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Sacrificial Cobalt–Carbon Bond Homolysis in Coenzyme B₁₂ as a Cofactor Conservation Strategy

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Abstract

A sophisticated intracellular trafficking pathway in humans is used to tailor vitamin B₁₂ into its active cofactor forms, and to deliver it to two known B₁₂-dependent enzymes. Herein, we report an unexpected strategy for cellular retention of B₁₂, an essential and reactive cofactor. If methylmalonyl-CoA mutase is unavailable to accept the coenzyme B₁₂ product of adenosyltransferase, the latter catalyzes homolytic scission of the cobalt–carbon bond in an unconventional reversal of the nucleophilic displacement reaction that was used to make it. The resulting homolysis product binds more tightly to adenosyltransferase than does coenzyme B₁₂, facilitating cofactor retention. We have trapped, and characterized spectroscopically, an intermediate in which the cobalt–carbon bond is weakened prior to being broken. The physiological relevance of this sacrificial catalytic activity for cofactor retention is supported by the significantly lower coenzyme B₁₂ concentration in patients with dysfunctional methylmalonyl-CoA mutase but normal adenosyltransferase activity.

The landmark accomplishment of elucidating the structure of vitamin B₁₂¹ was followed by clinical genetics studies on patients with inborn errors of B₁₂ metabolism, which hinted at a complex pathway for its intracellular trafficking.² These studies revealed that at least seven protein handlers assimilate and escort this reactive cofactor³ to the two enzymes that use it:

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Coordinates for the ATR structures have been deposited in the PDB (6D5X, 6D5K)

cob(II)alamin is formed under aerobic conditions was obtained by EPR spectroscopy. The large g spread and substantial Co hyperfine splittings are diagnostic of a square planar Co(II) coordination environment (Figures 2a and S3). Consistent with these results, the corresponding MCD spectrum showed an intense positively signed feature at $12\,500\text{ cm}^{-1}$ that is characteristic of 4C cob(II)alamin. This feature is considerably red-shifted from its counterpart in cob(II)inamide, which has an axial water ligand in solution (Figure 2b and S4).¹¹ The fate of Ado \cdot was investigated by NMR spectroscopy using [U- ^{13}C -Ado]-Cbl. The ^1H and ^{13}C chemical shifts of the product (Figure S5 and Tables S2 and S3) were nearly identical to those reported previously for 5'-hydroperoxyadenosine formed during aerobic photolysis of AdoCbl.¹² However, while 5'-hydroperoxyadenosine arises in aqueous solution from hydrolysis of a 5'-peroxy-AdoCbl intermediate and yields cob(III)alamin, 4C cob(II)alamin is produced in the ATR active site. Hence, 5'-hydroperoxyadenosine formed in the ATR reaction likely results from quenching of the initially formed alkylperoxy (Ado-OO \cdot) radical. The source of the hydrogen atom is not known.

We solved the structure of human ATR \cdot ATP crystals soaked with AdoCbl (Table S4). Electron density for AdoCbl was observed in two active sites (with occupancies of 1.00 and 0.86) and for ATP in the third site (Figures 2c and S6). The adenosine moieties in the sites containing ATP¹³ and AdoCbl are virtually superimposable (Figure 2d), held via electrostatic and hydrophobic interactions. Fortuitously, we also obtained a structure with AdoCbl and PPP_i bound (Figure 2e), which we ascribe to contaminating PPP_i in the ATP sample and to its high affinity for ATR \cdot AdoCbl (Table S1). The structures in the absence and presence of ATP are very similar, and at the current resolution, do not provide insights into how PPP_i labilizes the Co–C bond. AdoCbl is bound in a base-off state with Phe170 on a hydrophobic loop wedging between the DMB and the corrin ring, precluding water coordination (Figure 2f). The DMB tail in this structure is fully resolved in contrast to the *Lactobacillus reuteri* ATR structure where it is disordered.¹⁴ While AdoCbl transfer to MCM ($k = 0.63 \pm 0.06\text{ min}^{-1}$) and sacrificial formation of 5'-hydroperoxyadenosine and cob(II)alamin ($k = 0.082 \pm 0.01\text{ min}^{-1}$) both proceed slowly, the former is favored ~ 8 -fold over the latter. We note that CblC, a B₁₂ chaperone with decyanase and dealkylase activities, also exhibits low reaction rates ($\sim 0.003\text{--}0.2\text{ min}^{-1}$) that nevertheless support cellular B processing.^{15,16} Apparently, the low reaction rates are sufficient to support low flux through the B₁₂ trafficking pathway in which fidelity is prioritized over speed.¹⁷

