

Type A & B Niemann-Pick disease and acid sphingomyelinase structure

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B4 Ryota Matsukawa

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1. Sphingomyelin and Niemann-Pick disease (NPD) type A and B
2. Therapy for type A and B NPD
3. Crystal structures of acid sphingomyelinase
4. Summary

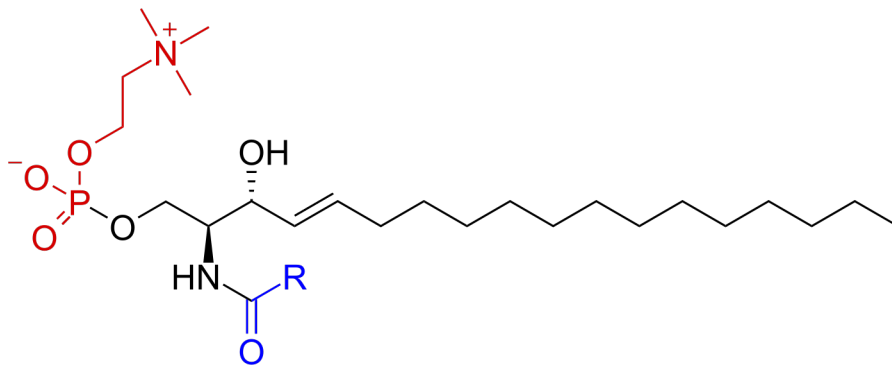
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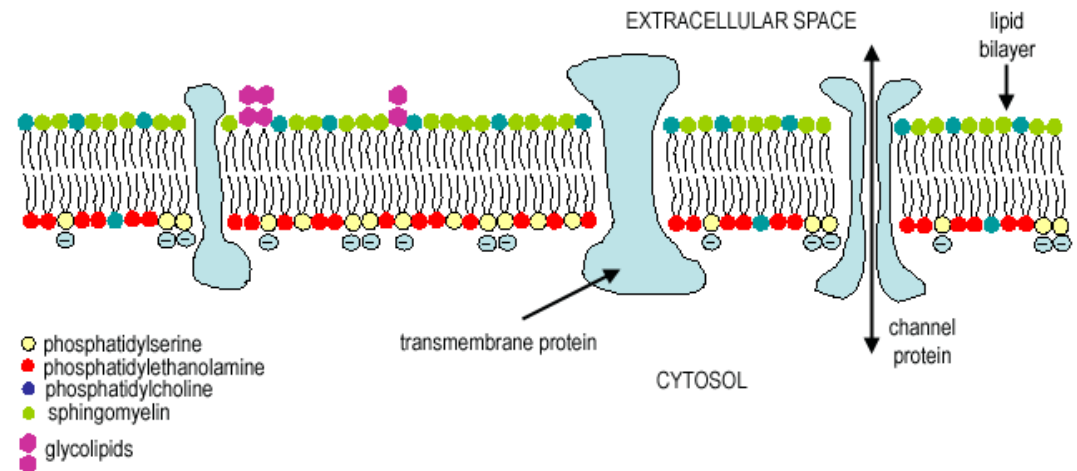
Sphingomyelin and acid sphingomyelinase (ASM)

Sphingomyelin

- Phosphate diester of **phosphocholine** and ceramide
- Ceramide: sphingosine + **fatty acid**
- A major component of the outer leaflet of cell membranes

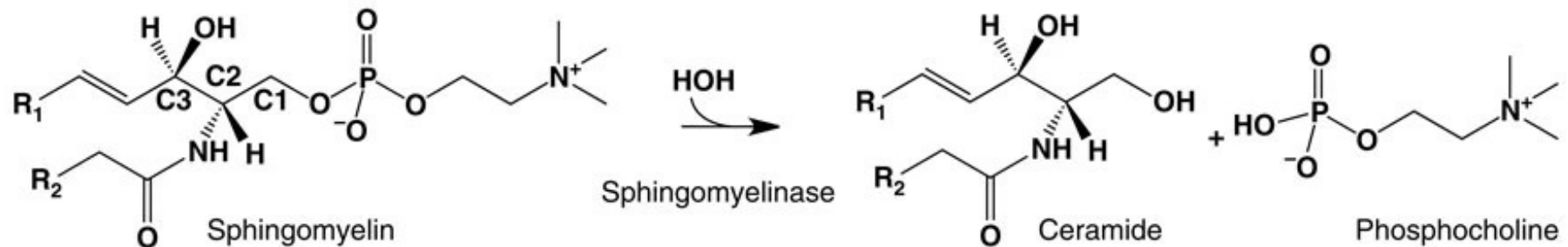


Wikipedia sphingomyelin
<https://en.wikipedia.org/wiki/Sphingomyelin>



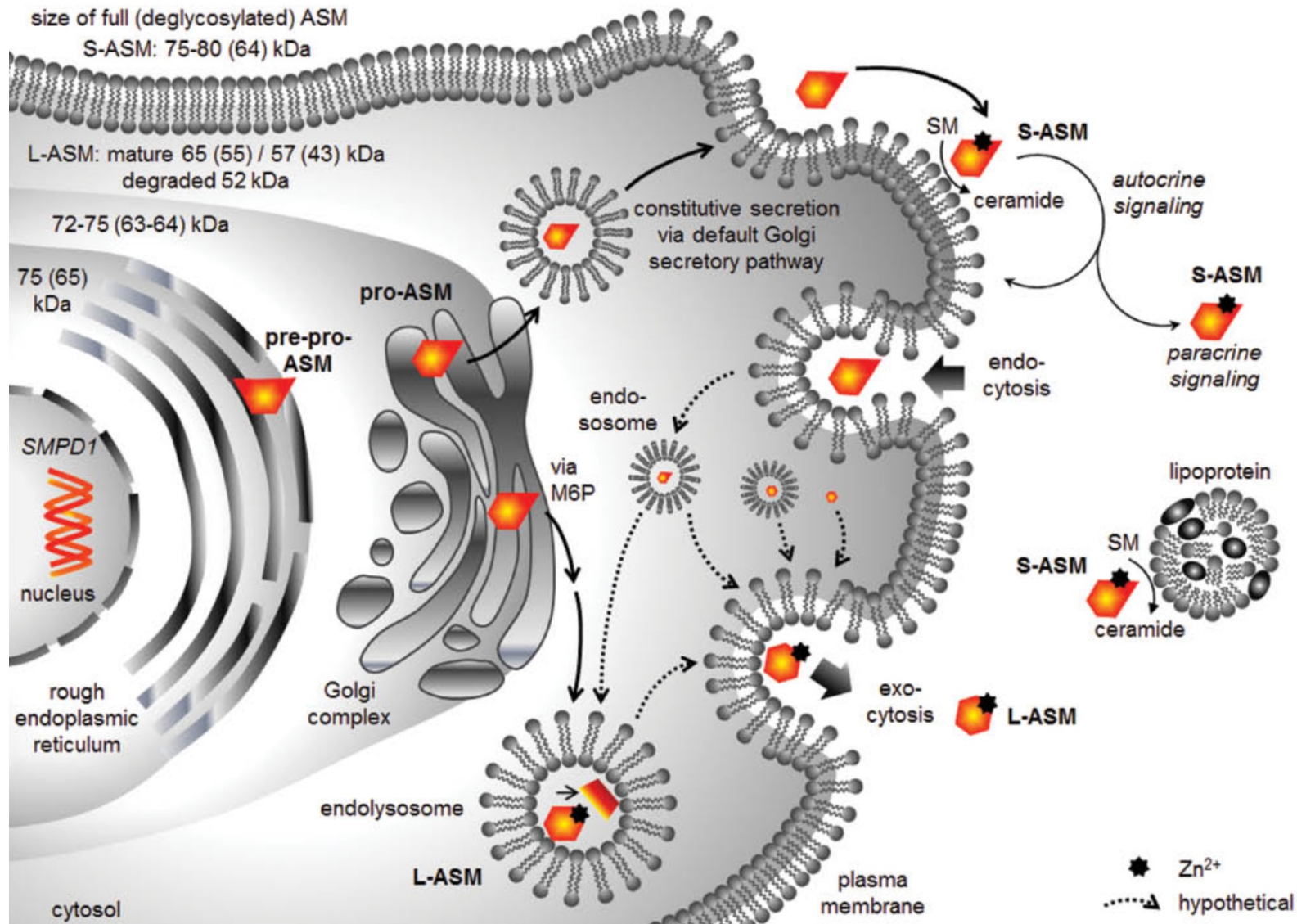
The Cell: The Histology Guide
https://www.histology.leeds.ac.uk/cell/plasma_membrane.php

- Sphingomyelin is hydrolyzed by acid sphingomyelinase (ASM)



Acid sphingomyelinase (ASM)

Pathway to hydrolysis of sphingomyelin



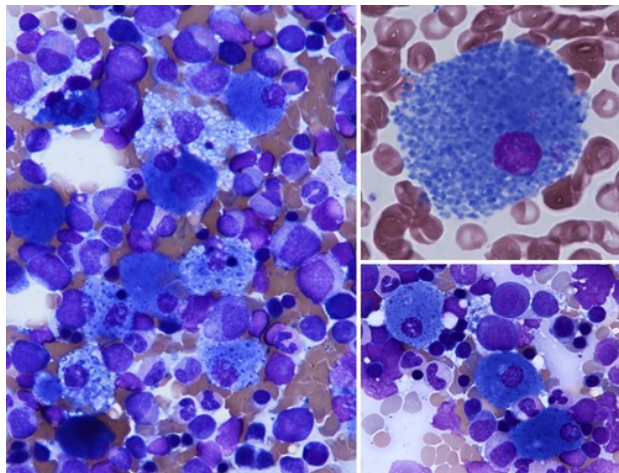
Niemann pick disease (NPD) type A and B

Niemann-Pick disease type A and B

- Acid sphingomyelinase deficiency (ASMD)
 - **Abnormal accumulation of sphingomyelin** in lysosomes or cell membrane in liver, spleen, lung and central nerve system due to mutations in SMPD1 which encoding ASM
- Clinical features and pathology
 - Type A: Hepatosplenomegaly (肝脾腫), hypotonia (筋緊張低下), progressive neurological symptoms

