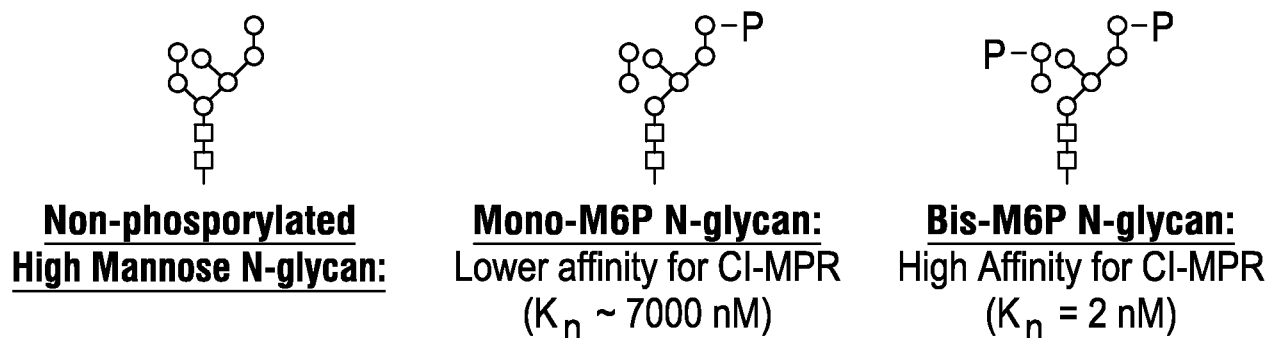


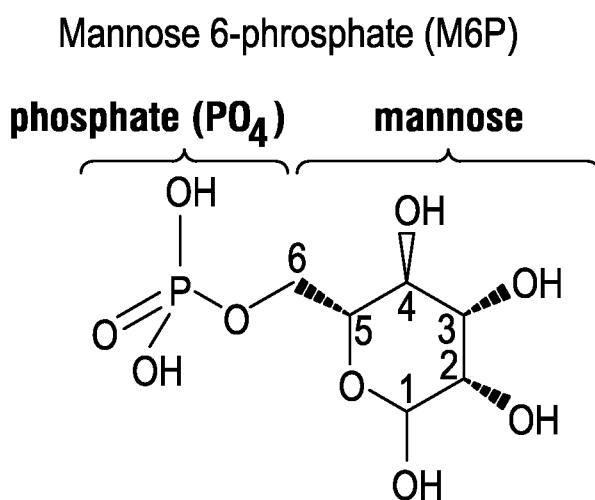
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Fig. 1A

Structure and Receptor Affinity for High Mannose and
Phosphorylated Oligosaccharides