What could be the physiological significance of AdoCbl synthesis by ATR at the expense of three ATP equivalents only to be followed by its cleavage in the absence of MCM? The kinetic choices facing the newly formed ternary ATR \cdot AdoCbl \cdot PPP_i complex in the absence of AdoCbl transfer to MCM are to form cob(II)alamin, as a strategy to sequester the cofactor or to release AdoCbl into solution. From a thermodynamic standpoint, binding of ATP and cob(II)alamin ($K_d = 0.08 \pm 0.01\text{ }\mu\text{M}$) to ATR is favored over AdoCbl ($K_d = 0.96 \pm 0.31\text{ }\mu\text{M}$) (Table S1). Our model predicts that AdoCbl levels should be reduced in MCM deficiency even though AdoCbl synthesis by ATR is unimpaired. To test this model, we examined AdoCbl levels in normal versus patient fibroblasts. In control fibroblasts ($n = 192$), $15.1 \pm 3.4\%$ of the intracellular B₁₂ pool is AdoCbl (Figure 3a); the majority exists as methylcobalamin. As expected for fibroblasts with ATR deficiency (due to mutations in the *cblB* locus), the AdoCbl pool size is reduced ($3.0 \pm 2.1\%$, $n = 45$, $p < 0.0005$). Consistent

with our model, the AdoCbl pool is smaller in patients with MCM (*mut*) deficiency, which is differentiated into groups containing either low ($8.3 \pm 6.9\%$ in *mut*⁻, $n = 53$, $p < 0.0005$) or undetectable ($8.1 \pm 4.4\%$ in *mut*⁰, $n = 195$, $p < 0.0005$) mutase activity.

Because of its low intracellular concentration, it is unlikely that free PPP_i binds to the binary $\text{ATR} \cdot \text{AdoCbl}$ complex ($K_d = 0.42 \pm 0.08 \mu\text{M}$, Figure S7) to trigger Co–C bond homolysis. Instead, we predict that the fate of AdoCbl is dictated by the kinetics of its transfer to MCM from the newly formed product complex versus Co–C bond homolysis. This model is indirectly supported by the properties of the R186Q patient mutation.¹⁸ The in vitro activity of R186Q ($11 \pm 3.6 \text{ min}^{-1}$) and wild-type ($14.8 \pm 3.5 \text{ min}^{-1}$) ATR are comparable. Arg186 forms an intersubunit salt bridge with Asp90 only when B_{12} is bound (Figure 2d). The mutant protein binds B_{12} in the base-on state as monitored by EPR and absorption spectroscopy (Figure 3b,c), revealing the tenuous hold of ATR on the base-off state. The homologous mutation in *L. reuteri* ATR also led to bound base-on B_{12} .¹⁹ The R186Q mutation destabilizes the ternary $\text{ATR} \cdot \text{AdoCbl} \cdot \text{PPP}_i$ complex but does not affect ATP binding (Figure S8 and Tables S1 and S5). Furthermore, while the affinity for cob(II)alamin is unaffected ($\leq 0.2 \mu\text{M}$), the affinity for AdoCbl is significantly diminished. The product of Co–C bond homolysis in the R186Q mutant resembles base-on 6C Np–Cbl (Figure 2c, inset) but is only seen when ATR active sites are present in vast excess over AdoCbl. Hence, the inability to sequester AdoCbl via direct transfer to MCM predisposes the R186Q mutant to cofactor release into solution (Figure 3d). We speculate that the twin challenges of reducing base-on cob(II)alamin (which has a lower redox potential than the base-off form²⁰), and weakened affinity for AdoCbl, contribute to methylmalonic aciduria in patients with the biallelic R186Q mutation. We recently reported that itaconyl-CoA inactivates MCM by rapid cob(II)alamin accumulation on the enzyme.²¹ Human MCM binds cob(II)alamin with a lower affinity than AdoCbl (Table S1), which begs the question as to how cob(II)alamin loss is averted from MCM into solution.

