

Study of the Individual Cytochrome b₅ and Cytochrome b₅ Reductase Domains of Ncb5or Reveals a Unique Heme Pocket and a Possible Role of the CS Domain

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Running Head: Unique heme pocket and possible role of CS in human Ncb5or

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SUPPELMENTAL DATA

FIGURE LEGENDS

Supplemental Figure 1. Sequence alignment of Cyb5A from vertebrates. Residue numbers and helices of human Cyb5A corresponding to those in Figure 1B are labeled. Conserved amino acid residues in each group are marked by “*” (identical, heme-ligands in red) or “-” (chemically similar). All are annotated from genomic sequences except those from human, mouse, rat, bovine, horse, pig, rabbit, Xenopus and Zebrafish are confirmed by transcript or protein sequences. GenBank accession numbers are: Human (NP_683725), Chimpanzee (XP_001135885), Monkey (XP_001083378), Orangutan (ENSPPYP00000010369), Guinea pig (ENSCPOP00000010893), Mouse (NP_080073), Rat (NP_071581), Bovine (NP_776458), Horse (NP_001153204), Pig (NP_001001770), Goat (ABQ12619), Dog (XP_533373), Rabbit (P00169), Opossum (XP_001373630), Zebrafish (XP_002195467), Chicken (NP_001001748), Xenopus laevis (NP_001086707), Xenopus tropicalis (NP_001015979), Rice fish (ENSORLT00000004278), Zebrafish (NP_998300), salmon (ACI66502), pufferfish (ENSTNIP00000008519), Fugu (ENSTRUP00000013474), Stickleback (ENSGACP00000002650), C. Armatus (CAE75863), Rainbow smelt (ACO09548). A 92% identity or a 96% similarity is found for human and rat Cyb5A sequences.

Supplemental Figure 2. Sequence alignment of Ncb5or-b₅ core from animals. Residue numbers and helices of human Ncb5or-b₅ corresponding to those in Figure 1B are labeled. Conserved amino acid residues in each group are marked by “*” (identical, heme-ligands in red) or “-” (chemically similar). All sequences are annotated from genomic sequences except sequences of human, mouse and rat have been confirmed by cloned cDNAs. Ncb5or is also named Cyb5R3, b5/b5R, and b5+b5R. GenBank accession numbers are: Human (NM_016230), Chimpanzee (XM_518614), Monkey (XM_001085835), Guinea pig

(EB369672), Mouse (NM_024195), Rat (NM_133427), Bovine (NM_001038159), Horse (XM_001499913), Sheep (DY519717), Dog (XM_532219), Squirrel (CO734025), Platypus (XM_001512881), Opossum (XM_001375853), Zebrafinch (XM_002188637), Chicken (XM_001233870), *Xenopus laevis* (NM_001016756), Little skate (CV222314), Rice fish (AM140533), Zebrafish (NM_001020660), Salmon (DY707237), Stickleback (DN714575), Pimephales (DT192112), Pea aphid (XM_001948299), Beetle (XM_963135), Honeybee (XM_394412), Jewel Wasp (XM_001601866), *Drosophila* (NM_137575), Louse (XM_002428283), Deer tick (XM_002401084), Mosquito (XM_001650886), Tunicate (XR_053035), Lancelet (XM_002603916), *C.elegans* (NM_001026613), *Teladorsagia* (CB038604), *Trichuris* (BM277379), Sea urchin (CD307914), Coral (EZ038676), Sea anemone (DV081463), *Trichoplax* (XM_002112883), Hydra (XM_002165807). A 93% identity or a 100% similarity is found for human and rat Ncb5or-b5 sequences.

Supplemental Figure 3. 2Fo-Fc electron density map contoured at 1σ showing the two orientations of the heme molecules in Ncb5or-b₅ associated with subunit A (left) and subunit B (right).

Supplemental Figure 4. Thermostability of wild-type Ncb5or-b₅ and its two mutants, b₅W114A and b₅R113A. The percent of heme loss (Y axis) was monitored by the decrease in A413 and plotted as a function of temperature. Thermal denaturation experiments were performed on a Varian Carey 100 Bio UV/Visible spectrophotometer equipped with a Peltier-thermostated multiple cell holder and a dedicated temperature probe accessory (± 0.1 °C). Solutions were buffered to pH 7.0 using 50 mM potassium phosphate. Experiments were performed in quartz cuvettes of 1 cm path length and 1 mL sample volume, equipped with tight-fitting PTFE lids. The temperature was increased in increments of 2 °C, and samples were equilibrated for 5 min after reaching each desired temperature. Thermal denaturation midpoints (T_m values) were obtained by fitting plots of absorbance at the Soret band λ_{max} (412 nm) vs. temperature to a previously described equation describing a two-state equilibrium (1). T_m (mid-point temperature) = 72.0 (Ncb5or-b₅), 73.4 (Ncb5or-b₅R113A), 71.5 (Ncb5or-b₅W114A), 73.5 (human Cyb5A).

