

An integrated study of the affinities of the A β 16 peptide for Cu(I) and Cu(II): implications for the catalytic production of reactive oxygen species†

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A new fluorescent probe A β 16wwa based upon the A β 16 peptide has been developed with two orders of magnitude greater fluorescence intensity for sensitive detection of interactions with Cu(II). In combination with the Cu(I) probe Ferene S, it is confirmed that the A β 16 peptide binds either Cu(I) or Cu(II) with comparable affinities at pH 7.4 ($\log K_D^I = -10.4$; $\log K_D^{II} = -10.0$). It follows from this property that the Cu–A β 16 complex is a robust if slow catalyst for the aerial oxidation of ascorbate with H₂O₂ as primary product (initial rate, $\sim 0.63 \text{ min}^{-1}$ for Cu–A β 16 *versus* $>2.5 \text{ min}^{-1}$ for Cu_{aq}²⁺). An integrated study of variants of this peptide identifies the major ligands and binding modes involved in its copper complexes in solution. The dependence of K_D^I upon pH is consistent with a two-coordinate Cu(I) site in which dynamic processes exchange Cu(I) between the three available pairs of imidazole sidechains provided by His6, His13 and His14. The N-terminal amine is not involved in Cu(I) binding but is a key ligand for Cu(II). Acetylation of the N-terminus alters the redox thermodynamic gradient for the Cu centre and suppresses its catalytic activity considerably. The data indicate the presence of dynamic processes that exchange Cu(II) between the three His ligands and backbone amide at physiological pH. His6 is identified as a key ligand for catalysis as its presence minimises the pre-organisation energy required for interchange of the two copper redox sites. These new thermodynamic data strengthen structural interpretations for the Cu–A β complexes and provide valuable insights into the molecular mechanism by which copper chemistry may induce oxidative stress in Alzheimer's disease.

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Introduction

While the underlying molecular causes of Alzheimer's disease remain unknown, mis-handling of the A β peptides derived from the amyloid precursor protein during recycling may be an initiating event ('the amyloid cascade').^{1–4} Aberrant metal ion homeostasis appears to contribute by promoting aggregation of the peptides and/or inducing toxic gain of function.^{5–7} In this context, the potential role of the trace metal copper has been emphasised (see ref. 8 for a review).

The affinity of A β peptides for Cu(II) remains a topic of discussion (see recent reviews^{9,10}) although a consensus of $K_D \sim 10^{-10} \text{ M}$ is building.^{11–13} On the other hand, the affinity for Cu(I) remains problematical.^{14,15} Spectroscopic data have provided extensive information on the structure of Cu–A β complexes and of those of the truncated form A β 16(DAEFRHDSGYEVHHQK), in particular. This fragment

appears to provide the copper binding sites of highest affinity. The two major coordination forms of monomeric Cu^{II}–A β are related by a $pK_a \sim 7.8$,^{16–22} while a single dominant Cu(I) form has been characterised spectroscopically.^{23,24} Rapid ligand exchange processes have been detected.^{21,25} The ability of these complexes to catalyse the production of H₂O₂ by reduction of O₂ by ascorbate (Asc) has been explored as a model for the production of reactive oxygen species that may be primarily responsible for inflammation responses.

The present work defines the dissociation constants of both Cu(I) and Cu(II) for the peptide A β 16 under the same conditions using chromophoric and fluorescence probes of appropriate affinities. A new probe for Cu(II) has been developed from the A β 16 peptide itself while those for Cu(I) were defined in recent work.²⁶ Application to variant forms of the A β 16 peptide has correlated the new thermodynamic data with existing spectroscopic structural data while the ability of the Cu complexes of the peptide and its variants to catalyse production of reactive oxygen species is explored.

Experimental section

Materials and general methods

Materials purchased from Sigma included ligands Ferene S (Fs) and Ferrozine (Fz) (as their sodium salts Na₂Fs and NaHFz),

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reductants NH_2OH (as its H_2SO_4 salt) and ascorbic acid, a copper standard (as a standard solution for calibration of atomic absorption spectroscopy), Amplex Red (also called Ampliflu Red) and horseradish peroxidase (HRP). They were all used as received. Proteins CopK and its variant CopK-H70F were expressed and isolated as reported previously.²⁷ Peptides A β 16 (sequence: DAEFRHDSGYEVHQQ), Ac-A β 16 (Ac-DAEFRHDSGYEVHQQ); A β 16-H13A (DAEFRHDSGYEVAHQK), A β 16-H6,13A (DAEFRADSGYEVAHQK); A β 16-H13,14A (DAEFRHDSGYEVAHQK) were purchased from GL Biochem (Shanghai) with purity estimated at >98%. Peptides A β 16-F4W,Y10W,H14A (denoted as A β 16wwa, DAEWRHDSGWEVHAQK); A β 16-H6A (DAEFRADSGYEVHQQ) and A β 16-H14A (DAEFRHDSGYEVAHQK) were synthesised on site by solid phase peptide techniques. Identity was verified by electrospray ionisation mass spectrometry (ESI-MS) while purity was confirmed to be >98% by HPLC. Peptide concentrations were estimated from absorbance maxima at ~ 276 nm using $\epsilon_{\text{max}} = 1410 \text{ M}^{-1} \text{ cm}^{-1}$ for those A β 16 peptides containing a single tyrosine residue and using $\epsilon = 11\,000 \text{ M}^{-1} \text{ cm}^{-1}$ at 280 nm for the A β 16wwa probe peptide containing two tryptophan residues. The concentrations obtained matched those estimated from fluorescence titrations with the copper standard assuming formation of a 1:1 complex.

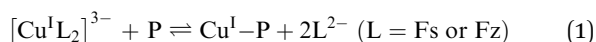
All ligand stock solutions, reaction buffers, reductant solutions and protein solutions were prepared in rigorously deoxygenated Milli-Q water and stored in an anaerobic glove-box (<1 ppm O_2). The working solution of ligand Fs was prepared freshly from aliquots of frozen stock solution stored in a freezer at temperature -80 °C.²⁶ All reactions involving Cu(i) were performed anaerobically in the glove-box and transported outside in a capped cuvette for spectroscopic characterisation.

UV-Vis and fluorescence titration

UV-visible spectra were recorded on a Varian Cary 300 spectrophotometer in dual beam mode with quartz cuvettes of 1.0 cm path length. All metal titrations were performed in appropriate buffers and corrected for baseline and dilution. Fluorescence emission spectra were obtained on a Varian Cary Eclipse spectrophotometer. The excitation wavelength was 280 nm with a band pass of 20 nm for both excitation and emission spectra. Spectra were recorded between 290–600 nm at a scale rate of 600 nm min^{-1} . The absorbance of solutions was maintained below $A_{280} = 0.1$ to minimise resorption effects.

Quantification of Cu(i) binding

Data of K_D^I for proteins and peptides P were obtained from the competition reaction of eqn (1) and analysed by eqn (2):²⁶



$$\frac{[\text{P}]_{\text{tot}}}{[\text{Cu}]_{\text{tot}}} = 1 - \frac{[\text{Cu}^I\text{L}_2]}{[\text{Cu}]_{\text{tot}}} + K_D\beta_2 \left(\frac{[\text{L}]_{\text{tot}}}{[\text{Cu}^I\text{L}_2]} - 2 \right)^2 [\text{Cu}^I\text{L}_2] \left(1 - \frac{[\text{Cu}^I\text{L}_2]}{[\text{Cu}]_{\text{tot}}} \right) \quad (2)$$

The term $[\text{Cu}^I\text{L}_2]$ is the equilibrium concentration of probe complex $[\text{Cu}^I\text{L}_2]^{3-}$ in eqn (1) and may be determined directly

from the solution absorbance under the condition that this complex is the only absorbing species. The other terms in eqn (2) are the known total concentrations of the relevant species. The dissociation constant K_D^I for $\text{Cu}^I\text{-P}$ was derived by curve-fitting of the experimental data to eqn (2) (*i.e.*, plots of $[\text{P}]_{\text{tot}}/[\text{Cu}]_{\text{tot}}$ versus $[\text{Cu}^I\text{L}_2]$) with $\beta_2 = 10^{13.7}$ and $10^{15.1} \text{ M}^{-2}$ for $\text{L} = \text{Fs}$ and Fz , respectively.²⁶ The detailed experimental protocol followed that reported recently.²⁶ The experiments were conducted anaerobically in deoxygenated MOPS buffer (50 mM, pH 7.4) containing reductants NH_2OH (0.5 mM) and/or Asc (0.5 mM) (denoted as buffer A) in a glovebox ($[\text{O}_2] < 1$ ppm). The samples were transferred in sealed containers for characterisation.

