

Unsymmetric or hybrid detergents for membrane protein structural study

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Abstract

Detergent micelles are widely used as a membrane-mimetic system for membrane protein extraction, isolation and structural study. Many recently developed detergents feature multiple tail and head groups, with architectures that are symmetric (i.e., the same alkyl chain) and non-hybrid (single head group type). Further diversification has involved incorporating structural differences in the tail groups (unsymmetric), head groups (hybrid), or both head and tail groups (unsymmetric hybrid). In this mini-review, we introduce these novel detergents, focusing on the relationships between their structural features, physical properties and performance in MP applications. The detergent design strategy utilizing unsymmetric/hybrid structures expands the detergent repertoire and the detergent structure-property-efficacy relationships presented offer valuable design guidelines, collectively advancing membrane protein research.

Introduction

Unveiling the structures of membrane proteins (MPs) is crucial for understanding their mechanisms of action and for developing effective protein specific therapeutic agents and [1,2]. However, MPs are inherently amphiphilic, containing both hydrophilic and hydrophobic groups. This amphiphilicity causes MPs to denature or aggregate when exposed to aqueous environments, making the investigation of MP structures challenging [3,4]. This challenge is particularly pronounced when studying eukaryotic MPs with multiple subunits or oligomeric architectures [5-7]. Consequently, the number of known MP structures is only a small fraction of that of total protein structures determined, although has recently increased dramatically in the last ten years, reaching approximately 1,800 unique structures as of February 20, 2025 (Figure 1a) [8]. This surge is largely due to the development of cutting-edge technologies, particularly single-particle cryo-electron microscopy (cryo-EM) [cryo-EM ref]. Additionally, recent advances in membrane-mimetic systems, including amphipathic polymers (APols), bicelles, and membrane scaffold protein (MSP)-, styrene-maleic acid copolymer (SMA)-, and saposin-based nanoassembly (nanodiscs (NDs), SMA lipid particles (SMALPs), and Salipro, respectively), have significantly contributed to MP structure determination (Figure 1b) [9-17]. Detergent micelles, as a

membrane-mimetic system, have been widely used for MP structural studies since the first crystal structure of *Rhodospseudomonas viridis* photosynthetic assembly was reported using lauryldimethylamine-*N*-oxide (LDAO) in 1985[18-20]. Unlike most other membrane mimetic systems, detergent micelles can be used throughout the entire course of MP manipulation, including protein extraction, purification and structural study[21,22]. However, one main issue associated with detergent micelles is their limited ability to stabilize MPs in aqueous media, likely due to their dynamic nature[23,24]. To increase the stability of MPs in detergent-based solution, various novel detergents have been developed over the past two decades[25-32]. In this review, we introduce recently developed detergents containing multiple tail and/or head groups, which we have categorized into four classes, based on the tail group symmetry and head group identity: detergents with the same or different alkyl chains (symmetric/unsymmetric) and detergents with identical or different head groups (non-hybrid/hybrid) (Figure 1c). We focus on the structural distinctions among these four detergent classes and their effects on physical properties, such as critical micellar concentrations (CMCs), micelle size, and hydrophilic-lipophilic balance (HLB). Importantly, this review also explores the relationship between the physical properties of these detergents and their protein stabilization efficacy. Overall, the detergent structure-property-efficacy relationships introduced in this review provide valuable insights for future detergent design.

Symmetric detergents

Conventional detergents widely used for MP studies, as exemplified by *n*-dodecyl- β -D-maltoside (DDM), *n*-octyl- β -D-glucoside (OG), LDAO and tetraethylene glycol monooctyl ether (C₈E₄), have a canonical architecture consisting of a single tail and single head group (Figure 2a). In this architecture, straight alkyl chains with various lengths serve as lipophilic groups, while polar groups, such as amine-*N*-oxide (LDAO), glucoside (OG), maltoside (DDM), and oligoethylene glycol (C₈E₄), act as hydrophilic groups. While the dynamic nature of micelles formed by conventional detergents may be favorable for protein extraction, many MPs in these micelles exhibit limited stability, posing a challenge for their structure determination[33,34]. To address this limitation, various novel detergents have been developed, many of which contain multiple alkyl chains (*ranging from two to four*) and multiple head groups (*ranging from two to eight*). Examples include maltose neopentyl glycols (MNGs), glucose neopentyl glycols (GNGs), TRIS linker-bearing triazine-based triglucosides (TTGs) and tandem malonate-derived glucosides (TMGs) (Figure 2b) [35-38]. The presence of multiple tail groups enhances MP stability by increasing *detergent-detergent* and *protein-detergent* interactions, as supported by MD simulations of LMNG[39]. As seen with these detergents, the presence of multiple tail groups necessitates inclusion of multiple head groups to achieve an optimal HLB in the range of 11 to 14 for MP studies [40]. All of these detergents feature identical tail and head groups, and are therefore classified as symmetric non-hybrid detergents. Due to the presence of multiple alkyl chains, these symmetric non-hybrid detergents have significantly lower CMCs than single alkyl chain detergents like DDM (Table 1) and are significantly more effective at stabilizing MPs.