***Fig. 1B***

Chemical Structure of Mannose 6-phosphate



Comparison of Productive and Non-Productive Targeting Glycan Specific Receptors

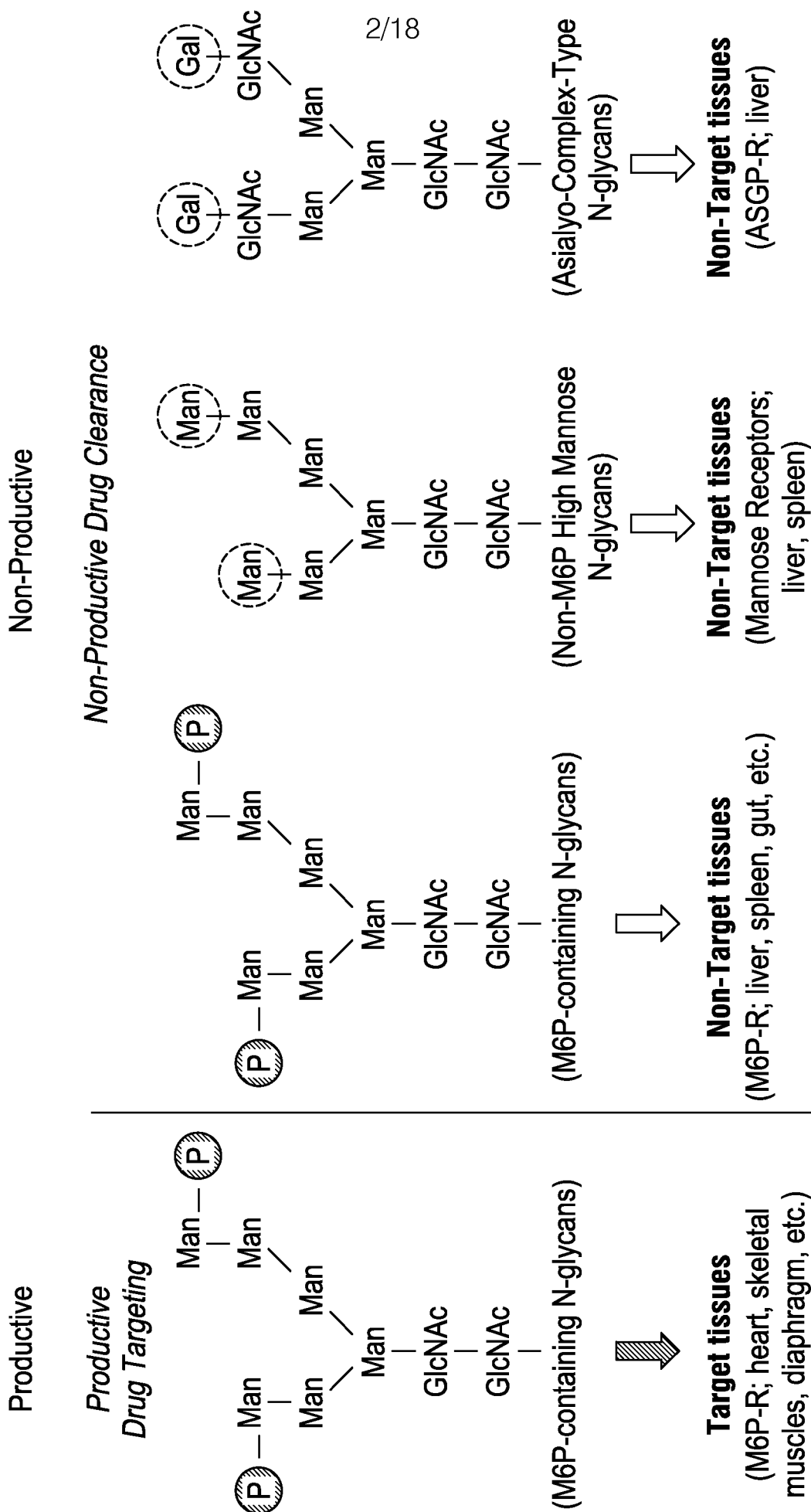


Fig. 2A

Fig. 2B

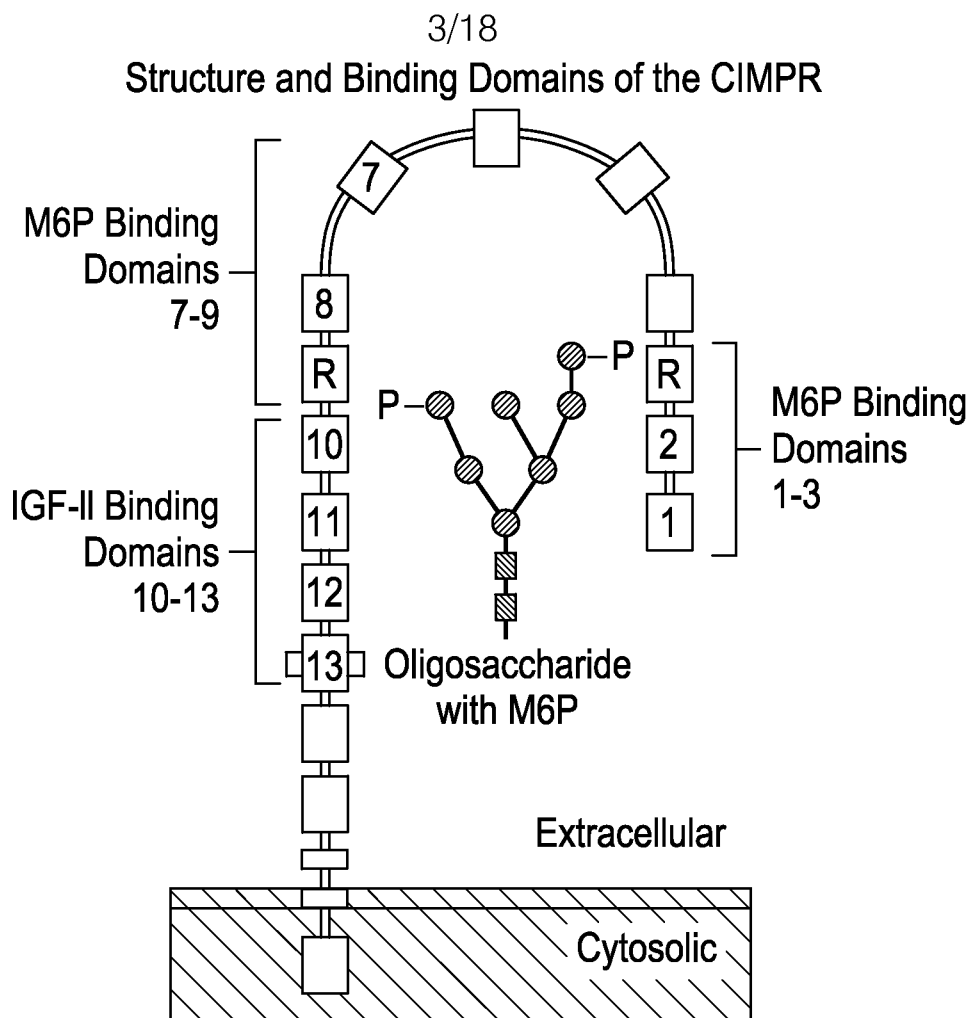


Fig. 3A

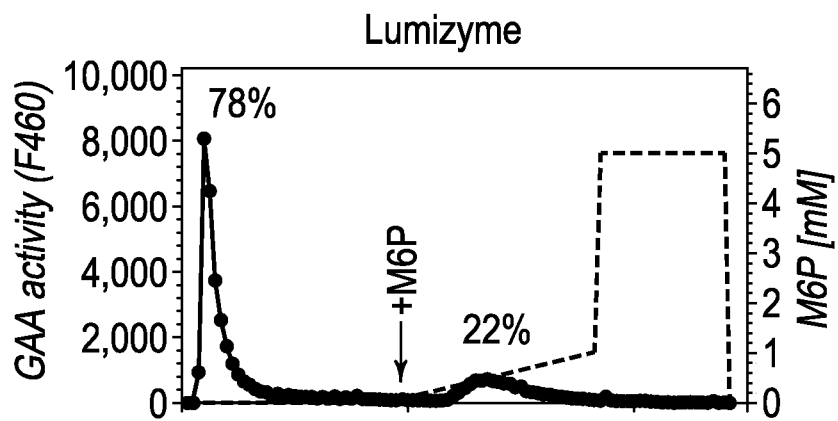
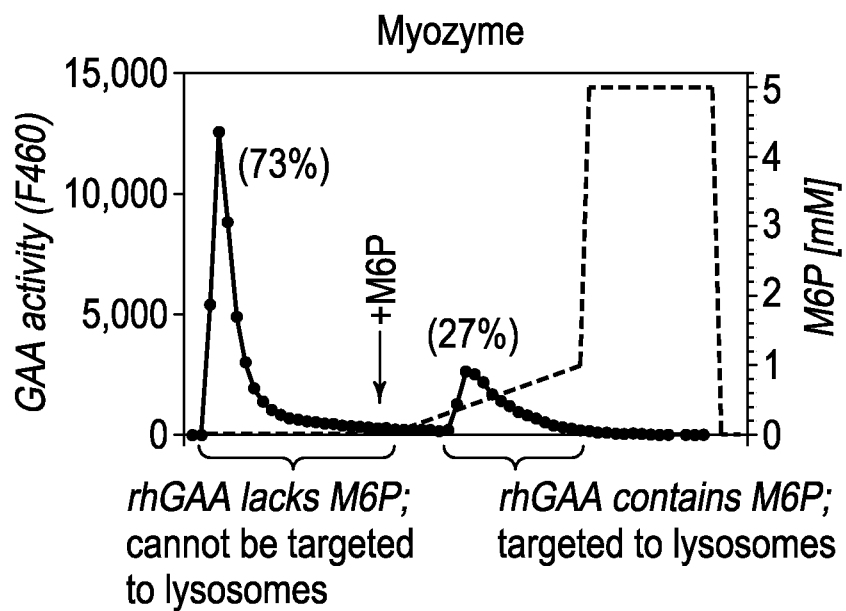
Ligands; Affinity and In Vivo Location of Three Glycoprotein Receptors

Ligand	Receptor	Affinity (nmolar)	Location
Bis-Phosphoylated Glycan	CIMPR	2	All Cells
Mono-Phosphorylated Glycan		7,000	
High Mannose Glycan	Mannose Receptor	20 ^b	Macrophages Dendritic Cells
De-sialylated Complex Glycan	Asialyoglycoprotein Receptor	7 ^c	Hepatocytes

