br>153<br>146<br>152<br>152<br>146<br>146<br>152  | RAH7407183.1<br>RAH7407183.1<br>RAT214442154.1<br>KAB8595570.1<br>KA72148595570.1<br>KA7214828.1<br>XF_033540912.1<br>KA7214828.1<br>XF_033540912.1<br>PSM69717.1<br>KA7264922.1<br>KA72634922.1<br>KA72634922.1<br>RAT1663762.1<br>RAT643936.1<br>RAT643936.1<br>RAT643936.1<br>RAH843936.1<br>RAH843936.1<br>RAH843937.1<br>RAH7063368.1<br>OAL44252.1<br>KA7263757.1<br>RAH7063357.1<br>RAH7063357.1<br>RAH7063357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH706357.1<br>RAH70637.1<br>RAH70637.1<br>RAH70637.1<br>RAH70637.1<br>RAH70637.1<br>RA  | TSTRS-TTSVRTTSAPAGESNGCKSHENDQCGGNDWKG PPTTSRTS   | 348<br>355<br>350<br>344<br>355<br>370<br>301<br>348<br>334<br>352<br>339<br>337<br>349<br>357<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>357<br>357<br>357<br>357<br>357<br>357<br>357<br>357<br>357 |
| KAH7407183.1<br>KAG442154.1<br>XF_031872955.1<br>KAH2595570.1<br>KAF2649221.1<br>KAF2649221.1<br>KAF2649221.1<br>KAF2649221.1<br>KAF2649220.1<br>XF_033608226.1<br>XKF2437396.1<br>KAF243796.1<br>KAF243796.1<br>KAF2634922.1<br>EF0964882.1<br>KAF183556.1<br>KAF183556.1<br>KAF183556.1<br>KAF183556.1<br>KAF183556.1<br>CAL4252.1<br>KAF17076357.1<br>KAF17076356.1<br>CAL4252.1<br>KAF250897.1<br>KAF250897.1<br>KAF2730897.1<br>KAF2750897.1<br>KAF2750897.1<br>KAF2750897.1<br>KAF2750897.1<br>KAF2750897.1<br>KAF2750897.1<br>KAF2750897.1<br>KAF2750897.1<br>KAF2750897.1<br>KAF2750897.1<br>KAF2750897.1<br>KAF2750897.1<br>KAF2750897.1<br>KAF2750897.1<br>KAF2750897.1<br>KAF2750897.1<br>KAF2750897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF25087.1<br>KAF25087.1<br>KAF25087.1<br>KAF25087.1<br>KAF25087.1<br>KAF   | YWLEVNINSWYELHTNEI (LAAR/GCDCVDPDHT DCY QP<br>YWLEVNINSWYELHTNEI (LAAR/GCDCVDPDHT DCY QP<br>YWLEVNISWYENEN (TAAR/GCDALDPDHT)<br>NIKLISSBWYENET (TAAR/GCDALDPDHT)<br>DCW QP<br>INKLYSSTYLEVNISWENET (LAAR/GCDALDPDHT)<br>DCW QP<br>INKLYSSTYLEVNISWENET (LAAR/GCDALDPDHT)<br>DCY QP<br>INKLYSSTYLENEN (TAAR/GCDALDPDHT)<br>DCY QP<br>INKLYSSSTYLENEN (TAAR/GCDALDPDHT)<br>DCY QP<br>INKLYSSSTYLENEN (TAAR/GCDALDPDHT)<br>DCY QP<br>INKLYSSSTYLENEN (TAAR/GCDALDPDHT)<br>DCY QP<br>INKLYSSSTYLENEN (TAAR/GCDALDPDHT)<br>DCY QP<br>INKLYSSSTYLENEN (TAAR/GCDALDPDHT)<br>DCY QP<br>INKLYSSSSTYLENEN (TAAR/GCDALDPDHT)<br>DCY QP<br>INKLYSSSS   | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>146<br>154<br>153<br>146<br>154<br>152<br>152<br>146<br>145<br>145<br>145<br>145<br>146   | RAH7407183.1<br>RAH442154.1<br>XP 01187395.1<br>RAH2549322.1<br>RAH2549322.1<br>RAF214428.1<br>XP 033540912.1<br>RAF2142821.1<br>FM089717.1<br>RAF2642820.1<br>XP 033588226.1<br>RAF264322.1<br>RAF264322.1<br>RAF2643422.1<br>RAF1661782.1<br>RAF1643722.1<br>RAH643562.1<br>XP 018387059.1<br>RAH7076357.1<br>RAH7076357.1<br>RAH7076357.1<br>RAH7076357.1<br>RAH7076357.1<br>RAH7076357.1<br>RAH7076357.1<br>RAH7076358.1<br>OAL44252.1<br>RAH72550897.1<br>RAH72550897.1<br>RAH725750897.1<br>RAH725750897.1<br>RAH725750897.1<br>RAH725750897.1<br>RAH725750897.1<br>RAH725750897.1   | TSTRS-TTSVRTTSAPAGESNGCKSKHMDQCGGNDWG PPTTSRTSTRS-STVRTTSAPAGESGCTSKHMDQCGGNDWG PTTVRT  | 348<br>355<br>350<br>344<br>355<br>370<br>301<br>348<br>352<br>362<br>337<br>349<br>337<br>349<br>349<br>3457<br>355<br>354<br>362<br>359<br>346<br>353<br>356<br>356<br>353<br>346<br>358<br>348<br>348<br>348<br>348<br>368   |
| KAH7407183.1<br>KAG442154.1<br>XH_03187295.1<br>KAH2595570.1<br>KAF261922.1<br>KAF2118428.1<br>XP_033540912.1<br>KAF2186221.1<br>PSN69717.1<br>KAF26200.1<br>XP_033688226.1<br>KAF243796.1<br>KAF243796.1<br>KAF24556.1<br>KAH6849362.1<br>KAH6849362.1<br>KAH6849362.1<br>KAH68493657.1<br>KAH697557.1<br>KAH7059368.1<br>OAL44252.1<br>KAF2750897.1<br>KAF2226012.1<br>KAF2266012.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF2266012.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1<br>KAF23807.1  | YWLRVINSWYRTRINN I QLAAARGCDGVDPDIT     DDY     QIP       YWLRVINSWYRTRYNSIN (QLAASRGCDGVDPDIT     DDY     QIP       YWLRVINSWYRTRYNSIN (QLAASRGCDGVDPDIT     DDY     QIP       IKMLISSOWYRTRYNSIN (QCAALDPDIT     DDY     QIP       IKMLISSOWYRTRYNSIN (QCAALDPDIT     DDY     QIP       IKMLISSOWYRTRYNSIN (QCAALDPDIT     DGY     QIP       IKMLISSOWYRTRYNSIN (QCAALDPDIT     DGY     QIP       IKMLINGSSIN (DMARRITLAADRIGCAALDPDIT     DGY     QIP       IKMLINGSGI (DMARRITLAADRIGCAALDPDIT     DGY     QIP </td <td><math display="block">148\\148\\155\\143\\157\\146\\145\\145\\145\\145\\145\\145\\146\\146\\146\\154\\154\\152\\152\\152\\146\\146\\145\\146\\145\\145\\152\\152\\152\\152\\152\\152\\146\\145\\152\\152\\152\\152\\152\\152\\152\\152\\152\\15</math></td> <td>RAH7407183.1<br/>RAH7407183.1<br/>RAT24442154.1<br/>XP 011872955.1<br/>RAT214829570.1<br/>RAT21482922.1<br/>RAT21482922.1<br/>RAT21482921.1<br/>RAT2148291.1<br/>RAT2621921.1<br/>RAT2621921.1<br/>RAT2631921.1<br/>RAT2631921.1<br/>RAT263192.1<br/>RAT263192.1<br/>RAT1637596.1<br/>RAT263192.1<br/>RAT1637596.1<br/>RAT87595.1<br/>RAT875951.1<br/>RAH7059588.1<br/>OAL44252.1<br/>RAT7059588.1<br/>OAL44252.1<br/>RAT705957.1<br/>RAT705957.1<br/>RAT27526012.1<br/>RAT2266012.1<br/>RAT2266012.1<br/>RAT228603.1</td> <td>TSTRS-TTSVRTTSAPAGGSNGCKSHENDQCGGNDWKG PPTTSRTG</td> <td>348<br/>355<br/>350<br/>344<br/>355<br/>301<br/>344<br/>352<br/>352<br/>352<br/>352<br/>352<br/>357<br/>355<br/>354<br/>362<br/>354<br/>355<br/>354<br/>355<br/>354<br/>355<br/>354<br/>355<br/>356<br/>356<br/>356<br/>356<br/>358</td>  | $148\\148\\155\\143\\157\\146\\145\\145\\145\\145\\145\\145\\146\\146\\146\\154\\154\\152\\152\\152\\146\\146\\145\\146\\145\\145\\152\\152\\152\\152\\152\\152\\146\\145\\152\\152\\152\\152\\152\\152\\152\\152\\152\\15$  | RAH7407183.1<br>RAH7407183.1<br>RAT24442154.1<br>XP 011872955.1<br>RAT214829570.1<br>RAT21482922.1<br>RAT21482922.1<br>RAT21482921.1<br>RAT2148291.1<br>RAT2621921.1<br>RAT2621921.1<br>RAT2631921.1<br>RAT2631921.1<br>RAT263192.1<br>RAT263192.1<br>RAT1637596.1<br>RAT263192.1<br>RAT1637596.1<br>RAT87595.1<br>RAT875951.1<br>RAH7059588.1<br>OAL44252.1<br>RAT7059588.1<br>OAL44252.1<br>RAT705957.1<br>RAT705957.1<br>RAT27526012.1<br>RAT2266012.1<br>RAT2266012.1<br>RAT228603.1   | TSTRS-TTSVRTTSAPAGGSNGCKSHENDQCGGNDWKG PPTTSRTG   | 348<br>355<br>350<br>344<br>355<br>301<br>344<br>352<br>352<br>352<br>352<br>352<br>357<br>355<br>354<br>362<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>356<br>356<br>356<br>356<br>358   |
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KAH7407183.1<br>KAG442154.1<br>XH_031872955.1<br>KAH7649322.1<br>KAF26149322.1<br>XH72118428.1<br>XM_033560912.1<br>KAF261202.1<br>PSN69717.1<br>KAF26200.1<br>XH_033688226.1<br>KAF2631922.1<br>EFQ94882.1<br>KAF2614922.1<br>EFQ94882.1<br>KAF163786.1<br>KAF263192.1<br>KAF26375.1<br>KAH705375.1<br>KAH705375.1<br>KAH70575.1<br>KAH70575.1<br>KAH70575.1<br>KAH70575.1<br>KAH70575.1<br>KAH72691.1<br>KAF2750897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF2602.1<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KAF202.2<br>KA 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03358021.1<br>RAF263280.1<br>KAF2631396.1<br>RAF2631396.1<br>RAF2631396.1<br>RAF2631396.1<br>RAF2631396.1<br>RAF163782.1<br>RAF163782.1<br>RAF163757.1<br>RAF17396479.1<br>RAF17395479.1<br>RAF2756897.1<br>RAF2256897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF2556897.1<br>RAF255  | TSTRS-TTSVRTTSAPAGESNCKSHENDQCCGNDWG PPTTSRTS   | 348<br>355<br>350<br>344<br>355<br>362<br>362<br>362<br>362<br>362<br>357<br>357<br>357<br>357<br>357<br>357<br>357<br>357<br>357<br>356<br>356<br>356<br>356<br>356<br>356<br>356<br>356<br>356<br>356   |
| 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| YWLRVINSIWELITNIR I QLAAARGCDGVDPDIT     DDY     QVP       YWLRVINSIWELITNIR I QLAAARGCDGVDPDIT     DDY     QVP       YWLRVINSIWELITNIR QLAARGCDGVDPDIT     DDY     QVP       INKLISSBWIRTE QUAARGCDALDPDIT     DDY     QVP       INKLISSBWIRTE QUAARGCDALDPDIT     DDY     QVP       INKLISSBWIRTE QUAARGCALARDDIT     DDY     QVP       INKLISSBWIRTE QUAARGCALARDDIT     DDY     QVP       INKLISSBWIRTE QUAARGCALARDDIT     DDY     QVP       INKLISSBWIRTE QUAARGCALARDDIT     DDY     QVP       INKLISSBWIRTE QUARKELLARDIGCOALDPDIT     DDY     QVP       INKLISSBWIRTERARTIGUARDIGCOALDPDIT     DDY     QVP       INKLISSBWIRTERARTIGUARDIGCOALDPDIT     DDY     QVP <td< td=""><td>148<br/>148<br/>155<br/>143<br/>157<br/>146<br/>145<br/>145<br/>145<br/>145<br/>145<br/>145<br/>146<br/>154<br/>152<br/>152<br/>152<br/>146<br/>146<br/>145<br/>145<br/>152<br/>152</td><td>RAH7407183.1<br/>RAH7407183.1<br/>RAP24492154.1<br/>XP 011872955.1<br/>KAP249322.1<br/>KAP249322.1<br/>KAP249322.1<br/>KAP249322.1<br/>KAP248221.1<br/>RAP248221.1<br/>RAP248221.1<br/>RAP248221.1<br/>RAP248231366.1<br/>RAP2431396.1<br/>RAP2431396.1<br/>RAP2431396.1<br/>RAP2431396.1<br/>RAP1243546.1<br/>RAP1243546.1<br/>RAH7053168.1<br/>RAH7053168.1<br/>RAH7053168.1<br/>RAH7051361.1<br/>RAP2256012.1<br/>RAP2266012.1<br/>RAP2266012.1<br/>RAP2266012.1<br/>RAP723603.1</td><td>TS       TRS-TTSVRTTSSA       PAGGSNGCKSHENDQCGGNDWKG         PPTTSITG       TKT-SSTVRTTSSA       PAGGSPGCTSHENDQCGGNDWKG         PTTTSITG       TPSTSTTSTTRFTT-TAGGGSGGGGGGCGCANDWKG         PTTTVRT       TPPTTS       TASTSHENDTSTSTRFTT-TAGGGSGGGGGGCGCANDWKG         PTTTIR       PTSSTRFTT       TAGGGSGGGGGGCGCANDWKG         PTTTIR       PSSTRFTTSTSTRFTT-TAGGGSGGGGGGCGCANDWKG         PTTTIR       PSSTRFFTSTSTSTPTS       TRGGGGGGGGGCGCANDWKG         PTTTIR       PSSTRFFTSTSTSTSTTT       TTMG         SIPPNPSTTSTSTRPTS       TMGCGGGGGGGCCANDWKG         PSTLARS       TAGGSGGGGGCCANDWKG         PSTLARS       TAGGGSGGGGCCANDWKG         PSTLARS       TAGGSGGGGGGCCANDWKG         PSTLARS       TAGGSGGCCANDWKG         PSTLARS       TAGGSGGCCANDWKG         PSTLARS       TTSTSTTUPTS         PSTLARS       TAGGSGGCCANDWKG         PTTTPSSVTRSOTTSTQUTTSTSTUPTS       GGGGCCANDWKG         VTTYSSVTRSOTTSTQUTTSTSTQUTTSTSTUPTS       GGGGGCCANDWKG         PSTVTST       HLP = STSSA-0000000000000000000000000000000000</td><td>348<br/>355<br/>350<br/>344<br/>355<br/>344<br/>355<br/>344<br/>355<br/>349<br/>357<br/>354<br/>359<br/>349<br/>349<br/>357<br/>354<br/>359<br/>349<br/>349<br/>355<br/>354<br/>359<br/>349<br/>343<br/>355<br/>354<br/>359<br/>344<br/>355<br/>356<br/>356<br/>356<br/>356<br/>356<br/>356<br/>356<br/>356<br/>356</td></td<>   | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>145<br>146<br>154<br>152<br>152<br>152<br>146<br>146<br>145<br>145<br>152<br>152  | RAH7407183.1<br>RAH7407183.1<br>RAP24492154.1<br>XP 011872955.1<br>KAP249322.1<br>KAP249322.1<br>KAP249322.1<br>KAP249322.1<br>KAP248221.1<br>RAP248221.1<br>RAP248221.1<br>RAP248221.1<br>RAP248231366.1<br>RAP2431396.1<br>RAP2431396.1<br>RAP2431396.1<br>RAP2431396.1<br>RAP1243546.1<br>RAP1243546.1<br>RAH7053168.1<br>RAH7053168.1<br>RAH7053168.1<br>RAH7051361.1<br>RAP2256012.1<br>RAP2266012.1<br>RAP2266012.1<br>RAP2266012.1<br>RAP723603.1   | TS       TRS-TTSVRTTSSA       PAGGSNGCKSHENDQCGGNDWKG         PPTTSITG       TKT-SSTVRTTSSA       PAGGSPGCTSHENDQCGGNDWKG         PTTTSITG       TPSTSTTSTTRFTT-TAGGGSGGGGGGCGCANDWKG         PTTTVRT       TPPTTS       TASTSHENDTSTSTRFTT-TAGGGSGGGGGGCGCANDWKG         PTTTIR       PTSSTRFTT       TAGGGSGGGGGGCGCANDWKG         PTTTIR       PSSTRFTTSTSTRFTT-TAGGGSGGGGGGCGCANDWKG         PTTTIR       PSSTRFFTSTSTSTPTS       TRGGGGGGGGGCGCANDWKG         PTTTIR       PSSTRFFTSTSTSTSTTT       TTMG         SIPPNPSTTSTSTRPTS       TMGCGGGGGGGCCANDWKG         PSTLARS       TAGGSGGGGGCCANDWKG         PSTLARS       TAGGGSGGGGCCANDWKG         PSTLARS       TAGGSGGGGGGCCANDWKG         PSTLARS       TAGGSGGCCANDWKG         PSTLARS       TAGGSGGCCANDWKG         PSTLARS       TTSTSTTUPTS         PSTLARS       TAGGSGGCCANDWKG         PTTTPSSVTRSOTTSTQUTTSTSTUPTS       GGGGCCANDWKG         VTTYSSVTRSOTTSTQUTTSTSTQUTTSTSTUPTS       GGGGGCCANDWKG         PSTVTST       HLP = STSSA-0000000000000000000000000000000000  | 348<br>355<br>350<br>344<br>355<br>344<br>355<br>344<br>355<br>349<br>357<br>354<br>359<br>349<br>349<br>357<br>354<br>359<br>349<br>349<br>355<br>354<br>359<br>349<br>343<br>355<br>354<br>359<br>344<br>355<br>356<br>356<br>356<br>356<br>356<br>356<br>356<br>356<br>356   |
| KAH7407183.1<br>KAG442154.1<br>XH_031872955.1<br>KAF26492955.1<br>KAF2649221.1<br>KAF218428.1<br>XT_033560912.1<br>KAF218428.1<br>XKF218620.1<br>XF_033688226.1<br>KAF2634922.1<br>EFQ9482.1<br>KAF2634922.1<br>EFQ94882.1<br>KAF2634922.1<br>EFQ94882.1<br>KAF1835456.1<br>KAF1835456.1<br>KAH705368.1<br>OAL44252.1<br>KAH705368.1<br>OAL4425.1<br>KAF7350897.1<br>KAF2750897.1<br>KAF7250897.1<br>KAF7250897.1<br>KAF2750897.1<br>KAF2261.1<br>KAF21.2<br>KAF7123803.1<br>KAF7407183.1<br>KAF7407183.1<br>KAF7407183.1<br>KAF7407183.1<br>KAF7407183.1  | YHLRYNNSWYR I NYNR I QLAAAR GCDGUDPDNT DCY WRLRYNNSWYR I NYNR I QLAAR AGCGUDPDNT DCY WRLRYNNSWYR WRLN I QLAAR AGCDUC YDDNT DCY WRLRYNNSWYR WRLN I QLAAR AGCDUC YDDNT DCY WRLRYNNSWYR WRLRYN GAAL AGCOL DDDNT DCY WRLRYN DAR AGCDUC YDDNT DCY WRLRYN DAR AGCUC YDDNT DCY WRLRYN DAR AGCUC YDDNT DCY WRLRYN DAR AGUN GCOL DDDNT DCY WRLRYN DAR AGUN GCOL DDDNT DCY WRLRYN DAR AGUN GCOL DDDNT DCY WRLRYN GARWR DAR AGUN GCOL DDDNT DCY WRLWYN GRAF AGUN GCOL DDDNT DCY WRLWN GCOL DDDNT DCY WRLWYN GRAF AGUN GCOL DDDNT DCY WRLWN GCOL DDDNT DCY WRLWYN GCOL DDDNT DCY WRLWN DCY WRLWYN GCOL DDDNT DCY WRLWYN GCOL DDDNT DCY WRLWN GCOL DDDNT DCY WRLWYN GCOL DDDNT DCY WRLWN GCOL DDDNT DCY WRLWYN GCOL DDDNT DCY WRLWYN GCOL DDDNT DCY WRLWN GCOL DDDNT DCY WRLWYN GCOL DDDNT DCY WRLWN GCOL DDNT DCY WRLWN GCOL DDDNT DCY WRLWN GCOL DDNT DCY WRLWN GCOL DDNT DCY WRLWN GCOL DDNT DCY WRLWN WRLWN GCOL DDNT DCY WRLWN WRLWN GUN GCOL DDNT DCY WRLWN WRLWN GUN GCOL DDNT DCY WRLWN WRLWN GCOL DDNT DCY WRLWN GCUN WRLWN GCOL DDNT DCY WRLWN GCUN WRLWN GCUN GCOL DDNT DCY  | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>154<br>153<br>146<br>154<br>153<br>146<br>152<br>152<br>146<br>146<br>152<br>152<br>146<br>146<br>145<br>152   | RAH7407183.1<br>RAH7407183.1<br>RAT214325.1<br>RAT214325.1<br>RAT214328.1<br>RAT214328.1<br>RAT214328.1<br>RAT214328.1<br>RAT214328.1<br>RAT24520.1<br>RAT2643221.1<br>RAT26320.1<br>RAT26320.1<br>RAT26320.1<br>RAT26320.1<br>RAT263422.1<br>RAT1653756.1<br>RAT1653756.1<br>RAT1653756.1<br>RAT1653757.1<br>RAT175537.1<br>RAT75537.1<br>RAT775587.1<br>RAT775587.1<br>RAT775587.1<br>RAT2750877.1<br>RAT25612.1<br>RAT250837.1<br>RAT250837.1<br>RAT275087.1<br>RAT250837.1<br>RAT275087.1<br>RAT250837.1<br>RAT275087.1<br>RAT250837.1<br>RAT275087.1<br>RAT275087.1<br>RAT25083.1   | TSTRS-TTSVRTTSAPAGESNGCKSHENDQCGGNDWG PPTTSRTS  | 348<br>355<br>350<br>301<br>301<br>301<br>302<br>302<br>302<br>302<br>302<br>302<br>302<br>302<br>302<br>302  |