Supplemental Figure 5. Circular dichroism (CD) spectra of human Ncb5or-b₅. (A) Far UV (190 – 250 nm) and (B) visible (350 – 500 nm) spectra of wild-type Ncb5or-b₅ and its two mutants, b₅W114A and b₅R113A, monitored at a concentration of 17.4, 14.5, and 15.3 μ M heme, respectively. CD spectra were recorded on a JASCO-815 spectropolarimeter equipped with a Peltier thermostated cell holder.(2) Solutions were buffered to pH 7.0 using 10 mM sodium phosphate. All spectra were obtained at 0.1 nm with a response time of 4 sec and a scan rate of 50 nm/min at room temperature. Final spectra represent the average of at least five scans. Background correction was accomplished by subtraction of a spectrum recorded at the same temperature and containing only buffer. Far-UV spectra are reported in terms of mean residue ellipticity ($[\theta]$, in $\text{deg}\cdot\text{cm}^2\cdot\text{dmol}^{-1}$), calculated as $[\theta] = [\theta]_{\text{obs}}[\text{MRW}/(10lc)]$ where $[\theta]_{\text{obs}}$ is the ellipticity measured in millidegrees, MRW is the polypeptide mean residue molecular weight (molecular weight divided by the number of amino acids), c = sample concentration in mg/mL, and l = optical path length of the cell in cm. Near-UV and visible region spectra are reported in terms of molar ellipticity ($[\theta]$, in $\text{deg}\cdot\text{cm}^2\cdot\text{dmol}^{-1}$), calculated as $[\theta] = [\theta]_{\text{obs}}[\text{MW}/(10lc)]$ where MW is the molecular weight of the polypeptide.

Supplemental Table 1. Crystallographic data for human Ncb5or-b₅ refined to 1.25 Å resolution.

| | |
|--|---|
| Data Collection | |
| Unit-cell parameters (Å, °) | $a = 38.48, b = 56.37, c = 42.56, \beta = 100.67$ |
| Space group | $P2_1$ |
| Resolution (Å) ¹ | 30.0-1.25 (1.28-1.25) |
| Wavelength (Å) | 1.0000 |
| Temperature (K) | 100 |
| Observed reflections | 185,062 |
| Unique reflections | 49,981 |
| $\langle I/\sigma(I) \rangle$ ¹ | 13.0 (1.9) |
| Completeness (%) ¹ | 99.0 (93.6) |
| Redundancy ¹ | 3.8 (3.1) |
| $R_{\text{sym}}(\%)$ ^{1,2} | 5.8 (72.4) |
| Refinement | |
| Resolution (Å) | 30.0-1.25 |
| Reflections (working/test) | 46,492 / 2,489 |
| $R_{\text{factor}} / R_{\text{free}}(\%)$ ³ | 14.7 / 17.3 |
| No. of atoms (protein (A:B) / Heme / sulfate /water) | 742:743 / 172 / 10 / 145 |
| Model Quality | |
| R.m.s deviations | |
| Bond lengths (Å) | 0.013 |
| Bond angles (°) | 1.477 |
| Average B factor (Å ²) | |
| All Atoms | 15.9 |
| Protein (chain A/B) | 15.2 / 15.3 |
| Heme | 11.0 |
| Sulfate | 27.7 |
| Water | 28.0 |
| Coordinate error based on R_{free} (Å) | 0.043 |
| Ramachandran Plot (chain A/B) | |
| Most favored (%) | 97.1 |
| Additionally allowed (%) | 2.9 |

1) Values in parenthesis are for the highest resolution shell.

2) $R_{\text{sym}} = \sum_{hkl} \sum_i |I_i(hkl) - \langle I(hkl) \rangle| / \sum_{hkl} \sum_i I_i(hkl)$, where $I_i(hkl)$ is the intensity measured for the i th reflection and $\langle I(hkl) \rangle$ is the average intensity of all reflections with indices hkl .

3) $R_{\text{factor}} = \sum_{hkl} ||F_{\text{obs}}(hkl)| - |F_{\text{calc}}(hkl)|| / \sum_{hkl} |F_{\text{obs}}(hkl)|$; R_{free} is calculated in an identical manner using 5% of randomly selected reflections that were not included in the refinement.

