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Computational-based structural, functional and phylogenetic analysis of *Enterobacter* phytases

Krishnendu Pramanik¹ · Shreyasi Kundu¹ · Sandipan Banerjee¹ · Pallab Kumar Ghosh¹ · Tushar Kanti Maiti¹

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Abstract

Myo-inositol hexakisphosphate phosphohydrolases (i.e., phytases) are known to be a very important enzyme responsible for solubilization of insoluble phosphates. In the present study, *Enterobacter* phytases have characterized by different phylogenetic, structural and functional parameters using some standard bio-computational tools. Results showed that majority of the *Enterobacter* phytases are acidic in nature as most of the isoelectric points were under 7.0. The aliphatic indices predicted for the selected proteins were below 40 indicating their thermostable nature. The average molecular weight of the proteins was 48 kDa. The lower values of GRAVY of the said proteins implied that they have better interactions with water. Secondary structure predicted 3D structure of *Enterobacter* phytases divulged that the proteins consisted of four monomeric polypeptide chains i.e., it was a tetrameric protein. The predicted tertiary model of *E. aerogenes* (A0A0M3HCJ2) was deposited in Protein Model Database (Acc. No.: PM0080561) for further utilization after a thorough quality check from QMEAN and SAVES server. Functional analysis supported their classification as histidine acid phosphatases. Besides, multiple sequence alignment revealed that "DG–DP–LG" was the most highly conserved residues within the *Enterobacter* phytases. Thus, the present study will be useful in selecting suitable phytase-producing microbe exclusively for using in the animal food industry as a food additive.

Keywords *Enterobacter* spp. \cdot Myo-inositol hexakisphosphate phosphohydrolases \cdot In silico analysis \cdot Histidine phosphatase superfamily \cdot Acidic phytases \cdot Thermostable

Abbreviations

UniProtKB	The Universal Protein Knowledgebase
MEGA	Molecular evolutionary genetics analysis
MW	Molecular weight
pI	Isoelectric point
EC	Extinction coefficient
AI	Aliphatic index
II	Instability index
GRAVY	Grand average of hydropathicities
QMEAN	Qualitative Model Energy ANalysis
SAVES	The structure analysis and verification server

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Tushar Kanti Maiti tkmbu@yahoo.co.in

¹ Microbiology Laboratory, Department of Botany, The University of Burdwan, Purba Bardhaman, West Bengal 713104, India

Introduction

Phytic acid is an indigestible organic form of phosphorus, which is found in cereal grains, legume plants, oilseeds, nuts, tubers and different types of seeds (Nakashima et al. 2007; Greiner and Konietzny 2016). Myo-inositol hexaki-sphosphate phosphohydrolases (i.e., phytases) belong to a subclass of phosphatase enzymes which break down the phytic acid by hydrolyzing the phosphate residues from phytic acid (myo-inositol hexakisphosphate). There are several types of phytases, such as 3-phytase (EC 3.1.3.8), 4-phytase (EC 3.1.3.26) and 5-phytase (EC 3.1.3.72) which are involved in the liberation of P moiety from phytic acid at the position C3, C4 and C5, respectively. These enzymes have a molecular mass between 40 and 70 kDa (Kumar et al. 2010; Afinah et al. 2010).

Ruminant animal utilized phytate through the action of phytases produced by microbial flora in the rumen. The anaerobic gut fungi and bacteria found in the ruminants are responsible for the phytate hydrolysis within the rumen.



The hydrolyzed inorganic phosphate from the phytate is utilized by both the microflora and the ruminant host (Yanke et al. 1998). However, the situation is quite different with monogastric animals such as chicken, swine, fish and birds are not able to utilize phytase phosphorus because they lack phytase-degrading enzymes or lack the insufficient amount of phytases in their digestive tracts (Gupta et al. 2015; Dahiya 2016). Hence, phytate in grains passed through the gastrointestinal tract without being digested properly (Niño-Gómez et al. 2017). Since phosphorus is an essential requirement for bone formation, deficiency of this mineral would cause of osteoporosis, tooth decay, narrow jaws, mental retardation, rickets, etc. (Berlyne et al. 1973). Phytic acid can inhibit the nutrient absorption by the intestine and also prevent the different types of ion uptake such as Zn^{2+} , Ca^{2+} , Mg^{2+} , Cu^{2+} and digestive enzymes such as pepsin, trypsin, amylase, etc. (Gupta et al. 2015). Here, phytic acid acts as an anti-nutritional agent (Escobin-Mopera et al. 2012; El-Toukhy et al. 2013). The phytase catalyzes the hydrolysis of phytic acid and converts the organic and insoluble form of phosphorus to more soluble form and ultimately improve and facilitate intestinal absorption (Wise 1982). Importance of the phytase protein can be evidenced by many earlier workers (Konietzny et al. 1994; Mullaney et al. 2000; He and Honeycutt 2001; Lei et al. 2007, 2013; Rodriguez et al. 2000; Tazisong et al. 2008; Yao et al. 2012; He et al. 2013; Gontia-Mishra and Tiwari 2013; Zajac et al. 2018).

Phytases have been reported in many fungi, e.g., Aspergillus niger (George et al. 2007), Aspergillus fumigatus (Zhang et al. 2007), Peniophora lycii (George et al. 2007), Penicillium simplicissimum (Tseng et al. 2000), Candida krusei (Quan et al. 2002), Debaryomyces castellii (Ragon et al. 2009) and Fusarium oxysporum (Gontia-Mishra et al. 2014). Moreover, a number of gram-positive- and gram-negative bacteria, e.g., Bacillus subtilis (Kerovuo et al. 1998; El-Toukhy et al. 2013), Bacillus licheniformis (Kumar et al. 2014), Pseudomonas spp. (Richardson and Hadobas 1997), Klebsiella pneumoniae (Escobin-Mopera et al. 2012), Klebsiella terrigena (Greiner et al. 1997), Enterobacter sp. (Kalsi et al. 2016), Serratia sp. (Zhang et al. 2011; Kalsi et al. 2016), and Yersinia mollaretii (Shivange et al. 2012) have also been reported earlier to possess this important enzyme.

Phytase enzyme has many beneficial roles in different industries, agriculture, poultry farm, etc. In poultry farm, phytase is used for overcoming the phosphorus deficiency (Elkhalil et al. 2007). Natuphos[®] and Ronozyme[®] are the two commercially available phytases derived from *Aspergillus*, one of the most abundant extracellular producers of phytase (Casey and Walsh 2004). This phytase was actually a recombinant phytase produced by the expression of the phyA gene of *Aspergillus ficuum* in *Aspergillus niger*, first produced in 1994 (Casey and Walsh 2004). However, few studies reported that bacterial phytases were also promising



for commercial phytase production (Konietzny and Greiner 2004; Kalsi et al. 2016; Niño-Gómez et al. 2017). In fact, bacterial phytases are reported to be more beneficial over the fungal phytases due to higher substrate specificity, better catalytic capacity and enhanced resistance to proteolysis (Konietzny and Greiner 2004). In addition, phytase-producing bacteria are known to involve in plant growth promotion also (Singh et al. 2014).

Apart from isolating and characterizing various types of phytases, extensive computational investigations of microbial phytases have been worked out to discover many unexplored features lying within the sequences (Kumar et al. 2012, 2014; Kumar and Agrawal 2014; Gontia-Mishra et al. 2014; Mathew et al. 2014; Verma et al. 2016; Ebrahimi et al. 2016; Niño-Gómez et al. 2017; Pramanik et al. 2018). The outcomes of these studies are biotechnologically advantageous to utilize them in agricultural and industrial perspectives.

This study describes the use of various bio-computational tools to perform the phylogenetic, structural and functional analyses of the phytase enzyme of *Enterobacter* spp. to understand its distinctive properties essential for its industrial application.

Materials and methods

Sequence retrieval and phylogenetic analysis

UniProtKB server is the knowledge base of Swiss Institute of Bioinformatics and a comprehensive source of protein sequences and annotation database (Apweiler et al. 2004). This proteomics-based source server (http://www.unipr ot.org) was used for retrieval of phytase sequences of different spp. of Enterobacter (Gram-negative-, rod-shaped bacteria). For this, Enterobacter aerogenes GN = ASV18 08060 (Protein Acc. no.: A0A0M3HCJ2) was first selected as the query sequence and BLAST search was done. A total of 16 sequences of different spp. of *Enterobacter* were selected (based on highest sequence identity, lowest E-value, maximum query coverage and bit score) and downloaded from UniProtKB in FASTA format for progressing to the computational investigation. Furthermore, the sequences were analyzed phylogenetically to decipher the evolutionary relationship among the selected proteins of interest by using MEGA7 software (Kumar et al. 2016). Percent similarity index within the sequences was calculated by Clustal Omega (https://www.ebi.ac.uk/Tools/msa/clustalo/).

Physiochemical characterization

ExPASy—ProtParam is a tool which is used for the calculation of different physical and chemical parameters for a protein (Gasteiger et al. 2005). This tool (http://www.espas y.org/protparam) was used to calculate physiochemical properties of retrieved sequences. Various computed parameters like amino acid composition, molecular weight (MW), isoelectric point (pI), molar extinction coefficient (EC), aliphatic index (AI), instability index (II) and grand average of hydropathicities (GRAVY) were calculated using this server.

Secondary structure prediction

Secondary structure (alpha-helix, 3₁₀ helix, pi helix, beta bridge, extended strand, beta-turn, bend region, random coil etc.) of a protein refers to the interaction of H-bond donor and acceptor residues of a polypeptide chain. Practically, secondary structural arrangements can be accurately done by nuclear magnetic resonance (NMR) spectroscopy (Meiler and Baker 2003). But some useful and easy computational tools used for in silico prediction of secondary structures of the protein. Here, secondary arrangements were predicted by SOPMA web-based server (Geourjon and Deleage 1995). For this, 16 protein sequences of different *Enterobacter* spp. were analyzed.

Homology protein modeling, its evaluation and submission

Homology 3D protein modeling of selected 16 sequences was performed using Swiss model workspace (Biasini et al. 2014) selecting its suitable and best-matched template. Evaluation of the predicted protein model was done in both QMEAN (Benkert et al. 2009) and SAVES server (http://services.mbi. ucla.edu/SAVES/). Based on the evaluation report the bestbuilt model was finally submitted to Protein Model Database (PMDB) (https://bioinformatics.cineca.it/PMDB/) and the PMDB ID was obtained.

Functional analysis and protein-protein interaction

To find out the functional motifs and superfamily of the protein sequence, Motif Finder (http://www.genome.jp/tools/motif/) was used for the analyses. Highly conserved domains among the sequences were analyzed by Clustal Omega (https://www.ebi.ac.uk/Tools/msa/clustalo/). To know the interaction of *Enterobacter* phytase with other closely associated proteins STRING v10.0 (http://string-db.org/) server was used and functional protein association network was generated.