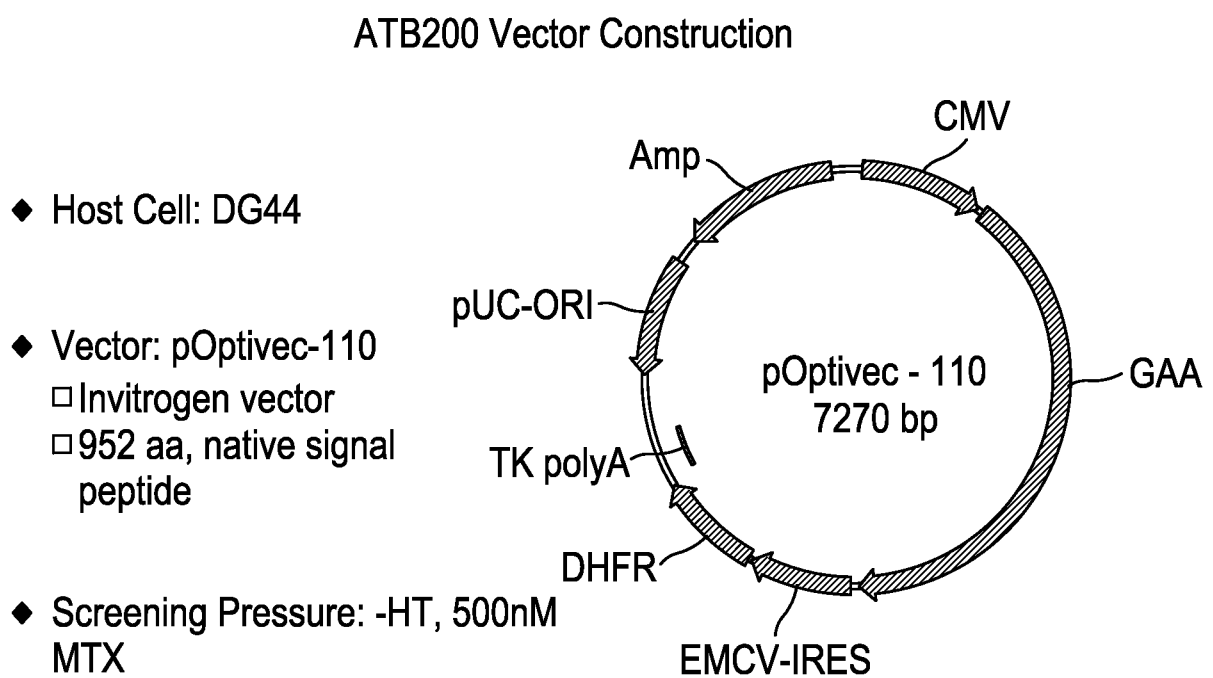
Reference: ^aTong *et al* 1989; ^bTaylor *et al* 1992; ^cSchwartz *et al* 1981

Fig. 3B

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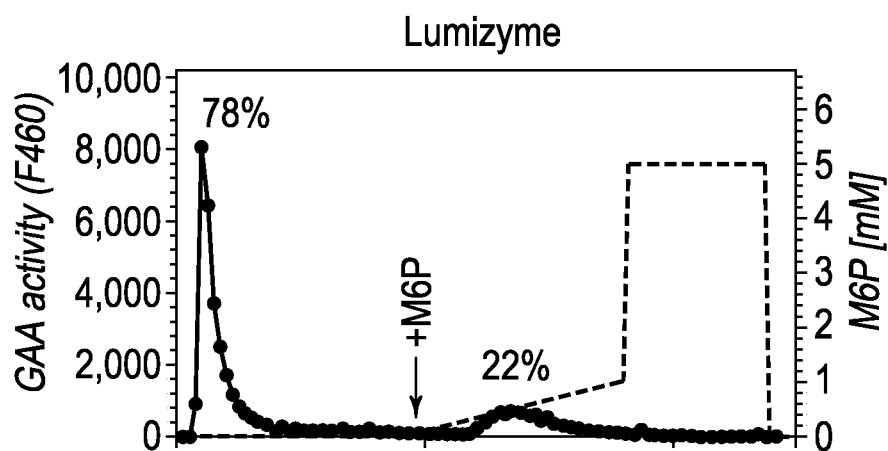
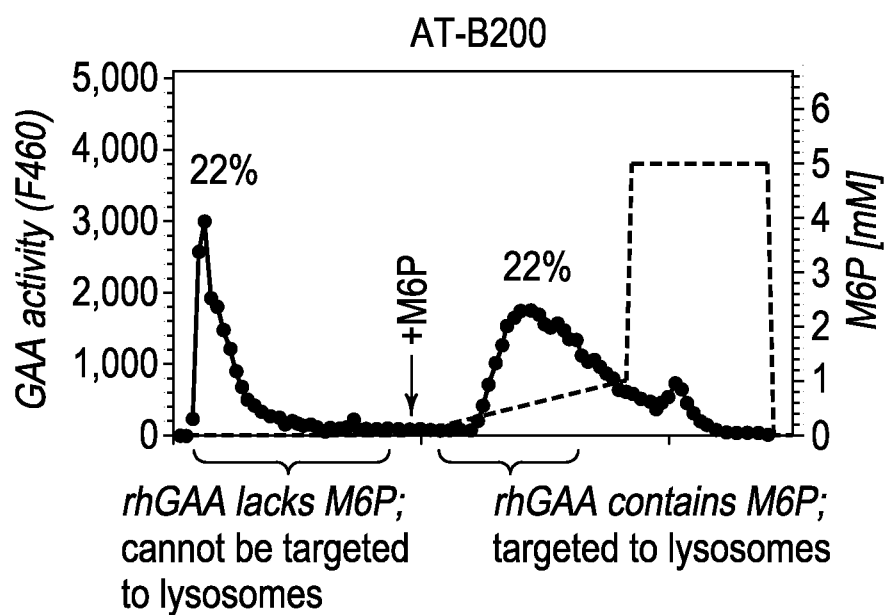
***Fig. 4A******Fig. 4B***

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***Fig. 5***

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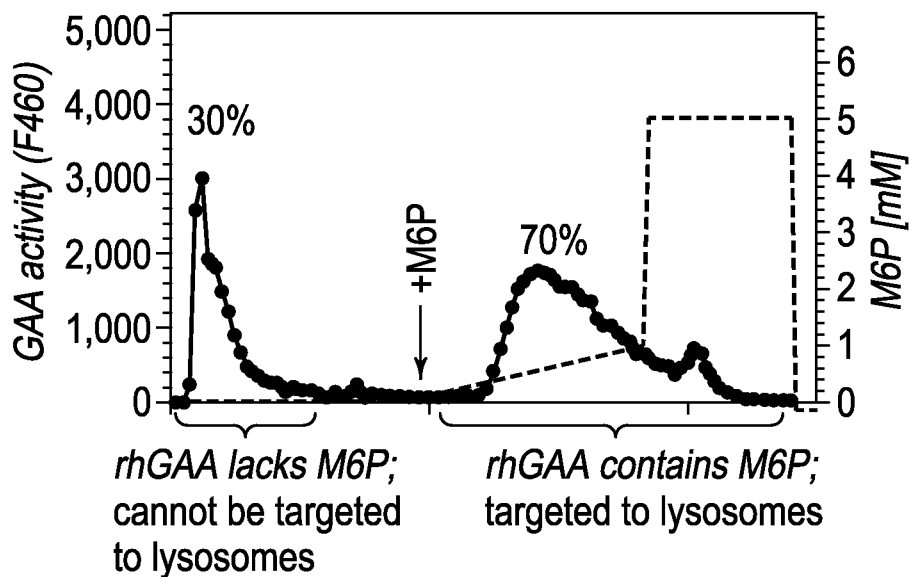
CIMPR Binding Profile of Lumizyme compared to that of ATB-200 rhGAA