Unsymmetric detergents

Despite their enhanced protein stabilization efficacy, symmetric detergents are often associated with issues related to MP studies. As exemplified by LMNG (also known as MNG-10,10), these symmetric

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detergents tend to form larger micelles (hydrodynamic diameter (D_h)=19.6 nm at 1.0 wt%). Small micelle-forming detergents are preferred for MP structural study via x-ray crystallography and cryo-EM[19,41]. In relation to large micelle formation, symmetric detergents often exhibit limited water-solubility when long alkyl chains are introduced to match the hydrophobic thickness of MPs (28–32 Å)[24,42]. For example, one-carbon extension versions of OGNG (GNG-6,6) and LMNG—GNG-7,7 and MNG-11,11, respectively—showed limited water-solubility (~1.0 wt%) (Table 1). Introducing unsymmetric hydrophobic groups effectively resolved these issues while retaining the favorable properties of the multiple alkyl chains. For the GNGs, the main chain length could be extended to C13/C14 without having water-solubility problems, and their micelle sizes decreased from 4.5 nm (GNG-6,6) to 3.2 nm upon introducing unsymmetric hydrophobic groups (Figure 2c & Table 1)[43]. Similar behaviors were observed for unsymmetric MNGs and TTGs, designated U-MNGs and U-TTGs, respectively (Figure 2c)[44,45]. The U-MNGs, which contain different alkyl chains (C9-C11, C8-C12, C6-C14, or C4-C16), form substantially smaller micelles and exhibit slightly lower CMCs compared to the symmetric LMNG (Table 1), potentially benefiting MP studies. The differences in micelle sizes and CMCs between LMNG and U-MNGs tend to increase as the difference in alkyl chain length (i.e. unsymmetry) increases. When evaluated with several model MPs (leucine transporter (LeuT), melibiose permease (MelB), human beta2 adrenergic receptor (β_2 AR), mouse μ -opioid receptor (MOR)), the U-MNGs outperformed LMNG in terms of protein stability, with the best performance observed for MNG-8,12[44]. These results demonstrate that the introduction of unsymmetric hydrophobic groups can improve not only detergent properties (water solubility, CMC and micelle size) but also enhance detergent efficacy for MP stabilization. Interestingly, the high efficiency of LMNG for MP extraction was well maintained even with their unsymmetric architecture[44]. Similar to the U-MNGs, the U-TTGs (e.g., TTG-9,11 and TTG-8,12) exhibited lower CMCs than TTG-10,10 (Table 1) and demonstrated improved MP stabilization compared to the latter when evaluated with the same set of MPs[45]. However, unlike the U-MNGs, the decrease in micelle size with increasing detergent unsymmetry was not as pronounced for the U-TTGs (Table 1), which may be due to the different ways the two alkyl chains are introduced into the detergent cores. Given the availability of many symmetric detergents[35-38,46,47], studies on their unsymmetric version will further clarify the advantages and disadvantages of unsymmetric detergents for MP studies.

The unsymmetric nature introduced into the TMG-Ps somewhat differs from that in the U-MNGs/U-TTGs, as an additional alkyl chain was inserted into the hydrophobic region between two alkyl chains of symmetrical TMGs (Figure 2c)[48]. Consequently, the TMG-Ps have higher hydrophobic density than the symmetrical counterparts, leading to decreased HLB values and enhanced MP stability. For example, TMG-P10,8 has a lower HLB value than TMG-A13 (11.3 vs. 11.9) (Table 1) and demonstrates enhanced efficacy in stabilizing LeuT, MelB and β_2 AR. Interestingly, this unsymmetric detergent exhibited higher MelB extraction efficiency compared to DDM and symmetric TMG-A13. However, the increase in the number of alkyl chains resulted in larger micelles (R_h = 8.7 nm for TMG-P10,8 vs. 3.6 nm for TMG-A13), explained by the increased hydrophobic volume (Table 1). This unfavorable property could be mitigated by making the detergent more unsymmetric. The unsymmetric strategy used for the TMG-Ps is likely to be useful in improving the physical properties and MP stabilization efficacy of symmetric detergents with a large inter-alkyl chain distance, due to enhanced hydrophobicity

and alkyl chain density.

Hybrid detergents

Two different types of head groups can be combined to generate hybrid detergents. The detergent's hydrophilic group is a key factor in determining overall molecular geometry and hydrophilicity, which in turn influence detergent packing parameter (i.e., micelle size) and HLB values, respectively[49]. By selecting and combining two head groups from glycerol (G0), tetraethylene glycol (E4), and glucoside (Glu), several non-hybrid or hybrid detergents were created, including G0-G0 ([G1]OGD), E4-G0, E4-E4, E4-Glu, Glu-Glu, and Gl-G1 (G2[OGD]) (Figure 2d)[50]. These non-hybrid/hybrid detergents provide a method to fine-tune both the HLB and packing parameter (Table 1). When tested with the outer membrane protease T (OmpT) from *E. coli*, a hybrid detergent (E4-Glu) was more effective than its non-hybrid counterparts (C8E4 and OG) at maintaining the protease's activity. The lower CMC of E4-Glu compared to the non-hybrid counterparts [0.5 mM vs. C8E4 (8 mM) and OG (23 mM)] allowed for the use of a smaller amount of detergent to maintain OmpT function (Table 1). A hybrid detergent containing maltoside (Mal) and E4 (i.e., Mal-E4) was used to investigate which factor, detergent concentration or detergent properties, most influences protein-lipid interaction[51,52]. When the amount of lipid molecules co-purified with the tetrameric aquaporin channel (AqpZ) was quantified by native mass spectrometry (MS), two low-CMC detergents, DDM (0.17 mM) and Mal-E4 (0.21 mM), showed increased retention of lipid molecules around tetrameric AqpZ than the high-CMC C8E4 (8 mM) (Table 1). This result demonstrates that protein-lipid interaction is primarily influenced by detergent concentration in purification buffers. As detergents are commonly used as multiples of their CMCs in purification buffers, low-CMC detergents (e.g., Mal-E4) can be favorably used for maintaining protein-lipid interaction.

