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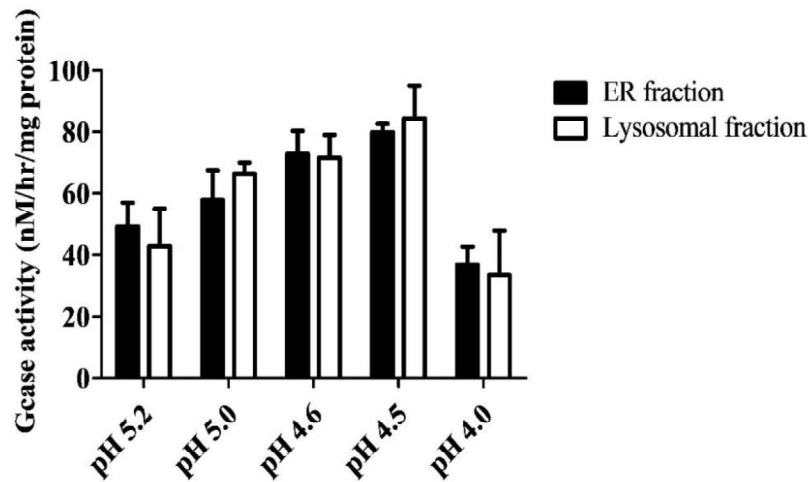
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# **Appendices**

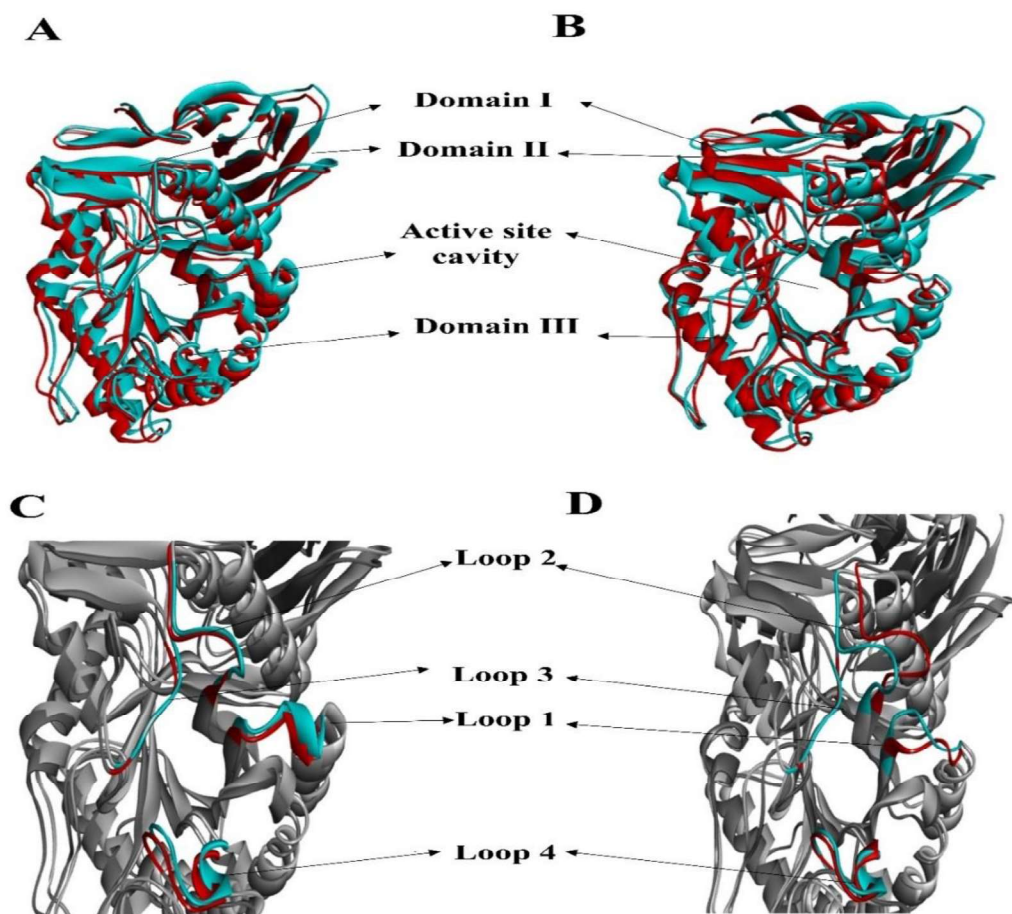
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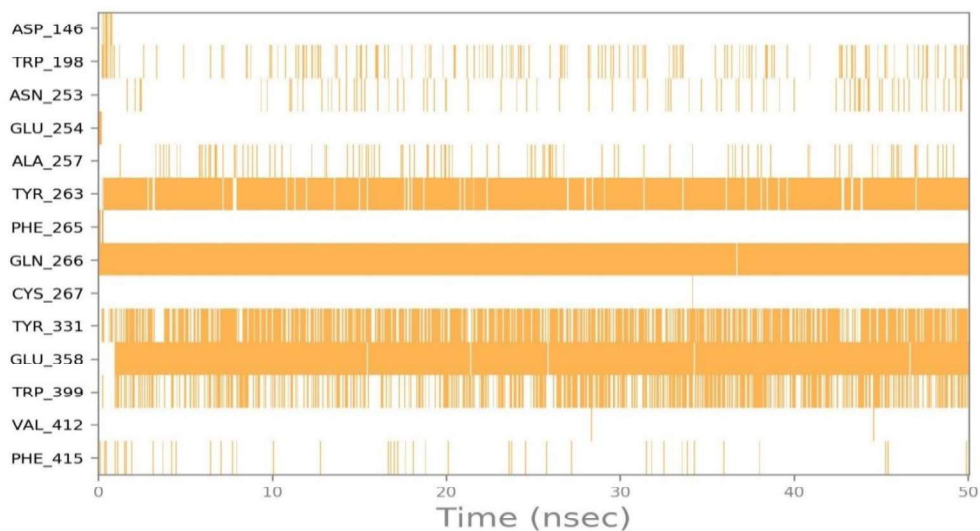
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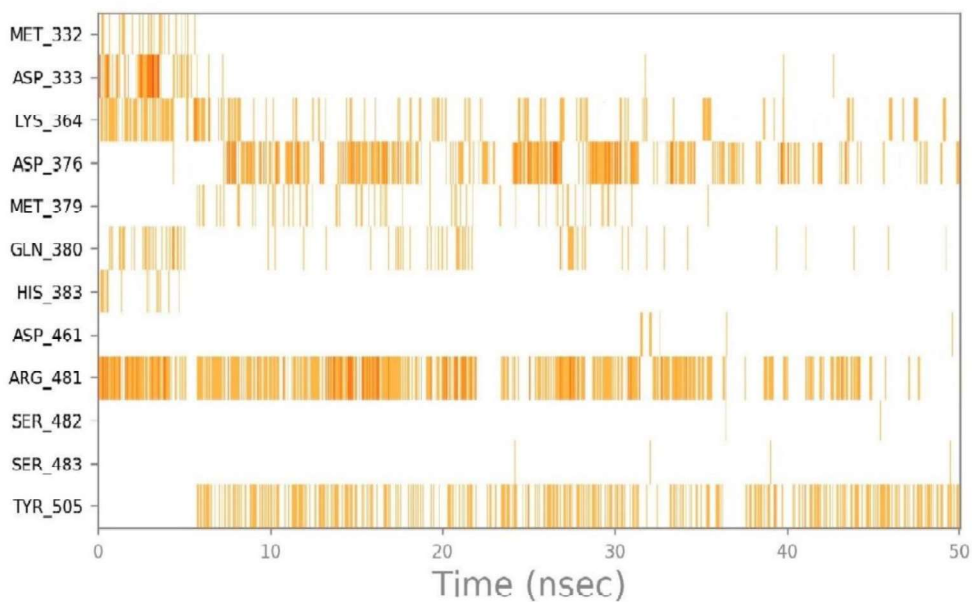
**Figure 2.1** rGCase activity of lysosomal fractions *versus* acidified ER fractions. There was no difference in the activity of rGCase was observed between acidic pH of lysosome and the acidified ER fractions All values are shown in the form of mean  $\pm$ SD; n = 3.



**Figure 2.2** Superimposition of the domain (A) and loops (C) of human-GCase protein (hGCse, PDB: 3NT1, colored red) over constructed rat- GCCase homology model (rGCCase, colored turquoise) at neutral pH (7.0). Superimposition of the domain (B) and loops (D) of hGCse (PDB: 3GXD, colored red) over constructed rGCCase homology model (colored turquoise) at acidic pH (4.5).



**Figure 2.3.** Timeline portrayal of the protein-ligand (rGCCase-AMB) contacts throughout the simulation on the pH 7.0.



**Figure 2.4** Timeline portrayal of the protein-ligand (rGCCase-AMB) contacts throughout the simulation on pH 4.5.

## Methods

### **2. Method of Isolation of GCase enriched Endoplasmic reticulum (ER) and lysosomal fractions**

**2.1 Requirements:** Tris-HCL was purchased from Merck. Triton X-100 and Protease inhibitor was acquired from Sigma-Aldrich (St. Louis, MO, USA). EGTA [ethylene glycol-bis (2-aminoethylether)-N,N,N',N'-tetraacetic acid], bovine serum albumin (BSA), sucrose, citric acid, sodium phosphate dibasic, and mannitol were supplied by Hi-media (Mumbai). All other reagents were analytical grade.

