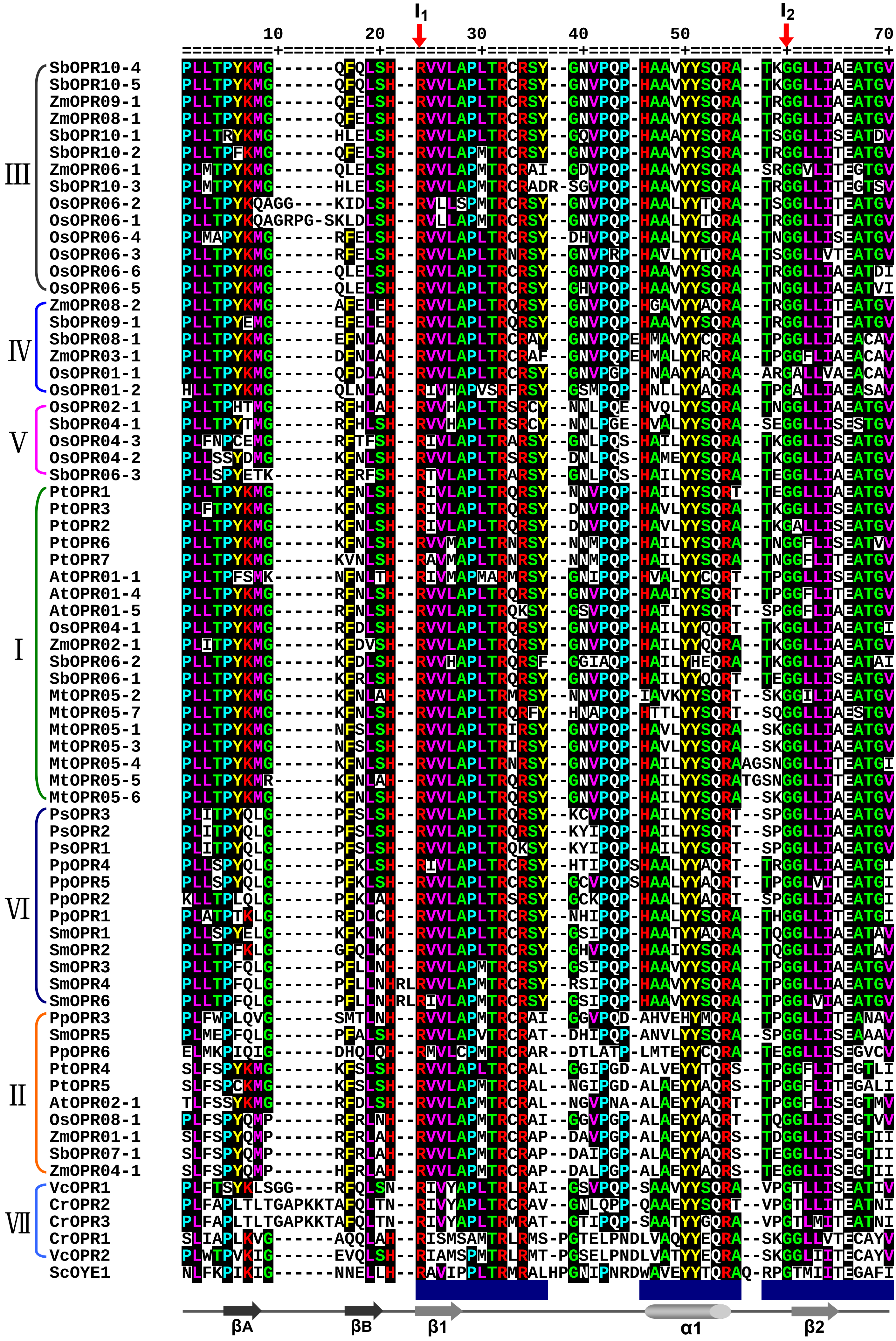

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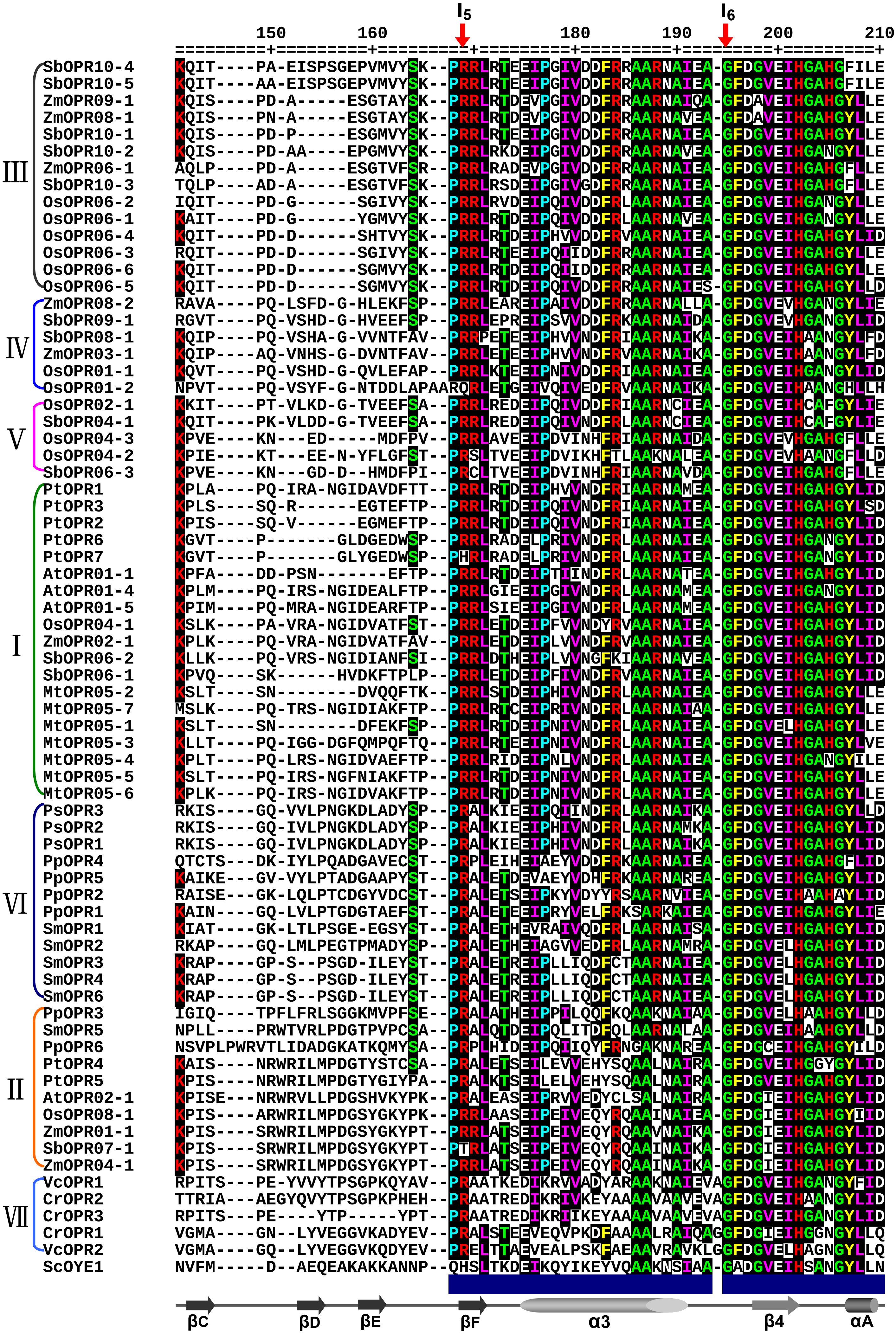

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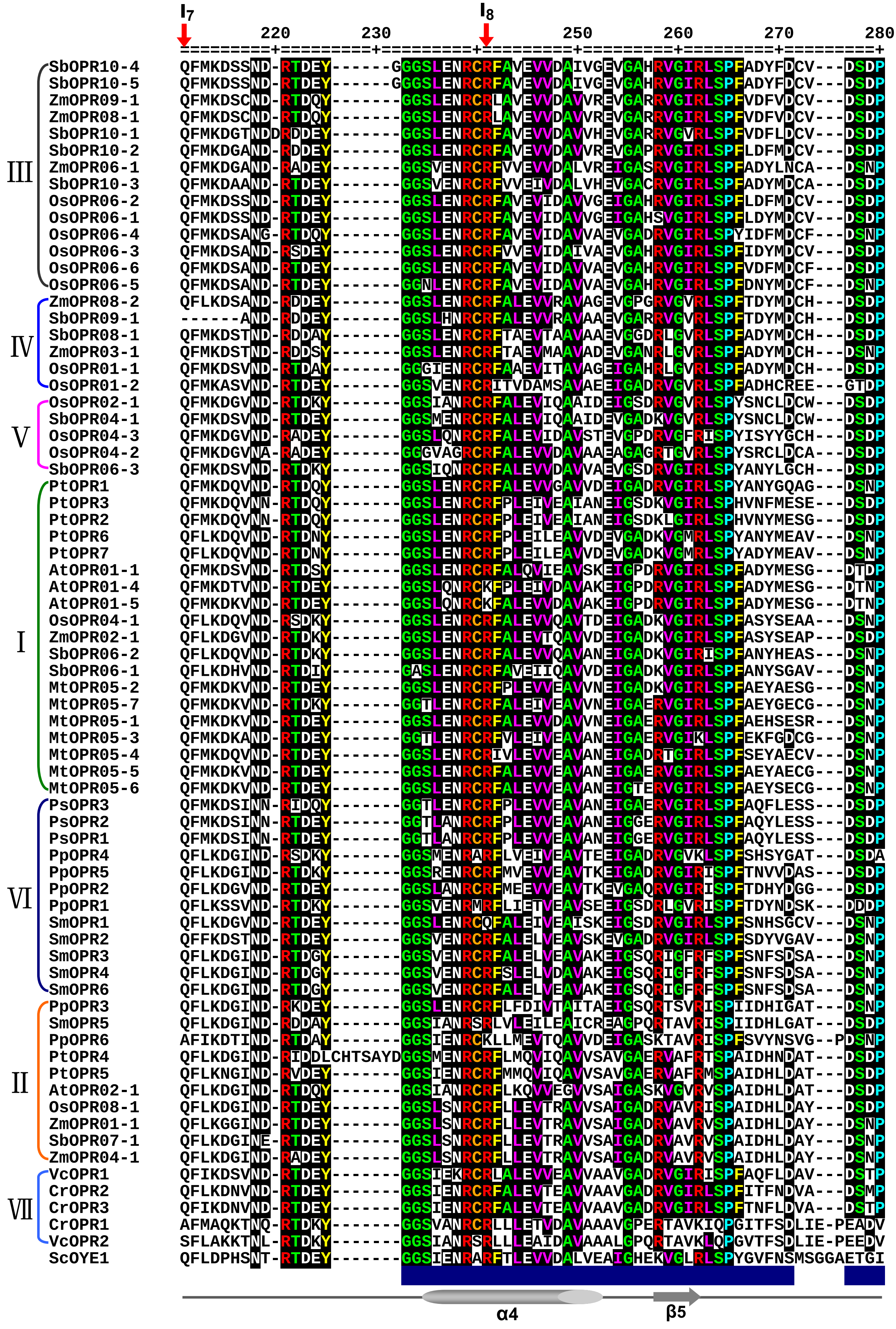

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ZmOPR09-1  QFMKDSCND-RTDQY-------GGSLENRCRLAVEVVDAVVREVGARRVGIRLSPFVDFVDCV---DSDP
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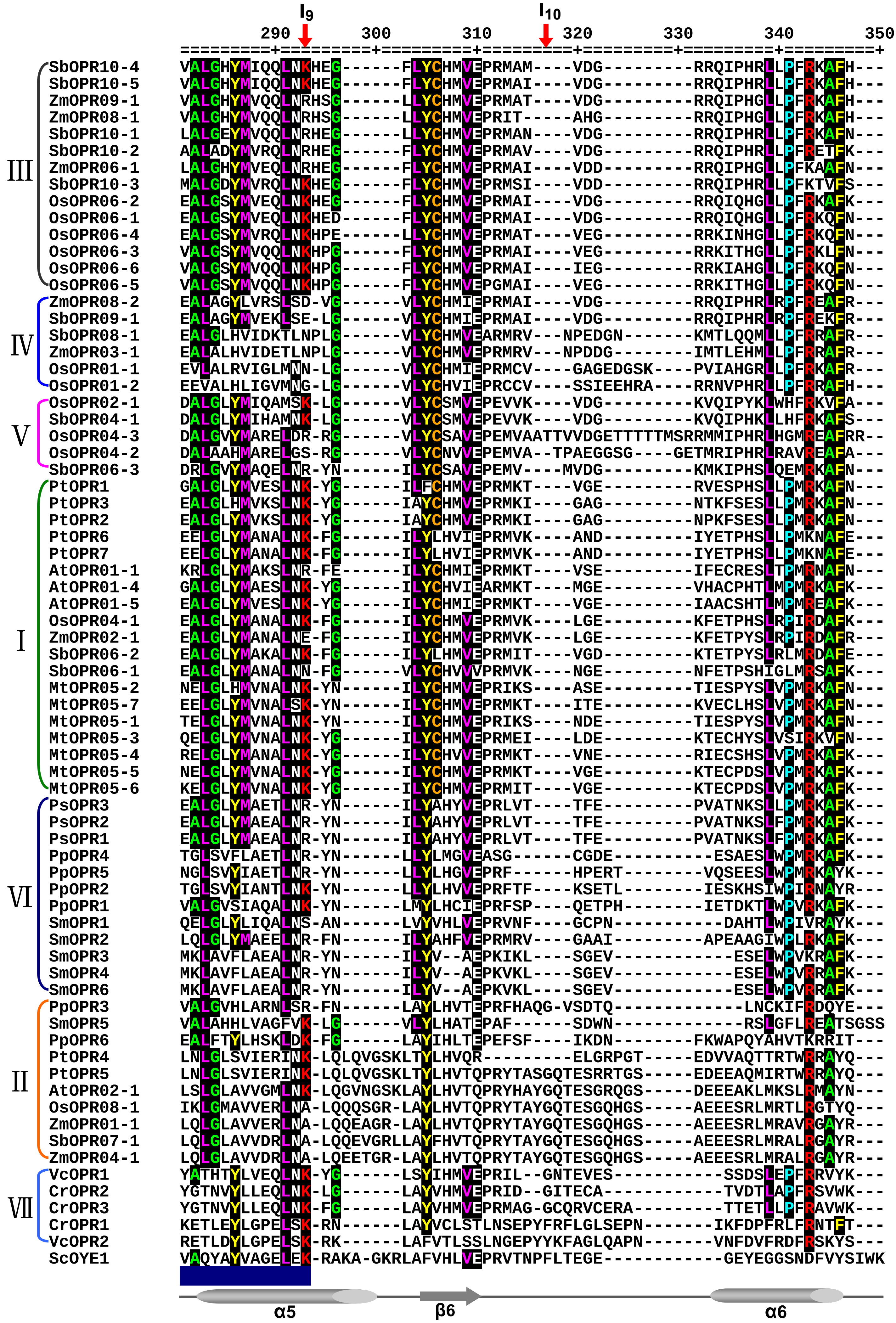
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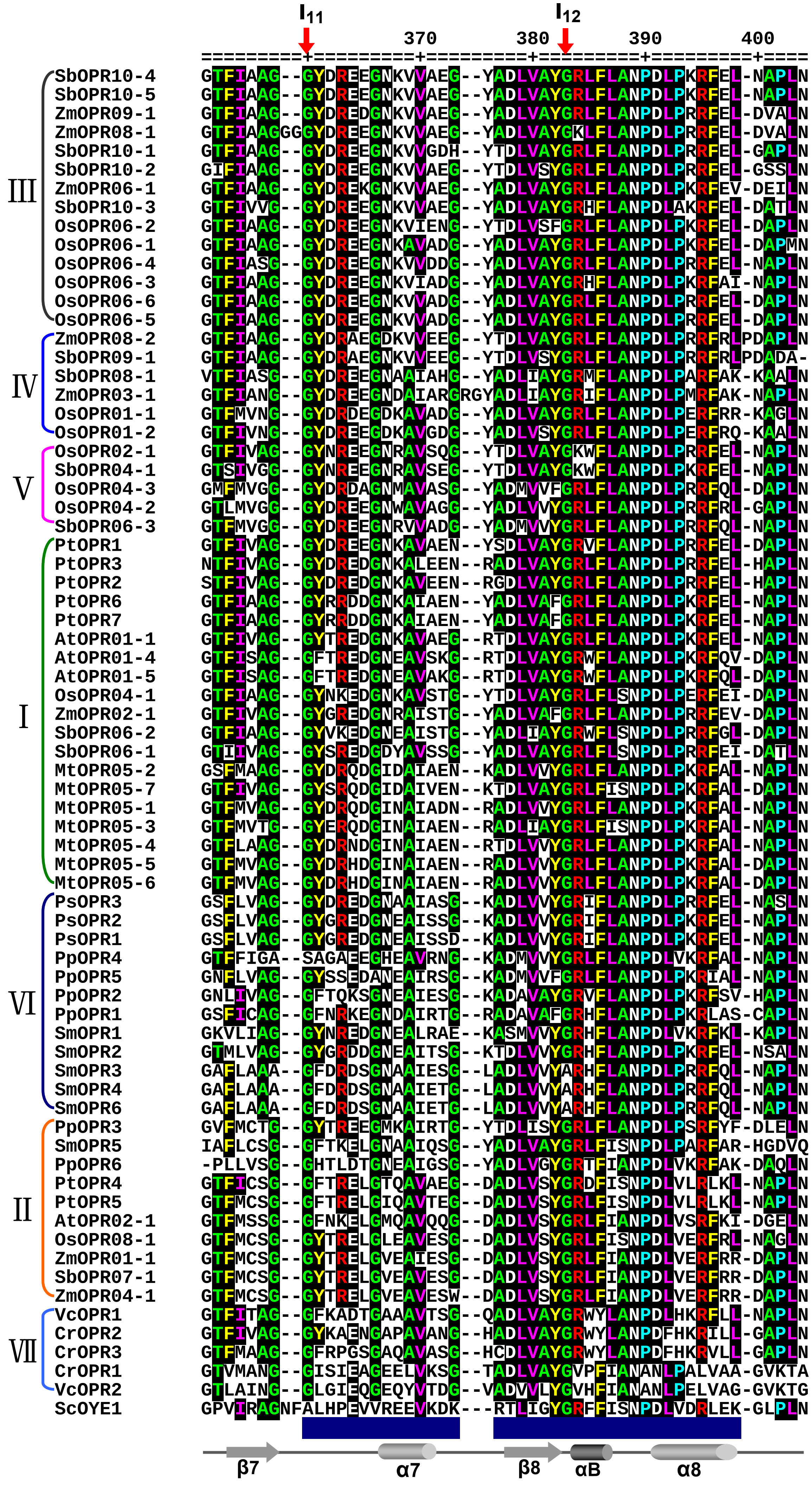
OsOPR08-1 IKLGMAVVERLNA-LQQQSGR-LAYLHVTQPRYTAYGQTESGQHGS-----AEEESRLMRTLRGTYQ---
ZmOPR01-1 LQLGLAVVERLNA-LQQEAGR-LAYLHVTQPRYTAYGQTESGQHGS-----AEEESRLMRAVRGAYR---
SbOPR07-1 LQLGLAVVDRLNA-LQQEVGRLLAYFHVTQPRYTAYGQTESGQHGS-----AEEESRLMRALRGAYR---