Different head groups can also be combined to utilize their respective merits for MP studies. For example, dicarboxylate-oxide detergents (DCODs) exploit the ability of a branched dicarboxylate group to form salt-bridges with basic residues present at the membrane-cytoplasm interfaces of MPs (Figure 2d)[53]. By combining the dicarboxylate group and a MP-stabilizing glucoside/maltoside group, the DCOD hybrid detergents (8b and 9b) preserved the function of BmrA, an ATP-binding cassette (ABC) pump, and achieved a high melting temperature for A2A adenosine receptor (A_{2A}AR). DCOD-9b was successfully applied to the purification and characterization of Cdr1, a protein responsible for azole resistance in *Candida glabrata*[54]. Furthermore, a related compound (3d) was used as an additive for crystal structure determination of BmrA [55]. These results suggest that hybrid detergent structures can be applied to a wide range of MP studies. In this context, the use of spermine as detergent head group is particularly interesting, as this polyamine group has been reported to effectively reduce protein surface charge, a useful feature for native MS (Figure 2d)[56]. Hypothetical hybrid detergents containing both spermine and maltoside groups are expected to not only stabilize MPs but also facilitate the mass analysis of MPs [Figure 3b].

Unsymmetric and hybrid detergents

As a logical extension, unsymmetric *and* hybrid detergents have been developed, such as triazole-linked pre-assembled detergents (T-PADs)[57]. Designed via cross-coupling reactions of two monomeric

detergents (OG and DDM analogs), the T-PAD architecture can be symmetric, unsymmetric, hybrid, or a combination of unsymmetric and hybrid (Figure 2e). The hybrid T-PADs generally exhibit lower CMCs than their non-hybrid counterparts, a trend similar to that observed for other hybrid detergents (Table 1). Micelle sizes formed by the T-PADs tend to decrease with increasing detergent unsymmetry, though no clear relationship was observed between the hybrid structure and micelle size in this system. Among the T-PADs, unsymmetric dimaltoside detergents (e.g., 13M9M and 13M10M) were most effective at maintaining the ATPase activity of an ABC transporter (MsbA), followed by the unsymmetric hybrid detergents (e.g., 14M8G) and the symmetric detergents (e.g., 12M12M and LMNG), confirming the beneficial effect of unsymmetric architecture on MP stability. Additionally, the unsymmetric non-hybrid (e.g., 10M14M and 13M11M) and unsymmetric hybrid detergents (14M8G and 14M9G) outperformed symmetric LMNG in retaining ligand binding of the A_{2A}AR. Notably, 14M8G and 14M9G were favorably used in EM studies of MsbA and NMR studies of A_{2A}AR, respectively, highlighting the potential of unsymmetric hybrid detergents for MP structural studies.

Various (pseudo) unsymmetric and/or hybrid architecture have also been generated by the Ugi four-component reaction, which requires amine, carboxylic acid, aldehyde and isocyanate as reactants (Figure 2e)[58]. When the resulting dipeptide-based U-PADs were tested with MsbA and four GPCRs [A_{2A}AR, the cannabinoid receptor type 2 (CB2R), the smoothened receptor (SMO), the glucagon-like peptide-1 receptor (GLP-1R)], the symmetric detergents, M-23-M and 12-M-12M, were generally more effective at stabilizing these MPs compared to the unsymmetric hybrid detergents (8-12M-G and 8-12M-E). One representative (M-23-M) was particularly effective for maintaining the homogeneity of GLP-1R and showed narrow signals in ¹⁹F NMR spectra of 2,2,2-trifluoroethanethiol-modified receptor, comparable to LMNG. This stands in contrast to the trends observed for other unsymmetric and/or hybrid detergents, such as the U-MNGs, Mal-E4, and T-PADs. The rigid dipeptide scaffold of the U-PADs likely accounts for this different trend, as it limits the flexibility of the detergent head and tail groups, making it difficult to achieve their optimal conformations for MP stability. Thus, the detergent scaffold is a key variable in detergent design for MP studies.

Beta-peptides (BPs) are another example of unsymmetric hybrid detergents, containing four head groups (two hydroxyl and two carboxylate groups) and four tail groups (two isobutyl and two octyl chains) (Figure 2e)[59]. BP-1 was highly effective at stabilizing various MPs; MsbA, bacteriorhodopsin, the tetrameric voltage-gated potassium channel, KcsA, and full-length glucagon receptor. This peptide-based detergent was also successfully applied to visualization of the dynamic conformation of MsbA through EM studies. These favorable properties are attributed to the formation of a hydrogen-bond network between the beta-peptide backbones. Recently, hybrid versions of the BPs with conventional detergents, designated AXBX detergents, were generated by conjugating OG/DDM to both ends of the BP-based scaffold (Figure 2e)[60]. Among the various AXBX detergents, A4B2, containing a head group of two maltosides and two carboxylic acids and a tail group of two C12 and two isobutyl chains, was shown to be most effective at stabilizing the three GPCRs (A_{2A}AR, SMO and GLP-1R) and demonstrated promising behavior for EM studies of A_{2A}AR. Furthermore, A4B2 outperformed BP-1 in extracting A_{2A}AR, indicating that well-designed unsymmetric hybrid detergents can be useful for MP extraction. However, due to their peptide scaffolds, these peptide-based detergents (BPs and AXBX)

may have issues with synthetic accessibility.

Conclusion

In summary, the emergence of LMNG has had a profound impact on membrane protein structural studies, leading to the development of various symmetric detergents with multiple head and tail groups. Over time, detergent architecture has evolved, incorporating variations in alkyl chain length or head group identity, which has spurred creation of unsymmetric and/or hybrid detergents. These unconventional detergents allow fine-tuning of key detergent properties, such as CMC, micelle size, and HLB values, all of which significantly influence MP stability. The introduction of unsymmetric hybrid detergents has dramatically expanded the detergent toolbox for MP research, but rational design and consideration of synthetic accessibility remain essential to ensure their practical application. Collectively, unsymmetric and/or hybrid detergents present vast potential for advancing MP structural studies.

Declaration of competing interest

The authors have declared no conflict of interest.

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Data availability

No data was used for the research described in the article.