The sidechains of the three histidine residues (His-6,13,14) in A β 16 peptides are likely to be involved in Cu(i) binding. Their $\text{p}K_a$ values in an A β 28 peptide have been estimated to be 6.5, 6.6 and 6.5, respectively.²⁸ Consequently, the apparent dissociation constants K_D^I for Cu(i) binding are likely to be sensitive to pH around pH 6.5. A quantitative analysis of the relationship between K_D^I and solution pH should provide information about the number of His residues being involved in the Cu(i) binding. For two- and three-His binding models, the relationship may be described by eqn (3) and (4), respectively:²⁹

$$K_D^I = K_D^I (1 + 10^{\text{p}K_a - \text{pH}} + 10^{2\text{p}K_a - 2\text{pH}}) \quad (3)$$

$$K_D^I = K_D^I (1 + 10^{\text{p}K_a - \text{pH}} + 10^{2\text{p}K_a - 2\text{pH}} + 10^{3\text{p}K_a - 3\text{pH}}) \quad (4)$$

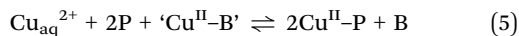
where K_D^I and K_D^I refer, respectively, to pH-dependent and pH-independent dissociation constants and $\text{p}K_a$ is the average proton dissociation constant for the sidechains of the three His residues, taken to be close to 6.5.²⁸ Note that eqn (3) and (4) address protonation equilibria of only those His sidechains that are involved in Cu(i) binding and assume negligible influence from other residues not involved directly in the binding to Cu(i).

The experiments were conducted within the pH range 5.5–7.8 in buffers MES ($\text{p}K_a = 6.1$) and MOPS ($\text{p}K_a = 7.2$) employing $[\text{Cu}^I(\text{Fs})_2]^{3-}$ as a chromophoric probe. The pH of each solution after an experiment was confirmed with a pH micro-electrode to ensure recording of an accurate value for each solution. The K_D^I values within this pH range were derived by curve-fitting of the experimental data to eqn (2), taking advantage of the low $\text{p}K_a$ value of ~ 3.2 for the probe ligand Fs. This means that the formation constant β_2 of $[\text{Cu}^I(\text{Fs})_2]^{3-}$ is essentially pH-independent at $\text{pH} > 5.5$.²⁶ This latter property was confirmed by determination of an essentially identical K_D^I , within experimental error, for control Cu(i) complexes of protein CopK and its variant H70F following the same approach, again using $[\text{Cu}^I(\text{Fs})_2]^{3-}$ as the determining probe (see Table S1, ESI[†]). The Cu(i) sites in both CopK proteins are defined by four methionine sidechains arranged tetrahedrally and so their Cu(i) binding affinities are expected to be pH-independent.²⁷

Quantification of Cu(II) binding via direct metal ion titration

Direct titration of Cu^{2+} into a solution of peptide P may induce reaction (5) where the fraction of bound Cu(II) is described by eqn (6):





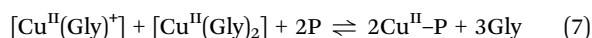
$$\frac{[\text{Cu}^{\text{II}}\text{-P}]}{[\text{Cu}(\text{II})]_{\text{tot}}} = \frac{[\text{P}]}{K_{\text{D}}^{\text{II}}(1 + K_{\text{A}}[\text{B}]) + [\text{P}]} \quad (6)$$

K_{D}^{II} is the dissociation constant of $\text{Cu}^{\text{II}}\text{-P}$ and K_{A} is the average association constant of the putative complex(es) $\text{Cu}^{\text{II}}\text{-B}$ (B = buffer and all other potential $\text{Cu}(\text{II})$ ligands except H_2O).

A pre-condition for a meaningful quantitative analysis *via* eqn (6) is that $K_{\text{D}}^{\text{II}}(1 + K_{\text{A}}[\text{B}]) \sim [\text{P}]$. To assist such analysis, an A β 16 variant A β 16wwa was designed and synthesised. Phe4 and Tyr10 were each replaced with Trp and His14 was replaced with Ala. Upon excitation at 280 nm, the fluorescence emitted by A β 16wwa at 360 nm was at least 100-fold more intense than that by A β 16. Binding of paramagnetic $\text{Cu}(\text{II})$ to A β 16wwa quenched this intense fluorescence sensitively. Consequently, the experimental concentration of P = A β 16wwa could be varied significantly to allow a possible detection of the equilibrium of eqn (5). This, in turn, allowed analysis under the conditions imposed by eqn (6). To minimise potential interference of putative $\text{Cu}^{\text{II}}\text{-B}$ complex(es) in eqn (5), the titration was conducted in a minimal concentration of MOPS or HEPES buffers, both of which exhibit a low affinity for $\text{Cu}(\text{II})$.

Quantification of $\text{Cu}(\text{II})$ binding *via* ligand competition

Reliable estimation of $\text{Cu}(\text{II})$ affinity by direct metal ion titration is restricted by the pre-condition $K_{\text{D}}^{\text{II}}(1 + K_{\text{A}}[\text{B}]) \sim [\text{P}]$ of eqn (6) and is subject to further uncertainties associated with the putative term $K_{\text{A}}[\text{B}]$ that cannot be evaluated reliably for most proton buffers. To lift the restriction (difficult to satisfy for K_{D}^{II} values much less than the experimental $[\text{P}]$) and to suppress the uncertainties, the $\text{Cu}(\text{II})$ buffer glycine (Gly; $K_{\text{A}1} = 1.17 \times 10^6 \text{ M}^{-1}$ and $K_{\text{A}2} = 6.76 \times 10^4 \text{ M}^{-1}$ at pH 7.4)^{12,30} was used to control the $\text{Cu}(\text{II})$ speciation (eqn (7) and (8)). Data was processed according to eqn (9) and (10):¹²



$$[\text{Cu}(\text{II})]_{\text{tot}} = [\text{Cu}^{\text{II}}(\text{Gly})^+] + [\text{Cu}^{\text{II}}(\text{Gly})_2] + [\text{Cu}^{\text{II}}\text{-P}] \quad (8)$$

$$[\text{Cu}_{\text{aq}}^{2+}] = \frac{[\text{Cu}(\text{II})]_{\text{tot}} - [\text{Cu}^{\text{II}}\text{-P}]}{K_{\text{A}1}[\text{Gly}] + K_{\text{A}1}K_{\text{A}2}[\text{Gly}]^2} \quad (9)$$

$$\frac{[\text{Cu}^{\text{II}}\text{-P}]}{[\text{P}]_{\text{tot}}} = \frac{[\text{Cu}_{\text{aq}}^{2+}]}{K_{\text{D}}^{\text{II}} + [\text{Cu}_{\text{aq}}^{2+}]} \quad (10)$$

where the term $[\text{Gly}]$ in eqn (9) is the free Gly concentration at equilibrium in eqn (7) and its calculation was detailed in ref. 12. Note that Gly is a neutral zwitterion in solution at pH 7.4 but is uni-negative when bound as a ligand to Cu^{II} . For simplicity, these protonation states are not reflected in the notation of eqn (7)–(9). A pre-condition for eqn (7) and (8) is that the contributions of both $\text{Cu}_{\text{aq}}^{2+}$ and the putative $\text{'Cu}^{\text{II}}\text{-B'}$ complexes to the total $\text{Cu}(\text{II})$ speciation are small enough to be ignored. Then $[\text{Cu}_{\text{aq}}^{2+}]$ may be estimated from eqn (9) based on known formation constants $K_{\text{A}1}$ and $K_{\text{A}2}$ at pH 7.4 and K_{D}^{II} for $\text{Cu}^{\text{II}}\text{-P}$ be derived from curve-fitting to eqn (10) of the variation of $[\text{Cu}_{\text{aq}}^{2+}]$ as a function of Gly addition (with consequent variation of $[\text{Cu}^{\text{II}}\text{-P}]$).

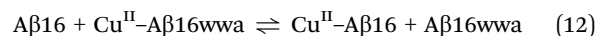
This approach was applied to determine K_{D}^{II} for the probe A β 16wwa *via* quenching of its intense fluorescence upon $\text{Cu}(\text{II})$ binding. Typically, a series of solutions in MOPS buffer (10 mM, pH 7.4) were prepared that contained A β 16wwa (2.0 μM), $\text{Cu}(\text{II})$ (1.6 μM ; 0.8 equiv.) and increasing concentrations of Gly. The fluorescence intensities at 360 nm (F) of the solutions increased with increasing concentrations of Gly and reached a constant value (F_0) that was >95% that of a control containing A β 16wwa (2.0 μM) only (see Fig. 6a below). The behaviour indicated that addition of Gly induced the reverse reaction of eqn (7) and that there is little inner filter effect under the conditions of low $\text{Cu}(\text{II})$ concentration. Consequently, $[\text{Cu}^{\text{II}}\text{-P}] = [\text{Cu}^{\text{II}}\text{-A}\beta 16\text{wwa}]$ may be estimated from eqn (11) and then $[\text{Cu}_{\text{aq}}^{2+}]$ and K_{D} from eqn (9) and (10):

$$\frac{[\text{Cu}^{\text{II}}\text{-P}]}{[\text{P}]_{\text{tot}}} = \frac{F_0 - F}{F_0 - F_{0.8}} \times 0.8 \quad (11)$$

An additional estimate of K_{D}^{II} for A β 16wwa was made by application of an independent $\text{Cu}(\text{II})$ competing ligand nitrilotriacetic acid (NTA). The details are given in the ESI† and Fig. S3.