***Fig. 6A******Fig. 6B***

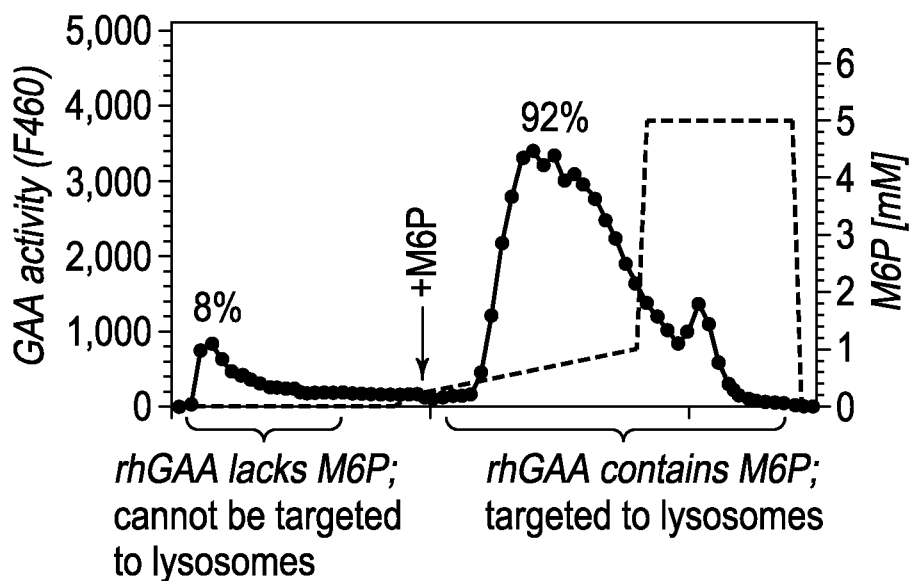
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Manufacturing Optimization for ATB200