A cytoplasmic strategy for cofactor sequestration is exemplified by MS, whose synthesis is translationally up-regulated by B_{12} .²² Prioritization of the B_{12} supply for MS, an essential enzyme, over MCM, which serves an anaplerotic function, is suggested by the prevalence of holo-MS ($\sim 100\%$)²³ versus fractional B_{12} saturation of MCM ($\sim 25\%$)²⁴ in liver. Furthermore, under conditions of B_{12} deficiency, the magnitude of cofactor loss from MCM is greater than from MS.²⁴ We now report a cellular strategy for B_{12} retention that exploits an unprecedented chemical versatility whereby AdoCbl is synthesized via nucleophilic chemistry but cleaved via radical chemistry within the same active site. The mechanism for mitochondrial import of B_{12} is unknown and the possibility that ATR-induced Co–C bond homolysis serves to return cob(II)alamin to the cytoplasm remains open.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

ACKNOWLEDGMENTS

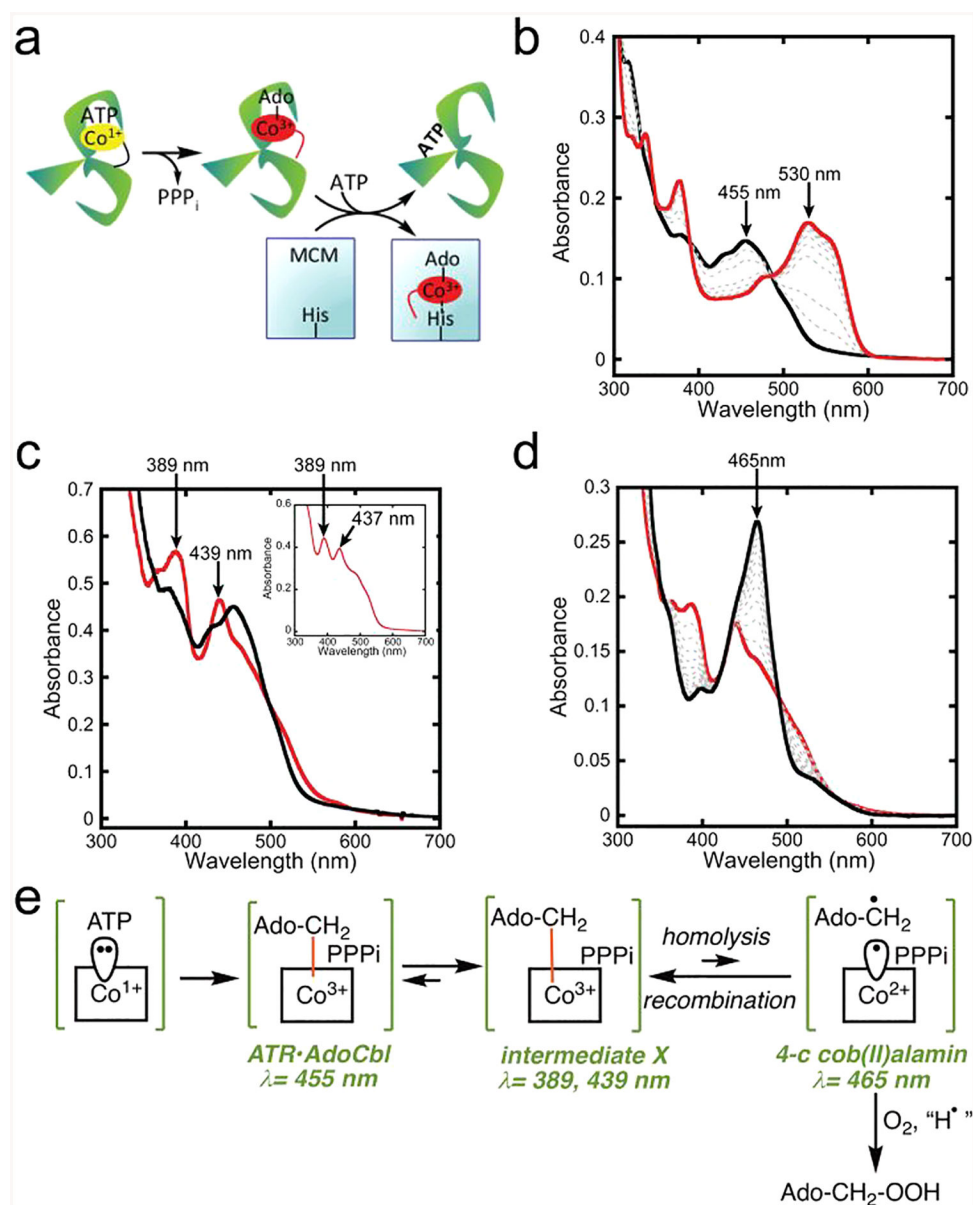
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REFERENCES