Quantification of $\text{Cu}(\text{II})$ -binding to selected A β 16 peptides with probe A β 16wwa

The $\text{Cu}(\text{II})$ affinities of A β 16 and its variants were determined conveniently based on competition for $\text{Cu}(\text{II})$ with the probe peptide A β 16wwa:



$$K_{\text{ex}} = \frac{[\text{Cu}^{\text{II}}\text{-A}\beta 16][\text{A}\beta 16\text{wwa}]}{[\text{A}\beta 16][\text{Cu}^{\text{II}}\text{-A}\beta 16\text{wwa}]} = \frac{K_{\text{D}}^{\text{II}}(\text{A}\beta 16\text{wwa})}{K_{\text{D}}^{\text{II}}(\text{A}\beta 16)} \quad (13)$$

At molar ratios A β 16:A β 16wwa < 3, the fluorescence intensity at 360 nm is dominated by that of A β 16wwa with negligible contribution from A β 16 (see Fig. 5a below). Consequently, the term $[\text{Cu}^{\text{II}}\text{-P}] = \text{Cu}^{\text{II}}\text{-A}\beta 16$ may be obtained from eqn (11) and then all other terms in eqn (12) from a mass balance at each known total concentration. This allows definition of K_{D}^{II} for A β 16 relative to that of A β 16wwa according to eqn (13).

The experiments were conducted as two types of complementary titrations. In the first, fluorescence intensity was quenched by titration of aliquots of CuSO_4 (10 μL , 80 μM) into a 2.0 mL solution in MOPS (10 mM, pH 7.4) containing either A β 16wwa (2.0 μM) alone or both A β 16wwa and the target peptide (each 2.0 μM). In the second, fluorescence intensity was recovered by titration of aliquots of the target peptide (4.0 μL , 500 μM) into a 2.0 mL solution in MOPS (10 mM, pH 7.4) containing A β 16wwa (2.0 μM) and $\text{Cu}(\text{II})$ (1.6 μM). The $\text{Cu}(\text{II})$ speciation was analysed *via* eqn (11) in both cases.

Catalytic aerobic oxidation of ascorbate and generation of H_2O_2

Generation of H_2O_2 by catalytic aerobic oxidation of Asc was monitored by UV-Vis spectroscopy *via* an assay based upon the dye Amplex Red³¹ using an experimental procedure



described recently.³² The solution conditions for a typical reaction were: $[\text{Asc}]_{\text{tot}} \sim 50 \mu\text{M}$, $[\text{Amplex Red}]_{\text{tot}} \sim 45 \mu\text{M}$; $[\text{HRP}] \sim 0.35 \text{ U mL}^{-1}$; $[\text{Cu}]_{\text{tot}} = 5.0 \mu\text{M}$ (if added) and $[\text{ligand}]_{\text{tot}} = 7.0 \mu\text{M}$. The reactions were started by addition of Asc into a solution containing all other components in air-saturated MOPS buffer (50 mM, pH 7.4). Spectral changes were recorded at intervals of 50 s. A control solution without Asc served for baseline correction. The initial absorbance observed at 265 nm was sensitive to the reaction rate and solution composition. Use of $\text{Cu}_{\text{aq}}^{2+}$ as catalyst led to considerably lower initial absorbance than the other test solutions due to its higher relative reaction rate.

The apparent reduction potentials of the copper centres in various Cu- β 16 complexes were estimated from the relative affinities of the peptides for Cu(I) and Cu(II) *via* the Nernst relationship of eqn (14):

$$E^{\circ'} (\text{mV}) = E^{\circ} + 59 \log \left(\frac{K_{\text{D}}(\text{Cu}^{\text{II}})}{K_{\text{D}}(\text{Cu}^{\text{I}})} \right) \quad (14)$$

where E° = 153 mV (*vs.* SHE) is the standard reduction potential of $\text{Cu}^{2+}/\text{Cu}^+$.³³

Results and discussion

β 16 binds Cu(I) with sub-nanomolar affinity

The chromogenic ligands Fs (Fig. 1a, inset) and Fz have been developed as quantitative probes for weaker Cu(I) binding.²⁶ When in excess, both react quantitatively to yield well-defined complex anions $[\text{Cu}^{\text{I}}(\text{Fs})_2]^{3-}$ ($\lambda_{\text{max}} = 484 \text{ nm}$; $\epsilon = 6700 \text{ cm}^{-1} \text{ M}^{-1}$; $\beta_2 = 10^{13.7} \text{ M}^{-2}$) and $[\text{Cu}^{\text{I}}(\text{Fz})_2]^{3-}$ ($\lambda_{\text{max}} = 470 \text{ nm}$, $\epsilon = 4320 \text{ cm}^{-1} \text{ M}^{-1}$; $\beta_2 = 10^{15.1} \text{ M}^{-2}$). This enables them to buffer free Cu_{aq}^+ concentrations (expressed hereafter as $\text{pCu}^+ = -\log[\text{Cu}_{\text{aq}}^+]$) in the respective ranges $\text{pCu}^+ = 8\text{--}12$ and $10\text{--}14$. However, the complexes are air-sensitive and subject to substitution by other weak Cu(I) ligands, especially for $[\text{Cu}^{\text{I}}(\text{Fs})_2]^{3-}$. Consequently, all reactions must be performed under anaerobic conditions in

MOPS buffer containing reductants NH_2OH and/or Asc with exclusion of all other potential Cu(I) ligands such as Cl^- .²⁶

A probe solution of $[\text{Cu}]_{\text{tot}} = 30 \mu\text{M}$ with a minimum molar ratio of $\text{Fs}/\text{Cu} \sim 2.3$ (to ensure the dominance of $[\text{Cu}^{\text{I}}(\text{Fs})_2]^{3-}$) was necessary to observe quantitative transfer of Cu(I) from $[\text{Cu}^{\text{I}}(\text{Fs})_2]^{3-}$ to the β 16 peptide (*i.e.*, eqn (1) goes to completion; see Experimental section). The peptide has a relatively weak affinity for Cu(I) and, even in this solution buffered at $\text{pCu}^+ \sim 8.2$, it is only able to extract Cu(I) from $[\text{Cu}^{\text{I}}(\text{Fs})_2]^{3-}$ quantitatively for β 16/Cu < 0.4 (Fig. 1a and b). Linear extrapolation of the data at low β 16/Cu ratios demonstrates that β 16 possesses a single site of highest affinity for Cu(I).

Increasing $[\text{Fs}]_{\text{tot}}$ to 180 μM under otherwise identical conditions constrained the free Cu_{aq}^+ concentration to $\text{pCu}^+ \sim 10.3$ and imposed an effective competition for Cu(I) according to eqn (1) (Fig. 1c). Dilution of each equilibrium solution resulted in partial transfer of Cu(I) from the complex to the peptide to reach a new equilibrium position, as shown by comparison with the dotted traces in (ii) of Fig. 1b and c, derived from simple 1 : 1 dilution of data sets (i). Eqn (2) (which assumes a single binding site) was used to fit the four sets of independent experimental data. This process allowed extraction of the equilibrium constant $K_{\text{ex}} = \beta_2 \times K_{\text{D}}^{\text{I}}$ and estimation of $K_{\text{D}}^{\text{I}} = 10^{-10.4} \text{ M}$ at pH 7.4. The estimate was the same for each data set, within experimental error.

Ligand Fz has a higher affinity for Cu(I) and, even at the minimum allowable molar ratio of $\text{Fz}/\text{Cu} \sim 2.3$, imposed an effective competition for Cu(I) between Fz and β 16. This allowed estimation of an indistinguishable $K_{\text{D}}^{\text{I}} = 10^{-10.4} \text{ M}$ at pH 7.4. This work substantiates preliminary results reported previously,²⁶ but contrasts considerably the other two earlier values ($K_{\text{D}}^{\text{I}} \sim 10^{-7} \text{ M}^{15}$ and 10^{-15} M^{14}). The present value was determined relative to $\beta_2 = 10^{15.1} \text{ M}^{-2}$ for $[\text{Cu}^{\text{I}}(\text{Fz})_2]^{3-}$ which, in turn, was derived based on $\beta_2 = 10^{17.2} \text{ M}^{-2}$ for $[\text{Cu}^{\text{I}}(\text{Bca})_2]^{3-}$ (Bca: bicinchoninic anion).^{26,34} The latter value was consolidated recently by an independent study.^{35,36}

