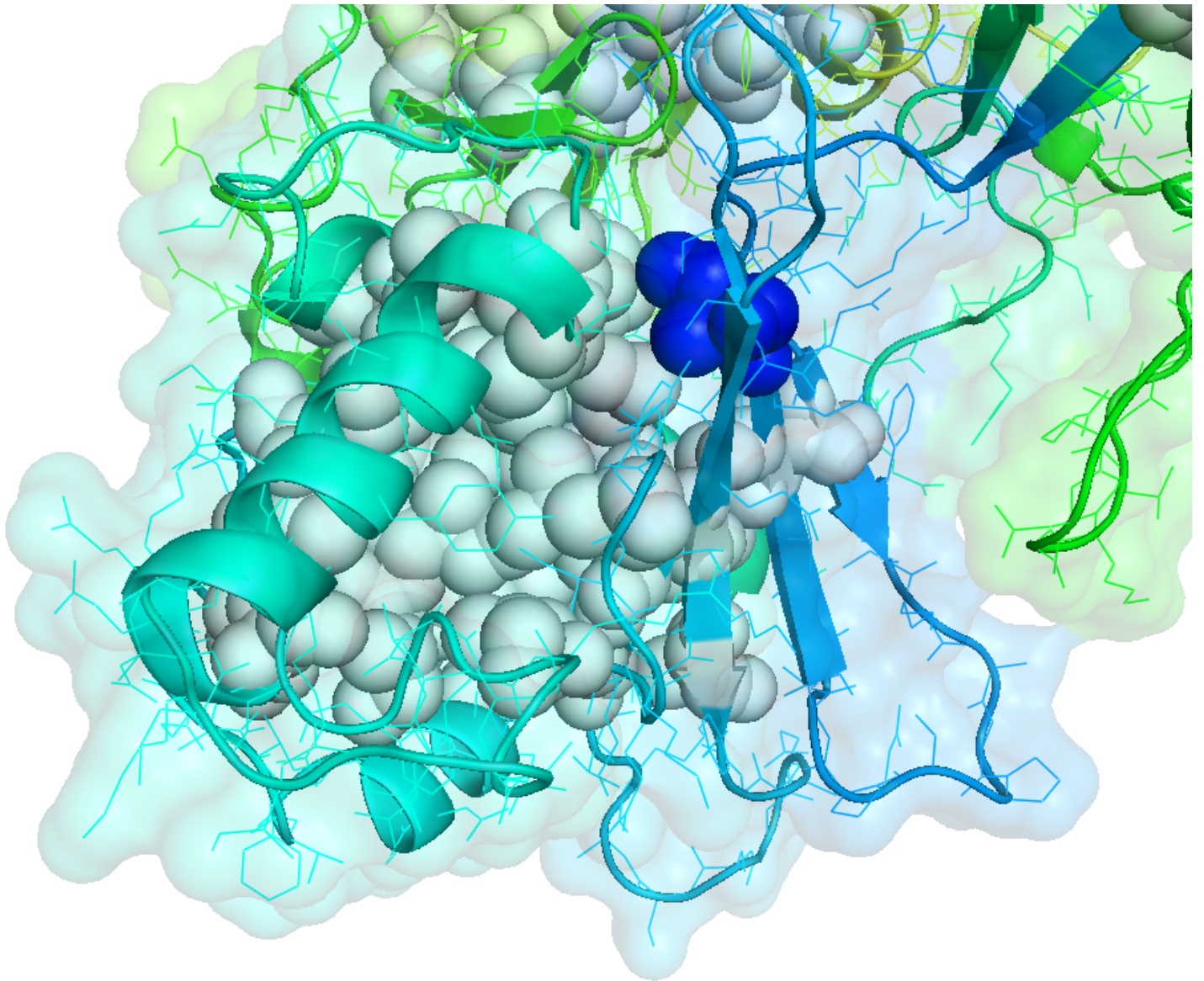
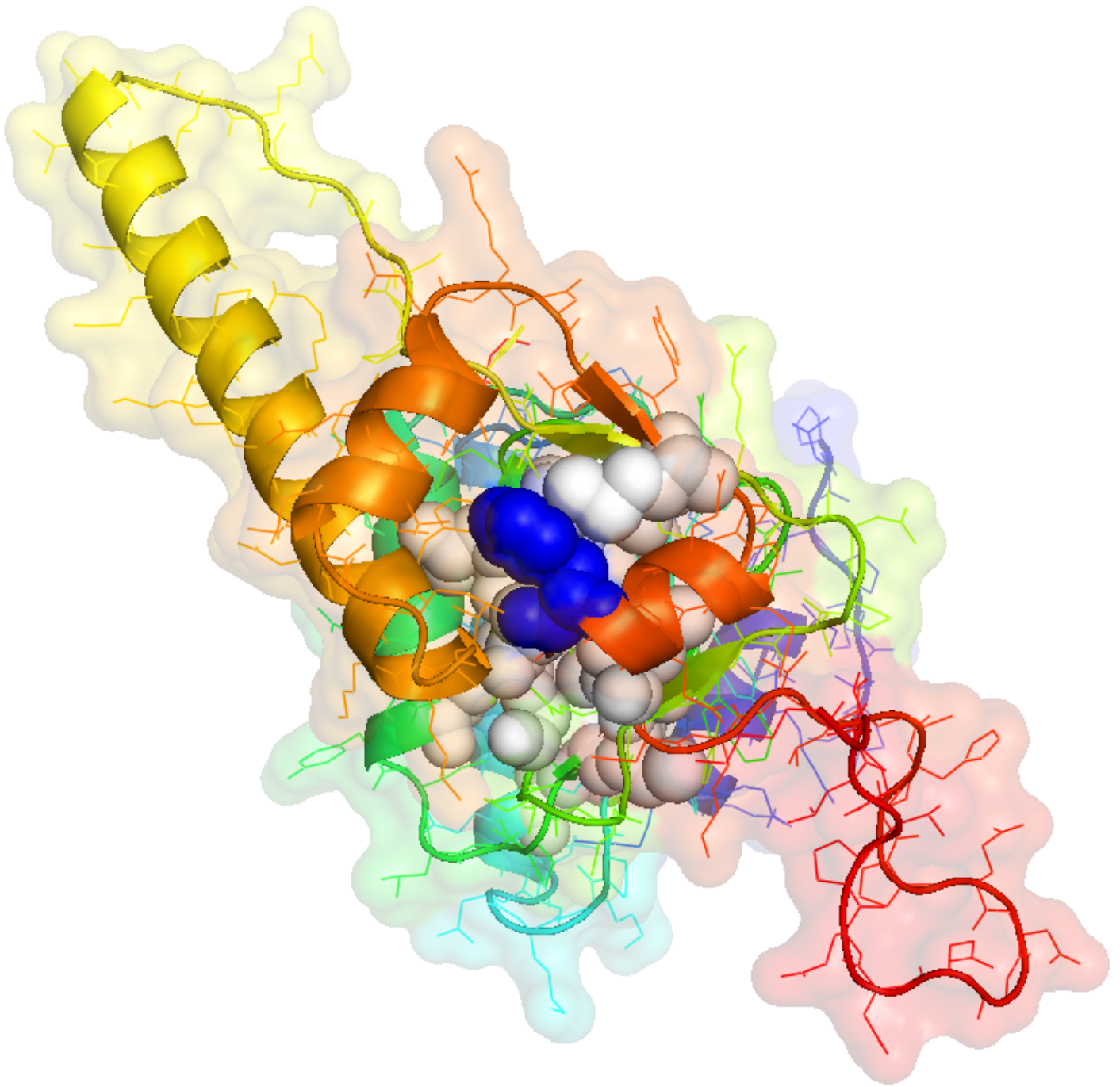


