

Organic & Biomolecular Chemistry

Accepted Manuscript



This is an *Accepted Manuscript*, which has been through the Royal Society of Chemistry peer review process and has been accepted for publication.

Accepted Manuscripts are published online shortly after acceptance, before technical editing, formatting and proof reading. Using this free service, authors can make their results available to the community, in citable form, before we publish the edited article. We will replace this *Accepted Manuscript* with the edited and formatted *Advance Article* as soon as it is available.

You can find more information about *Accepted Manuscripts* in the [Information for Authors](#).

Please note that technical editing may introduce minor changes to the text and/or graphics, which may alter content. The journal's standard [Terms & Conditions](#) and the [Ethical guidelines](#) still apply. In no event shall the Royal Society of Chemistry be held responsible for any errors or omissions in this *Accepted Manuscript* or any consequences arising from the use of any information it contains.

COMMUNICATION

Diaminodiacid-Based Solid-Phase Synthesis of all-Hydrocarbon Stapled α -helical Peptides

Cite this: DOI: 10.1039/x0xx00000x

Feng-Liang Wang,^a Ye Guo,^a Si-Jian Li,^b Qing-Xiang Guo,^a Jing Shi^{*a} and Yi-Ming Li^{*b}Received 00th January 2012,
Accepted 00th January 2012

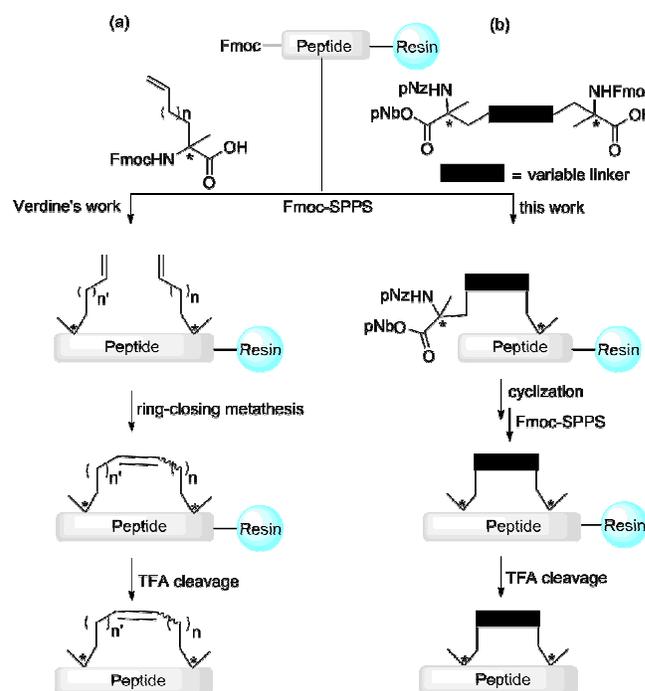
DOI: 10.1039/x0xx00000x

www.rsc.org/

An alternative stapling strategy was described herein by using Fmoc solid-phase peptide synthesis that employed pre-prepared diaminodiacid building blocks to introduce all-hydrocarbon staples into peptides by on resin cyclization. Compared to unstapled native peptides, diaminodiacid-based stapled peptides exhibited increased α -helicity ratio and stability toward protease. Moreover, the length of linkage was found to have impact on the bioactivity of the peptides on Wnt pathway inhibition. Therefore, the new stapling method provided an alternative way to obtain stapled peptides with tunable linkers of diaminodiacids.