Results and discussion

Sequence retrieval and phylogenetic analysis

Amino acid sequences of total 16 bacterial strains (Enterobacter kobei GN = ASV01_18150, Enterobacter sp. GN02225 GN = YA53_05950, Enterobacter sp. GN02186 GN = YA50 01625, Enterobacter sp. 35730 GN = SS33_10495, Enterobacter asburiae GN = ABF78_15640, Enterobacter sp. 35699 GN = SS37 20000, Enterobacter sp. 50588862 GN = APT89_19470, Enterobacter hormaechei GN = ASU65_02620, Enterobacter sp. GN02174 GN = YA49 02765, Enterobacter sp. 35027 GN = SS00_18385, Enterobacter sp. GN02616 GN = ABR35_11890, Enterobacter sp. 42324 GN = SS44 19905, Enterobacter sakazakii GN = AFK64_08585, Enterobacter agglomerans, Enterobacter cancerogenus GN = NH00_23800, Enterobacter *aerogenes* $GN = ASV18_{08060}$ were phylogenetically analyzed to predict their evolutionary interrelationship (Fig. 1). Enterobacter aerogenes (A0A0M3HCJ2) clustered only with E. cancerogenus (A0A0A3YJT6) and their closest neighbour is E. agglomerans (F2VRZ7) present in the same clade. Rest of the 13 taxa were in a separate clade showing interrelationships within them. This might be correlated with the percent similarity index of the phytase sequences of the strains with the selected query phytase protein, A0A0M3HCJ2 (Fig. 2). It was found (from the percent similarity index in Clustal Omega) that A0A0M-3HCJ2 showed the highest similarity with A0A0A3YJT6 (68.65%) and F2VRZ7 was next to it (66.43%). These percent similarity indices were also manifested by the closest clustering pattern of these three sequences (Fig. 1). Interestingly, rest 13 sequences showed percent similarity in between 19.46–24.11% with the A0A0M3HCJ2 sequence (Fig. 2). This was the principle reason behind forming a separate clade of 13 taxa from the rest three sequences in the phylogenetic tree of phytase proteins (Fig. 1). From this analysis, it can be interpreted that there might be a correlation among the selected taxa based on their protein sequences. The similar phylogenetic analysis was also made by some earlier workers to decipher the evolutionary significance of different taxa solely based on their protein sequences (Verma et al. 2016; Pramanik et al. 2017a, b, 2018).

Physicochemical characterization

Computational-based analysis about the physicochemical behavior of the proteins gives a theoretical overview of





Fig. 1 Phylogenetic classification of phytase proteins from 16 different Enterobacter spp



Fig. 2 Calculation of percent similarity index of the selected phytase proteins with the query protein (A0A0M3HCJ2)

the nature of the protein. In this study, all the 16 phytase sequences were physicochemically characterized by a number of bio-computational tools (Table 1; Fig. 3). The analysis revealed that the isoelectric point ranges from 5.03 to 8.90 which is said to be a wide range. The isoelectric point of the proteins below the neutral pH can be said to be acidic and above it can be regarded as alkaline. Here, 13 strains showed acid phytases and rest 3 phytases were basic/alkaline in nature. Acid phytases are evident in the work of Zhang et al. (2011) while basic one was reported by Tran et al. (2011) while working on other bacterial phytases. Acid phytases were also evident from



the in silico analysis of Aspergillus niger (Niño-Gómez et al. 2017). Except for the four strains (A0A0W2KF14, F2VRZ7, A0A0A3YJT6 and A0A0M3HCJ2), all strains showed instability index below 40 (Table 1). Thus, the majority of the proteins can be said as stable. Besides, higher ranges of aliphatic index prove the protein as thermostable in nature (Ikai 1980). Thermostable phytase from Enterobacter sp. was reported by Kalsi et al. (2016) which corroborated the present work. Besides higher aliphatic indices were also reported in Aspergillus niger (Niño-Gómez et al. 2017) while working on the prediction study of both 3-phytase A and 3-phytase B. Assuming all pairs of Cys residues form cystines, the molar extinction coefficients were calculated in water at 280 nm. However, EC ranges from 35,535 to $81,275 \text{ M}^{-1} \text{ cm}^{-1}$ (Table 1). The average molecular weight of the proteins is around 48 kDa. The GRAVY, calculated from ExPASy showed very low (Table 1) which implies that the proteins have better interactions with water. This interpretation was also corroborated by the work of Mathew et al. (2014), Verma et al. (2016). Moreover, the strains showed the difference in composition of amino acid residues of their respective proteins as presented graphically in Fig. 3.

Secondary structure prediction

The predicted secondary arrangements of different *Entero*bacter spp. revealed mainly four types of secondary elements which were alpha helices, random coils, extended strands and beta turns (Table 2). The alpha-helical content was the

Table 1	Physicochemical	features of	16	Enterobacter spp.	with	their r	respective	protein and	l gene accession	numbers
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Name of the bacteria	Protein Acc.no.	pI	II	AI	EC	MW	GRAVY
Enterobacter kobei GN=ASV01_18150	A0A0W2KF14	8.90	46.39	87.67	70,275	46.54	- 0.300
Enterobacter sp. GN02225 GN = YA53_05950	A0A0H0DDT8	5.80	22.35	86.15	37,025	48.61	- 0.330
Enterobacter sp. GN02186 GN=YA50_01625	A0A0H0DRS6	5.80	22.35	86.15	37,025	48.61	- 0.330
Enterobacter sp. 35,730 GN=SS33_10495	A0A0F0Y6K0	5.98	22.35	86.15	37,025	48.63	- 0.337
Enterobacter asburiae GN=ABF78_15640	A0A0J0G1R5	5.41	22.80	86.79	37,025	48.54	- 0.300
Enterobacter sp. 35,699 GN=SS37_20000	A0A0F1AJ70	5.51	21.62	87.04	37,025	48.54	- 0.314
Enterobacter sp. 50,588,862 GN=APT89_19470	A0A0V9DZB6	5.70	24.71	87.46	35,535	48.61	- 0.298
Enterobacter hormaechei GN=ASU65_02620	A0A0W2ZA64	5.41	19.74	88.74	37,025	48.63	- 0.287
Enterobacter sp. GN02174 GN=YA49_02765	A0A0H0CJX8	5.40	21.60	89.40	37,025	48.63	- 0.291
Enterobacter sp. 35,027 GN=SS00_18385	A0A0F1GTF1	5.79	23.90	90.07	35,535	48.49	- 0.255
Enterobacter sp. GN02616 GN=ABR35_11890	A0A0J0IC55	5.89	21.85	88.32	37,025	48.65	- 0.304
Enterobacter sp. 42,324 GN=SS44_19905	A0A0F0T849	5.89	21.85	88.32	37,025	48.65	- 0.304
Enterobacter sakazakii GN=AFK64_08585	A0A0K2MR18	5.03	31.44	89.58	38,515	48.84	- 0.338
Enterobacter agglomerans	F2VRZ7	8.42	46.84	92.22	80,245	46.30	- 0.238
Enterobacter cancerogenus GN=NH00_23800	A0A0A3YJT6	6.31	45.44	83.89	81,275	46.78	- 0.260
Enterobacter aerogenes GN=ASV18_08060	A0A0M3HCJ2	8.90	46.39	87.67	70,275	46.54	- 0.300

pI isoelectric point, MW molecular weight, II instability index, AI aliphatic index, EC extinction coefficient, GRAVY grand average of hydropathicity



Fig. 3 Graphical overview of composition difference of amino acids among the selected 16 strains of Enterobacter spp

highest (42.76%) as found in case of *E. aerogenes* (A0A0M-3HCJ2) among all of the *Enterobacter* spp. (Table 2, Suppl. 1). Niño-Gómez et al. (2017) also showed that 43 and 38%

 α -helices were found in the computational investigation of *Aspergillus niger* 3-phytase A and 3-phytase B, respectively. This indicated the thermostable nature of the protein



Tal	olo	e 2	C	Compari	son of	f seconda	arv and	tertiary	protein	structures	among	differe	nt spp.	of	Enterol	bacter

Serial no.	Name of the <i>Entero-</i> bacter spp.	Protein Acc. No.	Contents of elements	principal see	condary struc	Quality assessment of tertiary structure			
			Alpha-helix (%)	Extended strand (%)	Beta-turn (%)	Coil (%)	QMEAN score*	SAVES ERRAT overall quality factor	Amino acids in favoured region in Ramachan- dran plot (%)
1	Enterobacter kobei GN=ASV01_18150	A0A0W2KF14	14.38	30.53	11.95	43.14	- <u>6</u> .46	85.641	83.5
2	Enterobacter sp. GN02225 GN=YA53_05950	A0A0H0DDT8	15.27	29.87	11.95	42.92	- <u>6</u> .46	85.641	83.5
3	Enterobacter sp. GN02186 GN=YA50_01625	A0A0H0DRS6	15.27	29.87	11.95	42.92	-6.46 ©	85.641	83.5
4	Enterobac- ter sp. 35,730 GN=SS33_10495	A0A0F0Y6K0	15.27	29.87	12.39	42.48	-6.46 ©	85.641	83.5
5	Enterobacter asburiae GN=ABF78_15640	A0A0J0G1R5	14.82	32.30	12.83	40.04	-7.02	62.944	83.5
6	Enterobac- ter sp. 35,699 GN=SS37_20000	A0A0F1AJ70	16.59	30.75	12.83	39.82	-7.37 ©	72.959	84.8
7	Enterobacter sp. 50,588,862 GN=APT89_19470	A0A0V9DZB6	14.60	32.30	14.16	38.94	-7.71 ©	82.673	83.5
8	Enterobacter hormaechei GN=ASU65_02620	A0A0W2ZA64	17.48	30.31	12.39	39.82	-7.04	87.864	85.7
9	Enterobacter sp. GN02174 GN=YA49_02765	A0A0H0CJX8	17.92	30.53	12.39	39.16	-6.25 ©	77.885	82.6
10	Enterobac- ter sp. 35,027 GN=SS00_18385	A0A0F1GTF1	17.48	31.19	12.61	38.72	-7.38	72.959	84.8
11	Enterobacter sp. GN02616 GN=ABR35_11890	A0A0J0IC55	18.58	29.65	12.39	39.38	- <u>6.66</u>	78.218	82.2
12	Enterobac- ter sp. 42,324 GN=SS44_19905	A0A0F0T849	18.58	29.65	12.39	39.38	- <u>6.</u> 67	78.818	82.6
13	Enterobacter sakazakii GN=AFK64_08585	A0A0K2MR18	18.18	26.16	11.75	43.90	-6.11 ©	71.707	85.6
14	Enterobacter agglo- merans	F2VRZ7	39.95	15.55	9.57	34.93	0.32	96.026	96.1
15	Enterobacter cancerogenus GN=NH00_23800	A0A0A3YJT6	41.22	13.82	8.20	36.77	- <u>6</u> .67	87.080	94.9
16	Enterobac- ter aerogenes GN=ASV18_08060	A0A0M3HCJ2	42.76	11.16	8.79	37.29	0.25 1	96.141	97.9

* 🔥 indicates acceptable QMEAN score; 📭 indicates not-acceptable QMEAN score

as Kumar et al. (1999) indicated that α -helical conformations are abundant in case of thermophiles to withstand high temperatures. These types of structural findings were also performed by a number of bioinformatics researchers. A similar prediction of secondary structures of the residual interactions of *Aspergillus fumigatus* phytase was done by



Zhang et al. (2007) and *Bacillus* phytases were done by Verma et al. (2016).