References

Papers of particular interest, published within the period of review, have been highlighted as:

* of special interest ** of outstanding interest

1. Levental I, Lyman E: **Regulation of membrane protein structure and function by their lipid nano-environment.** *Nat Rev Mol Cell Biol* 2023, **24**:107-122.
2. Kockelkoren G, Lauritsen L, Shuttle CG, Kazepidou E, Vonkova I, Zhang Y, Breuer A, Kennard C, Brunetti RM, D'Este E, et al.: **Molecular mechanism of GPCR spatial organization at the plasma membrane.** *Nat Chem Biol* 2024, **20**:142-150.
3. Levesque I, Juliano BR, Parson KF, Ruotolo BT: **A Critical Evaluation of Detergent Exchange Methodologies for Membrane Protein Native Mass Spectrometry.** *J Am Soc Mass Spectrom* 2023, **34**:2662-2671.
4. Rampado R, Giordano F, Moracci L, Crotti S, Caliceti P, Agostini M, Taraballi F: **Optimization of a detergent-based protocol for membrane proteins purification from mammalian cells.** *J Pharm Biomed Anal* 2022, **219**:114926.
5. Yen HY, Jazayeri A, Robinson CV: **G Protein-Coupled Receptor Pharmacology-Insights from Mass Spectrometry.** *Pharmacol Rev* 2023, **75**:397-415.
6. Jain A, Liu R, Ramani B, Arauz E, Ishitsuka Y, Ragunathan K, Park J, Chen J, Xiang YK, Ha T: **Probing cellular protein complexes using single-molecule pull-down.** *Nature* 2011, **473**:484-488.
7. Walker G, Brown C, Ge X, Kumar S, Muzumdar MD, Gupta K, Bhattacharyya M: **Oligomeric organization of membrane proteins from native membranes at nanoscale spatial and single-molecule resolution.** *Nat Nanotechnol* 2024, **19**:85-94.
8. White SH: **Membrane proteins of known 3D structure.** <http://blanco.biomol.uci.edu/mpstruc/>.
9. Le Bon C, Michon B, Popot JL, Zoonens M: **Amphipathic environments for determining the structure of membrane**

- proteins by single-particle electron cryo-microscopy. *Q Rev Biophys* 2021, **54**:e6.
10. Woubshete M, Cioccolo S, Byrne B: **Advances in Membrane Mimetic Systems for Manipulation and Analysis of Membrane Proteins: Detergents, Polymers, Lipids and Scaffolds.** *Chempluschem* 2024, **89**:e202300678.
 11. Harrison PJ, Vecerkova T, Clare DK, Quigley A: **A review of the approaches used to solve sub-100 kDa membrane proteins by cryo-electron microscopy.** *J Struct Biol* 2023, **215**:107959.
 12. Young JW: **Recent advances in membrane mimetics for membrane protein research.** *Biochem Soc Trans* 2023, **51**:1405-1416.
 13. Faham S, Bowie JU: **Bicelle crystallization: a new method for crystallizing membrane proteins yields a monomeric bacteriorhodopsin structure.** *J Mol Biol* 2002, **316**:1-6.
 14. Tribet C, Audebert R, Popot J-L: **Amphipols: Polymers that keep membrane proteins soluble in aqueous solutions.** *Proceedings of the National Academy of Sciences* 1996, **93**:15047-15050.
 15. Bayburt TH, Grinkova YV, Sligar SG: **Self-assembly of discoidal phospholipid bilayer nanoparticles with membrane scaffold proteins.** *Nano letters* 2002, **2**:853-856.
 16. Frauenfeld J, Löving R, Armache J-P, Sonnen AF, Guettou F, Moberg P, Zhu L, Jegerschöld C, Flayhan A, Briggs JA: **A saposin-lipoprotein nanoparticle system for membrane proteins.** *Nature methods* 2016, **13**:345-351.
 17. Knowles TJ, Finka R, Smith C, Lin Y-P, Dafforn T, Overduin M: **Membrane proteins solubilized intact in lipid containing nanoparticles bounded by styrene maleic acid copolymer.** *Journal of the American Chemical Society* 2009, **131**:7484-7485.
 18. Choy BC, Cater RJ, Mancina F, Pryor EE, Jr.: **A 10-year meta-analysis of membrane protein structural biology: Detergents, membrane mimetics, and structure determination techniques.** *Biochim Biophys Acta Biomembr* 2021, **1863**:183533.
 19. Breibeck J, Rempel A: **Successful amphiphiles as the key to crystallization of membrane proteins: Bridging theory and practice.** *Biochim Biophys Acta Gen Subj* 2019, **1863**:437-455.
 20. Deisenhofer J, Epp O, Miki K, Huber R, Michel H: **Structure of the protein subunits in the photosynthetic reaction centre of Rhodospseudomonas viridis at 3 Å resolution.** *Nature* 1985, **318**:618-624.
 21. Tran NL, Senko S, Lucier KW, Farwell AC, Silva SM, Dip PV, Poweleit N, Scapin G, Catalano C: **High-Resolution Cryo-Electron Microscopy Structure Determination of Haemophilus influenzae Tellurite-Resistance Protein A via 200 kV Transmission Electron Microscopy.** *Int J Mol Sci* 2024, **25**.
 22. Ratkeviciute G, Cooper BF, Knowles TJ: **Methods for the solubilisation of membrane proteins: the micelle-aneous world of membrane protein solubilisation.** *Biochem Soc Trans* 2021, **49**:1763-1777.
 23. Krishnarajuna B, Sharma G, Im SC, Auchus R, Anantharamaiah GM, Ramamoorthy A: **Characterization of nanodisc-forming peptides for membrane protein studies.** *J Colloid Interface Sci* 2024, **653**:1402-1414.
 24. Chaptal V, Delolme F, Kilburg A, Magnard S, Montigny C, Picard M, Prier C, Monticelli L, Bornert O, Agez M, et al.: **Quantification of Detergents Complexed with Membrane Proteins.** *Sci Rep* 2017, **7**:41751.
 25. Brown KA, Guggen MK, Yu Z, Moreno D, Jin S, Ge Y: **Nonionic, Cleavable Surfactant for Top-Down Proteomics.** *Anal Chem* 2023, **10.1021/acs.analchem.2c03916**.
 26. Behnke JS, Urner LH: **Emergence of mass spectrometry detergents for membrane proteomics.** *Anal Bioanal Chem* 2023, **415**:3897-3909.
 27. Lee HJ, Lee HS, Youn T, Byrne B, Chae PS: **Impact of novel detergents on membrane protein studies.** *Chem* 2022, **8**:980-1013.
 28. Frotscher E, Danielczak B, Vargas C, Meister A, Durand G, Keller S: **A fluorinated detergent for membrane-protein applications.** *Angew Chem Int Ed Engl* 2015, **54**:5069-5073.
 29. Xue D, Xu T, Wang H, Wu M, Yuan Y, Wang W, Tan Q, Zhao F, Zhou F, Hu T, et al.: **Disulfide-Containing Detergents (DCDs) for the Structural Biology of Membrane Proteins.** *Chemistry* 2019, **25**:11635-11640.
 30. Chipot C, Dehez F, Schnell JR, Zitzmann N, Pebay-Peyroula E, Catoire LJ, Miroux B, Kunji ERS, Veglia G, Cross TA, et al.: **Perturbations of Native Membrane Protein Structure in Alkyl Phosphocholine Detergents: A Critical Assessment of NMR and Biophysical Studies.** *Chem Rev* 2018, **118**:3559-3607.
 31. Midtgaard SR, Darwish TA, Pedersen MC, Huda P, Larsen AH, Jensen GV, Kynde SAR, Skar-Gislinge N, Nielsen AJZ, Olesen C, et al.: **Invisible detergents for structure determination of membrane proteins by small-angle neutron scattering.** *FEBS J* 2018, **285**:357-371.
 32. Wycisk V, Wagner MC, Urner LH: **Trends in the Diversification of the Detergentome.** *Chempluschem* 2024, **89**:e202300386.