Protein-protein interactions (PPIs) mediate series of significant biological processes and it was regarded as next-generation of therapeutic targets.¹ In general, proteins interact with each other through secondary structure. Among them, α -helices are the most common protein secondary structures which are mostly found at the interface of a multitude of crucial PPIs.² It has been of great interest to explore this particular folding motif as modulator of PPIs.³ However, small peptide segments from proteins often show poor proteolytic stability, cell permeability and decreased biological activity because they own less helical property. Thus, stabilization of the helical conformation of peptides is indispensable for regulating of PPIs.⁴

Many strategies have been developed to stabilize peptide helices,^{1b,5} in which the mostly used is side-chain cross-linking, including disulfide bond formation,⁶ thioether ligation,⁷ lactam bridge,⁸ click chemistry,⁹ etc.¹⁰ Verdine group reported an all-hydrocarbon cross-linking system by ring-closing olefin metathesis (Scheme 1a).¹¹ In their work, the introduction of α -methyl group benefits α -helical conformation formation and the hydrophobic of all-hydrocarbon linker facilitates cellular uptake. Despite the great success, development of alternative stapling methods remains interesting as they may enable the introduction of more types of all-hydrocarbon staples.



Scheme 1 Metathesis-based (a) versus diaminodiacid-based (b) synthesis of all-hydrocarbon stapled peptide

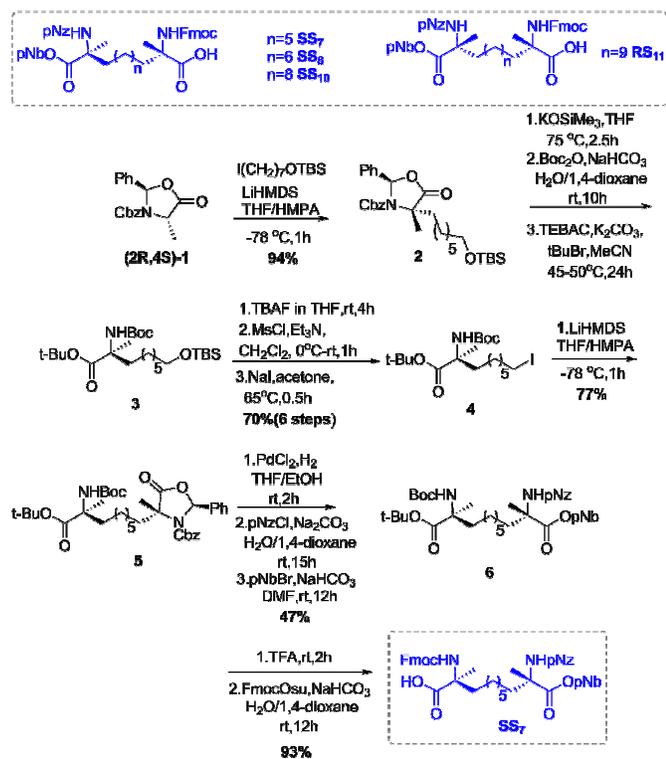
^a Department of Chemistry, University of Science and Technology of China, Hefei 230026, China. E-mail: shijing@ustc.edu.cn

^b School of Medical Engineering, Hefei University of Technology, Hefei, Anhui 230009, China. E-mail: lym2007@mail.ustc.edu.cn

†Electronic Supplementary Information (ESI) available: Experimental details. See DOI: 10.1039/b000000x/

Here we report an alternative all-hydrocarbon stapling strategy employing pre-prepared diaminodiacids to the solid-phase synthesis of stapled peptides (Scheme 1b). Various linkers with different structures could be introduced by the diaminodiacids strategy.¹² Pre-prepared diaminoacids have well-defined structures and therefore the isomer problem could be avoided. To our knowledge, it was the first time to employ diaminodiacids