| KAH7407183.1<br>KAG442154.1<br>XF_031872955.1<br>KAH2595570.1<br>KAF2649221.1<br>KAF2186921.1<br>XF_03150912.1<br>XF_03150912.1<br>XF_03150912.1<br>XF_033688226.1<br>XF_033688226.1<br>XF_033688226.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF183556.1<br>KAF183556.1<br>KAF183556.1<br>KAF183556.1<br>KAF18355.1<br>KAF17059368.1<br>OAL44252.1<br>KAF7059368.1<br>OAL44252.1<br>KAF725097.1<br>KAF226012.1<br>KAF7264781.3.1<br>KAF725303.1   | YWLRVINSIWELITNIR I QLAAARGCDGVDPDIT         DDY         QNP           YWLRVINSIWELITNIR I QLAARGCDGVDPDIT         DDY         QNP           YWLRVINSIWESIN (TO QLAARGCDGVDPDIT)         DDY         QNP           IRWLISSOWERT (TO QLAARGCDALDPDIT)         DDY         QNP           IRWLISSOWERT (TO QLAARGCDALDPDIT)         DDY         QNP           IRWLISSOWERT (TO QLAARGCDALDPDIT)         DDY         QNP           IRWLISSOWERT (TARGENT (TO ALDPDIT)         DDY         QNP           IRWLISSOWERT (TARGENT (TARGENT)         DDY         QNP           IRWLISSOWERT (TARGENT)         DDY         QNP           IRWLISSOWE  | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>145<br>146<br>154<br>152<br>152<br>152<br>152<br>146<br>146<br>145<br>145<br>152<br>152<br>152<br>152<br>152<br>152<br>152<br>152<br>152<br>15  | RAH7407183.1<br>RAH7407183.1<br>RA72449255.1<br>KA72449255.1<br>KA7244922.1<br>KA724922.1<br>KA72118428.1<br>KP_013540921.1<br>RA72184521.1<br>RA72184521.1<br>RA724520.1<br>KA724234922.1<br>E7094882.1<br>RA7124534922.1<br>RA71845456.1<br>RA71845456.1<br>RA71845456.1<br>RA718759.1<br>RA71765356.1<br>RA7705356.1<br>RA7705356.1<br>RA772557.1<br>RA7725607.1<br>RA772266012.1<br>RA772367.1<br>RA772367.1<br>RA772367.1<br>RA772367.1<br>RA772367.1<br>RA772367.1<br>RA772367.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA772357.1<br>RA77   | TS       TRS-TTSVRTTSSA       PAGGSNGCKSHENDQCGGNDWKG         PPTTSITG       TKT-SSTVRTTSSA       PAGGSPGCTSHENDQCGGNDWKG         PTTTSITG       TPSTSTTRATT       TADGGGSGCGGCGGCCCANDWKG         PTTTIN       TPSTTSTSTRATT       TADGGGGSGCGCGCGCCANDWKG         PTTTIN       TPSTTSTSTRATT       TADGGGGGGGGCCCANDWKG         PTTTIN       TSSTPART       TAGGGGGGGGGCCCANDWKG         PTTTIN       TSSTPARTSTSTSTTTTST       TGMT         PTTTIN       TSSTPARTSTSTSTTTTT       TGMT         PTTTIN       TSSTPARTSTSTSTTSTTTTTT       TGMT         PTTLAR       TSSTPARTSTSTTTTTTT       TGGGGGGGGCCCANDWGG         PTTLAR       TSSTTTSTTTSTTTTTT       TGCGGGGGCGCCCANDWGG         PTTLAR       TSSTPARTSTTTATSTTTTTTT       TGGGGGGCGCCANDWGGCCONDWGG         PTTTLAR       TSSTPARTSTTTATSTTTTTTT       TGGGGGCCCANDWGGCCONDWGG         PTTTLAR       TSSTPTSTTTATSTQATTSTSTPARTSTTTTTTT       TGGGGGCCCANDWGGCCONDWGG         PTTTLAR       TTTTSTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT  | 348<br>355<br>350<br>351<br>354<br>355<br>357<br>301<br>301<br>346<br>352<br>359<br>359<br>359<br>359<br>359<br>359<br>359<br>359<br>359<br>359   |
| KAH7407183.1<br>KAG442154.1<br>XH_031872955.1<br>KAH754182255.1<br>KAF2649227.1<br>KAF218428.1<br>XP_033540912.1<br>KAF218620.1<br>XF218620.1<br>XF2620.1<br>XF2620.1<br>XF2634922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF263492.1<br>KAF263492.1<br>KAF263492.1<br>KAF26375.1<br>KAF705356.1<br>CAL4252.1<br>KAF705357.1<br>KAF726957.1<br>KAF726957.1<br>KAF726957.1<br>KAF726957.1<br>KAF726957.1<br>KAF7250557.1<br>KAF7255.1<br>KAF7555.1<br>KAF5557.1   | YHLRVINSIVICI INTIN I QLAAAR GCDGVDPDIT DCY QP<br>YHLRVINSIVICI INTIN I QLAAAR GCDGVDPDIT DCY QP<br>YHLRVINSIVICI YHRVISIN QLAAAR GCDGVDPDIT DCY QP<br>YHLRVINSIVICI YHRVISIN QLAAAR GCDGVDPDIT DCY QP<br>YHLRVINSIVICI YHRVISIN QLAAAR GCDALDPDIT DCY QP<br>YHLRVISSIVICI INARRII ILAADR GCDALDPDIT DCY QP<br>YHLRVISSI YNDI YNN YN YNDI YNN YN   | 148<br>148<br>155<br>143<br>152<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>154<br>153<br>146<br>154<br>153<br>146<br>154<br>152<br>152<br>146<br>146<br>153<br>146<br>152<br>152<br>146<br>145<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>152<br>152<br>152<br>152<br>152<br>153<br>146<br>145<br>153<br>145<br>153<br>145<br>153<br>145<br>153<br>145<br>155<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>145   | RAH7407183.1<br>RAH7407183.1<br>RAT2148595570.1<br>RAT214828.1<br>RAT214828.1<br>RAT214828.1<br>RAT214828.1<br>RAT214828.1<br>RAT214828.1<br>RAT2649221.1<br>RAT2649221.1<br>RAT2649221.1<br>RAT264922.1<br>RAT264922.1<br>RAT264922.1<br>RAT1663762.1<br>RAT1663762.1<br>RAT163756.1<br>RAT163756.1<br>RAT705356.1<br>RAT705357.1<br>RAT705357.1<br>RAT7750897.1<br>RAT7750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT27555.1<br>RAT27555.1<br>RAT27555.1<br>RAT27555.1  | TS         TRS-TTSVRTTSA         PAGSINGLESHENDQCCGNDWKG           PPTTSRTS         THT-SSTURTTSTA         PAGGSPSCHSHENDQCCGNDWKG           PTTTSRTS         PFTTSSTRTRFT         PAGGSSCGCSMDWKG           PTTTSRTS         PFTTSSTRTRFT         PAGGSSCGCSMDWKG           PTTTIR         PFSTSTSTRTFT         PAGGSSCGCSMDWKG           PTTTIR         PFSTSTSTSTRFT         PAGGGSCGCGGCGCCSMDWKG           PTTTIR         PSSTPABPSSADTE         PTGGGGGGGGCCSCSHENDQCCGNDWKG           PTTTIR         PSSTPABPSSADTE         PTGGGGGGGGCCSCSHENDQCCGNDWKG           PTTTLR         PSSTPABPSSADTE         PTGGGGGGGCCSCSHENDQCCGNDWKG           PTTLR         SIPPNPSTTSTSTPPTS         PTGGGGGGGGCCSCSHENDQCCGNDWKG           PTTLR         SSTPATSASARTE         PTGNCGCCSHENDQCCGNDWKG           PTTLR         SSTPATSASARTE         PTGNCGCCSHENDQCCGNDWKG           PTTURPS         TH         GGGGCCSHENDQCCGNDWKG           SVTTYSSTVTSGTSTSTPTPTSTTFT         -GGGGCCSHENDQCCGNDWKG         -TTSTSTTSTSTSTSTSTPTS           SVTTYSSTVTSGTSTSTSTQFTSTSTSTPFT         -GGGGCCSHENDQCCGNDWKG         -TTSTSTTSTSTSTSTPTSTTSTSTSTPTSTTSTSTSTPTS           SVTTSST         HLPSITSSAQHTS -T-S         GGGGCCSHENDQCCGNDWKG         STTTSTSTQFTSTSTSTSTPPTS -TC           PSTTLRF         TTSSSAQHTS -T-S         GGGGCCSHENDQCCG   | 348<br>355<br>3300<br>301<br>304<br>304<br>304<br>304<br>304<br>304<br>304<br>304<br>304<br>305<br>305<br>305<br>305<br>305<br>305<br>305<br>305<br>305<br>305  |
| KAH7407183.1<br>KAG442154.1<br>XF_031872955.1<br>KAH2595570.1<br>KAF2649222.1<br>KAF218428.1<br>XF_031540912.1<br>KAF2186200.1<br>XF_033608226.1<br>XF_033608226.1<br>XF_033608226.1<br>KAF2634922.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835551.1<br>KAF226012.1<br>KAF226012.1<br>KAF226012.1<br>KAF226012.1<br>KAF22555.1<br>XAF249555.1<br>XAF25555.1<br>XAF25555.1<br>XAF2522.1   | YWLRVINSINGELTENET (JAAARGCGCVDPDIT     DOY     OVP       YWLRVINSINGENERT (JAARGCGCVDPDIT     DOY     OVP       YWLRVINSINGENERT (JAARGCGCDDPDIT     DOY     OVP       YWLRVINSINGENERT (JAARGCGCDDPDIT     DOY     OVP       YWLRVINSINGENERT (JAARGCGCDDPDIT     DOY     OVP       YWLRVINSINGENERT (JAARGCGDDDPDIT     DOY     OVP       YWLRVINSINGENERT (JAARGCGDDDPDIT     DOY     OVP       YWLRVINSINGENERT (JAARGCGDDDPDIT     DOY     OVP       YWLRVINSINGENERT (JAARGCGDDDPDIT     DOY     OVP       YWLRVINGENERT (JAARGCGDDDPDIT     DOY     OVP       YWLRVINGENERT (JAARGCGDDDPDIT     DOY     OVP       YWLRVINGENERT (JAARGCGDDDPDIT     DOY     OVP       YWLRVINGENERT (JAARGCGDDDDDIT     DOY     OVP       YWLRVINGENERT (JAARGCGDDDDDIT     DOY     OVP       YWLRVINGENERT (JAARGCGDDDDIT     DOY     OVP       YWLRVINGENERT (JAARGCGDDDDIT     DOY     OVP       YWWRINGENERT (JAARGCGDDDDIT     DOY     OVP <t< td=""><td>148<br/>148<br/>155<br/>143<br/>157<br/>146<br/>145<br/>145<br/>145<br/>145<br/>145<br/>145<br/>146<br/>153<br/>146<br/>154<br/>152<br/>152<br/>152<br/>146<br/>146<br/>145<br/>145<br/>152<br/>152<br/>152<br/>152<br/>146<br/>146<br/>145<br/>145<br/>152<br/>152</td><td>KAH7407183.1<br/>KAO442154.1<br/>XP 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KAH7407183.1<br>KAG442154.1<br>XL_031872955.1<br>KAH2595570.1<br>KAF2619322.1<br>KAF2118428.1<br>XD_033540912.1<br>KAF218621.1<br>PSN69717.1<br>KAF262800.1<br>XL_72061<br>KAF2621922.1<br>KAF2634922.1<br>KAT263796.1<br>KAF2634922.1<br>KA1663782.1<br>KAF263795.1<br>KAH7069368.1<br>OAL44225.1<br>KAF706937.1<br>KAF705937.1<br>KAF705937.1<br>KAF705937.1<br>KAF705937.1<br>KAF72612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2750897.1<br>KAF26012.1<br>KAF72612.1<br>KAF2750897.1<br>KAF26012.1<br>KAF27555.1<br>KAF705955.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612.1<br>KAF2612 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148<br>148<br>155<br>143<br>152<br>157<br>146<br>145<br>145<br>145<br>145<br>146<br>149<br>146<br>154<br>152<br>152<br>146<br>146<br>153<br>146<br>145<br>152<br>152<br>146<br>145<br>152<br>152<br>146<br>145<br>152<br>152<br>146<br>145<br>152<br>152<br>146  | RAH7407183.1<br>RAH7407183.1<br>RAP214442154.1<br>XP 011872955.1<br>RAP214428.1<br>XP 011872955.1<br>RAP214428.1<br>XP 013540912.1<br>XP 013540912.1<br>RAP2142821.1<br>RAP2142821.1<br>RAP24243921.1<br>RAP24243921.1<br>RAP14631796.1<br>RAP2434922.1<br>RA11663792.1<br>RA116637059.1<br>RA116637059.1<br>RA116637059.1<br>RA117059366.1<br>RA117059366.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA11705937.1<br>RA1170597.1<br>RA1170597.1<br>RA1170597.1<br>RA1170597.1<br>RA1170   | TSTRS-TTSVRTTSAPAGESNCKSHENDQCGONDWG PPTTSRTS   | 348<br>355<br>364<br>344<br>301<br>348<br>348<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362   |
| KAH7407183.1<br>KAG442154.1<br>XF_031872955.1<br>KAH2595570.1<br>KAF2649221.1<br>KAF264922.1<br>KAF2186921.1<br>XF_03360822.1<br>KAF2186200.1<br>XT_033688226.1<br>XT_033688226.1<br>KAF243796.1<br>KAF245796.1<br>KAF245796.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF183759.1<br>KAF1705356.1<br>CAF47597.1<br>KAF725371.1<br>KAF725371.1<br>KAF725371.1<br>KAF72555.1<br>KAF2550.1<br>KAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF2555.1<br>XAF25555.1<br>XAF25555.1<br>XAF25555.1<br>XAF25555.1<br>XAF25555.1<br>XAF25555.1<br>XAF25555.1<br>X                           | YWLRVINSINGELTENET (JAAARGCGCVDPDIT     DOY     OVP       YWLRVINSINGENERVELANG (JAARGCGCVDPDIT     DOY     OVP       YWLRVINSINGENERVELANG (GOALDPDIT     DOY     OVP       INKLISSEDWEITERVERVELANG (GOALDPDIT     DOY     OVP       INKLISSEDWEITERVERVELANG     DOY     OVP       INKLISSEDWEITERVERVELANG     DOY     OVP       INKLISSEDWEITERVERVELANG     DOY     OVP       INKLISSEDWEITERVERVERVELANG     DOY     OVP       INKLISSEDWEITERVERVERVELANG     DOY     OVP       INKLISSEDWEITERVERVERVERVERVERVERVERVERVERVERVERVERVE  | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>154<br>152<br>152<br>152<br>146<br>146<br>146<br>154<br>152<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>152<br>152<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>152<br>152<br>152<br>152<br>155<br>152<br>155<br>155   | KAH7407183.1<br>KAO442154.1<br>XP 011872955.1<br>KAP2649322.1<br>KAP2649322.1<br>KAP2649322.1<br>KAP2118428.1<br>XP 033540912.1<br>KAP2649322.1<br>KAP2649322.1<br>KAP2649322.1<br>KAP2649322.1<br>KAP2649322.1<br>KAP2649322.1<br>KAP1663769.1<br>KAP2649325.1<br>KAP16959.1<br>KAP70595.1<br>KAP2697.1<br>KAP26697.1<br>KAP2266012.1<br>KAP22657.0<br>KAP22657.0<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP226697.1<br>KAP22697.1<br>KAP22697.1<br>KAP22697.1<br>KAP22697.1<br>KAP22697.1<br>KAP22697.1<br>KAP22697.1<br>KAP22697.1<br>KAP22697.1<br>KAP22697.1<br>KAP22697.1<br>KAP22697.1<br>KAP22697.1<br>KAP22697.1<br>KAP22697.1<br>KAP2269   | TS         TS-TTSVRTTSA         PAGSINGLESHENDQCGGNDWKG           PPTTSITS         TKT-SSTVRTTSIA         PAGGSPGCTSHENDQCGGNDWKG           PTTTSITS         PFTTSITSTTRIPT         PAGGSSPGCTSHENDQCGGNDWKG           PTTTIN         TTSSTVRTT         PAGGSSPGCTSHENDQCGGNDWKG           PTTTIN         PSTRAFT         TARGGGSGCGGCGCCLENDQCGNDWKG           PTTTIN         PTSSTVRTT         PAGGSSCGGGGGCGCCLENDQCGNDWKG           PTTTIN         PSTRAFT         TRGGGSGCGGCGCCLENDQCGDDWKG           PTTTIN         PSTRAFT         TRGGGSGCGGCCCLENDQCGDDWKG           PTTLA         PSSTRAFT         TRGGGSGCGCCCLENDQCGDDWKG           PTTLA         PSSTRAFT         TRGGGSGCGCCCLENDQCGDDWKG           PTTLA         PSSTRAFT         TRGGGSGCGCCCLENDQCGGDWKG           PTTLA         PSSTRAFT         PSGGCGCDSSKENDQCCGDWKG           PTTLAP         STRAFTSTSTSTSTRAFT         TRGGGCGCCCLENDQCGCDWKG           PTTSSTSTSTSTSTSTSTSTSTTRAFTS         TRGGGGCGCGCCCLENDQCGCDWKG         PSSTRAFT           PSSTRAFT         MLP = STSSTARSTTRAFTS         STRMOQCGGCDWKG           PSSTRAFT         MLP = STSSTSTRAFTS         STRMOQCGGCDWKG         PSSTRAFT           PSSTRAFT         MLP = STSSTSTRAFTS         STRMOQCGCDWKG         PSSTRAFT           PSSTRAFT         ML  | 348<br>355<br>344<br>355<br>301<br>301<br>301<br>301<br>302<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>36  |