### **2.2 Compliance with ethical standards**

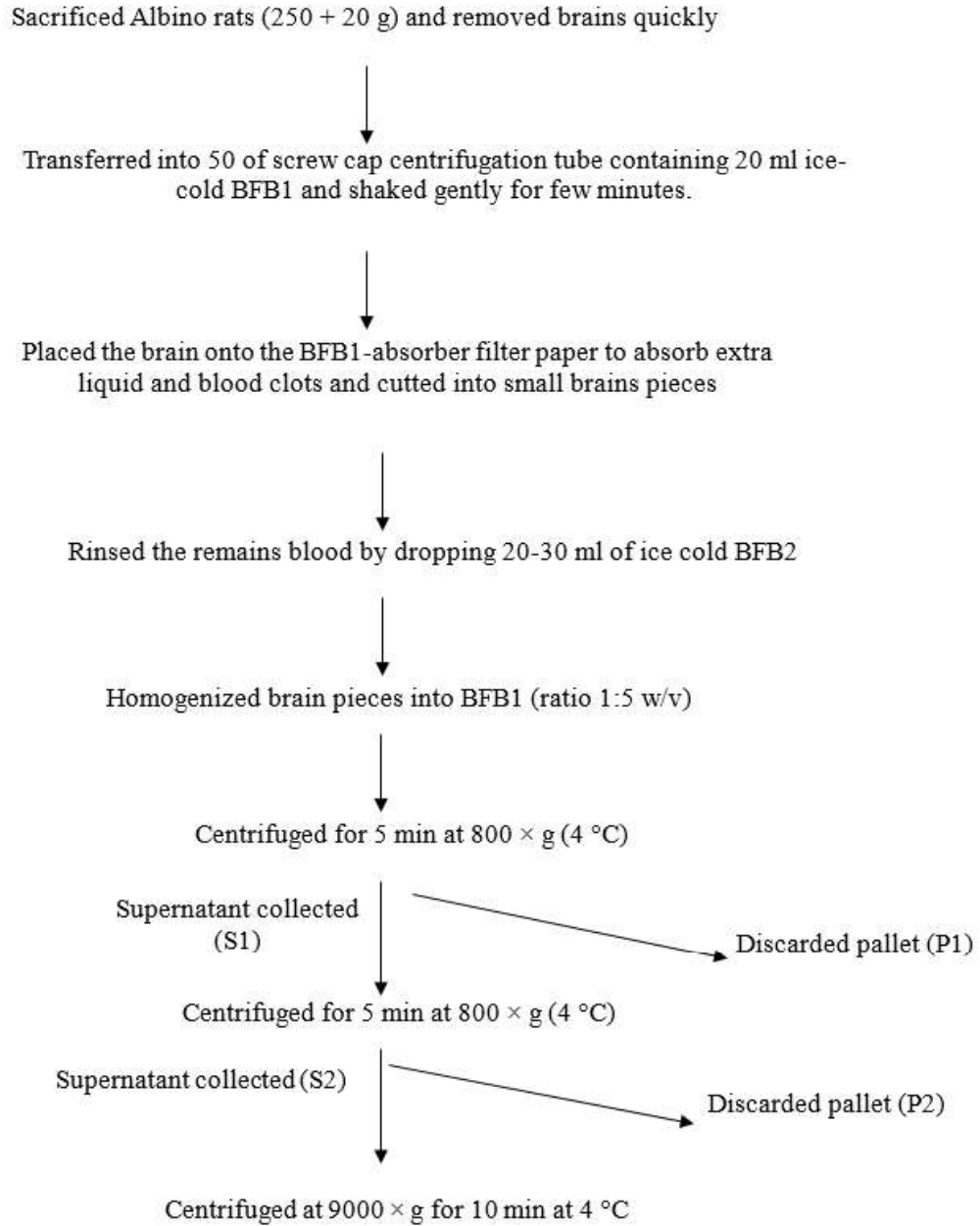
The experiments were conducted on the Charles-Foster strain of adult albino male rats (250 + 20 g), procured by Central Animal House of the Institute of Medical Sciences (IMS-BHU). All experimental protocols were carried out as per the approved guideline of principles of laboratory animal care (National Research Council US Committee for the Update of the Guide for the Care and Use of Laboratory Animals 2011) and approved by the Institutional animal ethical committee, Banaras Hindu University (Dean/2019/IAEC/1243).