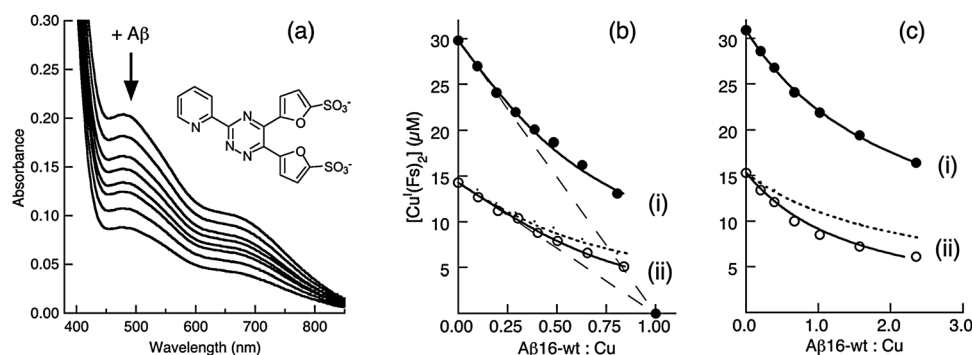


Fig. 1 Quantification of Cu(I) binding to the β 16 peptide in buffer A. (a) Changes in absorbance of $[\text{Cu}^{\text{I}}(\text{Fs})_2]^{3-}$ solution ($[\text{Cu}]_{\text{tot}} = 30 \mu\text{M}$; $[\text{Fs}]_{\text{tot}} = 70 \mu\text{M}$) with increasing molar concentration of β 16 peptide. The structure of the Fs ligand is shown in the inset; (b, c) variation of concentration of $[\text{Cu}^{\text{I}}(\text{Fs})_2]^{3-}$ with increasing molar ratio β 16 : Cu in Cu_{aq}^+ buffer of initial $\text{pCu}^+ = 8.2$ ($[\text{Cu}]_{\text{tot}} = 30 \mu\text{M}$; $[\text{Fs}]_{\text{tot}} = 70 \mu\text{M}$) in (b) and initial $\text{pCu}^+ = 10.3$ ($[\text{Cu}]_{\text{tot}} = 31 \mu\text{M}$; $[\text{Fs}]_{\text{tot}} = 180 \mu\text{M}$) in (c). The experimental data in solid circles were derived from the solutions prepared as described in the Experimental section. The data in empty circles was obtained after 1 : 1 dilution of the original solutions with proton buffer A. The two solid traces in (i, ii) are the fitting of the experimental data to eqn (2). The dotted traces in (ii) are the simple 1 : 1 dilutions of the data set (i). The two dashed lines intercepting β 16 : Cu = 1.0 in (b) allowed estimation of the binding stoichiometry.



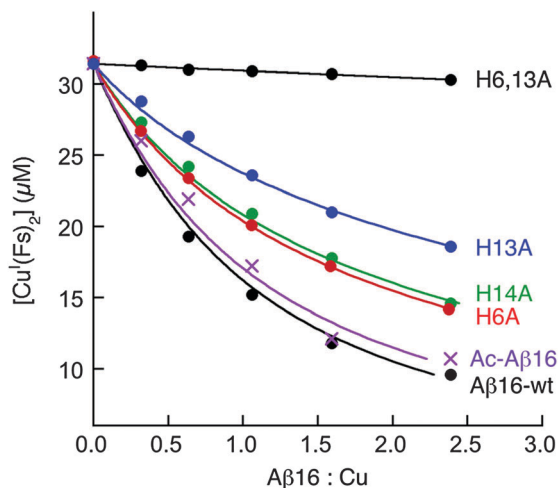


Fig. 2 Variation of Cu(I) binding affinity of the A β 16 peptide upon modification of individual peptide residues. Probe composition: [Cu]_{tot} ~ 31.4 μ M and [Fs]_{tot} = 140 μ M in proton buffer A. Within experimental error, pairs (A β 16-wt; Ac-A β 16) and (H6A; H14A) provided indistinguishable data.

At least two His are involved in Cu(I) binding to A β 16 but the N-terminal amine is not

Spectroscopic examination has implicated the His sidechains of the A β 16 peptide DAEFRHDSGYEVHHQK as Cu(I) ligands.^{21,23–25} The N-terminal amine and carboxylate sidechains may also be involved.

The affinities of a number of variants of A β 16 were investigated with probe Fs (Fig. 2 and Table 1). Probe Fz is less satisfactory in these systems as its affinity for Cu(I) is too high to allow effective competition. Substitution of any one of the three His residues with non-binding Ala reduced the affinities of the resultant peptides H6A, H13A and H14A by factors of between two and five. Removal of two His residues decreased the affinity of H6,13A and H13,14A by factors of >50 and >250, respectively. On the other hand, acetylation of the N-terminus (Ac-A β 16) did not alter the affinity of the peptide for Cu(I). The Cu(I) affinity of the triple mutant probe peptide F4W,Y10W,H14A (*i.e.*, A β 16wwa) is indistinguishable from that of the single mutant H14A (Table 1).

These experiments demonstrate that (i) at least two His sidechains are required for effective binding of Cu(I) but that all three His ligands contribute significantly; (ii) the N-terminal amine is not a Cu(I) ligand; (iii) substitution of residues not involved directly in Cu(I) binding (*e.g.*, aromatics F4,Y10) has little impact on the affinity, consistent with the structural flexibility of the peptide.

Variation of K_D^I with pH suggests that only two of the three His residues of A β 16 are involved simultaneously in Cu(I) binding

The sensitivity of the derived K_D^I values to the availability of the three His residues suggested that this parameter may be pH-dependent. His sidechains exhibit characteristic pK_a values of 6.0–6.5 and an average pK_a value of the three His sidechains in an A β 28 peptide was estimated to be 6.53.²⁸ Consequently, at pH < 7, protons may compete with Cu(I) for these sidechains.

K_D^I for A β 16 is sensitive to pH (black circles; Fig. 3a). With both K_D^I and pK_a as fitting parameters, the experimental data were fitted satisfactorily to eqn (3) assuming the availability of two His ligands only (black trace). Fitting to a model that assumes the availability of all three His ligands (eqn (4)) was less adequate (red dotted trace; Table 1). The essential difference is that the average pK_a = 6.5 derived from the two-His model is the same as that determined independently by NMR²⁸ while the value of 6.1 derived from the three-His model is significantly smaller (Table 1). However, when the parameter pK_a was constrained to the experimental value 6.5 so that K_D^I was the only fitting parameter, the curve fitting remained optimal for the two-His model but was unsatisfactory for the three-His model (Fig. 3a: black trace *versus* green dotted trace; Table 1).

Further support for the two-His model is provided by the equivalent experiments for the three A β 16 variants H6A, H13A and H14A (Fig. 3b(iii)–(v)). Their K_D^I values are also pH sensitive and the relationship in each case was described satisfactorily by the two-His model (eqn (3)) with both K_D^I and pK_a values derived from the curve-fitting matching those experimental values (Fig. 2 and Table 1). Each variant peptide features two His residues only and so can contribute a maximum of two His sidechains for Cu(I) binding.

The equivalent experiment for Ac-A β 16 (acetylated at the N-terminus) generated similar results to those for A β 16 itself

Table 1 Log K_D^I and pK_a for the A β 16 peptide and selected variants^a

Peptide	Log K_D^I ^b		$K_D^I/K_D^I(\text{wt})$	pK_a from curve fitting	Fitting R factor	Fitting curve in Fig. 3
	Direct det. at pH 7.4	From fitting pH variation				
A β 16	–10.4	–10.5 –10.4 ^c –10.8 ^d	1.0	6.5 6.1 ^c 6.5 (fixed) ^d	0.99 0.97 ^c 0.83 ^d	Black trace i Red dots ^c Green dots
Ac-A β 16	–10.4	–10.5	1.0	6.6	0.97	ii
H6A	–10.0	–10.1	2.5	6.5	0.99	iii
H14A	–9.95	–9.95	2.8	6.6	0.98	iv
A β 16wwa	–9.98	—	2.6	—	—	—
H13A	–9.76	–9.84	4.4	6.6	0.99	v
H6,13A	> –8 ^e	—	> 250	—	—	—
H13,14A	> –8.7 ^e	—	> 50	—	—	—

^a Unless otherwise indicated, the listed parameters were derived from curve-fitting of the experimental data to eqn (3) based on a Cu^I(His)₂ site model with both K_D^I and pK_a as fitting parameters. ^b Estimated experimental errors ± 0.05 unless indicated otherwise. ^c From curve-fitting to eqn (4) based on a Cu^I(His)₃ site model with both K_D^I and pK_a as fitting parameters. ^d From curve-fitting to eqn (4) (a Cu^I(His)₃ site model) with pK_a = 6.5 fixed and K_D^I as the only fitting parameter. ^e Approximate estimates only at the detection limit of Fs probe with large uncertainty.



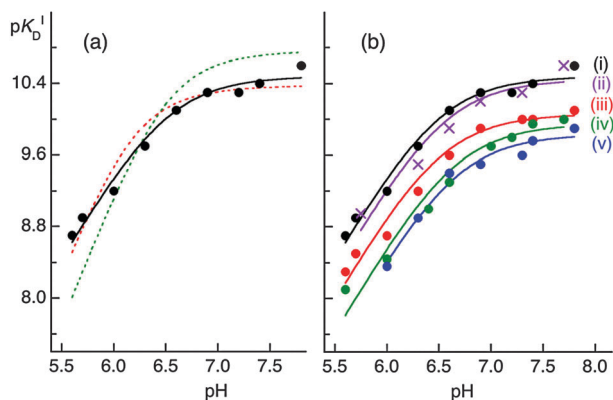


Fig. 3 Variation of pK_D^I ($= -\log K_D^I$) with solution pH: (a) comparison of curve-fittings of the experimental data for A β 16-wt to eqn (3) (black solid trace) or eqn (4) (red dotted trace) with fixed input of $pK_a = 6.5$ (green dotted trace); (b) curve-fittings of the experimental data to eqn (3) for: (i) A β 16 (black dots & trace); (ii) Ac-A β 16 (purple crosses & trace); (iii) H6A (red dots & trace); (iv) H14A (green dots & trace); (v) H13A (blue dots & trace). The fitting parameters in each case are given in Table 1.