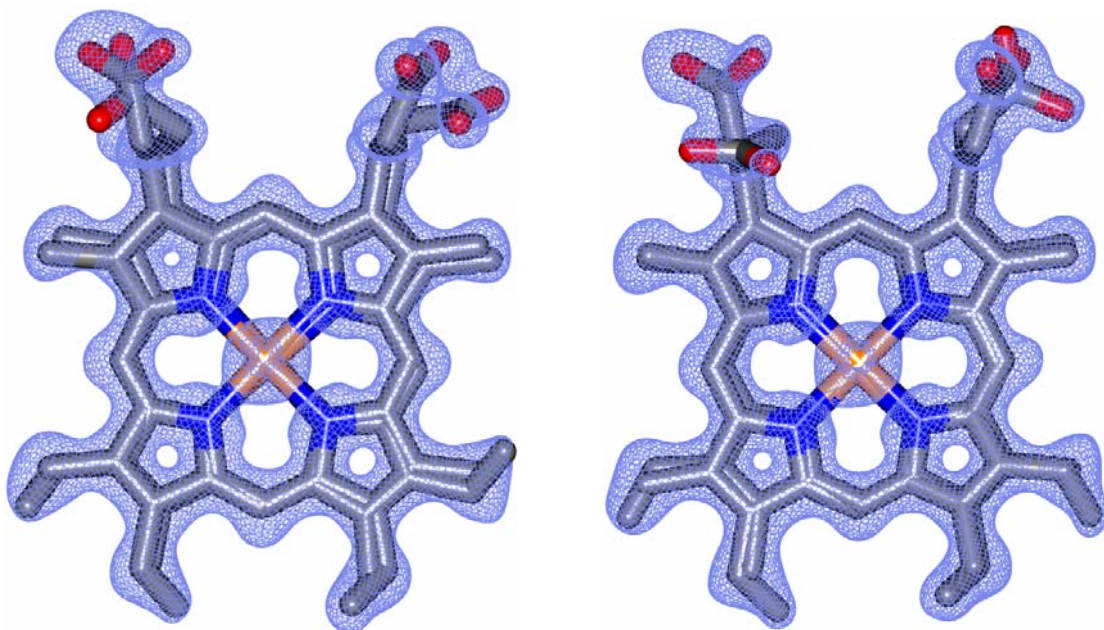
Supplemental Table 2. Summary of interplanar dihedral angles and EPR signals of Ncb5or and other members of the cytochrome b₅ superfamily. Interplanar dihedral angles of bis-histidine ligands were calculated with Mercury (<http://www.ccdc.cam.ac.uk/products/mercury/>). N/A: not available.

| Protein Name (source) | PDB # | g_{\max} or g_z | Interplanar dihedral angles | Reference |
|--|-------|---------------------|--|------------|
| Ncb5or (human) | 3LF5 | 3.56 | 83.2° / 81.3° (His ⁸⁹ ,His ¹¹²) | This study |
| Ncb5or (rat) | N/A | 3.54 | N/A | (3) |
| Cyb5A (human) | N/A | 3.09 | N/A | This study |
| Cyb5A (bovine) | 1CYO | 3.1 | 21.2° (His ⁴⁴ ,His ⁶⁸) | (4,5) |
| Cyb5A (rat) | N/A | 3.05 | N/A | (3) |
| Cyb5B (rat) | 1B5M | 3.03 | 11.9° (His ⁴² ,His ⁶⁶) | (6,7) |
| Cytochrome b ₅ (M. domestica) | 2IBJ | 3.07 | 23.8° (His ³⁹ ,His ⁶³) | (2,8) |
| Cytochrome b ₅ (A. suum) | 1X3X | N/A | 46.1° (His ³⁸ ,His ⁶²) | (9) |
| Cytochrome b558 (E. vacuolata) | 1CXY | N/A | 43.9° (His ⁴² ,His ⁷⁰) | (10) |
| Sulfite oxidase (chicken) | 1SOX | 2.93 | 9.6° (His ⁴⁰ ,His ⁶⁵) | (11,12) |
| Cytochrome b ₂ (yeast) | 1LTD | 2.99 | 42.3° (His ⁴³ ,His ⁶⁶) | (13,14) |
| Nitrate reductase (spinach) | N/A | 2.98 | N/A | (15) |