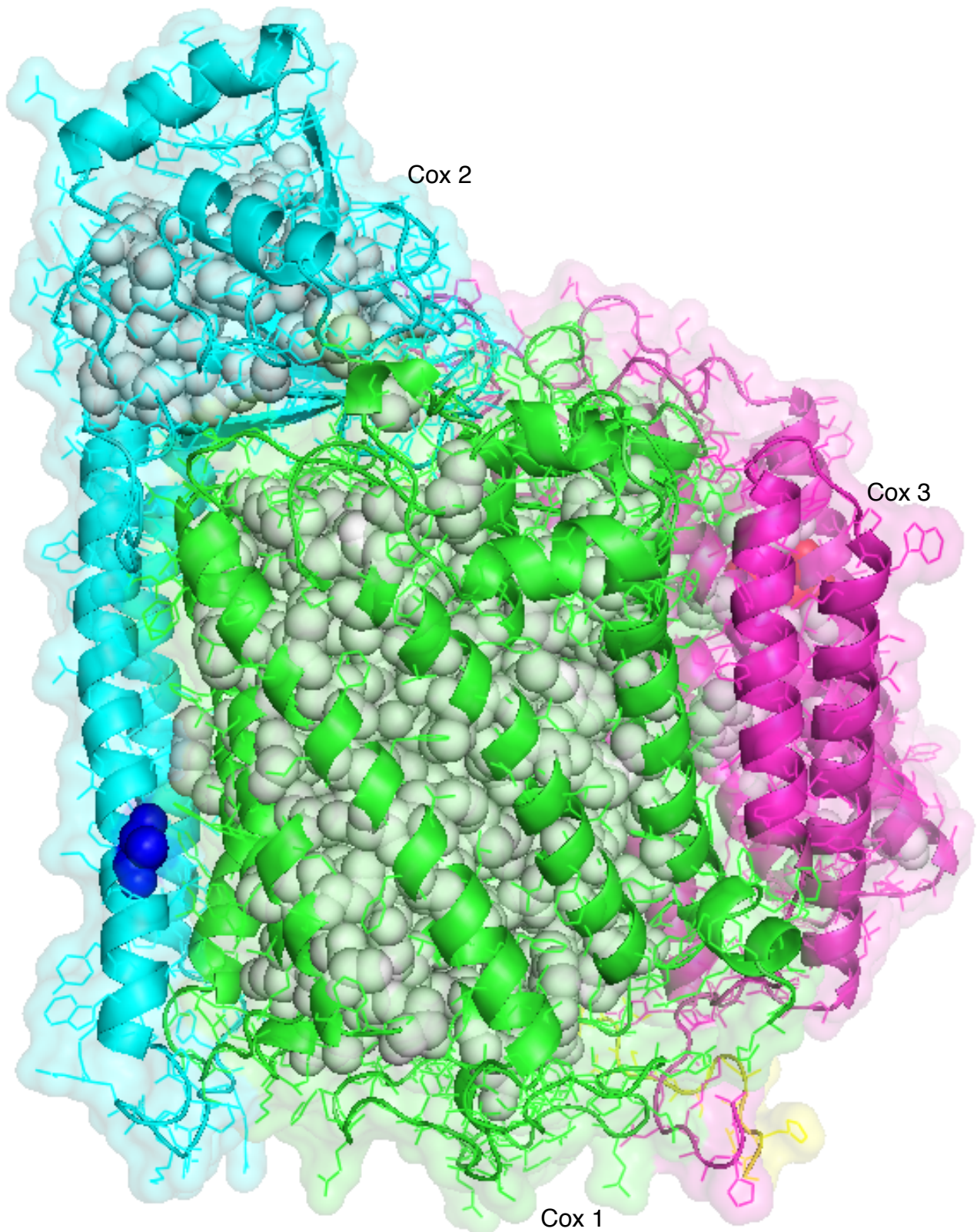
Supplemental Data 1. Three-dimensional structure of *Escherichia coli* RpoA N-terminal domain (PDB ID, 1BDF[B]). The backbone is depicted in ribbon model and residues forming structural core are in white space-filling model. The red residue is included in the core, and it is edited from Ser to Phe in *Arabidopsis thaliana* chloroplast. The residue is Ile61 in *E. coli* RpoA.