Homology protein modeling, its evaluation and submission

Although homology modeling was performed for all 16 proteins (Suppl. 1), Enterobacter aerogenes (A0A0M-3HCJ2) was selected as representative species (Fig. 4) to elucidate phytase protein structure of Enterobacter spp. based on QMEAN score, an overall quality factor from SAVES server and Ramachandran plot (Table 2, Suppl. 2). The predicted 3D protein modeling of Enterobacter aerogenes (A0A0M3HCJ2) divulged that the protein consisted of four monomeric polypeptide chains, i.e., it was a tetrameric protein (Fig. 4a). This structural finding was also corroborated by some earlier reports. Ragon et al. (2009) reported tetrameric phytase in fungal species-Debaryomyces castellii CBS 2923 and Shivange et al. (2012) reported in the bacterium-Yersinia mollaretii. Helix, sheet and loops are differentially coloured and presented in Fig. 4b. Besides distinct disulfide bridges were demarked as green spherical (s) in Fig. 4b. These disulfide bridges which are formed by the oxidation of thiol groups of the cystine residues (Trivedi et al. 2009) are one of the factors for the stability of a protein (Cheng et al. 2007). After the construction of 3D (.pdb) model, the evaluation and quality estimation of the model was performed (Table 2, Suppl. 2-3) and Ramachandran plot was built to show the positions allocated for each amino acid residues (Table 2, Suppl. 2). Analysis of Ramachandran plot for the PDB structure of E. aerogenes (A0A0M3HCJ2) protein showed that 97.9% residues were present in the most favoured region (Table 2, Suppl. 2). Presence of more than 90% residues in the favoured region of Ramachandran plot is the characteristics of the good quality model (Yadav et al. 2013). QMEAN4, QMEAN6 and Z-score calculated were 0.25, -0.26 and <1, respectively (Table 2, Suppl. 2). The desirable QMEAN scores and Z-score should be within 0-1 (Berman et al. 2000) and <1 Benkert et al. (2009), respectively, in comparison with a non-redundant set of PDB structures to obtain a high-quality model. Moreover, the overall quality factor by the SAVES ERRAT was 96.141% (i.e., >95%) (Suppl. 3). A good, high-resolution structure should score 95% or higher as an overall quality factor (Benkert et al. 2009). However, comprehensive evaluation of the predicted model proves to be a higher resolution model (> 3 Å) as determined by both QMEAN (Table 2, Suppl. 2) and SAVES server (Table 2, Suppl. 3). A similar type of model validation was also conducted by Pramanik et al. (2018) while working with *Klebsiella* phytases. Finally, the model (in .pdb format) was deposited in PMDB database and its accession number obtained is PM0080561 and the said model can be retrieved for any further investigations in future.



Fig. 4 Predicted 3D model structure of phytase of *Enterobacter aerogenes* (A0A0M3HCJ2) viewed by PyMol: **a** showing four distinct chains of the protein. **b** Tertiary structure showing prominent second-

ary elements and disulfides (red=helix, yellow=sheet, green=loop, green balls=disulfides)



Functional analysis and protein-protein interaction

From the functional analyses of the proteins, mainly two conserved motifs, i.e., His_Phos_1 and His_Phos_2 were found (Suppl. 4) both of which belong to the Histidine phosphatase superfamily (Suppl. 4). This superfamily is a vast functionally diverse group of proteins consisting of two clades sharing a finite sequence similarity (Rigden 2008). The multiple sequence alignment among all the 16 phytase protein sequences identified several fully

