Obesity is healthy for cetaceans: Evidence from pervasive positive selection in genes related to triacylglycerol metabolism

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Supplementary Table S1. The 88 genes of TAG metabolism Analyzed in this Study.

Synthesis		Lipolysis	Regulation
ACC1*	FABP5	AdPLA*	ABHD5
ACSL1*	FABP6*	ATGL*	ADIPOQ*
ACSL3	FABP7	HSL*	ADRP*
ACSL4*	GOT2(FABPpm)	LIPH	AMPK
ACSL5*	FAS*	LPL*	CAV1
ACSL6*	CD36(FAT)	MGLL*	CIDEA
ACSS1	FATP1*	PNLIP*	LXRa
ACSS2	FATP2*		LXRb
ACSS3	FATP3*		MLXIPL
AGPAT1*	FATP4		PDE3B*
AGPAT2	GNPAT		PLIN1*
AGPAT3*	GPAT1*		PLIN3
AGPAT4*	GPAT2*		PLIN4
AGPAT5*	MOGAT1*		PLIN5
AGPAT6*	MOGAT2*		PPARA*
DGAT1*	MOGAT3*		PPARD*
DGAT2*	PLCB1		PPARG*
DGKA	PLCB2		SERTAD2*
DGKB	PLCB3		SREBF1*
DGKE	PLCB4		SREBF2*
DGKG	PLCD3		APOB
DGKH	PLCD4		
DGKI	PLCE1		
DGKQ	PLCG1		
DGKZ	PLCG2		
FABP1*	PPAP2A		
FABP2*	PPAP2B		
FABP3	PPAP2C		
FABP4*			

* Forty-one genes were sequenced for five cetacean species (two mysticetes: common minke whale (*Balaenoptera omurai*), Omura's whale (*Balaenoptera acutorostrata*), and three odontocetes: Beluga (*Delphinapterus leucas*), Finless porpoise (*Neophocaena phocaenoides*), and Long-beaked common dolphin (*Delphinus capensis*)) in this study.

Abbreviations:

ACSL: Acyl-CoA Synthetase Long-chain family member; ACSS: Acyl-CoA Synthetase Short-chain family member; ACC1 (also known as ACACA): Acetyl-CoA Carboxylase Alpha

AGPAT: 1-Acylglycerol-3-Phosphate O-Acyltransferase; DGAT: Diacylglycerol O-Acyltransferase; DGKA: Diacylglycerol Kinase, Alpha; DGKB: Diacylglycerol Kinase, Beta; DGKG: Diacylglycerol Kinase, Gamma; DGKH: Diacylglycerol Kinase, Eta; DGKI: Diacylglycerol Kinase, Iota; DGKQ: Diacylglycerol Kinase, Theta; DGKZ: Diacylglycerol Kinase, Zeta; GNPAT: Glyceronephosphate O-Acyltransferase; GPAT: Glycerol-3-Phosphate

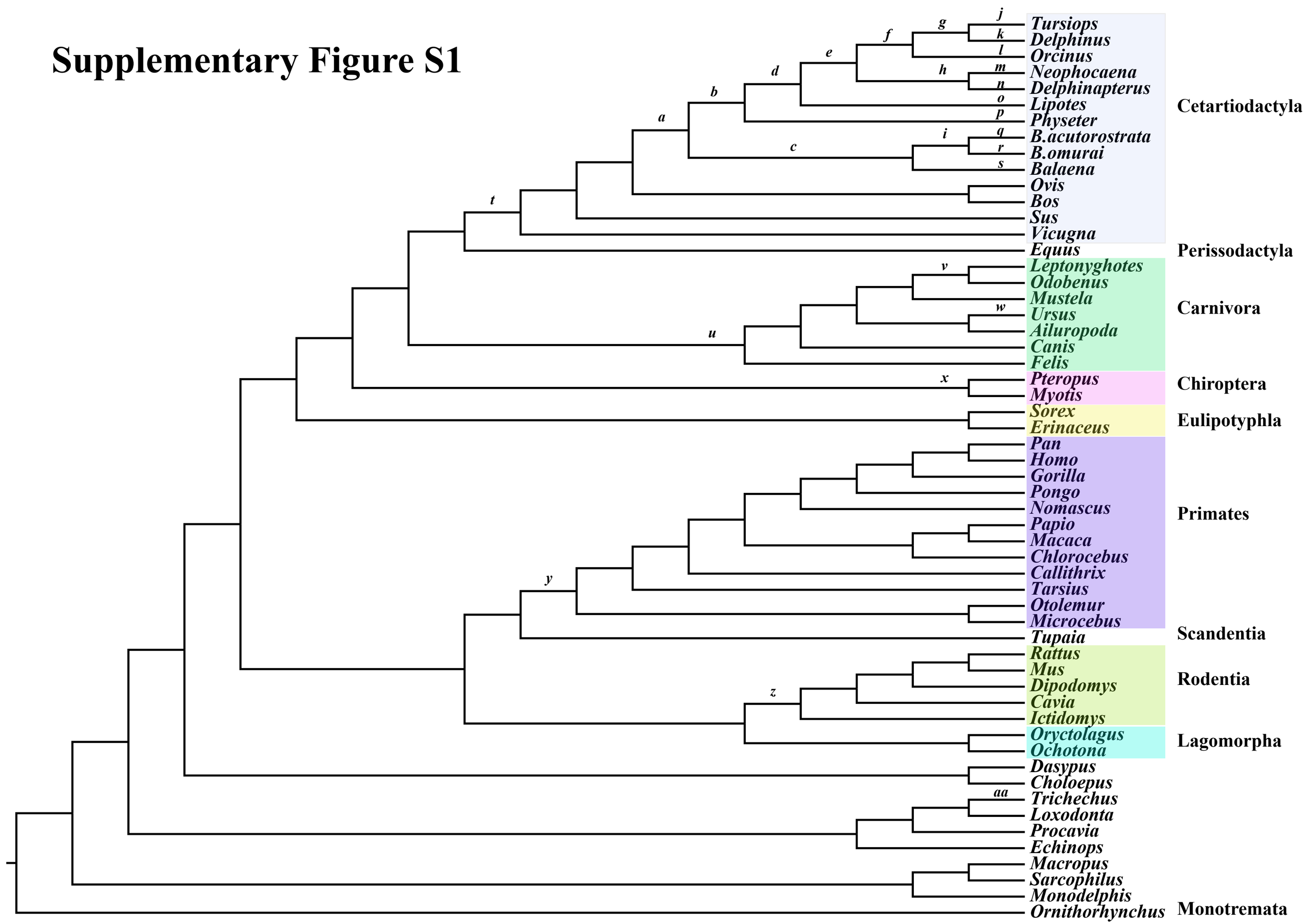
Acyltransferase; MOGAT: Monoacylglycerol O-Acyltransferase; FABP: Fatty Acid Binding Protein; FABPpm(also known as GOT2): Glutamic-Oxaloacetic Transaminase 2; FAS: Fatty Acid Synthase; FAT (also known as CD36): CD36 molecule (thrombospondin receptor); FATP: Solute Carrier Family 27 (Fatty Acid Transporter), member; PLCB: Phospholipase C, Beta; PLCD: Phospholipase C, Delta; PLCE: Phospholipase C, Epsilon; PLCG: Phospholipase C, Gamma; PPAP2A: Phosphatidic Acid Phosphatase type 2A; PPAP2B: Phosphatidic Acid Phosphatase type 2B; PPAP2C: Phosphatidic Acid Phosphatase type 2C; AdPLA: Adipose-Specific Phospholipase A2; ATGL: Adipose Triglyceride Lipase; HSL: Hormone-Sensitive Lipase; LIPH: Lipase, Member H; LPL: Lipoprotein Lipase; MGLL: Monoglyceride Lipase; PNLIP: Pancreatic Lipase
ABHD5: Abhydrolase Domain Containing 5; ADIPOQ: Adiponectin, C1Q and collagen domain containing; ADRP (also known as PLIN2): Adipose Differentiation-Related Protein; AMPK: AMP-activated protein kinase; CAV1: Caveolin 1, Caveolae Protein; CIDEA: Cell Death-Inducing DFFA-Like Effector A; LXRa: Liver X Receptor Alpha Protein; LXRb: Liver X Receptor Beta Protein; MLXIPL (also known as ChREBP): Carbohydrate Response Element Binding Protein; PDE3B: Phosphodiesterase 3B; PLIN: Perilipin; PPARA: Peroxisome Proliferator-Activated Receptor Alpha; PPARD: Peroxisome Proliferator-Activated Receptor Delta; PPARG: Peroxisome Proliferator-Activated Receptor Gamma; SERTAD2: SERTA domain-containing Protein 2; SREBF: Sterol Regulatory Element Binding Transcription Factor
APOB: Apolipoprotein B.

