

Supplemental Material

Fenretinide binding to the lysosomal protein Saposin D alters ceramide solubilization and hydrolysis

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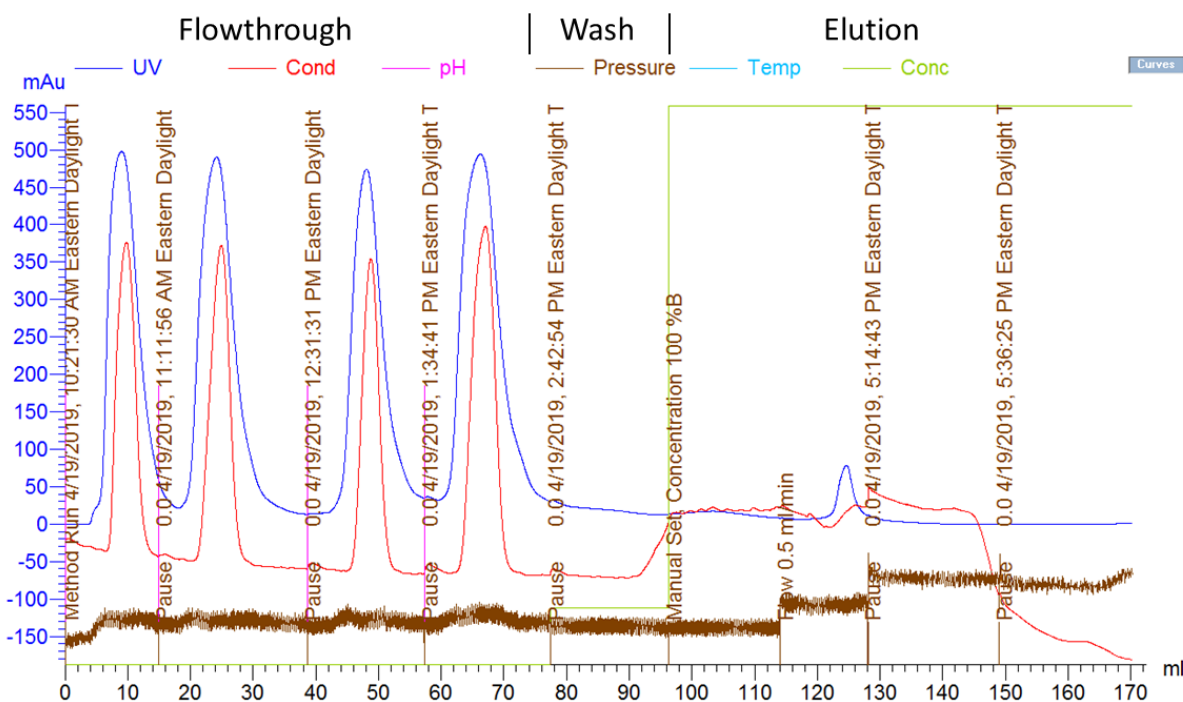


Figure S1. Purification of HIS-tagged SapD from concentrated lysate of *E. coli* by FPLC.

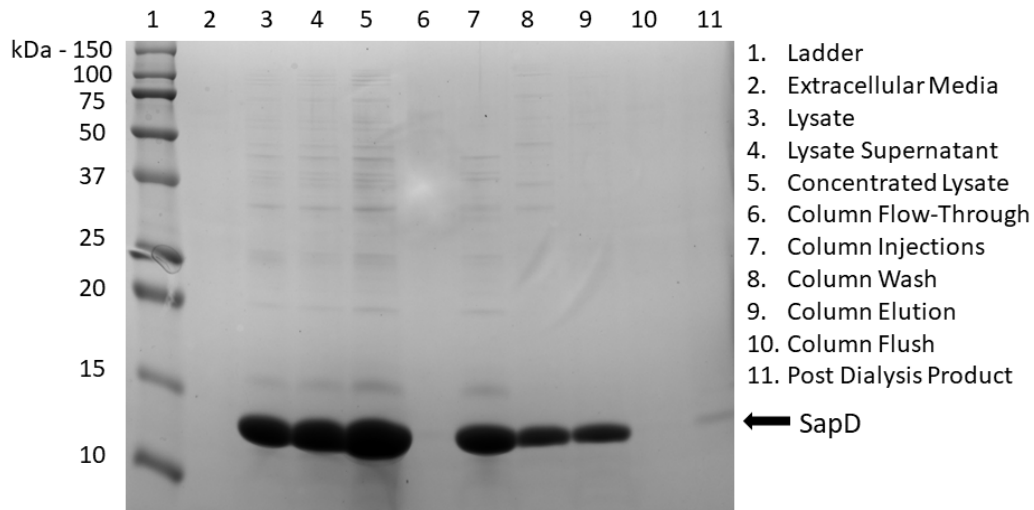


Figure S2. SDS-PAGE gel showing expression and purification of SapD induced with 400 μ M IPGT.