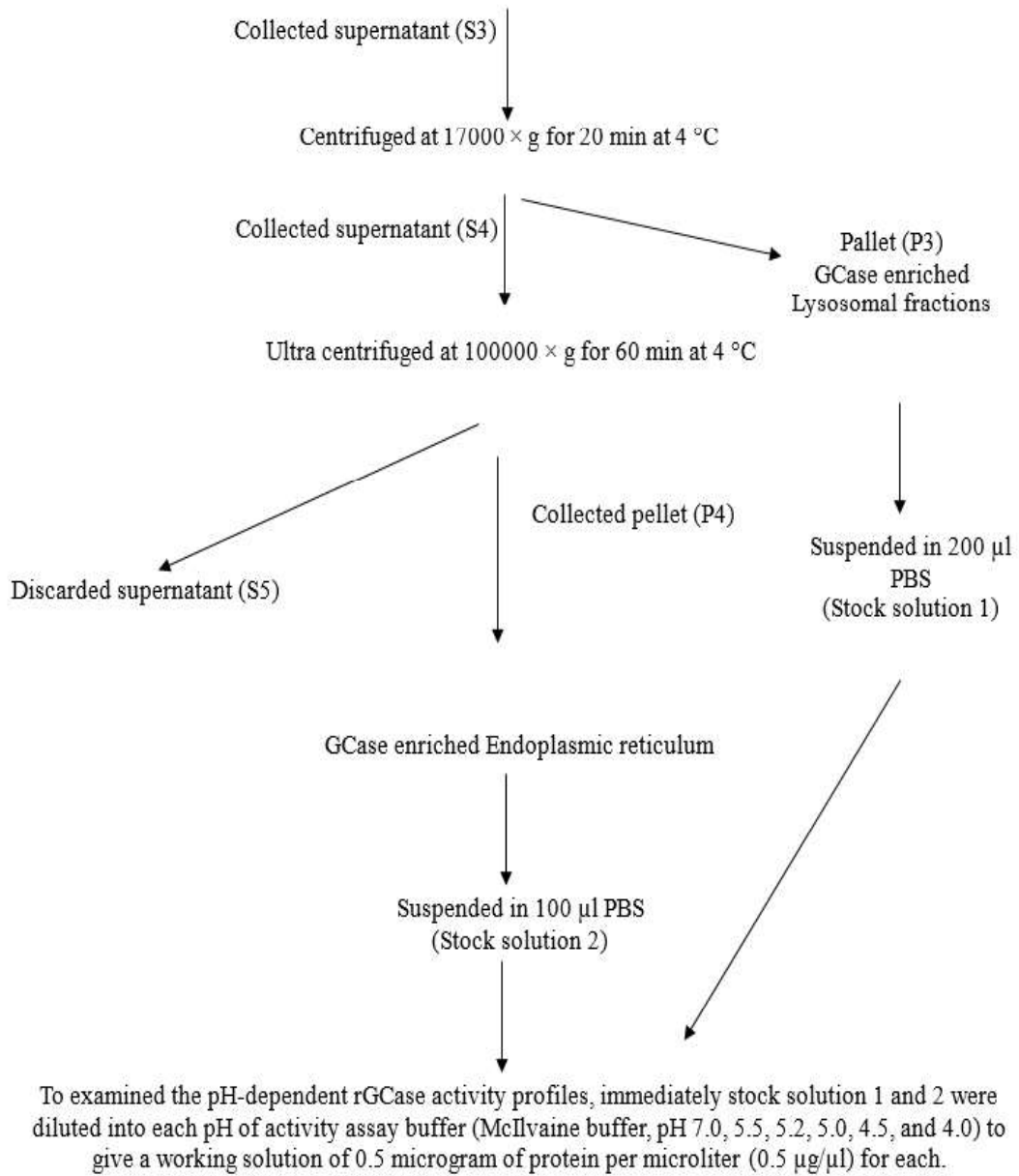
### **2.3 Preparation of Buffers:**

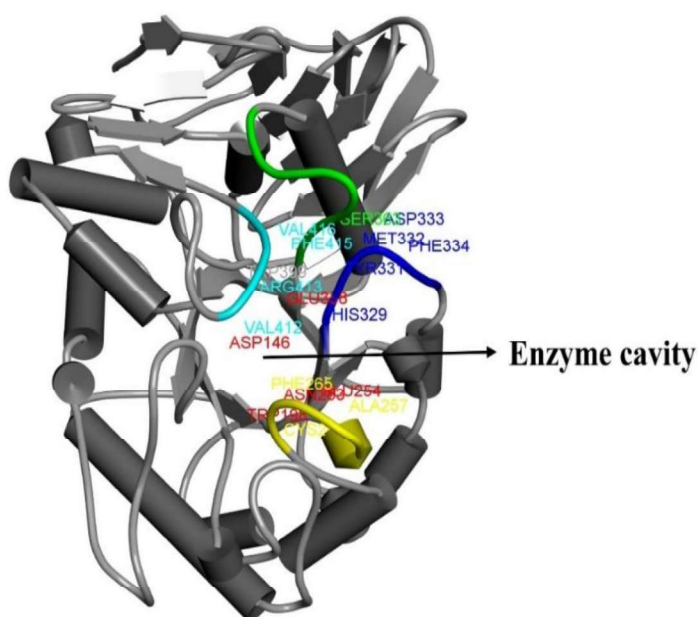
**2.3.1 Brain fractionation buffer 1 (BFB1):** 225 mM mannitol, 75 mM sucrose, 0.5 mM EGTA, 0.5% bovine serum albumin, 30 mM Tris-HCl, pH 7.4. Prepared in triple-distilled water (1 day before the experiments). To this, add a fresh protease inhibitor (dilution 1:100) to avoid sample proteolysis just before starting the experiments.

- 2.3.2 Brain fractionation buffer 2 (BFB2):** 225 mM mannitol, 75 mM sucrose, 30 mM Tris-HCl, pH 7.4. Prepared 1 day before the experiment in triple-distilled.
- 2.3.3 Enzyme activity assay buffer (McIlvaine buffer):** 100 mM sodium citrate, 200 mM sodium phosphate buffer, 0.2% TDC and 0.1% Triton-100, pH 7.0, 5.5, 5.2, 5.0, 4.5 and 4.0. Freshly prepared in triple-distilled water.
- 2.3.4 Note.** Isolation procedures must be carried out at 4°C. Equipment and solutions should be pre-cooled before use. Protein concentration was determined by the Lowry method (Lowry, Rosebrough et al. 1951, Hammond, Meador-Woodruff et al. 2012, Berger, Perkins et al. 2015, Schreiner and Ankarcróna 2017).