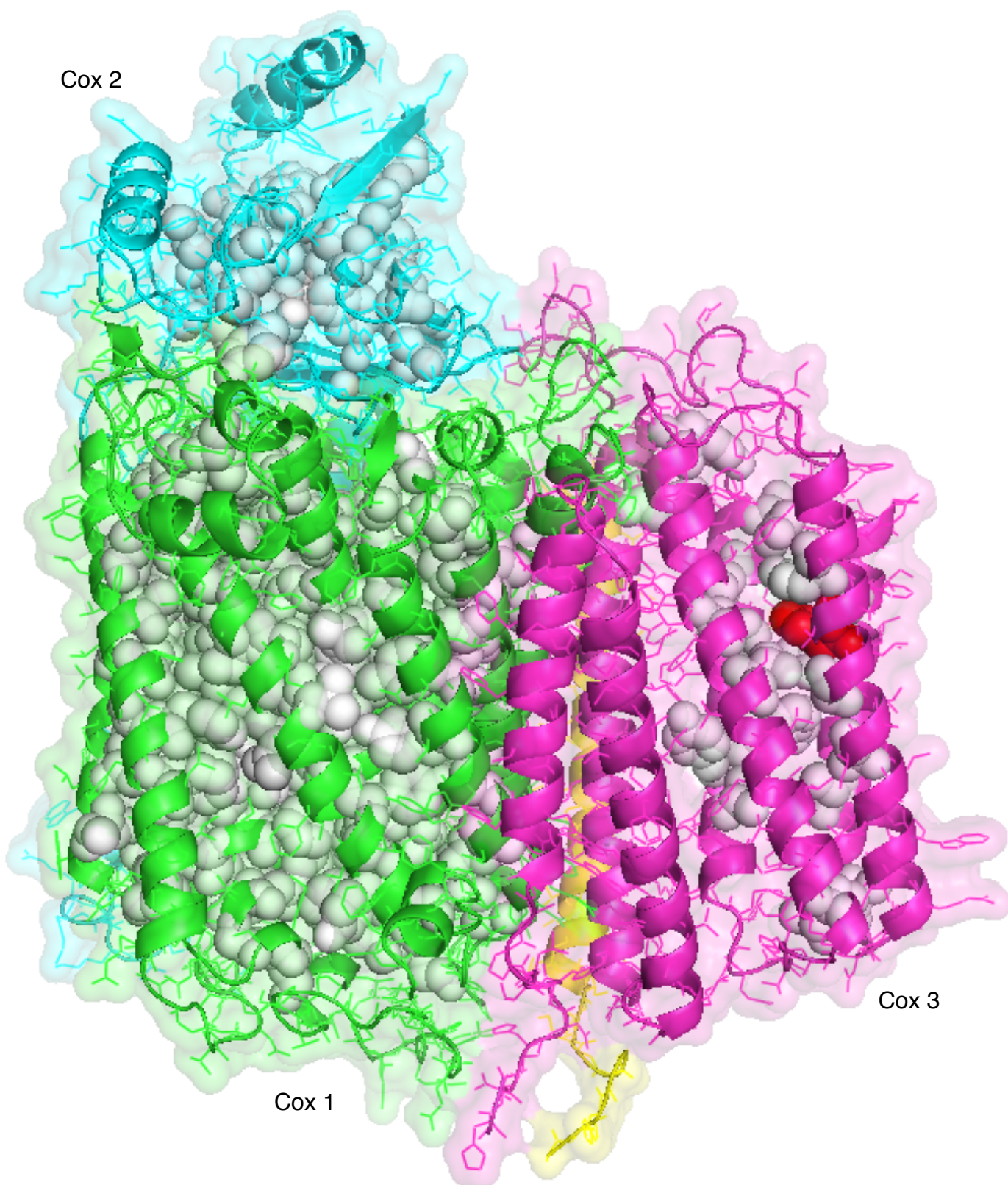
Supplemental Data 2. Three-dimensional structure of *Saccharomyces cerevisiae* RpoB C-terminal domain (PDB ID, 2E2I[B]). The backbone is depicted in ribbon model and residues forming structural core are in white space-filling model. The blue residue is not in the core, but located at the interface of two domains. It is edited from Ser to Phe in *Arabidopsis thaliana* chloroplast. The residue is Ile191 in *S. cerevisiae* RpoB.