- (1). Hodgkin DC; Kamper J; Mackay M; Pickworth J; Trueblood KN; White JG Structure of vitamin B₁₂. *Nature* (London, U. K.) 1956, 178, 64–66. [PubMed: 13348621]
- (2). Watkins D; Rosenblatt DS Inborn errors of cobalamin absorption and metabolism. *Am. J. Med. Genet., Part C* 2011, 157, 33–44.
- (3). Gherasim C; Lofgren M; Banerjee R Navigating the B₁₂ road: assimilation, delivery and disorders of cobalamin. *J. Biol. Chem* 2013, 288, 13186–13193. [PubMed: 23539619]
- (4). Banerjee R Radical carbon skeleton rearrangements: catalysis by coenzyme B₁₂-dependent mutases. *Chem. Rev* 2003, 103 (6), 2083–2094. [PubMed: 12797824]
- (5). Banerjee RV; Matthews RG Cobalamin-dependent methionine synthase. *FASEB J.* 1990, 4, 1450–1459. [PubMed: 2407589]
- (6). Padovani D; Labunska T; Palfey BA; Ballou DP; Banerjee R Adenosyltransferase tailors and delivers coenzyme B₁₂. *Nat. Chem. Biol* 2008, 4 (3), 194–196. [PubMed: 18264093]
- (7). Yamanishi M; Labunska T; Banerjee R Mirror “base-off” conformation of coenzyme B₁₂ in human adenosyltransferase and its downstream target, methylmalonyl-CoA mutase. *J. Am. Chem. Soc* 2005, 127, 526–527. [PubMed: 15643868]
- (8). Froese DS; Kochan G; Muniz JR; Wu X; Gileadi C; Ugochukwu E; Krysztofinska E; Gravel RA; Oppermann U; Yue WW Structures of the human GTPase MMAA and vitamin B₁₂- dependent methylmalonyl-CoA mutase and insight into their complex formation. *J. Biol. Chem* 2010, 285 (49), 38204–38213. [PubMed: 20876572]
- (9). Schrauzer GN; Grate JH Sterically induced, spontaneous cobalt-carbon bond homolysis and beta-elimination reactions of primary and secondary organocobalamins. *J. Am. Chem. Soc* 1981, 103, 541–546.
- (10). Waddington MD; Finke RG Neopentylcobalamin (Neopentyl-B₁₂) Cobalt-Carbon Bond Thermolysis Products, Kinetics, Activation Parameters, and Bond-Dissociation Energy - a Chemical-Model Exhibiting 10⁶ of the 10¹² Enzymatic Activation of Coenzyme-B₁₂s Cobalt-Carbon Bond. *J. Am. Chem. Soc* 1993, 115(11), 4629–4640.
- (11). Stich TA; Yamanishi M; Banerjee R; Brunold TC Spectroscopic evidence for the formation of a four-coordinate Co²⁺cobalamin species upon binding to the human ATP:cobalamin adenosyltransferase. *J. Am. Chem. Soc* 2005, 127 (21), 7660–7661. [PubMed: 15913339]
- (12). Schwartz PA; Frey PA 5'-Peroxyadenosine and 5'-peroxyadenosylcobalamin as intermediates in the aerobic photolysis of adenosylcobalamin. *Biochemistry* 2007, 46 (24), 7284–7292. [PubMed: 17503776]
- (13). Schubert HL; Hill CP Structure of ATP-Bound Human ATP:Cobalamin Adenosyltransferase. *Biochemistry* 2006, 45 (51), 15188–15196. [PubMed: 17176040]
- (14). St. Maurice M; Mera P; Park K; Brunold TC; Escalante-Semerena JC; Rayment I Structural characterization of a human-type corrinoid adenosyltransferase confirms that coenzyme B₁₂ is synthesized through a four-coordinate intermediate. *Biochemistry* 2008, 47 (21), 5755–5766. [PubMed: 18452306]
- (15). Kim J; Gherasim C; Banerjee R Decyanation of vitamin B₁₂ by a trafficking chaperone. *Proc. Natl. Acad. Sci. U. S. A* 2008, 105(38), 14551–14554. [PubMed: 18779575]
- (16). Kim J; Hannibal L; Gherasim C; Jacobsen DW; Banerjee R A human vitamin B₁₂ trafficking protein uses glutathione transferase activity for processing alkylcobalamins. *J. Biol. Chem* 2009, 284 (48), 33418–33424. [PubMed: 19801555]
- (17). Hannibal L; Kim J; Brasch NE; Wang S; Rosenblatt DS; Banerjee R; Jacobsen DW Processing of alkylcobalamins in mammalian cells: A role for the MMACHC (cblC) gene product. *Mol. Genet. Metab* 2009, 97 (4), 260–266. [PubMed: 19447654]
- (18). Lerner-Ellis JP; Gradinger AB; Watkins D; Tirone JC; Villeneuve A; Dobson CM; Montpetit A; Lepage P; Gravel RA; Rosenblatt DS Mutation and biochemical analysis of patients belonging to the cblB complementation class of vitamin B₁₂-dependent methylmalonic aciduria. *Mol. Genet. Metab* 2006, 87 (3), 219–225. [PubMed: 16410054]
- (19). Park K; Mera PE; Escalante-Semerena JC; Brunold TC Spectroscopic characterization of active-site variants of the PduO-type ATP:corrinoid adenosyltransferase from *Lactobacillus reuteri*:

insights into the mechanism of four-coordinate Co(II)corrinoid formation. *Inorg. Chem* 2012, 51 (8), 4482–4494. [PubMed: 22480351]

- (20). Lexa D; Saveant JM Electrochemistry of vitamin B₁₂. I. Role of the base-on/base-off reaction in the oxidoreduction mechanism of the B_{12r}-B_{12s} system. *J. Am. Chem. Soc* 1976, 98, 2652–2658. [PubMed: 4489]
- (21). Shen H; Campanello GC; Flicker D; Grabarek Z; Hu J; Luo C; Banerjee R; Mootha VK The Human Knockout Gene CLYBL Connects Itaconate to Vitamin B₁₂. *Cell* 2017, 171 (4), 771–782. [PubMed: 29056341]
- (22). Oltean S; Banerjee R A B₁₂-responsive IRES element in human methionine synthase. *J. Biol. Chem* 2005, 280 (38), 32662–8. [PubMed: 16051610]
- (23). Chen Z; Chakraborty S; Banerjee R Demonstration that the mammalian methionine synthases are predominantly cobalamin-loaded. *J. Biol. Chem* 1995, 270, 19246–19249. [PubMed: 7642596]
- (24). Kennedy DG; Cannavan A; Molloy A; O'Harte F; Taylor SM; Kennedy S; Blanchflower WJ Methylmalonyl-CoA mutase (EC 5.4.99.2) and methionine synthetase (EC 2.1.1.13) in the tissues of cobalt-vitamin B₁₂ deficient sheep. *Br. J. Nutr* 1990, 64 (3), 721–732. [PubMed: 1979918]

**Figure 1.**

PPP_i induces Co–C homolysis in ATR-bound AdoCbl. (a) Scheme showing the role of ATR (green) in AdoCbl synthesis and transfer to MCM. (b) Transfer of AdoCbl from ATR (black) to MCM (red). (c) Addition of PPP_i to AdoCbl bound to ATR (black) results in the formation of intermediate X (red) under anaerobic conditions. Inset shows the spectrum of base-off NpCbl. (d) Under aerobic conditions, X (red) converts to 4C cob(II)alamin (black). (e) Scheme showing conversion of ATR-bound AdoCbl to X and to 4C cob(II)alamin and 5'-hydroperoxyadenosine.