| KAH7407183.1<br>KAG442154.1<br>XF_03187295.1<br>KAH2595570.1<br>KAF251922.1<br>KAF218428.1<br>XP_033540912.1<br>KAF218428.1<br>XF218428.0<br>IXF218428.0<br>KAF2634922.1<br>EF094882.1<br>KAF2634922.1<br>KAF2634922.1<br>KAF263795.1<br>KAH5965.1<br>XH6849562.1<br>XH6849562.1<br>KAH7059368.1<br>OAL44252.1<br>KAF2750897.1<br>KAF264913.1<br>KAF266012.1<br>KAF26597.1<br>KAF266012.1<br>KAF26595.1<br>KAF275087.1<br>KAF2751825.1<br>KAF2751825.1<br>KAF2751825.1<br>KAF2751825.1<br>KAF2751825.1<br>KAF2751825.1<br>KAF2751825.1<br>KAF2751825.1<br>KAF2751825.1<br>KAF2751825.1<br>KAF2751825.1<br>KAF2751825.1<br>KAF2751825.1<br>KAF2751825.1<br>KAF2751822.1<br>KAF266012.1<br>KAF21825.1<br>KAF26512.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF21822.1<br>KAF   | YYLIVYINSIWYILIYNI I QLAAA'I COGVDPDIT DCY QP<br>YYLIVYINSIWYIN I QLAAS'I COALOPDIT DCY QP<br>YYLIVYINSIWYIN GLAAS'I COALOPDIT DCY QP<br>YNLIVYINSIWYIN I QLAAS'I COALOPDIT DCY QP<br>YNLIVYINSIWYIN I YNLIAGAI COALOPDIT DCY QP<br>YNLIVGSA'I YNLI YNLIAGAI COALOPDIT DCY QP<br>YNLIVGSA'I YNLI YNLI YNLI GAAL COALOPDIT DCY QP<br>YNLIYGSA'I YNLI YNLI YNLI GAAL COALOPDIT DCY QP<br>YNLIYGSA'I YNLI YNLI YNLI GAAL COALOPDIT DCY QP<br>YNLIYGSA'I YNLI YNLI YNLI YNLI GOAL DDYNT DCY QP<br>YNLIYGSA'I YNLI YNLI YNLI YNLI YNLI YNLI YNLI YNL  | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>149<br>146<br>154<br>153<br>146<br>153<br>146<br>153<br>152<br>152<br>146<br>145<br>152<br>152<br>146<br>145<br>152<br>152<br>146<br>145<br>152<br>152<br>152<br>146<br>145<br>152<br>152<br>152<br>152<br>152<br>152<br>152<br>152<br>152<br>15   | RAH7407183.1<br>RAH7407183.1<br>RAP24442154.1<br>XP 011872955.1<br>RAP22449322.1<br>RAP214282.1<br>XP 033540912.1<br>RAP214282.1<br>RAP2142821.1<br>RAP22428200.1<br>XP 03368226.1<br>RAP2437366.1<br>RAP2437366.1<br>RAP2437366.1<br>RAP2437366.1<br>RAP2437365.1<br>RAP1235456.1<br>RAP1235456.1<br>RAP1235456.1<br>RAP1235456.1<br>RAP123556.1<br>RAP123557.1<br>RAP123557.1<br>RAP123557.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12357.1<br>RAP12  | TS       TRS-TTSVRTTSSA       PAGSINGCKSHENDQCGGNDWKG         PPTTSIRTS       TRTSEPT       PFTTSSTRTRFT       PAGGSSGCKSHENDQCGGNDWKG         PTTTSIRTS       PFTTSSTRTRFT       PAGGSSGCKSHENDQCGGNDWKG         PTTTVNTT       TPSTTSTSTRFTSTST       PAGGSSGCKSHENDQCGGNDWKG         PTTTIR       PSSTABSSRDTS       TRGGGGGGGGCCCVSHENDQCGGNDWKG         PTTTIR       PSSTABSSRDTS       TRGGGGGGGCCCVSHENDQCGGNDWKG         PTTTLR       PSSTABSSRDTS       TRGGGGGGGCCVSHENDQCGQNDWKG         PTTTLP       TRAFTSTTSTSTRPTS       TRGGGGGGCCCVSHENDQCGQNDWKG         PTTTLP       TRAFTSTSTTIGPTS       TRGGGGGCCSHENDQCGQNWKG         PTTTLP       TRAFTSTGPTTSTSTRPTS       TRNGCHGGCCVSHENDQCGQNWKG         PTTTLP       STRTSTSTRTSTTSTTRPTS       TRNGCHGGCCVSHENDQCGQNWKG         SVTTYRSTTRSTSTRPTSTSTRPTSTTSTTRPT       GGGGGCCVSHENDQCGQNWKG       SVTTRSTSTTSTPPTSTSTRPTS         SVTTRSTSTSTSTPTPTSTSTRPTSTSTRPTS       TRAFTSTSHDQCGGNWKG       SVTTRSSCHENDQCGQNWKG         SVTTRSTSTSTSTSTPTPTSTSTRPTSTSTRPTS       TRAFTSTSTSTRPTSTSTRPTS       GGGGGCCVSHENDQCGQNWKG         SVTTRSTSTSTSTSTRPTSTSTRPTSTSTRPTS       TRAFTSTSTSTSTRPTSTSTRPTS       GGGGGCCVSHENDQCGGNWKG         PSTTLFST       STRTSTSTSTSTRPTSTSTRPTS       GGGGGCCVSHENDQCGGNWKG       STTTFSTSTSTSTSTSTSTRPTSTSTRPTS       GGGGGCCVSHENDQCGGNWKG   | 348<br>355<br>370<br>344<br>345<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>364<br>365<br>354<br>365<br>354<br>365<br>354<br>365<br>354<br>366<br>358<br>368  |
| KAH7407183.1<br>KAG442154.1<br>XF_031872955.1<br>KAH2595570.1<br>KAF2649221.1<br>KAF264922.1<br>KAF2186921.1<br>PSN69717.1<br>KAF2630922.1<br>KAF2186200.1<br>XF_033688226.1<br>XF_033688226.1<br>KAF243796.1<br>KAF245796.1<br>KAF245796.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF183556.1<br>KAF25379.1<br>KAF1705951.1<br>KAF7253971.1<br>KAF72555.1<br>KAF226012.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2649222.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF255555.1<br>KAF255555.1<br>KAF255555.1<br>KAF255555.1<br>KAF2555555555555555555555555555555555555  | YWLRVINSIWELHTNET (JAAARGCGVDPDNT     DOY     OVP       YWLRVINSIWELHTNET (JAARGCGALDPDNT     DOY     OVP       YWLRVINSIWESKELTER (JAARGCGALDPDNT     DOY     OVP       YWLRVINSIWERT (JAARGKGCALDPDNT     DOY     OVP       YWLRVINSIWERT (JAARGKGCALDPDNT     DOY     OVP       YWLRVINSIGUE (JAARGKGCALDPDNT     DOY     OVP       YWWRITGON (JAARGKELTAADIGCOALDPDNT     DOY     OVP       YWWRITGON (JAARGKELTAADIGCO  | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>154<br>152<br>152<br>152<br>146<br>146<br>154<br>152<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>152  | KAH7407183.1<br>KAO442154.1<br>XP 011872955.1<br>KAB25955.1<br>KAP2649322.1<br>KAP2118428.1<br>XF 033540912.1<br>KAP2649322.1<br>KAP218428.1<br>XF 033540912.1<br>KAP2634922.1<br>EV994882.1<br>KAP2634922.1<br>EV994882.1<br>KAP1643756.1<br>KAP2634922.1<br>KAP1663769.1<br>KAP163569.1<br>KAP1705356.1<br>OA144252.1<br>KAP705368.1<br>OA144252.1<br>KAP266913.1<br>KAP226697.1<br>KAP226697.1<br>KAP22657.0<br>KAP22657.0<br>KAP22557.0<br>KAP22557.0<br>KAP22557.0<br>KAP22557.0<br>KAP22557.0<br>KAP221.1<br>ZP01385970.1<br>KAP221.1<br>ZP01385970.1<br>KAP225570.1<br>KAP225570.1<br>KAP225570.1<br>KAP225570.1<br>KAP225570.1<br>KAP221.1<br>ZP01385970.1<br>KAP211428.1<br>XP01385970.1<br>KAP211428.1<br>XP01385970.1<br>KAP21428.1<br>XP01385970.1<br>KAP211428.1<br>XP01385970.1<br>KAP211428.1<br>XP01385970.1<br>KAP211428.1<br>XP01385970.1<br>KAP211428.1<br>XP01385970.1<br>KAP211428.1<br>XP01385970.1<br>KAP211428.1<br>XP01385970.1<br>KAP211428.1<br>XP01385970.1<br>KAP211428.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1<br>XP01385970.1   | TS       TRS-TTSVRTTSA       PAGSINGLESHENDQCGGNDWKG         PPTTSITS       TKT-SSTVRTTSIA       PAGGSPGCISHENDQCGGNDWKG         PTTTSITS       PFTTSITSTTRIPT       PAGGSSCGCGCGGGCGCANNKG         PTTTIN       PTSSTSTRIPT       PAGGSSCGCGCGGCGCANNKG         PTTTIN       PSSTVAPT       TABGGSGGGGGGCGCANNKG         PTTTIN       PSSTVAPT       PAGGSGGGGGGCCANNKG         PTTTIN       PSSTVAPT       TRGGGGGGGGCCANNKG         PTTTIN       PSSTVAPT       TRGGGGGGGGCCANNKG         PTTTIN       PSSTVAPT       TRGGGGGGGGCCANNKG         PTTLN       PSSTVAPT       TRGGGGGGGGCCANNKG         PSTVLNPSTVSTSTSSPTSTSSPTSTSTSSPTS       TRGGGGGGCGCCANNKG         PTTLNP       TSNTPTSTSSPTSTSSPTS       TRGGGCGCGCCANNKG         PTTLNP       TSNTPTSTSTSSPTSTSSPTSTSSPTS       TRGGCANGCANNKG         PTTLNP       STVTVSSTMSGTSTSTSVAPTSTSTSTRTSTSTSTSSPT       GGGCCCANNKG         PTTSSTTSSTSTSTSTSTSTSTSTTRTSTSTSTSTSSPT       GGGCCCANNKG       SVTTYSSTMSGTSTSTSTSTSTSTSTSSA         PSSTVTST       HLPSITSSA       GGGCCCANNKG       SVTTYSSTMSGTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTS   | 348<br>355<br>344<br>355<br>370<br>348<br>352<br>362<br>362<br>352<br>362<br>353<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>362<br>355<br>354<br>368<br>354<br>356<br>358<br>356<br>358<br>356<br>358<br>356<br>358<br>356<br>358<br>356<br>358<br>357<br>357<br>357<br>357<br>357<br>357<br>357<br>357<br>357<br>357                      |
| KAH7407183.1<br>KAG442154.1<br>XF_03187295.1<br>KAH2595570.1<br>KAF2618922.1<br>KAF2118428.1<br>XP_033540912.1<br>KAF2186221.1<br>PSN69717.1<br>KAF26200.1<br>XF_033688226.1<br>KAF247396.1<br>KAF247396.1<br>KAF247396.1<br>KAF247396.1<br>KAF247396.1<br>KAF247396.1<br>KAF24757.1<br>KAH7065368.1<br>OAL44225.1<br>KAF275087.1<br>KAF266012.1<br>KAF266012.1<br>KAF266012.1<br>KAF27501.1<br>KAF255.1<br>KAF275025.1<br>KAF275025.1<br>KAF275025.1<br>KAF2751.1<br>KAF2751.1<br>KAF2751.1<br>KAF27525.1<br>KAF2751.1<br>KAF27525.1<br>KAF2751.1<br>KAF255.1<br>KAF255.1<br>KAF255.1<br>KAF255.1<br>KAF255.1<br>KAF255.1<br>KAF255.1<br>KAF255.1<br>KAF26522.1<br>KAF26522.1<br>KAF26522.1<br>KAF26522.1<br>KAF26522.1<br>KAF2651.1<br>PSN5971.1<br>PSN5971.1<br>PSN5971.1<br>PSN5971.1  | YYLIVYINSIVIKIITYNI I QLAAR (CGCVDPDIT DCY QP<br>YYLIVYINSIVIKI WESIN (QLAAS (CGCVDPDIT DCY QP<br>YYLIVYINSIVIKIWESIN (QLAAS (CGCVDPDIT)<br>DCY QP<br>YNLIVSINSIVIKIWESIN (QLAAS (CGCVDPDIT)<br>DCY QP<br>YNLIVSIS (YNLIVSIKIT) (QLAAS (CGCVDPDI   | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>149<br>146<br>153<br>146<br>153<br>146<br>153<br>152<br>152<br>146<br>145<br>152<br>152<br>146<br>145<br>152<br>152<br>146<br>145<br>152<br>152<br>146<br>145<br>152<br>152<br>146<br>145<br>152<br>152<br>152<br>146<br>145<br>152<br>152<br>153<br>146<br>153<br>146<br>154<br>155<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>145   | RAH7407183.1<br>RAH7407183.1<br>RAP24442154.1<br>XP 011872955.1<br>RAP22449322.1<br>RAP214428.1<br>XP 033540912.1<br>RAP2142821<br>RAP2142821.1<br>RAP2428210.1<br>RAP242821.1<br>RAP2428200.1<br>RAP2437366.1<br>RAP2437366.1<br>RAP2437366.1<br>RAP2437366.1<br>RAP2437366.1<br>RAP243736.1<br>RAP243736.1<br>RAP243736.1<br>RAP243737.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP3537.1<br>RAP35   | TS       TRS-TTSVRTTSA       PAGSINGLESHENDQCGONDING         PPTTSIRTS       THT-SSTURTTTSA       PAGGSPGCISSHENDQCGONDING         PTTTSIRTS       PTTTSSTRTRATT       PAGGSSGCISSHENDQCGONDING         PTTTIR       PTSSTRTSTT       PAGGSGCGGGGGCGCCCURDINGG         PTTTIR       PSSTRAPPSSADPTS       PAGGGGGGGGGCGCCURDINGG         PTTTIR       PSSTRAPPSSADPTS       PAGGGGGGGGCCCURDINGG         PTTTIR       PSSTRAPPSSADPTS       PROGCGGGGGCCURDINGG         PTTTLR       PSSTRAPPSSADPTS       PROGCGGGGGCCURDINGCGQUDING         PTTTLR       PSSTRAPPSSADPTS       PROGCGGGGCGCURDINGCQUDING         PTTTLR       TTSTTTSTTGPTPTS       PCGCGGCGCCSHENDQCCGQUDING         PTTTLR       PSSTRAPPSTATTSTGPTTS       PCGCGGCGCSHENDQCGQUDING         PTTTLP       TTSTSTTGPTTSTTSTTSTTSTTTSTTTSTTTSTTTSTTT   | 348<br>355<br>370<br>344<br>345<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>365<br>364<br>365<br>354<br>365<br>354<br>365<br>354<br>365<br>354<br>366<br>8<br>368   |
| KAH7407183.1<br>KAG442154.1<br>XF_031872955.1<br>KAH2595570.1<br>KAF264922.1<br>KAF264922.1<br>KAF218622.1<br>KAF218622.1<br>KAF218620.1<br>XF_033608226.1<br>XF_033608226.1<br>KAF243796.1<br>KAF245796.1<br>KAF245796.1<br>KAF24579.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF25337.1<br>KAF1835456.1<br>KAF184759.1<br>KAF17076.9<br>KAF707697.1<br>KAF725371.1<br>KAF226012.1<br>KAF22557.1<br>KAF22557.1<br>KAF22557.1<br>KAF22557.1<br>KAF22557.1<br>KAF22557.1<br>KAF22557.1<br>KAF22557.1<br>KAF22557.1<br>KAF22557.1<br>KAF22557.1<br>KAF226012.1<br>KAF22557.1<br>KAF226012.1<br>KAF218422.1<br>KAF22557.1<br>KAF226012.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF2557.1<br>KAF264202.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF264222.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF26422.1<br>KAF264   | YWLRVINSIWELHTNET (JAAARGCGOUPDINT     DOY     OVP       YWLRVINSIWELHTNET (JAARGCGOUPDINT     DOY     OVP       YWLRVINSIWESKERT (JAARGCGOLDEDINT     DOY     OVP       YWLRVINSIWESKERT (VARANGCGOLDEDINT     DOY     OVP       YWLRVINSIWESKERT (VARANGCGOLDEDINT     DOY     OVP       YWLRVINSIWESKERT (VARANGCGOLDEDINT     DOY     OVP       YWLRVINSIWESKERT     OVP     OVP       YWLRVINSINGERAND     <   | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>154<br>152<br>152<br>152<br>152<br>146<br>146<br>155<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>152<br>120<br>206<br>201<br>217<br>207<br>207<br>207<br>207   | KAH7407183.1<br>KAO442154.1<br>XP 011872955.1<br>KAB25955.1<br>KAP2649322.1<br>KAP2118428.1<br>XF 033540912.1<br>KAP218428.1<br>XF 033540912.1<br>KAP2634922.1<br>KAP2634922.1<br>KAP2634922.1<br>KAP2634922.1<br>KAP2634922.1<br>KAP2634922.1<br>KAP1663769.1<br>KAP263492.1<br>KAP1663769.1<br>KAP1705356.1<br>OAL44252.1<br>KAP705368.1<br>OAL44251.1<br>KAP26613.1<br>KAP226613.1<br>KAP226570.1<br>KAP226570.1<br>KAP226570.1<br>KAP22550.1<br>KAP2266122.1<br>XP 01187570.1<br>KAP22550.1<br>KAP22550.1<br>KAP22550.1<br>KAP2266122.1<br>XP 01187570.1<br>KAP2266122.1<br>XP 01187270.1<br>XP2266122.1<br>XP 01187270.1<br>XP226612.1<br>XP211428.1<br>XP 0118282.1<br>XP 0118282.1<br>XP 01187270.1<br>XP211428.1<br>XP 0118282.1<br>XP 01182822.1<br>XP 0118282.1<br>XP 0118282.1<br>XP 0118282.1<br>XP 0182   | TS       TRS-TTSVRTTSSA       APGGSNGCKSHENDQCGGNDWKG         PPTTSITS       TKT-SSTVRTTSSA       PAGGSPGCTSHENDQCGGNDWKG         PTTTSITS       PFTTSITSTTRATT       TRDGGGSGCGGCGCCANNKG         PTTTVIRT       TPATTS       STRATTSTSTRATT       TRDGGGSGCGGCCCANNKG         PTTTIR       PTSSTRATT       TRGGGSGCGGCCCANNKG         PTTTIR       PSSTRATTSTSTRATTST       TRGGGSGCGCCCANNKG         PTTTIR       PSSTRATTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTS  | 348<br>355<br>364<br>375<br>370<br>375<br>370<br>377<br>377<br>377<br>377<br>377<br>377<br>377<br>377<br>377  |