ZmOPR04-1 LQLGLAVVDRLNA-LQEETGR-LAYLHVTQPRYTAYGQTESGQHGS-----AEEESRLMRALRGAYR---
VII
VcOPR1 YATHTYLVEQLNK-YG------LSYIHMVEPRIL--GNTEVES-----------SSDSLEPFRRVYK---
CrOPR2 YGTNVYLLEQLNK-LG------LAYVHMVEPRID--GITECA------------TVDTLAPFRSVWK---
CrOPR3 YGTNVYLLEQLNK-FG------LAYVHMVEPRMAG-GCQRVCERA---------TTETLLPFRAVWK---
CrOPR1 KETLEYLGPELSK-RN------LAYVCLSTLNSEPYFRFLGLSEPN-------IKFDPFRLFRNTFT---
VcOPR2 RETLDYLGPELSK-RK------LAFVTLSSLNGEPYYKFAGLQAPN-------VNFDVFRDFRSKYS---
ScOYE1 VAQYAYVAGELEK-RAKA-GKRLAFVHLVEPRVTNPFLTEGE------------GEYEGGSNDFVYSIWK
α5
β6
α6



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SbOPR10-5     GTFIAAG--GYDREEGNKVVAEG--YADLVAYGRLFLANPDLPKRFEL-NAPLN
ZmOPR09-1     GTFIAAG--GYDREDGNKVVAEG--YADLVAYGRLFLANPDLPRRFEL-DVALN