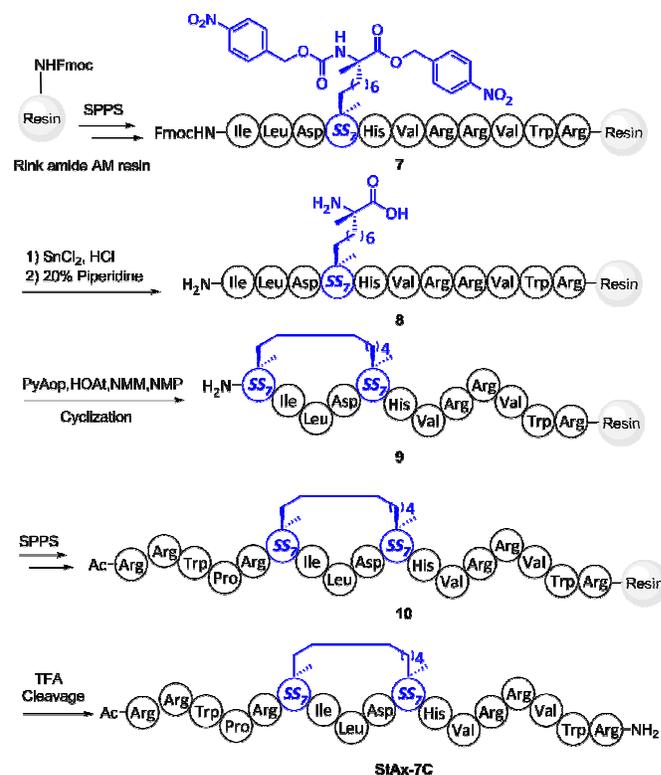
building blocks for the synthesis of all-hydrocarbon stapled peptides. To evaluate diaminodiacyd stapling strategy, we synthesized series of peptide inhibitors for Wnt signaling pathway. Compared to native unstapled peptide, diaminodiacyd-based stapled peptides showed increased helical propensity, proteolytic stability and inhibiting activity. Moreover, peptides with different lengths of linkers exhibited tunable inhibiting activity. Thus, our stapling strategy makes possible to increase the activity of stapled peptide by optimizing the linker of the diaminodiacyds.



Scheme 2 Structure and synthesis of diaminodiacyd building blocks (SS_7 as an example)

Our work began with the synthesis of diaminodiacyds building blocks (Scheme 2). For $i,i+4$ stapling, SS_7 , SS_8 , SS_{10} was synthesized and RS_{11} was obtained for $i,i+7$ stapling. As shown in Scheme 2 (SS_7 as an example), alkylation of *trans*-oxazolidinone (2*R,4S*)-**1** with tert-butyl((7-iodoheptyl)oxy)dimethylsilane and lithium hexamethyldisilazide (LiHMDS) afforded **2** in good yield (94%). 4-Disubstitutedoxazolidinone **2** could be cleaved with potassium trimethylsilylanolate (KOSiMe₃) to yield free quaternary amino acid, which was reacted with di-tert-butyl dicarbonate (Boc₂O) and tert-butylbromide (tBuBr)/N,N,N'-triethylbenzenemethanaminium chloride (TEBAC) successively. Then the resulting fully-protected amino acid **3** was treated with tetrabutylammonium fluoride (TBAF) to remove tert-butyl dimethylsilyl. Methylation and iodination of the resulting terminus hydroxyl gave **4** in high yield (70%, 6 steps). Then, alkylation of **1** with **4** generated **5** in 77% isolated yield. Compound **5** was subjected to hydrogenolysis and reacted with p-nitrobenzylchloroformate (pNZCl)/p-nitrobenzyl bromide

(pNbBr) to afford the fully-protected diaminodiacyd **6** (47%, 3 steps). We chose pNz/pNb as protecting groups because this couple was compatible with automated Fmoc-SPPS on peptide synthesizer. Deprotection of Boc/tBu and reaction with N-(9-Fluorenylmethoxycarbonyloxy)succinimide (Fmoc-Osu) afforded Fmoc-protected diaminodiacyd SS_7 (93%, 2 steps), which could be used for synthesis of stapled peptide. SS_8 and SS_{10} were synthesized in similar procedure as SS_7 , while *cis*-oxazolidinone (2*S,4S*)-**1** was used instead of (2*R,4S*)-**1** in the second alkylating step for RS_{11} . To verify the chiral purity of synthesized diaminodiacyds, we tested it with o-phthalaldehyde/N-Boc-cysteine.¹³