Supplementary Figure Legends

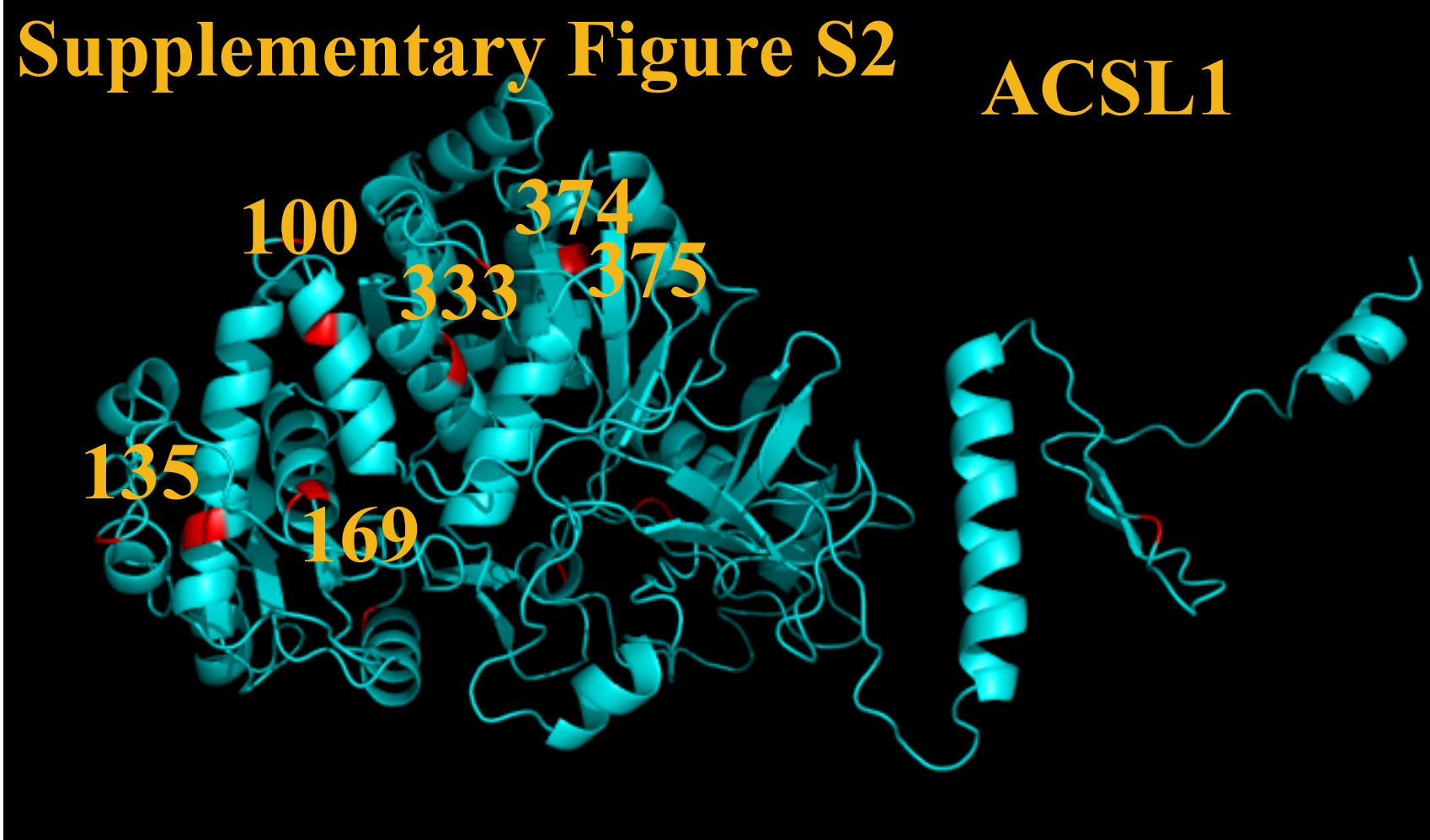
Supplementary Figure S1. A well supported phylogeny of mammals used for selective pressure analysis in PAML. Tree topologies of Laurasiatheria and primates were from Zhou et al. (2012)[52] and Perelman et al. (2011)[53], respectively. Different orders of mammals were marked with various colors. Branches a–aa in the tree are used in the branch-site models tests, and results are listed in Tables S2 and Tables S4.

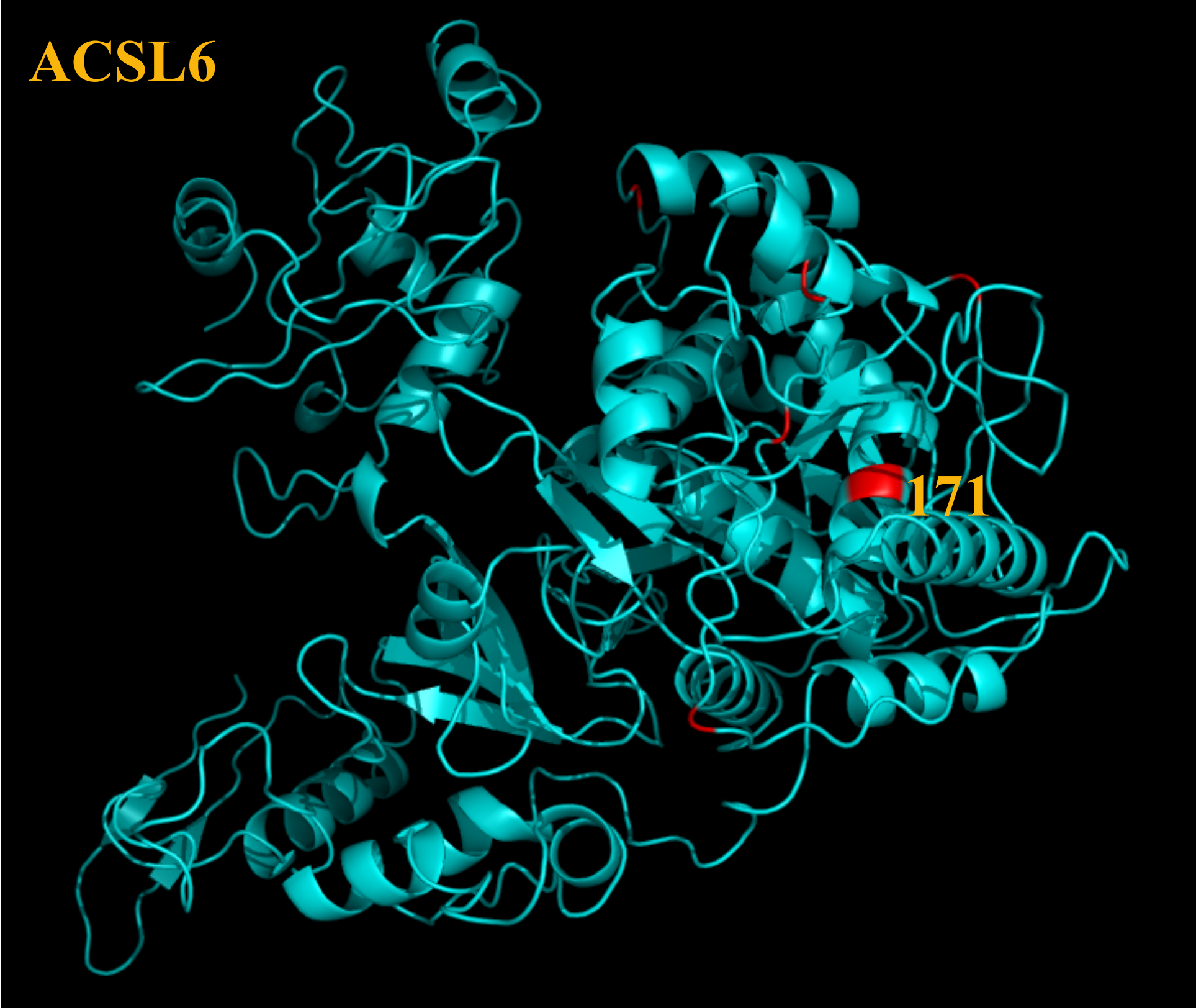
Supplementary Figure S2. Spatial distribution of positively selected sites in the three-dimensional (3D) structure of 15 genes related to TAG metabolism in cetaceans.

