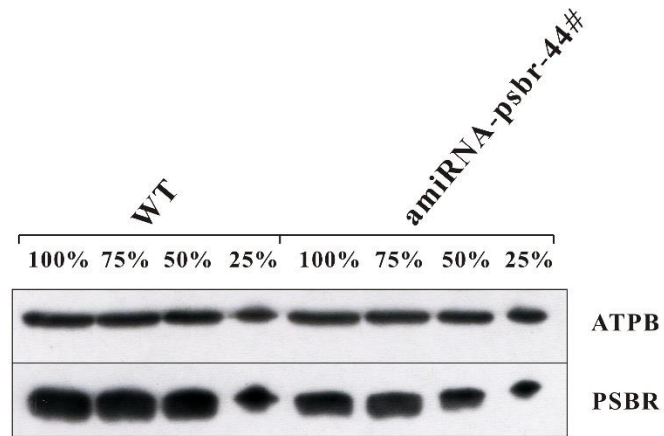
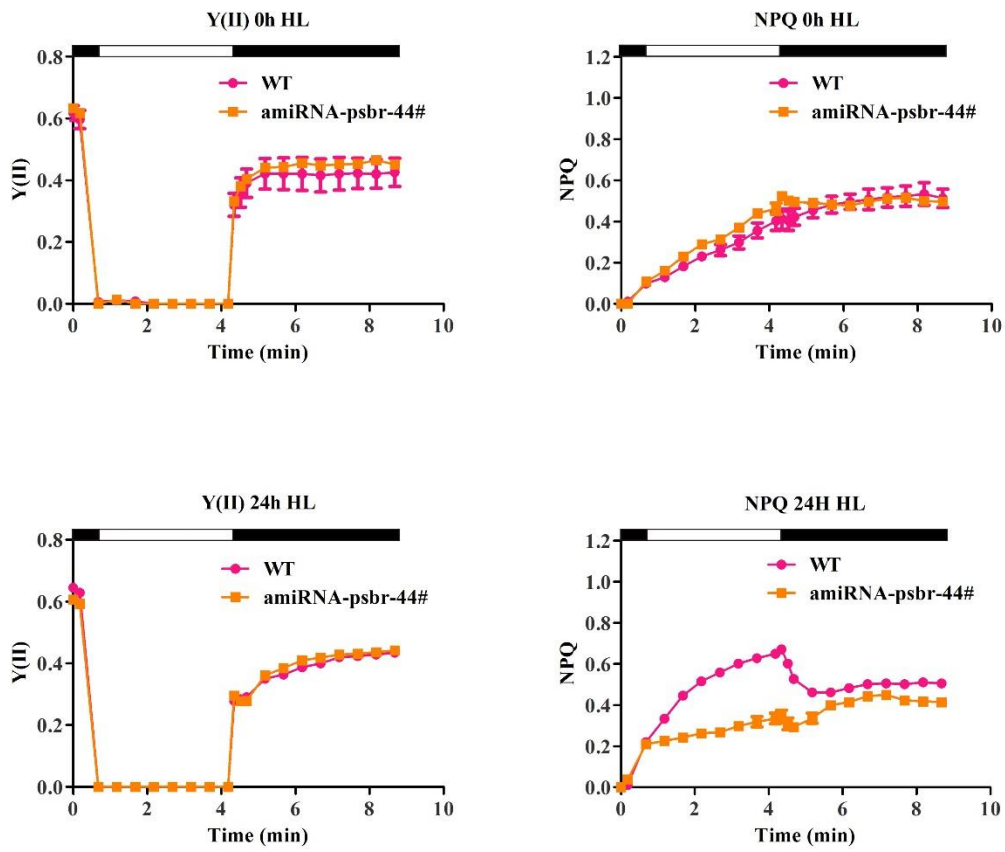