Scheme 3 Synthesis of stapled peptide via diaminodiacyds based strategy (StAx-7C as an example)

With protected diaminodiacyd building blocks in hand, we next evaluated the new stapling strategy by preparing Wnt/ β -Catenin signal pathway targeted peptides. The canonical Wnt pathway regulates cell differentiation, proliferation, and survival. Aberrant activation of this pathway was implicated in the development of variety of cancers.¹⁴ β -Catenin plays a key role in Wnt signaling by participating in critical PPIs. The sequence of stapled peptide synthesized here was confirmed to inhibit oncogenic Wnt signaling by directly targeting β -catenin/TCF interaction. By insertion of staple by Verdine's method, the peptide showed enhanced α -helicity and biological activity.¹⁵ The synthesis of stapled peptide by diaminodiacyds strategy was presented in Scheme 3. Peptide **7** containing SS_7 was first synthesized on Rink amide AM resin (0.33 mmol/g loading) following standard Fmoc-SPPS.

O-(7-Aza-1H-benzotriazole-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphate (HATU) was used as

coupling reagent instead of O-(1H-6-chlorobenzotriazol-1-yl)-1,1,3,3-tetramethyluroniumhexafluorophosphate (HCTU) when **SS₇** was incorporated. Next, deprotection of pNz/pNb group on **7** by SnCl₂ (2.5 M in DMF)/HCl and removal of the N-terminus Fmoc group afforded peptide **8**. Peptide **9** was obtained by cyclization of **8** by using (7-azabenzotriazol-1-yloxy)tripyrrolidinophosphoniumhexafluorophosphate (PyAop)/1-Hydroxy-7-azabenzotriazole (HOAt)/N-methylmorpholine (NMM). The remaining five amino acids were assembled onto **9** with a final acetylation procedure producing the N-terminus capped peptide **10**. After acidic cleavage and deprotection from the resin, crude **StAx-7C** was obtained.

High performance liquid chromatography (HPLC) was used to purify the diaminodiacid based crude **StAx-7C**. As shown in Figure 1a, crude peptide contained only a single major component and therefore can be conveniently purified to the desired stapled peptide **StAx-7C** (52% isolated yield). ESI-QTOF-MS further confirmed the identity of **StAx-7C** (Figure 1b). We conclude that the diaminodiacid based stapling strategy developed herein was efficient for the synthesis of stapled peptide. **StAx-8C**, **StAx-10C** and **StAx-11C** were prepared using the same approach with **N-35R**, while **StAx-35R** was synthesized by Verdine's RCM method for comparison (Table 1, isolated yield of each peptide is 38% for **StAx-8C**, 26% for **StAx-10C**, 37% for **StAx-11C**, 55% for **N-35R** and 35% for **StAx-35R**).

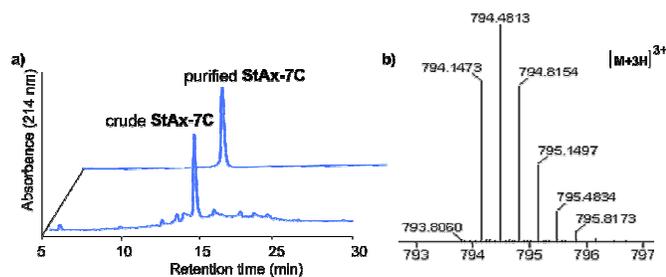


Fig. 1 (a) HPLC traces of crude and purified **StAx-7C** (Gradient: 20–50% of 0.08% TFA in CH₃CN). (b) ESI-QTOF-MS spectrum of **StAx-7C** (calc.: 2379.4141).

