

## LIST OF FIGURES

FIGURE NO.	TITLE	PAGE NO.
3.1	Digestive fates of carbohydrates, lipids, and proteins	15
3.2	Secondary structure of fungal alpha amylase	29
3.3a	PROMOTIF summary: Secondary structure of fungal alpha amylase	30
3.3b	PROMOTIF summary: Secondary structure of fungal alpha amylase	31
3.4	Catalytic mechanism of fungal alpha amylase involving three residues	36
3.5	LIGPLOT of metal's interactions with Taka-amylase	38
3.6	Structure of cyclodextrin	43
3.7	Dimensions of cyclodextrins	46
3.8	Structure of cellulose acetate phthalate	50
5.1	Indian Pharmacopoeial methods for estimation of fungal alpha amylase showing disappearance of the blue colour in the test medium indicates the completion of starch hydrolysis	156
5.2	Typical radial diffusion assay starch-agar plate showing clear zones of starch digestion produced by fungal alpha amylase and blue colour indicates the presence of undigested starch	166
5.3	Linearity plot of the radial diffusion method	167
5.4	The effect of pH on activity of fungal alpha amylase	170
5.5	Shelf life estimation for fungal alpha amylase powder	172
5.6	Shelf life estimation for fungal alpha amylase in mixed phosphate buffer pH 7.0	173
5.7	UV absorbance scan of fungal alpha amylase	177
5.8	UV absorbance scan of fungal alpha amylase in presence of calcium chloride	178
5.9	Fluorescence spectrum of fungal alpha amylase	179
5.10	Fluorescence spectrum of fungal alpha amylase with calcium chloride	180
5.11	FTIR spectrum of fungal alpha amylase	181
5.12	FTIR spectrum of fungal alpha amylase with calcium chloride	182

5.13	Comparison of oral liquid formulations stability data at 45°C	194
5.14	Comparison of dry syrup formulations stability data at 45°C	200
5.15	Comparison of oral drop formulations stability data at 45°C	204
5.16	Comparison of hard gelatin capsule formulations stability data at 45°C	209
5.17	Enteric sugar coated tablet showing complete disintegration of sugar coat and remaining intact enteric coated tablet in acidic medium	225
5.18	Stability data of enteric sugar coated tablet Batch ES-T-1 at 45°C	227
5.19	Graph representing the drug release from uncoated matrix tablets at buffer stage	235
5.20	Stability data of sugar coated matrix tablet Batch ES-MT-7 at 45°C	238
5.21	Figure A and B showing round shaped fungal alpha amylase enteric coated pellets	244
5.22	Figure showing disintegrated pepsin pellets and intact fungal alpha amylase enteric coated pellets	245
5.23	Stability data of hard gelatin capsule containing fungal alpha amylase enteric coated pellets and pepsin uncoated pellets Batch ESP- C-1 at 45°C	247
5.24	Particle size distribution of enteric coated powder of fungal alpha amylase Batch ECP-1 and ECP-2	251
5.25	Scanning electron micrograph A) Magnification X 1000 and B) Magnification X 1500 of enteric coated fungal alpha amylase Batch ECP-1	253
5.26	Scanning electron micrograph C) Magnification X 2000 and D) Magnification X 4000 of enteric coated fungal alpha amylase Batch ECP-1	254
5.27	Scanning electron micrograph A) Magnification X 1000 and B) Magnification X 1500 of enteric coated fungal alpha amylase Batch ECP-2	255
5.28	Scanning electron micrograph C) Magnification X 2000 and D) Magnification X 3500 of enteric coated fungal alpha amylase Batch ECP-2	256
5.29	Scanning electron micrograph E) Magnification X 6500 of enteric coated fungal alpha amylase Batch ECP-2	257
5.30	Stability data of hard gelatin capsule containing enteric coated fungal alpha amylase and pepsin powder-Batch	262

	ECP-C-1 at 45°C	
5.31	Stability data of tablets containing enteric coated fungal alpha amylase and pepsin powder-Batch ECP-T-1 at 45°C	267
5.32	Stability data of dry syrup containing enteric coated fungal alpha amylase and pepsin powder-Batch ECP-DS-1 at 45°C	272
5.33	Aggregation inhibition of fungal alpha amylase by beta-cyclodextrin	274
5.34	Recovery of fungal alpha amylase activity in excess of initial activity	276
5.35	Effect of enzyme concentration on inclusion complex	277
5.36	UV spectrum of fungal alpha amylase in Tris buffer	283
5.37	UV spectrum of inclusion complex of fungal alpha amylase with beta-cyclodextrin	284
5.38	UV absorbance of inclusion complex of fungal alpha amylase with beta-cyclodextrin at different molecular ratio	285
5.39	Fluorescence spectrum of inclusion complex of fungal alpha amylase with beta-cyclodextrin	286
5.40	FTIR spectrum of inclusion complex of fungal alpha amylase with beta-cyclodextrin	287
5.41	NMR spectrum of fungal alpha amylase	288
5.42	NMR spectrum of inclusion complex of fungal alpha amylase with beta-cyclodextrin	289
5.43	DSC thermograph of fungal alpha amylase	290
5.44	DSC thermograph of inclusion complex of fungal alpha amylase with beta-cyclodextrin	291
5.45	Stability data of oral liquid prepared with inclusion complex of fungal alpha amylase with beta-cyclodextrin of Batch IC-L-1 to IC-L-4 at 45°C	295
5.46	Structure of fungal alpha amylase taken from Brookhaven Protein Data Bank and structure was made by using Raswin Program	297
5.47	Structure of beta-cyclodextrin taken from Brookhaven Protein Data Bank and structure was made by using VMD Program	298

5.48	Binding pocket residues selected for docking are shown in Figure. Figure shows selected residues Arg 204, Glu 230, His 296 and Asp 297 from active site of fungal alpha amylase in Magenta Stick representation and fungal alpha amylase in orange space fill representation. Here remainder selected binding pocket residue His 122, Asp 206 are inside the pocket. The figure was made using Insight II program.	299
5.49	Ramachandran plot for fungal alpha amylase	302
5.50	Ramachandran plot for inclusion complex of fungal alpha amylase with beta-cyclodextrin	303
5.51	Fungal alpha amylase residues that were found to form hydrogen bonding with beta-cyclodextrin are shown in stick representation and beta-cyclodextrin shown in line representation using VMD program	306
5.52	The plot of total solvent accessible surface area for fungal alpha amylase	307
5.53	The plot of total solvent accessible surface area for beta-cyclodextrin- fungal alpha amylase inclusion complex is shown.	308
5.54	Solid surface diagram of the fungal alpha amylase pocket with final docking results of the beta-cyclodextrin (Pymol program used for structural presentation)	311
5.55	Final docked structure represented in form A) cartoon and B) dots using VMD program	312
5.56	Final docked structure represented in form C) surface and D) line using VMD program	313
5.57	Final docked structure represented in form E) mesh and F) ribbon using VMD program	314
5.58	Final docked structure represented in form G) sphere and H) stick using VMD program	315

---