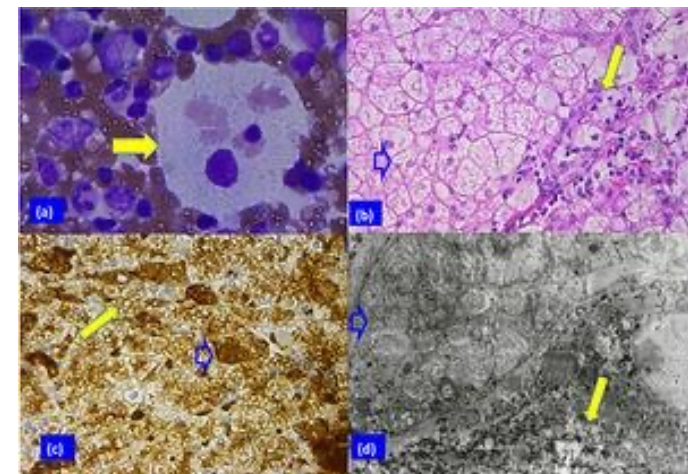
Type B: Hepatosplenomegaly (肝脾腫), liver failure (肝不全), decreased pulmonary function (肺機能の低下)

Splenomegaly (脾腫)



Jesús, V. *et al.*, *Br. J. Haematol.*, **2016**, 172, 840.

Foam cells (泡沫細胞)



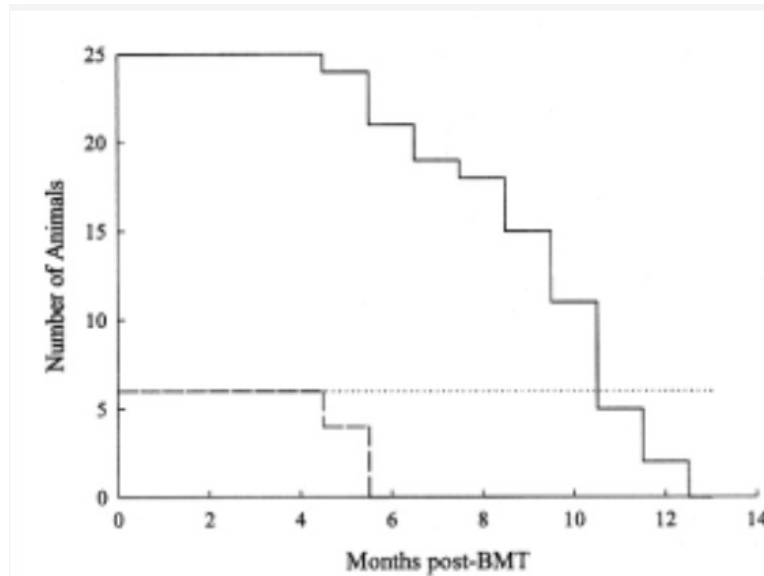
M. Cerón-Rodríguez *et al.*, *Ann. Hepatol.*, **2019**, 18, 613.
E.H. Schuchman, *et al.*, *Mol. Genet. Metab.*, **2017**, 120, 27.

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2. Therapy for type A and B NPD
 - Bone marrow transplantation
 - Enzyme replacement therapy
 - Gene therapy
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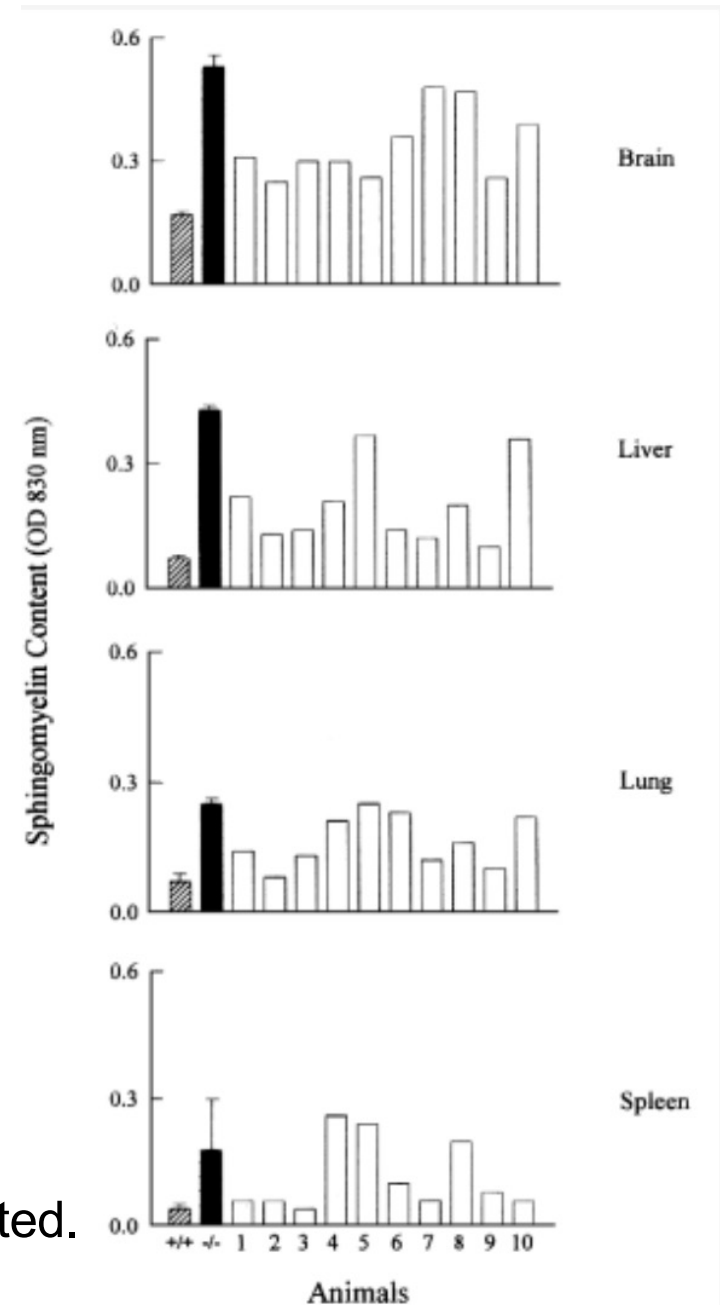
Bone marrow transplantation (BMT)

Bone marrow transplantation for ASM knock-out mouse model



Dotted line: Controls (+/+)
Hatched line: ASMKO controls (-/-)
Solid line: Transplanted ASMKO

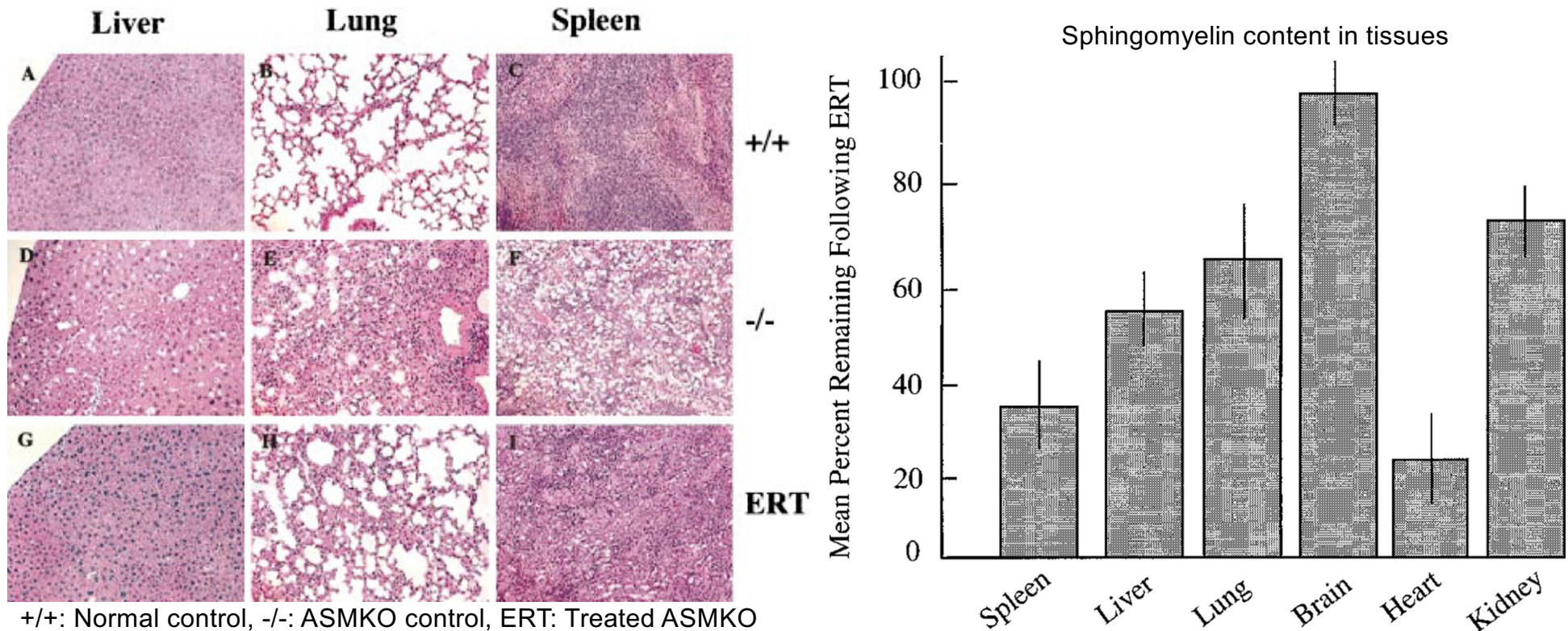
- Sphingomyelin levels in the spleen and liver decreased significantly.
- The effect on the brain was moderate and the progressive neurological disease was not prevented.