Supplementary Figure S1



Supplementary Figure S2

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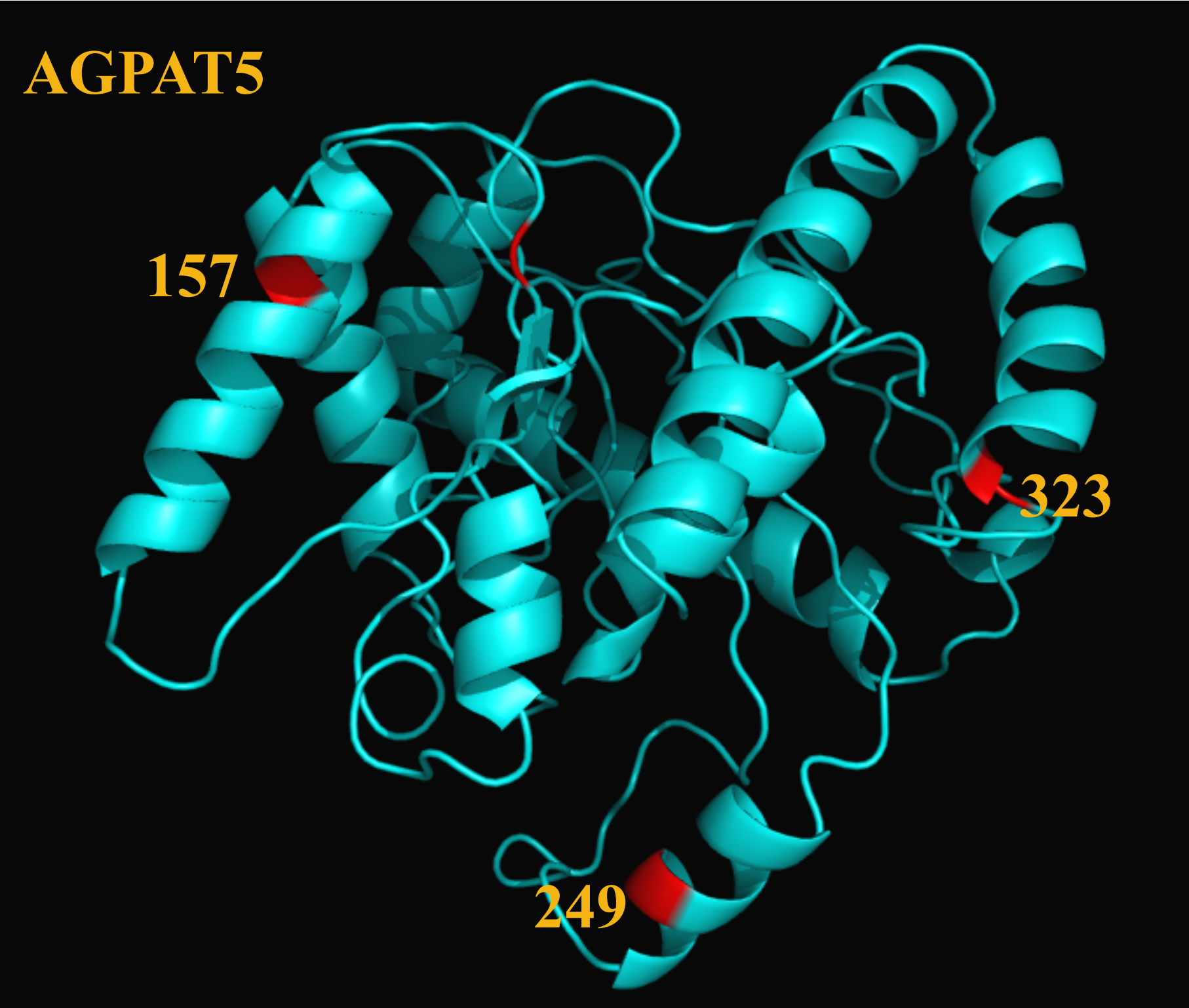
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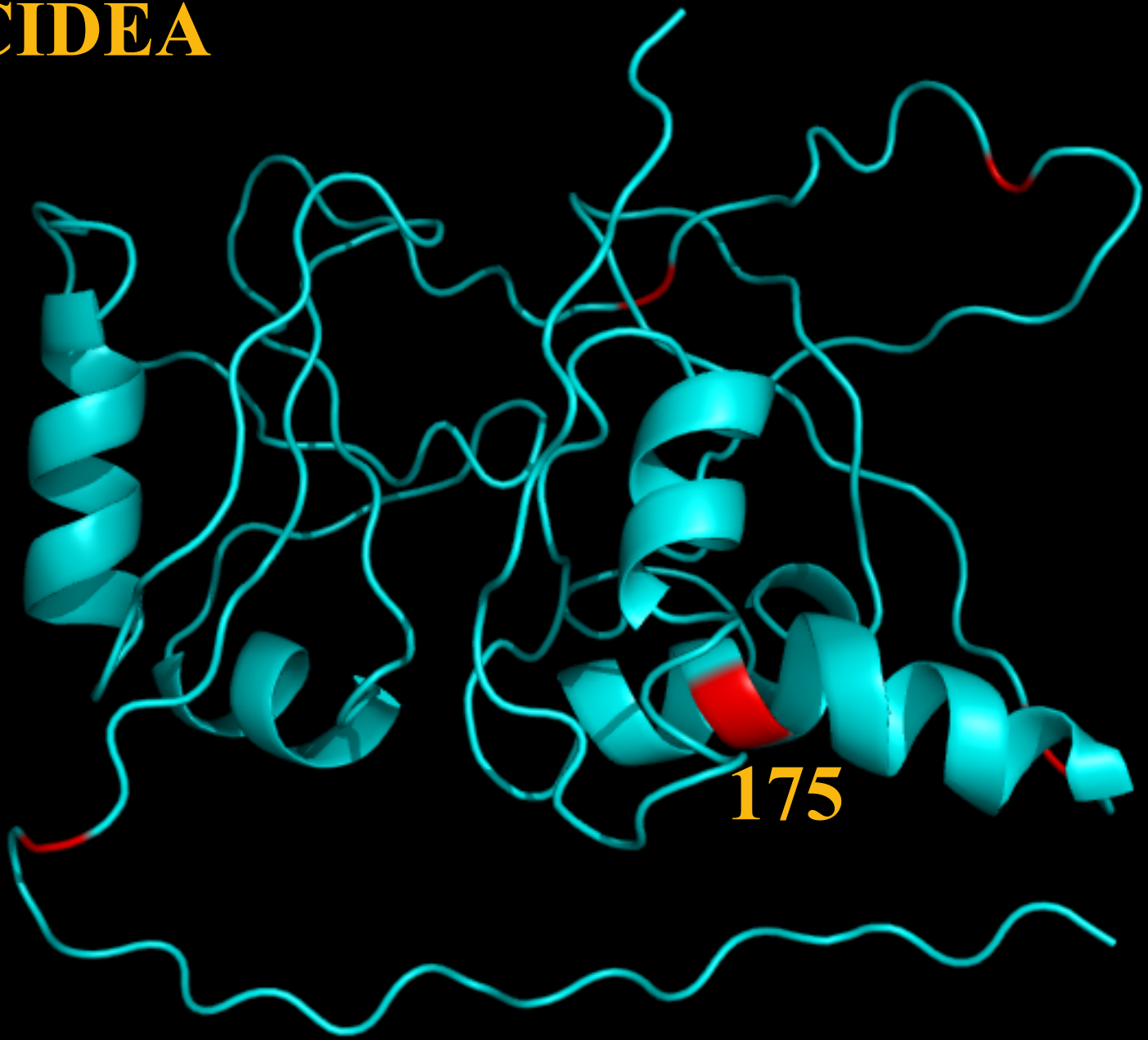
323
249