(Fig. 3b, (i) vs. (ii); Table 1), although the former carries one less positive charge than does the native peptide. This supports the condition set previously for derivation of pH dependence *via* eqn (3) and (4): protonation of other non-metal-binding sites has minimal impact on the observed K_D^I . It also re-affirms that the N-terminus is not involved in Cu(I) binding.

Taken together, these experiments provide strong evidence that the Cu(I) site in A β 16 includes two only of the three available His ligands. This conclusion is supported by X-ray absorption spectroscopy and theory.^{21,23,24,37} On the other hand, the data of Fig. 2 and 3 and Table 1 demonstrate that replacement of any one of the three His residues in A β 16 led to a marginal decrease only in Cu(I) binding affinity (*i.e.*, any two will do) but that replacement of any two His ligands disabled the binding site. When combined with the NMR study,²¹ the data are consistent with the presence of solution dynamic processes that exchange Cu(I) between the three available pairs of His ligands (Fig. 4). This dynamic nature proves to be

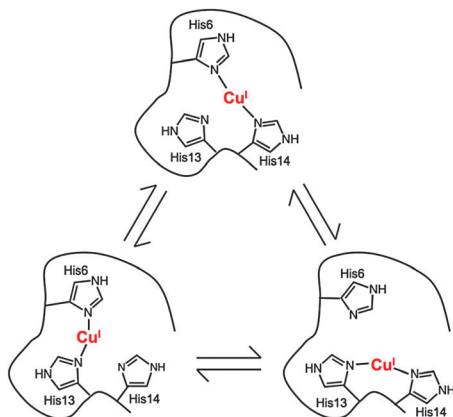


Fig. 4 Model of Cu(I) binding in A β 16 peptide derived from the experimental data in Fig. 2 and 3.

important for redox cycling in the catalytic production of H_2O_2 (*vide infra*).

Development of a highly fluorescent peptide probe for estimation of Cu(II) affinities

The well-characterised Cu(II) ligand Gly has been used as an affinity standard to determine the Cu(II) affinities of A β peptides. Spectroscopic approaches have relied on the fluorescence emission of the single Tyr residue in A β peptides as the detection probe. However, both detection sensitivity and specificity are compromised by the relatively weak emission intensity of Tyr and interference from secondary Cu(II) binding sites.¹³

A probe based upon the A β peptide was designed by replacement of aromatic residues Phe4 and Tyr10 with Trp to increase detection sensitivity and of His14 by Ala to suppress secondary Cu(II) binding. The resultant peptide A β 16wwa exhibited excellent properties as a probe for quantification of Cu(II) binding to other A β peptides: (i) it binds either Cu(I) or Cu(II) with affinities indistinguishable from those of H14A (see Tables 1 and 2); (ii) it emits fluorescence (λ_{ex} , 280 nm; λ_{em} 360 nm) that is an order of magnitude more intense than that of the A β 16 peptide at 310 nm or more than two orders of magnitude more intense than that at 360 nm (Fig. 5a); (iii) at a concentration of 20 μ M, it responds sensitively to Cu(II) binding with a distinct turning point at one equivalent of Cu(II) with evidence of further binding to a second equivalent (Fig. 5b, blue trace). In contrast, the response of A β 16 to Cu(II) binding is much less sensitive and poorly defined with up to three equivalents of Cu(II) binding detectable under the same conditions (Fig. 5b, red trace).¹³

Quantification of Cu(II) binding to Aβ16wwa probe

Addition of bis(2-hydroxyethyl)amino-tris(hydroxymethyl)-methane (BisTris) (1.0 mM) into the MOPS buffer (50 mM; pH 7.4) for the Cu^{2+} titration eliminated Cu(II) binding to the weaker site in A β 16wwa (20 μ M; Fig. S1, ESI⁺) and induced competition between BisTris and the stronger peptide binding site for Cu(II) according to eqn (5) ($P = A\beta 16wwa$; $B = BisTris$; $K_D = 10^{-5.2} M^{-1}$ for Cu^{II} -BisTris at pH 7.4³⁸ while MOPS has little Cu(II) affinity). After addition of one equivalent of Cu(II), >90% of total added Cu(II) was bound by the peptide. Consequently, an affinity of $K_D^{II} < 10^{-9} M$ may be

Table 2 Selected $\log K_D^{II}$ for Cu^{II} -A β complexes estimated *via* ligand competition^a

Peptide	Log K_D^{II}	Affinity std.	Det. probe	Ref.
A β 16wwa	-9.8	Gly	A β 16wwa	This work
A β 16wwa	-9.8	NTA	A β 16wwa	This work
A β 16	-10.0	Gly	A β 16wwa	This work
A β 28	-10.0 ^b	Gly	Tyr in A β	13
A β 42	-10.2	Gly	Tyr in A β	11
A β 16/40	-9.6	Gly	ITC	41
A β 16	-9.0 ^c	ACES	ITC	42
A β 28	-8.8 ^c	ACES	ITC	42

^a Refer to ref. 13 for a summary of more extensive literature values estimated *via* various approaches. ^b Estimated at pH 7.6. ^c Estimated using *N*-(2-acetamido)-2-aminoethanesulfonic acid (ACES) as both proton buffer and Cu(II) affinity standard.



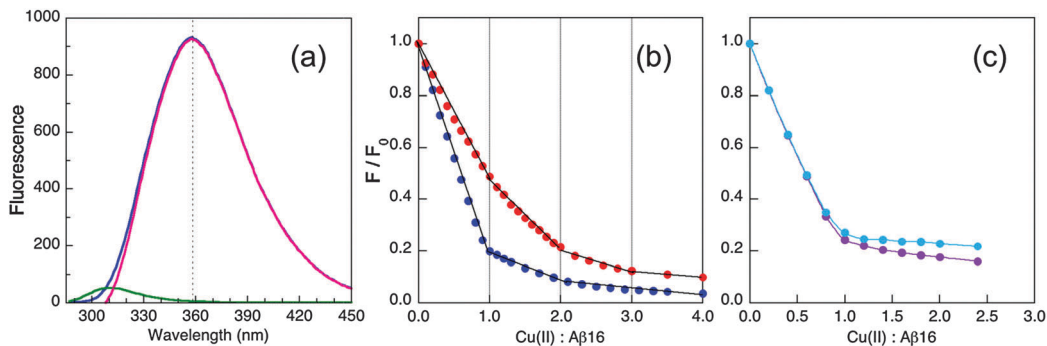


Fig. 5 Comparison of A β 16 peptides (20 μ M) in MOPS (50 mM, pH 7.4): (a) fluorescence spectra of A β 16wt (green trace), A β 16wva (blue trace) and their difference (pink trace) under the same conditions; (b) plot of normalised fluorescence (F/F_0) versus Cu(II) : A β 16 ratio for A β 16wva (blue) and A β 16wt (red); (c) same plot as (b) but for A β 16wva at 2.0 μ M (purple) and 0.20 μ M (cyan) in MOPS (1.0 mM, pH 7.4).

estimated from eqn (6) based on the above K_D for Cu^{II}-BisTris.³⁸ On the other hand, the high emission intensity of the A β 16wva probe allows its experimental concentration to be reduced significantly. At concentrations between 0.2 and 2.0 μ M,³⁹ Cu(II) binding to the weaker site was suppressed while that to the stronger site remained dominant (Fig. 5c). Even at the lowest peptide concentration of 0.20 μ M, $\geq 94\%$ of total added Cu(II) was estimated to be bound by the peptide after addition of one equivalent of Cu(II) titration. Consequently, an affinity of $K_D^H \leq 10^{-9.1}$ M may be estimated from eqn (6) without consideration of the possible contribution of Cu(II) binding to the MOPS buffer at 1.0 mM. However, in either case, the degree of complex formation was too high (>90%) to allow a reliable estimation of K_D^H .⁴⁰

These experiments demonstrate that: (i) the second binding site for Cu(II) in A β 16wva is relatively weak ($K_D^H \geq 10^{-6}$ M); (ii) direct metal ion titration defines the binding stoichiometry of Cu(II):A β 16wva = 1.0 for the stronger site but can provide an approximate value only for the binding affinity: $K_D^H \leq 10^{-9.1}$ M at its lowest experimental concentration of 0.2 μ M. The detection sensitivity for the parent A β 16 peptide is lower by a factor of ~ 100 , thereby setting estimation limit of its affinity to $K_D^H < 10^{-7}$ M with high uncertainty. This provides an answer to the puzzle of why the Cu(II) affinities acquired in the past for A β peptides *via* direct metal ion titration were scattered so widely around $K_D^H \sim 10^{-7}$ M.^{11,13,20}

It is apparent that the Cu(II) affinity of the A β 16wva probe is too high (*i.e.*, K_D^H is too small) to be determined by direct metal ion titration and a ligand competition approach is required for reliable estimation.¹² Glycine (Gly) and nitrilotriacetic acid (NTA) are two suitable competing ligands. Experimental results with Gly are described below and those with NTA are given in the ESI[†] and Fig. S3.