AØAØK2MR18	MKIKPLTLVFAALFPLCSLAAAPQVERYVVTFPQEDHVVYSGNYASAFPNG
AØAØHØCJX8	MKRKIIPVLIGCVLSFSALAAQPTAERYVVSFPEGTHVNYTGAFASAFPNG
A0A0J0IC55	MKRKIIPVLIGCVLSESALAAOPTAERYVVSEPEGTHVNYTGAFASAEPNG
A0A0E0T849	MKRKTTPVI TGCVI SESALAAOPTAERVA/SEREGTHVNVTGAEASAERNG
A0A0101040	
AUAUWZZA04	PIKEKIIPVLIGCALSFSGLAAQPTACKTIVSFPDASHVKTSGAFADAFPNG
AØAØF1GTF1	MKRKIIPVLIGCALSFSGLAAQPTAERYVVTFPEGSHIKYSGAFASAFPNG
AØAØV9DZB6	MKRKIIPVLIGCTLSFSGLAAQPTAEHYVVSFPDGSHVKYSGAFAGAFPNG
AØAØF1AJ70	MKRKIIPALIGCALSESGLAAOPTAERYVVSEPDGSHVKYSGAFADAEPNG
A0A0106185	MKRKTTPVI TGCTI SESGI AAOPTAERXW/SEPEGSHVSVSGAFASAERDG
AGAGGOVEKO	
AUAUFUTOKU	PIKEKIIPVLVQCALSFSQLAAQPTAEKTVVSFPEQSRVWTSQAFASAFPWQ
AØAØW2KFI4	MKRKIIPVLVGCAFSFSGLAAQPTAERYVVSFPEGSHVNYSGAFASAFPNG
AØAØHØDDT8	MKRKIIPVLVGCALSFSGLAAQPTAERYVVSFPEGSHVNYSGAFASAFPNG
AØAØHØDRS6	MKRKIIPVLVGCALSFSGLAAOPTAERYVVSFPEGSHVNYSGAFASAFPNG
E21/R77	MTLPGLVRCALTESELWE-ESPASOAADVOLEKWEESRHGVRPPTPGNR
1201027	
AGAGADYOTC	
AUAUA3YJI6	MNACKNQINA-GLLIAGILMMSASPAHAEAQYQLEKVVELSKHGIKPPIPGNK
	* *
AØAØK2MR18	LPVGVGSGLLELRKEGDDLTEATVTDRGPNADSPKMGKOESKTEASPEYTPLMMTTRVSK
A0A0H0C1X8	L PVGTGSGL L ETGVOGDAL TEATTTDDGDNADSDVVGVNEAVTEVTDDEADL LMTTDVON
AGAGIOCIAG	L POLOSOCI I DECKOCOAL TEATITORCHIMOSEN/UCKNEAKTEVTEDEAPLLI'I I NVUM
AGAGIGIC22	LE VOTO SOLLE LORQUDAL LEATTID KOPNAD SPKVGKNEAKTEV TPDEAPLLMTTRVQN
AØAØFØT849	LPVGIGSGLLFTGKQGDALTFATITDRGPNADSPKVGKNEAKIFVTPDFAPLLMTIRVQN
AØAØW2ZA64	LPVGMGSGLLFTGKQGDALTFATVTDRGPNADSPKMGKNDAKIFVTPDFAPLLMTIRVON
AØAØF1GTF1	LPVGIGSGLLFTGKOGDALTFATVTDRGPNADSPKMGKNDAKIEVTPDFAPLIMTTRVON
4040V9D786	I PVGTGSGLI ETGKOGDAL TEATVTDRGDNADADVMGVMEAVTEVTDGEADLI MTTRVOM
A0A0V30200	L POLOSOCI I DECKOCOAL TEATUTOROFINADAD ADVACANEANTENTEDESADI UNTERVIDA
AGAGE TAT 10	LE VOTO SOLLE TO KUODALTEATVID KOPNADAPKMGKNEAKTEVTPDEAPLLMTIRVQN
A0A0J0G1R5	LPVGIGSGLLFTGKQGDTLTFATVTDRGPNADAPKMGKNEAKIFVTPDFAPLLMTIRVQN
AØAØFØY6KØ	LPVGIGSGLLFTGKQGDALTFATVTDRGPNADAPKMGKNEAKIFVTPDFAPLLMTIRVQN
AØAØW2KFI4	LPVGIGSGLLFTGKOGDALTFATVTDRGPNADAPKMGKNEAKIFVTPDFAPLLMTIRVON
AAAAHADDTS	L PVGTGSGL L ETGKOGDAL TEATVTDPGPNADAPKMGKNEAKTEVTPDEADL L MTTPVON
AGAGHODDIG	LEVOLOSOLLET CKOCEAL TEATOTERCENADARKINGKNEAKTEVTEDEADLENTTENON
AUAUHUDKSO	LPVGIGSGLLFIGKQGDALIFATVIDKGPNADAPKMGKNEAKIFVIPDFAPLLPHIKVQN
F2VRZ7	
AØAØM3HCJ2	
AØAØA3YJT6	
A0A0A3YJT6	
A0A0A3YJT6	
AØAØA3YJT6 AØAØK2MR18	DQAQASDPMPLHDDKGNISGLPLPAGLIGATNELALNDALQTLTGDKRGLDTEGITPDGK
A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8	DQAQASDPMPLHDDKGNISGLPLPAGLIGATNELALNDALQTLTGDKRGLDTEGITPDGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK
A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A0J0IC55	DQAQASDPMPLHDDKGNISGLPLPAGLIGATNELALNDALQTLTGDKRGLDTEGITPDGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK
A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A0J0IC55 A0A0F0T849	DQAQASDPMPLHDDKGNISGLPLPAGLIGATNELALNDALQTLTGDKRGLDTEGITPOGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPOGK
A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A0J0IC55 A0A0F0T849 A0A0W2ZA64	DQAQASDPMPLHDDKGNISGLPLPAGLIGATNELALNDALQTLTGDKRGLDTEGITPDGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEXVDARPLHDDKGAINGLPLESDVIGSTNEVALSDTLKRLKGDNRGLDTEGITPDGK
A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A0J0IC55 A0A0F0T849 A0A0F0T849 A0A0F0T6TE1	DQAQASDPMPLHDDKGNISGLPLPAGLIGATNELALNDALQTLTGDKRGLDTEGITPDGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKVLKGDNRGLDTEGITPOGK
A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A0J0IC55 A0A0F0T849 A0A0F0T849 A0A0F1GTF1 A0A0F1GTF1	DQAQASDPMPLHDDKGNISGLPLPAGLIGATNELALNDALQTLTGDKRGLDTEGITPOGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVALSDTLKVLKGDNRGLDTEGITPOGK GKAEVDARPLHDDKGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPOGK
A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A0H0CJX8 A0A0J0IC55 A0A0F0T849 A0A0H0ZA64 A0A0F1GTF1 A0A0V9DZB6	DQAQASDPMPLHDDKGNISGLPLPAGLIGATNELALNDALQTLTGDKRGLDTEGITPDGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLGSGVIGSTNEVAFSDTLKLKKDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLGSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLGSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPOGK
A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A0J0IC55 A0A0F0T849 A0A0W2ZA64 A0A0W2ZA64 A0A0F1GTF1 A0A0Y9DZB6 A0A0F1AJ70	DQAQASDPMPLHDDKGNISGLPLPAGLIGATNELALNDALQTLTGDKRGLDTEGITPOGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVALSDTLKRLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK
A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A0H0CJX8 A0A09J0IC55 A0A0F07849 A0A0W2ZA64 A0A0F1GTF1 A0A0V9D286 A0A0F1AJ70 A0A090G1R5	DQAQASDPMPLHDDKGNISGLPLPAGLIGATNELALNDALQTLTGDKRGLDTEGITPDGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEAVDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK
A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A090IC55 A0A0F0T849 A0A0WIZZA64 A0A0F1GTF1 A0A0V9DZ86 A0A0F1AJ70 A0A090Z185 A0A0FY6K0	DQAQASDPMPLHDDKGNISGLPLPAGLIGATNELALNDALQTLTGDKRGLDTEGITPOGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK
A0A0A3YJT6 A0A0K2MR18 A0A040CJX8 A0A0301C55 A0A0F0T849 A0A0F0T849 A0A0F1GTF1 A0A0F0T864 A0A0F1GTF1 A0A0902D86 A0A096185 A0A096185 A0A096V6K0 A0A09V6K714	DQAQASDPMPLHDDXGNISGLPLPAGLIGATNELALNDALQTLTGDXRGLDTEGITPDGX GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEANDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEANDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEANDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEANDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX
A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A00J0IC55 A0A0F0T849 A0A0WIZZA64 A0A0F1GTF1 A0A0V9DZ86 A0A0F1AJ70 A0A090CIR5 A0A0F1X770 A0A090Y6K0 A0A0WZKT14 A0A0H0DT8	DQAQASDPMPLHDDKGNISGLPLPAGLIGATNELALNDALQTLTGDKRGLDTEGITPDGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEANDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEANDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEANDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEANDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEANDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEANDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEANDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK
A0A0A3YJT6 A0A0K2MR18 A0A040CJX8 A0A0301C55 A0A0F0T849 A0A0401C55 A0A0F0T849 A0A04F1GTF1 A0A049D2B6 A0A0F1AJ70 A0A030G1R5 A0A0F0Y6K0 A0A0402KF14 A0A0402KF14 A0A0402KF14	DQAQASDPMPLHDDXGNISGLPLPAGLIGATNELALNDALQTLTGDXRGLDTEGITPDGX GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAPSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAPSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLCSDVIGSTNEVAPSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEAVDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEANDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEANDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEANDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARDLDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX
A0A0A3YJT6 A0A0K2/MR18 A0A0H0CJX8 A0A0301C55 A0A0F0T849 A0A0F1C55 A0A0F1TF1 A0A0YDZ86 A0A0F1AJ70 A0A0Y0DZ86 A0A0F1AJ70 A0A090C1R5 A0A0F0Y6K0 A0A0H0CR56 C3/072	DQAQASDPMPLHDDKGNISGLPLPAGLIGATNELALNDALQTLTGDKRGLDTEGITPDGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEANDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEANDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEANDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEATDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEATDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEATDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEATDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEATDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK
A0A0A3YJT6 A0A0K2MR18 A0A040CJX8 A0A0401C55 A0A0F0T849 A0A0401C55 A0A0F0T849 A0A0401C751 A0A040702064 A0A04014770 A0A090C185 A0A0400078 A0A0400078 A0A0400078 F2VR27	DQAQASDPMPLHDDKGNISGLPLPAGLIGATNELALNDALQTLTGDKRGLDTEGITPOGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK
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A0A0A3YJT6 A0A0K2MR18 A0A040EJX8 A0A040EIX55 A0A0F0T849 A0A04012C55 A0A0F0T849 A0A04F1476 A0A04F1476 A0A04F1476 A0A0F1476 A0A0F0456 A0A0F0456 A0A0F0456 F2VR27 A0A08056 F2VR27 A0A0843VJT6	DQAQASDPMPLHDDKGNISGLPLPAGLIGATNELALNDALQTLTGDKRGLDTEGITPOGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPOGK GKAEAIDARPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPOGK GKAEAIDARAPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPOGK GKAEAIDARAPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPOGK GKAEAIDARAPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPOGK GKAEAIDARAPLHDDKGEINGLPLCSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPOGK GKAEAIDARAPLHDDKGEINGLPLCSGUIGSTNEVARAIDTEGLTGHGVAAVAN
A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A0301C55 A0A0F0T849 A0A0F0T849 A0A0F16TF1 A0A0F16TF1 A0A0F1AJ70 A0A0F076K0 A0A0F076K0 A0A0H0DR56 F2VR27 A0A0H0DR56 F2VR27 A0A0M3HCJ2 A0A0A3YJT6	DQAQASDPMPLHDDXGNISGLPLPAGLIGATNELALNDALQTLTGDXRGLDTEGITPDGX GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAFSDTLXRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGINGLPLESDVIGSTNEVAFSDTLXRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLXVLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLXVLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLXVLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLKGDNRGLDTEGITPDGX GKAEAADARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLKGDNRGLDTEGITPDGX GKAEAADARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLKGDNRGLDTEGITPDGX GKAEAADARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLKGDNRGLDTEGITPDGX GKAEAADARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLKGDNRGLTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLKGDNRGLTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLKGDNRGLTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLXGNRGLTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLXGNRGLTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLXGNRGLTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLXGNRGLTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLXGNRGLTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLXGNRGLTEGITPDGX CKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLXTLXGNRGLTGATGYAAVNN CKEI CONGAUAAT