Embodiment 1

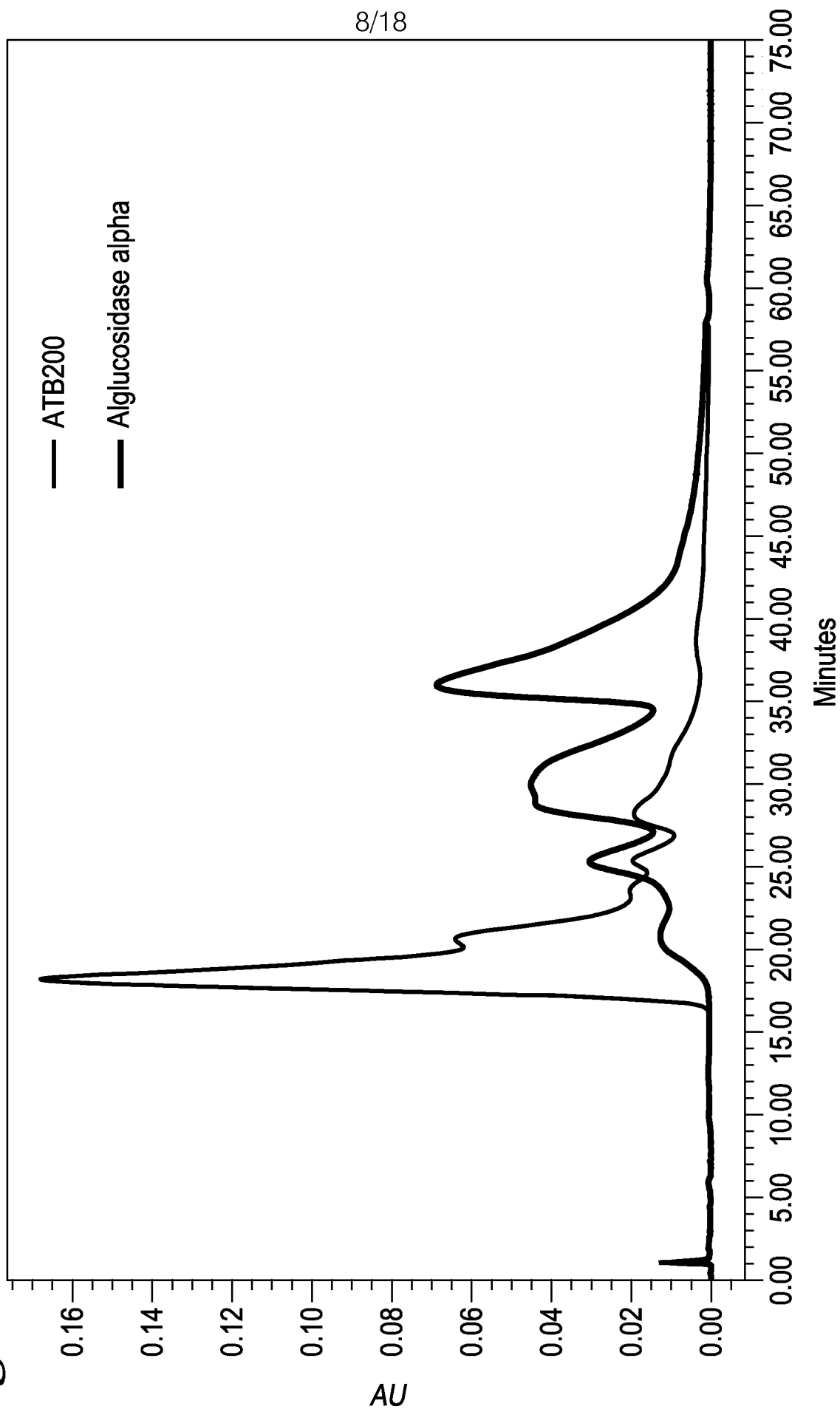
**Fig. 7A**

Embodiment 2

**Fig. 7B**

Polywax elution profiles of Alglucosidase alpha and ATB200 rhGAAs

Fig. 8



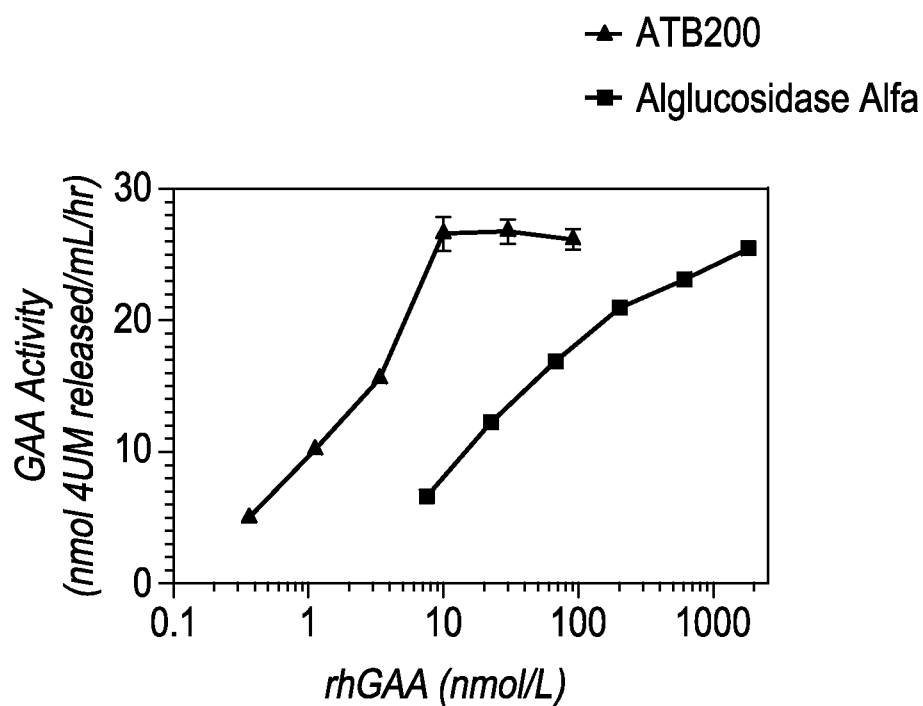
Distribution of N-Glycans on rhGAA Preparations

	Lumizyme	BP-rhGAA *	ATB200	
			1	2
Complex Type N-Glycans	70.7%	48.9%	51.0%	47.5%
Hybrid Type N-Glycans	6.7%	9.7%	4.4%	3.7%
High Mannose Type N-Glycans:				
Non-phosphorylated	15.8%	23.7%	14.0%	9.9%
Mono-M6P	5.2%	10.4%	13.4%	14.2%
Bis-M6P	1.6%	6.8%	17.2%	24.7%

Fig. 9

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Measurement of CIMPR Binding Affinity

**Fig. 10A**

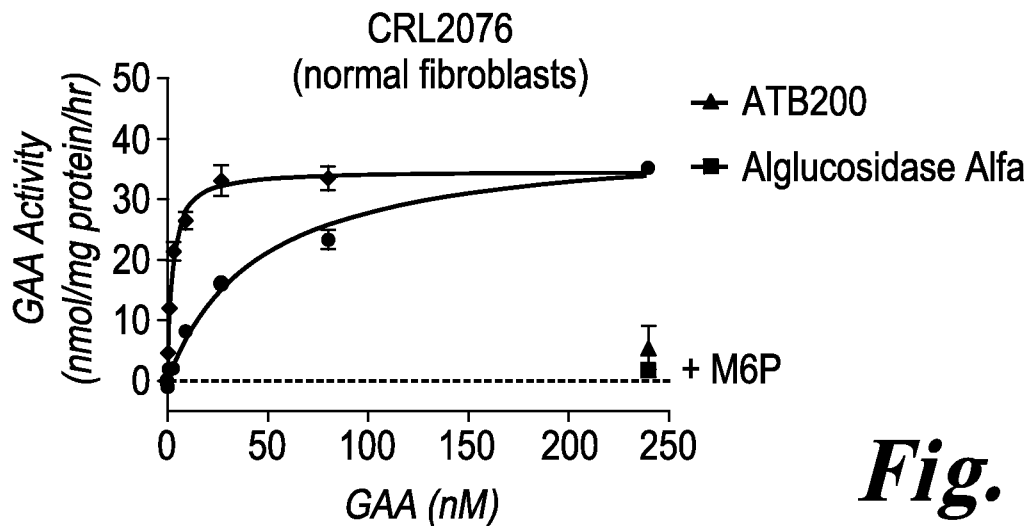
Bis-Phosphorylated Oligosaccharides Comparison

Glycan	Alglucosidase Alfa (mol bis-glycan/ mol protein)	ATB200 (mol bis-glycan/ mol protein)
Bis-M6P	0.1	1.3

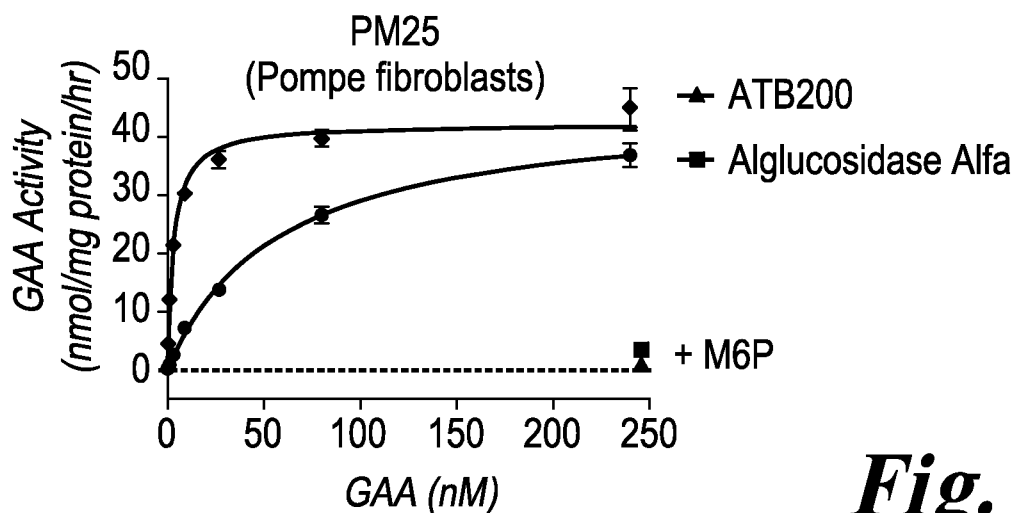
Fig. 10B

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CIMPR Uptake in Normal Fibroblasts

**Fig. 11A**

CIMPR Uptake in Pompe Fibroblasts

**Fig. 11B** K_{uptake} Comparison in Normal and Pompe Fibroblasts

Cell Line	K_{uptake} (nM)	
	AT200	Lumizyme
normal	2	56
Pompe	3	57

Fig. 11C

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Comparative glycogen clearance by ATB-200 rhGAA and Lumizyme rhAGG
in Heart, Quadriceps and Tricep muscles