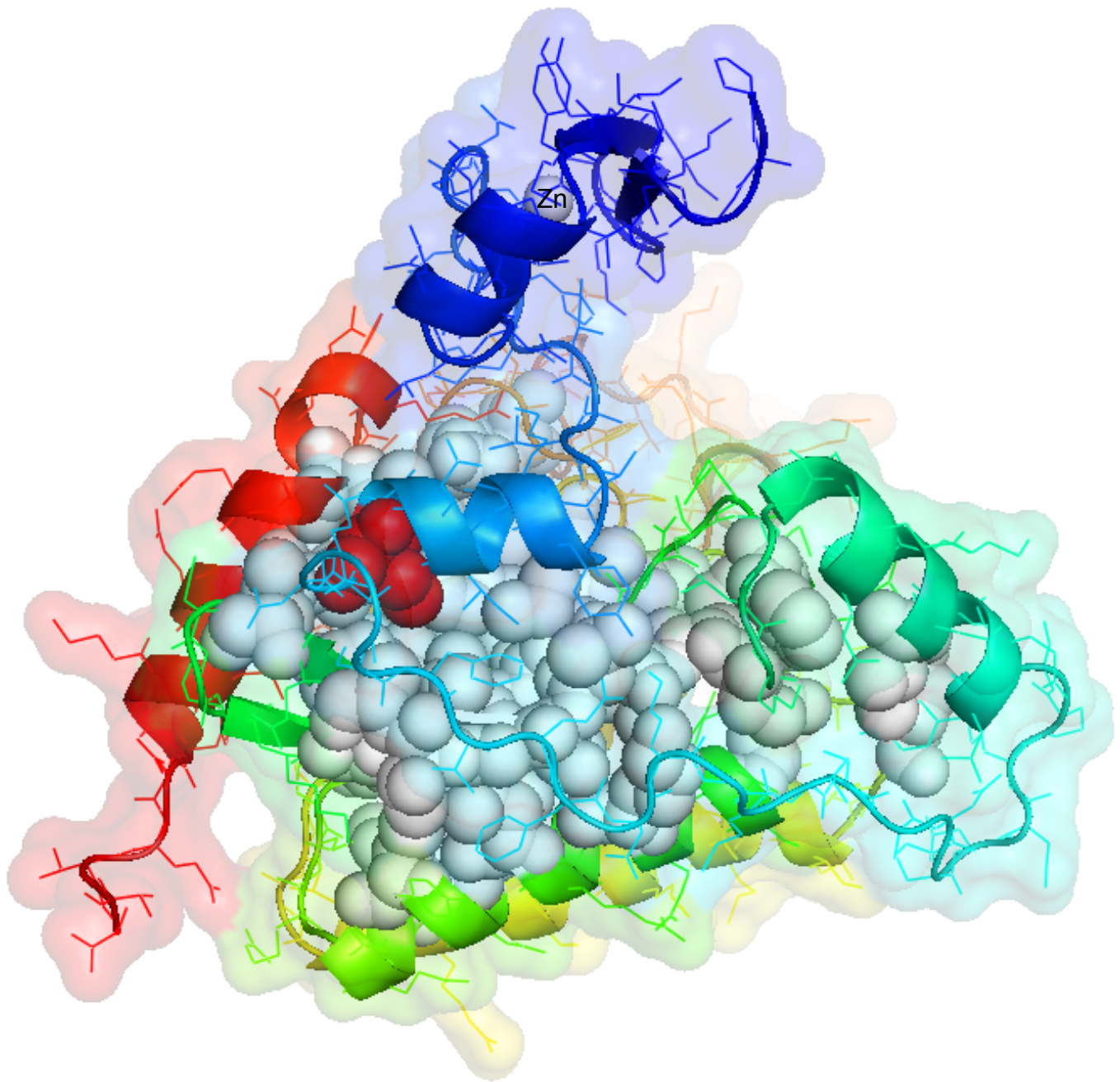
Supplemental Data 3. Three-dimensional structure of *Homo sapiens* ClpP (PDB ID, 1TG6[E]). The backbone is depicted in ribbon model and residues forming structural core are in white space-filling model. The blue residue is not in the core, but located close to the surface of the protein. It is edited from His to Tyr in *Arabidopsis thaliana* chloroplast. The residue is Phe173 in *H. sapiens* ClpP.



Supplemental Data 4. Three-dimensional structure of *Rhodobacter sphaeroides* cytochrome oxidase (PDB ID, 1M56). The backbone is depicted in ribbon model and each chain is in different color. Residues forming structural core are in white space-filling model. The blue residue in Cox2 is not in the core, but located at the interface to the membrane. It is edited from Ser to Leu in *Oryza sativa* mitochondrion. The residue is Thr44 in *R. sphaeroides* Cox2.