A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A030IC55 A0A0F0T849 A0A0W2ZA64 A0A0F1GTF1 A0A0V9DZB6 A0A0F1AJ70 A0A09DZB6 A0A0F1AJ70 A0A09CK0 A0A0W2KF14 A0A0H0DT86 F2VRZ7 A0A0H0DT86 F2VRZ7 A0A0A3YJT6	DQAQASDPMPLHDDKGNISGLPLPAGLIGATNELALNDALQTLTGDKRGLDTEGITPDGK GKAEAIDARPLHDDKGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEAADARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK MAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK MAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK MAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK MAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK MAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK MAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK MAEAIDARPLHDDKGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK MAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGK MAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGK MAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGK MAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGK MAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGK MAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPGK MAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTGEITPGK MAEAIDARPLHDDXGEINGLPLGSGVIGSTNEVAFSDTLKTLKGDNRGLTGEITGGVAAVNN MAEANANGANANANANANANANANANANANANANANANANA
A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A0301C55 A0A0F0T849 A0A0F0T849 A0A0F1GTF1 A0A0F1GTF1 A0A0F1GTF1 A0A0F076K0 A0A0F076K0 A0A0F076K0 A0A0H0DT8 A0A0A0H0DT8 A0	DQAQASDPMPLHDDXGNISGLPLPAGLIGATNELALNDALQTLTGDXRGLDTEGITPDGX GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPGGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTGGTPGXAVXN * * * * * * * * * * * * * * * * * * *
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A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A0301C55 A0A0F0T849 A0A0F0T849 A0A0F0T849 A0A0F0T847 A0A0F0T847 A0A0F076K0 A0A0F076K0 A0A0F076K0 A0A0F076K0 A0A0H0DT8 A0A	DQAQASDPMPLHDDXGNISGLPLPAGLIGATNELALNDALQTLTGDXRGLDTEGITPDGK GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAPSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGINGLPLESDVIGSTNEVAPSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLGSGVIGSTNEVAPSDTLKTLKGDNRGLTGHGTVAAVAN * * * * * * * * * * * * * * * * * * *
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A0A0A3YJT6 A0A0K2/MR18 A0A0H0CJX8 A0A0301C55 A0A0F0T849 A0A0F1C55 A0A0F0T849 A0A0F1C55 A0A0F1C55 A0A0F1C55 A0A0F1AJ70 A0A04002186 A0A0400786 F2VR27 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0CJX8 A0A00H0CJX8 A0A00H0CJX8 A0A00H0CJX8 A0A00H0CJX8 A0A00H0CJX8 A0A00H0CJX8	DQAQASDPMPLHDDXGNISGLPLPAGLIGATNELALNDALQTLTGDXRGLDTEGITPDGX GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GGVHLCDEVGPFIINDSGXILAHGPQAAEGEKAIAGGLPNILKURQNRGFEGLTRM GGVHLCDEVGPFIINIDSKGXILAIHGPQAAEGEKAIAGGLPNILKURQNRGFEGLTRM GGVHLCDEVGPFIINIDSKGXILAIHGPQAAEGEKAIAGGLPNILKURQANNGFEGLTRM GGVHLCDEVGPFIINIDSKGXILAIHGPQAAEGEKAIAGGLPNILKURQANNGFEGLTRM GGVHLCDEVGPFIINIDSKGXILAIHGPQAAEGEKAIAGGLPNILKURQANNGFEGLTRM GGVHLCDEVGPFIINIDSKGXILAIHGPQAAEGEKAIAGGLPNILKURQANNGFEGLTRM
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A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A0301C55 A0A0F0T849 A0A09D1C55 A0A0F0T849 A0A09D1256 A0A0F1AJ70 A0A09D256 A0A0F1AJ70 A0A0902155 A0A0F0Y6K0 A0A0W2KF14 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0CJX8 A0A0H0CJX8 A0A0H0CJX8 A0A0F1GTF1 A0A0A0F1GTF1 A0A0A0F1GTF1	DQAQASDPMPLHDDXGNISGLPLPAGLIGATNELALNDALQTLTGDXRGLDTEGITPDGX GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLTEGITPDGX GGYWLLDEVGPFIINIDSXKILAIHGPQAAEGEXAIAGGLPNILKWRQANRGFEGITRM GGYWLLDEVGPFIINIDSXKILAIHGPQAAEGEXAIAGGLPNILKWRQANRGFEGITRM GGYWLLDEVGPFIINIDSXKILAIHGPQAAEGEXAIAGGLPNILKWRQANRGFEGITRM GGYWLLDEVGPFIINIDSXKILAIHGPQAAEGEXAIAGGLPNILKWRQANRGFEGITRM GGYWLLDEVGPFIINIDSXKILAIHGPQAAEGEXAIAGGLPNILKWRQANRGFEGITRM GGYWLLDEVGPFIINIDSXKILAIHGPQAAEGEXAIAGGLPNILKWRQANRGFEGITRM
A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A0301C55 A0A0F0T849 A0A0401C155 A0A0F0T849 A0A0401C151 A0A0401256 A0A0F1A70 A0A030G1R5 A0A0F0Y6K0 A0A0402056 F2VR27 A0A040DR56 F2VR27 A0A040DR56 F2VR27 A0A0400DR56 F2VR27 A0A04055 A0A0610255 A0A040CJX8 A0A040755 A0A040755 A0A040755 A0A047151 A0A04757 A0A0757 A0A0757 A0A0757 A0A0757 A0A0757 A0A0757 A0A0757 A0A0757 A0A0757 A0A0757 A0A0757 A0A0757 A0A0757 A0A0757 A0A0757 A0A0757 A0A0757 A0A07577 A0A07577 A0A07577 A0A075777 A0A075777 A0A07577777 A0A0757777777777	DQAQASDPMPLHDDXGNISGLPLPAGLIGATNELALNDALQTLTGDXRGLDTEGITPDGK GKAEATDARPLHDDXGAINGLPLESDVIGSTNEVAPSDTLKRLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGBINGLPLESDVIGSTNEVAPSDTLKRLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKRLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGK GKAEATDARPLHDDXGEIXLAIHGPQAAEGEKAIAGGLPNILKHRQANRGFEGLTRM GGYWLCDEVGPFLINIDSKGXTLAIHGPQAAEGEKAIAGGLPNILKWRQANRGFEGLTRM GGYWLCDEVGPFLINIDSKGXTLAIHGPQAAEGEKSIAGGLPNILKWRQANRGFEGLTRM GGFWLLCDEVGPFLINNDSKGXTLAIHGPQAAEGEKSIAGGLPNILKWRQANRGFEGLTRM GGFWLCDEVGPFLINNDSKGXTLAIHGPQAAEGEKSIAGGLPNIXKWRQANRGFEGLTRM GGFWLCDEVGPFLINNDSKGXTLAIHGPQAAEGEKSIAGGLPNIXKWRQANRGFEGLTRM
A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A0301C55 A0A0F0T849 A0A0912C55 A0A0F0T849 A0A09702B6 A0A0F1AJ70 A0A0902B6 A0A0F0Y6K0 A0A0002KF14 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0T84 A0A0	DQAQASDPMPLHDDXGNISGLPLPAGLIGATNELALNDALQTLTGDXRGLDTEGITPDGX GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGX GGVBLCDEVGPFLINIDSKGXILAIHGPQAAEGEKAIAGGLPNILKMRQNNGFEGITRM GGYWLCDEVGPFLINIDSKGXILAIHGPQAAEGEKAIAGGLPNILKMRQANNGFEGITRM GGYWLCDEVGPFLINIDSKGXILAIHGPQAAEGEKAIAGGLPNILKMRQANNGFEGITRM GGYWLCDEVGPFLINIDSKGXILAIHGPQAAEGEKAIAGGLPNILKMRQANNGFEGITRM GGYWLCDEVGPFLINIDSKGXILAIHGPQAAEGEKAIAGGLPNILKMRQANNGFEGITRM GGYWLCDEVGPFLINIDSKGXILAIHGPQAAEGEKAIAGGLPNILKMRQANNGFEGITRM GGYWLCDEVGPFLINIDSKGXILAIHGPQAAEGEKAIAGGLPNIKKMRQANNGFEGITRM GGYWLCDEVGPFLINIDSKGXILAIHGPQAAEGEKAIAGGLPNIKKMRQANNGFEGITRM GGYWLCDEVGPFLINIDSKGXILAIHGPQAAEGEKSIAGGLPNIKKMRQANNGFEGITRM
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A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A0301C55 A0A0F0T849 A0A0870T849 A0A08716TF1 A0A0F16TF1 A0A0F16TF1 A0A0F16J70 A0A0F1070 A0A0F076K0 A0A00K2KF14 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0T55 A0A0A155 A0A0F16TF1 A0A040CJX8 A0A0F16TF1 A0A0407266 A0A0F1AJ70 A0A09C155 A0A0761549 A0A09C155 A0A0761549 A0A09C155 A0A07655 A0A07755 A0A075555 A0A075555 A0A075555 A0A075555 A0A075555 A0A075555 A0A075555 A0A075555 A0A075555 A0A075555 A0A075555 A0A075555 A0A075555 A0A075555 A0A0755555 A0A07555555 A0A075555555555	DQAQASDPMPLHDDXGNISGLPLPAGLIGATNELALNDALQTLTGDXRGLDTEGITPDGK GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAPSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGINGLPLESDVIGSTNEVAPSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKVLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKTLKGDNRGLTEGITPDGK GGVWLCDEVGPFLINIDSKKILAIHGPQAAEGEKAIAGGLPNILKWRQANRGFEGITRM GGVWLCDEVGPFLINIDSKKKILAIHGPQAAEGEKAIAGGLPNILKWRQANRGFEGITRM GGVWLCDEVGPFLINIDSKKKILAIHGPQAAEGEKAIAGGLPNILKWRQANRGFEGITRM GGVWLCDEVGPFLINIDSKKILAIHGPQAAEGEKSIAGGLPNIKKRQANRGFEGITRM GGVWLCDEVGPFLINNDSKKILAIHGPQAAEGEKSIAGGLPNIKKRQANRGFEGITRM GGVWLCDEVGPFLINNDSKKILAIHGPQAAEGEKSIAGGLPNIKKRQANRGFEGITRM GGVWLCDEVGPFLINNDSKKILAIHGPQAAEGEKSIAGGLPNIKKRQANRGFEGITRM GGVWLCDEVGPFLINNDSKKILAIHGPQAAEGEKSIAGGLPNIKKRQANRGFEGITRM GGVWLCDEVGPFLINNDSKKILAIHGPQAAEGEKSIAGGLPNIKKRQANRGFEGITRM GGVWLCDEVGPFLINNDSKKILAIHGPQAAEGEKSIAGGLPNIKKRQANRGFEGITRM GGVWLCDEVGPFLINNDSKKILAIHGPQAAEGEKSIAGGLPNIKKRQANRGFEGIT
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A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A0301C55 A0A0F0T849 A0A0301C55 A0A0F0T849 A0A0401C751 A0A0471471 A0A0471471 A0A04756 A0A047147 A0A04774 A0A04774 A0A04774 A0A04774 A0A04774 A0A04774 A0A04775	DQAQASDPMPLHDDXGNISGLPLPAGLIGATNELALNDALQTLTGDXRGLDTEGITPDGX GKAEATDARPLHDDXGAINGLPLESDVIGSTNEVAPSDTLKRLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGAINGLPLESDVIGSTNEVAPSDTLKRLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKRLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKRLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKRLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKRLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKRLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGX GKAEATDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLTGHGYAAVNN * * * * * * * * * * * * * * * * * * *
A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A03J01C55 A0A0F0T849 A0A03J01C55 A0A0F0T849 A0A0A012TF1 A0A049D2B6 A0A049D2B6 A0A049D2B6 A0A0402515 A0A040D256 A0A040D256 A0A040D256 A0A04002X8 A0A040002X8 A0A040000X8 A0A040000X8 A0A040000X8 A0A04000X8 A0A04000X8 A0A04000X8 A0A04000X8 A0A04000X8 A0A04000X8 A0A04000X8 A0A04000X8 A0A04000X8 A0A04000X8 A0A0400X8 A0A0400X8 A0A0400X8 A0A0400X8 A0A00X8 A0000X8 A0A000X8 A0A000X8 A0A00X8 A0000X8 A00	DQAQASDPMPLHDDXGNISGLPLPAGLIGATNELALNDALQTLTGDXRGLDTEGITPDGK GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAPSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAPSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKRLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVALSDTLKLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGLDTEGITPDGK GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAPSDTLKTLKGDNRGEITRDGK GGVMLCDEVGPFLINIDSKGKILAIHGPQAAEGEKAIAGGLPNILKMRQANRGFEGITRM GGVMLCDEVGPFLINIDSKGKILAIHGPQAAEGEKSIAGGLPNILKMRQANRGFEGITRM GGVMLCDEVGPFLINIDSKGKILAIHGPQAAEGEKSIAGGLPNILKMRQANRGFEGITRM GGVMLCDEVGPFLINNDSKGKILAIHGPQAAEGEKSIAGGLPNIKKMRQANRGFEGITRM GGVMLCDEVGPFLINNDSKGKILAIHGPQAAEGEKSIAGGLPNIKKMRQNNRGFEGITRM GGVMLCDEVGPFLINNDSKGKILAIHGPQAAEGEKSIAGGLPNIKKMRQNNRGFEGITRM GGVMLCDEVGPFLINNDSKGKILAIHGPQAAEGEKSIAGGLPNIKKMRQNNRGFEGITRM GGVMLCDEVGPFLINNDSKGKILAIHGPQAAEGEKSIAGGLPNIKKMRQNNRGFEGITRM GGVMLCDEVGPFLINNDSKGKILAIHGPQAAEGEKSIAG
A0A0A3YJT6 A0A0K2MR18 A0A0H0CJX8 A0A030EC55 A0A0F0T849 A0A030EC55 A0A0F0T849 A0A040EC75 A0A0F0T849 A0A040276 A0A040276 A0A040276 A0A0402018 A0A0402018 A0A0402018 A0A0402018 A0A0402018 A0A040275 A0A00275 A000275 A0A00275 A0A00275 A	DQAQASDPMPLHDDXGNISGLPLPAGLIGATNELALNDALQTLTGDXRGLDTEGITPDGX GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGAINGLPLESDVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKRLKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GKAEAIDARPLHDDXGEINGLPLQSGVIGSTNEVAFSDTLKILKGDNRGLDTEGITPDGX GGVULCDEVGPFLINIDSXGXILAIHGPQAAEGEXAIAGGLPNILKMRQANRGFEGITRM GGVULCDEVGPFLINIDSXGXILAIHGPQAAEGEXAIAGGLPNILKMRQANRGFEGITRM GGVULCDEVGPFLINIDSXGXILAIHGPQAAEGEXAIAGGLPNILKMRQANRGFEGITRM GGVULCDEVGPFLINIDSXGXILAIHGPQAAEGEXSIAGGLPNIXKMRQANRGFEGITRM GGVULCDEVGPFLINIDSXGXILAIHGPQAAEGEXSIAGGLPNIXKMRQANRGFEGITRM GGVULCDEVGPFLINIDSXGXILAIHGPQAAEGEXSIAGGLPNIXKMRQANRGFEGITRM GGVULCDEVGPFLINIDSXGXILAIHGPQAAEGEXSIAGGLPNIXKMRQANRGFEGITRM GGVULCDEVGPFLINIDSXGXILAIHGPQAAEGEXSIAGGLPNIXKMRQANRGFEGITRM GGVULCDEVGPFLINIDSXGXILAIHGPQAAEGEXSIAGGLPNIXKMRQANRGFEGITRM GGVULCDEVGPFLINIDSXGXILAIHGPQAAEGEXSIAGGLPNIXKMRQANRGFEGITRM GGVULCDEVGPFLINIDSXGXILAIHGPQAAEGEXSIAGGLPNIXKMRQANRGFEGITRM GGVULCDEVGPFLINIDSXGXILAIHGPQAAEGEXSIAGGLPNIXKMRQANRGFEGITRM GGVULCDEVGPFLINIDSXGXILAIHGPQAAEG