| KAH7407183.1<br>KAG442154.1<br>XF_03187295.1<br>KAF2649255.1<br>KAF264922.1<br>KAF2118428.1<br>XP_033540912.1<br>KAF2186921.1<br>PSN69717.1<br>KAF26200.1<br>XF_033688226.1<br>KAF247396.1<br>KAF24795.1<br>KAF24795.1<br>KAF24795.1<br>KAF24795.1<br>KAF24795.1<br>KAF247913.1<br>KAF255.1<br>KAF2555.1<br>KAF266012.1<br>KAF21859557.0<br>KAF26012.1<br>KAF2185955.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF2750897.1<br>KAF2255.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF2   | YHLIYINSIWIKI IMTNI QLAAA/GCGVDPDNT     DDY     QIP       YHLIYINSIWIKI INTO QLAAS/GCGVDPDNT     DDY     QIP       YHLIYINSIWIKI INTO QLAAS/GCGVDPDNT     DDY     QIP       INHLISSIWIKI INTA QUAAS/GCGALDPDNT     DDY     QIP       INHLIYISSIWIKI INTA QUAAS/GCGALDPDNT     DDY     QIP       INHLIYISSIWIKI INTA QUAAS/GCALDPDNT     DDY     QIP       INHLIYISSIWIKI INAAS/GCALDPDNT     DGY     QIP       INHLIYISSIWIKI INAAS/GCALDPDNT     DGY     QIP       INHLIYISSIWIKI INAAS/GCALDPDNT     DGY     QIP       INHIYGGSI INDARK/ILAAD/GCALDPDNT     DGY     QIP       INHIYGGSI INDAKKIILAAD/G  | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>145<br>146<br>154<br>153<br>146<br>154<br>152<br>152<br>146<br>145<br>145<br>152<br>152<br>146<br>145<br>145<br>152<br>152<br>146<br>145<br>145<br>152<br>152<br>146<br>145<br>152<br>152<br>152<br>152<br>152<br>152<br>152<br>152<br>152<br>15  | RAH7407183.1<br>RAH7407183.1<br>RAP2442154.1<br>XP 011872955.1<br>RAP218595570.1<br>RAP2182922.1<br>XAP2118428.1<br>XP 033540512.1<br>RAP228210.1<br>XP 033540512.1<br>RAP228210.1<br>RAP228210.1<br>RAP228210.1<br>RAP228210.1<br>RAP228210.1<br>RAP228210.1<br>RAP22821.1<br>RAP2355.1<br>RAP2355.1<br>RAP2355.1<br>RAP2355.1<br>RAP2357.1<br>RAP255.1<br>RAP255.1<br>RAP2357.1<br>RAP255.1<br>RAP2357.1<br>RAP255.1<br>RAP22857.1<br>RAP22857.1<br>RAP2255.1<br>RAP22857.1<br>RAP228557.1<br>RAP2255.1<br>RAP228557.1<br>RAP228557.1<br>RAP228557.1<br>RAP228557.1<br>RAP228557.1<br>RAP228557.1<br>RAP228557.1<br>RAP228557.1<br>RAP228557.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP22857.1<br>RAP2285  | TS       TRS-TTSVRTTSSA       PAGSINGLESHENDQCGGNDWKG         PPTTSISTS       TRTSPT       FR-TSSTRTRFT       PAGGSSGCISHENDQCGNDWKG         PTTTSISTS       PTTTSSTRTRFT       PAGGSSGCISHENDQCGNDWKG         PTTTIR       PTSSTRTSTT       PAGGSSGCISHENDQCGNDWKG         PTTTIR       PTSSTRTRFT       PAGGGSGCGCINENDQCGNDWKG         PTTTIR       PSSTRASPSSADTS       TRGGCGGGGGCCISHENDQCGNDWKG         PTTTIR       PSSTRASPSSADTS       TRMP   | 348<br>355<br>370<br>344<br>335<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362   |
| KAH7407183.1<br>KAG442154.1<br>XF_031872955.1<br>KAH2595570.1<br>KAF2649221.1<br>KAF264922.1<br>KAF2186921.1<br>PSN69717.1<br>KAF263200.1<br>XF_033688226.1<br>KAF243796.1<br>KAF243796.1<br>KAF243796.1<br>KAF2455.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1847553.37.1<br>KAF1835456.1<br>KAF1847553.1<br>KAF184755.1<br>KAF17076.357.1<br>KAF17076.357.1<br>KAF17076.1<br>KAF12360.1<br>KAF25370.1<br>KAF2557.1<br>KAF226612.1<br>KAF22557.1<br>KAF226570.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF26220.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF24373   | YWLRVINSIWELHTNET (JAAARGCGVDPDNT     DOY     OVP       YWLRVINSIWELHTNET (JAARGCGALDPDNT     DOY     OVP       YWLRVINSIWESKERT (JAARGCGALDPDNT     DOY     OVP       YWLRVINSIWESKERT (VARANGCGALDPDNT     DOY     OVP       YWLRVINSIWESKERT (VARANGCGALDPDNT     DOY     OVP       YWLRVINSIWESKERT (VARANGCGALDPDNT     DOY     OVP       YWLRVINSIWESKERT (VARANGCGALDPDNT     DOY     OVP       YWLRVINSIWESKERT     OVP     OVP       YWLRVINSINGERAND     OVP       YWLRVINSINGERAND     OV  | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>154<br>152<br>152<br>152<br>146<br>146<br>154<br>152<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>120<br>206<br>201<br>210<br>217<br>204<br>203<br>203<br>203<br>203<br>203   | KAH7407183.1<br>KAO442154.1<br>XP 011872955.1<br>KAB25955.1<br>KAP2649322.1<br>KAP2118428.1<br>XF 033540912.1<br>KAP218428.1<br>XF 033540912.1<br>KAP2634922.1<br>KAP2634922.1<br>KAP2634922.1<br>KAP1663785.1<br>KAP2634922.1<br>KAP1663769.1<br>KAP263492.1<br>KAP16356.1<br>0A144252.1<br>KAP705357.1<br>KAP705368.1<br>0A144252.1<br>KAP26612.1<br>KAP2647813.1<br>KAP26570.1<br>KAP226570.1<br>KAP226570.1<br>KAP226612.1<br>KAP226612.1<br>KAP22550.1<br>KAP226612.1<br>KAP226612.1<br>KAP226612.1<br>KAP226612.1<br>KAP226612.1<br>KAP226612.1<br>KAP226612.1<br>KAP226612.1<br>KAP226612.1<br>KAP226612.1<br>KAP226612.1<br>KAP226612.1<br>KAP226612.1<br>KAP221.1<br>ZP21842.1<br>KAP221.1<br>ZP21842.1<br>KAP221.1<br>ZP31577.1<br>KAP221.1<br>ZP31577.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP2   | TS         TS-TTSVRTTSA         PAGSNGCKSHENDQCGGNDWKG           PPTTSITS         TKT-SSTVRTTSIA         PAGGSSGCCSKHENDQCGGNDWKG           PTTTSITS         PFTTSISTSTRRTT         PAGGSSGCCSKHENDQCGGNDWKG           PTTTVIRT         TPTTSI-TSARTSTSSTVTTTSIA         PAGGSSGCCSKHENDQCGGNDWKG           PTTTIA         PSTRIATT-TASKRTSTSSLPTTSI         PGGGGGGGGGCCCVSHENDQCGGNDWKG           PTTTIA         PSSTRAPSSADUTS         TFGGGGGGGGCCCVSHENDQCGGNDWKG           PTTTIA         PSSTRAPSSADUTS         TFGGGGGGGGCCCVSHENDQCGGNDWKG           PTTLAR         PSSTRAPSSADUTS         TFGGGGGGGGCCCVSHENDQCGGNDWKG           PTTLARS         TSSTRAPTS-TRANCARGGCCVSHENDQCGGNDWKG           PTTLARS         SSTRAPSSADUTS         TFGHCARGCCVSHENDQCGGNDWKG           PTTLARS         SSTRAPSSADUTSTSTRAPS-TFGHCARGCVSHENDQCGGNDWKG         -TTSSTRAPSTSTRAPSTSTRAPSTSTRAPS-TFGHCARGCVSHENDQCGGNDWKG           PTTLARS         STRAPSSADUTSTSTRAPTSTSTRAPS-TFGHCARGCVSHENDQCGGNDWKG         -TTSSTRAPSTSTRAPSTSTRAPSTSTRAPSTSTRAPSTSTRAPSTSTRAPSDCCOMWKG           PSSTRTST         MLP-SSTSSAD-QRTFS-T-S-SGGGGCCCSHENDQCGGNDWKG         PSSTRTSTSTWEDPS-STRAPSTSTRAPSTSTRAPDCCGNDWKG           PSSTRTSTSTRAPPTSTSTRAPSTTSTRAPSTS-TFG-GGGGCCCARHAPQCGNDWKG         PSSTRTAPST         -TFG-GGGGCCCARHAPQCGNDWKG           PSSTRTSTSTRAPTSTSTSTRAPSTSTSTRAPSTS-TFG-GGGGCCCARHAPQCGNDWKG         PSTRTAPSTAPPTSTSTSTSTRAPSTS-TFG-GGGGCCARHAPQCGNDWK   | 348<br>355<br>364<br>375<br>370<br>314<br>315<br>352<br>362<br>362<br>353<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>356<br>355<br>356<br>356<br>356<br>356<br>356<br>356<br>356  |
| KAH7407183.1<br>KAG442154.1<br>XF_03187295.1<br>KAF2619255.1<br>KAF261922.1<br>KAF2118428.1<br>XF_03187921.1<br>KAF2186921.1<br>PSN59717.1<br>KAF26200.1<br>XF_033688226.1<br>KAF243796.1<br>KAF243796.1<br>KAF243796.1<br>KAF243796.1<br>KAF243796.1<br>KAF1835456.1<br>KAH6849362.1<br>KAH6849362.1<br>KAF1835557.1<br>KAF2750897.1<br>KAF2266012.1<br>KAF2266012.1<br>KAF2184221.1<br>KAF2184221.1<br>KAF2184221.1<br>KAF2184221.1<br>KAF2184221.1<br>KAF2184221.1<br>KAF2184221.1<br>KAF2184221.1<br>KAF2184221.1<br>KAF2184221.1<br>KAF2184221.1<br>KAF2184221.1<br>KAF2184221.1<br>KAF2184221.1<br>KAF2184221.1<br>KAF2184221.1<br>KAF2184221.1<br>KAF2184221.1<br>KAF2184221.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF243795.1<br>KAF263422.1<br>KAF243795.1<br>KAF263422.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF2437775.1<br>KAF2437775.1<br>KAF2437775.1<br>KAF2437775.1<br>KAF24   | YHLRYNNSWYR I MYNR I QLAAAR GCDGVDPDYT     DDY     QMP       YHLRYNNSWYR I MYNR I QLAAR GCDGVDPDYT     DDY     QMP       YMLRYNNSWYR I MYNR I QLAAR GCDALDPDNT     DDY     QMP       I KALLSEN KHERFE (QAAR KECOLDPDNTWENLTLINHELDCY     QMP       I KALLSEN KHERFE (QAAR KECOLDPDNT     DDY     QMP       I KALLSEN KHERFE (QAAR KECOLDPDNT     DDY     QMP       I KALLSEN KHERFE (QAAR KECOLDPDNT     DDY     QMP       I KALLSEN KERFE (QAAR KECOLDPDNT     DDY     QMP       I KALLSEN KERFE (LAAB KECOLDPDNT     DDY     QMP       I KHLRYSSEN KEN KERFE (LAAB KECOLDPDNT     DDY     QMP       I KHLRYSSEN KERFE (LAAB KECOLDPDNT     DDY     QMP       I KHLRYSSEN KERFE (LAAB KECOLNPDNT     DDY     QMP       I KHLRYSSEN KERFE (LAAB KECOLDPDNT     DDY     QMP       I KHLRYSSEN KERFE (LAAB KECOLDPDNT     DDY     QMP       I KHLRYSSEN KERFE (LAAB KECOLDPDNT     DDY     QMP <t< td=""><td>148<br/>148<br/>155<br/>143<br/>157<br/>146<br/>145<br/>145<br/>145<br/>145<br/>145<br/>146<br/>146<br/>154<br/>153<br/>146<br/>154<br/>152<br/>152<br/>146<br/>146<br/>145<br/>152<br/>152<br/>146<br/>145<br/>145<br/>152<br/>152<br/>146<br/>206<br/>206<br/>201<br/>201<br/>201<br/>201<br/>201<br/>201<br/>201<br/>207<br/>203<br/>203<br/>203<br/>204</td><td>RAH7407183.1<br/>RAH7407183.1<br/>RAP24442154.1<br/>XP 011872955.1<br/>RAP2184522.1<br/>RAP2118428.1<br/>XP 033540512.1<br/>RAP218428.1<br/>RAP2184281.1<br/>PSM65717.1<br/>RAP2428210.1<br/>RAP2434922.1<br/>RAP2434922.1<br/>RAP145456.1<br/>RAP145456.1<br/>RAP145456.1<br/>RAP145456.1<br/>RAP145456.1<br/>RAP145456.1<br/>RAP145456.1<br/>RAP145456.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP14557.1<br/>RAP145</td><td>TSTRS-TTSVRTTSAPAGESNCKSHENDQCGNDWKG PPTTSRT2</td><td>348<br/>355<br/>370<br/>344<br/>335<br/>362<br/>362<br/>362<br/>362<br/>362<br/>362<br/>362<br/>362<br/>362<br/>362</td></t<>   | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>154<br>153<br>146<br>154<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>146<br>145<br>145<br>152<br>152<br>146<br>206<br>206<br>201<br>201<br>201<br>201<br>201<br>201<br>201<br>207<br>203<br>203<br>203<br>204   | RAH7407183.1<br>RAH7407183.1<br>RAP24442154.1<br>XP 011872955.1<br>RAP2184522.1<br>RAP2118428.1<br>XP 033540512.1<br>RAP218428.1<br>RAP2184281.1<br>PSM65717.1<br>RAP2428210.1<br>RAP2434922.1<br>RAP2434922.1<br>RAP145456.1<br>RAP145456.1<br>RAP145456.1<br>RAP145456.1<br>RAP145456.1<br>RAP145456.1<br>RAP145456.1<br>RAP145456.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP14557.1<br>RAP145   | TSTRS-TTSVRTTSAPAGESNCKSHENDQCGNDWKG PPTTSRT2   | 348<br>355<br>370<br>344<br>335<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362   |
| KAH7407183.1<br>KAG442154.1<br>XF_031872955.1<br>KAH2595570.1<br>KAF264922.1<br>KAF264922.1<br>KAF2186921.1<br>PSN69717.1<br>KAF263200.1<br>XF_033688226.1<br>KAF243796.1<br>KAF243796.1<br>KAF243796.1<br>KAF243796.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1847553.37.1<br>KAF1835456.1<br>KAF1847553.37.1<br>KAF184755.31<br>KAF17076355.1<br>KAF725397.1<br>KAF725371.1<br>KAF226012.1<br>KAF22555.1<br>KAF226012.1<br>KAF218428.1<br>XF225550.1<br>KAF218428.1<br>XF218428.1<br>KAF218428.1<br>KAF218428.1<br>KAF218428.1<br>KAF253350.1<br>KAF26280.1<br>KAF262820.1<br>KAF262820.1<br>KAF262820.1<br>KAF262820.1<br>KAF262820.1<br>KAF26220.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF26422.1<br>EF094882.1   | YWLRVINSIWELHTNET (JAAARGCGVDPDNT     DOY     OVP       YWLRVINSIWELHTNET (JAARGCGALDPDNT     DOY     OVP       YWLRVINSIWESTERTER (JAARGCGALDPDNT)     DOY     OVP       YWLRVINSIWESTERTER (JAARGCGALDPDNT)     DOY     OVP       YWLRVINSIWESTERTAR (JAARGCGALDPDNT)     DOY     OVP       YWLRVINSIGUESTERTAR (JAARGCGALDPDNT)     DOY     OVP       YWWLRGGGETERTAR (JAARGCGALDPDNT)     DOY     OVP  | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>154<br>152<br>152<br>152<br>146<br>146<br>154<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>152<br>152<br>146<br>146<br>152<br>152<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>145  | KAH7407183.1<br>KAO442154.1<br>XP 011872955.1<br>KAB25955.1<br>KAP2649322.1<br>KAP2649322.1<br>KAP2118428.1<br>XF 033540912.1<br>KAP2649322.1<br>KAP2649322.1<br>KAP2649322.1<br>KAP2649322.1<br>KAP2649322.1<br>KAP2649322.1<br>KAP1663769.1<br>KAP2649321.1<br>KAP2649321.1<br>KAP2649321.1<br>KAP2649321.1<br>KAP2649321.1<br>KAP266971.1<br>KAP2266971.1<br>KAP2266971.1<br>KAP2266971.1<br>KAP2266971.1<br>KAP2266971.1<br>KAP2266971.1<br>KAP2266971.1<br>KAP2266971.1<br>KAP2266971.1<br>KAP2266971.1<br>KAP2266971.1<br>KAP2266971.1<br>KAP2266971.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP22266012.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP221.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP222.1<br>KAP22.1<br>KAP22.1<br>KAP222.1<br>KAP22.1   | TS         TRS-TTSVRTTSA         PAGSINGLESHENDQCGGNDWIG           PPTTSITS         TRT.SPT         PAGSPGCLSHENDQCGGNDWIG           PTTTSITS         PPTTSITSTRIPT         PAGGSSGCGGGGGCGCANNENDQCGGNDWIG           PTTTIN         PTTTINT         PAGSTRADCGGGGGGGCGCANNENDQCGGNDWIG           PTTTIN         PSTRIPTS         TASTSRTPTTSI           PTTTIN         PSTRIPTS         TASTSRTPTTSI           PTTTIN         PSTRIPTS         TASGGGGGGGGGCCANNENDQCGGNDWIG           PTTTIN         PSTRIPTS         TASGGGGGGGGGCCANNENDQCGGNDWIG           PTTLA         PSSTRIPTS         TROMANDCGGGGGGGGCCANNENDQCGGNDWIG           PTTLA         PSSTRIPTS         TROMANDCGGNDWIG           PTTLA         TSSTRIPTSTSTSTSTSTSTRIPTS         TROMANDCGGNDWIG           PTTLAPS         STATATSSTRAD         TROMANDCGGNDWIG           PTTLAPS         STATATSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTS  | 348<br>355<br>364<br>375<br>370<br>314<br>315<br>352<br>362<br>362<br>353<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>354<br>355<br>356<br>356<br>356<br>356<br>356<br>356<br>356<br>356<br>356  |
| KAH7407183.1<br>KAG442154.1<br>XF_03187295.1<br>KAF2649225.1<br>KAF218428.1<br>XF_03187295.1<br>KAF218428.1<br>XF_031540912.1<br>KAF2186220.1<br>XF_033688226.1<br>KAF2634922.1<br>EF004882.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF63782.1<br>KAF1835456.1<br>KAF1835557.1<br>KAF7059368.1<br>OAL44225.1<br>KAF725097.1<br>KAF226012.1<br>KAF72307.1<br>KAF226012.1<br>KAF72355.1<br>KAF72355.1<br>KAF7235012.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF2255.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF2255.1<br>KAF218422.1<br>KAF218422.1<br>KAF218422.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF2437474.1<br>KAF2437474.1<br>KAF2437474.1<br>KAF2437474.1<br>KAF24374.1<br>KAF24   | YMLRVINSINGLINTINI QLAAR/GCGVDPDNT     DDY     QIP       YMLRVINSINGLINTINI QLAAR/GCGVDPDNT     DDY     QIP       YMLRVINSINGLINTINI QLAAR/GCGADDPNT     DDY     QIP       INKLISSINGLINTIPRIQAR/GCGADDPNT     DDY     QIP       INKLISSINGLINTIPRIQAR/GCGADDPNT     DDY     QIP       INKLINGSINGLINTIPRIQAR/GCADDPNT     DDY     QIP       INKLINGSINGLINTIRAGN/GCADDPNT     DGY     QIP       INKLINGSINGLINTAR/GLAUGCADDPNT     DGY     QIP       INKLINGSINGLINAR/GLAUGCADDPNT     DGY     QIP       INKLINGSQITALAAR/GLAUAR/GCADDPNT     DGY     <  | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>146<br>154<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>146<br>206<br>201<br>201<br>201<br>201<br>201<br>201<br>201<br>201<br>201<br>201  | <ul> <li>RAH7407183.1</li> <li>RAH7407183.1</li> <li>RAA442154.1</li> <li>XP 01187295.1</li> <li>RAB72184292.1</li> <li>RAP2118428.1</li> <li>XP 033540912.1</li> <li>RAP218428.1</li> <li>RAP218428.1</li> <li>RAP218428.1</li> <li>RAP218428.1</li> <li>RAP218428.1</li> <li>RAP218428.1</li> <li>RAP218456.1</li> <li>RAP2437376.1</li> <li>RAP243737.1</li> <li>RAP2434922.1</li> <li>RAP218456.1</li> <li>RAP243737.1</li> <li>RAP2543922.1</li> <li>RAP26377.1</li> <li>RAP26377.1</li> <li>RAP26377.1</li> <li>RAP2637.1</li> <li>RAP2637.1</li> <li>RAP2637.1</li> <li>RAP2637.1</li> <li>RAP2637.1</li> <li>RAP2726097.1</li> <li>RAP226012.1</li> <li>RAP2755.1</li> <li>RAP2186957.0</li> <li>RAP2186921.1</li> <li>RP0348012.1</li> <li>RAP2186921.1</li> <li>RAP2186922.1</li> <li>RAP2186922.1</li> <li>RAP2186922.1</li> <li>RAP2643022.1</li> <li>RAP264322.1</li> <li>RAP2437396.1</li> <li>RAP264322.1</li> <li>RAP264352.1</li> <li>RAP264352.1</li> <li>RAP264356.1</li> <li>R</li></ul>   | TS       TRS-TTSVRTTSA       PAGSINGLESHENDQCGGNDWKG         PPTTSISTG       TRTSEPT       PFTTSSTRTRFTT       PAGGSSGCISHENDQCGNDWKG         PTTTSISTG       PFTTSSTRTRFTT       PAGGSSGCISHENDQCGNDWKG         PTTTIR       PTSSTRTSTTSTSTRFTTSISA       PAGGSSGCISHENDQCGNDWKG         PTTTIR       PSSTRASSSANDTS       TRMP       PAGGSGCGGCGCCUSHENDQCGNDWKG         PTTTIR       PSSTRASSSANDTS       TRMP       PGGGGGGGGCGCUSHENDQCGQDWKG         PTTTLR       PSSTRASSSANDTS       TRMP       PGGGGGGGGCGCUSHENDQCGQDWKG         PTTLR       TASTTIOPTS       TRMP       PGGGGGGGCGCUSHENDQCGQDWKG         PTTLR       STRTSTSTRPTSSTTOPTS       TRMP       GGGGGCGCNENDQCGQDWKG         PTTLR       STRTSTSTRPTSSTTOPTS       TRMP       GGGGCGCNENDQCGQDWKG         PTTTLP       STRTSTSTRPTSSTTOPTS       GGGGGCCNENDQCGQDWKG       TTTSSTTTPTS         VTTNSVTRSOTSTPRPTSSTTRFTSTTTFTS       GGGGGCCNENDQCGQDWKG       SVTTRSTSTRNDPTSSTRPTS       GGGGCCNENDQCGQDWKG         SVTTNSTSTVRSTSTRPTSSTRPTSTSTRPTS       TTC       GGGGGCCNENDQCGQDWKG       SVTTRSTTMDQCGQDWKG         SVTTNSTSTRSTRPTSSTRPTSTSTRPTS       TTC       GGGGCCNENDQCGQDWKG       SVTTRSTSTRPTSTSTRPTSTSTRPTS       GGGGCCNENDQCGQDWKG         PSTTLRST       MLP<-SRTSSTORPTS   | 348<br>355<br>370<br>344<br>335<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362   |