Supplemental Data 5. Three-dimensional structure of *Rhodobacter sphaeroides* cytochrome oxidase (PDB ID, 1M56). The backbone is depicted in ribbon model and each chain is in different color. Residues forming structural core are in white space-filling model. The red residue in Cox3 is in the core and is edited from Ser to Leu in *Oryza sativa* mitochondrion. The residue is Phe177 in *R. sphaeroides* Cox3.



Supplemental Data 6. Three-dimensional structure of *Staphylococcus aureus* AccD (PDB ID, 2F9I[B]). The backbone is depicted in ribbon model and residues forming a structural core are in white space-filling model. The red residue is included in the core, and it is edited from Ser to Leu in *Arabidopsis thaliana* chloroplast. The residue is Ile45 in *S. aureus* AccD.

Supplementary Data 7. Multiple amino acid sequence alignments showing identical RNA editing sites in genes derived from different organelles. The summary of the data is shown in Table 2.

Color scheme in the alignment:

- X: no letter is edited.
- X: 1st letter is edited.
- X: 2nd letter is edited.
- X: 3rd letter is edited.
- X: 1st and 2nd letters are edited.
- X: 1st and 3rd letters are edited.
- X: 2nd and 3rd letters are edited.
- +: Corresponding RNA editing sites between genes from chloroplasts and genes from mitochondria

Data 1: amino acid alignment (partial) of *rps7*

(the original data at <http://cib.cf.ocha.ac.jp/RNAEDITING/align.php?id=g0003>)

- 1:chloroplast *Adiantum capillus-veneris* [AY178864_67]
- 2:chloroplast *Anthoceros formosae* [AB086179_73]
- 3:mitochondrion *Beta vulgaris* [AB008450_1]
- 4:mitochondrion *Brassica napus* (rape) [AP006444_26]
- 5:mitochondrion *Cycas taitungensis* [AP009381_41]
- 6:mitochondrion *Daucus carota* (carrot) [AY521591_1]
- 7:mitochondrion *Oryza sativa Japonica* Group [BA000029_6]

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1:..SDPIYRNRLANMLVDRLKNGKKSLAYQIFYQAMKRIRQKTNRNPLSVLRQAVRGVTPDVVTETKRVGGSTYRVPIEVVPAKGKA 93
2:..PDPIYRNRLVNLVNRILRNGKKSLAYRILYGAMRNIRRA TKKNPLSVLRQAVRRVTPNVTVKARRVGGSTYQVPIEIESSQGKA 98
3:..GLDSEQQLIKKLVNFRMKEGKRTRVRAIVYQTFHRLAR-TEGDVIKLMIDAVENIKPICKVEKVRVAGTIYDVPGIVARDRQQT 86
4:..GLDGEQQLIKKLVNFRMKEGKRTRVRAIVYQTFHRPAR-TERDVIKLMVDAVENIKPICEVAKVGVAGTIYDVPGIVARDRQQT 86
5:..GLDGKQKQLINKSVNFRITIDGKRTRKARAIAYQTFHRPAR-TERDVIKLLVNAVENIKPICEAGKVRVAGTTYNVPEIVARDRQQT 169
6:..DLDGEQQLIKKLVNFRMKEGKRTRVRAIVYKTLHRLGR-TERDVIKLMVDALENIKPICKVERVGRAGTIYDVPGIVARDRQQT 86
7:..DFDGEQKELIKKLVNFRMIDGKRTRVRAIVYKTFHRLAR-TERDVIKLMVDAVDNIKPICEVVKVGVAGTIYDVPGIVARDRQQT 86

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+ (195)

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1:LAIRWLLIACRKR---GRSMALRLSDELIDAARNSGSAIRKKEETHKVAEANKAFAHFR*-- 151
2:LAIRWLLVASKKRP---GRNMAFKLSYELIDAARDNGNAVRKREETHRMAEANRAFAHFR*-- 156
3:LAIRWILEAAFKRRISYRISLEKCLFDEILDAYRKRGISRKKRENLHGLASANRSFAHFRWW* 149
4:LAIRWILEAAFKRRISYRISLEKCLFAEILDAYQKRGSAARRKRENLHGLASTNRSFAHFRWW* 149
5:LAIRWILGAAFKRRISNGIGSDKCLSAETLDAHRKRGIARKKRDPHEPASTNRSFAHLRWW* 232
6:LAIRWTLEAAFKRRISYRISLEQCLFDEILDAYRKRGIIVRKKRGNLHRLASTNRSIAHFRWW* 149
7:LAIRWIFGAAFKRRISYRISLEKCLFAEILDAYRKRGISRKKRGNLHGLASTNRSFAHFRWW* 149

```

Data 2: amino acid alignment of *rps19*

(the original data at <http://cib.cf.ocha.ac.jp/RNAEDITING/align.php?id=g0014>)

- 1:chloroplast *Adiantum capillus-veneris* [AY178864_64]
- 2:chloroplast *Anthoceros formosae* [AB086179_69]
- 3:mitochondrion *Cycas revoluta* [AY345867_1]
- 4:mitochondrion *Oenothera berteriana* [X61030_1]
- 5:mitochondrion *Oryza sativa Japonica Group* [BA000029_37]
- 6:mitochondrion *Petunia x hybrida* [X57283_1]

+ (16)