Supplemental figure S1

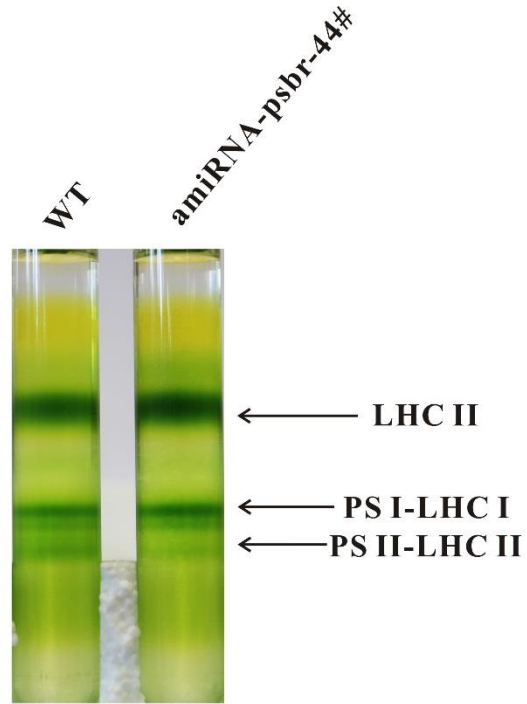
A



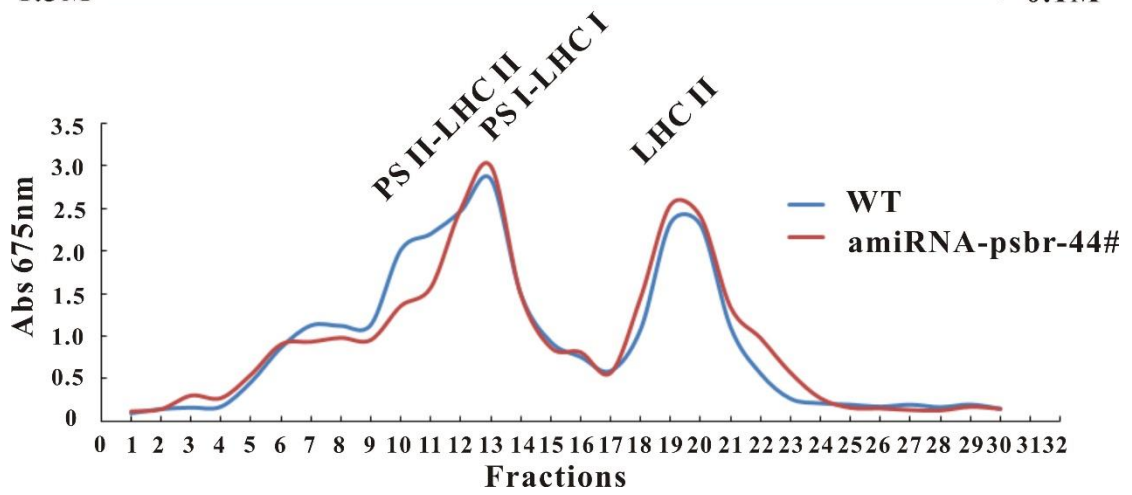
B



C



1.3M → 0.1M



D

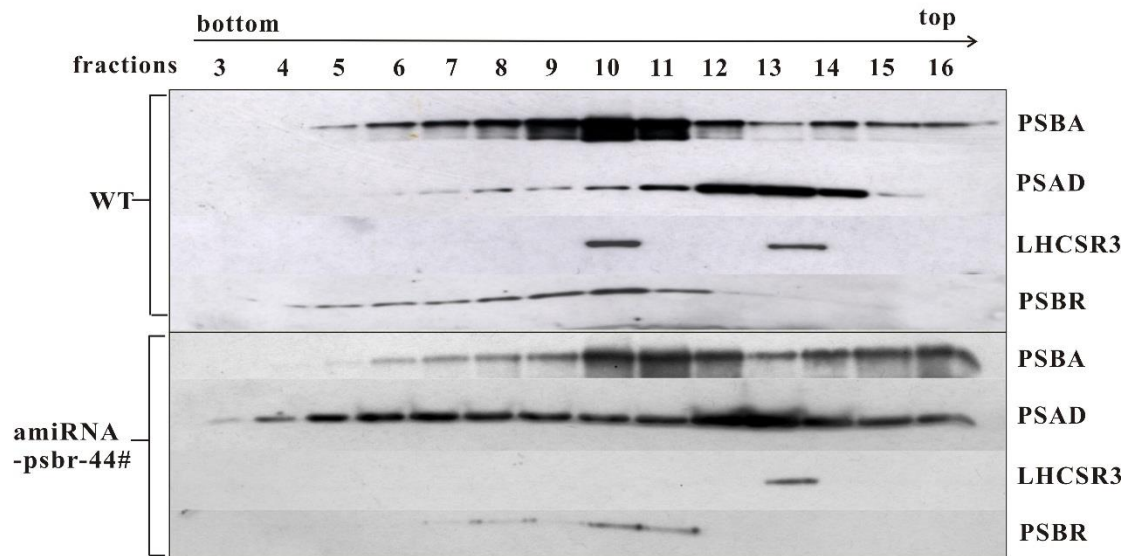