CIDEA




DGAT2
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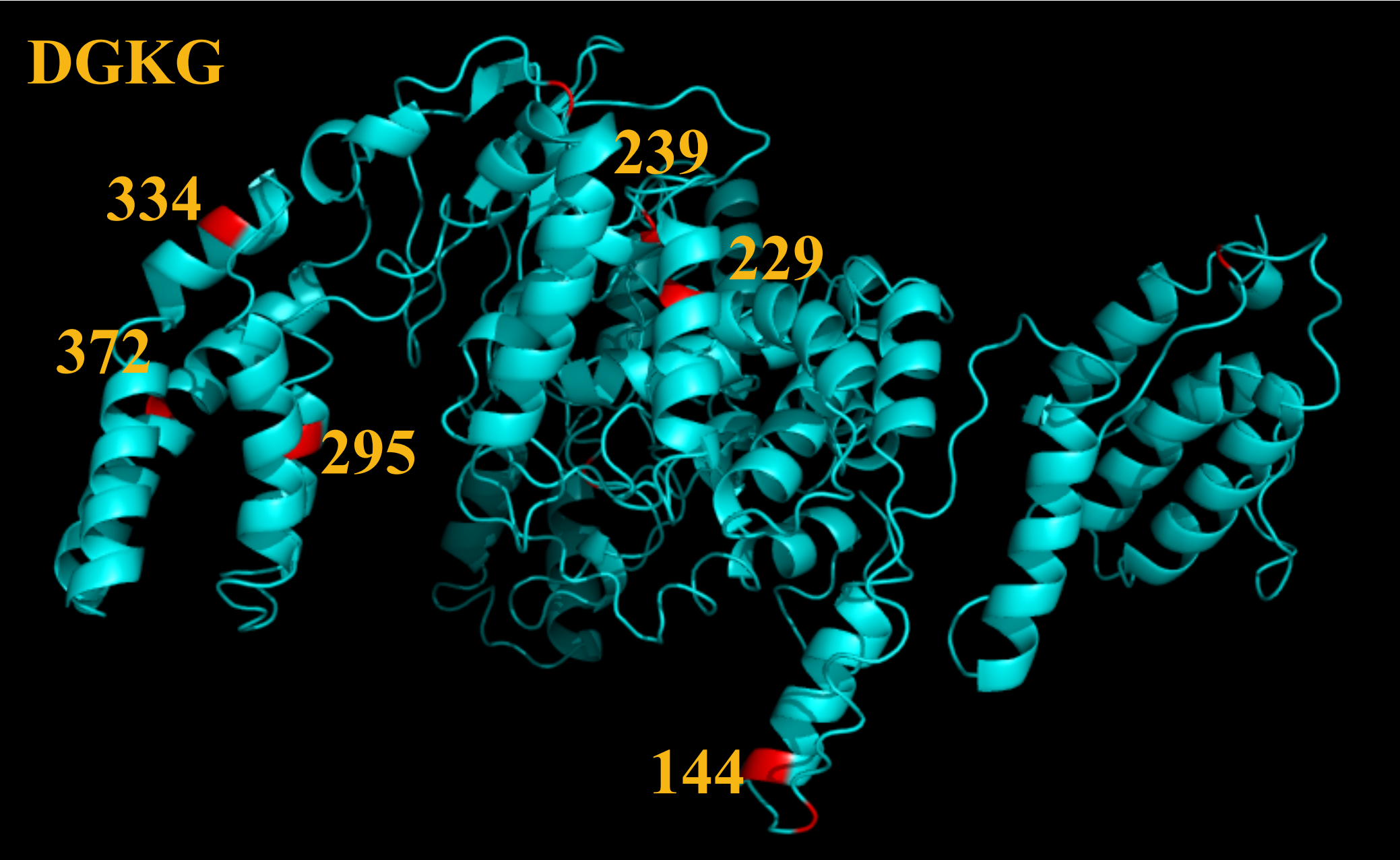
223
177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372
295
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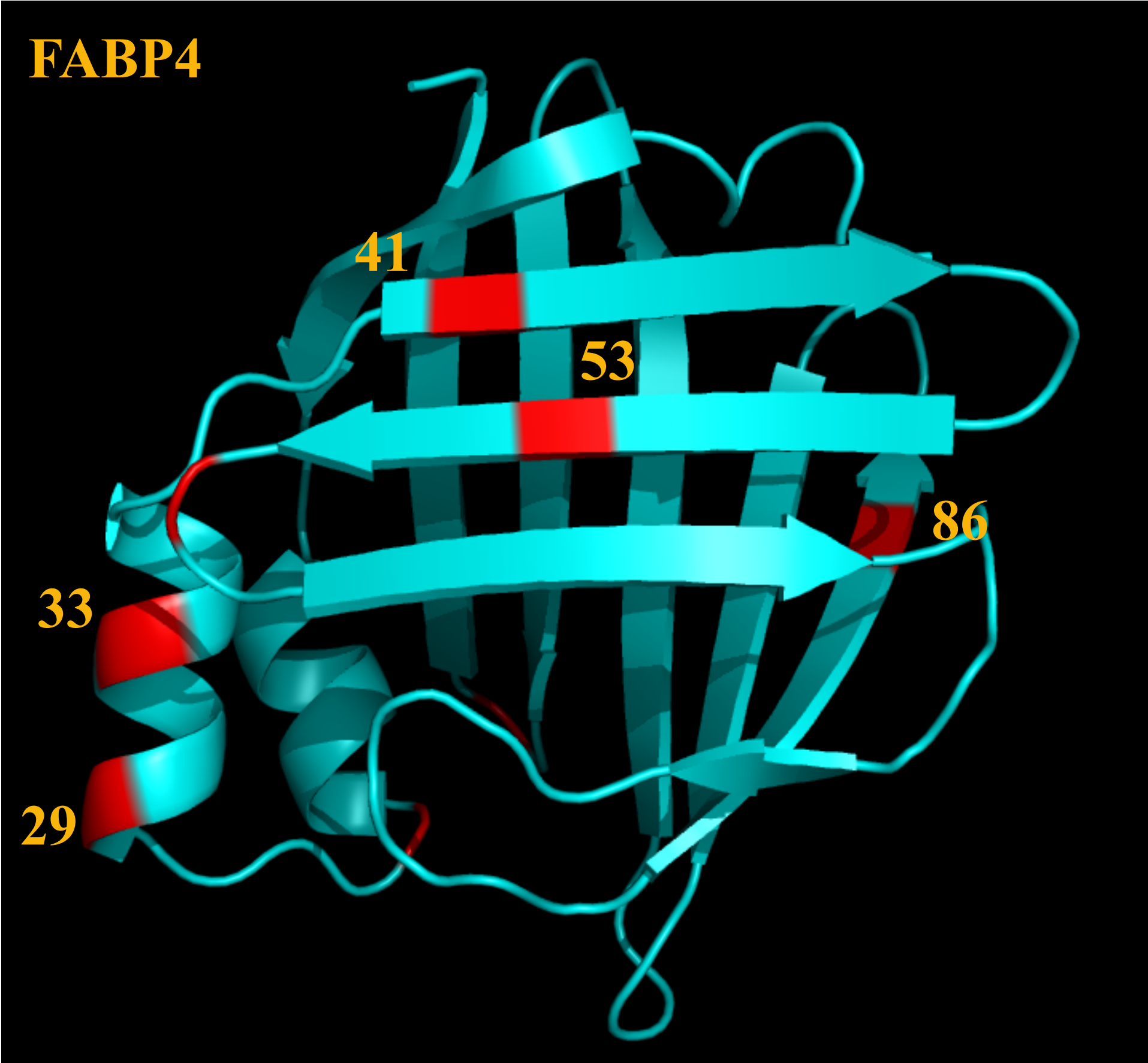