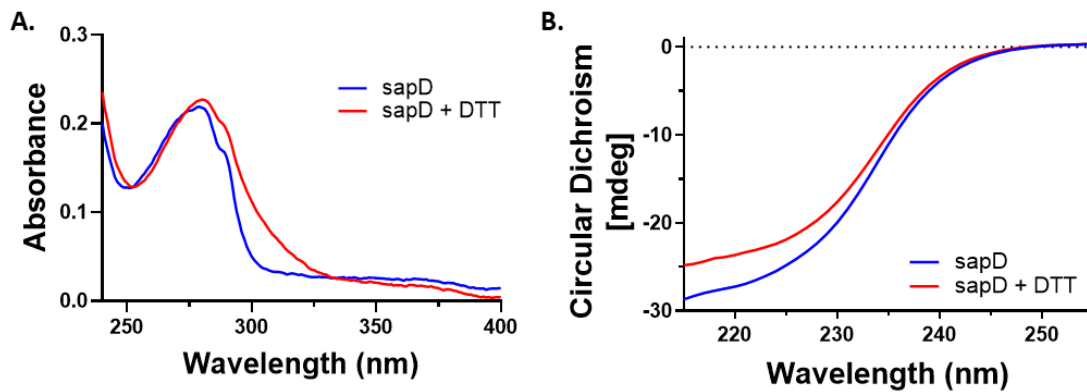


Figure S3. Evaluation for the presence of disulfide-bond formation. (a) Absorbance and (b) Circular Dichroism (CD) for 20 μ M sapD initially evaluated. Sample was then spiked with >3 eq. of DTT and reevaluated.

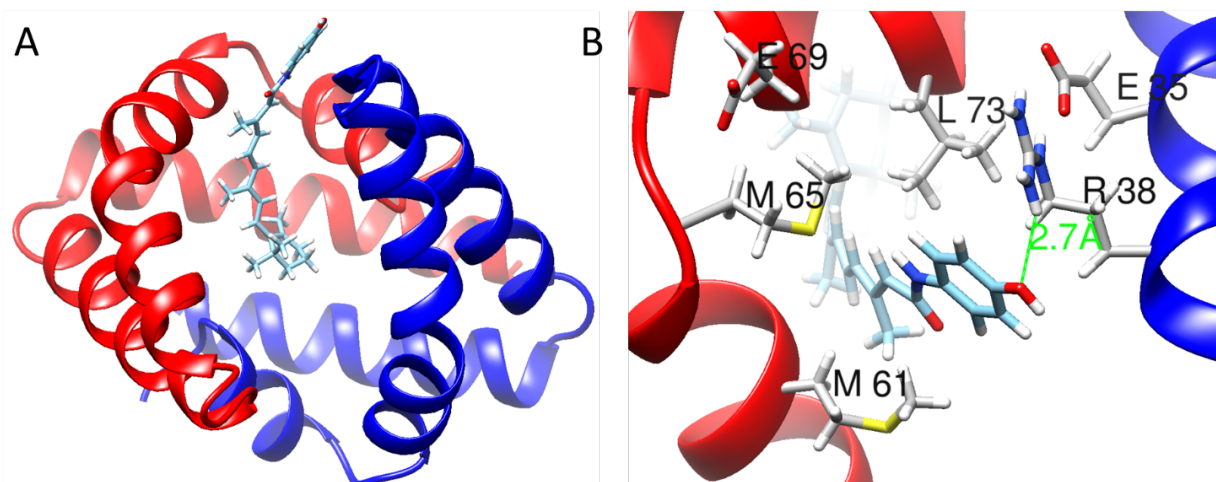


Figure S4. SwissDock molecular modeling for sapB (PDB:4V2O)¹³ and Fen. Docking images were generated using the SwissDock modeling in Chimera 1.14. SwissDock Estimated ΔG (kcal/mol) -8.12.

Ligand	Residue	Bond	Distance (Å)
18:1 ceramide-1-phosphate	Tyr54	Van der Waals	3.8
	Pro56	Van der Waals	4.1
	Val57	Van der Waals	3.8
	Glu60	Van der Waals	4.3
	Ile61	Van der Waals	4.2
	Lys74	Van der Waals	4.4
Fenretinide	Glu53	Van der Waals	5.2
	Tyr54	Van der Waals	3.4
	Pro56	Van der Waals	5.3
	Val57	Van der Waals	3.9
	Ile73	Van der Waals	3.9
	Lys74	Van der Waals	4.0
	Lys74	Hydrogen	3.8
	Ile75	Van der Waals	5.6
Tamoxifen	Glu53	Van der Waals	4.4
	Tyr54	Van der Waals	3.9
	Pro56	Van der Waals	4.4
	Val57	Van der Waals	3.7
	Ile75	Van der Waals	4.6
	Ser80	Hydrogen	3.7

Table S1. Summary of SwissDock modeling interactions for sapD and ligands.