| KAH7407183.1<br>KAG442154.1<br>XF_031872955.1<br>KAH5595570.1<br>KAF264922.1<br>KAF264922.1<br>KAF264922.1<br>KAF264922.1<br>KAF263200.1<br>XF_033608226.1<br>XF_033608226.1<br>KAF263795.1<br>KAF263795.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF183755.1<br>KAF183756.1<br>KAF183759.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF273087.1<br>KAF25087.1<br>KAF25087.1<br>KAF25087.1<br>KAF2649322.1<br>KAF21182855.1<br>KAF2649322.1<br>KAF21182822.1<br>KAF21182822.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF2649322.1<br>KAF264932.1<br>KAF264942.1<br>KAF264942.1<br>KAF264942.1<br>KAF264942.1<br>KAF264944.1<br>KAF2644   | YWLRVINSIWELITNIR I QLAAR GCOCUPDINT     DOY     OVP       YWLRVINSIWELITNIR I QLAAR GCOCUPDINT     DOY     OVP       YWLRVINSIWESKI TO CAAR GCOLUPDINT     DOY     OVP       YWLRVINSIWESKI THIR ROAR GCOLUPDINT     DOY     OVP       YWLRVINSIWESKI THIR ROAR GCOLUPDINT     DOY     OVP       YWLRVINSIWESKI THARD ROAR GCOLUPDINT     DOY     OVP       YWLRVINSIWESKI THARD ROAR GCOLUPDINT     DOY     OVP       YWLRVINSIWESKI THARD ROAD GCOLUPDINT     DOY     OVP       YWLRVINGSOLID TAARRETLAAD ROCOLUPDINT     DOY     OVP       YWLRVINGSOLID TAARRETLAAD ROCOLUPDINT     DOY     OVP       YWLRVINGSOLITAARRETLAAD ROCOLUPDINT     DOY     OVP       YWLRVINGSOLITAARRETLAAD ROCOLUPDINT     DOY     OVP       YWRRVINGSOLITAARRETLAAD ROCOLUPDINT     DOY  | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>154<br>153<br>146<br>154<br>152<br>152<br>152<br>152<br>146<br>146<br>146<br>146<br>154<br>153<br>146<br>152<br>152<br>152<br>146<br>145<br>145<br>152<br>152<br>146<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>154<br>152<br>157<br>146<br>146<br>154<br>155<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>145  | RAH7407183.1<br>RAH7407183.1<br>RAT2144215.1<br>RAT214428.1<br>RAT214428.1<br>RAT214428.1<br>RAT214428.1<br>RAT214428.1<br>RAT214428.1<br>RAT2645122.1<br>RAT2645122.1<br>RAT2645122.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1<br>RAT264512.1   | TSTRS-TTSVRTTSAPAGSNGCKSHENDQCGGNDWG PPTTSITSTR-SSTVRTTSAPAGGSSCGCCORDWG PTTYIR   | 348<br>355<br>364<br>375<br>370<br>314<br>315<br>352<br>362<br>362<br>359<br>337<br>357<br>354<br>357<br>354<br>356<br>353<br>354<br>354<br>354<br>354  |
| KAH7407183.1<br>KAG442154.1<br>XF_031872955.1<br>KAF26492255.1<br>KAF2649221.1<br>KAF218428.1<br>XF_031540912.1<br>KAF2186221.1<br>PSN59717.1<br>XF226200.1<br>XF_033688226.1<br>KAF2437956.1<br>KAF2437956.1<br>KAF1835456.1<br>KAF1835456.1<br>KAH74051831.1<br>KAF17339679.1<br>KAF25317.1<br>KAF25317.1<br>KAF25317.1<br>KAF2526012.1<br>KAF226012.1<br>KAF226012.1<br>KAF22555.1<br>KAF226012.1<br>KAF226012.1<br>KAF226012.1<br>KAF22555.1<br>KAF226012.1<br>KAF226012.1<br>KAF22551.1<br>KAF262801.1<br>KAF262801.1<br>KAF262801.1<br>KAF262801.1<br>KAF262801.1<br>KAF2634822.1<br>KAF262801.1<br>KAF2634822.1<br>KAF262801.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF2634822.1<br>KAF263482.1<br>KAF263482.1<br>KAF263482.1<br>KAF263482.1<br>KAF263482.1<br>KAF263482.1<br>KAF263482.1<br>KAF263482.1<br>KAF263482.1<br>KAF263482.1<br>KAF263482.1<br>KAF263482.1<br>KAF263482.1<br>KAF263482.1<br>KAF263482.1<br>KAF263482.1<br>KAF263482.1<br>KAF263482.1<br>KAF263482.1<br>KAF263482.1<br>KAF263482.1<br>KAF2   | YWLRVINSIWELITNIR I QLAAR/GCG/UPDNT     DOY     OVP       YWLRVINSIWERIN (QLAAR/GCG/UPDNT)     DOY     OVP       I WLRJSDWINSIWERIN (QLAAR/GCG/UPDNT)     DOY     OVP       I WLRYSDWINSIWERIN (LAAR/GCG/UPDNT)     DOY     OVP       I WLRYSDWINSIWERIN (LAAR/GCG/UPDNT)     DOY     OVP       I WLRYGSSIWERIN MARKITLAAD/GCG/UPDNT     DOY     OVP       I WLRYGSSIWERINAR/SCG/UPDNT     DOY     OVP       I WLRYGSSIERINAR/SCG/UPDNT     DOY     OVP </td <td>148<br/>148<br/>155<br/>143<br/>157<br/>146<br/>145<br/>145<br/>145<br/>145<br/>145<br/>146<br/>146<br/>146<br/>153<br/>146<br/>146<br/>153<br/>152<br/>152<br/>152<br/>146<br/>146<br/>145<br/>152<br/>152<br/>152<br/>146<br/>206<br/>201<br/>201<br/>217<br/>201<br/>217<br/>201<br/>201<br/>217<br/>203<br/>3<br/>195<br/>207<br/>203<br/>203<br/>203<br/>203<br/>203<br/>203<br/>203<br/>204<br/>207<br/>204<br/>204<br/>204<br/>204<br/>204<br/>204<br/>204<br/>204<br/>204<br/>204</td> <td><ul> <li>RAH7407183.1</li> <li>RAH7407183.1</li> <li>RAA442154.1</li> <li>XP 01187295.1</li> <li>RAB7188595570.1</li> <li>RAP2118428.1</li> <li>XP 0137395.1</li> <li>RAP218428.1</li> <li>XP 0137396.1</li> <li>RAP2248210.1</li> <li>RAP218428.1</li> <li>RAP218428.1</li> <li>RAP218428.1</li> <li>RAP243796.1</li> <li>RAP243795.1</li> <li>RAP2447813.1</li> <li>RAP245957.1</li> <li>RAP2266012.1</li> <li>RAP2266012.1</li> <li>RAP21869957.01</li> <li>RAP22859.11</li> <li>RAP21869957.01</li> <li>RAP22640912.1</li> <li>RAP21869957.01</li> <li>RAP22640912.1</li> <li>RAP2186921.1</li> <li>RAP233492.1</li> <li>RAP23492.2</li> <li>RAP234362.1</li> <li>RAP343456.1</li> <li>RAP343456.1</li> <li>RAP343456.1</li> <li>RAP34356.1</li> <li>RAP34356.1</li> <li>RAP34356.1</li> <li>RAP34356.1</li> <li>RAP23456.</li></ul></td> <td>TS       TRS-TTSVRTTSA       PAGSINGLESHENDQCGGNDWKG         PPTTSISTG       TRTSEP       PFTTSSTRTRFTT       PAGGSSGCISHENDQCGGNDWKG         PTTTSISTG       PFTTSSTRTRFTT       PAGGSSGCISHENDQCGGNDWKG         PTTTIR       PTSSTRTSTTSTSTRFTT       PAGGSGCGGGGGCGCANDWKG         PTTTIR       PSSTRTSSTSTRFTT       PAGGGSGCGGGGGCGCANDWKG         PTTTIR       PSSTRTSSTSTRFTT       PAGGGGGGGGCGCANDWKG         PTTTIR       PSSTRTSSTSRPTS       PTGGGGGGGGCGCANDWGG         PTTTIR       PSSTRTSTSTSTSTSTTSTSTRFTT       PGGGGGGGGCGCANDWGG         PTTTLP       TSSTTTSTSTUPPTS       PGGGGGGCGCANDWGGCGGGGGGGCGCANDWGG         PTTTLP       TSSTTTSTSTTSTSTTSTSTSTSTSTSTSTSTSTSTST</td> <td>348<br/>355<br/>370<br/>344<br/>334<br/>334<br/>337<br/>335<br/>362<br/>362<br/>362<br/>362<br/>362<br/>362<br/>363<br/>364<br/>355<br/>355<br/>355<br/>355<br/>355<br/>355<br/>355<br/>355<br/>355<br/>35</td>   | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>146<br>153<br>146<br>146<br>153<br>152<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>152<br>146<br>206<br>201<br>201<br>217<br>201<br>217<br>201<br>201<br>217<br>203<br>3<br>195<br>207<br>203<br>203<br>203<br>203<br>203<br>203<br>203<br>204<br>207<br>204<br>204<br>204<br>204<br>204<br>204<br>204<br>204<br>204<br>204   | <ul> <li>RAH7407183.1</li> <li>RAH7407183.1</li> <li>RAA442154.1</li> <li>XP 01187295.1</li> <li>RAB7188595570.1</li> <li>RAP2118428.1</li> <li>XP 0137395.1</li> <li>RAP218428.1</li> <li>XP 0137396.1</li> <li>RAP2248210.1</li> <li>RAP218428.1</li> <li>RAP218428.1</li> <li>RAP218428.1</li> <li>RAP243796.1</li> <li>RAP243795.1</li> <li>RAP2447813.1</li> <li>RAP245957.1</li> <li>RAP2266012.1</li> <li>RAP2266012.1</li> <li>RAP21869957.01</li> <li>RAP22859.11</li> <li>RAP21869957.01</li> <li>RAP22640912.1</li> <li>RAP21869957.01</li> <li>RAP22640912.1</li> <li>RAP2186921.1</li> <li>RAP233492.1</li> <li>RAP23492.2</li> <li>RAP234362.1</li> <li>RAP343456.1</li> <li>RAP343456.1</li> <li>RAP343456.1</li> <li>RAP34356.1</li> <li>RAP34356.1</li> <li>RAP34356.1</li> <li>RAP34356.1</li> <li>RAP23456.</li></ul>   | TS       TRS-TTSVRTTSA       PAGSINGLESHENDQCGGNDWKG         PPTTSISTG       TRTSEP       PFTTSSTRTRFTT       PAGGSSGCISHENDQCGGNDWKG         PTTTSISTG       PFTTSSTRTRFTT       PAGGSSGCISHENDQCGGNDWKG         PTTTIR       PTSSTRTSTTSTSTRFTT       PAGGSGCGGGGGCGCANDWKG         PTTTIR       PSSTRTSSTSTRFTT       PAGGGSGCGGGGGCGCANDWKG         PTTTIR       PSSTRTSSTSTRFTT       PAGGGGGGGGCGCANDWKG         PTTTIR       PSSTRTSSTSRPTS       PTGGGGGGGGCGCANDWGG         PTTTIR       PSSTRTSTSTSTSTSTTSTSTRFTT       PGGGGGGGGCGCANDWGG         PTTTLP       TSSTTTSTSTUPPTS       PGGGGGGCGCANDWGGCGGGGGGGCGCANDWGG         PTTTLP       TSSTTTSTSTTSTSTTSTSTSTSTSTSTSTSTSTSTST   | 348<br>355<br>370<br>344<br>334<br>334<br>337<br>335<br>362<br>362<br>362<br>362<br>362<br>362<br>363<br>364<br>355<br>355<br>355<br>355<br>355<br>355<br>355<br>355<br>355<br>35   |
| KAH7407183.1<br>KAG442154.1<br>XF_031872955.1<br>KAH2595570.1<br>KAF264922.1<br>KAF264922.1<br>KAF264922.1<br>KAF264922.1<br>KAF263200.1<br>XF_033608226.1<br>XF_033608226.1<br>KAF263795.1<br>KAF263795.1<br>KAF183555.1<br>KAF183556.1<br>KAF183755.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF27112807.1<br>KAF27112807.1<br>KAF27112807.1<br>KAF27112807.1<br>KAF27112807.1<br>KAF27112807.1<br>KAF27112807.1<br>KAF27112807.1<br>KAF2712852.1<br>KAF27112807.1<br>KAF2712852.1<br>KAF2612822.1<br>EF094882.1<br>KAF2612822.1<br>EF094882.1<br>KAF2612822.1<br>EF094882.1<br>KAF2613782.1<br>KAF2613782.1<br>KAF2613782.1<br>KAF2613782.1<br>KAF2613782.1<br>KAF26320.1<br>Y_013387052.1<br>Y_013387052.1<br>Y_013387052.1<br>Y_013387052.1<br>Y_013387052.1  | YWLRVINSIWELITNIR I QLAAR GCOCUPDIT     DOY     OVP       YWLRVINSIWELITNIR I QLAAR GCOCUPDIT     DOY     OVP       YWLRVINSIWESINE TREAT GOAL TO COLLED DIT     DOY     OVP       YWLRVINSIWESINE TRAESE GOAL TO DIT     DOY     OVP       YWLRVINSIWESINE TA DIT GOAL TO DIT     DOY     OVP       YWLRVINSINE TA DIT GARRELI LA DIT GOAL TO DIT     DOY     OVP       YWLRVINSINE TA DIT GARRELI LA DIT GOAL TO DIT     DOY     OVP       YWLRVINSINE TA DIT GARRELI LA DIT GOAL TO DIT     DOY     OVP       YWLRVINSINE TA DIT GARRELI LA DIT GOAL TO DIT     DOY     OVP       YWLRVINSINE TA DIT GARRELI LA DIT GOAL TO DIT     DOY     OVP       YWWLRVINSINE TA DIT GARRELI LA DIT GOAL TO DIT     DOY     OVP       YWWLRVINSINE TA DIT GARRELI LA DIT GOAL TO DIT     DOY     OVP       YWWLRVINSINE TA DIT GARRELI LA DIT GOAL TO DIT     DOY     OVP       YWWLRVINSINE TA DIT GARRELI LA DIT GOAL TO DIT     DOY     OVP       YWWLRVINSINE TA DIT GOAL TO DIT  | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>154<br>153<br>146<br>154<br>152<br>152<br>152<br>152<br>146<br>146<br>146<br>146<br>154<br>153<br>146<br>145<br>152<br>152<br>146<br>145<br>145<br>152<br>146<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>154<br>152<br>152<br>146<br>146<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>145   | RAH7407183.1<br>RAH7407183.1<br>RAT2144215.1<br>RAT214428.1<br>RAT214428.1<br>RAT214428.1<br>RAT214428.1<br>RAT214428.1<br>RAT214428.1<br>RAT245200.1<br>RAT245200.1<br>RAT245200.1<br>RAT24520.1<br>RAT24520.1<br>RAT24520.1<br>RAT24520.1<br>RAT24520.1<br>RAT24520.1<br>RAT24520.1<br>RAT24520.1<br>RAT24520.1<br>RAT24520.1<br>RAT24520.1<br>RAT250897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT255897.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT255.1<br>RAT255.1<br>RAT2557.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT555.1<br>RAT2555.1<br>RAT2555.1<br>RAT2555.1<br>RAT2555.1<br>RAT2555.1<br>RAT25555.1<br>RAT25555.1<br>RAT25555.1<br>RAT25555.1<br>RAT25555.1<br>RAT255555.1<br>RAT255555.1<br>RAT25555.1<br>RAT255555.1<br>RAT255555.1<br>RAT25555.1<br>RAT255555.1<br>RAT255555.1<br>RAT255555.1<br>RAT255555.1<br>RAT255555.1<br>RAT255555.1<br>RAT255555.1<br>RAT255555.1<br>RAT255555.1<br>RAT255555.1<br>RAT255555.1<br>RAT255555.1<br>RAT2555555.1<br>RAT2555555.1<br>RAT25555555.1<br>RAT25555555.1<br>RAT2555555555555555555555555555555555555  | TS       TRS-TTSVRTTSA       PAGSNGCKSHENDQCGGNDWKG         PPTTSITS       TKT-SSTVRTTSIA       PAGGSSGCCSUBNCCONDWKG         PTTTSITS       PFTTSSTRTRTT       PAGGSSGCCSUBNCCONDWKG         PTTTVIRT       TPPTTS       TSSTVRTTSISTSTRTTT       PAGGSSGCCSUBNCCONDWKG         PTTTVIRT       TPPTS       TSSTVRTTSISTSTRTTT       PAGGGSGCGCGCCCVSUBNCCONDWKG         PTTTIA       PSSTVAPS       TSSSTVTSSSCGCCCCCCONDWKG         PTTTIA       DSSTVAPS       TRGGGSGCGCCCCVSUBNCCCONDWKG         PTTLAP       TSSTVAPS       TRGGGSGCGCCCCVSUBNCCCONDWKG         PTTLAP       TSSTVAPS       TRGGGSGCGCCCCVSUBNCCCONDWKG         PTTLAP       TSSTVAPS       TRGGGSGCGCCCVSUBNCCCONDWKG         PTTLAP       TSSTVAPS       TRGGGSCGCCCCVSUBNCCCONDWKG         PTTLAP       STANTSTSTSTVAPS       TRGGGSCGCCCCCVSUBNCCCONDWKG         TTVVSTVTNSTVTNSTSTVAPS       TTGCCCQUBNCCCONDWKG       TTTVNSTVTNSTSTVAPSTSTVAPS         SVTTVSSTVTNSTSTVAPSTSTVAPSTSTSTVAPS       TFGCCCQUBNCCCONDWKG       TTTSTVTPS         PSSTVTSST       MLP = STSSSTQPPST = TS = GGGCCCCCCCONDWKG       STTTVSSTVPPS         PSSTVTSTSTVAPS       TTSSTSTVAPST = TTC = GGGCCCCCNNWCG       TTSVPPS         PSSTVTSTSTVAPS       TSTSSTQPPST = TTC = GGGCCCCNNWCG       TSTVTSSTSTVAPSTSTSTRAPST = TTC = GGGCCCCNNWCG       TSTVT  | 348<br>355<br>364<br>375<br>370<br>314<br>315<br>362<br>362<br>352<br>352<br>354<br>357<br>355<br>354<br>356<br>353<br>356<br>353<br>356<br>353<br>354<br>356<br>354  |