Enzyme replacement therapy (ERT)

Olipudase alfa (Xenpozyme) for ASMKO mouse

Olipudase alfa: Recombinant human ASM

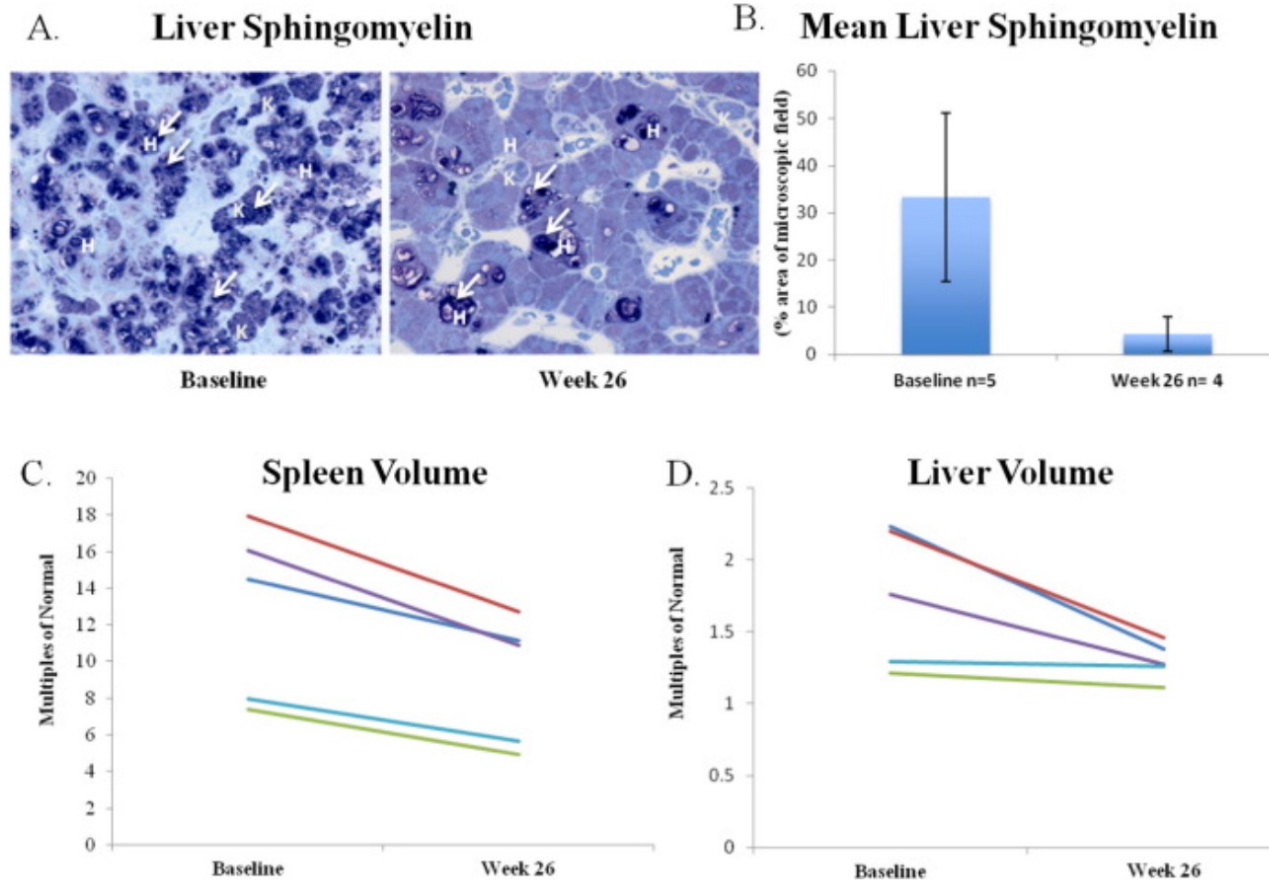


- Histological improvement was observed by infusion of rhASM.

Enzyme replacement therapy (ERT)

Olipudase alfa (Xenpozyme) for NPD type B patients

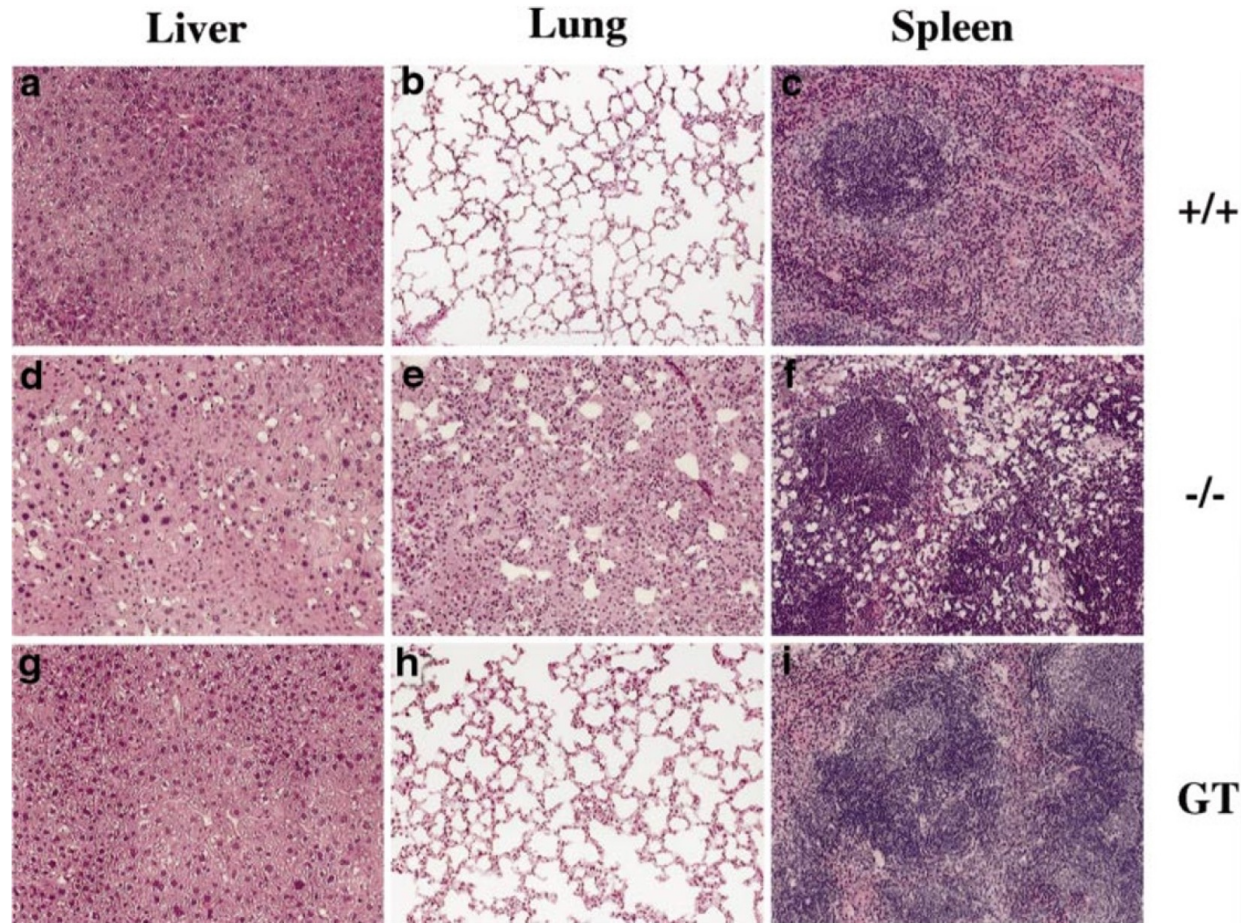
Olipudase alfa: Recombinant human ASM



- Accumulated sphingomyelin was debulked and histological improvement was observed by treatment of Olipudase alfa.