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33
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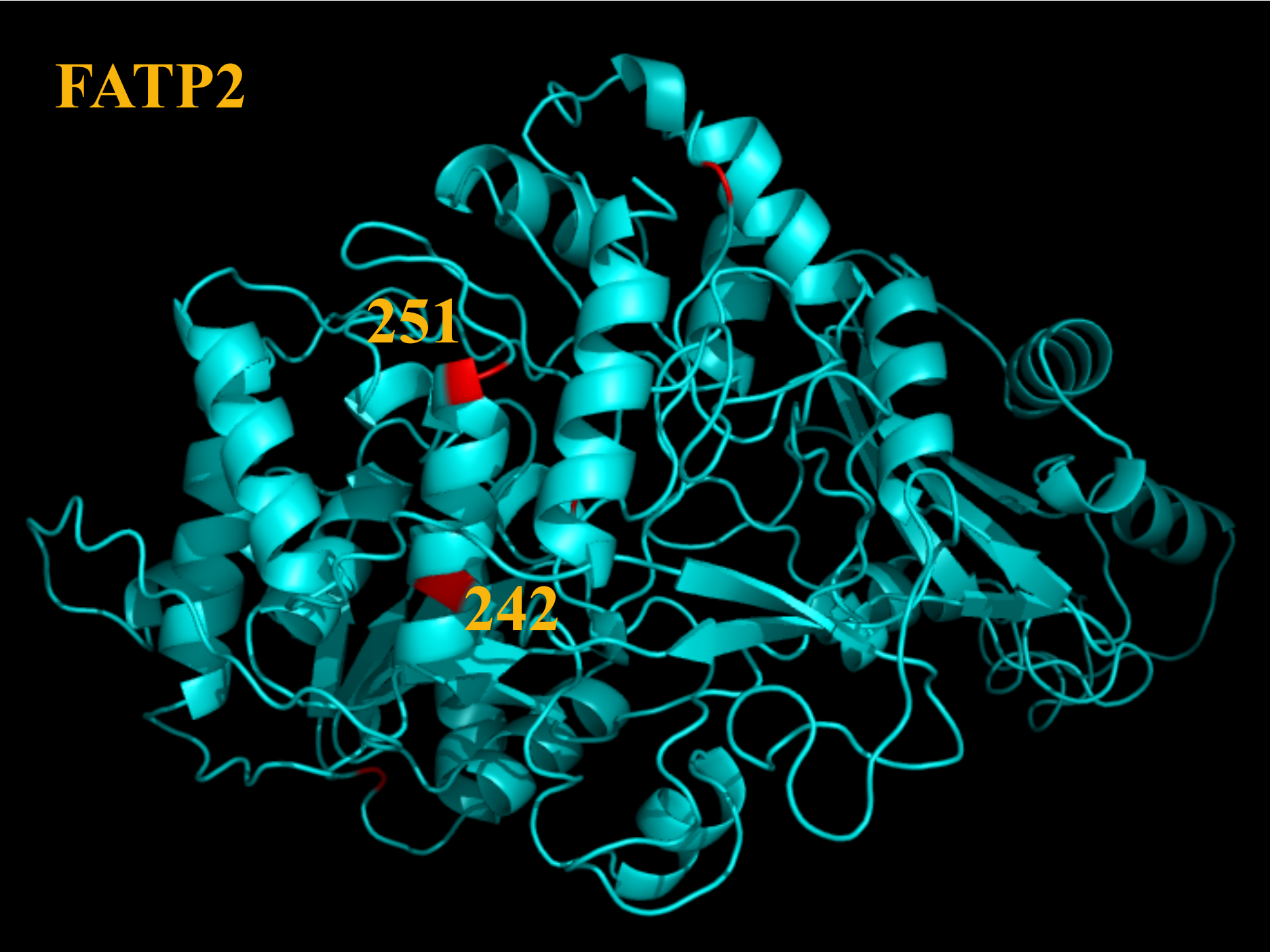
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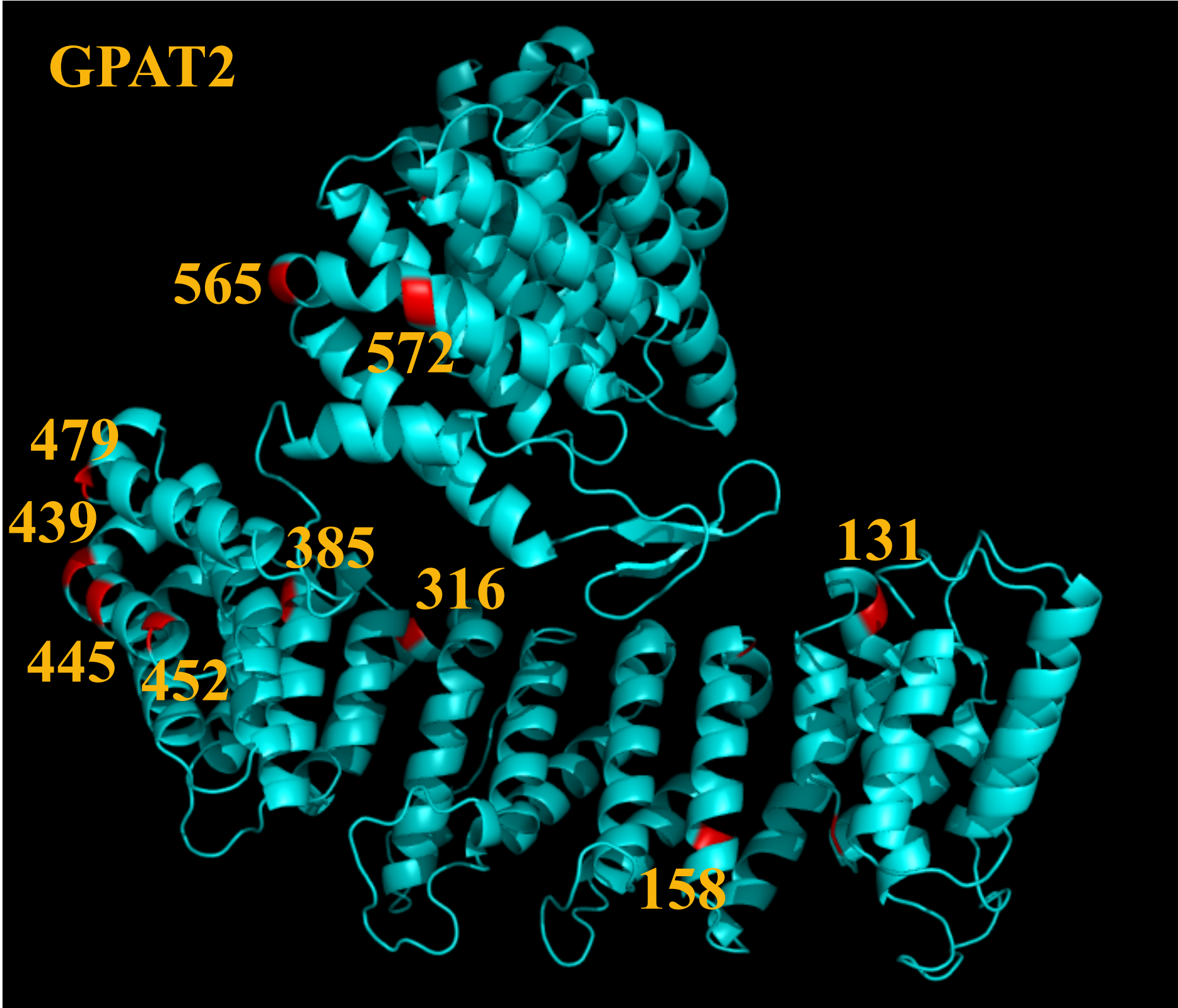