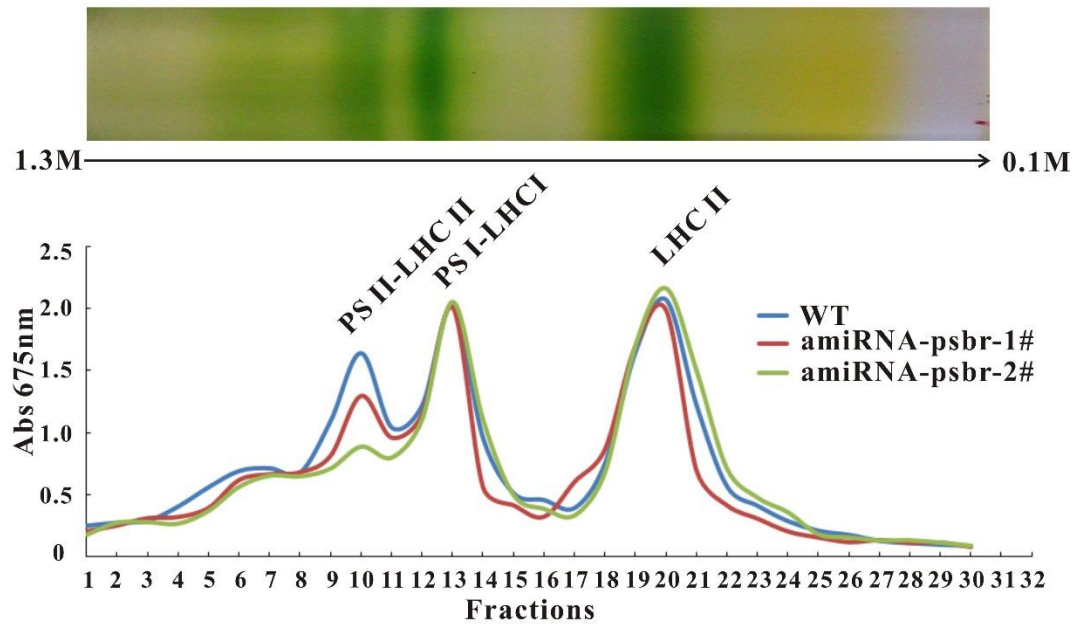


Figure S1. Immunoblot analysis of thylakoid membrane and sucrose density gradients and PSII quantum yield and NPQ induction of WT and *amiRNA-psbr-44#*