| KAH7407183.1<br>KAG442154.1<br>XF_031872955.1<br>KAF26492255.1<br>KAF264922.1<br>KAF218428.1<br>XF_03187295.1<br>KAF218428.1<br>XF_033540912.1<br>XF_033688226.1<br>XF_033688226.1<br>KAF243796.1<br>KAF24551.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF17399679.1<br>KAF25337.1<br>KAF17399679.1<br>KAF25317.1<br>KAF25557.1<br>KAF2266012.1<br>KAF725551.1<br>KAF2266012.1<br>KAF22555.1<br>KAF218422.1<br>KAF218422.1<br>KAF2256012.1<br>KAF226012.1<br>KAF22555.1<br>KAF2262801.1<br>XF_033888226.1<br>XF_033868226.1<br>KAF2455557.1<br>KAF2628012.1<br>KAF264222.1<br>KAF25557.1<br>KAF2628012.1<br>KAF264222.1<br>KAF2628012.1<br>KAF263822.1<br>KAF25557.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF263822.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1<br>KAF26382.1   | YMLRVINSINGLINTNI I QLAAR/GCGVDPDNT     DDY     QIP       YMLRVINSINGLINTNI QLAAR/GCGVDPDNT     DDY     QIP       YMLRVINSINGLINTRY QLAAR/GCGADDPNT     DDY     QIP       INKLISSON/SINTRY RUSSINGCADDPNT     DDY     QIP       INKLISSON/SINTRY RUSSINGCADDPNT     DDY     QIP       INKLISSON/SINTRY RUSSINGCADDPNT     DDY     QIP       INKLINGSTAVADIARS/LIAAD/GCADDPNT     DGY     QIP       INKLINGSGATANARS/LIAAD/GCADDPNT   | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>146<br>153<br>146<br>146<br>153<br>146<br>146<br>153<br>152<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>152<br>146<br>206<br>201<br>201<br>217<br>201<br>201<br>217<br>203<br>207<br>203<br>203<br>203<br>204<br>207<br>203<br>203<br>204<br>207<br>204<br>204<br>204<br>204<br>204<br>204<br>204<br>204<br>204<br>204  | RAH7407183.1<br>RAH7407183.1<br>RAP24442154.1<br>XP 011872955.1<br>RAP2188295570.1<br>RAP2184282.1<br>XP 0137955.1<br>RAP2242821.1<br>PSN69717.1<br>RAP2262810.1<br>XP 03368226.1<br>RAP2243796.1<br>RAP2243796.1<br>RAP2434922.1<br>RAP1243546.1<br>RAH16437454.1<br>RAH16437457.1<br>RAH2763587.1<br>RAH7765358.1<br>0AL44225.1<br>RAP2247813.1<br>RAP2247813.1<br>RAP226112.1<br>RAP226012.1<br>RAP2247813.1<br>RAP2260371.1<br>RAP2260371.1<br>RAP2260371.1<br>RAP2260371.1<br>RAP2260371.1<br>RAP2260371.1<br>RAP2260371.1<br>RAP2260371.1<br>RAP2260371.1<br>RAP2260371.1<br>RAP2260371.1<br>RAP2260371.1<br>RAP2260371.1<br>RAP2260371.1<br>RAP2260371.1<br>RAP2260371.1<br>RAP2260371.1<br>RAP2260371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226372.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP226371.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP3737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP3737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP3737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP2377.1<br>RAP377   | TS       TRS-TTSVRTTSA-       PAGSINGLESHENDQCGGNDWKG         PPTTSISTG       TRTSEP       PFTTSSTRTRFTT-TRADGGSSGCGCGGUGCUSCHONKG         PTTTVNTT-       TPPTTS-TSARTSTSPTTTSID-       CONCOMING         PTTTIR       PTSSTRTSTTT-TRANCTSKARCGGGGGGGCCCVSHENDQCGGNDWKG         PTTTIR       PSSTRASSSARTS-TRAGGSGGGGGGCCVSHENDQCGGNDWKG         PTTTIR       PSSTRASSSARTS-TRAGGSGGGGGGCCVSHENDQCGGNDWKG         PTTTIR       PSSTRASSSARTS-TRAGGSGGGGGCCVSHENDQCGGNDWKG         PTTTLRP       TASTSTUDPTS-TRAFT-TRAFT-FYGGGCGGGGGCCVSHENDQCGGNDWKG         PTTLRP       TASTSTUDPTS-TRAFT-TRAFT-FYGGGCGGCGCCVSHENDQCGGNDWKG         PTTTLRP       STRAFTSTUDPTS-TP-TCHC-GCGGGCGCCSHENDQCGGNDWKG         PTTTLRP       STRAFTSTRTSTSTRFTSTTSTTPT-STRFTPTS-TP-GCGCCGKSHENDQCGGNDWKG         SVTTYRSTVTRSOTSTPRETSTSTRFTTSTTTTTTS-TFTCHC-GGGGGGCCSHENDQCGGNDWKG       SVTTRSTTMSTTSTSTRFTSTSTSTRFTS-TP-GCGCGGCGCCSHENDQCGGNDWKG         SVTTYRSTVTRSOTSTPRETSTSTRFTSTTTTTS-TFC-WGGCGGCGCCNHENDQCGGNDWKG       SVTTRSTTMSTTSTSTRFTSTSTSTRFTS-TPC-GGGGGGCCCNHENDQCGNDWKG         PSTTVTST       MLP-SRTSSTQPTTS-TFC-SCGGGCGCCNHENDQCGCNDWKG       SVTTRSTTSTSTRFTSTTTTTSTSTSTRFTS-TPC-GGGGGCGCNHENDQCGNDWKG         PSTTVFST       MLP-SRTSSTQPTTS-TFC-GGGGGCCCNHENDQCGNDWKG       STTRFTSTSTSTSTSTRFTS-TPC-GGGGGCCCNHENDQCGNDWKG         PSTTPHP1       PTFSS-STSTSTSTSTSTSTSTSTSTS-TFC-GGGGGCCCNHENDQCGNDWKG       STTRFTSTSTSTSTSTSTSTSTSTSTSTSTS-TFC-GGGGGCCCNHENDQCGNDWKG  | 348<br>355<br>370<br>344<br>334<br>334<br>337<br>335<br>336<br>339<br>337<br>335<br>335<br>335<br>335<br>335<br>335<br>335<br>335<br>335  |
| KAH7407183.1<br>KAG442154.1<br>XF_031872955.1<br>KAH5595570.1<br>KAF264922.1<br>KAF264922.1<br>KAF264922.1<br>KAF26128620.1<br>XF_033608226.1<br>XF_033608226.1<br>KAF263795.1<br>KAF263795.1<br>KAF2634922.1<br>EF094882.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF183759.1<br>KAF183759.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF17076357.1<br>KAF250897.1<br>KAF250897.1<br>KAF250897.1<br>KAF2649322.1<br>KAF2118428.1<br>XF_033540912.1<br>KAF21186921.1<br>KAF25091.1<br>KAF2649322.1<br>EF094882.1<br>KAF2649322.1<br>EF094882.1<br>KAF2619822.1<br>EF094882.1<br>KAF261972.1<br>KAF261932.1<br>KAF261932.1<br>KAF261932.1<br>KAF261932.1<br>KAF261932.1<br>KAF261932.1<br>KAF261932.1<br>KAF261932.1<br>KAF261932.1<br>KAF261932.1<br>KAF261932.1<br>KAF261932.1<br>KAF261932.1<br>KAF261972.1<br>KAF261972.1<br>KAF261972.1<br>KAF261972.1<br>KAF261972.1<br>KAF261972.1<br>KAF261972.1<br>KAF261972.1<br>KAF261972.1<br>KAF261977.1<br>KAF261977.1<br>KAF261977.1<br>KAF261977.1<br>KAF261977.1<br>KAF261977.1<br>KAF261977.1<br>KAF261977.1<br>KAF261977.1<br>KAF261977.1<br>KAF261977.1<br>KAF261977.1<br>KAF261977.1<br>KAF261977.1<br>KAF261977.1<br>KAF261977.1<br>KAF261777.1<br>KAF261777.1<br>KAF261777.1<br>KAF261777.1<br>KAF2777.1<br>KAF2777.1<br>KAF27777.1<br>KAF2777.1<br>KAF27777.1<br>KAF27777.1<br>KAF27777.1<br>KAF27777.1<br>KAF27777.1<br>KAF27777.1<br>KAF27777.1<br>KAF27777.1<br>KAF27777.1<br>KAF27777.1<br>KAF277777.1<br>KAF27777.1<br>KAF27777.1<br>KAF27777.1<br>KAF27777.1<br>KAF27777.1<br>KAF27777.1<br>KAF27777.1<br>KAF27777.1<br>KAF277777.1<br>KAF277777.1<br>KAF277777.1<br>KAF277777.1<br>KAF277777.1<br>KAF2777777777777777777777777777777777777   | YMLIVINISIWICH THIN I QLAAR GCOCUDPDT     DOY     OVP       YMLIVINISIWICH THIN I QLAAR GCOCUDPDT     DOY     OVP       YMLIVINISIWICH THIN I QLAAR GCOCUDPDT     DOY     OVP       YMLIVINISIWICH THIN I QLAAR GCOLD DDT     DOY     OVP       YMLIVINISIWICH THIN I ALGONG COLD DDT     DOY     OVP       YMLIVISIWICH THIN I ALGONG COLD DDT     DOY     OVP       YMLIVISIWICH THAR I TLAAD GCOLD DDT     DOY     OVP       YMLIVISIWICH THAR I TLAAD GCOLD DDT     DOY     OVP       YMLIVIGSAVID HARRI TLAAD GCOLD DDT     DOY     OVP       YMVIGSQUIT HARRI TLAAD GCOLD DDT     DOY     OVP   | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>154<br>153<br>146<br>154<br>152<br>152<br>152<br>152<br>146<br>146<br>146<br>154<br>153<br>146<br>152<br>152<br>146<br>145<br>145<br>152<br>152<br>146<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>152<br>146<br>146<br>145<br>145<br>146<br>146<br>146<br>145<br>145<br>146<br>146<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>145  | RAH7407183.1<br>RAH7407183.1<br>RAT2144215.1<br>RAT214428.1<br>RAT214428.1<br>RAT214428.1<br>RAT214428.1<br>RAT214428.1<br>RAT214428.1<br>RAT214428.1<br>RAT245200.1<br>RAT245200.1<br>RAT245200.1<br>RAT24520.1<br>RAT24520.1<br>RAT24520.1<br>RAT24520.1<br>RAT24520.1<br>RAT24520.1<br>RAT24520.1<br>RAT24520.1<br>RAT24520.1<br>RAT24520.1<br>RAT250897.1<br>RAT7557.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT25587.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT255.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT557.1<br>RAT55  | TS       TS-TTSVRTTSA       PAGSNOCKSHENDQCCGNDWKG         PPTTSITS       TKT-SSTVRTTSIA       PAGGSSOCKSHENDQCCGNDWKG         PTTTSITS       PFTTSITSTRTTTT-TARGGSSOCGCOCCUMPUTADQCCGNDWKG         PTTTIN       PTSTSTSTRTTT-TARGGSSOCGCOCCUMPUTADQCCGNDWKG         PTTTIN       PTSTSTSTSTSTSTSTTTTSIA         PTTTIN       PSSTRTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST  | 348<br>355<br>360<br>344<br>355<br>370<br>348<br>352<br>362<br>362<br>359<br>337<br>357<br>354<br>356<br>354<br>356<br>354<br>356<br>354<br>356   |
| KAH7407183.1<br>KAG442154.1<br>XF_031872955.1<br>KAH2595570.1<br>KAF2649221.1<br>KAF218428.1<br>XF_0318724821.1<br>KAF218428.1<br>XF_033688226.1<br>XF_033688226.1<br>KAF2634922.1<br>EF094882.1<br>KAF1835456.1<br>KAF1835456.1<br>KAH7463782.1<br>KAF1835456.1<br>KAH7059368.1<br>0AL44252.1<br>KAF275097.1<br>KAF226012.1<br>KAF226012.1<br>KAF226012.1<br>KAF2255.1<br>KAF226012.1<br>KAF226012.1<br>KAF2262801.1<br>KAF2262801.1<br>KAF2285.1<br>KAF236422.1<br>KAF236422.1<br>KAF236422.1<br>KAF236422.1<br>KAF236422.1<br>KAF236422.1<br>KAF236422.1<br>KAF236422.1<br>KAF236422.1<br>KAF24781.1<br>KAF25557.1<br>KAF2642801.1<br>KAF26422.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF243795.1<br>KAF25337.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.   | YMLIVINISIWICHTNICTIQLAAR/GCGVDPDNT     DDY     OVP       YMLIVINISIWICHTNICTIQLAAR/GCGVDPDNT     DDY     OVP       YMLIVINISIWICHTVINISIAR/GCGADDPNT     DDY     OVP       YMLIVISIWICHTVINISIVINICTIALSONGCADDPNT     DDY     OVP       YMLIVISIWICHTVINISITIANG     DDY     OVP       YMLIVISIWICHTVINISIVINICTIALSONGCADDPNT     DDY     OVP       YMLIVISIWICHTVINISITIANG     DDY     OVP       YMLIVISINISITIANG     DDY     OVP       YMLIVISINISITIANG     OVP     OVP       YMUTISISTIANG     OVP     OVP <td< td=""><td>148<br/>148<br/>155<br/>143<br/>157<br/>146<br/>145<br/>145<br/>145<br/>145<br/>145<br/>146<br/>146<br/>146<br/>146<br/>146<br/>153<br/>146<br/>146<br/>146<br/>146<br/>146<br/>146<br/>145<br/>152<br/>152<br/>152<br/>146<br/>146<br/>145<br/>152<br/>152<br/>152<br/>152<br/>152<br/>146<br/>146<br/>145<br/>152<br/>152<br/>152<br/>152<br/>152<br/>152<br/>152<br/>152<br/>152<br/>15</td><td>RAH7407183.1<br/>RAH7407183.1<br/>RAP24442154.1<br/>XP 011872955.1<br/>KAP2188595570.1<br/>KAP2184222.1<br/>XAP2118428.1<br/>XP 033540512.1<br/>RAP2242821.1<br/>PSN69717.1<br/>RAP2262810.1<br/>XP 033688226.1<br/>RAP243736.1<br/>RAP2434922.1<br/>EXP193456.1<br/>RAP2434922.1<br/>RAP124356.1<br/>RAP124356.1<br/>RAP124357.1<br/>RAP1705356.1<br/>RAP2437937.1<br/>RAP1705358.1<br/>0AL44225.1<br/>RAP2247813.1<br/>RAP2246113.1<br/>RAP224570.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP22478031.1<br/>RAP2246012.1<br/>RAP2245012.1<br/>RAP2245012.1<br/>RAP2245012.1<br/>RAP2245012.1<br/>RAP2245012.1<br/>RAP2245012.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP2255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1<br/>RAP255.1</td><td>TS       TRS-TTSVRTTSSA       PAGSINGLESHENDQCGGNDWKG         PPTTSISTG       TRTS-STVRTTTSSA       PAGGSPGCISSHENDQCGGNDWKG         PTTTSISTG       PTTSSTRTRFTT-TARGGSSGCGGGGGCGCANNENDQCGGNDWKG         PTTTIR       PTSSTRTSTTSTSTRFTT-TARGGSSGCGGGGGCGCANNENDQCGGNDWKG         PTTTIR       PTSSTRTSTTSTSRPTSS-TPGM-GGGGGGGCGCGCSNNNKG         PTTTIR       PSSTRTSTSTSRPTS-TRANGT-TARGGSGGGGGCGCANNENDQCGQDWKG         FITTLAP       PSSTRTSTSTSRPTS-TRANGT-REGGGGGGGCGCANNENDQCGQDWKG         PTTTLAP       TARSTTDIPTS-THANT-FUNCT-FUGGCGGGGGCGCCANNENDQCGQDWKG         PTTLAP       TTSSTTTPTS-TPT-GTP-GCGGGGGCGCCANNENDQCGQDWKG         PTTTLAP       STRTSTSTDIPTS-TT-GTP-GCGGGGGCGCSKENDQCGQDWKG         TTTS-TTARSTTTPTS-TPT-GTP-GCGCGCKSKHDQCGQDWKG       TTTSSTTTPTS-TP-GCGGGGGCGCSKHDQCGQDWKG         SVTTYRSVTRSOTSTPDIPTSTSTSPRTS-TRSSTPRETS-TS-S-GGGGGCGCKSKHDQCGQDWKG       SVTTRSSTWRSOTSTPDIPTSTSTSPRTS-TFG-WGGGGGGGCGCMKHDQCGDWKG         PSTVTST       MLP-SRTSSA-GRTS-T-S-GGGGGGCGCKSKHDQCGGDWKG       SVTTRSTWRSOTSTPDIPTSTSTSPRTS-TFG-WGGGCGGCCMKHDQCGGNWKG         PSTVTRSTWRSOTSTPDIPTSTSTSPRTS-TFG-WGGGCGGCCCANKDQCGGNWKG       SVTTRSTSTSTDIPTSTSTRTFTSTTRTKTSTS-TFG-WGGGCGGCCCANKG         PSTVTRSTSTSSTDIPTS-TFG-WGGGCGCCCANKDQCGGNWKG       SVTTRSTSTSTDIPTS-TFG-WGGGCGGCCCANKDQCGNWKG         PSTVTRSTSTSTSTSTSTSTSTSTSTSTRTFTS-TFG-GGGGGCGCCANKDQCGNWKG       STTRSTSTSTSTSTSTDIPTS-TFG-WGGGCGCCANKDQCGNWKG         PSTTPHP1-PTTSSTSTSTSTSTSTSTP</td><td>348<br/>355<br/>370<br/>344<br/>334<br/>334<br/>337<br/>335<br/>336<br/>339<br/>337<br/>335<br/>335<br/>335<br/>335<br/>335<br/>335<br/>335<br/>335<br/>335</td></td<> | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>146<br>146<br>146<br>153<br>146<br>146<br>146<br>146<br>146<br>146<br>145<br>152<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>152<br>152<br>152<br>146<br>146<br>145<br>152<br>152<br>152<br>152<br>152<br>152<br>152<br>152<br>152<br>15  | RAH7407183.1<br>RAH7407183.1<br>RAP24442154.1<br>XP 011872955.1<br>KAP2188595570.1<br>KAP2184222.1<br>XAP2118428.1<br>XP 033540512.1<br>RAP2242821.1<br>PSN69717.1<br>RAP2262810.1<br>XP 033688226.1<br>RAP243736.1<br>RAP2434922.1<br>EXP193456.1<br>RAP2434922.1<br>RAP124356.1<br>RAP124356.1<br>RAP124357.1<br>RAP1705356.1<br>RAP2437937.1<br>RAP1705358.1<br>0AL44225.1<br>RAP2247813.1<br>RAP2246113.1<br>RAP224570.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP22478031.1<br>RAP2246012.1<br>RAP2245012.1<br>RAP2245012.1<br>RAP2245012.1<br>RAP2245012.1<br>RAP2245012.1<br>RAP2245012.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP2255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1<br>RAP255.1   | TS       TRS-TTSVRTTSSA       PAGSINGLESHENDQCGGNDWKG         PPTTSISTG       TRTS-STVRTTTSSA       PAGGSPGCISSHENDQCGGNDWKG         PTTTSISTG       PTTSSTRTRFTT-TARGGSSGCGGGGGCGCANNENDQCGGNDWKG         PTTTIR       PTSSTRTSTTSTSTRFTT-TARGGSSGCGGGGGCGCANNENDQCGGNDWKG         PTTTIR       PTSSTRTSTTSTSRPTSS-TPGM-GGGGGGGCGCGCSNNNKG         PTTTIR       PSSTRTSTSTSRPTS-TRANGT-TARGGSGGGGGCGCANNENDQCGQDWKG         FITTLAP       PSSTRTSTSTSRPTS-TRANGT-REGGGGGGGCGCANNENDQCGQDWKG         PTTTLAP       TARSTTDIPTS-THANT-FUNCT-FUGGCGGGGGCGCCANNENDQCGQDWKG         PTTLAP       TTSSTTTPTS-TPT-GTP-GCGGGGGCGCCANNENDQCGQDWKG         PTTTLAP       STRTSTSTDIPTS-TT-GTP-GCGGGGGCGCSKENDQCGQDWKG         TTTS-TTARSTTTPTS-TPT-GTP-GCGCGCKSKHDQCGQDWKG       TTTSSTTTPTS-TP-GCGGGGGCGCSKHDQCGQDWKG         SVTTYRSVTRSOTSTPDIPTSTSTSPRTS-TRSSTPRETS-TS-S-GGGGGCGCKSKHDQCGQDWKG       SVTTRSSTWRSOTSTPDIPTSTSTSPRTS-TFG-WGGGGGGGCGCMKHDQCGDWKG         PSTVTST       MLP-SRTSSA-GRTS-T-S-GGGGGGCGCKSKHDQCGGDWKG       SVTTRSTWRSOTSTPDIPTSTSTSPRTS-TFG-WGGGCGGCCMKHDQCGGNWKG         PSTVTRSTWRSOTSTPDIPTSTSTSPRTS-TFG-WGGGCGGCCCANKDQCGGNWKG       SVTTRSTSTSTDIPTSTSTRTFTSTTRTKTSTS-TFG-WGGGCGGCCCANKG         PSTVTRSTSTSSTDIPTS-TFG-WGGGCGCCCANKDQCGGNWKG       SVTTRSTSTSTDIPTS-TFG-WGGGCGGCCCANKDQCGNWKG         PSTVTRSTSTSTSTSTSTSTSTSTSTSTRTFTS-TFG-GGGGGCGCCANKDQCGNWKG       STTRSTSTSTSTSTSTDIPTS-TFG-WGGGCGCCANKDQCGNWKG         PSTTPHP1-PTTSSTSTSTSTSTSTSTP  | 348<br>355<br>370<br>344<br>334<br>334<br>337<br>335<br>336<br>339<br>337<br>335<br>335<br>335<br>335<br>335<br>335<br>335<br>335<br>335  |