** This review articles presents an overview of synthetic strategies and various building blocks utilized in the preparation of detergent molecules, highlighting the approaches that facilitate the design and synthesis of optimized detergents for potential applications in further research and industrial use.

33. Lee S, Mao A, Bhattacharya S, Robertson N, Grishammer R, Tate CG, Vaidehi N: **How Do Short Chain Nonionic Detergents Destabilize G-Protein-Coupled Receptors?** *J Am Chem Soc* 2016, **138**:15425-15433.
34. Ganapathy S, Opdam L, Hontani Y, Frehan S, Chen Q, Hellingwerf KJ, de Groot HJM, Kennis JTM, de Grip WJ: **Membrane matters: The impact of a nanodisc-bilayer or a detergent microenvironment on the properties of two eubacterial rhodopsins.** *Biochim Biophys Acta Biomembr* 2020, **1862**:183113.
35. Chae PS, Rasmussen SG, Rana RR, Gotfryd K, Chandra R, Goren MA, Kruse AC, Nurva S, Loland CJ, Pierre Y, et al.: **Maltose-neopentyl glycol (MNG) amphiphiles for solubilization, stabilization and crystallization of membrane proteins.** *Nat Methods* 2010, **7**:1003-1008.
36. Chae PS, Rana RR, Gotfryd K, Rasmussen SG, Kruse AC, Cho KH, Capaldi S, Carlsson E, Kobilka B, Loland CJ, et al.: **Glucose-neopentyl glycol (GNG) amphiphiles for membrane protein study.** *Chem Commun (Camb)* 2013, **49**:2287-2289.
37. Hussain H, Mortensen JS, Du Y, Santillan C, Ribeiro O, Go J, Hariharan P, Loland CJ, Guan L, Kobilka BK, et al.: **Tandem malonate-based glucosides (TMGs) for membrane protein structural studies.** *Sci Rep* 2017, **7**:3963.
38. Ghani L, Zhang X, Munk CF, Hariharan P, Lan B, Yun HS, Byrne B, Guan L, Loland CJ, Liu X, et al.: **Tris(hydroxymethyl)aminomethane Linker-Bearing Triazine-Based Triglucoisides for Solubilization and Stabilization of Membrane Proteins.** *Bioconjug Chem* 2023, **34**:739-747.
39. Lee S, Ghosh S, Jana S, Robertson N, Tate CG, Vaidehi N: **How Do Branched Detergents Stabilize GPCRs in Micelles?** *Biochemistry* 2020, **59**:2125-2134.
40. Urner LH, Junge F, Fiorentino F, El-Baba TJ, Shutin D, Nolte G, Haag R, Robinson CV: **Rationalizing the Optimization of Detergents for Membrane Protein Purification.** *Chemistry* 2023, **29**:e202300159.
- ** The authors assessed the utility of hydrophilic-lipophilic balance (HLB) concept in optimizing detergent properties, thereby facilitating the rational detergent selection based on the optimal HLB values for membrane protein studies.
41. Jiko C, Li J, Moon Y, Tanaka Y, Gopalasingam CC, Shigematsu H, Chae PS, Kurisu G, Gerle C: **NDT-C11 as a Viable Novel Detergent for Single Particle Cryo-EM.** *Chempluschem* 2024, **89**:e202400242.
- * This report employed NDT-C11 to investigate the EM structures of cyanobacterial photosystemI (PSI) and mammalian F-ATP synthase, demonstrating the promising utility of this symmetric detergent for single particle Cryo-EM study.
42. Lee AG: **Lipid-protein interactions in biological membranes: a structural perspective.** *Biochim Biophys Acta* 2003, **1612**:1-40.
43. Bae HE, Cecchetti C, Du Y, Katsube S, Mortensen JS, Huang W, Rehan S, Lee HJ, Loland CJ, Guan L, et al.: **Pendant-bearing glucose-neopentyl glycol (P-GNG) amphiphiles for membrane protein manipulation: Importance of detergent pendant chain for protein stabilization.** *Acta Biomater* 2020, **112**:250-261.
44. Bae HE, Du Y, Hariharan P, Mortensen JS, Kumar KK, Ha B, Das M, Lee HS, Loland CJ, Guan L, et al.: **Asymmetric maltose neopentyl glycol amphiphiles for a membrane protein study: effect of detergent asymmetry on protein stability.** *Chem Sci* 2019, **10**:1107-1116.
45. Ehsan M, Ghani L, Lan B, Katsube S, Poulsen IH, Zhang X, Arslan M, Byrne B, Loland CJ, Guan L, et al.: **Unsymmetric Triazine-Based Triglucoiside Detergents for Membrane Protein Stability.** *Chembiochem* 2025, **10**:1002/cbic.202400958:e202400958.
- ** This publication introduces unsymmetric variants of triazine-based triglucoisides (TTGs) and confirms the advantageous roles of detergent unsymmetry in enhancing membrane protein stability as demonstrated through evaluation with multiple proteins including two GPCRs.
46. Sadaf A, Mortensen JS, Capaldi S, Tikhonova E, Hariharan P, de Castro Ribeiro O, Loland CJ, Guan L, Byrne B, Chae PS: **A Class of Rigid Linker-bearing Glucosides for Membrane Protein Structural Study.** *Chem Sci* 2016, **7**:1933-1939.
47. Ghani L, Kim S, Ehsan M, Lan B, Poulsen IH, Dev C, Katsube S, Byrne B, Guan L, Loland CJ, et al.: **Melamine-cored glucosides for membrane protein solubilization and stabilization: importance of water-mediated intermolecular hydrogen bonding in detergent performance.** *Chem Sci* 2023, **14**:13014-13024.
- * Melamine-cored symmetric glucoside detergents were found to form water-mediated intramolecular hydrogen bond network when associated with membrane proteins, a feature responsible for enhanced protein stabilization efficacy of this class of detergents.
48. Yoon S, Bae HE, Hariharan P, Nygaard A, Lan B, Woubshete M, Sadaf A, Liu X, Loland CJ, Byrne B, et al.: **Rational Approach to Improve Detergent Efficacy for Membrane Protein Stabilization.** *Bioconjug Chem* 2024, **35**:223-231.
- ** The authors introduced an additional chain between two symmetric alkyl chains in tandem malonate-derived glucosides (TMGs) to generate unsymmetric TMGs (i.e., TMG-Ps). These unsymmetric variants have smaller HLB values compared to the symmetric counterparts, which partly explains high membrane protein stabilizing efficacy.
49. Israelachvili J: **The science and applications of emulsions—an overview.** *Colloids and Surfaces A: Physicochemical*