```
1:-MARSSKRGPFVANHLIREIRNLNIQKKRKLITWRSASAIVPIMIGHTIAVHNGREHLPIYVTD1DRMVGHKLGEFVPT2RNFRGHA 84
2:-MTRL3LKKGPFVAYHLL4EKIEDLN5IKREK6IIVTWSR1ASTIVPTMIGHTIAVYNGQEHLPIYITDRMVGHKLGEFALTRVFKGHA 84
3:MPRRSIW1KG2SFVDA3FL4LKMR5SKREN6ISSR1KI---WSRR2SSILPE3FVDC4FVRIYNGKT5FVRCKITEGKVGHK6FGEFA1FARKRKPSR 82
4:MPRRSIW1KG2SFVDA3FL4LRM5KKKRD6LLNRKI---WLR1RSIL2LE3FVNC4SVRIYNGKT5PVRCKITEEKVGHK6F*EFA1FTRKRR2CSR 82
5:MPRRSIW1KG2SFVDA3FL4FR5IKKNRES6LSR1KI---WSRR2SSILPE3FVDC4SVLIYNGKT5FVRCKITEGKVGHK6FGEFA1FTRRRR2RPYQ 82
6:MPRR1SIW2KG3SFVDA4FL5LRM6KKKRD1LLENR2KI---WSRR3SSILPE4FVDC5FVRIYNGKT6FVRCKITEGKVGHK1FGEFA2FTRKRR3PSR 82
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1:KSDKGSRR*---- 93
2:KSDKKSRR*---- 93
3:TDIGPGRK-GKR* 94
4:TNIGLGRKRGKK* 95
5:TNRGKGRK-GKK* 94
6:TNIGPGRKRGKK* 95
```


Data 3: amino acid alignment (partial) of *ndhB/nad2*
 (the original data at <http://cib.cf.ocha.ac.jp/RNAEDITING/align.php?id=g0075>)

- 01:chloroplast *Adiantum capillus-veneris* [AY178864_2]
- 02:chloroplast *Anthoceros formosae* [AB086179_72]
- 03:chloroplast *Arabidopsis thaliana* (thale cress) [AJ002490_1]
- 04:chloroplast *Hordeum vulgare* [X90650_1]
- 05:chloroplast *Thuja plicata* (giant arborvitae) [EF421241_1]
- 06:mitochondrion *Arabidopsis thaliana* (thale cress) [X96535_2]
- 07:mitochondrion *Megaceros aenigmaticus* [EU660574_34]
- 08:mitochondrion *Plagiopus oederi* [AJ299548_1]
- 09:mitochondrion *Triticum aestivum* (bread wheat) [Y14433_1]
- 10:mitochondrion *Triticum aestivum* (bread wheat) [Y14435_1]

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+ (186)                                     + (242)
01: ... LSGYTKRDMRSNEATMKFLMSGASSSILLYGFSILLYGLSGGQL--QLDKIVDGI-IFNR-YGSI-IYLSAAFTTAGTAFKLSLF 230
02: ... LSGYTKKDVRSNEAAMKYLLMGGASSSILAYGFSWLYGLSGGKI--QLQEIFNGL-INTQMYNSTSISIVLIFIIAGIAFKLSLV 229
03: ... LSGYTKKDIRSNEATMKYLLMGGASSSILVYGFWSWLYGSSGGEI--ELQEI V NGL-INTQMYNSPGISIALIFITVVGIGFKLSLA 247
04: ... LSGYTKRDLRSNEATMKYLLMGGASSSILVYGFWSWLYGLSGGEI--ELQEI V NGL-INTQMYNSPGISIALIFITVGLGFKLSLA 247
05: ... LSGYTKRDIRSNEAIMKYLLMGGTSSSILAYGLSWLYGLSGGEI--EIQEI ANGL-INTQMYNSPGIWIALLSVTVGIAFKLSLV 229
06: ... IAASKRKSEFSTEAGLKYLILGAFSSGILLFGCSMIYGSTGATHFDQLAKILTGYEIT--GARSSGIFMGILFIAVGFLFKITAV 244
07: ... IAASKRDSEFSTEAGLKYFILGAFSSGILLFGCSMIHGFTGVTNFEELAKIFTGYEITLFGAQSSGIFMGILFIAVGFLFKITAV 232
08: ... IAASKRDSEFSTEAGLKYFILGAFSSGILLFGCSMIYGFTGVTNFEELAKIFTGYEITLFGAQSSGIFMGILFIAVGFLFKITAV 201
09: ... IAASKRKSEFSTEAGLKYLILGAFSSGILLFGCSMIYGSTGATHFDQLAKILTGYEIT--GARSSGIFMGILFIAVGFLFKITAV 233
10: ... IAASKRKSEFSTEAGLKYLILGAFSSGILLFGCSMIYGSTGATHFDQLAKILTGYEIT--GARSSGIFMGILFIAVGFLFKITAV 233

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+ (285)
01: PFHQWTPDVYEGSPTPVVAFFSVTSKVAAPASFTRLFGLIFPYFSNEWHVAVGLLATFSMILGNLIAVTQRSVKRMLAYPSISQI... 315
02: PFHQWTPDVYEGAPTSVIAFFSVTSKIAGLALATRIFNTVFFSSLNEWHLILEIIAILSMILGNFIAITQTSMKRMLAYSSISQI... 314
03: PFHQWTPDVYEGSPTPVVAFLSVTSKVAALALATRIFDIPFYFSSNEWHLLEILAILSMIFGNLIAITQTSMKRMLAYSSISQI... 332
04: PFHQWTPDVYEGSPTPVVAFLSVTSKVAALALATRILDIPFYFSSNEWHLLEILAILSMILGNLIAITQTSMKRMLAYSSISQI... 332
05: PFHQWTPDVYEGSPTPVVAFISVISKVAALALVTRIFDIIIFYFSLNEWHLLEVSAILSMILGNLIAITQTSIKRMLAYSSISQI... 314
06: PPHMWAPDIYEGSPTPVTAFLSIAPKISISANILRVFIYGSYGAT--LQQIFFFCSIASMILGALAAMAQTKVKRLLAYSSIGHV... 327
07: PPHMWAPDVYEGSPTLVTAFFPIAPKISILANMLRVFIYSFYDPT--WQQLFFFCSIASMILGALAAMAQNKVKRLLAYSSIGHV... 315