To explore the impact of diaminodiacid building blocks with various chain lengths for helix stability, circular dichroism (CD) spectroscopy of each peptide was tested. As shown in Figure S9, we concluded that long chain (**StAx-10C**, **StAx-11C**) exerted more impact on helix stability than short one (**StAx-7C**). Moreover, Table 1 indicated that the helical ratio of **N-35R** and **StAx-7C** were calculated to 5% and 7% according to the method described by Fairlie.¹⁶ These values were lower than other peptides, such as 19% for **StAx-35R**, 12% for **StAx-8C**, 17% for **StAx-10C**, 20% for **StAx-11C**. The results also suggested that diaminodiacid based stapling method acts similar as ring-closing metathesis-based stapling strategy in stabilizing the α -helix structure of peptide.

Table 1. Sequences of peptides and the corresponding α helicity.

Compound	Sequence	α helicity
N-35R	Ac-RRWPRSILDQHVRVWR-NH ₂	5%
StAx-35R	Ac-RRWPRS ₅ ILDS ₅ HVRRVWR-NH ₂	19%
StAx-7C	Ac-RRWPRS ₇ ILDS ₇ HVRRVWR-NH ₂	7%
StAx-8C	Ac-RRWPRS ₈ ILDS ₈ HVRRVWR-NH ₂	12%
StAx-10C	Ac-RRWPRS ₁₀ ILDS ₁₀ HVRRVWR-NH ₂	17%
StAx-11C	Ac-RRWPRS ₁₁ ILDS ₁₁ HVRRVWR-NH ₂	20%

To further study the activity of stapled peptides on inhibiting Wnt pathway, we measured the transcriptional activity of Wnt/ β -catenin pathway by using Topflash reporter assay. We found that all stapled peptides treatment inhibited the reporter expression in the presence of Wnt3a (Figure 2). **StAx-10C** shows higher efficiency for the inhibition of Wnt3a-induced Top-flash reporter than **StAx-35R**, which own the same stapled position. It was worth to note that **StAx-11C**, with stapled position at i, i+7, has the highest activity (50% transcriptional suppression), possibly due to the highest ratio of α -helicity. This result indicated that the linker of stapled bridge has important impact on activity of stapled peptide. Thus, we consider that diaminodiacid based stapling strategy may lead to peptides with higher bioactivity by optimizing the linker.

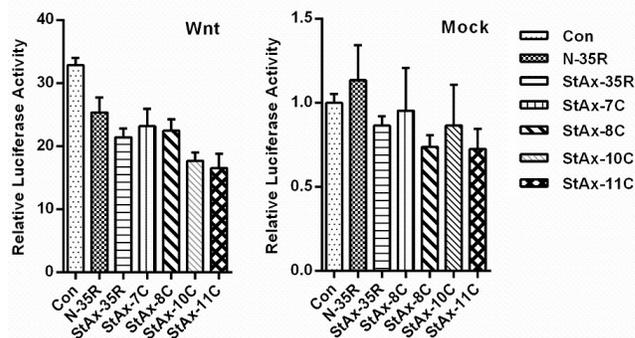


Fig. 2 Stapled peptides inhibit TOP flash luciferase reporter activity in Wnt3a-stimulated HeLa cells.

Finally, we evaluate the protease stability of **StAx-10C** and **StAx-11C** for inhibiting Wnt pathway as model. **StAx-10C** and **StAx-11C** (25 μ M) were subjected to chymotrypsin (0.5 ng/ μ L, pH 7.4) which mostly cleaves after Phe, Tyr, Trp, Leu, Met.¹⁷ The kinetic degradation of each peptide was monitored by HPLC (Figure 3). For **N-35R**, the half-life time was only 15 min, while **StAx-10C** and **StAx-11C** were measured to 38 and 106 min. This result was consistent with previous studies that protease stability of peptides can be increased after stapling. Compared to

N-35R, StAx-11C showed 7-fold increased stability against chymotrypsin-mediated degradation, StAx-10C exhibited only 2-fold increase. This difference could be explained that higher helicity of StAx-11C own more compact structure than StAx-10C, possibly leading to less protease cleavage site exposed. These results demonstrated that protease stability of peptide could be improved by using diaminiacid based stapling strategy. Moreover, we identified that all three peptides were cleaved at the C-terminus Trp-Arg site (SI).