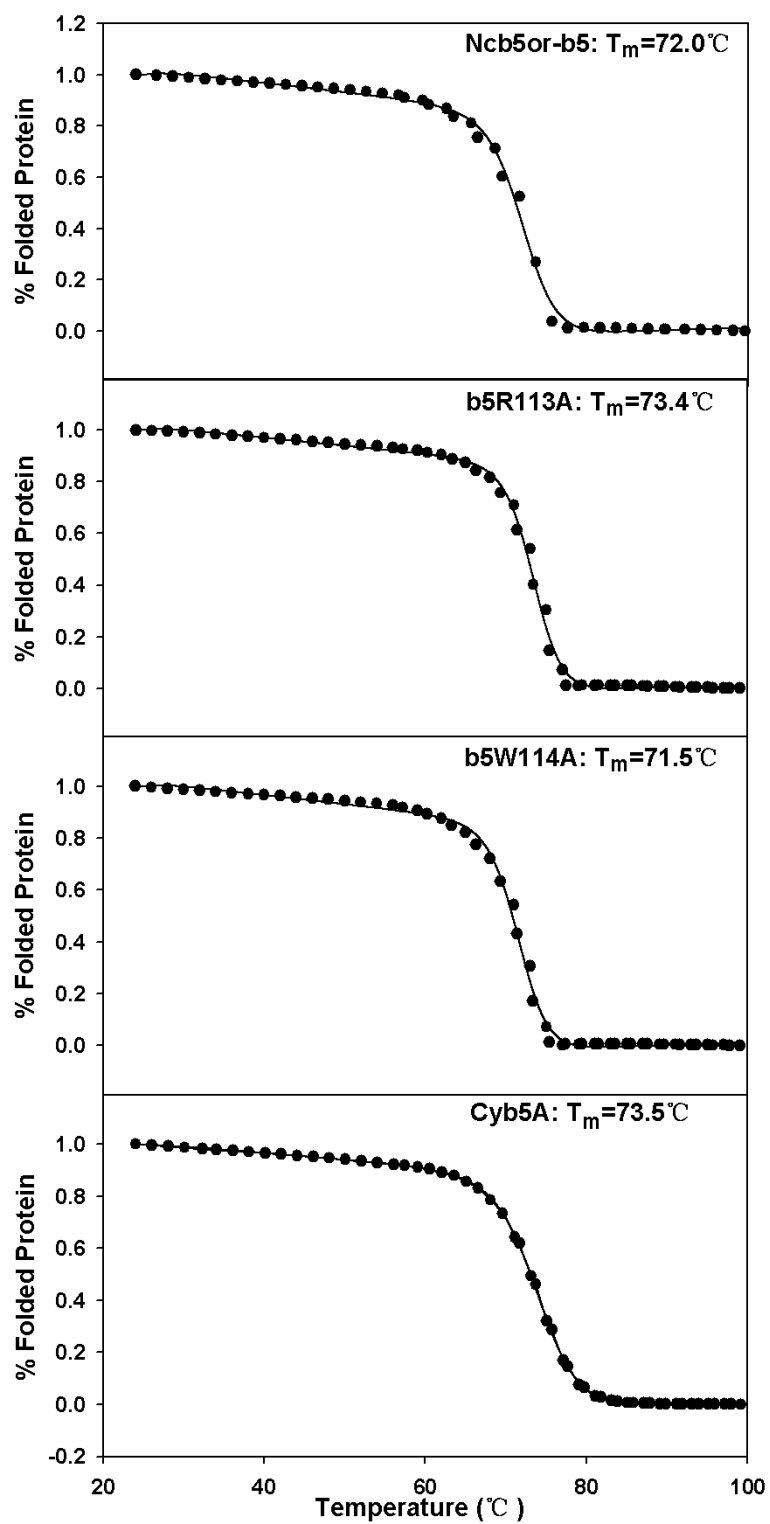
Supplemental Table 3. Kinetic properties of Cyb5A mutants tested for electrostatic interaction with Cyb5R3. Heme ligands are His⁴⁴ and His⁶⁸ in Cyb5A, corresponding to His⁸⁹ and His¹¹² in Ncb5or, respectively. ^a Both k_{cat} and K_M values are the ratio against that of wild-type Cyb5A. ^b N116 is displaced relative to D71 given the difference in local secondary structure, but it is the closest residue spatially and is pointed generally in the same direction.