| KAH7407183.1<br>KAG442154.1<br>XF_031872955.1<br>KAH5595570.1<br>KAF2649221.1<br>KAF264922.1<br>KAF264922.1<br>KAF264922.1<br>KAF264922.1<br>KAF2632802.1<br>XF_033688226.1<br>XKF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1231545.1<br>KAF1231545.1<br>KAF1231545.1<br>KAF1231545.1<br>KAF1231545.1<br>KAF2537.1<br>KAF2537.1<br>KAF2557.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF243739.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF257.1<br>KAF                 | YMLRVINSINGLINTNET (LAAR/GCG/UPDNT     DOY     OVP       YMLRVINSINGLINTNET (LAAR/GCGA/UPDNT     DOY     OVP       INKLISSINGLINTRY (LAAR/GCA/UPDNT     DOY     OVP       INKLISSINGLINKRIFTLAAD/GCA/UPDNT     DOY     OVP       INKLISSINGLINKRIFTLAAD/GC  | 148 148 155 143 157 146 145 145 145 145 145 145 145 146 146 154 153 146 146 154 152 152 146 146 146 145 145 152 206 201 210 217 204 203 201 217 204 203 203 204 203 204 203 204 203 204 203 204 204 203 204 204 203 204 204 204 201 201 201 201 201 201 201 201 201 201  | RAH7407183.1<br>RAH7407183.1<br>RAT21442154.1<br>XP 011872955.1<br>RAT214428.1<br>XP 01372643322.1<br>RAT211428.1<br>XP 033540912.1<br>PSN69717.1<br>RAT22463221.1<br>RAT224520.1<br>XP 03368226.1<br>RAT2634922.1<br>RAT2634922.1<br>RAT2634922.1<br>RAT26349362.1<br>RAT26349362.1<br>RAT26349362.1<br>RAT26357.1<br>RAT705356.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2750897.1<br>RAT2264122.1<br>RAT211428.1<br>RAT218612.1<br>RAT218571.1<br>RAT22612.1<br>RAT21836.1<br>RAT21836.1<br>RAT2356.1<br>RAT2356.1<br>RAT2356.1<br>RAT2357.1<br>RAT2365.1<br>RAT2357.1<br>RAT2357.1<br>RAT2357.1<br>RAT2357.1<br>RAT2357.1<br>RAT2357.1<br>RAT2357.1<br>RAT2357.1<br>RAT2357.1<br>RAT2357.1<br>RAT2357.1<br>RAT2357.1<br>RAT2357.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1  | TS       TS-TTSVRTTSA       PAGSNGCKSHENDQCGGNDWKG         PPTTSITS       TKT-SSTVRTTSIA       PAGGSSGCCSUBNCCONDWKG         PTTTSITS       PFTTSSTRTRTT       PAGGSSGCCSUBNCCONDWKG         PTTTVIRT       TPTTS-TSSTRTTTSITS       PAGGSSGCCSUBNCCONDWKG         PTTTIN       PTSSTSTSTRTTTSIS       PAGGSSGCCSCCSUBNCCONDWKG         PTTTIN       PSTRLAPS       PSTRLAPS         PTTTIN       PSTRLAPS       PSTRLAPS         PTTTIN       TASTSTSTSTSTSTSTSTSTSTSTS       PSTRLAPS         PTTLAP       SSTTIDSPGT1-TCGCCGCCCCCSUBNCG         PSTRLAPS       TSSTTTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST  | 348<br>355<br>350<br>344<br>355<br>362<br>362<br>362<br>362<br>359<br>357<br>364<br>357<br>359<br>359<br>357<br>354<br>356<br>353<br>356<br>353<br>356<br>353<br>356<br>354<br>356<br>356<br>356<br>356<br>356<br>356<br>356<br>356<br>356<br>356   |
| KAH7407183.1<br>KAG442154.1<br>XF_03187255.1<br>KAH5555570.1<br>KAF264922.1<br>KAF218622.1<br>KAF218622.1<br>KAF218622.1<br>PSN59717.1<br>XGF263220.1<br>XF_033688226.1<br>XF_033688226.1<br>KAF263792.1<br>KAF263792.1<br>KAF263792.1<br>KAF25377.1<br>KAF25375.1<br>KAH71059361.1<br>KAF2537.1<br>KAF2537.1<br>KAF226012.1<br>KAF226012.1<br>KAF226012.1<br>KAF226012.1<br>KAF226012.1<br>KAF226012.1<br>KAF226012.1<br>KAF226012.1<br>KAF226012.1<br>KAF226012.1<br>KAF226012.1<br>KAF226012.1<br>KAF226012.1<br>KAF226012.1<br>KAF218422.1<br>KAF262800.1<br>XF_0336822.1<br>KAF262820.1<br>KAF2639012.1<br>KAF264820.1<br>KAF264822.1<br>KAF264822.1<br>KAF2437396.1<br>KAF264822.1<br>KAF2437396.1<br>KAF264822.1<br>KAF264822.1<br>KAF2437396.1<br>KAF264822.1<br>KAF2437396.1<br>KAF25337.1<br>KAF25537.1<br>KAF25557.1<br>KAF25557.1<br>KAF264820.1<br>XF_0356555.1<br>KAF264822.1<br>KAF264822.1<br>KAF264822.1<br>KAF264822.1<br>KAF264823.1<br>KAF25337.1<br>KAF25557.1<br>KAF2555.1<br>KAF264825.1<br>KAF2537.1<br>KAF2555.1<br>KAF2555.1<br>KAF2555.1<br>KAF25555.1<br>KAF264825.1<br>KAF2537.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF2555555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF255555.1<br>KAF255555.1<br>KAF255555.1<br>KAF25555.1<br>KAF255555.1<br>KAF255555.1<br>KAF255555.1<br>KAF255555.1<br>KAF255555.1<br>KAF255555.1<br>KAF2555555.1<br>KAF2555555.1<br>KAF2555555.1<br>KAF255555555.1<br>KAF25555555.1<br>KAF2555555555.1<br>KAF25555555.1<br>KAF25555555555.1<br>KAF25555555555.1<br>KAF2555555555555.1<br>KAF2555555555555555555555555555555555555  | YMLIVINISIWICHTNICTIQLAAR/GCGVDPDNT     DOY     OVP       YMLIVINISIWICHTNICTIQLAAR/GCGVDPDNT     DOY     OVP       YMLIVINISIWICHTRUGAAR/GCGDUPDNT     DOY     OVP       YMLIVISIWICHTRUGAAR/GCGDUPDNT     DOY     OVP       YMLIVISIWICHTRUGAAR/GCGDUPDNT     DOY     OVP       YMLIVISIWICHTRUGAAR/GCGDUPDNT     DOY     OVP       YMLIVISIWICHTAKERTIAAD/GCDUPDNT     DOY     OVP       YMUTOGSTIVINAKERTIAAD/GCDUPDNT     DOY     OVP       YMVTOSOGTIDTAKERTITAAD/GCDUPDNT     DOY     OVP       YMVTOSOGTIDTAKERTITAAD/GCDUPDNT     DOY     OVP       YMVTOSOGTIDTAKERTITAAD/GCDUPDNT     DOY     OVP       YMVTOSOGTIDTAKERTITAAD/GCDUPDNT     DOY     OVP       YMTOSOGTIDTAKERTITAAD/GCDUPDNT     DOY     OVP       YMTOSOGTIDTAKERTITAAD/GCDUPDNT     DOY     OVP       YMTOSOGTIDTAKERTITAAD/GCDUPDNT     DOY     OVP       YMTOSOGTIDTAKERTITAAD/GCDUPDNT     DOY     OVP       YMTTOSOGTITAKERTITAAD/GCDUPDNT     DOY     <  | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>146<br>146<br>146<br>146<br>146<br>146<br>146<br>146  | RAH7407183.1<br>RAH7407183.1<br>RAP4442154.1<br>XP 011872955.1<br>KAP2148292.1<br>KAP2148292.1<br>KAP214822.1<br>XP 033540912.1<br>RAP2242821.1<br>PSN69717.1<br>RAP2262810.1<br>XP 03368226.1<br>RAP2243796.1<br>RAP2243796.1<br>RAP2243796.1<br>RAP2243796.1<br>RAP23736.1<br>RAP23736.1<br>RAP23736.1<br>RAP23736.1<br>RAP23736.1<br>RAP23736.1<br>RAP23736.1<br>RAP23736.1<br>RAP23736.1<br>RAP23736.1<br>RAP23736.1<br>RAP23736.1<br>RAP3737.1<br>RAP3737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP23737.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1<br>RAP337.1   | TS         TRS-TTSVRTTSSA         PAGSNOCKSHENDQCGONDWG           PPTTSITS         TRT-STTVTTTSIT         PAGGSSOCCSURPQCGONDWG           PTTTSITS         PTTTISTSTRAFT         TRDGGGSCGCGOCGCANNG           PTTTIR         PTTTISTSTRAFT         TRDGGGSCGGGGCGCCANNG           PTTTIR         PTTTISTSTRAFT         TRDGGGSCGGGGCGCANNG           PTTTIR         PTTTIR         PSTRAFTSTSTSRPTS           PTTTIR         PSTRAFTSTSTSPTTST         TRMT-FXGGCGGGGGCCCANNG           PTTTIR         PSTRAFTSTSTSPTS         TRMT-FXGGCGGGGGCCCANNG           PTTTIR         PSTRAFTSTSTTSTTSTT         TRMT-FXGGCGGGGGCCCANNG           PTTTIR         TTSTSTTTSTSTTSTTSTTSTT         TRMT-FXGGCGGCGCCCANNG           PTTTRFSTTRAFTSTSTSTSTTSTSTTSTSTTSTTSTTSTTSTTSTTSTTS   | 348<br>355<br>350<br>364<br>355<br>370<br>367<br>367<br>367<br>367<br>367<br>367<br>367<br>367<br>367<br>367  |
| KAH7407183.1<br>KAG442154.1<br>XF_03187255.1<br>KAH5555570.1<br>KAF2649221.1<br>KAF2649221.1<br>KAF2649221.1<br>KAF2649221.1<br>KAF2649220.1<br>XF_033668226.1<br>XF_033668226.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF25337.1<br>KAF25397.1<br>KAF25397.1<br>KAF2557.1<br>KAF264922.1<br>KAF264922.1<br>KAF264922.1<br>KAF264922.1<br>KAF264922.1<br>KAF264922.1<br>KAF264922.1<br>KAF2621.1<br>KAF26220.1<br>XAF26220.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF2437396.1<br>KAF26220.1<br>KAF26220.1<br>KAF26220.1<br>KAF26220.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF26377.1<br>KAF   | YMLIVINISIWICI INTRI QLAAR/GCG/UPDNT     DOY     OVP       YMLIVINISIWICI INTRI QLAAR/GCG/UPDNT     DOY     OVP       YMLIVINISIWICI INTRI QLAAR/GCG/UPDNT     DOY     OVP       YMLIVISIWICI INTRI TAAD/GCALIPONT     DOY     OVP       YMLIVISIWICI INTRI TAAD/GCALIPONT     DOY     OVP       YMLIVIGSA IND INARE ILLAAD/GCALIPONT     DOY     OVP       YMLIVIGSA INTAKKE ILLAAD/GCALIPONT     DOY     OVP   | 148 148 155 143 157 146 145 145 145 145 145 145 145 146 146 154 153 146 146 154 152 152 152 152 146 146 146 145 145 145 145 145 145 145 145 145 145  | RAH7407183.1<br>RAH7407183.1<br>RAT2148295570.1<br>RAT2148295570.1<br>RAT2148295570.1<br>RAT2148295570.1<br>RAT214829.1<br>RAT214829.1<br>RAT214829.1<br>RAT214829.1<br>RAT214829.1<br>RAT264922.1<br>RAT264922.1<br>RAT264922.1<br>RAT1663762.1<br>RAT63756.1<br>RAT63757.1<br>RAT705356.1<br>RAT705356.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705350.1<br>RAT26422.1<br>RAT26422.1<br>RAT26422.1<br>RAT26570.9<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705350.1<br>RAT27356.1<br>RAT2622.1<br>RAT2622.1<br>RAT2622.1<br>RAT2622.1<br>RAT2622.1<br>RAT27357.1<br>RAT27357.1<br>RAT27355.1<br>RAT27355.1<br>RAT26422.1<br>RAT2622.1<br>RAT21435.1<br>RAT26357.1<br>RAT26357.1<br>RAT26357.1<br>RAT26357.1<br>RAT26357.1<br>RAT26357.1<br>RAT26357.1<br>RAT26357.1<br>RAT26357.1<br>RAT26357.1<br>RAT26357.1<br>RAT26357.1<br>RAT26357.1<br>RAT26357.1<br>RAT26357.1<br>RAT2557.1<br>RAT2557.1<br>RAT70535.1<br>RAT70535.1<br>RAT70535.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT70537.1<br>RAT70537.1<br>RAT70537.1<br>RAT70537.1   | TS  | 348<br>355<br>350<br>344<br>355<br>362<br>362<br>362<br>362<br>359<br>357<br>364<br>357<br>356<br>359<br>357<br>356<br>359<br>357<br>356<br>359<br>357<br>356<br>357<br>356<br>358<br>356<br>353<br>356<br>353<br>356<br>355<br>356<br>356<br>356<br>356  |
| KAH7407183.1<br>KAG442154.1<br>XF_03187255.1<br>KAH2595570.1<br>KAF2649221.1<br>KAF2186921.1<br>PSN5917.1<br>XF_03186921.1<br>XF_033688226.1<br>XF_033688226.1<br>XF_033688226.1<br>KAF2634922.1<br>EF294882.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835557.1<br>KAF1705356.1<br>CAL4252.1<br>KAF226012.1<br>KAF226012.1<br>KAF226012.1<br>KAF226012.1<br>KAF226012.1<br>KAF22537.1<br>KAF22555.1<br>KAF22555.1<br>KAF22555.1<br>KAF218622.1<br>KAF21855557.1<br>KAF22555.1<br>KAF22555.1<br>KAF22555.1<br>KAF218622.1<br>KAF2185555.1<br>KAF22555.1<br>KAF262200.1<br>XF_031872555.1<br>KAF2471396.1<br>KAF2471396.1<br>KAF2471396.1<br>KAF2471396.1<br>KAF2471396.1<br>KAF25337.1<br>KAF25557.1<br>KAF25557.1<br>KAF25555.1<br>KAF2471396.1<br>KAF2537.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF2555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF255555.1<br>KAF25555.1<br>KAF255555.1<br>KAF255555.1<br>KAF25555.1<br>KAF25555.1<br>KAF25555.1<br>KAF255555.1<br>KAF25555.1<br>KAF255555.1<br>KAF255555.1<br>KAF25555.1<br>KAF25555.1<br>KAF255555.1<br>KAF255555.1<br>KAF25555.1<br>KAF255555.1<br>KAF255555.1<br>KAF255555.1<br>KAF255555.1<br>KAF255555.1<br>KAF255555.1<br>KAF255555555.1<br>KAF2555555555.1<br>KAF2555555555555555555555555555555555555  | YHLIVINSIVICI TYNI I QLAAR (CGCVDPDNT       DCY       QIP         YHLIVINSIVICI TYNI I QLAAR (CGCVDPDNT)       DCY       QIP         YHLIVINSIVICI TYNI I QLAAR (CGCVDPDNT)       DCY       QIP         YHLIVISSIVICI TYNI RUNT (CGANTROCK)       DCY       QIP         YHLIVISSIVICI TYNI TYNI CAN (CGANTPDNT)       DCY       QIP         YHLIVISSIVICI TYNI TYNI TYNI CGANTROCK)       DCY       QIP         YHLIVISSIVICI TYNI TYNI TYNI CGANTPONTON (CGANTPDNT)       DCY       QIP         YHLIVISSIVICI TYNI TYNI TYN CGANTPONTON (CGANTPDNT)       DCY       QIP         YHLIVISSIVICI TYNI TYN CGANTPONTON (CGANTPDNT)       DCY       QIP         YHLIVISSIVICI TYN TYN CGANTPONTON (CGANTPDNT)       DCY       QIP         YHLIVISSIVICI TANARTI TAADI (CGANTPDNT)       DCY       QIP         YHLIVISSIVICI TANARTI TAADI (CGANTPDNT)       DCY       QIP         YHVITSSIVICI TANARTI TAADI (CGANTPDNT)       DCY       QIP  | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>146<br>146<br>146<br>146<br>146<br>146<br>146<br>146<br>146  | RAH7407183.1<br>RAH7407183.1<br>RAH4442154.1<br>XP 011872955.1<br>KAT8595570.1<br>KAT2482922.1<br>KAT2148292.1<br>RAT2148292.1<br>RAT2148292.1<br>RAT214822.1<br>RAT2148242.1<br>RAT2145241.1<br>RAT24541922.1<br>RAT24541922.1<br>RAT1637596.1<br>RAT87557.1<br>RAT87557.1<br>RAT87557.1<br>RAT87557.1<br>RAT705368.1<br>0AL44252.1<br>RAT705358.1<br>0AL44252.1<br>RAT705358.1<br>RAT705358.1<br>RAT70555.1<br>RAT70555.1<br>RAT70555.1<br>RAT70555.1<br>RAT70555.1<br>RAT70555.1<br>RAT70555.1<br>RAT70555.1<br>RAT24322.1<br>RAT70555.1<br>RAT24322.1<br>RAT70555.1<br>RAT24322.1<br>RAT70555.1<br>RAT24322.1<br>RAT70555.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT243237.1<br>RAT243237.1<br>RAT24322.1<br>RAT24325.1<br>RAT24322.1<br>RAT24325.1<br>RAT24322.1<br>RAT243237.1<br>RAT24322.1<br>RAT24322.1<br>RAT243237.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT24322.1<br>RAT743356.1<br>RAT74337.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75357.1<br>RAT75377.1<br>RAT75357.1<br>RAT75357.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT7557.1<br>RAT755   | TS       TRS-TTSVRTTSA       PAGSINGLESHENDQCGGNDWKG         PPTTSISTG       TRTSPT       PAGSINGLESHENDQCGGNDWKG         PTTTSISTG       TRSSTRTRTT       TRDGGGSCGCGCGCCCCNDWKG         PTTTVRT       TPTTTSTARNTT       TRDGGGSCGCGCGCCCNDWKG         PTTTIR       PTSSTRTSTT       TRGGGSCGGGGCCCCNDWKG         PTTTIR       PSSTRAPPSSNDTS       TRGGGGGGGCCCNDWKG         PTTTIR       PSSTRAPPSSNDTS       TRMT-WGGCCQCGCCCCNNWKG         PTTTIR       PSSTRAPSSNDTS       TRMT-WGGCCQCGCCCCNNWKG         PTTTIR       TRSSTTDPTSTSTRPTS       TRMT-WGGCCQCCNNWG         PTTTLAP       TRSSTTDPTSTSTRAPST       TRMT-WGGCCQCNWKG         PTTTLAPS       STRAPSSTRTSTTNPTSTTPT       -GGCGCCNSHPDQCCQCNWKG         VTTVSVTRSOTSTPRIPTSTSTRAPSTSTTRTTSTTSTTTT       -GGCGGCCNSHPDQCCQCNWKG         SVTTYSSVTRSOTSTPRIPTSTSTRAPSTSTRTWTSTSTTRTTSTSTTMT       -GGCGGCCNSHPDQCCQCNWKG         SVTTYSSVTRSOTSTPRIPTSTSTRTWTSTSTTRTTSTSTTT       -GGCGGCCNSHPDQCCQCNWKG         PSTTURPT       HLP-SRTSSA-RPTS-TS-S-GGGGGCCNSHPDQCCQNWKG         PSTTVRPT       -FNS-GGGGGCCNSHPDQCCQNWKG         PSTTVRPT       -FNS-SGGGGGCCNSHPDQCCQNWKG         PSTTVRPT       -FNS-SGGGGCCNSHPDQCCQNWKG         PSTTVRPT       -FNS-SGGGGCCNSHPDQCCQNWKG         PSTTVRPT       -FNS-SGGGGCCNSHPDQCCG  | 348<br>355<br>370<br>344<br>355<br>370<br>352<br>362<br>352<br>354<br>355<br>354<br>355<br>355<br>354<br>355<br>355<br>355<br>355   |