conserved amino acid residues (marked as * in Fig. 5) among which "DG–DP–LG" sequence was found to be the highly conserved sequences (Fig. 5). Similarly, Niño-Gómez et al. (2017) while working with 3-Phytase A and 3-Phytase B from *Aspergillus niger* found that RHGXRXP-HD were the highly conserved sequences as revealed from the multiple sequence alignment study. In addition, the protein–protein interaction network produced through STRING server depicted that the query protein interacts with ten different proteins directly or

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AØAØK2MR18	PDGRIIAAVOSTLDI	DGKTKNTAR	FTRLVSR	IDPATG	KTAMYGYPIE	DIDVYKKAKDAK
10100001778	PDGPTTA/WOSTLDT	DEVENUENT	ETDIVCC	DDACG	VTAMVGVDT	
AGAGHOCIXO	PUGKTIAAVQSTEDI	DURUKKKAL	FIREVSI	UP ADO	KIAPITOTP11	JOHAT DRIIDUAR
A0A0J0IC55	PDGRIIAAVQSTLDI	DGKSKKKAL	FTRLVSF	DPASG	KTAMYGYPIE	DSAAYSKNSDAK
1010E0T840	PDGPTTAAVOSTI DT	DEVENUAL	FTDIVSP	nphse	TAMVGVDT	NEAAVSEVISDAV
A0A0101045	P DOMITIANY OST COL	DURDRINGE	TINE VOI	0100	CIACITATI LL	JORATOKIODAK
AØAØW2ZA64	PDGRIIAAVQSTLDI	DGKSKKQAL	FTRLVSH	DPATG	KTAMYGYPVL	JSAAYSKNSDAK
A0A0E1GTE1	PDGRTTAAVOSTLDT	DGKSKKOAL	ETRLVSE	DPATG	KTAMVGVPT	DSAAVSKNSDAK
AGAGI IGTI I	- Built I Antigot Los	our sintere	1112 123			
A0A0V9D2B6	PDGRIIAAVQSTLDI	DGKSKNQAL	FIRLVSP	DPAIG	KTAPIYGYPIL	JSAAYSKNSDAK
4040F14170	PDGRTTAAVOSTLDT	DGKSKKOAL	ETRLVSE	DPATG	KTAMVGVPT	
AGAGI 1AG70	1 DONTIANTOSTED	our sintere	THE VE		CINCILL 21	JART DIVINIORI
AØAØJØGIR5	PDGRIIAAVQSTLDI	DGKSKKQAL	FIRLVSF	DPAIG	KTAPIYGYPIL	JSAAYSKINSDAK
Δαδαέανεκα	PDGRTTAAVOSTI DT	DGKSKKOAL	ETRLVSE	DPATG	KTAMVGVPT	NSAAVSKNSDAK
101010101010						
AØAØW2KF14	PDGRIIAAVQSTLDI	DGKSKKQAL	FIRLVSH	DPAIG	KTAPIYGYPIL	JSAAYSKNSDAK
ΔΘΔΘΗΘΟΟΤS	PDGRTTAAVOSTI DT	DGKSKKOAL	ETRLVSE	DPATG	KTAMVGVPT	DSAAVSKNSDAK
				_		
AØAØHØDRS6	PDGRIIAAVQSTLDI	DGKSKKQAL	FTRLVSP	DPATG	KTAMYGYPIL	dsaaysknsdak
F2\/P77	PLOPTRATASALT	DGAERGCGV	D/HHVAGD	DPI FO	SEKL TVTHT	PAREL AAKOOK
201627	r Egitha tabact	Jan Geav	, villivados	v	JERCIVIIII	ANELAANQQI
AØAØM3HCJ2	PLQRTRATAQALV	DGAFPGCGV	AIHYVSGDA	DPLFQ	TDKFSATQTE	JPARQLAEV KAK
404043V1T6	PLORTRATAGALV-	DGAEPGCGV	TVHHVAGED	DPJ FO	ΤΕΔΕΡΔΤΝΤΓ	ΡΔΟΟΙ ΔΔΥΤΔΤ
1010101010		out rocur				
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AØAØK2MR18	GDIVALDDHRILLIE	QGGDKNKTM	RNRVYVVDL	SNATD.	LSTLDKT-EF	PEFDDAEKLNA
A0A0H0C1X8	GDTVAL DNOHTLL TE	OGSDVNDGM	DMI TV/VDI	SKASD	I SGEDVDGEN	VPEEDDEKTLAG
AdAdhocoxo	dormebnighteere	Quadratica				IT ET DOERTENQ
A0A0J01C55	GDIVALDNQHILLIE	QGSDKNDGM	RNLIYKVDL	SKASD	LSGEDKPGEN	(PEFDDEK I LAQ
4040F0T849	GDTVALDNOHTLL TE	OGSDKNDGM	RNI TYKVDI	SKASD	I SGEDKPGEN	PEEDDEKTI AO
	CONTRACTOR OF CONTRACTOR	2000 Milliour				IN ER DOERNERQ
AØAØW2ZA64	GDIVALDNHTILLIE	QGEDKNDAM	RNLIYRVDL	SKASD	LAAFDKPGEY	rpefiddektlaq
A0A0F1GTF1	GDIVALGNHTTL ! TF	OGEDKNDAM	RNLTYRVDI	SKASD	LAAEDKPGEN	PEEDDEKTI AO
1010110111	COTVAL DOOLT	OCCDIMENT OF	DALL TACOUT	CKACC	LTARDUCET	A CODE CITERO
AØAØV9DZB6	GDIVALDDQHILLIE	QGEDKNDAM	RNLIYKVDL	SKASD	LIAFDKPGEY	rpefiddektlaq
A0A0F1A170	GDTVALDNOHTUUTE	OGSDKNDGM	RNI TYKVDI	SKASD		PEEDDEKTI AO
AGAGI 1A370	doi vacongnicci c	QUODINIDU	INVELTING DE		CARLOR DE	IT ET DOEKTERQ
AØAØJØG1R5	GDIVALDDQHILLIE	QGSDKNDGM	RNLIYKVDL	SKASD	LTAFDKPGEY	PEFDDEKTLAQ
Δαδαέανεκα	GDTVAL DDOHTLL TE	OGSDKNDGM	RMI TYKVDI	SKASD	I SAED//PGEN	PEEDDEKTI KO
AdAdi di di dico	doivacoogniccie	Quadranda	INVEL TROUC		EDAT DIG GET	IT ET DOEKTERQ
AØAØW2KFI4	GDIVALDDQHILLIE	QGSDKNDGM	RNLIYKVDL	SKASD	LSAFDKPGEY	/PEFDDEK TLKQ
	GDTVAL DDOHTLL TE	OGSDKNDGM	DNI TVVVDI	SKASD	I SAED/ PGEN	PEEDDEKTI KO
AGAGHODDTO	doi vacoo Quiterie	2020ininodi	NIVELTINVOL		EDAI DIGI GEI	IT ET DOEKTERQ
AØAØHØDRS6	GDIVALDDQHILLIE	QGSDKNDGM	RNLIYKVDL	SKASD	LSAFDKPGEY	PEFDDEKTLKQ
F2\/P77	GDLARLOOOL OPTTO	0	I KAAM	DDATD	CDI ENTOUSE	POTRIGNTVIV
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AØAØM3HCJ2	GDLAKRRQALAPTIQ	L	LKAAVC	.QQDKP	CPIFDKPWQ\	/EQNQSGKTTIS
404043V1T6	GNI VAROOAL OPAVO	4	I KSAVC	OPGSD	CSVEDKPW01	EKOSKSGKTVVO
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A0A0K2MP18		GUODEKAEG				EDOGDYVENDD
AØAØK2MR18	GVQLATKQLAVDLRE	.GNQQEKAEG	LALIDPQTL	- AVIND	DFGLQSELL	EPQGDKKEMDD
AØAØK2MR18 AØAØHØCJX8	GVQLATKQLAVDLREL	GVQQEKAEG	LALIDPQTL	- AVINDI AVANDI	NDFGLQSELL	EPQGDKKEMDD HPVE-GKKLKD
AØAØK2MR18 AØAØHØCJX8		GNQQEKAEG	LALIDPQTL LALIDSKTL	AVINDI AVANDI		EPQGDKKEMDD HPVE-GKKLKD
A0A0K2MR18 A0A0H0CJX8 A0A0J0IC55	GVQLATKQLAVDLREL GITLAQKTQVVDLRAL GITLAQKTQVVDLRAL	GVQQEKAEG GVQQEKAEG GVQQEKAEG	LALIDPQTL LALIDSKTL LALIDSKTL	- AVINDI AVANDI AVANDI	NDFGLQSELL NDFGVKVAMQ NDFGVKVAMQ	EPQGDKKEMDD HPVE-GKKLKD HPVE-GKKLKD
A0A0K2MR18 A0A0H0CJX8 A0A0J0IC55 A0A0F0T849	GVQLATKQLAVDLREL GITLAQKTQVVDLRAL GITLAQKTQVVDLRAL GITLAQKTQVVDLRAL	GVQQEKAEG GVQQEKAEG GVQQEKAEG GVQQEKAEG	LALIDPQTL LALIDSKTL LALIDSKTL LALIDSKTL	AVINDI AVANDI AVANDI AVANDI	NDFGLQSELL NDFGVKVAMQ NDFGVKVAMQ NDFGVKVAMO	EPQGDKKEMDD HPVE-GKKLKD HPVE-GKKLKD HPVE-GKKLKD
A0A0K2MR18 A0A0H0CJX8 A0A0J0IC55 A0A0F0T849 A0A0F0T849	GVQLATKQLAVDLREL GITLAQKTQVVDLRAL GITLAQKTQVVDLRAL GITLAQKTQVVDLRAL GITLAQKTQVVDLRAL	GVQQEKAEG GVQQEKAEG GVQQEKAEG GVQQEKAEG GVQQEKAEG	LALIDPQTL LALIDSKTL LALIDSKTL LALIDSKTL	AVINDI AVANDI AVANDI AVANDI AVANDI	NDFGLQSELL NDFGVKVAMQ NDFGVKVAMQ NDFGVKVAMQ	EPQGDKKEMDD HPVE-GKKLKD HPVE-GKKLKD HPVE-GKKLKD
A0A0K2MR18 A0A0H0CJX8 A0A0J0IC55 A0A0F0T849 A0A0W2ZA64	GVQLATKQLAVDLREL GITLAQKTQVVDLRAL GITLAQKTQVVDLRAL GITLAQKTQVVDLRAL GITLAQKTQVVDLRAL	GVQQEKAEG GVQQEKAEG GVQQEKAEG GVQQEKAEG GVQQEKAEG	LALIDPQTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL	AVINDI AVANDI AVANDI AVANDI AVANDI AVANDI	NDFGLQSELL NDFGVKVAMQ NDFGVKVAMQ NDFGVKVAMQ NDFGVKVAMQ	EPQGDKKEMDD HPVE-GKKLKD HPVE-GKKLKD HPVE-GKKLKD NPVE-GKKLKD
A0A0K2MR18 A0A0H0CJX8 A0A0J0IC55 A0A0F0T849 A0A0W2ZA64 A0A0W2ZA64	GVQLATKQLAVDLRE GITLAQKTQVVDLRAL GITLAQKTQVVDLRAL GITLAQKTQVVDLRAL GITLAEKTQVVDLRAL GITLAEKTQVVDLRAL	GVQQEKAEG GVQQEKAEG GVQQEKAEG GVQQEKAEG GVQQEKAEG GVQQEKAEG GVQQEKAEG	LALIDPQTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL	AVINDI AVANDI AVANDI AVANDI AVANDI AVANDI AVANDI	NDFGLQSELL NDFGVKVAMQ NDFGVKVAMQ NDFGVKVAMQ NDFGVKVAMQ NDFGVKVAMQ	EPQGDKKEMDD HPVE-GKKLKD HPVE-GKKLKD HPVE-GKKLKD NPVE-GKKLKD NPVE-GKKLKD
A0A0K2MR18 A0A0H0CJX8 A0A0J0IC55 A0A0F0T849 A0A0M2ZA64 A0A0F1GTF1 A0A0M0JZ66	GVQLATKQLAVDLRA GITLAQKTQVVDLRA GITLAQKTQVVDLRA GITLAQKTQVVDLRA GITLAQKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA	GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG	LALIDPQTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKRL	AVINDI AVANDI AVANDI AVANDI AVANDI AVANDI AVANDI	NDFGLQSELL NDFGVKVAMQ NDFGVKVAMQ NDFGVKVAMQ NDFGVKVAMQ NDFGVKVAMQ	EPQGDKKEMDD HPVE-GKKLKD HPVE-GKKLKD HPVE-GKKLKD NPVE-GKKLKD NPVE-GKKLKD HPVE-GKKLKD