08: PPHMWAPDVYEGSPTLVTAFFSIAPKISILANMVRVFIYSFYDPT--WQQLFFFCSIASMILGALAAMAQNKVKRLLAYSSIGHV... 284
09: PPHMWAPDIYEGSPTPVTAFLSIAPKISIFANMLRVFIVASYGGT--LQQIFFFCSIASMILGALAAMAQTKVKRLLAYSSIGHV... 316
10: PPHMWAPDIYEGSPTPVTAFLSIAPKISIFANMLRVFIVASYGGT--LQQIFFFCSIASMILGALAAMAQTKVKRLLAYSSIGHV... 316

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Data 5: amino acid alignment (partial) of *petB/cob*

(the original data at <http://cib.cf.ocha.ac.jp/RNAEDITING/align.php?id=g0061>)

- 01:chloroplast *Adiantum capillus-veneris* [AY178864_53]
- 02:chloroplast *Anthoceros formosae* [AB086179_58]
- 03:chloroplast *Takakia lepidozoioides* [AB254134_6]
- 04:mitochondrion *Beta vulgaris* subsp. *vulgaris* [BA000009_69]
- 05:mitochondrion *Brassica napus* (rape) [AP006444_75]
- 06:mitochondrion *Cucumis sativus* (cucumber) [AF288044_1]
- 07:mitochondrion *Equisetum arvense* (field horsetail) [FJ376600_1]
- 08:mitochondrion *Megaceros aenigmaticus* [EU660574_44]
- 09:mitochondrion *Oryza sativa Japonica Group* [BA000029_40]
- 10:mitochondrion *Pfiesteria piscicida* [AF357519_1]
- 11:mitochondrion *Prorocentrum minimum* [AY030286_1]
- 12:mitochondrion *Vitis vinifera* [AY727902_1]

(64)+ + (68)

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01:-----MSKVYDWFEEERLEIQAIADDITSKYVPPHVNIIFYCLGGITLTCFLVQIATGFAMTFYYRPTVTEAFSSVQYIMTE 75
02:-----MGKVYDWFEEERLEIQAIADDITSKYVPPHVNIIFYCLGGITLTCFLVQVASGFAMTFYYRPTVTEAFASVQYIMTE 75
03:-----MGKVYDWFEEERLEIQAIADDITSKYVPPHVNIIFYCLGGITLTCFLVQVATGFAMTFYYRPTVTEAFASVQYIMTE 75
04:-----MSLRNQRFSLKQPIFSTLNQHLIDYPTPSNLSYWWGFGSLAGICLVIQIVTGVEFLAMHYTPHVDLAFNSVEHIMRD 77
05:-----MTIRNQRFSLKQPISSSTLNQHLVDYPTPSNLSYWWGFGPLAGICLVIQIVTGVEFLAMHYTPHVDLAFNSVEHIMRD 77
06:-----MTKRKQRFSLKQPISSSTLNQHLIDYPTPSNLSYWWGFGSLAGICLVIQIVTGVEFLAMHYTPHVDLAFNSVEHIMRD 77
07:-----HLIDYPTPSNLSYWWGFGSLAGLRSVIQMITGVLLAQHYTPHVDLAFHSVEHIMRD 56
08:-----MARRLSILKQPIFSTVNNSIDYPTLSNLSYWWGFGSLAAIRLVTQIITGVSLAMHHTPHVDLAFLSVEHIMRD 74
09:-----MTIRNQRFSLKQPIYSTLNQHLIDYPTPSNLSYWWGFGSLAGICLVIQIVTGVEFLAMHYTPHVDLAFNSVEHIMRD 77
10:-----LLIPNFSFYCIYRITYFVLLMKSHLQSYPCPLQINFFWNEGFLLGVAIILQIITGILLALHYTSDLNSAYFSLFFLIRE 79
11:-----MKSHLQTYPCPLQINSEFWNLGFLGTLITLQIITGIFLGLHYTSDLNSAYYQIFFFIRE 59
12:-----MTIRNQRFSLKQPISSSTLNQHLIDYPTPSNLSYWWGFGSLAGICLVIQIVTGVEFLAMHYTPHVDLAFNSVEHVMRD 77
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+ (116)

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01:VNFGWLIRSVHRWSASMMVLMILHVFVRVYLTGGFKKPRELTTWVTGVILAVLTVSFGVGTGYSLEPWDQIGYWAVKIVTGVPEAIPF 160
02:VNFGWLIRSVHRWSASMMVLMILHVFVRVYLTGGFKKPRELTTWVTGVILAVLTVSFGVGTGYSLEPWDQIGYWAVKIVTGVPEAIPF 160
03:VNFGWLIRSVHRWSASMMVLMILHVFVRVYLTGGFKKPRELTTWVTGVILAVLTVSFGVGTGYSLEPWDQIGYWAVKIVTGVPEAIPV 160
04:VEGGWLLRYMHANGASMFFIVVYLHIFRGLYYSYSSPREFVWCLGVVIFLLMIVTAFIGYVLPWGQMSFWGATVITSLASAIPIV 162
05:VEGGWLLRYMHANGASMFFIVVYLHIFRGLYYSYSSPREFVWCLGVVIFLLMIVTAFIGYVLPWGQMSFWGATVITSLASAIPIV 162
06:VSGGWLLRYMHANGASMFFIVVYLHIFRGLYYSYSSPREFVWCLGVIIFLLMIVTAFIGYVLPWGQMSFWGATVITSLASAIPIV 162
07:VRGGWLLRYMHANGASMFFMIVVYLHIFRGLYYSYSSPREFVWCLGVVIFLLMIVTAFIGYVLPWGQMSFWGATVITSLASAIPI 141
08:VKGGWLLRYMHANGASMFFITVYLHILRGLYYSYASPRELWVCLGVVILLMIITAFIGYVLPWGQMSFWGATVITSLASAIPIV 159
09:VEGGWLLRYMHANGASMFFIVVYLHIFRGLYYSYSSPREFVWCLGVVIFLLMIVTAFIGYVLPWGQMSFWGATVITSLASAIPIV 162
10:VFYGWCLRYFHSSGASVFLFLFLHLGRAMFYGSYFYNPNTWFSGIILFLFLMAIAFMGYVLPWGQMSFWGATVITNLLSPFP- 162
```