Gly binds Cu(II) to yield 1:1 and 1:2 complexes with formation constants $K_{A1} = 10^{6.07}$ and $K_{A2} = 10^{4.77}$ M⁻¹ at pH 7.4.⁴³ The fluorescence intensity of an A β 16wva solution (2.0 μ M) in MOPS buffer (10 mM, pH 7.4) was quenched markedly by addition of Cu²⁺ (0.80 equiv.) but was recovered almost quantitatively (>95%) by titration of a large excess of Gly (>10 mM; Fig. 6a). This demonstrates that: (i) Cu(II) bound to the peptide can be removed reversibly; (ii) Gly imposes no discernable inner-filter effect; (iii) the inner-filter effect of Cu^{II}-Gly complex(es) at low concentrations (≤ 1.6 μ M) is negligible. Consequently, at each point of the titration, the occupancy $[Cu^{II}-P]/[P]_{tot}$ can be estimated *via* eqn (11) and the corresponding free Cu_{aq}²⁺ concentration analysed *via* eqn (7)–(9). Curve-fitting to eqn (10) led to $K_D = 10^{-9.8}$ M at pH 7.4 for Cu^{II}-A β 16wva. This data is supported by equivalent and independent experiment with NTA as a competing ligand that provided the same $K_D^H = 10^{-9.8}$ M at pH 7.4 within the experimental error (see Table 2 and Fig. S3, ESI[†]).

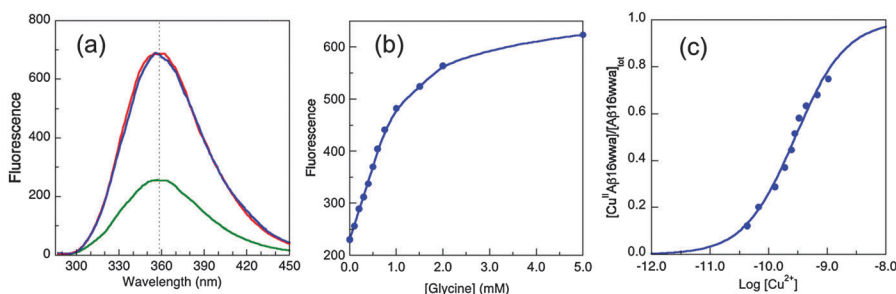


Fig. 6 Determination of Cu(II) affinity of A β 16wva in MOPS buffer (10 mM, pH 7.4): (a) fluorescence spectra of A β 16wva (2.0 μ M; blue trace); A β 16wva (2.0 μ M) plus Cu(II) (1.6 μ M) (green trace); A β 16wva (2.0 μ M) plus Cu(II) (1.6 μ M) plus ≥ 10 mM Gly (red trace); (b) recovery of fluorescence intensity for Cu^{II}_{0.8}-A β 16wva (2.0 μ M) with increasing Gly concentration; (c) curve fitting of $[Cu^{II}-P]/[P]_{tot}$ versus $\log[Cu_{aq}^{2+}]$ to eqn (10) derived an estimate of $K_D = 10^{-9.8}$ M for Cu^{II}-A β 16wva.



Estimation of the affinities of A β 16 peptides for Cu(II) using the A β 16wwa probe

As the affinity of the probe peptide A β 16wwa for Cu(II) is comparable to those of many other A β peptides, two complementary approaches based on eqn (12) and (13) were employed: (i) monitoring of fluorescence quenching by direct titration of Cu_{aq}²⁺ into a solution containing A β 16wwa and the target peptide in equimolar concentrations (2.0 μ M) relative to a control that contained A β 16wwa only (Fig. S4, ESI[†]); (ii) monitoring the fluorescence recovery of the probe by titration of the target peptide into a solution containing A β 16wwa (2.0 μ M) and 0.8 equiv. of Cu(II) (1.6 μ M) (Fig. 7a and b). The Cu(II) speciation in eqn (12) and (13) may be analysed reliably *via* eqn (11) as the fluorescence intensity of the probe at 360 nm is more than 100 fold greater than those A β peptides that contain a single Tyr residue only (Fig. 5a, Fig. S5a, ESI[†]). Approach (ii) may be compromised in cases where a large excess of target peptide is required to impose competition. Then, despite their low extinction coefficient around the excitation position (ϵ_{276} 1410 M⁻¹ cm⁻¹) and low emission intensity at the detection position (360 nm), the target peptides may still impact on the observed fluorescence intensity when in large excess (Fig. S5b, ESI[†]). This follows from a combination of inner-filter and fluorescence effects of the target peptides. However, in the present systems, the impact was negligible when the target peptide was restricted to no more than two equivalents relative to A β 16wwa (Fig. 5a, Fig. S5a, ESI[†]).

At pH 7.4, both approaches estimated $K_D^{\text{II}} = 10^{-10.0}$ M for A β 16 based on $K_D^{\text{II}} = 10^{-9.8}$ M for A β 16wwa. This value is in an excellent agreement with the recent consensus value of $K_D \sim 10^{-10}$ M (Table 2).^{11,13} Substitution of any one of the three His residues by Ala decreased the affinity for Cu(II) marginally (by 2–3 fold; Fig. 7a and b, Fig. S4, ESI[†]; Table 3). In addition, K_D^{II} values for H14A and A β 16wwa were the same within experimental error, confirming that removal of the aromatic residues has little impact on the copper binding chemistry. It appears that, as for the case of Cu(I), any two of the three His ligands can contribute to binding of Cu(II) and that a dynamic

Table 3 Cu(II) affinities of A β 16/28 peptides relative to those of the wild type forms

A β 16	Log K_D^{II}		$K_D^{\text{II}}/K_D^{\text{II}}(\text{wt})$		$K_D^{\text{II}}/K_D^{\text{II}}(\text{wt})$	
	pH 7.4	pH 7.4	pH 9.0	A β 28	pH 7.4 ^a	pH 7.8
wt	-10.0	1.0	1.0	wt	1.0	1.0
Ac-A β 16	-8.3	50	10	Ac-A β 28	10.6	7.9
H6A	-9.5	3.2	3.2	H6A	1.3	2.5
H13A	-9.7	2.0	1.6	H13A	0.8	1.3
H14A	-9.7	2.0	1.3	H14A	0.9	1.3
A β 16wwa	-9.8	1.6	—	—	—	—
H6,13A	-9.0	10	3.2	—	—	—
H13,14A	-9.5	3.2	1.6	—	—	—
Ref.	This work	This work	This work		42	11

^a Estimated using *N*-(2-acetamido)-2-aminoethanesulfonic acid (ACES) as both proton buffer (20 mM, pH 7.4) and Cu(II) affinity standard and ITC as detection probe.

exchange equilibrium is present. However, the K_D^{II} value of H13,14A is identical to that of H6A but is three-fold smaller than that of H6,13A (Table 3). This is consistent with His6 playing a more important role than either His13 or His14 in Cu(II) binding. These observations are in agreement with a current Cu(II) binding model that suggests that His6 is an essential equatorial ligand while a second equatorial ligand is provided interchangeably by either His13 or His14 (Fig. 8).⁸ On the other hand, acetylation of the N-terminal nitrogen leads to a dramatic decrease of affinity by more than an order of magnitude (Fig. 7a and b, Fig. S4, ESI[†]; Table 3), demonstrating that the N-terminal nitrogen is another key Cu(II) ligand (Fig. 8). These data support previous analysis of relative affinities,^{11,42} but provide a sensitive and reliable basis for detection of these differences experimentally (Table 3).

Analysis of the relative affinities for Cu(II) in CHES ((cyclohexylamino)ethanesulfonic acid) buffer at pH 9.0 provides a somewhat different story (Fig. 7b). Overall, His ligands and the N-terminal nitrogen appear to make lesser contributions to the Cu(II) binding than those at pH 7.4 although the influence of His6 remains unchanged (Fig. 7 and Table 3). This suggests that increasing pH promotes deprotonation of the Ala2 backbone amide for Cu(II) coordination and formation of the so-called component II (Fig. 8).⁸ Consistent with this model, variant peptides H13A, H14A and H13,14A all display affinities for Cu^{II} that are only marginally weaker than that of the wild-type peptide (Fig. 7b and Table 3). It appears that neither His13 nor His14 are crucial ligands in component II. In contrast, both H6A and H6,13A variants show a significant reduction in affinity (Fig. 7b and Table 3). Current models require only one His ligand for component II,⁸ and our data suggests that the identity of this ligand is His6 – perhaps due to its proximity to the N-terminal chelate ring. The significant loss of affinity upon acetylation indicates that the N-terminal nitrogen remains as an essential Cu(II) ligand at this pH. Thus the observed changes in the relative affinities of A β 16 variants at pH 9.0 (Table 3) supports the proposed change in coordination environment in component II (Fig. 8), as observed by a variety of spectroscopic techniques⁴⁴ including EPR, CD and NMR.^{16,45}

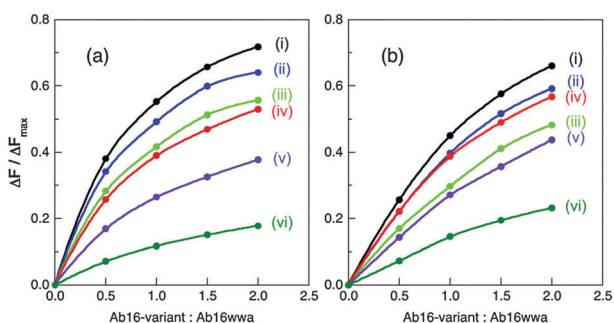


Fig. 7 Determination and comparison of Cu(II) dissociation constants for A β 16 peptides using A β 16wwa as a probe at pH 7.4 (a) and 9.0 (b): (i) A β 16wt; (ii) H14A or H13A; (iii) H6A; (iv) H13,14A; (v) H6,13A; (vi) Ac-A β 16. All experiments were conducted by titration of target peptide (4.0 μ L, 500 μ M) into a solution (2.0 mL) containing A β 16wwa (2.0 μ M) and Cu(II) (1.6 μ M) in either MOPS buffer (10 mM, pH 7.4) or CHES buffer (10 mM, pH 9.0). The complete set of derived K_D^{II} values is given in Table 3.