A0A0K2MR18 A0A0H0CJX8 A0A0J0IC55 A0A0F0T849 A0A0W2ZA64 A0A0F1GTF1 A0A0V9DZB6	GVQLATKQLAVDLRE GITLAQKTQVVDLRAL GITLAQKTQVVDLRAL GITLAQKTQVVDLRAL GITLAGKTQVVDLRAL GITLAAKTQVVDLRAL GITLAAKTQVVDLRAL	GWQQEKAEG GWQQEKAEG GWQQEKAEG GWQQEKAEG GWQQEKAEG GWQQEKAEG GWQQEKAEG GWQQEKAEG	LALIDPQTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDGKRL LALIDGKRL	AVINDI AVANDI AVANDI AVANDI AVANDI AVANDI AVANDI	NDFGLQSELL NDFGVKVAMQ NDFGVKVAMQ NDFGVKVAMQ NDFGVKVAMQ NDFGVKVAMQ NDFGVKVAMQ	EPQGDKKEMDD HPVE-GKKLKD HPVE-GKKLKD HPVE-GKKLKD NPVE-GKKLKD NPVE-GKKLKD HPVE-GKKLKD
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A0A0K2NR18 A0A0H0CJX8 A0A0F0IC55 A0A0F0IC55 A0A0F0ICF1 A0A0F0ICF1 A0A0F0ICF1 A0A0F0ICF1 A0A0F0ICF1 A0A0F0ICF1 A0A0F0ICF1 A0A0F0ICF1 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0CJX8 A0A0	GVQLATKQLAVDLRE GITLAQKTQVVDLRA GITLAQKTQVVDLRA GITLAQKTQVVDLRA GITLAAKTQVVDLRA SIGN	GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNSENLPAD HSSNLP	LALIDPQTL LALIDSKTL LALIDS	AVINDI AVANDI AVANDI AVANDI AVANDI AVANDI AVANDI AVANDI AVANDI AVANDI AVANDI AVANDI S1 : : : : : : : :	NDFGLQSELL NDFGVI:VANQ NDFGVI:V	EPQGDKKEMDD HPVE-GKLLKD HPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD TANYDLSNDVL .:
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A0A0K2MR18 A0A0H0CJX8 A0A0F0ITS5 A0A0F0ITS49 A0A0K70IT51 A0A0F0ITF1 A0A0V9DZB6 A0A0F1AJ70 A0A030G1R5 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0CJX8 A0A0H0CJX8 A0A0F1GT51 A0A0F1GT	GVQLATKQLAVDLRE GITLAQKTQVVDLRA GITLAQKTQVVDLRA GITLAQKTQVVDLRA GITLAAKTQVVDLRA SILA	GIQQEIKAEG GIQUEKAEG GI	LALIDPQTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL QLANGKITH QLANGKITH DKPASQNEL EKPESDSEL EKPESDSEL KKPESDSEL KKPESDSEL KKPESDSEL KKPESDSEL KKPESDSEL KKPESDSEL KKPESDSEL	AVANDI AV	NDFGLQSELL NDFGVIXAANQ NDFGVIXA	EPQGDKKEMDD HPVE-GKILKD HPVE-GKILKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLCD NPV
A0A0K2MR18 A0A0H0CJX8 A0A0F0T849 A0A0F0T849 A0A0WJZA64 A0A0F1GTF1 A0A0Y0ZB6 A0A010GIR5 A0A0F0Y6K0 A0A0102KF14 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0T8 A	GVQLATKQLAVDLRE GITLAQKTQVVDLRA GITLAQKTQVVDLRA GITLAQKTQVVDLRA GITLAKTQVVDLRA GITLAKTQVVDLRA GITLAKTQVVDLRA GITLAAKTQVVDLRA WNVDGQGHLTDDKP YRWAAGKLTLDDKP	GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNQQEKAEG GNSENLPJA SKIGIKPL YETLSVKPL YETLSVKPL YETLSVKPL YETLSVKPL YETLSVKPL YETLSVKPL YETLSVKPL YETLSVKPL YETLSVKPL YETLSVKPL YETLSVKPL YETLSVKPL YETLSVKPL	LALIDPQTL LALIDSKTL KIPESDSEL KIPESDSEL KIPESDSEL KIPESDSEL KIPESDSEL KIPESDSEL KIPESDSEL KIPESDSEL KIPESDSEL KIPESDSEL KIPESDSEL	AVIND AVANDI AVANDI AVANDI AVANDI AVANDI AVANDI AVANDI AVANDI AVANDI AVANDI AVANDI S	NDFGLQSELL NDFGVI/VANQ NDFGVI	EPQGDKKEMDD HPVE-GKLLKD HPVE-GKLLKD NPVE-GKLKLKD NPVE-GKLKD NPVE-GKLKD
A0A0K2MR18 A0A0H0CJX8 A0A0701C55 A0A0701849 A0A0701849 A0A0191871 A0A0190286 A0A0190286 A0A0190286 A0A0190286 A0A0190286 A0A019018 A0A0400018 A0A0400018 A0A0400128 A0A0400128 A0A0401275 A0A047111 A0A0401271 A0A041271 A0A03155 A0A071671 A0A07171 A0A071671 A0A0717171 A0A0717171 A0A0717171 A0A0717171 A0A0717171 A0A0717171 A0A0717171 A0A0717171 A0A07171717171 A0A07171	GVQLATKQLAVDLRE GITLAQKTQVVDLRA GITLAQKTQVVDLRA GITLAQKTQVVDLRA GITLACKTQVVDLRA GITLAKTQVVDLRA GITLAAKTQVVDLRA SILAAKTQVVDLRA SILAAKTQVVDLRA SILAAKTQVVDLRA SILAAKTQVVDLRA SILAAKTQVVDLRA SILAAKTQVVDLRA SILAAKTQVVDLRA SILAAKTQVVDLRA SILAAKTQVVDLRA SILAAKTQVVDLRA SILAAKTQVVDLRA SILAAKTQVVDLRA SILAAKTQVVDLRA SILAAKTQVDLRA SILAAKTQVLRA SILAAKTQVDLRA SILAAKTQVDLRA SILAAKTQVDLRA SILAAKTQVDLRA SILAAKTQVDLRA SILAAKTQVDLRA SILAAKTQVLRAAKTQVDLRA SILAAKTQVDLRA SILAAKTQVDLR	GNQQEKAEG GNQ GNQ GNQ GNQ GNQ GNQ GNQ GNQ GNQ GN	LALIDORTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL QLANGKITH QLANGKITH QLANGKITH DKPASQNEL EKPESDSEL KKPESDSEL KKPESDSEL KKPESDSEL KKPESDSEL KKPESDSEL KKPESDSEL KKPESDSEL	AVANDI AV	NDFGLQSELL NDFGVIVAANQ NOTTAVING NDFGUTAL NOTANNG	EPQGDKKEMDD HPVE-GKLLKD HPVE-GKLLKD NPVE-GKLLD NP
A0A0K2NR18 A0A0H0CJX8 A0A0F0IGT55 A0A0F0IGT51 A0A0F0IGTF1 A0A0F0IGTF1 A0A0V9DZB6 A0A0F1GTF1 A0A0V9DZB6 A0A0H21AJ70 A0A0W2KF14 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0CJX8 A0A0H0CJX8 A0A0H0CJX8 A0A0F0IGTF1 A0A0H0CJX8 A0A0F0IGTF1 A0A0H0CJX8 A0A0F1GTF1 A0A0H0CJX8 A0A0F1GTF1 A0A0H0CJX8 A0A0F1GTF1 A0A0H0CJX8 A0A0F1GTF1 A0A0H0CJX8 A0A0F1GTF1 A0A0H0CJX8 A0A0F1GTF1 A0A0H0DT8 A0A0F1GTF1 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0D56 F2VRZ7	GVQLATKQLAVDLRE GITLAQKTQVVDLRA GITLAQKTQVVDLRA GITLAQKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVDLRA GITLAAKTQVDLRA GITLAAKTQVDLRA GITLAAKTQVDLRA GITLAKTQVDLRA GITLAKTQVDLRA GITLAKTQVDLRA GITLAKTQVDLRA GITLAKTQVDLRA GITLAKTQVDLRA GITLAKTQVDLRA GITLAKTQVDLRA GITLAKTQVDLRA GITLAKTQVDLRA GITLAKTQVDLRA GITLAKTQVDLRA GITLAKTQVDLRA GITLAKTQVDLRA GITLAKTQVDLRA GITLAKTQVDLRA GITLAKTQVDLRA GITLAKTQVDLRA SITLAKTQVDLR	GIQQEIXAEG GIQEIXAEG GIUZEIXAEG GIUZEIXAEG	LALIDPQTL LALIDSKTL LALIDS	AVANDI AV	IDFGLQSELL IDFGVICVANQ IDFGVICV	EPQGDKKEMDD HPVE-GKLLKD HPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLKD NPVE-GKLD NPVE
A0A0K2MR18 A0A0H0CJX8 A0A0F0T849 A0A0F0T849 A0A0F0T849 A0A0FJGTF1 A0A0FJGTF1 A0A0FJGTF1 A0A0FJGTF1 A0A0FJGTF1 A0A0FJGTF3 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0DT8 A0A0H0CJX8 A0A0FJGTF1 A0A0K2MR18 A0A0FJGTF1 A0A0FJ	GVQLATKQLAVDLRE GITLAQKTQVVDLRA GITLAQKTQVVDLRA GITLAQKTQVVDLRA GITLAKTQVVDLRA GITLAKTQVVDLRA GITLAKTQVVDLRA GITLAKTQVVDLRA GITLAKTQVVDLRA GITLAKTQVVDLRA GITLAKTQVVDLRA GITLAKTQVVDLRA GITLAKTQVVDLRA GITLAKTQVVDLRA CILAKTQVVDLRA GITLAKTQVVDLRA CILAKTQVVDLRA GITLAKTQVVDLRA SITLAKTQVVDLRA CILAKTQVVDLRA GITLAKTQVVDLRA SITLAKTQVVDLRA SITLAKTQVVDLRA SITLAKTQVDLRA SITLAK	GNQQEKAEG GNQEKAEG GN	LALIDPQTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL LALIDSKTL QLANGKITTS QLANGKITTS QLANGKITTS DKPASQNEL EKPESDSEL KKPESDSEL KKPESDSEL KKPESDSEL KKPESDSEL KKPESDSEL KKPESDSEL KKPESDSEL KKPESDSEL KKPESDSEL KKPESDSEL	AVANDI AV	NDFGLQSELL NDFGVIVAANQ UDFGVIVAANQ UDFGVIVA	EPQGDKKEMDD HPVE-GKLLKD HPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD NPVE-GKLLKD TANYDLSNDVL .:
A0A0K2MR18 A0A0H0CJX8 A0A070IC55 A0A0F0IT49 A0A0R10IC51 A0A0F10IT1 A0A070IC11 A0A070IC11 A0A070IC11 A0A070IC11 A0A070IC11 A0A070IC11 A0A070IC11 A0A070IC15 A0A0402XR14 A0A040CJX8 A0A040CJX8 A0A040CJX8 A0A070IC55 A0A070IC5	GVQLATKQLAVDLRE GITLAQKTQVVDLRA GITLAQKTQVVDLRA GITLAQKTQVVDLRA GITLAAKTQVVDLRA SILAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA SILAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA SILAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA GITLAAKTQVVDLRA SILAAKTQVVDLRA GITLAAKTQVVDLRA SILAAKTQVVDLRA	GIQQEIXAEG GIQQEIXAEG GIQQEIXAEG GIQQEIXAEG GIQQEIXAEG GIQQEIXAEG GIQQEIXAEG GIQQEIXAEG GIQQEIXAEG GIQQEIXAEG GIQQEIXAEG GIQQEIXAEG GIQQEIXAEG GIQQEIXAEG GIQQEIXAEG GIQQEIXAEG GIQQEIXAEG GIQQEIXAEG GIQQEIXAEG GISENLPLS GISENLP	LALIDOSTI LALIDOSTI LALIDOSTI LALIDOSTI LALIDOSTI LALIDOSKI LALIDOSKI LALIDOSKI LALIDOSKI LALIDOSKI LALIDOSKI UALIDO	AVINDI AVANDI AV	IDFGLQSELL IDFGVIXANQ ID	EPQGDKKEMDD HPVE-GKILKD HPVE-GKILKD NPVE-GKLD NPVE-GKLKD NPVE-GKLD NPVE-GK