Glycogen Reduction in Heart

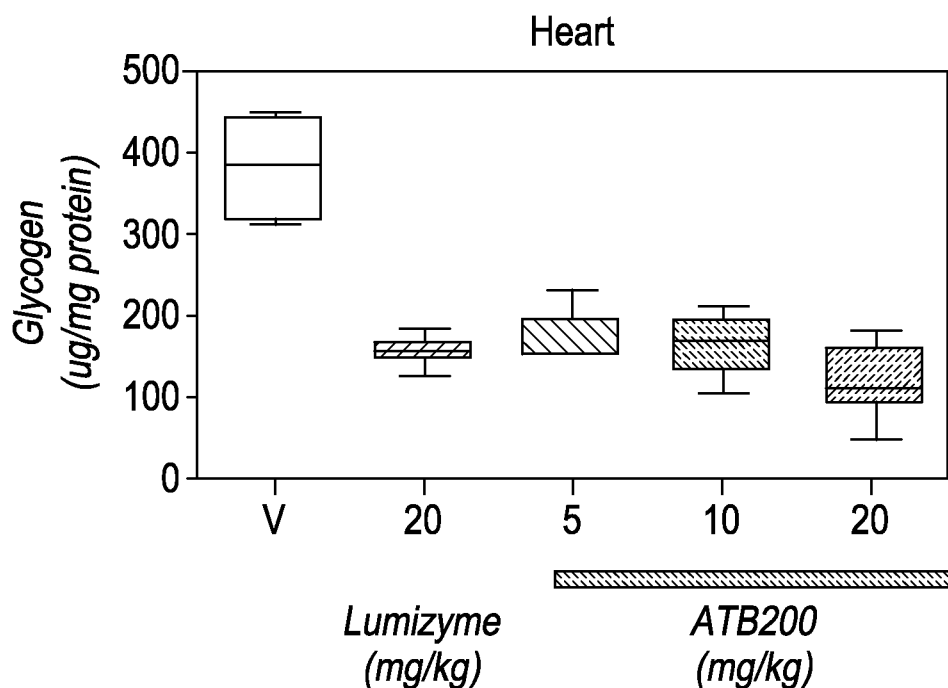


Fig. 12A

Glycogen Reduction in Quadriceps

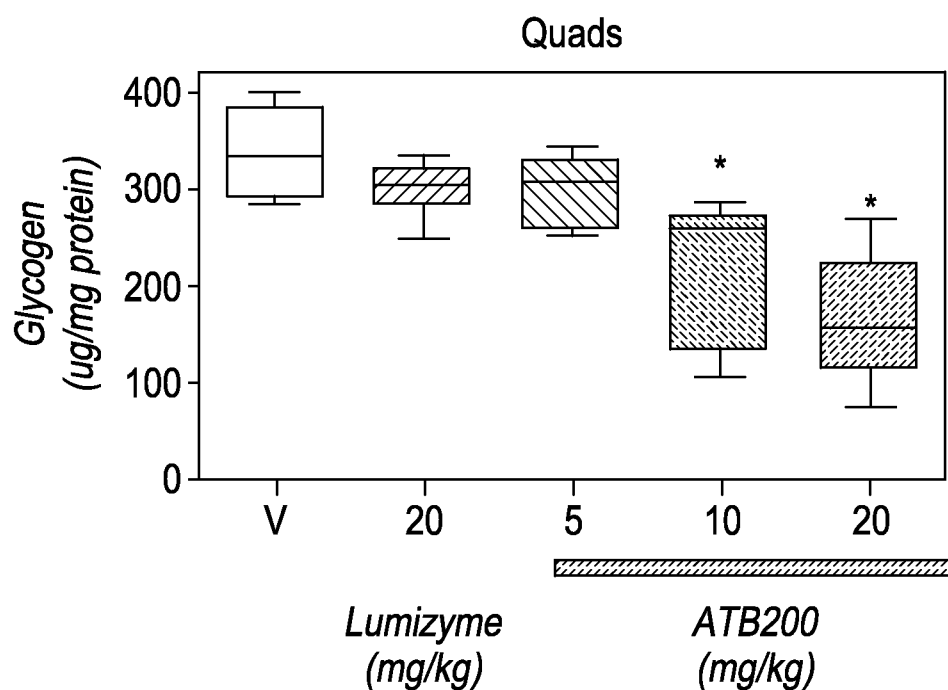
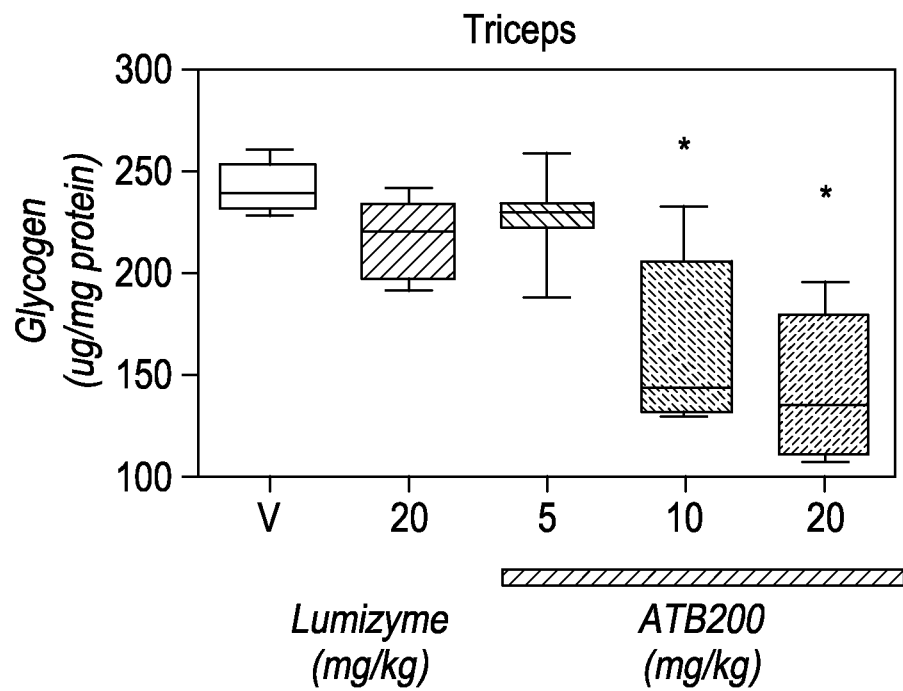


Fig. 12B

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Glycogen Reduction in Quadriceps

**Fig. 12C**

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Effects of temperature on ATB-200 rhGAA folding
in presence of chaperone AT2221