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KAH7407183.1<br>KAG442154.1<br>KU-3187255.1<br>KAH2595570.1<br>KAF2649221.1<br>KAF2649221.1<br>KAF2649221.1<br>KAF2649221.1<br>KAF2649221.1<br>KAF2649221.1<br>KAF264922.1<br>EP054882.1<br>KAF2634922.1<br>EP054882.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF1835456.1<br>KAF28377.1<br>KAF29286012.1<br>KAF2928601.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF284712.1<br>KAF2750877.1<br>KAF706877.1<br>KAF706877.1<br>KAF706877.1<br>KAF706877.1<br>KAF706877.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697.1<br>KAF70697   | YULIYUNSIWELIYINI QLAARIGCOGVDPDIT       DOY       QIP         YULIYUNSIWESINI QLAARIGCOGVDPDIT       DOY       QIP         YULIYUNSIWESINI TURAQARIGCOLUPDIT       DOY       QIP         INULISSIWESINI TURAQARIGCOLUPDIT       DOY       QIP         INULISSIWESINI TURAQARIGCOLUPDIT       DOY       QIP         INULISSIWESINI TURAQARIGCOLUPDIT       DOY       QIP         INULIYUSSIWESINI TURAQARIGCOLUPDIT       DOY       QIP         INULIYUSSIWENI TURARI TURAQARIGCOLUPDIT       DOY       QIP         INUTIYOGANUD HARRI TURADOGCOLUPDIT       DOY       QIP         INUTIYOGANUTARARI TURADOGCOLUPDIT       DOY       QIP         INUTYOGANUTARARI TURADOGCOLUPDIT       DOY       QIP         INUTYOGANUTARARI TURADOGCOLUPDIT       DOY       QIP         INUTYOGANUTARARI TURADOGCOLUPDIT       DOY       QIP         INUTYOGANUTARARI TURADOGCOLUPDIT       DOY       QIP         INVITYOGANUTARARI TURADOGCOLUPDIT       DOY       QIP         INVITYOGANUTARARI TURADOGCOLUPDIT       DOY       QIP         <  | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>146<br>154<br>152<br>152<br>146<br>153<br>146<br>154<br>152<br>152<br>146<br>146<br>154<br>152<br>152<br>146<br>145<br>152<br>152<br>146<br>145<br>152<br>152<br>146<br>145<br>152<br>152<br>146<br>145<br>152<br>152<br>146<br>145<br>152<br>152<br>146<br>145<br>152<br>152<br>152<br>146<br>145<br>152<br>152<br>152<br>146<br>145<br>155<br>152<br>152<br>152<br>152<br>152<br>155<br>146<br>145<br>155<br>152<br>155<br>146<br>155<br>155<br>155<br>146<br>155<br>155<br>155<br>146<br>155<br>155<br>155<br>146<br>155<br>155<br>155<br>155<br>146<br>145<br>155<br>155<br>155<br>155<br>146<br>145<br>155<br>155<br>146<br>145<br>155<br>155<br>155<br>146<br>146<br>155<br>155<br>155<br>146<br>146<br>155<br>155<br>155<br>155<br>146<br>145<br>155<br>155<br>155<br>146<br>145<br>155<br>155<br>155<br>146<br>145<br>145<br>155<br>155<br>155<br>146<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>155<br>155 | RAH7407183.1<br>RAH7407183.1<br>RAT2148295570.1<br>RAT2148295570.1<br>RAT2148295570.1<br>RAT2148295570.1<br>RAT2148295570.1<br>RAT214829.1<br>RAT214829.1<br>RAT214829.1<br>RAT214829.1<br>RAT2649221.1<br>RAT264922.1<br>RAT264922.1<br>RAT1663756.1<br>RAT26349362.1<br>RAT663757.1<br>RAH7075357.1<br>RAH7075357.1<br>RAH7075357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT705357.1<br>RAT264021.1<br>RAT21869577.1<br>RAT264021.1<br>RAT21869577.1<br>RAT264322.1<br>RAT2186921.1<br>RAT264392.1<br>RAT263492.1<br>RAT263492.1<br>RAT263492.1<br>RAT263492.1<br>RAT263492.1<br>RAT263492.1<br>RAT263492.1<br>RAT263492.1<br>RAT263492.1<br>RAT263492.1<br>RAT263492.1<br>RAT26357.1<br>RAT705958.1<br>RAT705957.1<br>RAT705957.1<br>RAT705957.1<br>RAT705957.1<br>RAT705957.1<br>RAT705957.1<br>RAT705957.1<br>RAT22647813.1<br>RAT225607.1<br>RAT222607.1<br>RAT222607.1<br>RAT222607.1<br>RAT222607.1<br>RAT222607.1<br>RAT222607.1<br>RAT222607.1<br>RAT222607.1<br>RAT222607.1<br>RAT222607.1<br>RAT222607.1<br>RAT222607.1<br>RAT222607.1<br>RAT27226012.1<br>RAT27226012.1<br>RAT27226012.1<br>RAT27226012.1<br>RAT27226012.1<br>RAT27226012.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT27257.1<br>RAT2725  | TS TS TTS TTS AT SATURATES AN APGGSNOCK SHEND CCGNDWG<br>PTTS:RTP TS -TS STVRTTS SAN PROGSSOC SHEND CCGNDWG<br>PTTYINT TS PTTS -TS STVRTTTS IN PROGGSOC CONSTRUCT CONSTRUCT<br>PTTYINT TS PTTS -TASTS:RTPTTS IN PTS STURDECCNDWG<br>PTTYINT TS PTS -TRANSITS STVRTTS IN PROGSSOC SHEND CCGNDWG<br>PTTYIN TS TS STVRTTS TS PTS -TPCN -GGCGCCCCUSHNCG<br>PTTYINT TS TTASTS:TS PTS -TPCN -GGCGCCCUSHND CCGNDWG<br>PTTIL STURPTS -TRANSITS STVRTTS -TO COGGGCCCUSHND CCGNDWG<br>PTTY STVTS TTASTS:TS PTS -TPCN -GGCGCCCUSHND CCGNDWG<br>PTTS:PT -TTS STTIPTS -TPCN -GGCGCCCUSHND CCGNDWG<br>PTTS:PT -TTS STTIPTS -TPCN -GGCGCCCUSHND CCGNDWG<br>SVTTYS STVTS STRATS -TRUE -GGCGCCUSHND CCGNDWG<br>-TTS -TTS STTIPTS -TPC -GGCGCCUSHND CCGNDWG<br>SVTTYS STVTS STRATS -TRUE -GGCGCCUSHND CCGNDWG<br>SVTTYS STVTS STRATS -TS STRATS -TS -GGCGGCCUSHND CCGNDWG<br>PSTTLP - STASTS STRATS -TS -GGCGGCCUSHND CCGNDWG<br>SVTTYS STVTS STRATS STRATS -TS -GGCGGCCUSHND CCGNDWG<br>PSTTLP - STASTS STRATS STRATS -TS -GGCGGCCUSHND CCGNDWG<br>PSTTLP - STASTS STRATS STRATS -TS -GGCGGCCUSHND CCGNDWG<br>PSTTLP - STASTS STRATS STRATS -TS -GGCGGCCUSHND CCGNDWG<br>PSTTLP - TTS - STTS STASTS -TS -GGCGGCCUSHND CCGNDWG<br>PSTTLP - TTS - STASTS STRATS -TTGGGCGCCUSHND CCGNDWG<br>PSTTLP - TTS - STASTS STRATS -TTGGGCCCUSHNC COMMG<br>PSTTLP - TTS - STASTS STRATS -TTGGGCCCUSHNC COMMG<br>PSTTLP - TTS STASTS ORT - TSGGGGCCCUSHNC COMMG<br>PSTTLP - TTS STASTS ORT - TSGGGCGCCUSHNC COMMG<br>PSTTLP - TTS STASTS ORT - TSGGGCGCCUSHNC COMMG<br>PSTTLP - TTS - STASTS STRATS -TTGGGCCCUSHNC COMMG<br> | 348<br>355<br>370<br>344<br>334<br>334<br>337<br>335<br>352<br>354<br>359<br>354<br>354<br>354<br>354<br>354<br>354<br>354<br>356<br>356<br>356<br>358<br>358<br>358  |
| KAH7407183.1<br>KAG442154.1<br>XF_03187255.1<br>KAH5555570.1<br>KAF2649221.1<br>KAF2186921.1<br>XF_031870912.1<br>KAF2186200.1<br>XF_033688226.1<br>XF_033688226.1<br>KAF263795.1<br>KAF2634922.1<br>EF2034882.1<br>KAF1835551.1<br>KAF1835557.1<br>KAF1705356.1<br>KAF1705356.1<br>KAF7059368.1<br>OL44252.1<br>KAF21859557.1<br>KAF725337.1<br>KAF725307.1<br>KAF226012.1<br>KAF21859557.1<br>KAF2253012.1<br>KAF21859557.1<br>KAF2628001.1<br>KAF2628012.1<br>KAF2638012.1<br>KAF25337.1<br>KAF2628012.1<br>KAF25337.1<br>KAF2628012.1<br>KAF25337.1<br>KAF2628012.1<br>KAF25337.1<br>KAF2537.1<br>KAF25337.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF2537.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF25387.1<br>KAF2337.1<br>KAF25387.1<br>KAF2337.1<br>KAF25387.1<br>KAF25387.1<br>KAF2337.1<br>KAF25387.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF2337.1<br>KAF237                                       | VYLEVINSIVELITNI I QLAAR GCOCUPDNT DCY QP<br>VYLEVINSIVELITNI I QLAAR GCOCUPDNT DCY QP<br>VYLEVINSIVENI WENT QLAAR GCOLUPDNT DCY QP<br>VXLEVINSIVENI WENT QLAAR GCOLUPDNT DCY QP<br>VXLEVINSIVENI WENT QLAAR GCOLUPDNT DCY QP<br>VXLEVINSIVELITNI VXLEVICOLUPDNT DCY QP<br>VXLEVINSIVELITNI VXLEVICOLUPDNT DCY QP<br>VXLEVISITVE QARAELIAAD GCOLUPDNT DCY QP<br>VXLEVISQUITE VXLEVISITIADE GCOLUPDNT DCY QP<br>VXLEVISQUITE VXLEVISITIADE GCOLUPDNT DCY QP<br>VXVETCOGUITUAREELIAAD GCOLUPDNT DCY QP<br>VXVETCOGUITUAREELIAA  | 148<br>148<br>155<br>143<br>157<br>146<br>145<br>145<br>145<br>145<br>145<br>145<br>146<br>154<br>152<br>152<br>152<br>154<br>146<br>154<br>152<br>152<br>152<br>152<br>154<br>146<br>146<br>146<br>145<br>145<br>152<br>152<br>152<br>152<br>152<br>152<br>152<br>152<br>152<br>15  | RAH7407183.1<br>RAH7407183.1<br>RA4442154.1<br>XP 011872955.1<br>KA72643922.1<br>RA72148292.1<br>RA7214822.1<br>RA7214822.1<br>RA7214822.1<br>RA7214822.1<br>RA7214822.1<br>RA7214522.1<br>RA7214523.1<br>RA724534922.1<br>RA71463756.1<br>RA71453556.1<br>RA71453556.1<br>RA7145355.1<br>RA71705356.1<br>RA71705357.1<br>RA7705357.1<br>RA7705357.1<br>RA7705357.1<br>RA7705357.1<br>RA7705357.1<br>RA7705357.1<br>RA7705357.1<br>RA7705357.1<br>RA7705357.1<br>RA7705357.1<br>RA724247813.1<br>RA724392.1<br>RA72437355.1<br>RA7243725.1<br>RA7243725.1<br>RA72118425.1<br>RA72118425.1<br>RA7243725.1<br>RA72118425.1<br>RA7243725.1<br>RA72118425.1<br>RA7243725.1<br>RA7243725.1<br>RA7243725.1<br>RA7243725.1<br>RA7252.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725.1<br>RA725 | TS       TRS-TTSVRTTSA       PAGSINGLISHENDQCGGNDWIG         PYTTSIT       TRTSPT       TRTSSTRIPT       PAGGSSGCISHENDQCGGNDWIG         PTTTIA       PFTTIS-TSARTETSTRIPT       PAGGSSGCISHENDQCGGNDWIG         PTTTIA       PSTRIPTS-TARGETSGCGGGGGGCGCUSHENDQCGGNDWIG         PTTTIA       PSTRIPTS-TRANPT-STANGGGGGGGGGCGCUSHENDQCGGNDWIG         PTTTIA       PSTRIPTS-TSTSPPTS-TPGN-GGGGGGCGCUSHENDQCGGNDWIG         PTTTIA       PSTRIPTSTSTSPPTS-TPGN-GGGGGGGCGCUSHENDQCGGNDWIG         PTTTLAP       TASTITIOPTS-TTANTS-THANT-ATGGGGGGGGCCUSHENDQCGGNDWIG         PTTLAP       STRATSTIOPTS-TTANTS-THANT-ATGGGGGGGCGCUSHENDQCGGNDWIG         PTTLAP       STRATSTINFTSTRIPTS-TP-GCGCGGGCGCUSHENDQCGGNDWIG         PTTTAP       STRATSTINFTSTSTUPTS-TP-GCGCGGGGCGCUSHENDQCGGNDWIG         STTTYSSTUTSSTSTUPTSTSTUPTS-TP-GCGGGGGCUSHENDQCGGNDWIG       TTSSTTPTPTS-TP-GCGGGGCGCUSHENDQCGGNDWIG         STTTYSSTUTSSTUTTSTSTUPTS-TTC-GCGGGGCCUSHENDQCGGNDWIG       PSTTLAPS-STRATSSA-QHTS-T-S-GGGGGGCCUSHENDQCGGNDWIG         PSTTTYST <hlp-sttsstsa-qhts-tfc-gcgggccushendqcggndwig< td="">       PSTTLAPS-STRATSSA-QHTS-TFC-GCGGGGCCUSHENDQCGGNDWIG         PSTTLAPS-TTTSSTSA-SA-STRATSSA-STRATSSA-STRATS-TTC-GCGGGGCCUSHENDQCGGNDWIG       PSTTLAPS-STRATSSA-GHTS-TFC-GCGGGGCCUSHENDQCGGNDWIG         PSTTLAPS-TTTSSTSTSTSTSTSTSTSTSTSTSTSTTTS-TTC-GCGGGCCUSHENDQCGGNDWIG       TTSTVPTS-STRATSSA-GHTS-TTC-GCGGGGCCUSHENDQCGGNDWIG         PSTTLAPS-STRATSSA-STRATS-TTC-GCG</hlp-sttsstsa-qhts-tfc-gcgggccushendqcggndwig<>  | 348<br>355<br>370<br>344<br>355<br>370<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>362<br>363<br>364<br>355<br>354<br>355<br>354<br>355<br>354<br>356<br>353<br>354<br>356<br>353<br>354<br>356<br>356<br>356<br>356<br>356<br>356<br>356<br>357<br>357<br>357<br>357<br>357<br>357<br>357<br>357<br>357<br>357   |

Figure 12. Multiple sequence alignment of endo- $\alpha$ -1,4-polygalactosaminidase from *L. ingoldianus* with its orthologues.

closer look at the alignment of the sequences of the proteins showed that both proteins differ from the rest of their orthologues in terms of the lacking and/or varying amino acid residues at their terminal ends (black box; Figure 12). Although, all these orthologous proteins obviously contain several conserved sequences making up the same domain architectures.

Finally, the BLASTp analysis did not reveal any similar protein sequences that are found on the same strain of species studied. Thus, analysis of paralogous genes embedded within the same genome of *L. ingoldianus* or any fungal species that produce endo  $\alpha$ -1,4 polygalactosaminidase would be an interesting topic for future research.

# Conclusion

This study confirms the translation of an BDR25DRAFT 381691 uncharacterized protein (Accession No.: XP 033540912) from an mRNA (Accession No.: XM 033697727) expressed by an scaffold BDR25scaffold 49 unplaced genomic (Accession No.: NW 022985210). This protein has 370 amino acid residues and is predicted to have a neutral charge and unstable and non-polar characteristics. It consists of a signal peptide, GH114, low complexity, and fCBD Structural characterization regions. and phylogenetic analysis revealed that this protein is an endo- $\alpha$ -1,4-polygalactosaminidase enzyme with unique domain architecture. This protein was also found to contain 36 active sites and was predicted to be secreted extracellularly. Lastly, molecular docking analysis showed that it could bind galactosaminogalactan in its active site much better than Ega3 from A. fumigatus. Suggesting that this enzyme produced by L. ingoldianus could be potentially used for more efficient degradation of biofilms or other polymers composed of galactosaminooligosaccharides. Finally, his endo- $\alpha$ -1,4polygalactosaminidase from L. ingoldianus was found to be closely related to its orthologue from a plant pathogenic fungus Zopfia rhizophila.

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Not Applicable.

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## **Author Contribution**

JGB: Conceptualization, Data curation, Formal analysis, Methodology, Software, Visualization, writing – Original Draft Preparation; MDS: Conceptualization, Methodology, Project Administration, Supervision, Validation, Writing – Review & Editing

## **Conflict of Interest**

The authors declare that they have no known competing financial or non-financial, professional, or personal conflicts that could have appeared to influence the work reported in this paper.

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