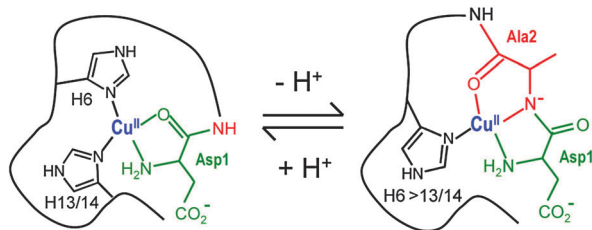


Fig. 8 Equilibrium of Cu(II) binding modes in solution ($pK_a \sim 7.8$) without considering possible axial coordination.⁸

Catalytic aerobic oxidation of ascorbate and generation of H₂O₂

A common feature in Alzheimer's disease is oxidative stress caused by reactive oxygen species (ROS). It has been proposed that one source is undesirable redox chemistry imposed by Cu bound to the disease proteins/peptides including, most importantly, the A β peptides.⁴⁶ Ascorbic acid is an abundant physiological reductant in the central nerve system (CNS) and is important as a neuromodulator and/or neuroprotective agent in the brain.^{47,48} Its oxidation by dioxygen can produce H₂O₂ that, if uncontrolled, may undergo further reduction *via* Haber-Weiss and related reactions to generate the hydroxyl radical OH, a likely source of oxidative stress and inflammation.⁴⁹ However, the oxidation is intrinsically slow and must be catalysed by redox-active couples such as Cu^{II}/Cu^I. The Cu ion bound in A β peptides has been demonstrated capable of assuming such a catalytic role.^{32,50} The present work has characterised the thermodynamic properties of a range of Cu centres in selected A β 16 peptides and, in particular, compared their relative Cu(I) and Cu(II) binding affinities reliably under the same conditions. This provides an unprecedented opportunity for an integrated study to correlate these thermodynamic properties with their efficiencies for generation of H₂O₂ *via* catalytic aerobic oxidation of Asc.

The catalytic reaction was followed by UV-visible spectroscopy (Fig. 9).³¹ While the 'free Cu_{aq}²⁺ ion' is a robust catalyst,

the redox-inactive complex [Cu^{II}(EDTA)]²⁻ was not (Fig. 9b and c(i) vs. (vii)). All metal-free A β 16 peptides were catalytically inactive. As observed previously,^{32,50} binding of 'free Cu_{aq}²⁺ ion' by A β 16 diminishes but does not silence the catalytic activity of the Cu centre (Fig. 9b and c(v); Table 4). Overall, the catalytic activity decreases in the following order of ligand environments (relative to that for A β 16-wt taken as unity):

$$\begin{aligned} \text{H}_2\text{O} (>4) > \text{H6,13A} \sim \text{H13,14A} (2.8) > \text{H13A} \sim \text{H14A} (1.5) \\ > \text{wt} (1.0) > \text{H6A} (0.8) > \text{Ac-A}\beta\text{16} (0.3) > \text{EDTA} (0) \end{aligned} \quad (15)$$

Aerobic oxidation of ascorbate may be represented by two redox half-reactions: two-electron oxidation of Asc to dehydroascorbate (D-Asc) coupled to two-electron reduction of O₂ to H₂O₂ (Fig. 10). Their respective reduction potentials at pH 7.0 are about +50 mV⁵¹ and +300 mV⁵² and hence the oxidation is a thermodynamically favored process. However, the reaction is very slow without a catalyst and the catalytic activity of a Cu centre depends on the efficiency of redox cycling between its Cu^I and Cu^{II} forms. This, in turn, is determined by both thermodynamic and kinetic factors. The molecular basis of the order of catalytic activity defined by eqn (15) may be analysed with regard to both factors.

Thermodynamically, the reduction potential of a favoured catalyst must fall within the range +50 and +300 mV. 'Free Cu²⁺ ion' is a robust catalyst likely due to its reduction potential (+153 mV vs. SHE) falling about midway in this range and the presence of exchangeable aqua ligands only. The formal reduction potential of a copper centre is linked *via* the Nernst equation (eqn (14)) to the *relative* binding affinities of the different oxidation states. Both Cu(I) and Cu(II) affinities in selected A β 16 peptides have been determined at the same pH = 7.4 in this work and are listed in Table 4. The calculated reduction potential for the copper centre in A β 16 ($E^{O'}$ = +178 mV) closely matches an experimental value ($E_{1/2}$ = +180 mV)²¹ determined by direct electrochemistry and predicts

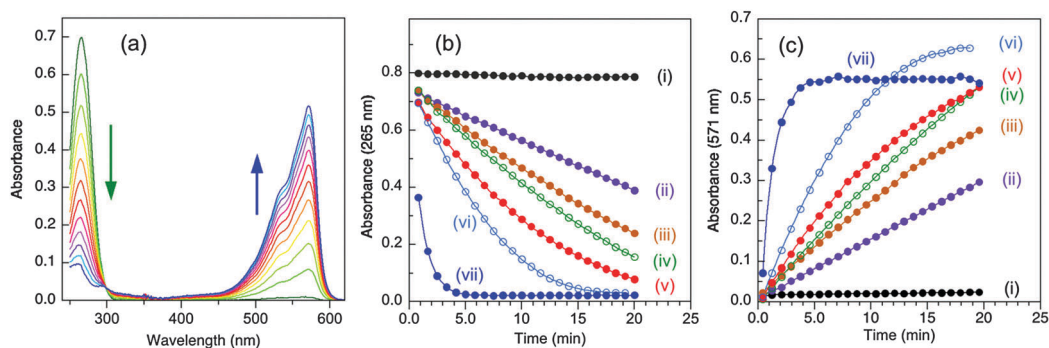


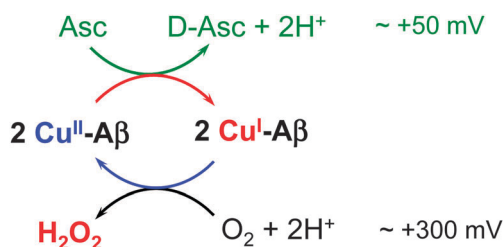
Fig. 9 Catalytic aerobic oxidation of Asc and production of H₂O₂. (a) UV-Vis monitoring of Asc consumption and resorufin formation that monitors H₂O₂ production. The spectrum of initial solution containing all components except Asc was subtracted from each recorded spectrum; (b) monitoring of Asc consumption at 265 nm and (c) resorufin production at 571 nm (proportional to H₂O₂ production), in the presence of Cu (5.0 μM) and Cu ligand (7.0 μM). Ligands are: (i) EDTA, (ii) Ac-A β 16; (iii) A β 16wt plus Ac-A β 16 (in 1 : 1 molar ratio); (iv) H6A; (v) A β 16wt; (vi) H13A (indistinguishable from H14A); (vii) free Cu²⁺ (note: the lower end absorbance and thus less final resorufin production in (c) was due to more extensive extra consumption of Asc by the rapidly produced Amplex Red radicals; see ref. 31). Other initial reaction conditions: [Amplex Red] = 45 μM , [HRP] = 0.35 U mL⁻¹, [Asc] = 50 μM . The reactions were conducted in air-saturated MOPS buffer (20 mM, pH 7.2–7.3) and started by introduction of catalyst.



Table 4 Copper binding affinities and relative catalytic rates of the Cu-Aβ16^a

Aβ16 peptide	Log K_D^I	Log K_D^{II}	E'_{calc} ^b (mV) (vs. SHE)	Relative catalytic rate	
				Asc consumption	H ₂ O ₂ production
wt	-10.4 ~ -7 ^c ~ -15 ^d	-10.0	+178 ~-24 ^e ~+448 ^e	1.00	1.00
Ac-Aβ16	-10.4	-8.3	+277	0.37	0.34
H6A	-10.0	-9.5	+183	0.75	0.78
H13A	-9.76	-9.7	+157	1.42	1.51
H14A	-9.95	-9.7	+168	1.42	1.52
H6,13A	> -8	-9.0	< +94	~ 2.8	~ 2.7
H13,14A	> -8.7	-9.5	< +106	~ 2.8	~ 2.7
Cu _{aq} ²⁺			+153	> 4 ^f	> 5 ^f

^a All data were acquired in MOPS buffer (10–50 mM, pH 7.4). ^b Calculated from eqn (14) using $E^0 = +153$ mV for the redox couple Cu²⁺/Cu⁺. ^c From ref. 15. ^d From ref. 14. ^e The consensus $K_D^I = 10^{-10.0}$ M was used for the calculation. ^f Reactions were too fast to estimate the initial rates reliably.