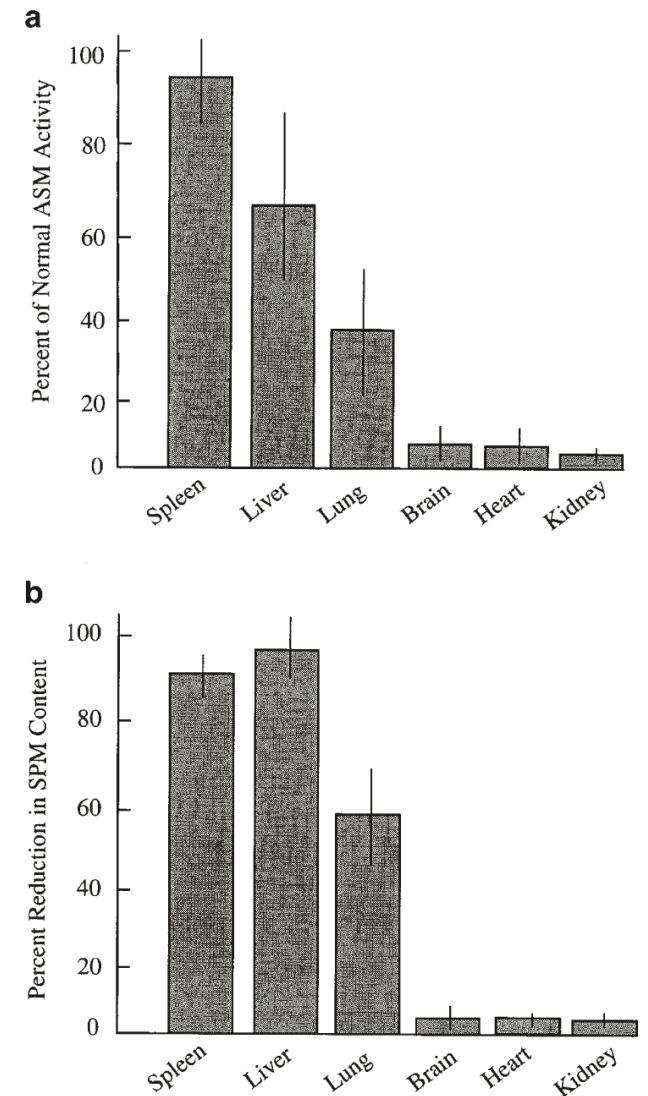
Gene therapy

Hematopoietic stem cell gene therapy



+/+ : Normal control, -/- : ASMKO control, GT: Treated ASMKO

- Tissues from the treated mice show markedly less lipid accumulation than ASMKO control.



Gene therapy

Hematopoietic stem cell gene therapy

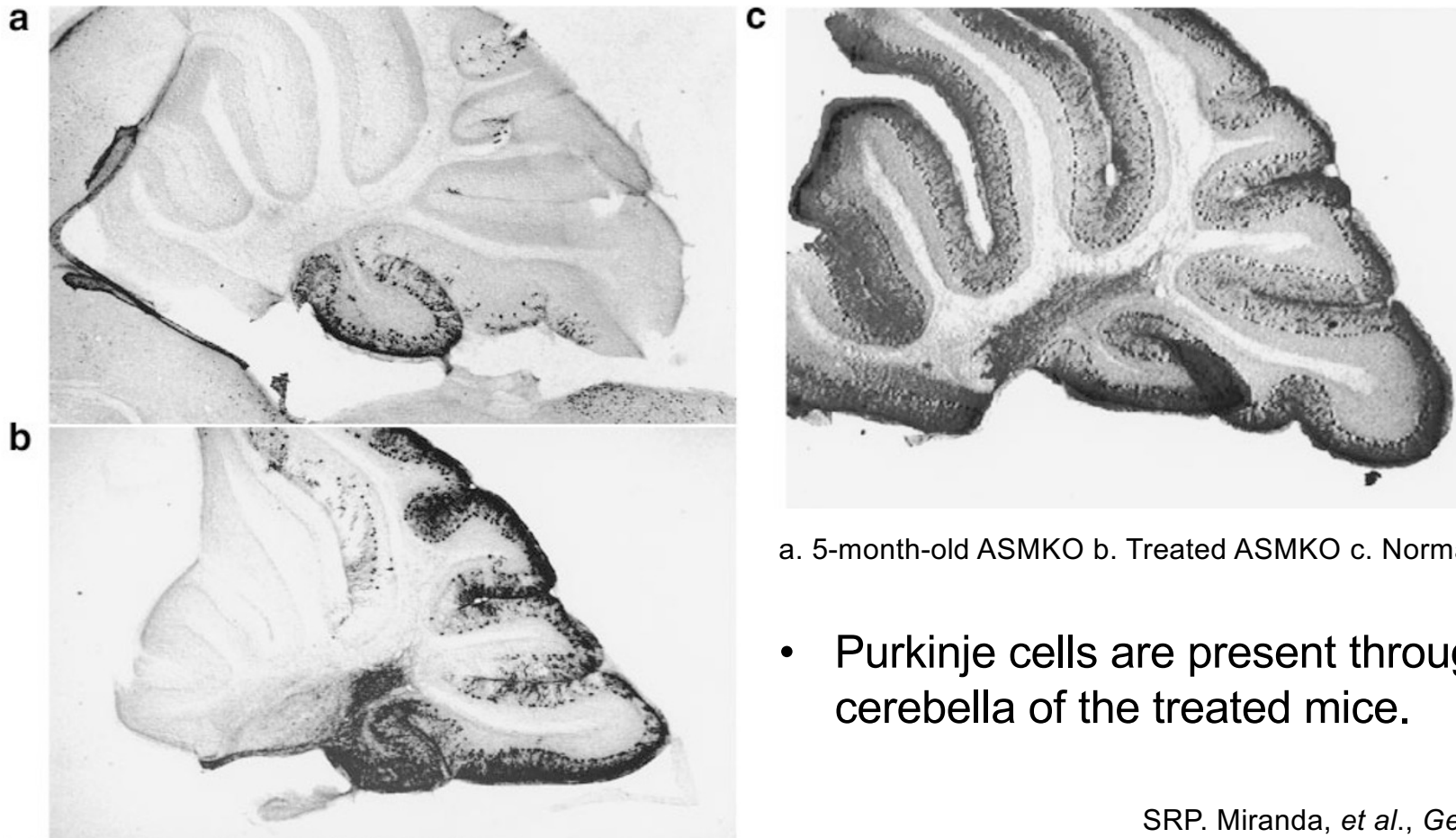
- It has been reported that Purkinje cells are reduced in the cerebellum in the ASMKO mouse model.

K. Horinouch, *et al.*, *Nat. Genet.*, **1995**, *10*, 288-293.

Gene therapy



Purkinje cell immunohistochemistry



a. 5-month-old ASMKO b. Treated ASMKO c. Normal control

- Purkinje cells are present throughout the cerebella of the treated mice.

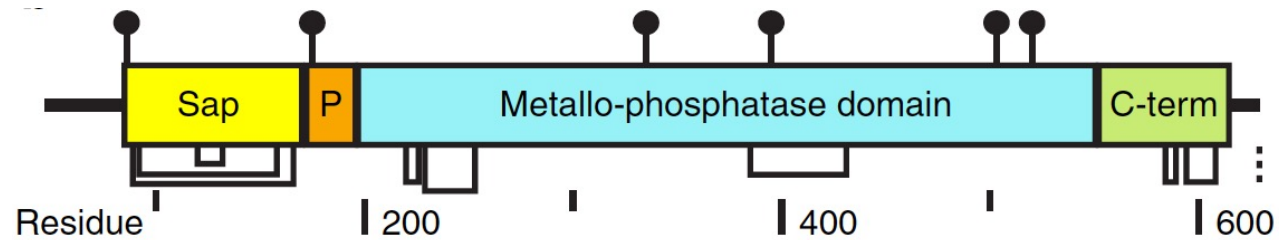
SRP. Miranda, *et al.*, *Gene Ther.*, **2000**, *7*, 1768.

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ASM structures

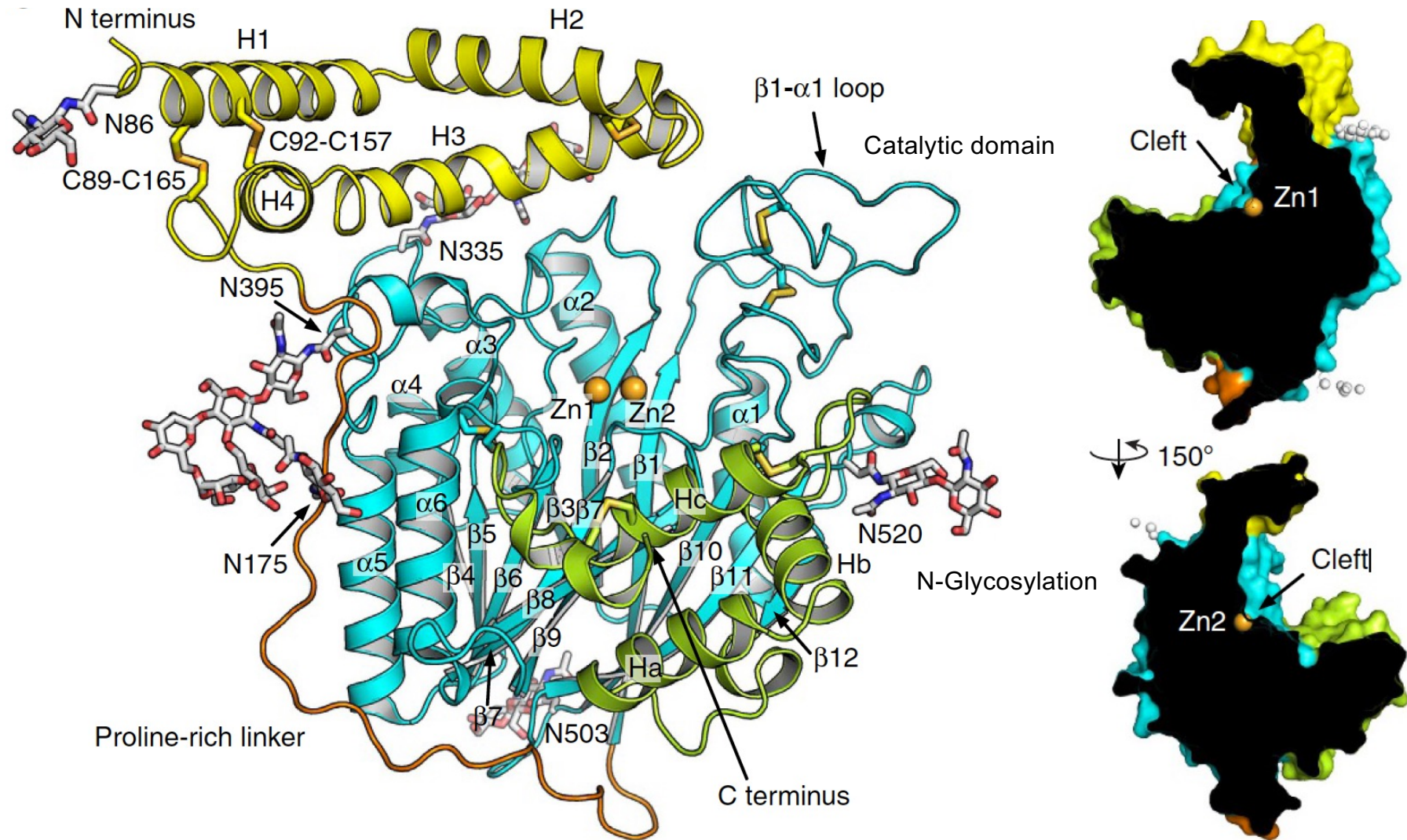
Diagram of ASM domains



- Yellow: Saposin domain (*N-terminal*)
Sphingomyelin activator that recognize and locate lipids on the active site
- Orange: Proline-rich linker
The connection between the saposin and the catalytic domain
- Blue: Metallo-dependent phosphatase catalytic domain
Active site for hydrolysis of sphingomyelin
- Green: *C-terminal* domain (ill-defined)