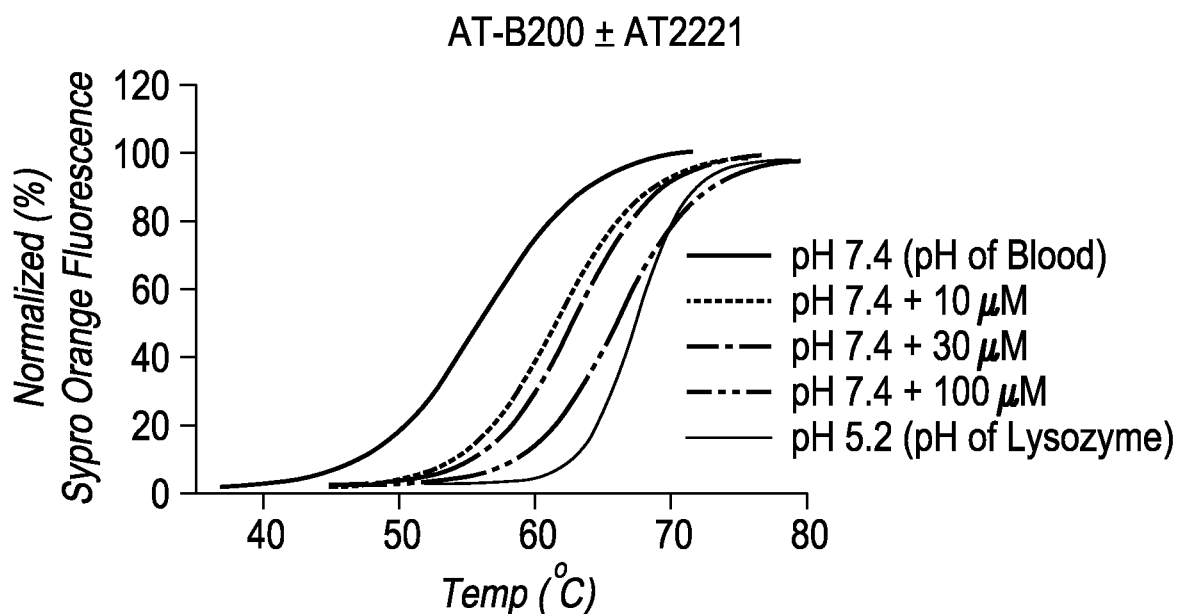


Fig. 13A

Summary of Melting Temp of ATB200 with increasing amounts of AT2221

Buffer	$T_m(^{\circ}\text{C})$ of ATB200
pH 7.4	56.2
pH 7.4 + 10 mM AT2221	61.6
pH 7.4 +30 mM AT2221	62.9
pH 7.4 + 100 mM AT2221	66.0
pH 5.2	67.3

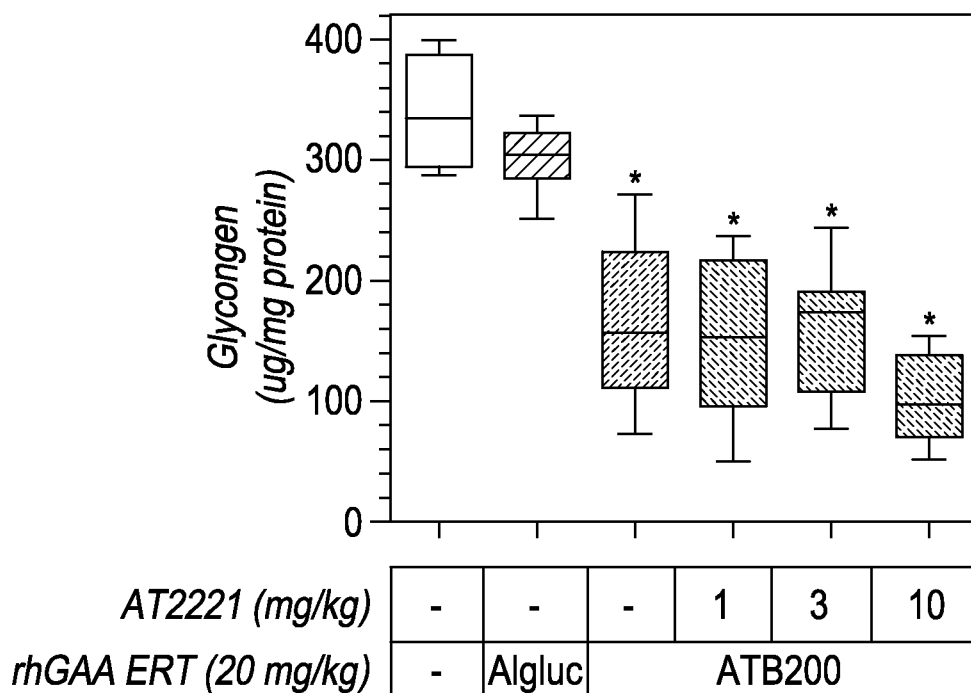
Fig. 13B

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Comparison of % glycogen reduction in <i>Gaa</i> KO mice after Lumizyme or ATB200 administration (with or without miglustat)		
Enzyme $\pm$ Chaperone	Quadriceps	Triceps
Lumizyme alone (20 mg/Kg)	14	14
ATB200 alone (20 mg/kg)	74	62
ATB200 + Miglustat (AT2221) (20 mg/kg) + (10 mg/kg)	94	73

Fig. 14

Glycogen clearance in quadriceps muscle by ATB-200 rhGAA and AT-2221 chaperone

***Fig. 15***

PAS Glycogen staining and EM of skeletal muscle tissue from GAA KO mice treated with conventional rhGAA or ATB-200 rhGAA and AT2221