Fig. 5 Multiple sequence alignment of 16 phytase sequences of *Enterobacter* spp. showing highly conserved amino acid residues. An * (asterisk) indicates single, fully conserved residue, a : (colon) indicates conservation between groups of strongly similar properties and

مدينة الملك عبدالعزيز KACST للعلوم والتفنية KACST a. (period) indicates conservation between groups of weakly similar properties. Therefore, the hierarchy of conservation using these symbols is * (identical) > : (colon) >. (period). Highlighted area in the sequence alignment indicates highly conserved sequences

AØAØK2MR18	
A0A0H0CJX8	
A0A0J0IC55	
AØAØFØT849	
AØAØW2ZA64	
AØAØF1GTF1	
AØAØV9DZB6	
A0A0F1AJ70	
AØAØJØG1R5	
AØAØFØY6KØ	
AØAØW2KFI4	
AØAØHØDDT8	
AØAØHØDRS6	
F2VRZ7	YSRGNIPPGSSLVLERWRDTRSGKRFLRIYFQAQSLDGIRQLQPLDDKHPLLRQEWHQPD
AØAØM3HCJ2	YSRGNIPPGSSLVIERWRNSKNGERYLRVYFQAQSLDDLRRLQMPDQQHPMLQQEWRQPD
AØAØA3YJT6	YTRGNIPPGSSLVFERWRDKQSGERWLHVYFQAQSLDDLRRLQSVDQAHPLLREEWRTPD
AØAØK2MR18	
AØAØHØCJX8	
A0A0J0IC55	
AØAØFØT849	
AØAØW2ZA64	
AØAØF1GTF1	
AØAØV9DZB6	
AØAØF1AJ70	
AØAØJØG1R5	
AØAØFØY6KØ	
AØAØW2KFI4	
AØAØHØDDT8	
AØAØHØDRS6	
F2VRZ7	CRVTDVGLLCPYQSTLTQLRKNLDNSAVLPVSVILP
AØAØM3HCJ2	CQQTSVGTLCPYQSALEALSKQIDKSAVPPVNMVL-
AØAØA3YJT6	CRVTEVGTI CPMASTI AKEGOOI DPTATTPTSVAP-
	chi referenci aggebri meri estin

Fig. 5 (continued)

indirectly (Fig. 6). Occupying the central position, the query protein interacts with bifunctional riboflavin kinase/FMN adenylyltransferase, alpha subunit of riboflavin synthase, NAD(P)H-dependent FMN reductase, FMN reductase, major facilitator superfamily protein, spore coat U domain-containing protein, lipoprotein, TonBdependent receptor, a hypothetical protein of 117 amino acid residues and putative universal stress family protein as shown in Fig. 6. STRING analysis is very important in terms of system-level understanding of cellular processes in a computer-based way. The interacting network can be used for filtering and assessing functional genomics data as well to provide an instinctive platform for annotating evolutionary properties of proteins in addition to structure–function aspects (Schwartz et al. 2008). Exploring this type of STRING generated predicted interaction networks can suggest important directions for future experimental research, e.g., prediction of the possible pathway of the protein of interest. Similar protein–protein interaction study was previously worked out by Goñi et al. (2008), Gao et al. (2012), Guney and Oliva (2012), Quan et al. (2014), Zhang et al. (2016), Pramanik et al. (2017a, b, 2018) etc.

Hence, this elaborative study will be very helpful in selecting commercial phytases in future derived from *E. aerogenes* as potential phytases in animal feed additive. In addition, direct application of *E. aerogenes*, in cultivated fields will help crops to grow better by soluble P uptake released due to phytase activity of the strain.

Conclusion

In silico characterization of *Enterobacter* phytases revealed that the 48 kDa proteins were tetrameric, thermostable and acidic in nature belonging to the histidine phosphatase superfamily. This types of thermostable, acidic phytases derived from *E. aerogenes* might be beneficial in terms of application in various industrial fields such as monogastric animals, poultry farms, etc., by solubilized phosphorus supplement in their food essential for their normal growth and development. Besides phytase containing *E. aerogenes* can be directly applied in the agricultural field to meet up the phosphorus deficiency in crop plants. Hence, this study will help researchers to understand the essential structure–function properties of *Enterobacter* phytases.





Your Input:	po co su su
■ EAE_02525 putative 3-phytase (421 aa)	borho ^L usior wrenc ressic ments ases ining ining
Predicted Functional Partners:	Neighl Gene I Gene I Coexp Datab Datab Datab Datab Datab Score
e EAE_10840 bifunctional riboflavin kinase/FMN adenylyltransferase (312 aa)	• 0.907
e EAE_17765 riboflavin synthase subunit alpha (211 aa)	• 0.900
EAE_15285 NAD(P)H-dependent FMN reductase (191 aa)	• 0.900
fre FMN reductase (233 aa)	• 0.900
EAE_02530 major facilitator superfamily protein (452 aa)	• 0.771
EAE_22750 spore coat U domain-containing protein (317 aa)	• 0.718
e EAE_13570 lipoprotein (206 aa)	• 0.665
EAE_01755 TonB-dependent receptor (783 aa)	• 0.653
EAE_00310 hypothetical protein (117 aa)	• 0.652
⊜ EAE_23715 putative universal stress family protein (140 aa)	• 0.642

Fig. 6 Protein-protein interaction map including the predicted interacting proteins with phytase protein (A0A0M3HCJ2)

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Compliance with ethical standards

Conflict of interest Authors declare no conflict of interest.

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