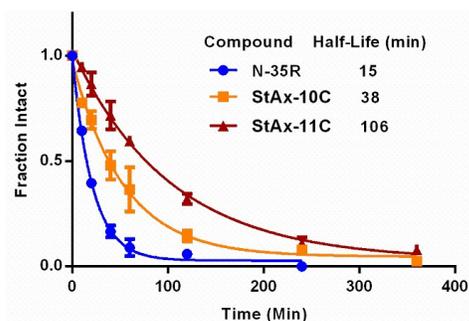


Fig. 3 Time-course degradation curve of N-35R, StAx-10C and StAx-11C under the treatment of chymotrypsin. StAx-10C and StAx-11C exhibited longer half time compared to native unstapled peptide.

In summary, we present a practical method for Fmoc-SPPS of all-hydrocarbon stapled peptides by using pre-prepared diaminiacid building blocks. Peptides stapled exhibited increased property of helicity and protease stability than unstapled one. Moreover, its Wnt pathway inhibitory effect could be tuned by the change of linker. The main advantage of this strategy is the potential introduction of crosslinks that are not accessible via ring-closing metathesis. Therefore the diaminiacid based stapling method provides a new way to optimize biological activity of stapled peptides by introducing different types of linkers.

Acknowledgements

This work was supported by the National Natural Science Foundation of China (21372058 to Y. M. Li; 21272223 to Q. X. Guo).

Notes and references

- (1) (a) L. G. Milroy, T. N. Grossmann, S. Hennig, L. Brunsveld and C. Ottmann, *Chem. Rev.*, 2014, 4695. (b) A. J. Wilson, *Chem. Soc. Rev.*, 2009, 3289.
- (2) M. Guharoy and P. Chakrabarti, *Bioinformatics*, 2007, 1909.
- (3) V. Azzarito, K. Long, N. S. Murphy and A. J. Wilson, *Nat. Chem.*, 2013, 161.
- (4) L. K. Henchey, A. L. Jochim and P. S. Arora, *Curr. Opin. Chem. Biol.* 2008, 692.
- (5) (a) R. N. Chapman, G. Dimartino and P. S. Arora, *J. Am. Chem. Soc.* 2004, 12252. (b) D. Y. Wang, W. Liao and P. S. Arora, *Angew. Chem.*