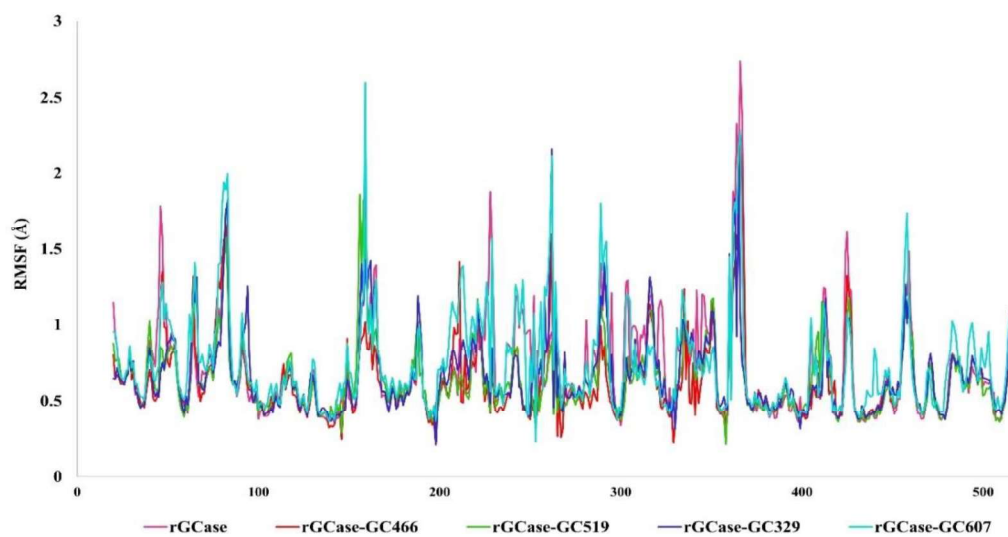
**2.4 Procedure:**



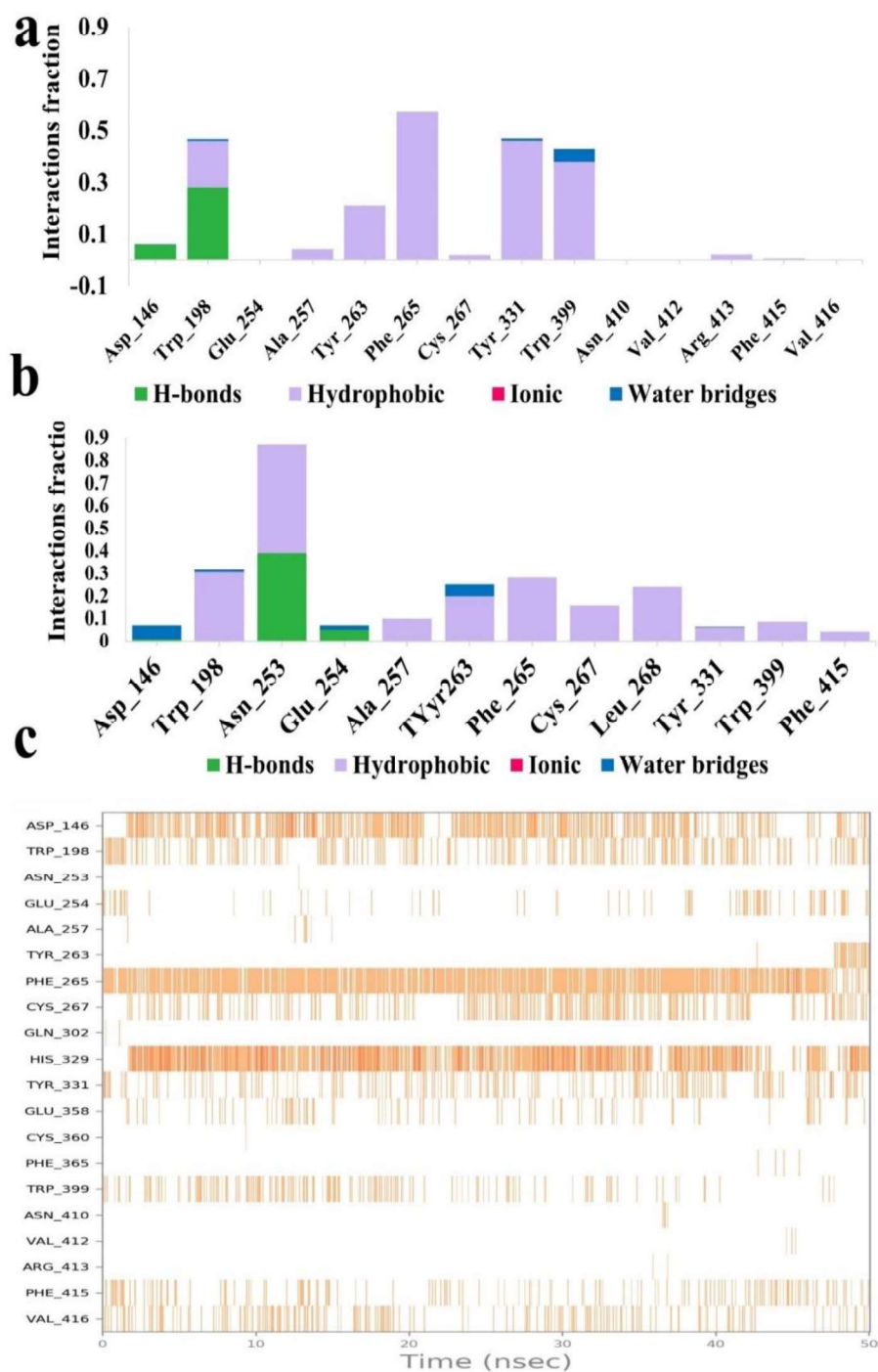




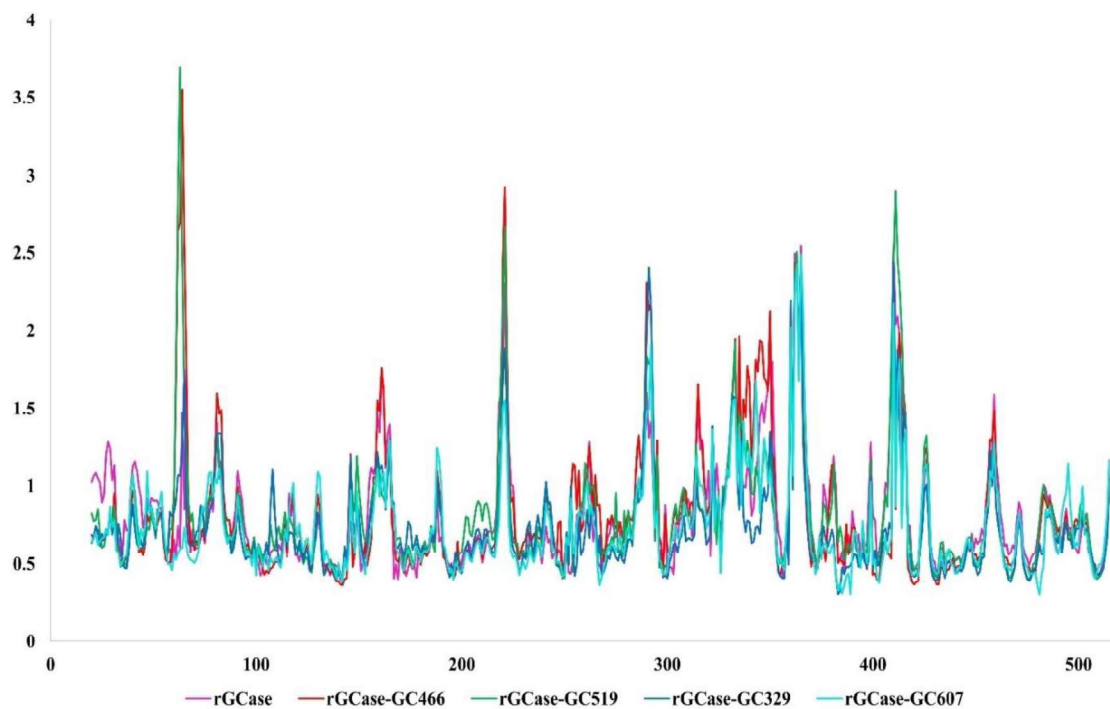
**Figure 3.1** rGCCase active site residues. Loop 1, loop 2, loop 3, and loop 4 are denoted by Blue, Green, Turquoise, and Yellow colour, respectively.



**Figure 3.2** Influence of pH 7.0 on protein (C- $\alpha$  atoms) RMSF plots before and after ligand binding during a 50 ns simulation.

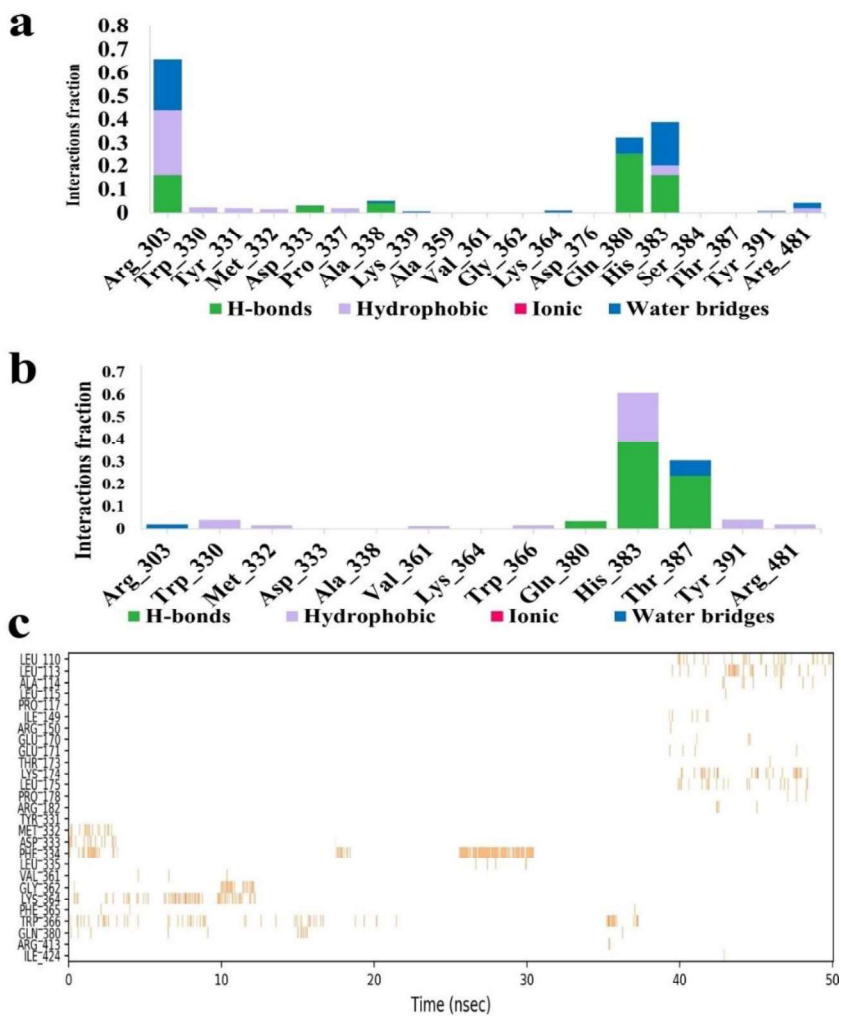


**Figure 3.3** GC329 (a) and GC607 (b) 50 ns PL-contact time frame plots at pH 7.0. A value of 0.8 indicates that the specific interaction is maintained 80% of the time during the simulation.

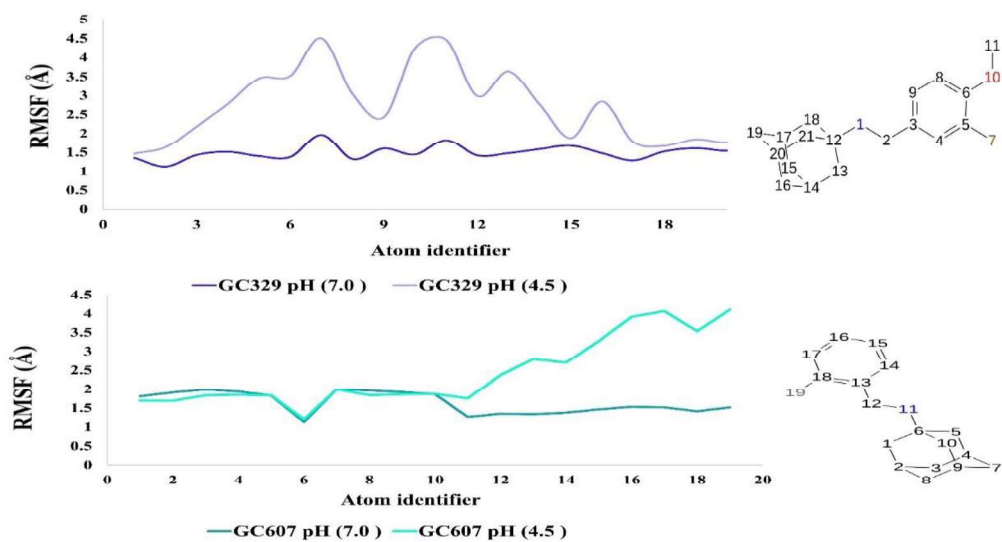


**Figure 3.4** Effect of pH 4.5 on protein (C- $\alpha$  atoms) RMSF plots before and after ligand binding during a 50 ns simulation.

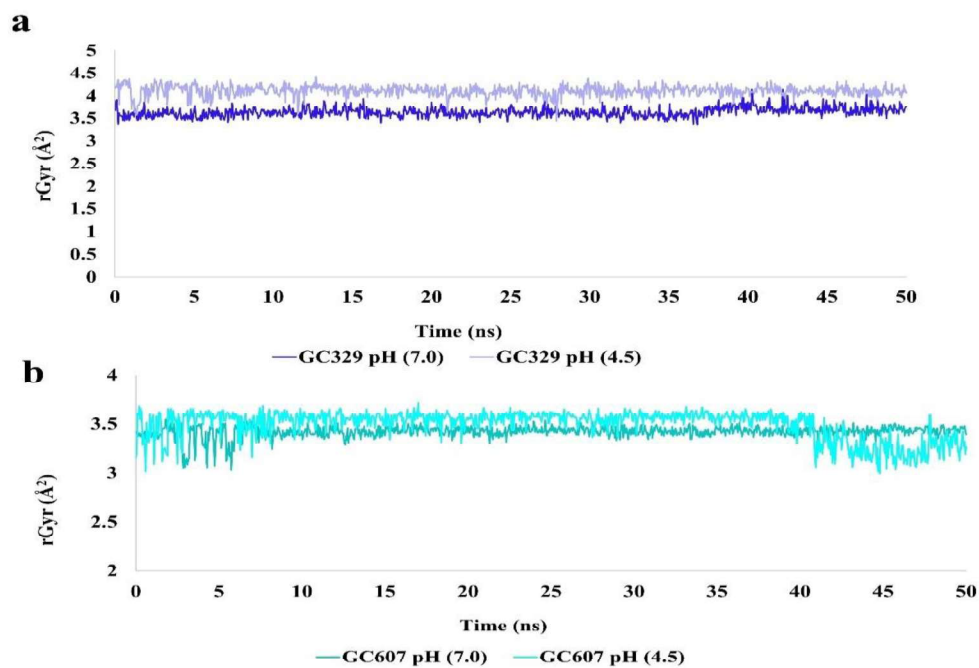
Contacts timeline representation (c) of the top ligand (GC466) with protein throughout the trajectory (50 ns) at pH 7.0.