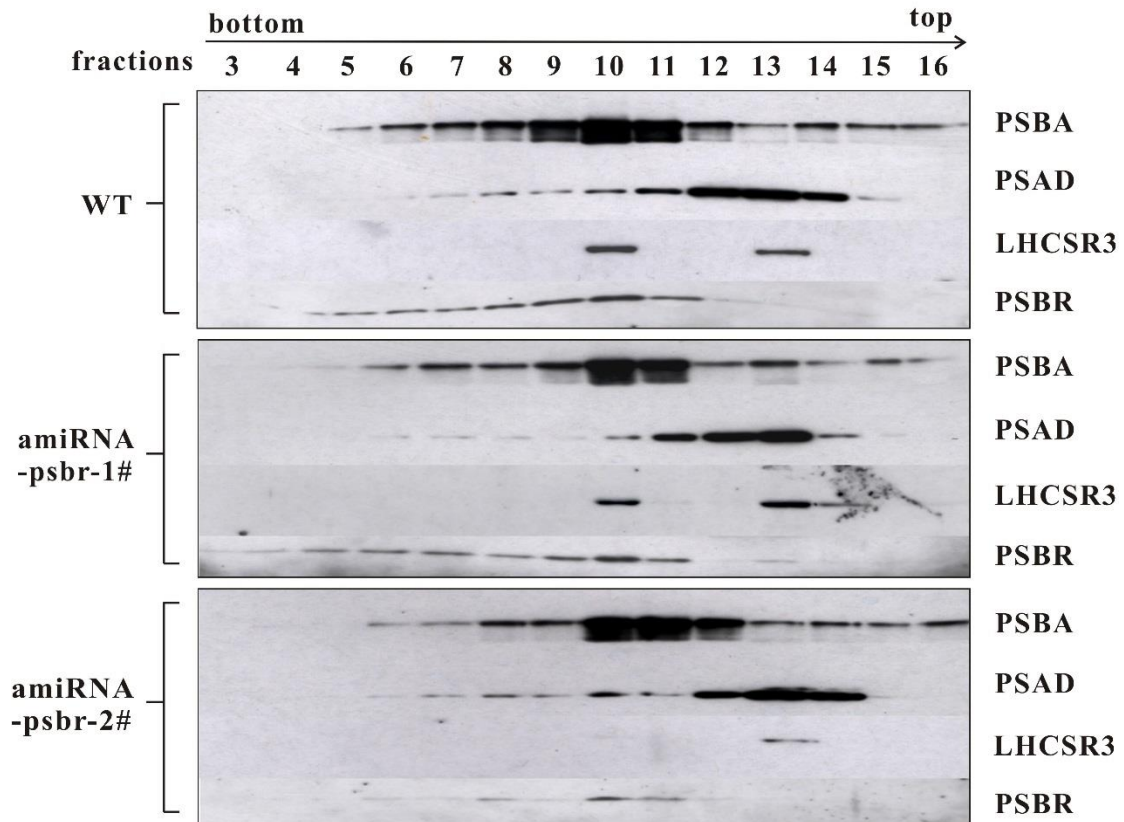
(A) WT and *amiRNA-psbr-44#* were grown in TAP medium at LL ($20 \mu\text{E m}^{-2} \text{s}^{-1}$) and then shifted to HL ($200 \mu\text{E m}^{-2} \text{s}^{-1}$) in HSM medium for 24h. Afterwards, isolated thylakoids were separated on a 13 % SDS-PAGE and analyzed by immunoblotting using anti-PsbR antibodies. 6 μg chlorophyll equals 100 %, ATPB served as loading control. (B) Cells were grown in TAP medium under LL and then shifted to HL and HSM for 24h. Y(II) and NPQ were measured after 0h and 24h HL treatment. (C) Sucrose density gradients of thylakoid membranes from WT and *amiRNA-psbr-44#*. Thylakoid isolated from 24h HL treatment cells were solubilized with 1.0 % α -DM and separated by sucrose density gradient ultracentrifugation. SDGs were fractionated and measured as (Figure 5 B). (D) Immunoblot analysis of SDG fractions 3-16 from 24h HL of WT and *amiRNA-psbr-44#*. Sample preparation and Immunoblotting were performed as in (Figure 6 A)

