iJRASET
International Journal For Research in Applied Science and Engineering Technology

INTERNATIONAL JOURNAL FOR RESEARCH

IN APPLIED SCIENCE & ENGINEERING TECHNOLOGY

Volume: 9 **Issue:** VI **Month of publication:** June 2021

DOI: https://doi.org/10.22214/ijraset.2021.34874

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International Journal for Research in Applied Science & Engineering Technology (IJRASET)
ISSN: 2321-9653; IC Value: 45.98; SJ Impact Factor: 7.429
Volume 9 Issue VI Jun 2021- Available at www.ijraset.com

Phospholipase A2 (PLA2) Sequences in *Rattus norvegicus* Genome

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Abstract— Phospholipase A2 is enzyme that hydrolyses phospholipids at sn-2 position. This class of enzymes are significant due to their ability to cleave membrane phospholipids and hence causing inflammation. The PLA2 enzymes present in Rattus norvegicus is extensively studied to predict its properties. The Protparam analysis was performed to predict the physical properties like number of amino acids, Theoretical pH, stability index value, aliphatic index value and GRAVY value. The SOPMA analysis predicted its structural properties like the number of alpha-helices and beta-strands. Hence the focus of the present study was to perform a preliminary in silico analysis to identify the PLA2 protein sequences in the genome of Rattus norvegicus.

Keywords— Phospholipase A2, Secretory PLA2, Rattus norvegicus, Protparam, SOPMA,

I. INTRODUCTION

Phospholipase A2 (PLA2) are enzymes that cleave fatty acid in the position two of phospholipids. It hydrolyses the bond between the second fatty acid tail and the glycerol molecule. The sn-2 acyl bond of phospholipids is specifically recognized by this particular phospholipase and catalytically hydrolyses the bond to generate arachidonic acid and lysophosphatidic acid. Arachidonic acid (AA) is a precursor of eicosanoids including prostaglandins and leukotrienes that induce inflammation. PLA2 enzymes are commonly found in mammalian tissues, arachnid, insect, and snake venom.

The types of PLA2 enzymes include sPLA2, cPLA2 and iPLA2. The families in PLA2 superfamily include Calcium dependent, Calcium independent and Secretory PLA2. sPLA2s possess anti-bacterial and anti-viral activity. Macrophages, monocytes, T cells, mast cell and neutrophils produce sPLA2. sPLA2s also play a role in development of atherosclerosis. cPLA2α is reportedly involved in embryo implantation and fertility, pathophysiology of allergic inflammation, asthma, lung cancer metastasis, spinal cord injury, Alzheimer's disease. The PLA2 enzymes are involved in the sites of inflammation and hence can serve as potential targets for inflammatory disorders. The usual rodent model is the rat (*Rattus norvegicus*), which is used for evaluating toxicity of various classes of chemicals and has a large database. Hence, in this study the Calcium dependent, Calcium independent and Secretory PLA2 sequences were retrieved from genome of *Rattus norvegicus* and their properties were predicted.

II. METHODOLOGY

The genome of Rattus norvegicus was analyzed for phospholipase A2 protein sequences. From the PLA2 genes obtained, the Calcium dependent, Calcium independent and Secretory PLA2 sequences were retrieved from NCBI. They were analyzed using ProtParam tool from the SIB ExPASy Bioformatics Resources Portal. The number of amino acids, Theoretical pH, stability index value, aliphatic index value and GRAVY value were predicted using the tool. SOPMA [Self-Optimized Prediction Method with Alignment] from PRABI was used to predict the Secondary structure of protein. The number of beta-strands, Alpha helices, Total residue and their percentage were retrieved.

III. RESULTS AND DISCUSSION

A. Identification of PLA2 Sequences

The identified Phospholipase A2 protein sequences from the genome of *Rattus norvegicus* are shown in Table-1.

	Family	Protein Sequence	Name
A	Calcium dependent	NP_058870.1	Calcium-dependent phospholipase A2 group V precursor
B	Calcium independent	NP_001005560.1	85/88 kDa calcium-independent phospholipase A2 isoform 1
C		NP_001257725.1	85/88 kDa calcium-independent phospholipase A2 isoform 2