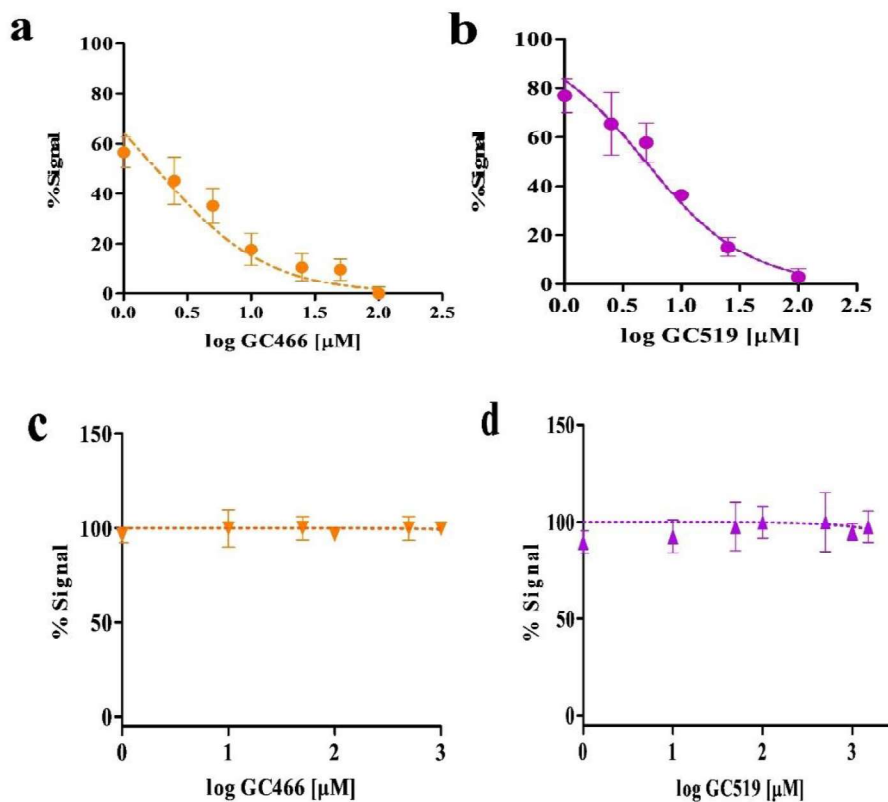
**Figure 3.5** GC329 (a) and GC607 (b) 50 ns PL-contact time frame plots at pH 4.5. A value of 0.1 indicates that the specific interaction is maintained 10% of the time during the simulation. Contacts timeline representation (c) of the top ligand (GC466) with protein throughout the trajectory (50 ns) at pH 4.5.



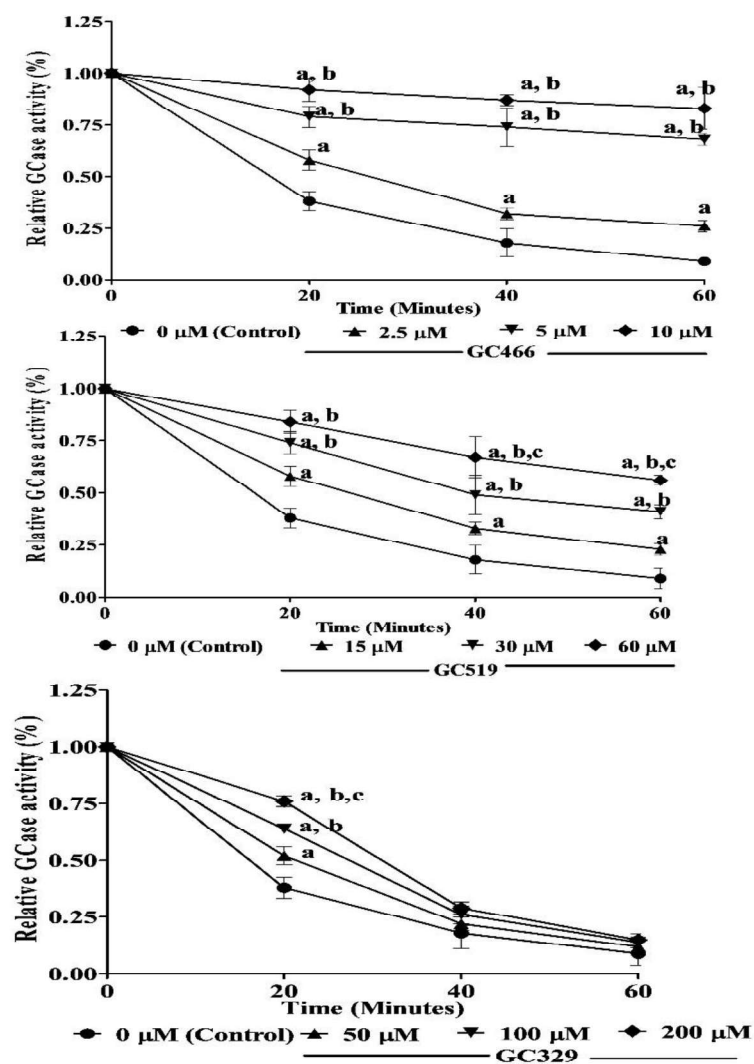
**Figure 3.6.** A comparative RMSF plot between pH 7.0 and 4.5 of ligands GC329 (blue) and GC607 (turquoise).



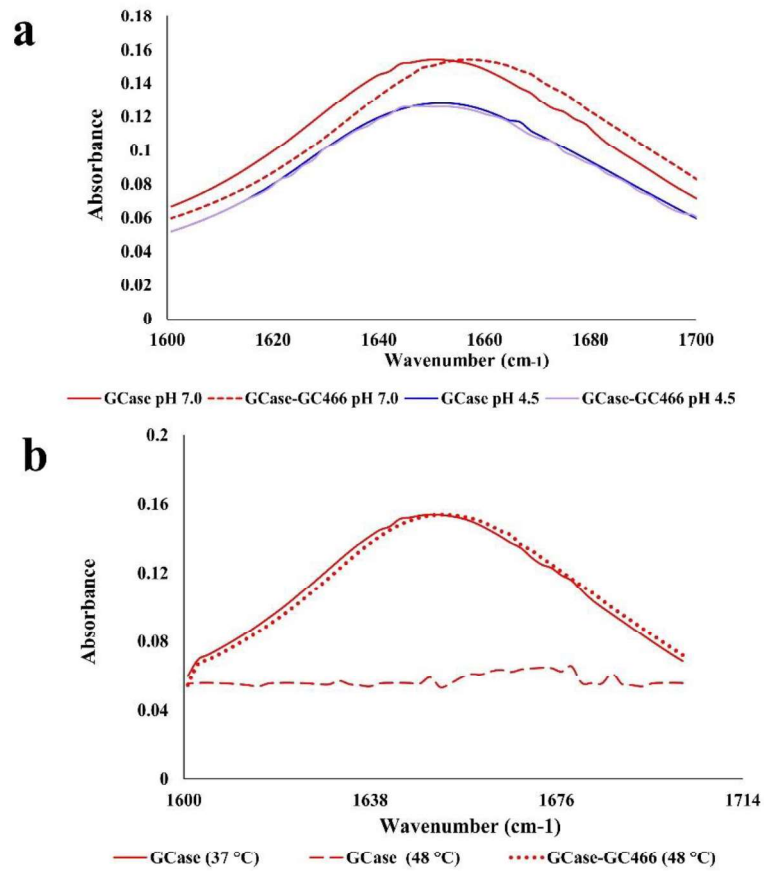
**Figure 3.7** A comparative radius of gyration (rGyr) plots between pH 7.0 and 4.5 of ligands GC329 (blue) and GC607 (turquoise).



**Figure 3.8** The concentrations and pH-dependent sigmoidal plots of top two ligands for rGCCase are depicted graphically. a and b, plots depict for pH 7.0. c and d, show for pH 4.5. rGCCase activity is represented as a % of the fluorescent signal. rGCCase isolated from Charles-Foster strain of adult albino male rats (250 + 20 g) provided by Central Animal House of the Department of Zoology, Institute of Science, Banaras Hindu University. The Institutional Animal Ethical Committee approves experimental protocol (IAEC, Reference No; BHU/DoZ/IAEC/2021-2022/047).



**Figure 3.9** Relative GCase activity after thermal denaturation (TD, 48 °C) during 1 hr at the indicated compounds concentrations (μM), compared to the corresponding 0 °C (control) assay. All values are shown in the form of mean ± SD; n = 3. <sup>a</sup>p < 0.05 compared to the corresponding time of the untreated group (control). <sup>b</sup>p < 0.05 compared to the corresponding time of 2.5 μM, 15 μM, and 50 μM for GC466, GC519, and GC329, respectively. <sup>c</sup>p < 0.05 compared to the corresponding time of 30 μM and 100 μM for GC519 and GC329, respectively [Two-way ANOVA followed by Bonferroni multiple comparison tests, Graph Pad Prism 5.1 Software, Inc].