Supplemental figure S2

A



B



C

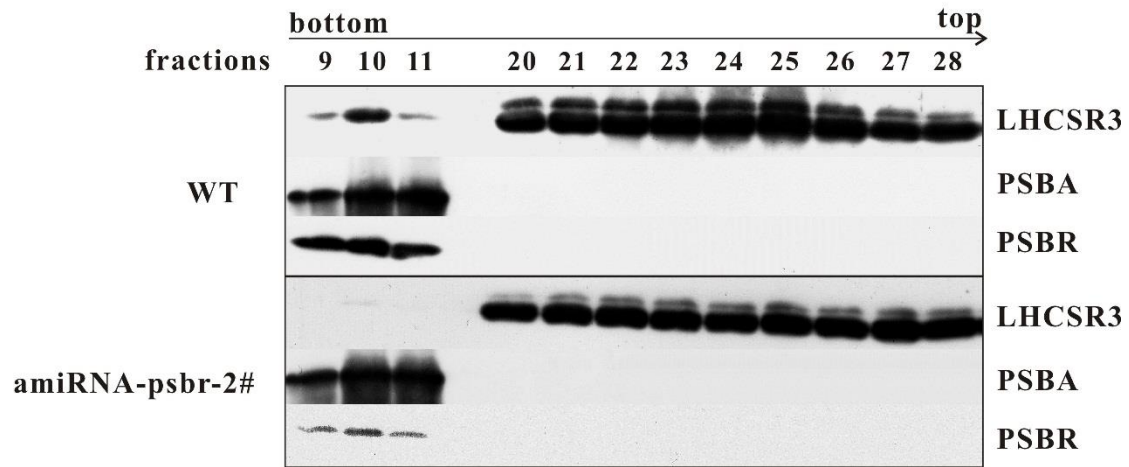


Figure S2. Absorbance measurement and immunoblot analysis of SDG fractions from 24h HL WT and PSBR Knock-down strains

(A) SDGs of 24h HL of WT, *ami-RNA-psbr-1#* and *ami-RNA-psbr-2#* were fractionated and measured as (Figure 5 B). (B) Immunoblot analysis of SDG fractions 3-16 from 24h HL of WT and *ami-RNA-psbr* lines. Sample preparation and Immunoblotting were performed as in (Figure 6 A). (C) 24h (fractions 9-11 and 20-18) HL of WT and *ami-RNA-psbr-2#* were subjected to immunoblotting with an anti-LHCSR3, PSBA PSBR antibody. Sample preparation was performed as in (B).

Supplemental figure S3

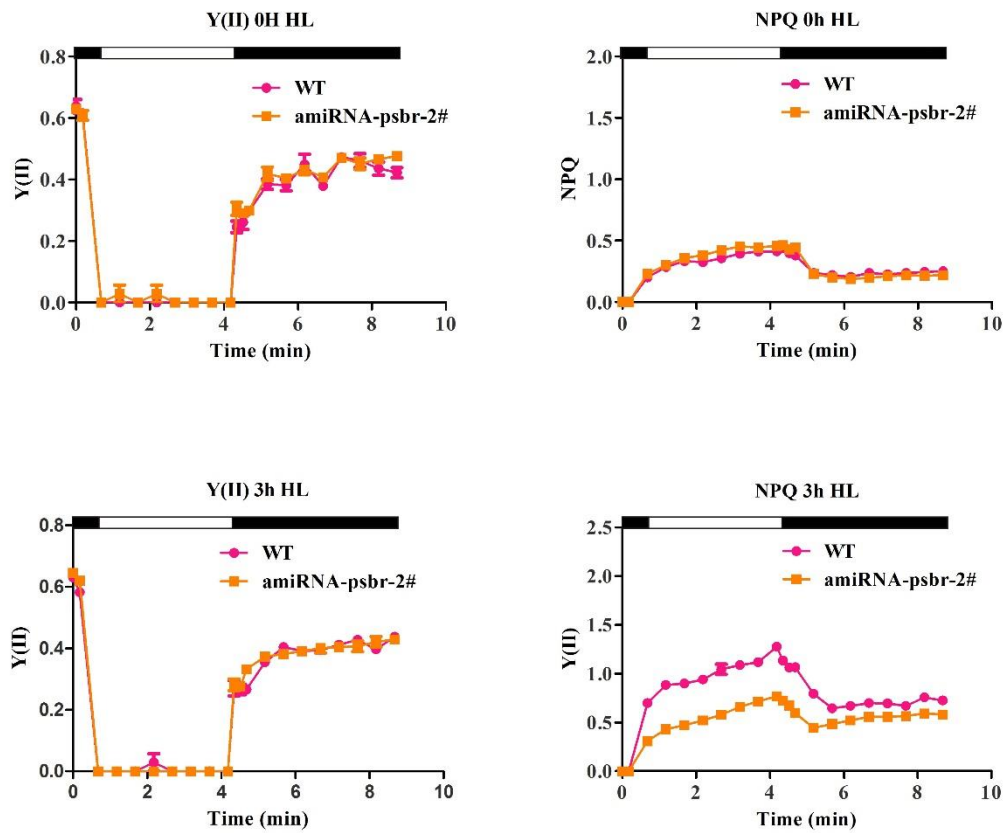


Figure S3. PSII quantum yield and NPQ induction of WT and *ami-RNA-psbr-2#* from 3h HL cells