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452
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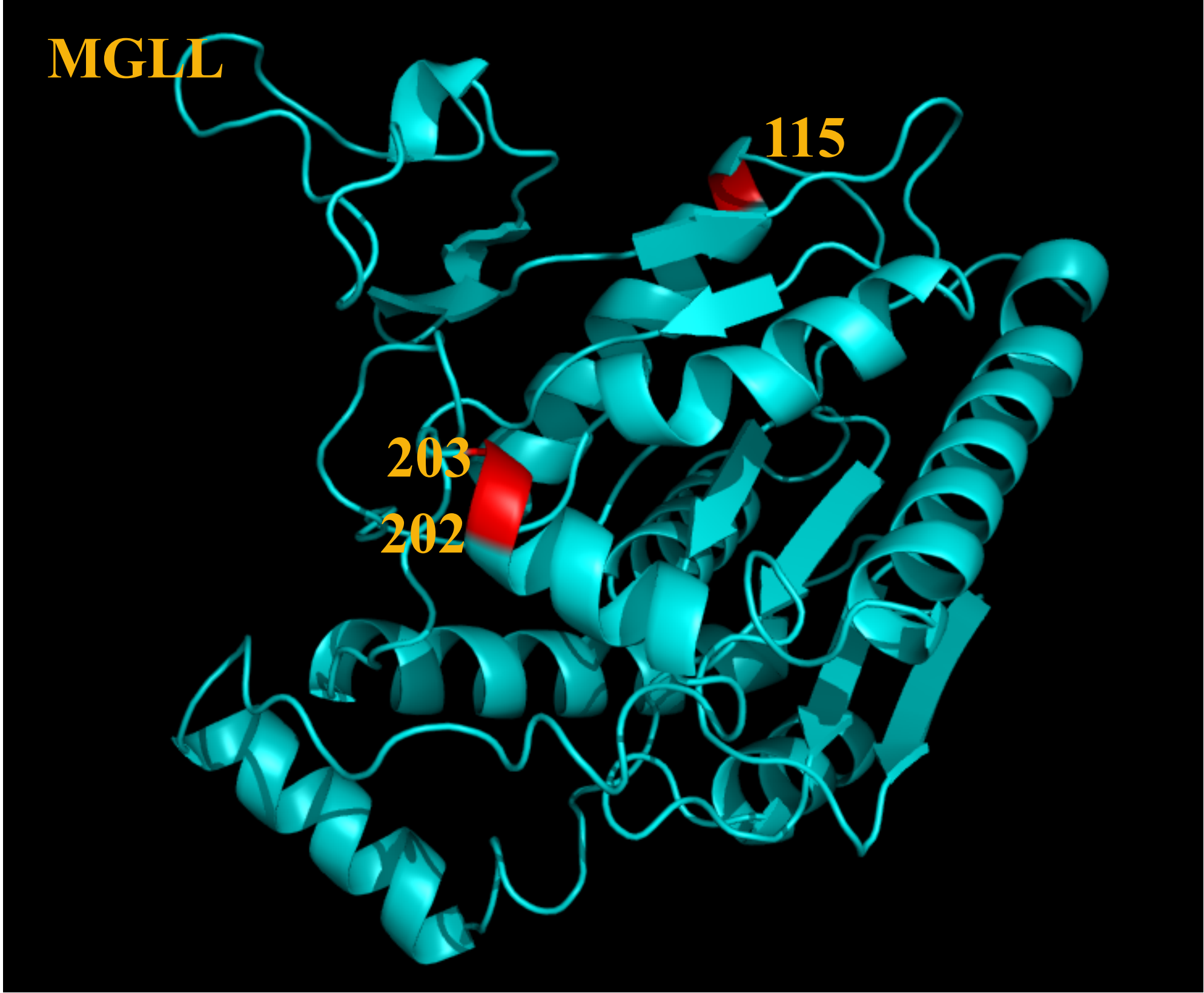
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