Fig. 10 Scheme for catalytic aerobic oxidation of Asc and production of H₂O₂.

it to be a competent catalyst. In contrast, the same calculations based on $\log K_D^I = -7^{15}$ or -15^{14} and the consensus $\log K_D^{II} = -10.0$ led to estimates of $E^0 = -24$ and $+448$ mV, respectively. Neither predicts catalytic function. The Cu-Aβ complexes, indeed, catalyse the aerial oxidation of Asc effectively although less actively than does Cu_{aq}²⁺. The structures of Cu(I) and Cu(II) complexes of the Aβ16 peptide are distinctly different: redox cycling will require energy input for structural reorganisation (Fig. 11). On the other hand, free Cu ions are under tight control in living cells and are present in tightly-bound forms only.

Acetylation of the N-terminal nitrogen has little impact on Cu(I) binding but removes a key Cu(II) ligand and consequently

shifts the predicted reduction potential positively to a value ($E^0 = +277$ mV) that promotes oxidation of Asc but does not favour reduction of O₂. This is consistent with the catalytic activity of Ac-Aβ16 being ~30% of that of Aβ16-wt (eqn (15)). Notably, addition of Cu²⁺ into an equimolar mixture of Aβ16 and Ac-Aβ16 produced an activity that was about the average of the combined activities of Aβ16 and Ac-Aβ16 (Fig. 9b and c; compare traces (ii), (iii) and (v)). The affinities of these two peptides for Cu(I) are identical but their affinities for Cu(II) differ considerably. These experiments suggest that the resting state of the catalyst in the presence of Asc is dominated by the Cu(I) form and that the catalytic activity of Cu-Aβ16 is suppressed by Ac-Aβ16. These results are also consistent with the properties of a copper centre bound to the second domain of the amyloid precursor protein (APP-D2): it exhibits similar affinities and catalytic activities to those of the copper centre in Ac-Aβ16.³²

Interestingly, APP may be processed *in vivo* by two enzymes, the α/β secretases, in two different pathways (*i.e.*, so called non-amyloidogenic and amyloidogenic pathways) to secrete two soluble forms of APP N-terminal fragments, sAPPα and sAPPβ. The former cleaved site is within the Aβ sequence between the position 16 and 17 whereas the latter is located right before the N-terminus of the Aβ sequence. Consequently, while both fragments contain Cu site in APP-D2, sAPPα differs from sAPPβ by having a C-terminal 16 amino acid extension equivalent to Ac-Aβ16 in term of Cu binding sites. Our experiments suggest that the Cu sites in APP-D2 and Ac-Aβ16 may be neuroprotective in a sense that ROS generation in the CNS by the Cu-Aβ catalyst may be suppressed partially by competitive Cu(I) binding with APP-D2 and Ac-Aβ16 (Fig. 9b and c, (iii) vs. (v)).³² Notably, it has been reported that sAPPα shows a range of neuroprotective and growth factor properties, including reduction of neuronal injury and improvement in memory performance, in contrast to the generally less potent sAPPβ.^{53–56}

Intriguingly, the predicted reduction potential for the copper centre in each of the three single His variants H6A, H13A and H14A is similar to that in the original Aβ16 peptide. However, mutation on His6 decreased activity by >20% while mutation of either of the other two increased the activity by ~50%, *i.e.*, the copper centres in the H13A and H14A copper

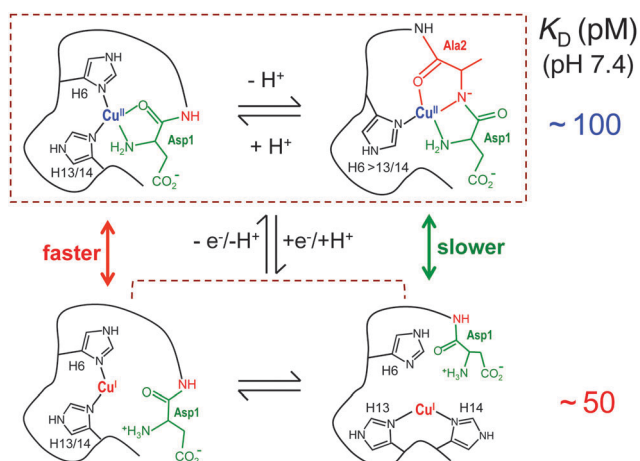


Fig. 11 Some chemical equilibria in solution at physiological pH.



complexes are twice as active as that in H6A (Fig. 9 and Table 4). An electrochemical study has proposed a pre-organisation mechanism for electron exchange between the Cu(I) and Cu(II) forms.⁵⁷ His6 is an important ligand for both Cu(I) and Cu(II) at pH 7.4 while either His13 and His14 can contribute but play a more important role in binding to Cu(I) than to Cu(II). The data suggests that retention of the His6 ligand is important for optimisation of the rate of electron exchange at pH 7.4 (Fig. 11).

Copper ions in the presence of the double His variants (H6,13A and H13,14) exhibit higher catalytic activities (Table 4). However, these data need to be interpreted cautiously, as the binding affinities of these variants are significantly weaker, in particular for Cu(I) (Table 4). The observed high activities may be related to a significant level of unbound or partially aquated Cu under the conditions. Addition of EDTA ($K_D = 10^{-15.9}$ M at pH 7.4) sequesters the copper into non-redox active Cu^{II}-EDTA that inhibits the catalytic activity completely.

Summary and concluding remarks

The A β peptides of 40–42 residues are the primary components of the extracellular senile plaques deposited in the AD brain and are proposed as a source of toxicity. The plaques are rich in transition metals Cu, Zn and Fe and the toxicity may be linked to oxidative stress induced by catalytic oxidation mediated *via* redox-active metal ions and copper ions in particular. The thermodynamic viability of a copper centre as a redox catalyst is linked to its reduction potential that, in turn, is determined by the relative stabilities of the two oxidation states (eqn (14)). However, these stabilities, as measured by dissociation constants K_D (affinities) for Cu(I) and Cu(II) bound to A β peptides, have remained controversial, primarily due to a lack of reliable detection probes and affinity standards.

All essential metal ligands in A β peptides are located within the first 16 residues and the fundamental Cu binding properties of A β 16 peptides have proven to be representative of those of other longer A β peptides. This work undertook a systematic quantitative investigation of the Cu(I) and Cu(II) binding properties of various A β 16 peptides by employing the Fs probe established recently for weaker Cu(I) binding²⁶ and a new highly fluorescent probe A β 16wwa introduced in this work for weaker Cu(II) binding. The key results are summarised following:

(i) A β 16 binds Cu(I) in three exchangeable two-coordinate sites defined by two His ligands out of the total of three (Fig. 4). The apparent binding affinity is pH dependant at pH < 7.5 and is estimated to be $K_D^I = 10^{-10.4}$ M for wild type A β 16 at pH 7.4. The N-terminal amine and backbone amides are not involved in Cu(I) binding.

(ii) The N-terminal nitrogen is a key Cu(II) ligand and appears to be part of a chelate ring ligand at pH 7.4 (Fig. 8). All three His ligands and at least one backbone amide are involved in Cu(II) binding but not simultaneously and only in several dynamic exchange modes (Fig. 8). His6 appears to play a

more important role in Cu(II) binding than does either His13 or His14. The apparent binding affinity for wild type A β 16 was estimated to be $K_D^{II} = 10^{-10.0}$ M at pH 7.4, consolidating the consensus data reported in several recent studies.

(iii) The dissociation constants K_D^I and K_D^{II} allow estimation of the formal reduction potential for the Cu-A β 16 complex as $E^{O'}/ = 178$ mV (*vs.* SHE).³⁶ This value matches $E_{1/2} = 180$ mV determined directly by cyclic voltammetry.²¹ Consequently, the complex is predicted to be a robust redox catalyst for oxidation of Asc ($\sim +50$ mV) by dioxygen ($\sim +300$ mV) to generate H₂O₂ and thus other ROS. Its catalytic activity is about 25% that of 'free Cu_{aq}²⁺' ($E^{O'}/ = +153$ mV), consistent with the distinct Cu(I) and Cu(II) binding modes present in A β 16 and the consequent pre-organisation energy required for the redox switching.

These new thermodynamic data consolidate the structural interpretations for the Cu-A β complexes deduced previously by spectroscopic investigations and provide molecular insight into the mechanism of ROS production by copper chemistry and of oxidative stress in Alzheimer's disease.

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- difference will be passed on to the Cu(I) affinities determined based on different potential standards and thus the reduction potential back-estimated *via* eqn (14) from K_D^I and K_D^{II} unless the same standard reduction potential (+164 mV or +130 mV) is used. For consistency, we choose to adopt the IUPAC value $E^\circ = +153$ mV for all applications and calculations.
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