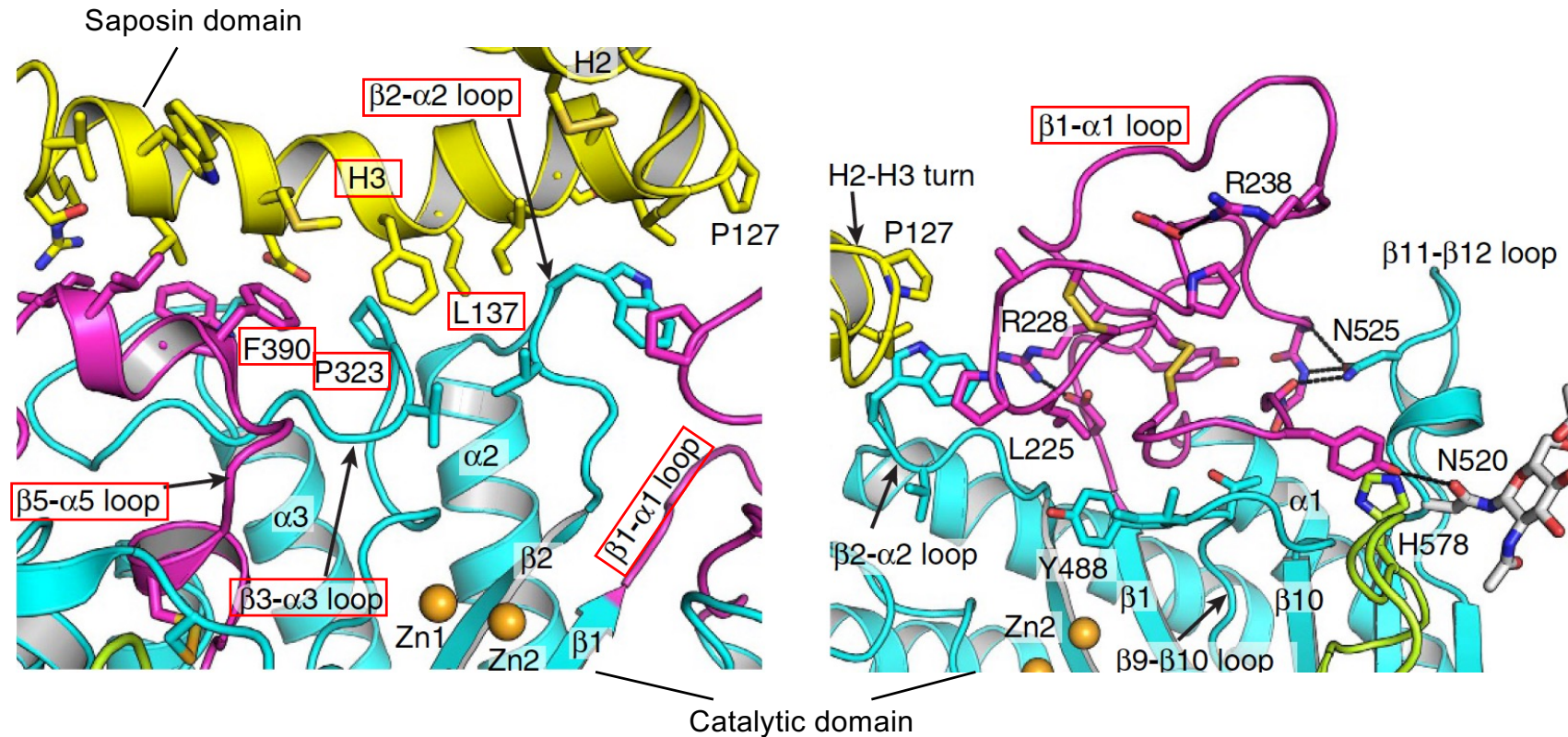
ASM structures

Overall structure of ASM



ASM structure: Domain interactions

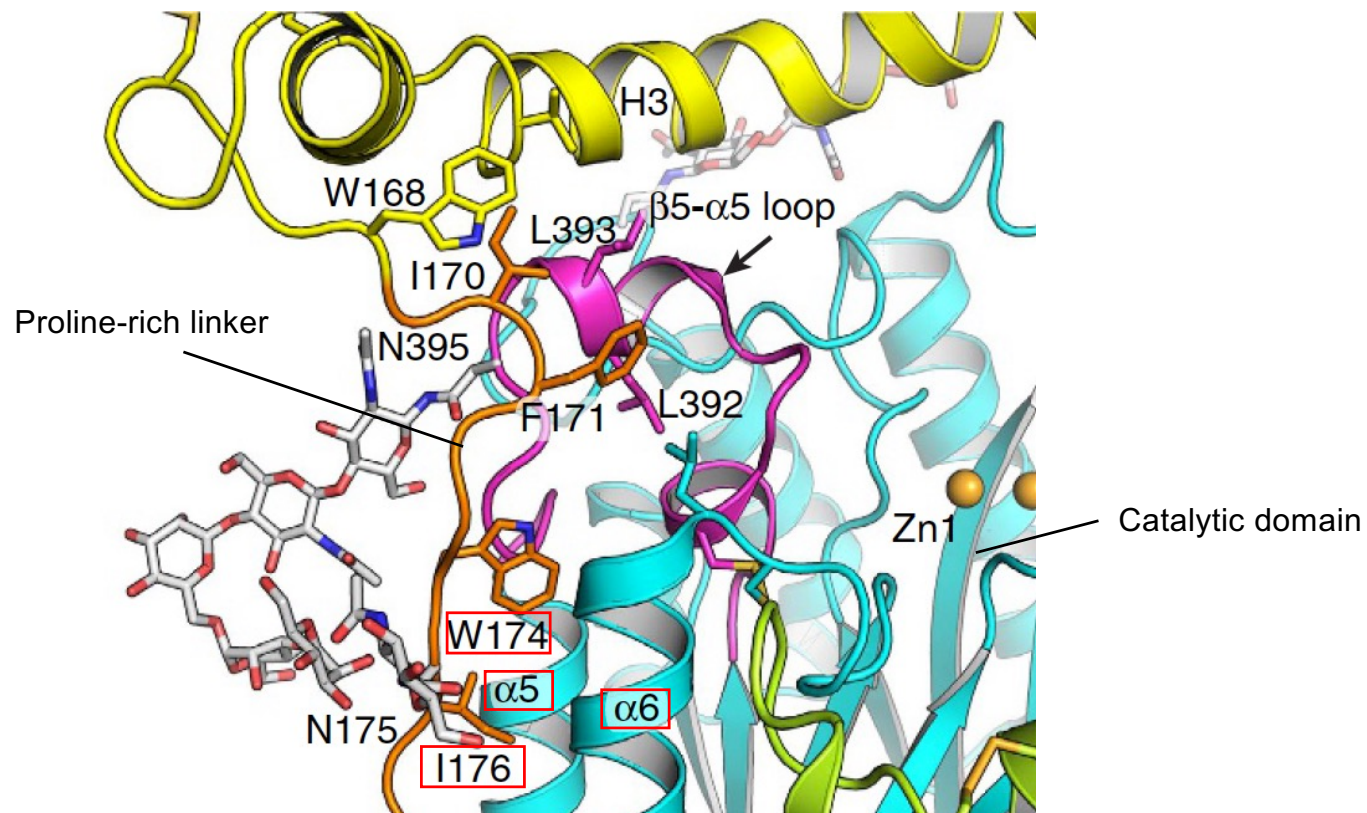
Interactions between the saposin domain and catalytic domain



- H3 helix in saposin domain extensively contacts with $\beta 1-\alpha 1$, $\beta 2-\alpha 2$, $\beta 3-\alpha 3$, $\beta 5-\alpha 5$ loop.
- Many mutations occur on the interface residues, such as L137P in H3, P323A on the $\beta 3-\alpha 3$ loop, Δ F390 on the $\beta 5-\alpha 5$ loop.