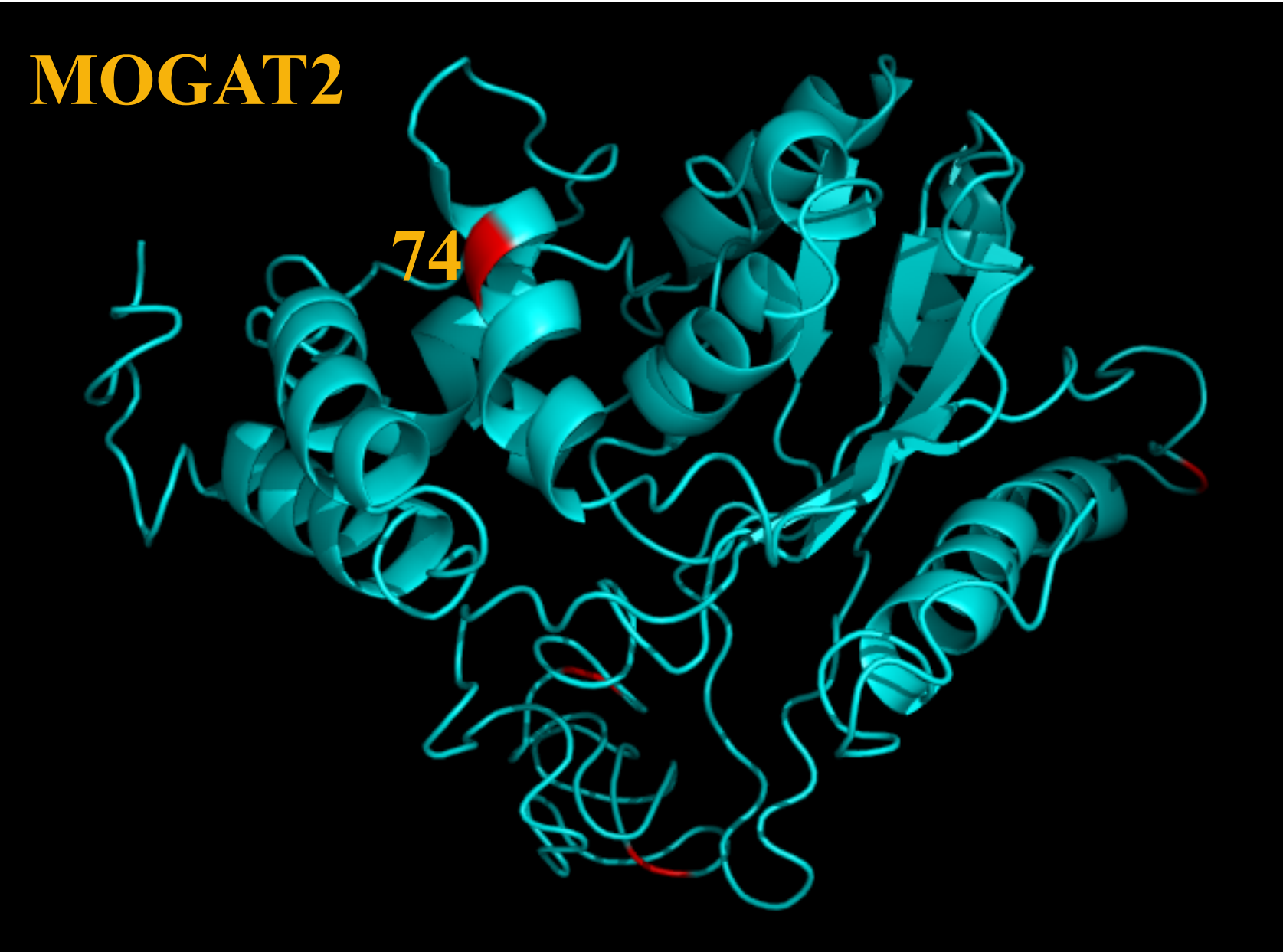
MOGAT2
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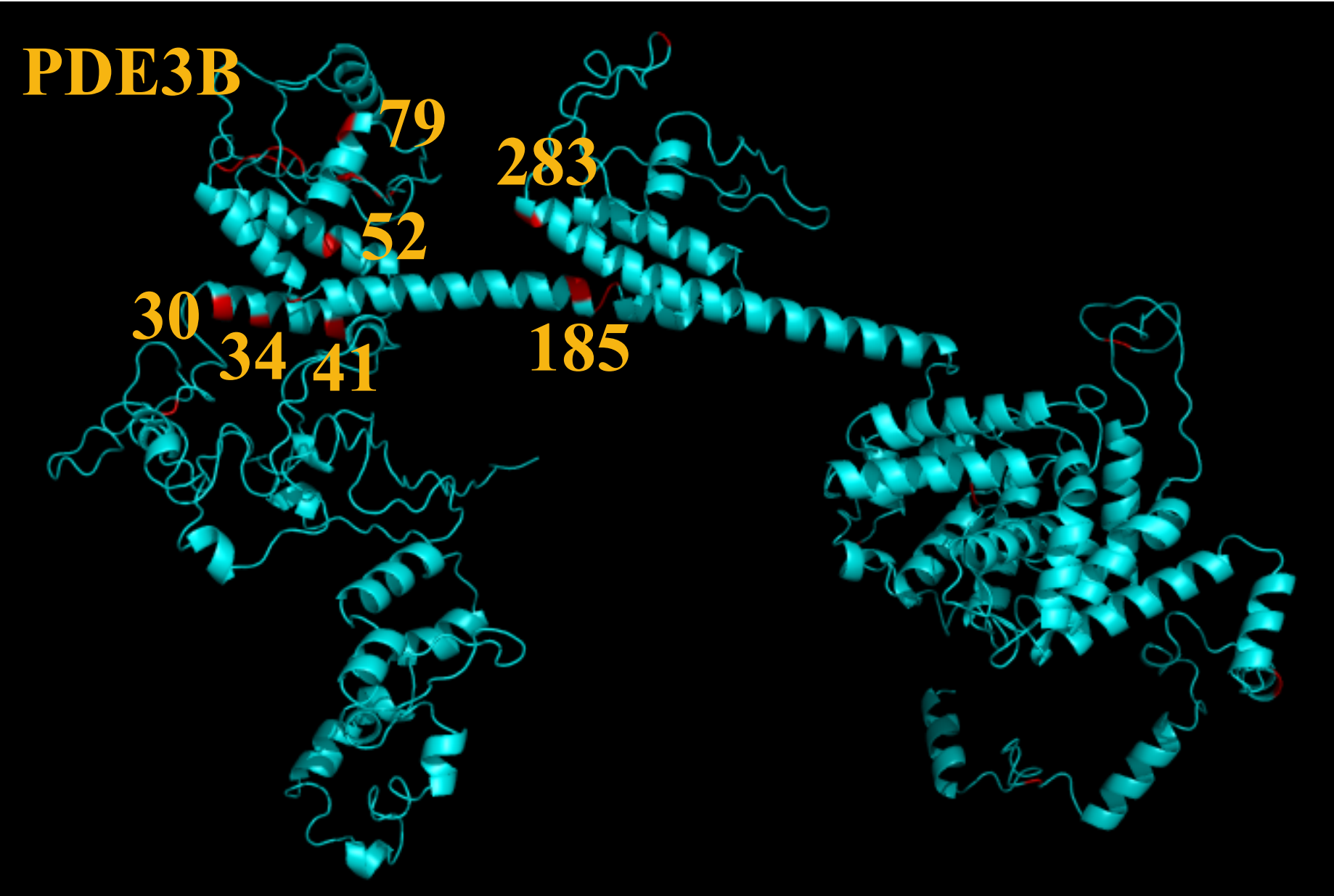
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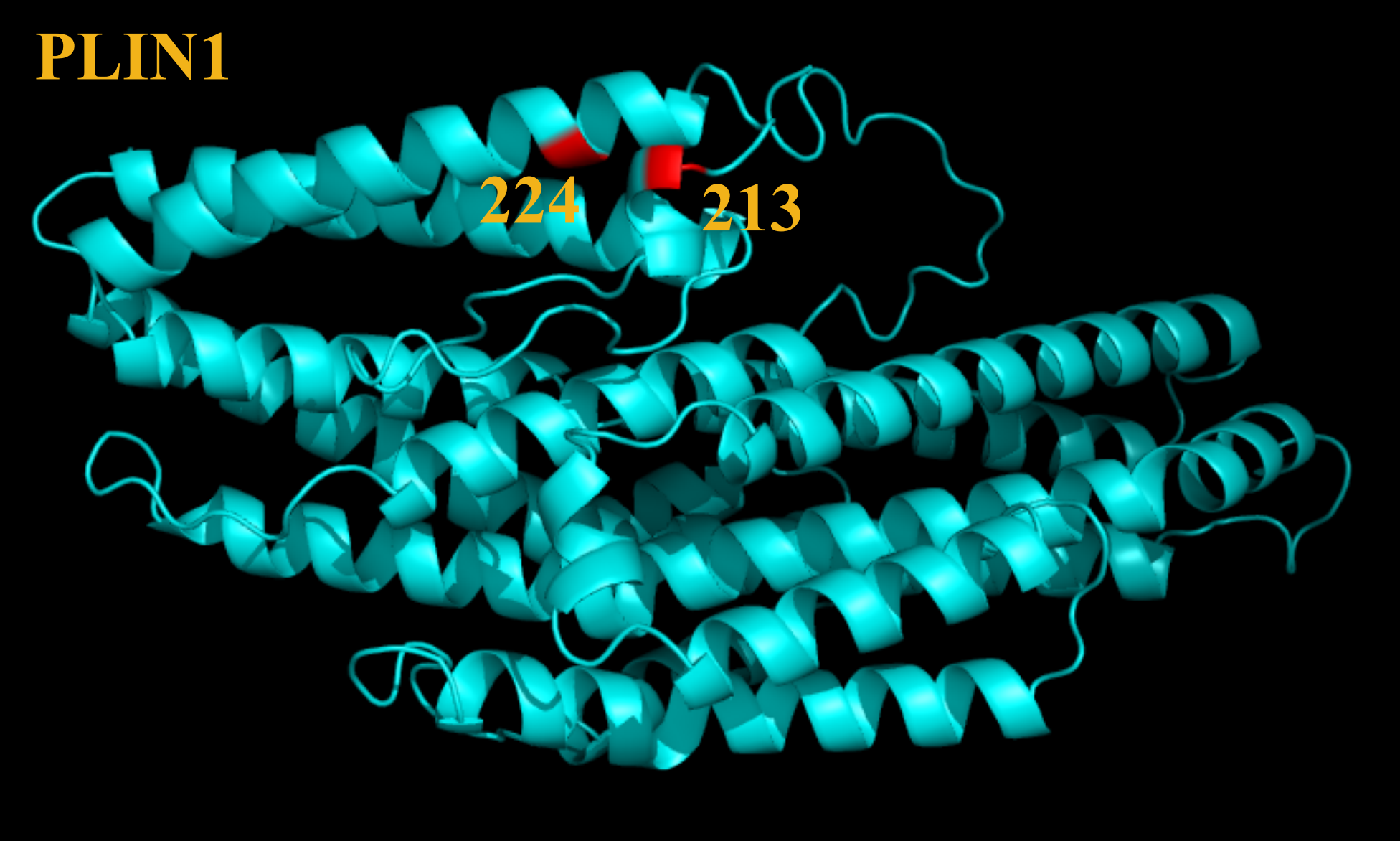