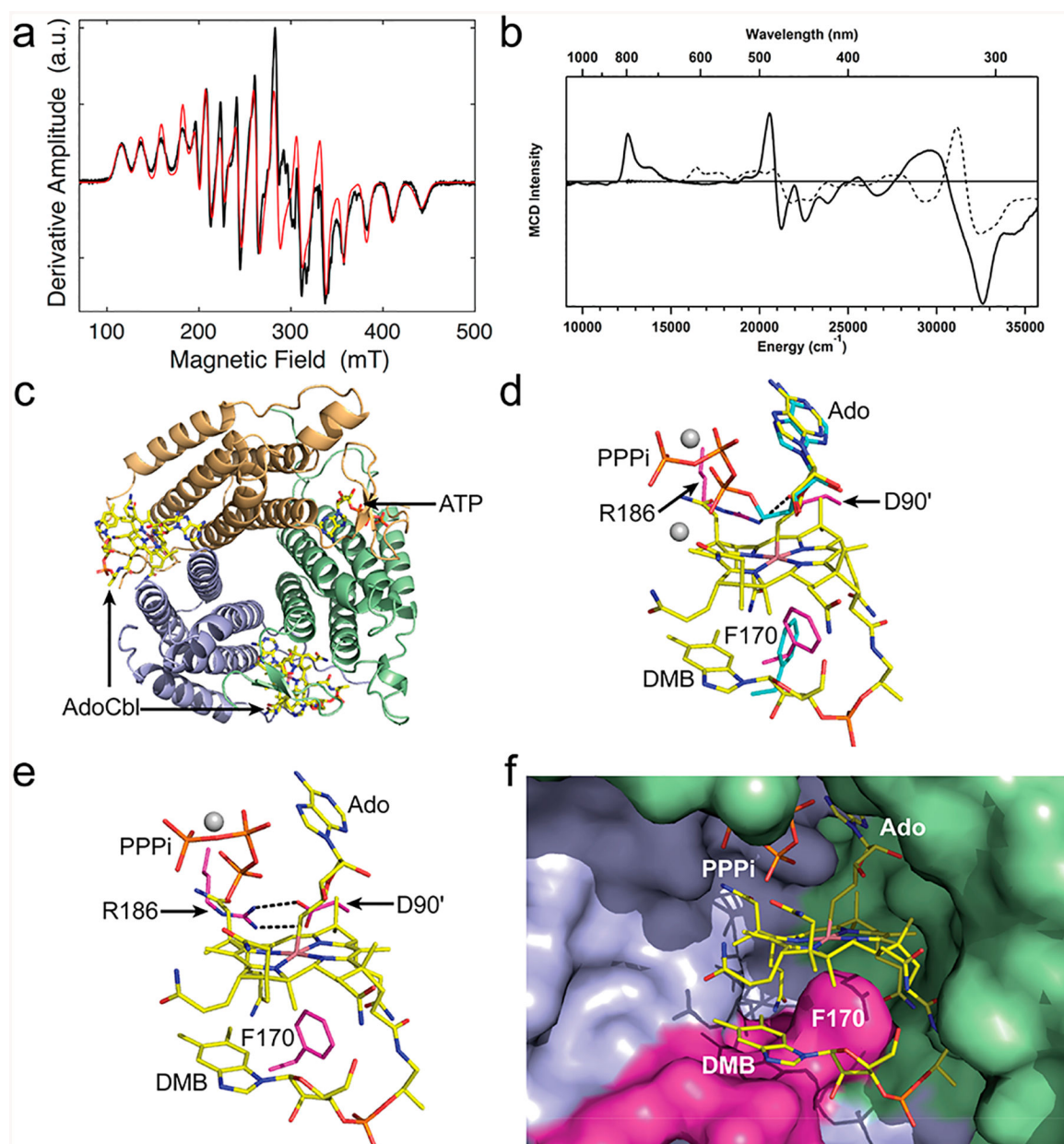


Figure 2.

Spectroscopic and structural characterization of B_{12} bound to ATR. (a) EPR spectrum of 4C cob(II)alamin formed after addition of $PPPi$ under aerobic conditions (black). The red line corresponds to the simulated spectrum. (b) MCD spectra of 4C cob(II)alamin (solid line) generated under the same conditions as (a) and of 5C cob(II)inamide (dashed lines) as a reference. (c) Structure of human ATR showing two subunits occupied by AdoCbl and a third by ATP. (d) Superposition of the adenosine rings in ATP (cyan, PDB: 21DX) and AdoCbl (yellow, PDB: 6D5K, this study) bound to ATR. (e) Close-up of the ATR·AdoCbl· $PPPi$ active site structure (PDB: 6D5X, this study). (f) Close-up of human ATR showing that the DMB tail, tucked below the corrin ring, is kept from coordinating to the

cobalt by Phe170 on a hydrophobic loop (pink). Adjacent subunits that form the active site are in blue and green. The gray spheres in panels d and e represent magnesium.