ASM structure: Domain interactions

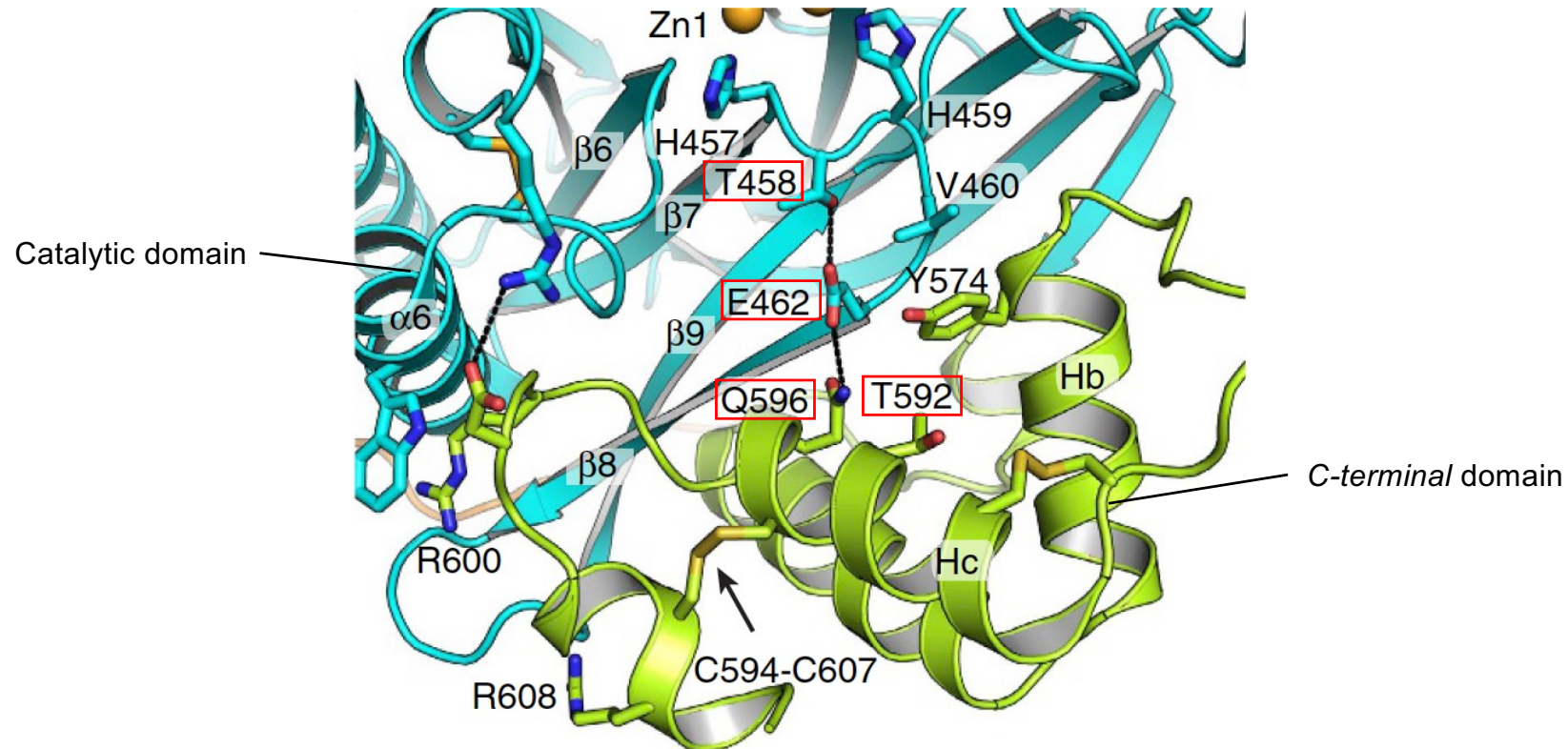
Interactions between the proline linker and catalytic domain



- The proline-rich linker is stabilized by hydrophobic interactions between W174, I176, L178 in the proline-rich linker and $\alpha 5$, $\alpha 6$ helices in the catalytic domain.

ASM structure: Domain interactions

Interactions between the proline linker and C-terminal domain



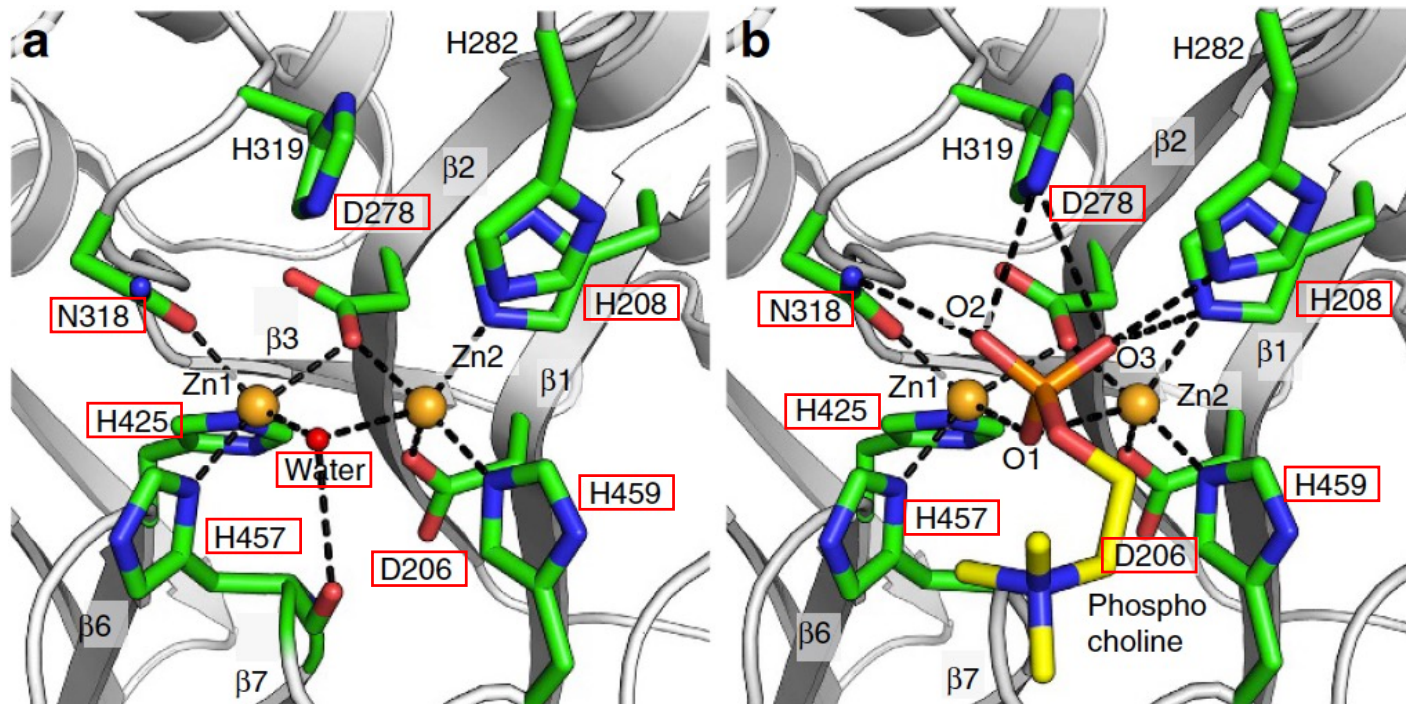
- The *C-terminal* domain contributes to stabilization of the active site, especially $\beta 7$ - $\beta 8$ loop.
- It has been reported that $\Delta T592$ mutation causes severe ASMD.
→ $\Delta T592$ mutation has a severe impact on ASM folding?

Rodriguez-Pascau, L. *et al.*, *Hum. Mutat.*, **2009**, 30, 1117.

Zhou, YF. *et al.*, *Nat. Commun.*, **2016**, 7, 13082.

ASM structure: Zinc and phosphocholine binding in the active site

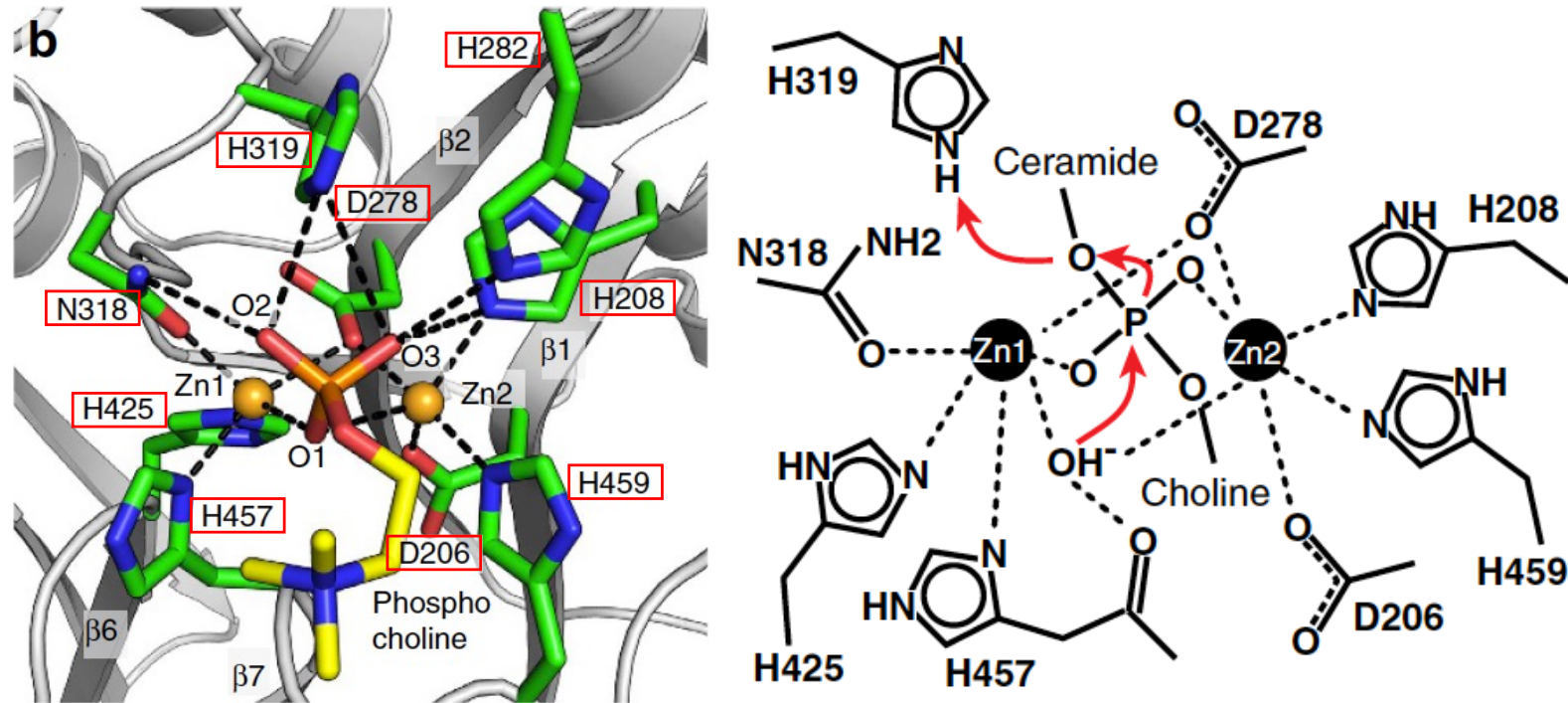
- Active site of holo ASM structure
- Phosphocholine bound structure