Cells were grown in TAP medium under LL and then shifted to HL and HSM for 3h.

Supplemental Table S1. Quantitative proteomics data of Figure 7A

Protein	Peptides	Ratio mean (¹⁴ N/ ¹⁵ N)	SD
PSBA	ANLGMEVMHER	1.285723	0.127054
	ETTENESANEGYR		
	FGQEEETYNIIVAAHGYFGR		
	LIFQYASFNNSR		
	VLNTWADIINR		
PSBD	AAEDPEFETFYTK	1.200534	0.121991
	AFNPTQAEETYSMTANR		
	AWMAAQDQPHER		
	AYDFVSQEIR		
	LVFPEEVLPR		
	FWSQIFGVAFSNK		
	TWFDDADDWLR		
PSBH	VNSDFQEPGLVTPGLTLLR	1.253401	0.055727
	VNSDFQEPGLVTPGLTLLRPLNSEAGK		
PSBO	EDDGIDYAATTVQLPGER	1.286167	0.260808
	GDFLVPSYR		
	GGSTGYDNAVALPAR		
	GGSTGYDNAVALPARADAEELLKENVK		
	LYTLDAMSGSFK		
	VDPVTGEIAGVFESIQPSDIDLAKPPK		
	VGSDGSAELKEDDGIDYAATTVQLPGER		
	VTGLWYAQLK		
PSBP	ENDFPGVILR	1.811229	0.073269
	FLESVSYLLGK		
	QAYSGETQSEGGFAPNR		
	SGFVVPYAGDGFALLPAK		
	VSAASLLDVSTTTDKK		
	YEDNFDVNNLVIAQDITDKK		
PSBQ	DLDLPQNR	1.717382	0.391841
	EFIQAVEDLDFALR		
	KEFIQAVEDLDFALR		
	GFDLIYEAR		
	IDADLDVFIQK		
PSBW	DLGDFEDADDGLKL	1.250466	0.034870
	DLGDFEDADDGLK		
LHCB4	FADGLNNGK	1.189483	0.162436
	FPTPPGTQK		
	GFDPLGLSKPSEFVVIGVDENDQNAAK		
	KYQGDALWLPNTRPEWLDGSLPGDR		
LAMVSFFGYGVQALSTGEGALGSLAK			

Protein	Peptides	Ratio mean (¹⁴ N/ ¹⁵ N)	SD
LHCB4	LAPYSEVFGLAR PEWLDGSLPGDR PSEFVVIGVDENDQNAAK YQGDALWLPNTRPEWLDGSLPGDR	1.189483	0.162436
LHCB5	ENELLHAR GWLGGQGAADLDK GWLGGQGAADLDK WYGPDR HVADPFYNYLLTVLGAEER LFLPSGLYDR NGTGPAGYSPGIGK WAMLAAGILPEGLQANGANIK SEIPEYLNAGELAGDYGYDPLGLGK YRENELLHAR	1.207260	0.167547
LHCBM1	ASTPDSFWYGPDR GPLQNLSDHLANPGTNNAFAYATK LYPGGSFDPLGLADDPDTFAELK VNGGPLGEGLDK	1.026265	0.198301
LHCBM3	GPIQNLDDHLSNPTVNNAFAFATK QAPASSGIEFYGPNR SGTQFGEAVWFK	0.973797	0.241609
LHCBM4 and LHCBM6	GPVQNLDDHLANPTVNNAFAFATK	1.317567	0.076375
LHCBM2 and LHCBM7	ANGGPLGEGLDPLHPGGAFDPLGLADDPDTFAELK NGIPFGEAVWFK	1.164885	0.440862
LHCBM5	VNGGPAGEGLDK	1.037268	0.327399
CP43	FDEPVLSMR AMYFGGVYDTWAPGGGDVDR DQETTGFVWWSGNAR FDEPVLSMRPLD GIDRFDEPVLSMRPLD GPWLEPLR LGANVASAQGPTGLGK LKNDIQPWQER NDIQPWQER SPTGEIIFGGETMR VITNPTTNAAVIFGYLVK	1.358915	0.288501
CP47	AQLGEIFEFDK DVFAGIDDDINDQVEFGK KAQLGEIFEFDK KLGDTSSLR	1.292974	0.247392