- Int. Ed.* 2005, 6525. (c) D. Y. Wang, K. Chen, J. L. Kulp III and P. S. Arora, *J. Am. Chem. Soc.* 2006, 9248.
- (6) A. M. Leduc, J. O. Trent, J. L. Wittliff, K. S. Bramlett, S. L. Briggs, N. Y. Chirgadze, Y. Wang, T. P. Burris and A. F. Spatola, *Proc. Natl. Acad. Sci. U.S.A.* 2003, 11273.
- (7) (a) F. M. Brunel and P. E. Dawson, *Chem. Commun.* 2005, 2552. (b) A. Muppidi, Z. Y. Wang, X. L. Li, J. D. Chen and Lin, Q. *Chem. Commun.* 2011, 9396. (c) H. Jo, N. Meinhardt, Y. B. Wu, S. Kulkarni, X. Z. Hu, K. E. Low, P. L. Davies, W. F. DeGrado and D. C. Greenbaum, *J. Am. Chem. Soc.* 2012, 17704. (d) A. M. Spokoyny, Y. K. Zou, J. J. Ling, H. T. Yu and Y. S. Lin, *J. Am. Chem. Soc.* 2013, 5946.
- (8) (a) G. Osapay and J. W. Taylor, *J. Am. Chem. Soc.* 1992, 6966. (b) J. C. Phelan, J. S. Nicholas, A. C. Braisted and R. S. McDowell, *J. Am. Chem. Soc.* 1997, 455. (c) E. Schievano, A. Bisello, M. Chorev, A. Bisol, S. Mammi and E. Peggion, *J. Am. Chem. Soc.*, 2001, 2743. (d) K. Fujimoto, N. Oimoto, K. Katsuno and M. Inouye, *Chem. Commun.* 2004, 1280. (e) N. E. Shepherd, H. N. Hoang, G. A. Abbenante, D. P. Fairlie, *J. Am. Chem. Soc.* 2005, 2974. (f) K. Fujimoto, M. Kajino, and M. Inouye, *Chem. Eur. J.* 2008, 857.
- (9) (a) S. Cantel, A. L. C. Isaad, M. Scrima, J. J. Levy, R. D. DiMarchi, P. Rovero, J. A. Halperin, A. M. D'Ursi, A. M. Papini, and M. Chorev, *J. Org. Chem.* 2008, 5663. (b) M. M. Madden, C. I. R. Vera, W. J. Song and Q. Lin, *Chem. Commun.* 2009, 5588. (c) S. A. Kawamoto, A. Coleska, X. Ran, H. Yi, C. Y. Yang and S. M. Wang, *J. Med. Chem.* 2012, 1137.
- (10) (a) E. Cabezas and A. C. Satterthwait, *J. Am. Chem. Soc.* 1999, 3862. (b) M. J. Kelso, R. L. Beyer, H. N. Hoang, A. S. Lakdawala, J. P. Snyder, W. V. Oliver, T. A. Robertson and D. P. Fairlie, *J. Am. Chem. Soc.* 2004, 4828. (c) C. M. Haney, M. T. Loch and W. S. Horne, *Chem. Commun.* 2011, 10915.
- (11) (a) C. E. Schafmeister, J. Po, G. L. Verdine, *J. Am. Chem. Soc.* 2000, 5891. (b) F. Bernal, A. F. Tyle, S. J. Korsmeyer, L. D. Walensky, and G. L. Verdine, *J. Am. Chem. Soc.* 2007, 2456. (c) L. D. Walensky, A. L. Kung, I. Escher, T. J. Malia, S. Barbuto, R. D. Wright, G. Wagner, and G. L. Verdine and S. J. Korsmeyer, *Science* 2004, 1466. (d) R. E. Moellering, M. Cornejo, T. N. Davis, C. D. Bianco, J. C. Aster, S. C. Blacklow, A. L. Kung, D. G. Gilliland, G. L. Verdine and J. E. Bradne, *Nature* 2009, 182. (e) K. W. Kim, P. S. Kutchukian and G. L. Verdine, *Org. Lett.* 2010, 3046. (f) Y. W. Kim, T. N. Grossmann and G. L. Verdine, *Nat. Protoc.* 2011, 761. (g) G. L. Verdine and G. L. Hilinski, *Methods Enzymol.* 2012, 3.
- (12) H. K. Cui, Y. Guo, Y. He, F. L. Wang, H. N. Chang, Y. J. Wang, F. M. Wu, C. L. Tian and L. Liu, *Angew. Chem. Int. Ed.* 2013, 9558.
- (13) L. Liu, M. Rozenman and R. Breslow, *Bioorg. Med. Chem.* 2002, 3973.
- (14) H. Clevers, R. Nusse, *Cell* 2012, 1192.
- (15) (a) T. N. Grossmann, J. T. H. Yeh, B. R. Bowman, Q. Chu, R. E. Moellering and G. L. Verdine, *Proc. Natl. Acad. Sci. USA.* 2012, 17942. (b) H. K. Cui, B. Zhao, Y. H. Li, Y. Guo, H. Hu, L. Liu, Y. G. Chen, *Cell Res.* 2013, 581.
- (16) N. E. Shepherd, H. N. Hoang, G. Abbenante and D. P. Fairlie, *J. Am. Chem. Soc.* 2005, 2974.
- (17) G. H. Bird, F. Bernal, K. Pitter and L. D. Walensky, *Methods Enzymol.* 2008, 369.