**Figure 3.10** The FT-IR spectra of free rGCCase and rGCCase-GC466 complex at 37 °C (under body temperature condition, Fig. a) and thermal denaturation condition (48 °C, Fig b) at the region of 1700–1600 cm<sup>-1</sup>. rGCCase protein kept at 37 °C (body temperature) is considered a control for thermal denaturation conditions.

### 3.1 Circular dichroism (CD) spectroscopy studies

Circular dichroism (CD) spectroscopy (Jasco J-810 Analytical Instruments) was used to examine changes in the secondary structure of the rGCCase protein induced by pHs or ligands in accordance with a procedure previously described with a few modifications (Xiao, Gu et al. 2014, Li, Hu et al. 2018, Dai, Chen et al. 2019). There were two different sets of experiments run. In the first set, we determined the rGCCase's spectra (10  $\mu\text{g}$ , 0.5  $\mu\text{g} / \mu\text{l}$ ) from 190 to 250 nm at pH 7.0 and 4.5 of McIlvaine buffer (100 mM citric acid, 200 mM sodium phosphate buffer) in the presence or absence of the test compound GC466 (0.65  $\mu\text{M}$ , concentration selected based on our *in vitro* kinetics study where we found 0.65  $\mu\text{M}$  have good binding affinity for rGCCase], after subtracting the background spectra of the corresponding test buffer solution. The top compound selected for this study was based on our *in silico* and *in vitro* study. This experiment was performed under normal conditions (37  $^{\circ}\text{C}$ , body temperature).

The second series of experiments, however, involved recording CD spectra at pH 7.0 after thermally exposing the rGCCase (200  $\mu\text{g}$ , 20  $\mu\text{l}$ ) at 48  $^{\circ}\text{C}$  for 60 min in either the presence or absence of GC466 (10  $\mu\text{M}$ ). rGCCase protein kept at 37  $^{\circ}\text{C}$  (body temperature) is considered as control GCCase. Our thermal denaturation assay experiment (section 2.2.4.2) served as the basis for selecting the temperature, concentration, and time. The instrument was set at a 1 mm path-length cell, 100 nm/min scanning speed, 1 nm bandwidth, 4 s response time, and a 1.0 nm data pitch. Nitrogen was continually pumped through all samples during all of the measurements. Each spectrum represented the average of three scans. The CD spectroscopic data were analyzed using the online

BESTSEL software (<https://bestsel.elte.hu/index.php>) to determine the secondary structure, such as  $\alpha$ -helix,  $\beta$ -sheet, and random coil.

### 3.1.1 Observations

The investigation of the secondary conformation forms of proteins using CD spectroscopy has been proven to be a trustworthy technique. In light of this, it may be possible to better comprehend how pH variations or the presence of ligands affect protein conformation (Xiao, Gu et al. 2014, Dai, Chen et al. 2019). With these facts in mind, in the first set, we discovered changes in the structure of the rGCCase protein at lysosomal pH 4.5 in comparison to ER pH 7.0 in both the presence and absence of the test substance GC466 at normal body temperature (37 °C). At pH 7.0, two negative bands, characteristic of helix structures, were discernible in the rGCCase CD profile. They were located around 209 and 222 nm (**Figure 3.16a in Chapter 3**). When the pH was altered from 7.0 to 4.5, the values of %  $\alpha$ -helix (pH 7:0 to 4.5:  $18.40 \pm 0.15\%$  to  $15.42 \pm 0.13\%$ ) and negative ellipticity decreased, but the % random coil increased (pH 7:0 to 4.5:  $22.01 \pm 0.25\%$  to  $25.72 \pm 0.16\%$ ), indicating alterations in the rGCCase secondary structure at pH 4.5 as compared to 7.0. Similarly, in our *in silico* work, we observed conformational alterations when comparing rGCCase pH 7.0 to 4.5 (**Figure 3.1 in appendices**). Also, similar observations were found in our earlier study (Tripathi, Ganeshpurkar et al. 2022). As previously described, changes in the position of hydrogen bond formation may cause changes in the secondary structure of proteins (Zhao, Wen et al. 2020). In the meantime, the protein-ligand interaction in terms of protein's structural alterations in the presence of GC466 at both pHs has also been examined. The contents of the  $\beta$ -sheet and random coil in rGCCase at pH 7.0 after the addition of GC466 increased from  $21.20 \pm 0.14\%$  to  $23.18$

$\pm 0.16\%$  and  $22.01 \pm 0.25\%$  to  $26.20 \pm 0.17\%$ , respectively. In contrast, the contents of the  $\alpha$ -helix significantly decreased from  $18.4 \pm 0.15\%$  to  $17.5 \pm 0.26\%$ . These findings suggested that the binding of GC466 may cause conformational changes in the rGCase, characterized by a decrease in the  $\alpha$ -helix and an increase in the random coil, as reported in other studies (Zhao, Wen et al. 2020). This research-backed with our findings from the MD simulation, where we observed stable interactions between rGCase and GC466. According to an *in vitro* investigation, this persistent association may also be the cause of the enzyme's inhibition at pH 7.0 (**Section 3.3.4 and Table 3.2 in chapter 3 and, Figure 3.8 in appendices**). However, at pH 4.5, the contents of rGCase protein secondary structure in either free or complex form were similar [ $\alpha$ -helix:  $15.42 \pm 0.13\%$  (rGCase) and  $15.41 \pm 0.17\%$  (rGCase –GC466);  $\beta$ -sheet:  $20.5 \pm 0.18\%$  (rGCase) and  $20.51 \pm 0.12\%$  (rGCase –GC466; random coil:  $25.72 \pm 0.16\%$  (rGCase) and  $25.70 \pm 0.14\%$  (rGCase –GC466)]. These results demonstrated no persistent interactions between them at pH 4.5, as discovered in our MD simulation. This might be the result of the enzyme activity losing its inhibition around pH 4.5, according to *in vitro* research.

In the second series of tests (**Figure 3.16a in Chapter 3**), using CD spectroscopy and thermal denaturation conditions, we assessed the stability of interactions of the rGCase-GC466 complex by evaluating rGCase secondary structural changes under thermal conditions. In this context, free rGCase and rGCase-GC466 complex were thermally exposed at  $48\text{ }^{\circ}\text{C}$  for 60 min. The rGCase Since GC466 only interacts with rGCase in stable ways at pH 7.0; thus, we have chosen this pH. The structural alterations or denaturation of the protein by CD spectra was evaluated online for a free or complex form of rGCase by the online BESTSEL software approach. We observed that the rGCase was denatured after being exposed to heat ( $48\text{ }^{\circ}\text{C}$ ) for 60 minutes, as seen by a very low elliptical negative peak at 210 nm and a negative band close to 198 nm while compared

to its control rGCCase (37 °C, body temperature) (Greenfield 2006). These data indicated a complete loss in  $\alpha$ -helix structures. On the other hand, the complex form was able to retain the  $\alpha$ -helix structures even after 60 minutes of thermal denaturation, as evidenced by two sharp negative bands at approximately 209 and 222 nm. These observations are enough to comprehend that GC466 may have the ability to bind with rGCCase and stabilize it before it becomes denatured. The chaperoning capacity of GC466 is demonstrated by its ability to bind to rGCCase and stabilize it. This result corroborated the findings of our MD simulation and *in vitro* thermal denaturation assay.

### **3.2 Fourier transform infrared (FT-IR) spectra measurements**

The FT-IR spectra of rGCCase and its GC466 complex were measured for the first set of the experiment in the range of 1700–1400  $\text{cm}^{-1}$  at pH 7.0 and 4.5. However, the second set involved recording FT-IR spectra at pH 7.0 after thermally exposing the rGCCase at 48 °C for 60 min in either the presence or absence of the GC466 (**detailed in Section 3.1**). The ATR method of the FT-IR spectrometer (Bruker Optics, Germany) was employed for detection at wavenumbers between 1600 and 1700  $\text{cm}^{-1}$  with a resolution of 4  $\text{cm}^{-1}$  and 60 scans. Meanwhile, the corresponding absorbance values of free GC466 and buffer solutions were recorded and subtracted with the same instrumental parameters. Data were analyzed using Origin software (version 6.0, Origin Lab, Northampton, MA, USA (Han, Fang et al. 2017)).