Protein	Peptides	Ratio mean (¹⁴ N/ ¹⁵ N)	SD
CP47	LAFYDYIGNNPAK LGD TSSLR MPTFFETFPVLLLDK MPTFFETFPVLLLDKDGIVR QGMFVLPFMTR RMPTFFETFPVLLLDK STLQSDGVFR TGAMNSGDGIAGWLGHASFK VHTVVINDPGR VQASLAEGASLSDAWSR YQWDQGFFQQEIQK	1.292974	0.247392
LHCSR3	DLGLPVTPLPDNLK EAILELDDIER	2.305342	0.127054
PSBR	VGLNSIEDPVVK YGANVDGYSPIYTPDLWTESGDSYTLGTK	3.297521	0.317235
α-CF1 "	AIESPAPGIVAR SVYEPLATGLVAVDAMIPVGR TAIAVDTILNQK TPEELSNLIK IAEIPVGEAYLGR	0.939444	0.077343
β-CF1	DGSITSIQAVYVPADDLTDPA PATTF AHL DATTVLSR ELQDIIAILGLDELSEEDR FVQAGAEVSALLGR GMEVVDTGKPLSVPVGK IFAGELDDLPEQAFYLVGNITEAISK IFNVLGEPVDNMGNVK MPSAVGYQPTLATEMGG LQER QDV LFFIDNIFR TAPAFV DLDTR TVLIMELINNI AK VALTALTMAEYFR VVDLLAPYR	0.995517	0.155767

Supplemental Table S2. Quantitative proteomics data of Figure 7B

Protein	Peptides	Ratio mean (¹⁴ N/ ¹⁵ N)	SD
PSBA	ANLGMEVMHER	1.351819	0.223429
	FGQEEETYNIVA AHGYFGR		
	LIFQYASFNNSR		
	VLNTWADIINR		
PSBD	AAEDPEFETFYTK	1.106439	0.099573
	AFNPTQAEETYSMVTANR		
	AYDFVSQEIR		
	LVFPPEVLPR		
	NILLNEGIR		
	TWFDDADDWLR		
PSBH	VNSDFQEPGLVTPGLTLLR	0.989421	0.217864
PSBO	ADAEELLKENVK	1.273401	0.292776
	EDDGIDYAATTVQLPGER		
	GDFLVPSYR		
	GGSTGYDNAVALPAR		
	LYTLDAMSGSFK		
	VAFLFYTK		
	VDPVTGEIAGVFESI QPSDTDLGAKPPK		
	VGSDGSAELKEDDGIDYAATTVQLPGER		
	VTGLWYAQLK		
	VTGLWYAQLK		
PSBP	ENDFPGVILR	1.467983	0.131825
	FLESVSYLLGK		
	QAYSGETQSEGGFAPNR		
	SGFVPYAGDGFALLPAK		
	VSAASLLDVSTTTDKK		
	YEDNFDVNNLVVIAQDQDKK		
PSBQ	DLDLQNVNR	1.237611	0.106663
	EFIQAVEDLDFALR		
	FDLNLTASTK		
	IDADLDVFIQK		
PSBW	DLGDFEDADDGLK	1.221623	0.051973
LHCB4	GFDPLGLSKPSEFVVIGVDENDQNAAK	1.088816	0.114001
	GSVEAIVQATPDEVSSNR		
	KYQGDALWLPNTRPEWLDGSLPGDR		
	LAPYSEVFLAR		
	PSEFVVIGVDENDQNAAK		
YQGDALWLPNTRPEWLDGSLPGDR			
LHCB5	FDSSVFDGLDPLYPGGPFDPGLLADDPEVLQELK	1.072036	0.255306
	GWLGGQGGAADLDK		
	HVADPFGYNLLTVLGAEER		