ZmOPR08-1     GTFIAAGGGYDREEGNKVVAEG--YADLVAYGKLFLANPDLPRRFEL-DVALN
SbOPR10-1     GTFIAAG--GYDREEGNKVVGDH--YTDLVAYGRLFLANPDLPRRFEL-GAPLN
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SbOPR10-3     GTFIVVG--GYDREEGNKVVAEG--YADLVAYGRHFLANPDLAKRFEL-DATLN
OsOPR06-2     GTFIAAG--GYDREEGNKVIENG--YTDLVSFGRLFLANPDLPKRFEL-DAPLN
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ZmOPR08-2     GTFIAAG--GYDRAEGDKVVEEG--YTDLVAYGRLFLANPDLPRRFRLPDAPLN
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ZmOPR03-1     GTFIANG--GYDREEGNDAIARGRGYADLIAYGRIFLANPDLPMRFAK-NAPLN
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SbOPR06-3     GTFMVGG--GYDREEGNRVVADG--YADMVVYGRLFLANPDLPRRFQL-NAPLN
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AtOPR01-5     GTFISAG--GFTREDGNEAVAKG--RTDLVAYGRWFLANPDLPKRFQL-DAPLN
OsOPR04-1     GTFIAAG--GYNKEDGNKAVSTG--YTDLVAYGRLFLSNPDLPERFEI-DAPLN
ZmOPR02-1     GTFIVAG--GYGREDGNRAISTG--YADLVAFGRLFLANPDLPRRFEV-DAPLN
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OsOPR08-1     GTFMCSG--GYTRELGLEAVESG--DADLVSYGRLFISNPDLVERFRL-NAGLN
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CrOPR3        GTFMAAG--GFRPGSGAQAVASG--HCDLVAYGRWYLANPDFHKRVLL-GAPLN
CrOPR1        GTVMANG--GISIEAGEELVKSG--TADLVAYGVPFIANANLPALVAA-GVKTA
VcOPR2        GTLAING--GLGIEQGEQYVTDG--VADVVLYGVHFIANANLPELVAG-GVKTG
ScOYE1        GPVIRAGNFALHPEVVREEVKDK---RTLIGYGRFFISNPDLVDRLEK-GLPLN
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Additional file 3