D		XP_003754218.1	PREDICTED: calcium-independent phospholipase A2-gamma
E	Secretory	NP_001013446.1	group IID secretory phospholipase A2 precursor
F		NP_001094307.1	secretory phospholipase A2 receptor precursor
G		NP_001099485.1	group 3 secretory phospholipase A2 precursor
H		NP_001100166.1	group IIE secretory phospholipase A2
I		NP_001102035.1	group XIIA secretory phospholipase A2 precursor
J		NP_001103057.1	group IIF secretory phospholipase A2
K		NP_058872.1	group 10 secretory phospholipase A2 precursor
L		NP_062075.1	group IIC secretory phospholipase A2
M		XP_001053976.3	PREDICTED: group XIIB secretory phospholipase A2-like protein isoform X1
N		XP_006223959.1	PREDICTED: group XIIB secretory phospholipase A2-like protein isoform X2
O	Others	NP_001004277.1	group XV phospholipase A2 precursor
P		NP_001139454.1	phospholipase A2, group IVC
Q		NP_113773.1	phospholipase A2 precursor
R		NP_113786.3	phospholipase A2, membrane associated precursor

TABLE-1: PHOSPHOLIPASE A2 SEQUENCES IDENTIFIED FROM *Rattus norvegicus* GENOME

B. Protparam Analysis

The analysis of phospholipase A2 protein sequences from genome of Rattus norvegicus was done using Protparam and the results are depicted in Table-2.

	Protein Sequence	No. of Amino acids	Theoretical pI	Stability Index (II) value	Aliphatic index value	GRAVY value (Grand average of hydropathicity)
A	NP_058870.1	137	8.67	46.45 (Unstable)	73.28	-0.225
B	NP_001005560.1	807	6.69	35.61 (Stable)	86.27	-0.212
C	NP_001257725.1	752	6.65	35.94 (stable)	85.57	-0.229
D	XP_003754218.1	776	9.19	44.58 (Unstable)	84.19	-0.453
E	NP_001013446.1	144	8.80	27.77 (Stable)	65.76	-0.397
F	NP_001094307.1	1461	6.12	40.45 (Unstable)	72.49	-0.398
G	NP_001099485.1	506	8.95	54.73 (Unstable)	70.63	-0.470
H	NP_001100166.1	147	10.71	52.26 (Unstable)	81.09	-0.135
I	NP_001102035.1	114	9.18	45.53 (Unstable)	82.28	-0.365
J	NP_001103057.1	210	7.09	38.68 (Stable)	60.33	-0.525
K	NP_058872.1	151	6.18	51.07 (Unstable)	78.87	-0.138
L	NP_062075.1	158	8.54	26.37 (Stable)	64.18	0.070
M	XP_001053976.3	195	6.56	43.17 (Unstable)	69.03	-0.186
N	XP_006223959.1	194	6.56	43.34 (Unstable)	68.87	-0.196
O	NP_001004277.1	413	5.73	47.99 (Unstable)	87.75	-0.214
P	NP_001139454.1	587	5.26	35.18 (Stable)	79.25	-0.469
Q	NP_113773.1	146	7.89	13.70 (Stable)	66.16	-0.434

R	NP_113786.3	146	9.22	33.88 (Stable)	59.45	-0.248

TABLE-2: PREDICTED PHYSICOCHEMICAL AND BIOLOGICAL PROPERTIES

C. SOPMA Analysis

The results of SOPMA [Self-Optimized Prediction Method with Alignment] is depicted in Table-3. From the SOPMA results it is evident that the predicted secondary structure of the proteins possesses greater number of alpha-helices than beta-strands.

	Protein Sequence ID	Beta-strand		Alpha-helices		Others		Total Residues
		Number	(%)	Number	(%)	Number	(%)	
A	NP_058870.1	12	8.76	64	46.72	61	44.53	137
B	NP_001005560.1	58	7.19	321	39.78	428	53.04	807
C	NP_001257725.1	56	7.45	313	41.62	383	50.93	752
D	XP_003754218.1	32	4.12	309	39.82	435	56.05	776
E	NP_001013446.1	3	2.08	59	40.97	82	56.95	144
F	NP_001094307.1	58	3.97	321	21.97	1082	74.06	1461
G	NP_001099485.1	6	1.19	141	27.87	359	70.94	506
H	NP_001100166.1	8	5.44	40	27.21	99	67.35	147
I	NP_001102035.1	12	10.53	43	37.72	59	51.75	114
J	NP_001103057.1	4	1.90	64	30.48	142	67.62	210
K	NP_058872.1	6	3.97	59	39.07	86	56.95	151
L	NP_062075.1	10	6.33	62	39.24	86	54.43	158
M	XP_001053976.3	4	2.05	90	46.15	101	51.8	195
N	XP_006223959.1	3	1.55	96	49.48	95	48.96	194
O	NP_001004277.1	23	5.57	147	35.59	243	58.84	413
P	NP_001139454.1	18	3.07	295	50.26	274	46.68	587
Q	NP_113773.1	8	5.48	52	35.62	86	58.9	146
R	NP_113786.3	2	1.37	67	45.89	77	52.74	146

TABLE-3: SECONDARY STRUCTURE SUMMARY OF PHOSPHOLIPASE A2 AND RELATED PROTEINS

IV. CONCLUSIONS

Calcium dependent, Calcium independent and Secretory Phospholipase A2 sequences were identified from the genome of *Rattus norvegicus*. This study reports the various physical and structural properties of the identified sequences predicted using different computational tools. The entire study will help for the prediction of structure and function of Phospholipase A2 at a preliminary level.