#### **3.2.1 Observations**

Further evidence for conformational changes in rGCCase and protein-ligand interactions affected by pHs was further confirmed by FT-IR spectroscopy. In the IR region, proteins exhibit a number of amide bands in different ranges of wavenumbers, representing different vibrations of the peptide moiety. Among these amide bands of protein, amide I bands of IR spectra, which mainly originated from the C = O stretching vibration

severally and occur in the region 1700–1600  $\text{cm}^{-1}$ , have been extensively used in the characterization of protein-ligand interactions and conformational studies of proteins (Han, Fang et al. 2017). Thus, in the first set (**Figure 3.10 in appendices**), the FT-IR spectra of free rGCase and rGCase-GC466 complex in the region of 1700–1600  $\text{cm}^{-1}$  were investigated at pH 7.0 and 4.5. It can be seen that the peak position of the amide I band of free rGCase was shifted from 1654 to 1657  $\text{cm}^{-1}$  after shifting the pH from 7.0 to 4.5. The spectral ranges between 1650–1660  $\text{cm}^{-1}$  are ascribed to the  $\alpha$ -helix by the well-known assignment criterion (Han, Fang et al. 2017). In light of this, the changes above in peak positions, particularly in these areas, might be the result of changes to the rGCase  $\alpha$ -helix conformation. This conclusion is supported by the results of the CD spectroscopy and MD simulation (**Figure 3.10 in chapter I and 3.1 appendices**), in which a change in  $\alpha$ -helix has been observed while lowering the pH from 7.0 to 4.5. Meanwhile, the protein-ligand stability in terms of protein's structural alterations in the presence of GC466 at both pHs have also been examined. At pH 7.0, upon the addition of GC466 to rGCase, the peak position of the amide I band shifted from 1654 to 1658  $\text{cm}^{-1}$ . This phenomenon suggested that GC466 makes a stable complex with rGCase by interacting with the C=O group in the protein structure subunits. However, no shifts in peaks were observed at pH 4.5 after the addition of GC466 to rGCase (free rGCase: 1656  $\text{cm}^{-1}$ ; rGCase-GC466 complex: 1656  $\text{cm}^{-1}$ ), indicating no interaction between them at this pH. A similar observation was also found in our MD study, where GC466 has only stable interaction with rGCase at pH 7.0.

In the second set (**Figure 3.10 in appendices**), using FT-IR spectroscopy, we measured the stability of interactions of the rGCase-GC466 complex in terms of structural changes at pH 7.0 in either presence or absence of GC466 under thermal denaturation (48  $^{\circ}\text{C}$ ) conditions. We have found that the peak position of the amide I band for control rGCase

(kept at 37 °C) was 1654 cm<sup>-1</sup> which displayed the characteristic feature of the  $\alpha$ -helix structure. However, the protein was denatured after being exposed to heat for 60 min at 48 °C, as seen by the loss in intensity of the amide I band between 1650-1660 cm<sup>-1</sup> position. With the addition of GC466 to rGCase, a sharp amide I band can be seen at the position of 1656 cm<sup>-1</sup>, indicating the retaining of amide I. However, when this peak position was compared to its control GCase (37 °C) peak (1654 cm<sup>-1</sup>), a shift in the amide I band (1656 to 1654 cm<sup>-1</sup>) was noticed. The changes in these peak positions signified that GC466 makes a stable complex with rGCase at pH 7.0 by interacting with the C=O group of protein subunits and stabilizing it before denatured under thermal denaturation. Similar findings were made in our MD investigation, which showed that GC466 interacts with rGCase most consistently at pH 7.0.

### **3.3. RAMAN spectra measurements**

Raman (Witec alpha 300R, WITEC-RAMAN instrument) spectra of both sets of experiments (**detailed mentioned in section 3.1 in appendices**) at pH 7.0 and 4.5 were determined in the ranges of 400–3050 cm<sup>-1</sup> (Xu, Han et al. 2011, Kang, Li et al. 2017). The protein samples were spread on a glass slide during the measurement and focused on the excitation laser beam (785 nm). The spectra were recorded in the range of 400–3050 cm<sup>-1</sup>. Each spectrum was obtained under the following conditions: 3 scans, 60 s exposure time and 2 cm<sup>-1</sup> resolution. The time required for the acquisition of 1 spectrum was about 2 min. Raman spectral data were averaged over multiple scans, smoothed, baseline corrected, and were plotted using Origin software.

#### **3.3.1 Observations**

Raman spectroscopy further confirmed the pH-dependent conformational changes in rGCase protein and protein-ligand interactions seen in CD, FT-IR, and MD simulation studies. Amide I is the most useful Raman band for determining the secondary structure

of proteins in Raman. Unambiguously, the amide I vibrational mode, which primarily consists of C=O stretching vibrations, has been ascribed to the strong Raman band in the area 1645–1685 cm<sup>-1</sup> (Xu, Han et al. 2011). Thus, in both sets of experiments, we focus on this region (1645-1685 cm<sup>-1</sup>) to investigate protein-ligand interactions and pH-dependent conformational changes of the protein. In the first set (**Figure 3.10b in chapter 3**) it can be seen that when pH changed from 7.0 to 4.5, the amide I band of the Raman spectra of pH 7.0 was displaced from 1656 to 1650 cm<sup>-1</sup>. However, it is well known, the Raman spectral ranges from, 1650–1660 cm<sup>-1</sup> are assigned to  $\alpha$ -helix (Xu, Han et al. 2011, Kang, Li et al. 2017). As a result, the shift in Raman spectra could be attributed to conformational changes in the  $\alpha$ -helix structure of rGCCase, as observed in our MD simulation (**Figure 3.1 in appendices**). In the meantime, the protein-ligand interaction at both pHs has also been examined in terms of structural alteration. At pH 7.0, after mixing the GC466 to rGCCase, the Raman spectrum of the amide I band shifted from 1656 to 1652 cm<sup>-1</sup>, signifying that GC466 interacted with the C=O group in the protein structure subunits and made a stable complex with it, which also seen in MD simulation. This persistent association may also be the cause of the enzyme's inhibition at pH 7.0 (**Section 3.3.4 and Table 3.2 in chapter 3 and, Figure 3.8 in appendices**). However, no changes in the Raman shift of amide I band were visible at pH 4.5 when comparing free rGCCase (1650 cm<sup>-1</sup>) Raman shift to rGCCase-GC466 complex (1650 cm<sup>-1</sup>) Raman shift, indicating no interaction between them. The MD simulation produced results that were very similar; interactions were only seen at pH 7.0. Also, an *in vitro* study suggests that this may be caused by the enzyme activity losing its inhibition around pH 4.5. To dig further, we measured the stability of interactions between rGCCase and GC466 at pH 7.0 under thermal denaturation conditions (**Figure 3.10b in Chapter 3**). pH 7.0 was chosen for this study because GC466 has only stable interaction with rGCCase

at this pH. For control rGCCase (kept at 37 °C), we found sharp Raman spectra of the amide I band at 1656 cm<sup>-1</sup>, which displayed the characteristic feature of  $\alpha$ -helix structure as previously reported (Xu, Han et al. 2011, Kang, Li et al. 2017). However, after heat exposure for 60 min, the loss in Raman spectral of amide I band between 1645- 1685 cm<sup>-1</sup> has been seen signified protein denaturation under thermal exposure conditions. In the addition of GC466 to rGCCase under thermal denaturation conditions, a sharp amide I Raman spectral band can be seen at 1650 cm<sup>-1</sup>. A shift in the amide I (1656 to 1650 cm<sup>-1</sup>) band was observed when this Raman spectral peak position was compared to that of the control GCCase (37 °C). The changes in these peak positions signified that GC466 may interact with the C=O group of protein subunit and stabilize it before being denatured under thermal denaturation. A stable interaction between rGCCase protein and GC466 has also been seen in our MD simulation.

**Table 4.1** Effect of single-dose oral administration of compound GC466 at a dose of 2000 mg/kg on hematological parameters of rats after their death on Day -1

Rats	Hb (g/dL)	RBC (x 10 <sup>6</sup> cells/mL)	WBC (x 10 <sup>3</sup> Cell/mL)	PLT Platelets (x 10 <sup>5</sup> Cells/mL)
1	11.71	5.45	6.01	7.72
2	10.60	4.24	4.11	3.65
3	11.32	6.21	5.78	3.52
4	7.82	2.74	3.58	4.24
5	8.47	4.56	3.88	3.77

**Table 4.2** Effect of single-dose oral administration of compound GC466 at a dose of 2000 mg/kg on the liver, kidneys and heart coefficient of the rats after their death on Day -1

<b>Rats</b>	<b>Liver (g)</b>	<b>Kidneys (g)</b>	<b>Heart (g)</b>
<b>1</b>	4.62	0.74	0.45
<b>2</b>	6.10	0.47	0.37
<b>3</b>	4.23	0.28	0.38
<b>4</b>	5.72	0.54	0.45
<b>5</b>	5.88	0.42	0.35

**Table 4.3** Effect of single-dose oral administration of compound GC466 at a dose of 2000 mg/kg on the lungs, brain and spleen coefficient of the rats after their death on Day -1