and Engineering Aspects 1994, **91**:1-8.

50. Urner LH, Ariamajd A, Weikum A: **Combinatorial synthesis enables scalable designer detergents for membrane protein studies**. *Chem Sci* 2022, **13**:10299-10307.

51. Urner LH, Liko I, Pagel K, Haag R, Robinson CV: **Non-ionic hybrid detergents for protein delipidation**. *Biochim Biophys Acta Biomembr* 2022, **1864**:183958.

52. Wycisk V, Urner LH: **Protocol to test the utility of detergents for E. coli membrane protein extraction and delipidation**. *STAR Protoc* 2023, **4**:102146.

** This report outlines a protocol for extracting *E. coli* membrane proteins using detergents and determining the lipid contents associated with these proteins. This methodology is valuable for investigating the capacity of hybrid detergents to retain lipid molecules copurified with membrane proteins.

53. Nguyen KA, Peuchmaur M, Magnard S, Haudecoeur R, Boyere C, Mounien S, Benammar I, Zampieri V, Igonet S, Chaptal V, et al.: **Glycosyl-Substituted Dicarboxylates as Detergents for the Extraction, Overstabilization, and Crystallization of Membrane Proteins**. *Angew Chem Int Ed Engl* 2018, **57**:2948-2952.

54. Pata J, Moreno A, Wiseman B, Magnard S, Lehlali I, Dujardin M, Banerjee A, Hogbom M, Boumendjel A, Chaptal V, et al.: **Purification and characterization of Cdr1, the drug-efflux pump conferring azole resistance in Candida species**. *Biochimie* 2024, **220**:167-178.

55. Chaptal V, Zampieri V, Wiseman B, Orelle C, Martin J, Nguyen K-A, Gobet A, Di Cesare M, Magnard S, Javed W: **Substrate-bound and substrate-free outward-facing structures of a multidrug ABC exporter**. *Science Advances* 2022, **8**:eabg9215.

56. Zhu Y, Peng BJ, Kumar S, Stover L, Chang JY, Lyu J, Zhang T, Schrecke S, Azizov D, Russell DH, et al.: **Polyamine detergents tailored for native mass spectrometry studies of membrane proteins**. *Nat Commun* 2023, **14**:5676.

* This publication reports spermine head group-bearing detergents that were exceptionally effective at reducing surface charges of proteins, thereby being useful for native MS studies of membrane proteins.

57. Zhao F, Zhu Z, Xie L, Luo F, Wang H, Qiu Y, Luo W, Zhou F, Xue D, Zhang Z, et al.: **Two-Dimensional Detergent Expansion Strategy for Membrane Protein Studies**. *Chemistry* 2022, **28**:e202201388.

**The authors designed and synthesized unsymmetric hybrid detergents by linking two amphiphilic units via an azide-alkyne click reaction. This approach offers an effective strategy to expand detergent repertoires with synthetic convenience.

58. Yang M, Luo W, Zhang W, Wang H, Xue D, Wu Y, Zhao S, Zhao F, Zheng X, Tao H: **Ugi Reaction Mediated Detergent Assembly for Membrane Protein Studies**. *Chem Asian J* 2022, **17**:e202200372.