| Cyb5A | k_{cat} ^a | K_M ^a | Helix | Residue in Ncb5or | Ref. |
|---------------------------------------|------------------------|--------------------|----------------|-------------------|------|
| E42A | 1.0 | 1.2 | $\alpha 2$ | E87 | (16) |
| E43A | 1.0 | 3.1 | $\alpha 2$ | Y88 | (16) |
| E48A | 1.3 | 1.7 | $\alpha 3$ | E93 | (17) |
| E49A | 0.8 | 0.6 | $\alpha 3$ | D94 | (17) |
| E48A/E49A | 1.3 | 1.1 | $\alpha 3$ | - | (17) |
| E53A | 1.2 | 1.2 | $\alpha 3$ | R98 | (17) |
| E61A | 1.3 | 1.4 | $\alpha 4$ | E106 | (17) |
| E64A | 1.0 | 1.0 | $\alpha 4$ | D109 | (16) |
| D65A | 1.0 | 1.5 | $\alpha 4$ | Q110 | (17) |
| D71A | 0.7 | 6.4 | $\alpha 5$ | N116 ^b | (16) |
| E74A | 1.1 | 1.8 | $\alpha 5$ | S119 | (16) |
| E48/E49/E53/E61/D65→A | 0.9 | 1.4 | $\alpha 3,4$ | - | (17) |
| E42/E43/E48/E49/E53/D58/E61/E64/D65→A | 0.9 | 6.1 | $\alpha 2,3,4$ | - | (17) |

Supplemental Figure 3.

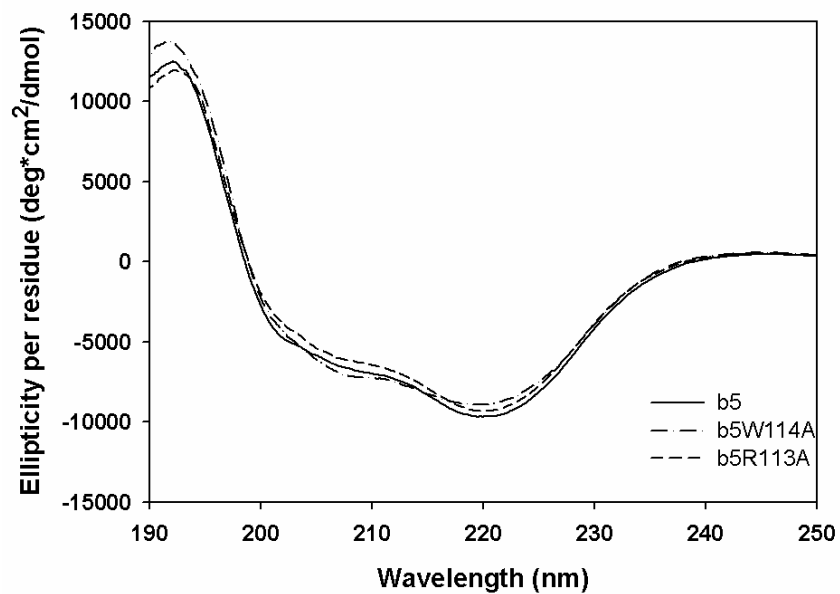


Supplemental Figure 4.

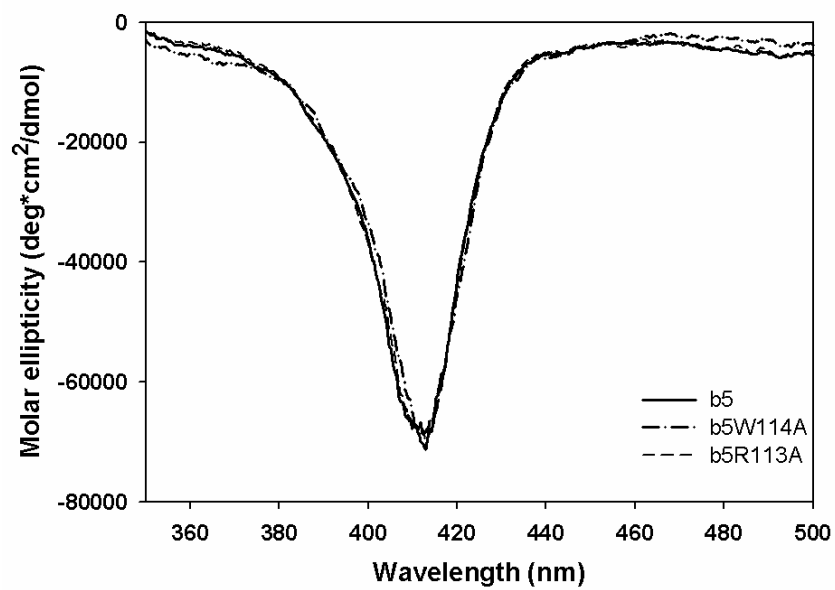


Supplemental Figure 5.

A.



B.



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