11: IYYGRCLRYLHSTGASFVFLFLEFLHLGRAISYGSYFYSSS-TWFSGILLFFFLMATAFIGYVLPFGQMSFWGATVITNLLSPFP- 142
 12: VEGGWLLRYMHANGASMFIVVYLHIFRGLYASYSSPREFVWCLGVVIFLLMIVTAFIGYVLPWGQMSFWGATVITSLASAIPV 162

+ (209)

01: IGSSIVELLRGSVSVGQSTLTRFYSLHTFVLP LLTAVFMLMHFLMIRKQGISGPI*-----... 216
 02: VGSSIVELLRGSVSVGQSTLTRFYSLHTFVLP LLTAVLMLMHFLMIRKQGISGPI*-----... 216
 03: IGSPIVELLRGSVSVGQSTLTRFYSLHTFVLP LLTAVFMLMHFLMIRKQGISGPI*-----... 216
 04: VGDSIVTWLWGGFSVDNATLNRFFSLH-YLLPFILVGASLLHLAALHQYGSNNPLGV-----HSEMDKIAFYYPYFYVKDLVG... 238
 05: VGDTIVTWLWGGFSVDNATLNRFFSLH-YLLPFILVGASLLHLAALHQYGSNNPLGV-----HSEMDKIAFYYPYFYVKDLVG... 238
 06: VGDTIVTWLWGGFSVDNATLNRFFSLH-YLLPFLLAGASLLHLAALHQYGSNNPLGV-----HSEMDKIAFYYPYFYVKDLVG... 238
 07: VGDTIVTWLWGGFSVDNATLNRFFSLH-YLFPFIAGASLIHLAALHQYGSNNPLGI-----HSSVDKIAFYPIYVKDLVG... 217
 08: VGDTIVTRLWGGFPVDNATLNRFFSLH-HLPPFLIAGVSILHPAALHQYGSNNPLGI-----NSSVDKIASYLYSYVKDPVG... 235
 09: VGDTIVTWLWGGFSVDNATLNRFFSLH-YLLPFILVGASLLHLAALHQYGSNNPLGV-----HSEMDKIAFYYPYFYVKDLVG... 238
 10: ---SLIEWVSGGYCVHSPTLKRFFLFH-YQLPFLVCGFSILHLFYLFHFLSSNNPLR-----NSTNNKIPFFPLIFDKDFFG... 234
 11: ---SLIEWVCGGHYVYPTLKRFFLIH-FIFPFLLCGFLFIHLFYLFHFLSSNNPLR-----NSTNNKIPFFPFIKDFDFFG... 214
 12: VGDTIVTWLWGGFSVDNATLNRFFSLH-YLLPFILVGASLLHLAALHQYGSNNPLGV-----HSEMDKISFYYPYFYVKDLVG... 238