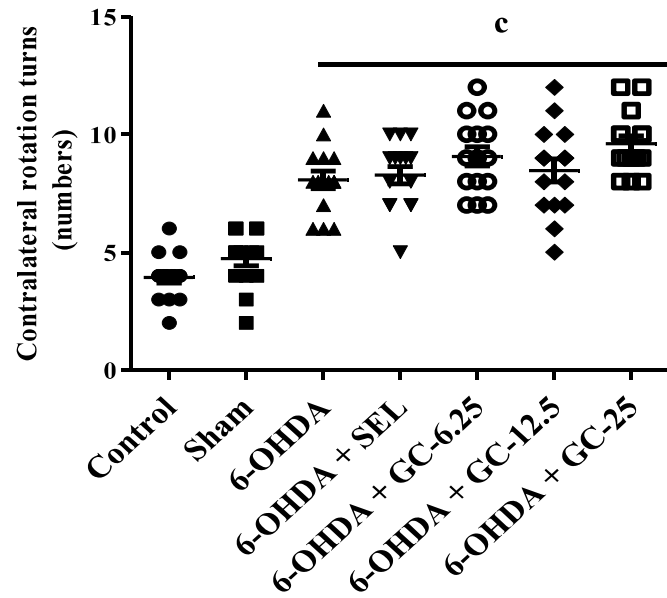
<b>Rats</b>	<b>Lung (g)</b>	<b>Brain (g)</b>	<b>Spleen (g)</b>
<b>1</b>	1.31	1.11	0.49
<b>2</b>	1.25	1.34	0.52
<b>3</b>	0.78	0.84	0.56
<b>4</b>	0.98	1.03	0.39
<b>5</b>	1.60	0.75	0.56

**Table 4.4** Effect of single-dose oral administration of compound GC466 at a dose of 2000 mg/kg on serum hepatic enzyme parameters of the rats after their death on Day -1

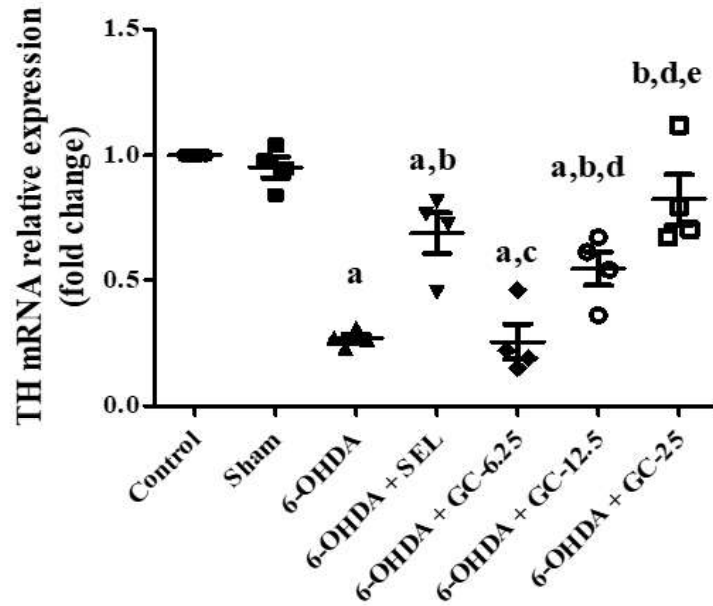
<b>Rats</b>	<b>AST(IU/L)</b>	<b>ALT(IU/L)</b>	<b>ALP (IU/L)</b>
<b>1</b>	126.54	50.72	150.86
<b>2</b>	154.32	42.14	144.72
<b>3</b>	290.52	34.82	200.70
<b>4</b>	210.65	56.57	168.91
<b>5</b>	286.85	61.22	131.43

**Table 4.5** Effect of single-dose oral administration of compound GC466 at a dose of 2000 mg/kg on the serum creatinine and CK-MB (heart) parameters of the rats after their death on Day -1.

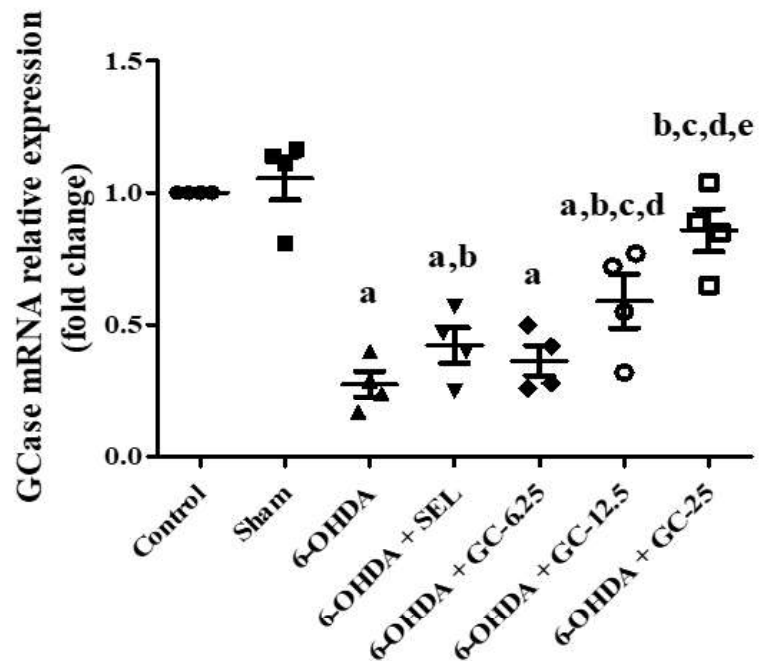
<b>Rats</b>	<b>Creatinine (mmol/L)</b>	<b>CK-MB (ng/mL)</b>
<b>1</b>	70.82	22.27
<b>2</b>	91.53	40.60
<b>3</b>	76.32	36.65
<b>4</b>	80.06	48.71
<b>5</b>	76.53	42.62



**Figure 5.1** Effect of GC466 on 6-OHDA-induced alteration in apomorphine-induced rotations on Day-4. All values are shown as mean  $\pm$  SD; n = 16; <sup>c</sup>p < 0.05 compared to control and sham [One-way ANOVA followed by Tukey Post-hoc test, Graph Pad Prism 5.1 Software, Inc].



**Figure 5.2** Effect of GC466 on 6-OHDA-induced alteration in Tyrosine hydroxylase (TH) mRNA level. Results are expressed as mean  $\pm$  SD; n = 4; <sup>a</sup>p < 0.05 compared to sham, <sup>b</sup>p < 0.05 compared to 6-OHDA and <sup>c</sup>p < 0.05 compared to 6-OHDA + SEL, <sup>d</sup>p < 0.05 compared to 6-OHDA + GC-6.25 and <sup>e</sup>p < 0.05 compared to 6-OHDA + GC-12.5 [One-way ANOVA followed by Tukey post-hoc test, Graph Pad Prism 5.1 Software, Inc].



**Figure 5.3** Effect of GC466 on 6-OHDA induced alterations in glucocerebrosidase (GCCase) mRNA levels in PD rats. Results are reported as mean  $\pm$  SD;  $n = 4$ ; <sup>a</sup> $p < 0.05$  compared to sham, <sup>b</sup> $p < 0.05$  compared to 6-OHDA and <sup>c</sup> $p < 0.05$  compared to 6-OHDA + SEL, <sup>d</sup> $p < 0.05$  compared to 6-OHDA + GC-6.25 and <sup>e</sup> $p < 0.05$  compared to 6-OHDA + GC-12.5 [One-way ANOVA followed by Tukey post-hoc test, Graph Pad Prism 5.1 Software, Inc].

- **List of publications from thesis:**
- **Pratigya Tripathi**, Ankit Ganeshpurkar, Sushil Kumar Singh, S. Krishnamurthy, Generation of wild-type rat Glucocerebrosidase homology modeling: Identification of putative interactions site and mechanism for chaperone using combined in silico and invitro studies, *Bioorganic Chemistry* 126 (2022) 105871. DOI: 10.1016/j.bioorg.2022.105871.
- **Pratigya Tripathi**, Ankit Ganeshpurkar, Sushil Kumar Singh, S. Krishnamurthy, Identification of novel glucocerebrosidase chaperone for potential treatment of Parkinson's disease: An approach using *in silico* virtual screening, molecular docking and molecular dynamics, and *in vitro* studies. *International Journal of Biological macromolecules*, 228(4) (2023) 453-466. DOI: 10.1016/j.ijbiomac.2022.12.217.
- **List of publications during Ph.D**
- Ankit Ganeshpurkar, Ravi Singh, **Pratigya Tripathi**, Qadir Alam, Sairam Krishnamurthy, Ashok Kumar, Sushil Kumar Singh, Effect of sulfonamide derivatives of phenylglycine on scopolamine-induced amnesia in rats" *Ibrain*, 9(2023) 13-31. DOI: [doi.org/10.1002/ibra.12092](https://doi.org/10.1002/ibra.12092).
- **Under review from the Thesis**
- **Pratigya Tripathi**, Ela Mishra, Mahendra Kumar Thakur, and Sairam Krishnamurthy, Modulation of ER stress- glucocerebrosidase pathway involved in the neuroprotective effect of novel compound GC466 in the 6-OHDA-induced Parkinson's disease model: A new molecular mechanism and treatment approach for Parkinson's disease is under review in "*Progress of Neurobiology*."

- **Under review from the other projects during PhD**
- Ankit. Ganeshpurkar, Ravi. Singh, **Pratigya Tripathi**, Qadir Alam, Sairam Krishnamurthy, Ashok Kumar, Sushil Kumar Singh, Effect of sulfonamide derivatives of para-aminobenzoic acid on scopolamine-induced amnesia in rats communicated in “*Experimental Brain Research*”