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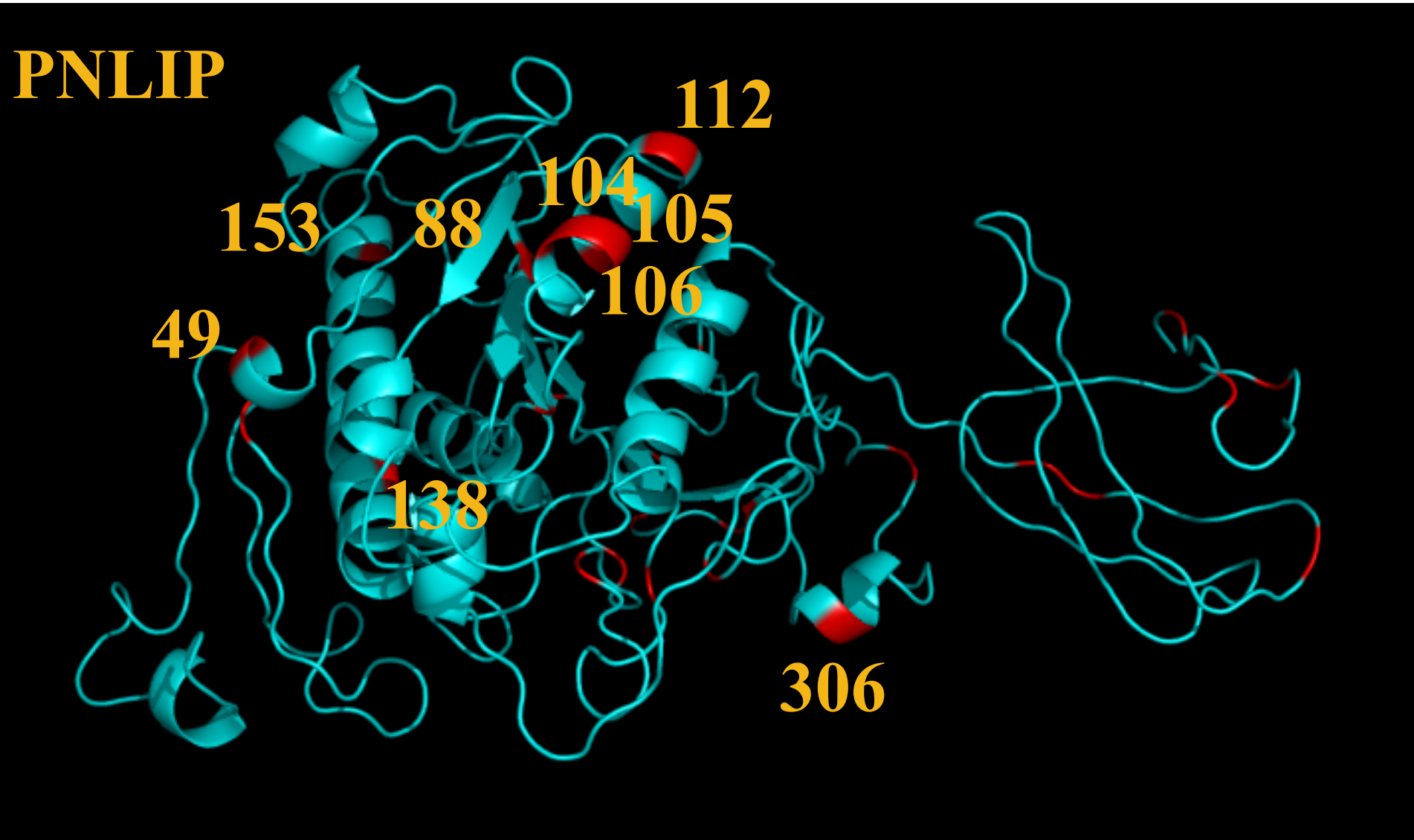
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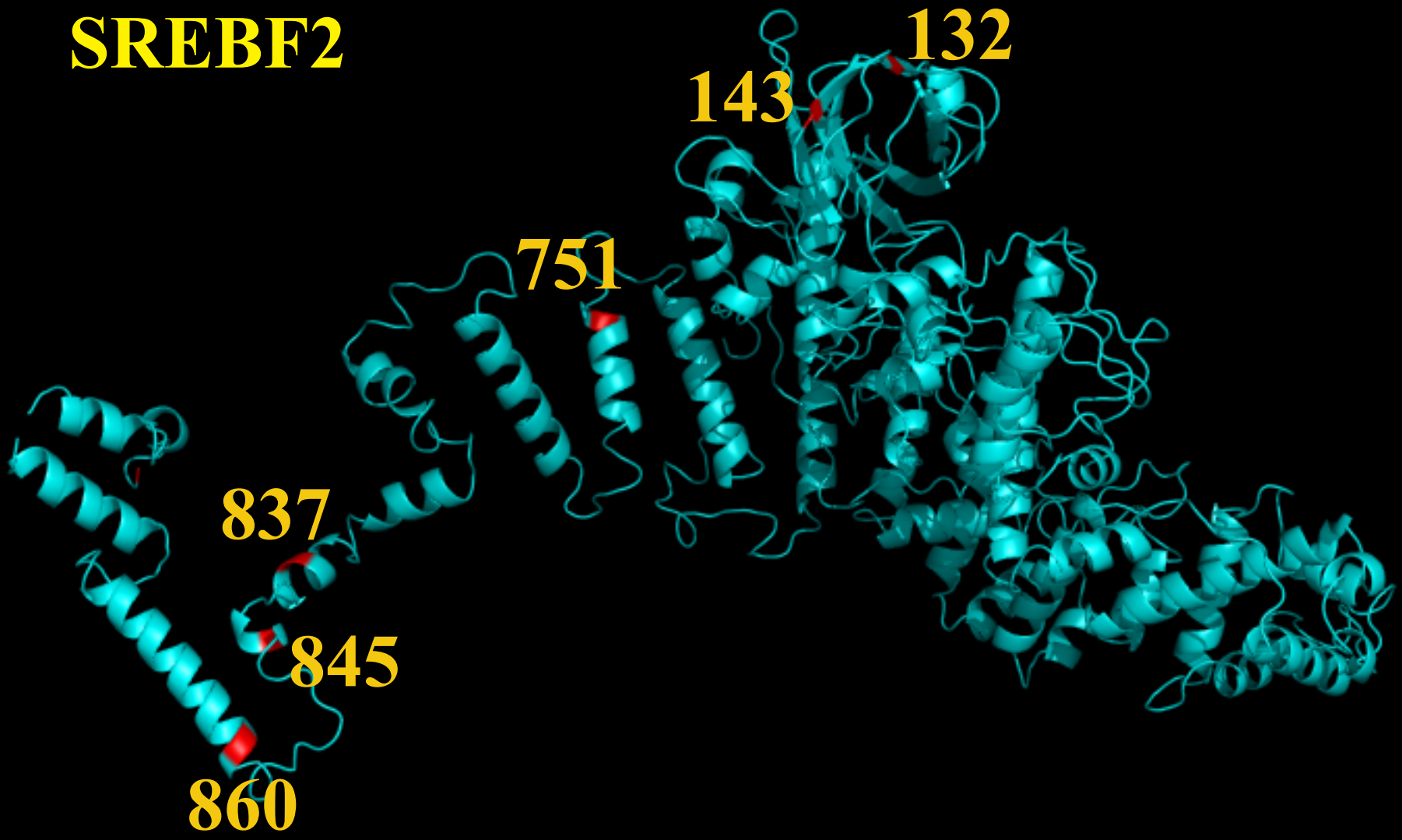
SREBF2
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