Amino acid sequences alignment of Oxidored_FMN domain in OPR genes from eleven species representing six major lineages within the green plants: the green algae (*Chlamydomonas reinhardtii* and *Volvox carteri*), the mosses (*Physcomitrella patens*), the lycophytes (*Selaginella moellendorffii*), the gymnosperms (*Picea sitchensis*), the monocotyledoneous angiosperms (*Oryza sativa*, *Sorghum bicolor* and *Zea mays*) and the dicotyledoneous angiosperms (*Arabidopsis thaliana*, *Populus trichocarpa* and *Medicago truncatula*). Only 3 of 74 OPR genes (AtOPR01-2/3 and SbOPR06-4) without complete Oxidored_FMN domain are excluded, while the outgroup ScOYE1 from yeast (Saito et al., 1991) is included in the alignment. The blue blocks below the alignment represent the fragments selected by the Gblocks program (Castresana, 2000; Talavera and Castresana, 2007) with default parameters underlined. Positions of the alignments where more than 50% of the sequences are identical are shown with black boxes. The secondary structure elements are represented at the bottom of the alignment as tubes or arrows shown in gray based on structural information from OPR proteins AtOPR1 (Fox et al., 2005), AtOPR3 (Malone et al., 2005) and LeOPR3 (Breithaupt et al., 2006). The intron positions of putative ancestral OPR are represented at the top of the alignment as red vertical arrows, and I_1~I_{12} represent intron 1~12. The seven conserved OPR subfamilies are represented as Ⅰ, Ⅱ, Ⅲ, Ⅳ, Ⅴ, Ⅵ and Ⅶ at the left side of the alignment.

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