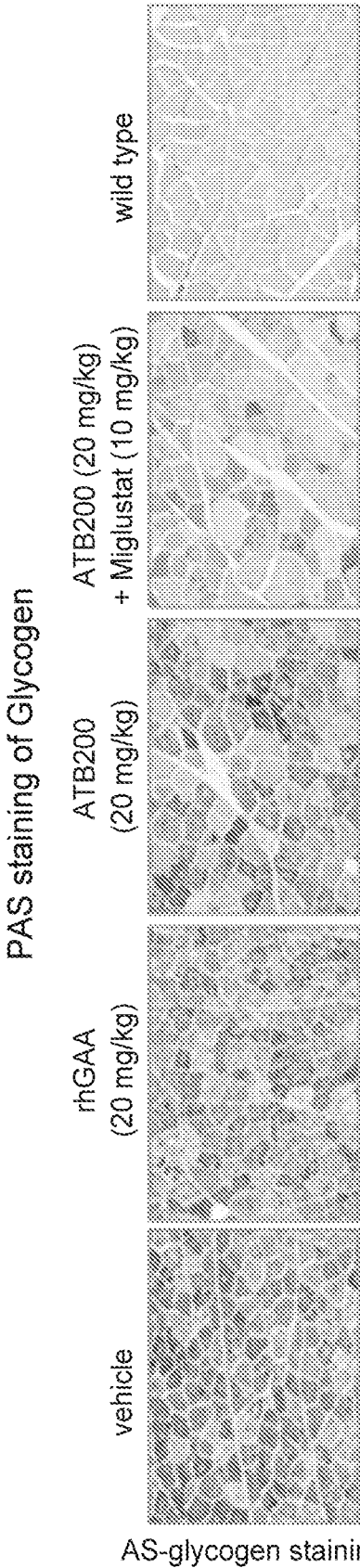


Fig.16A

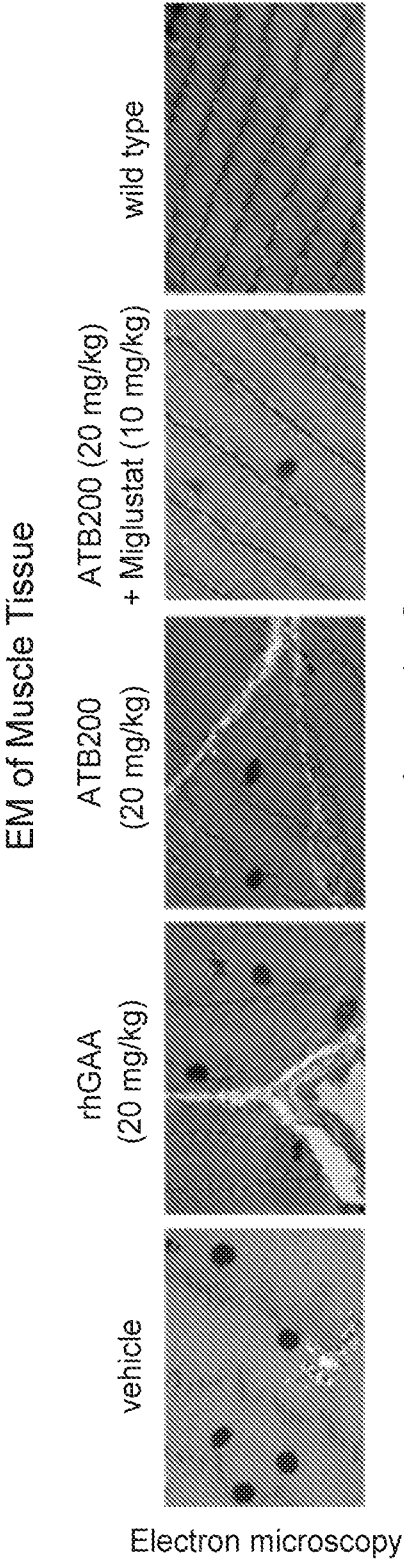


Fig.16B

Glycogen staining and EM of skeletal muscle tissue from GAA KO
Mice treated with conventional rhGAA or ATB-200 and AT2221

Evaluation of Lysosomal Proliferation by LAMP-1 marker

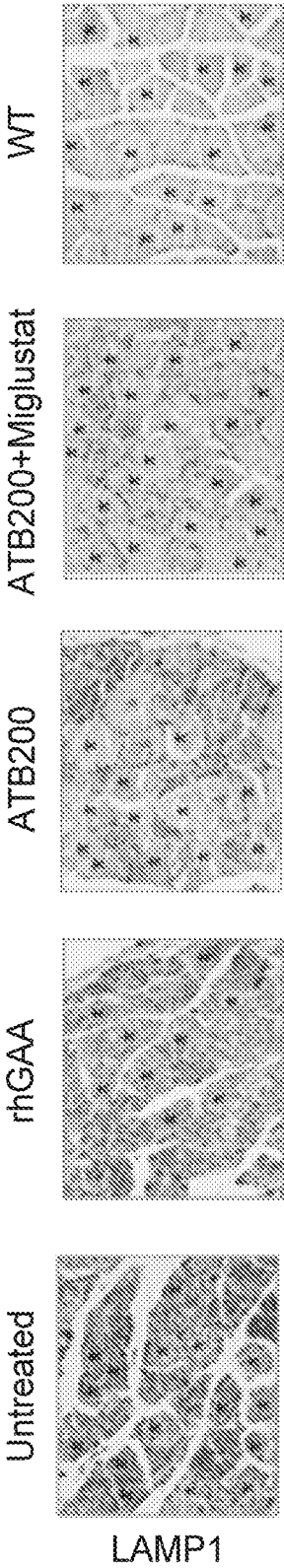


Fig.16C

Identification of Type I and Type II muscle fibers



Fig.16D

PAS glycogen staining and EM of Cardiac muscle tissue from GAA KO mice treated with conventional rhGAA or ATB-200 rhGAA and Miglustate (AT-2221)

PAS Staining of Glycogen

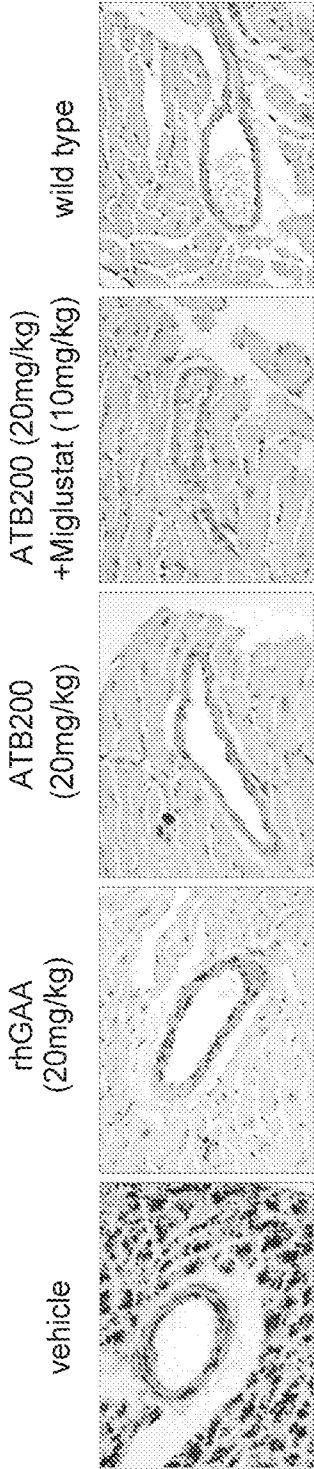


Fig.17A

Evaluation of Lysosomal Proliferation by LAMP-1 marker

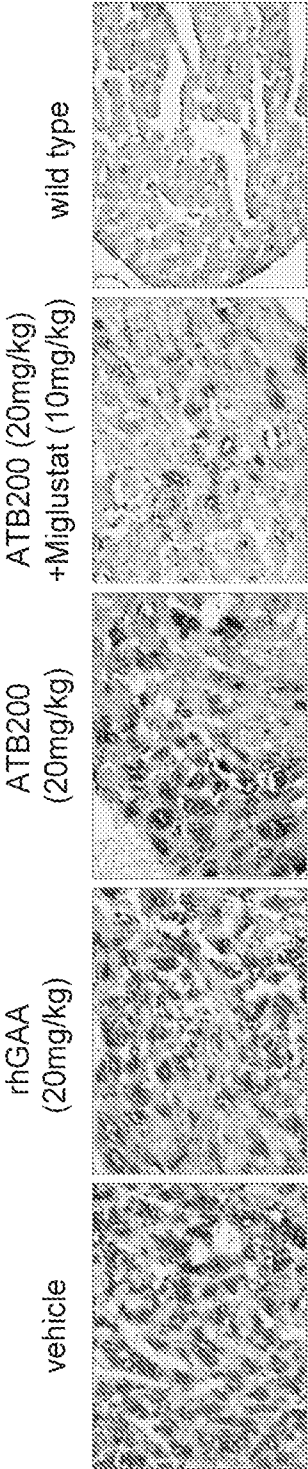


Fig.17B