- Both zincs have trigonal bipyramidal geometry.
- A water molecule bridges between Zn1 and Zn2 and is stabilized by hydrogen bonding to the main chain carbonyl of H457.
- Oxygen (O1) in the phosphoryl group replaces the position of the water molecule in the holo ASM structure.

Hydrolysis of sphingomyelin

Mechanism of hydrolysis of sphingomyelin



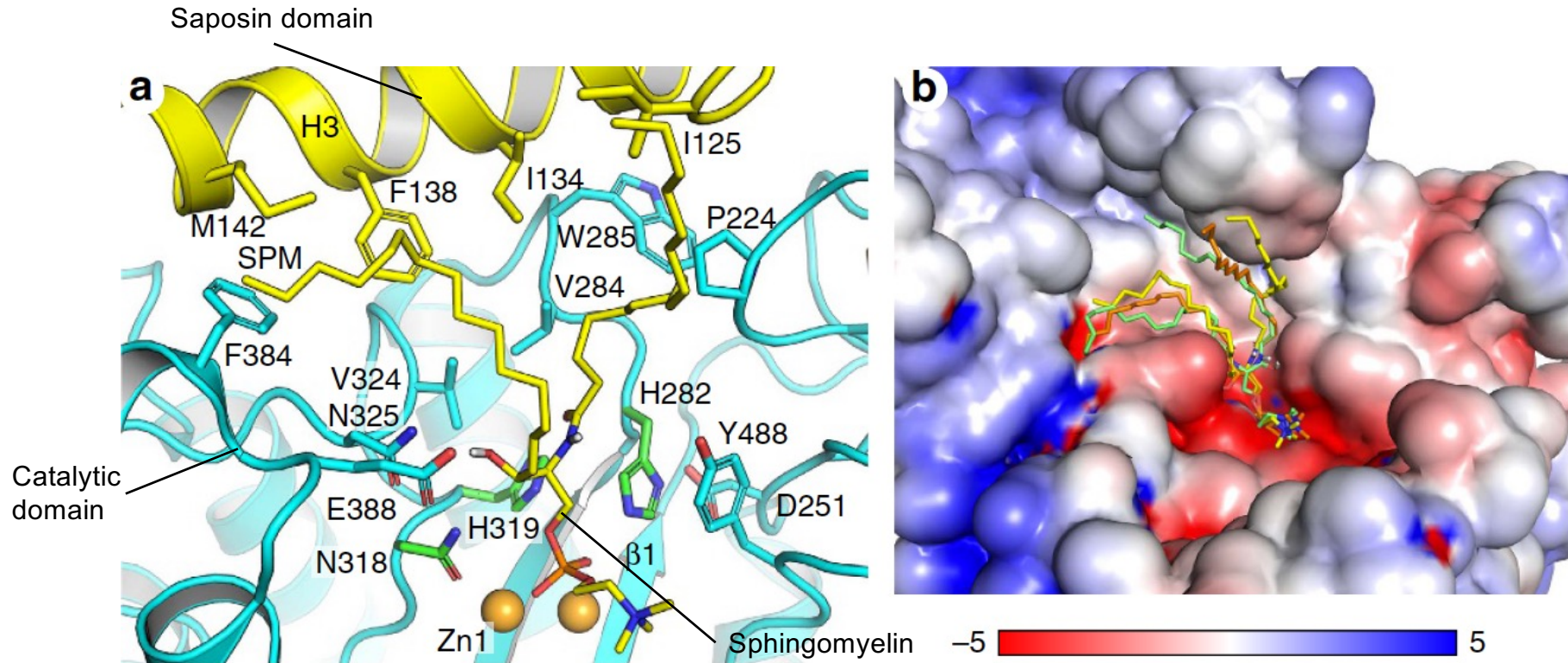
- The coordinated water is deprotonated to hydroxide due to the activation by two zinc ions, and the hydroxide attacks on the phosphorus of sphingomyelin.
- The phosphorus oxygen on the ceramide side extracts a proton from H319.
- Mutation of H319Y causes severe ASMD.

Sikora, J. *et al.*, *Ann. Hum. Genet.*, **2003**, 67, 63.

Zhou, YF. *et al.*, *Nat. Commun.*, **2016**, 7, 13082.

Docking model of sphingomyelin on ASM

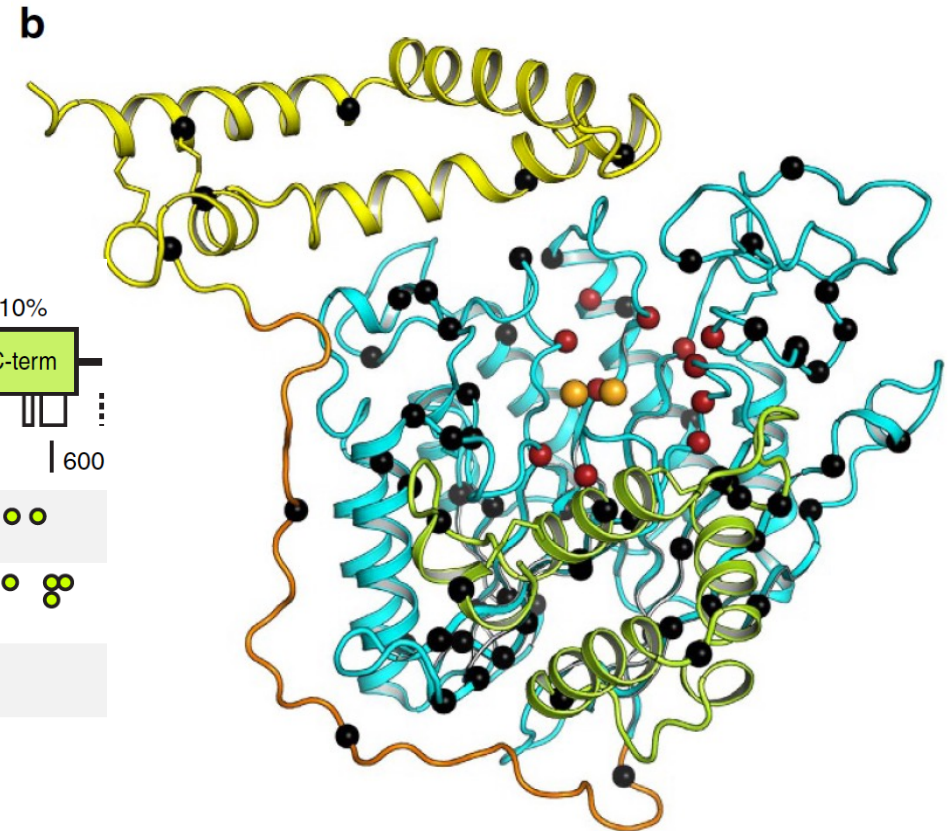
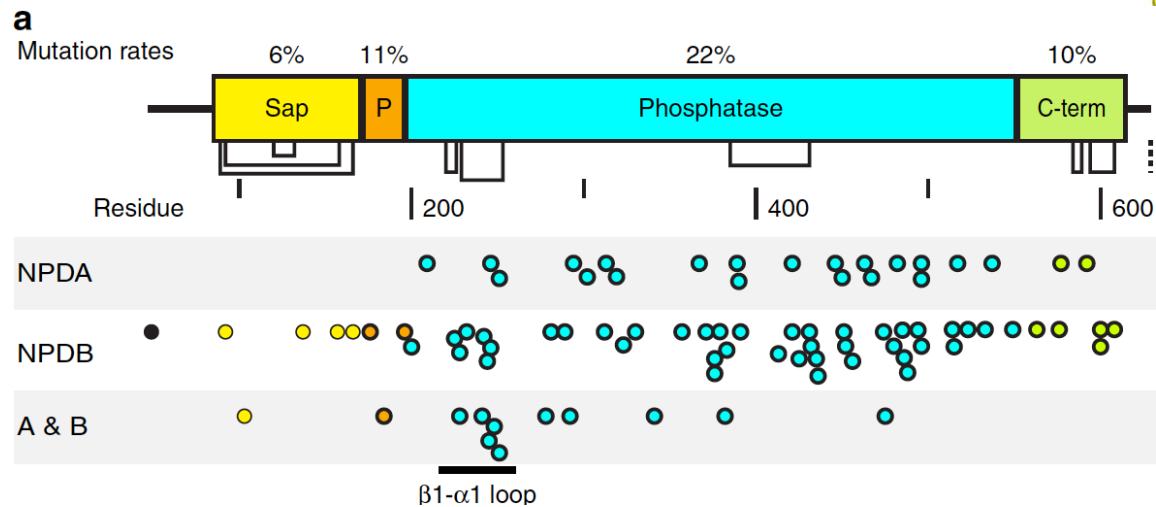
- Surface residues around C-16 sphingomyelin
- Electrostatic potential maps



- The hydrophobic ceramide chains in sphingomyelin is accommodated in the saposin concave surface which is rich in hydrophobic residues and not highly charged.