ACKNOWLEDGMENT

Authors thank the management of Kalasalingam Academy of Research and Education.

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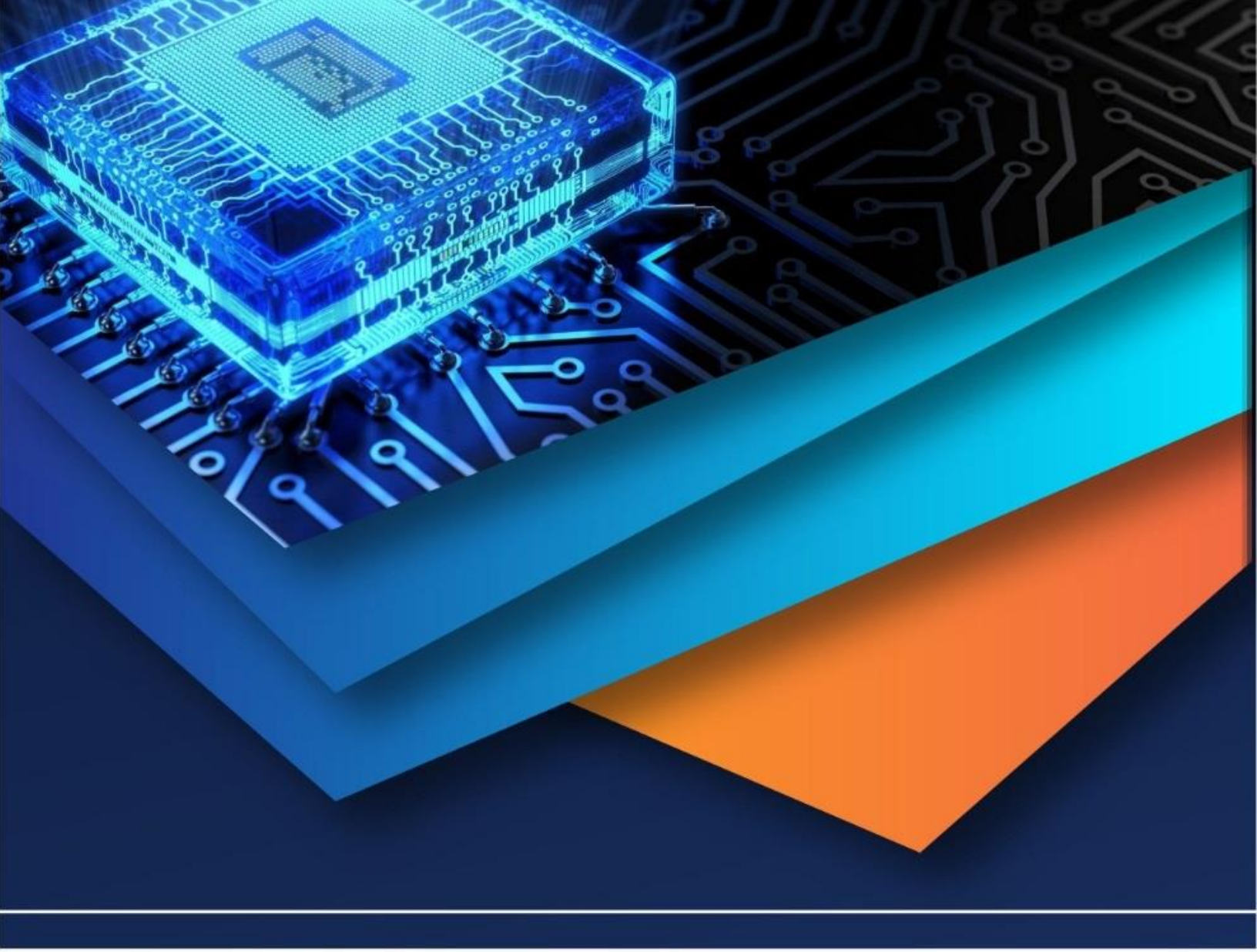

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