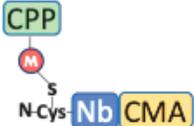
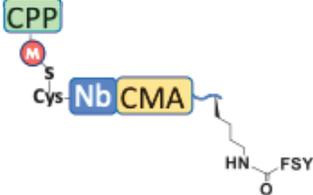
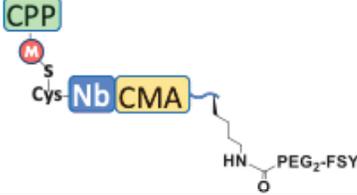
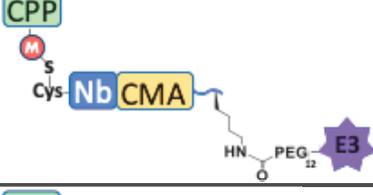
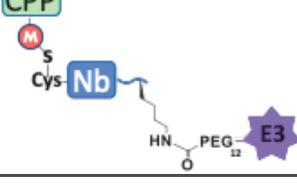
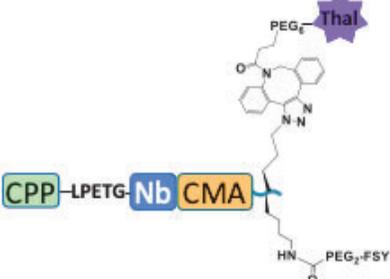
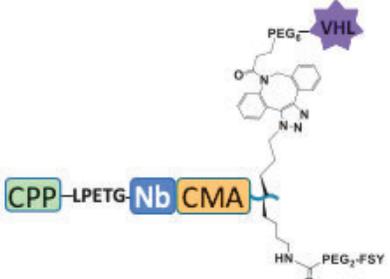


ND ^a -syn	Functional groups	Degradation %	Spine recover %
 <p>CPP M S N-Cys Nb CMA</p>	lysosomal	41.50	97.39
 <p>CPP M S Cys Nb CMA HN PEG₂-FSY</p>	lysosomal, covalent binding	65.97	74.66
 <p>CPP M S Cys Nb CMA HN PEG₂-FSY</p>	lysosomal, covalent binding	69.52	108.1
 <p>CPP M S Cys Nb CMA HN PEG₁₂-E3</p>	lysosomal, proteasomal	40.89	47.39
 <p>CPP M S Cys Nb HN PEG₁₂-E3</p>	proteasomal	37.83	52.41
 <p>CPP-LPETG-Nb CMA PEG₇-Thal HN PEG₂-FSY</p>	lysosomal, proteasomal, covalent binding	52.05	56.58
 <p>CPP-LPETG-Nb CMA PEG₇-VHL HN PEG₂-FSY</p>	lysosomal, proteasomal, covalent binding	46.67	59.10