59. Tao H, Lee SC, Moeller A, Roy RS, Siu FY, Zimmermann J, Stevens RC, Potter CS, Carragher B, Zhang Q: **Engineered nanostructured beta-sheet peptides protect membrane proteins**. *Nat Methods* 2013, **10**:759-761.

60. Yang M, Dai Y, Zhou F, Zhou X, Qiu Y, Tan Y, Zhao S, Xue D, Zhao F, Tao H: **Peptide-Scaffolded Detergents for Membrane Protein Studies**. *Chemistry* 2025, **10**.1002/chem.202404520:e202404520.

**This publication describes the design and synthesis of peptide-DDM hybrid detergents by conjugating DDM with amphiphilic β -peptide scaffolds via click chemistry. The resulting DDM-peptide conjugate exhibited superior membrane protein stabilization efficacy compared to LMNG.

Commented [BB2]: In part a) the text next to the blue box at the top should read "number". Also I don't think I would use the term "Stephen White Lab"-rather I would use "Membrane Proteins of Known 3D structure" and then maybe put the specific details of the website and the fact that this is curated by Stephen White in the figure legend.

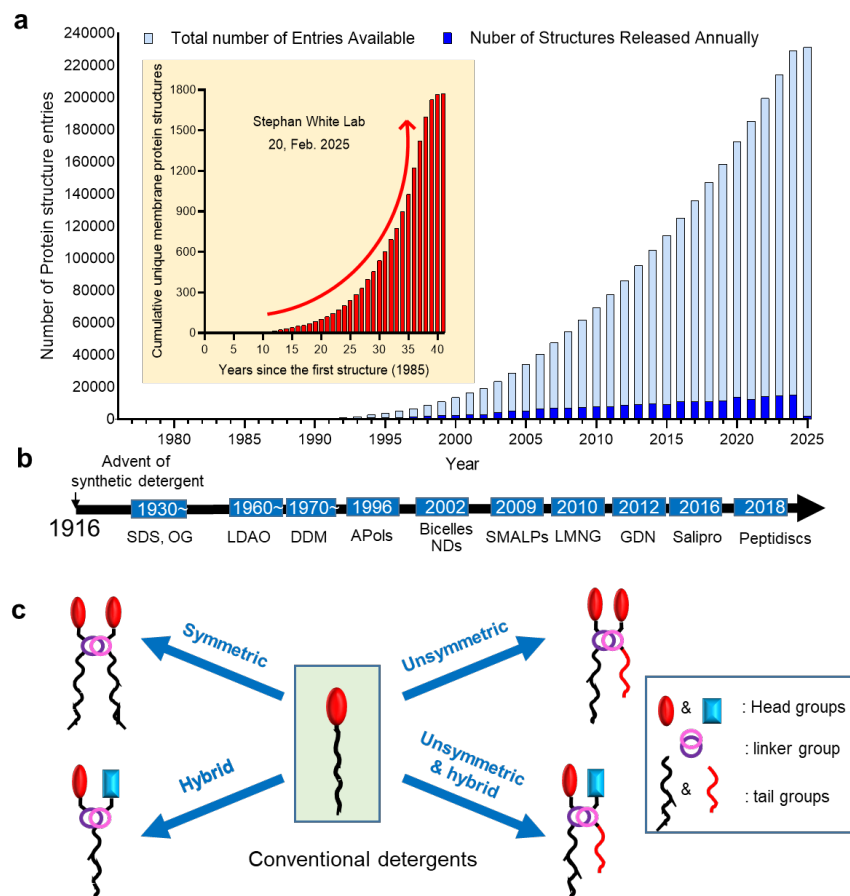
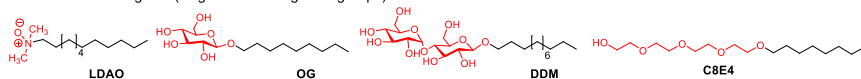
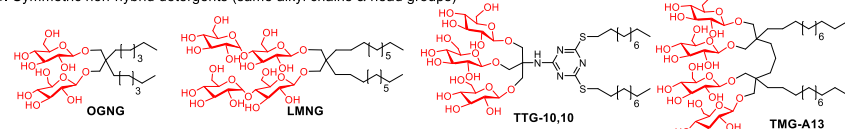


Figure 1. (a) Cumulative numbers of total protein structures (data obtained from the PDB; <https://www.rcsb.org/>). and unique membrane protein structures (inset, obtained from <https://blanco.biomol.uci.edu/mpstruc/> with the data curated by the Stephen White laboratory). (b) Timeline for development of membrane-mimetic systems, including detergents, amphipols (APols), bicelles, nanodiscs (NDs), styrene-maleic acid-based lipid particles (SMALPs), Salipro and Peptidiscs. (c) Schematic representation of new detergent classes derived from conventional detergents (*center*): symmetric non-hybrid detergents (*top left*), unsymmetric detergents (*top right*), hybrid detergents (*bottom left*), and unsymmetric hybrid detergents (*bottom right*).