Mutation in ASM

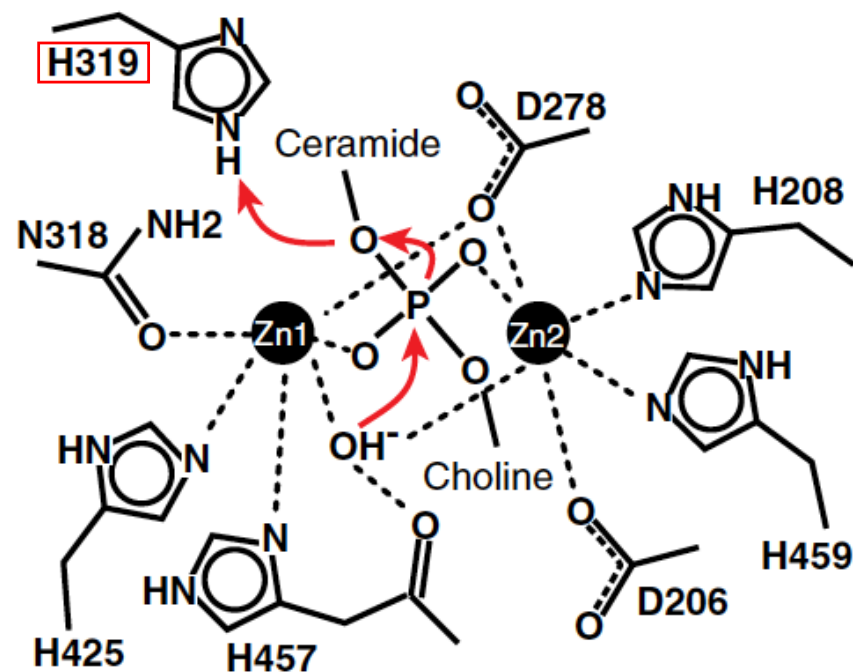
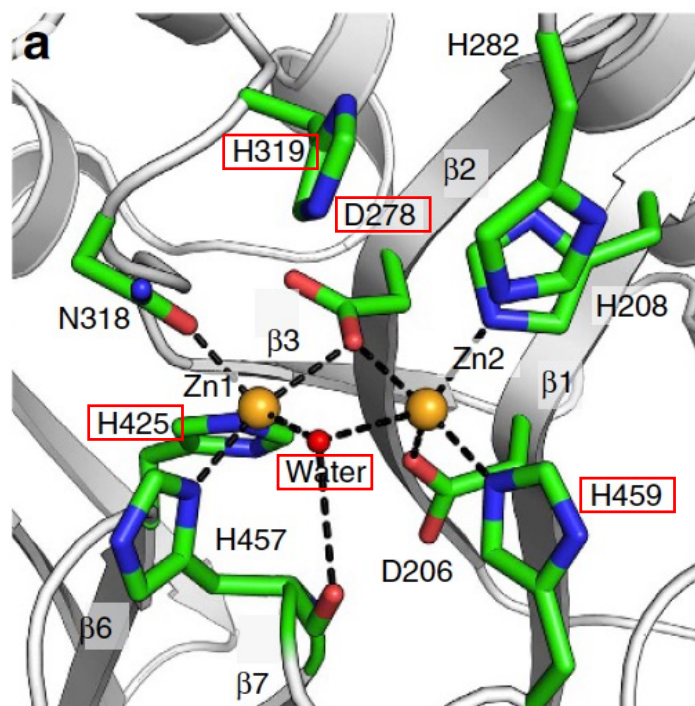
- Distribution of mutations on ASM sequence
- Distribution of mutations on 3D structure



- 82% of mutations are located in the catalytic domain.
- Those mutations are categorized into two groups, according to their disruptive effects on catalytic activity and protein folding.

Mutation affecting catalytic activity

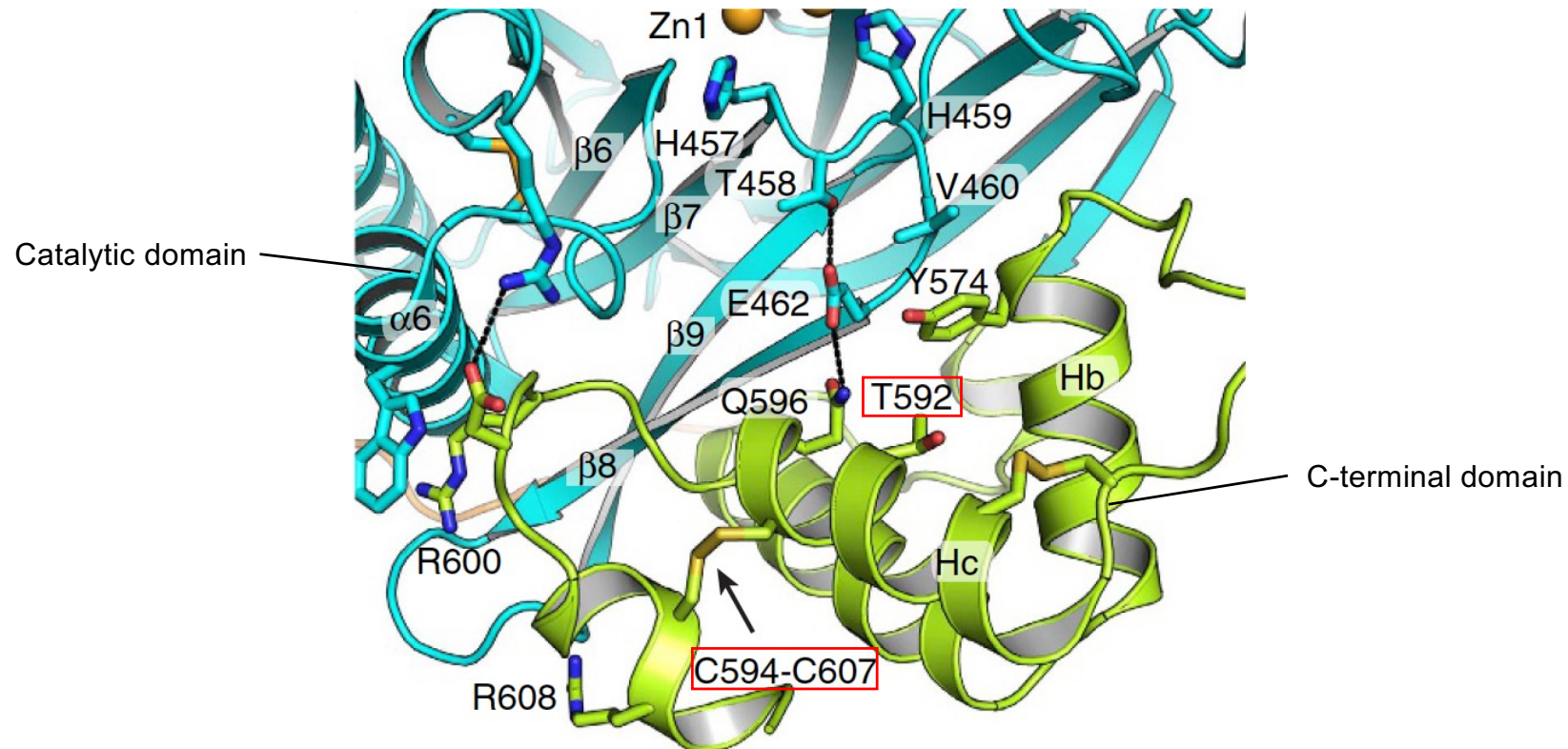
D278A, H329Y, H425R mutations



Mutation	NPD ^{\$}	RSA [*]	Interpretation of mutations based on structure	Category [†]
D278A	A, B	0.00	Carboxylic acid group coordinate binding of both zinc atoms.	Active
H319Y	A	0.09	Essential imidazole ring for catalysis. Long side chain of tyrosine disrupts catalytic reaction.	Active
H425R	B	0.00	Direct coordination with zinc. Mutation disrupts zinc binding and catalytic reaction.	Active

Mutation affecting protein folding

ΔT592 mutations



Mutation	NPD [§]	RSA*	Interpretation of mutations based on structure	Category [¶]
delT592	A	0.09	In the middle of Hc helix. A deletion not only breaks the C594-C607 disulfide, but also interferes the interactions between C-terminal domain and catalytic domain. .	Folding

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Summary

- NPD type A and B present abnormal accumulation of sphingomyelin due to deficient activity of ASM.
- NPD type A present progressive neurological symptoms.
- There are no approved therapies for ASMD except for enzyme replacement therapy, which is effective only in NPD type B.
- Crystal structures of ASM revealed the mechanism of hydrolysis of sphingomyelin, in which two zinc ions activate a water molecule for nucleophilic attack of phosphodiester bond.
- Saposin, proline-rich linker, catalytic and *C-terminal* domain together create a cleft specific for sphingomyelin binding.