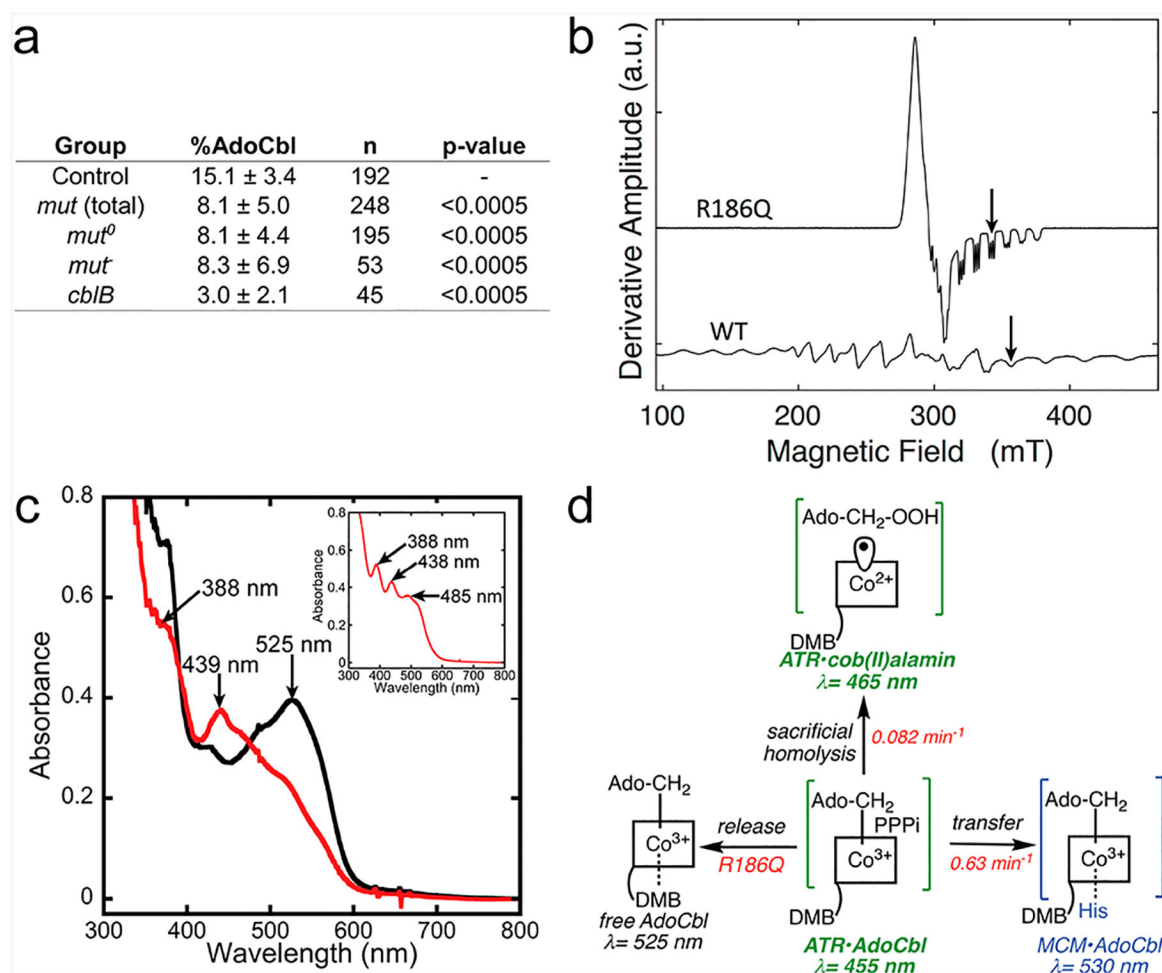


Figure 3.

Impact of ATR deficiency on AdoCbl synthesis. (a) AdoCbl as a percent of total cobalamin in fibroblasts from ATR (*cbIB*) or MCM (*mut*) deficiency versus control individuals. The *mut*⁻ and *mut*⁰ subgroups represent fibroblasts with diminished or undetectable MCM activity, respectively. (b) Comparison of the EPR spectra of cob(II)alamin bound to R186Q versus wild-type (WT) ATR. The presence of the triplet superhyperfine splittings in the high-field lines of the R186Q spectrum is caused by the presence of axial nitrogen coordination (absent in WT). (c) Absorbance spectrum of 6C AdoCbl bound to R186Q ATR (black). Addition of PPP_i under anaerobic conditions gives rise to a spectrum (red) that resembles “base-on” NpCbl (inset). (d) Intermediate X partitions between transfer to MCM, release into solution or undergoes sacrificial Co–C bond homolysis leading to retention of tightly bound cob(II)alamin.