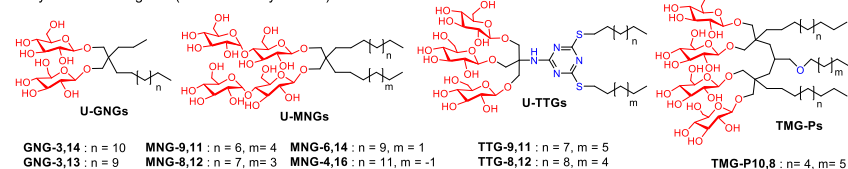
a. Conventional detergents (single head & single tail groups)



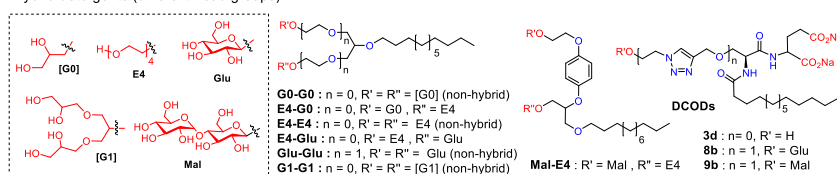
b. Symmetric non-hybrid detergents (same alkyl chains & head groups)



c. Unsymmetric detergents (different alkyl chains)



d. Hybrid detergents (different head groups)



e. Unsymmetric hybrid detergents (different alkyl chains & head groups)

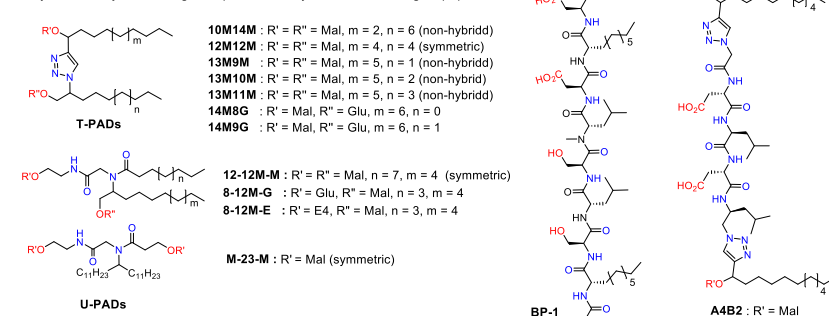


Figure 2. Chemical structures of (a) conventional detergents and (b-e) newly developed detergents with the symmetric alkyl chains and non-hybrid head groups (b), unsymmetric alkyl chains and non-hybrid head groups (c), hybrid head groups (d), and unsymmetric alkyl chains and hybrid head groups (e).

Table 1. Molecular weights (MW), critical micelle concentrations (CMC) of detergents and the hydrodynamic radii (R_h) of their micelles in water at room temperature.

Detergent	MW	CMC (mM)	R_h (nm) ^a	Solubility (%)	HLB ^b	Ref
DDM	510.6	~ 0.17	3.4	> 10	13.4	[27]
C8E4	306.4	~ 8.0	2.4	> 10	12.6	[50] ^d
OG	292.4	~ 25	2.6	> 10	12.3	[27]
LDAO	229.4	1-2	-	> 10	22.3 ^c	[27] [Mdlar et al., 1986]
LMNG	1005.2	~ 0.010	10.6	~ 10	13.6	[27]
MNG-11,11	1033.3	-	-	~ 1.0	13.2	-
OGNG	568.7	~ 1.0	4.4	> 10	12.6	[27]
GNG-7,7	596.8	-	-	~ 1.0	12.0	-
TTG-10,10	1031.3	~ 0.005	3.6	> 10	11.8	[44]
TMG-A13	1205.5	~ 0.006	3.6	> 10	11.9	[47]
GNG-3,13	624.8	~ 0.022	3.1	> 10	3.1	[42]
GNG-3,14	638.8	~ 0.023	3.2	> 10	3.2	[42]
MNG-9,11	1005.2	~ 0.008	8.3	> 10	13.6	[43]
MNG-8,12	1005.2	~ 0.008	6.0	> 10	13.6	[43]
MNG-6,14	1005.2	~ 0.006	3.8	> 10	13.6	[43]
MNG-4,16	1005.2	~ 0.004	3.5	> 10	13.6	[43]
TTG-9,11	1031.3	~ 0.004	3.7	> 10	11.8	[44]
TTG-8,12	1031.3	~ 0.003	3.6	> 10	11.8	[44]
TMG-P10,8	1263.6	~ 0.01	8.7	~ 10	11.3	[47]
G0-G0	408.5	~ 0.5	-	-	11.7	[49]
E4-G0	510.7	~ 0.4	-	-	13.3	[49]
E4-E4	612.8	~ 0.5	-	-	14.4	[49]
E4-Glu	642.8	~ 0.5	-	-	14.7	[49]
Glu-Glu	672.8	~ 0.5	-	-	14.9	[49]
G1-G1	704.5	~ 0.7	-	-	15.2	[49]
E4-Mal	880.5	~ 0.21	2.8~3.8	-	12.1	[50]
DCOD-8b	775.8	~ 1	0.3-1.0	-	-	[52]
DCOD-9b	1008.1	~ 2	0.5-1.8	-	-	[52]
10M14M	1086.3	~ 0.005	4.2	-	13.8	[56]
12M12M	1086.3	~ 0.004	4.7	-	13.8	[56]
13M9M	1058.2	~ 0.004	3.6	-	14.2	[56]
13M10M	1072.3	~ 0.004	3.7	-	14	[56]
13M11M	1086.3	~ 0.004	3.7	-	13.8	[56]
14M8G	896.1	~ 0.002	3.6	-	13.1	[56]
14M9G	910.1	~ 0.002	3.6	-	12.9	[56]
8-12M-G	928.5	~ 0.008	3.8	-	11.2	[57]
8-12M-E	942.6	~ 0.02	3.1	-	11.3	[57]
12-12M-M	1146.7	~ 0.002	3.7	-	11.9	[57]
M-23-M	1160.7	~ 0.003	13.6	-	11.8	[57]
BP-1	1042.3	< 0.001	3.0 ^d	~ 0.1	-	[58]
A4B2	1313.6	0.01	2.6 ^e	> 5	-	[59]

^a Hydrodynamic radius of micelles measured at a detergent concentration ^b Calculated by Griffin's method. ^c Calculated by Davies' Method. ^d Length of filamentous structure measured by electron microscopy. ^e Gyration radius (R_g) determined in 5.0 mM in phosphate buffer (20 mM, pH 6.2, 150 mM NaCl).