S.No.	Description	For Normal Date	a in Rs. (up to 200 NS)		
1.	Molecular Docking - Ligand preparation, Protein Preparation				
	Server Processing, GPU Utilization & Memory usage	Memory Usage			
		For up to 1 MB	500		
		More than 1MB	5 per MB		
		For up to 1 GB	1000		
		More than 1 GB	1000 per GB		
		GPU Utilization	time		
		For up to 24	100		
		hours	5 per hour		
		More than 24 hours			
2.	ADME Profiling	200 (up to 50 con	npounds)		
3. Molecular and High Throughput Virtual Screening					
		Memory Usage			
	Server Processing, GPU Utilization & Memory usage	For up to 1 MB	500		
		More than 1MB	5 per MB		
		For up to 1 GB	1000		
U		More than 1 GB	1000 per GB		
		GPU Utilization	time		
		For up to 24	100		

hours

5 per hour

More	than	24
hours		

4. Active site prediction

200 per protein

5. Protein Structure Prediction

3. Trotein Structure Trediction					
	Server Processing, GPU Utilization & Memory usage	Memory Usage			
		For up to 1 MB	500		
		More than 1MB	5 per MB		
		For up to 1 GB	1000		
		More than 1 GB	1000 per GB		
		GPU Utilization time			
		For up to 24 hours	100		
		More than 24 hours	5 per hour		
6.	QSAR				
	If structural analogs to be prepared	5000			
	If they bring structural analogs (100 Nos)	1000			
7.	and simulation				
	(i) Minimum charges(up to 24 hrs computer	2500			
	time) (ii) Every additional hour of computer time	50 per hour			
8.	Service Charges	25 per hour			