Protein	Peptides	Ratio mean (¹⁴ N/ ¹⁵ N)	SD
LHCB5	KLFLPSGLYDR LFLPSGLYDR NGTGPAGYSPGIGK SEIPEYLNAGELAGDYGYDPLGLGK WAMLAAAGILPEGLQANGANIK	1.072036	0.255306
LHCBM1	ASTPDSFWYGPER PLQNSDHLANPGTNNAFAYATK LYPGGSFDPLGLADDPDTFAELK VNGGPLGEGLDK	1.303171	0.251581
LHCBM3	GPIQNDDHLSNPTVNNAFAFATK QAPASSGIEFYGNR SGTQFGEAVWFK	1.181249	0.276587
LHCBM4 and LHCBM6	GPVQNDDHLANPTVNNAFAFATK	1.476974	0.009663
LHCBM2 and LHCBM7	ANGGPLGEGLDPLHPGGAFDPLGLADDPDTFAELK FLGPFSEGDTPAYLTGEFPGDYGWDTAGLSADPETFK GPIQNDDHLANPTAVNAFAYATK NGIPFGEAVWFK	1.569313	0.191636
LHCBM5	VNGGPAGEGLDK	1.150154	0.345649
CP43	AAEYMTHAPLGLSLNSVGGVATEINAVNFVSPR AMYFGGVYDTWAPGGGDVDR DQETTGFVWWSGNAR FDEPVLSMR GIDRFDEPVLSMRPLD GPWLEPLR LGANVASAQGPTGLGK LKNDIQPWQER NDIQPWQER SPTGEIIFGGETMR VITNPTTNAAVIFGYLVK	1.183454	0.200762
CP47	AQLGEIFEFDK DVFAGIDDDINDQVEFGK KAQLGEIFEFDK LAFYDYIGNNPAK MPTFFETFPVLLLDK QGMFVLPFMTR STLQSDGVFR TGAMNSGDGIAVGWLGHASFK VQASLAEGASLSDAWSR YQWDQGGFFQEIQK YSIEQVGVSVTFYGGELDGLTFTDPATVK	1.151346	0.117750

Protein	Peptides	Ratio mean (¹⁴ N/ ¹⁵ N)	SD
LHCSR3	DLGLPVTPLPDNLK	2.256318	0.364134
PSBR	VGLNSIEDPVVK	2.887469	0.534016
α -CF1 "	AIESPAPGIVAR IAEIPVGEAYLGR QAINELYEEFK SVYEPLATGLVAVDAMIPVGR TAIAVDTILNQK TPEELSNLIK	1.065211	0.175358
β -CF1	ELQDIHAILGLDELSEEDR TAPAFVDLDTR	1.120346	0.033946

Supplemental Table S3. Quantitative proteomics data of Figure 7C

Protein	Peptides	Ratio mean (¹⁴ N/ ¹⁵ N)	SD
PSBA	FGQEEETYNIVA AHGYFGR VLNTWADIINR	0.915335	0.018279
PSBD	AAEDPEFETFYTK AFNPTQAEETYSMTANR AWMAAQDQPHER AYDFVSQEIR LVFPEEVLPR NILLNEGIR TWFD DADDWLR	0.895616	0.038690
PSBH	VNSDFQEPGLV TPLGLLLR VNSDFQEPGLV TPLGLLLRPLNSEAGK	0.945221	0.045258
PSBO	ADAEELLKENVK EDDGIDYAATT VQLP GGER GDFLVPSYR GGSTGYD NAVALPAR GSAVFSVAK GSSFLDPK GTLDNIK GDFLVPSYR LTYTLDAMSGSFK VAFLFTIK VDPVTGEIAGVFESIQPSDTDLGAKPPKDIK VGS DGS AELKEDDGIDYAATT VQLP GGER VTGLWYAQLK	0.954203	0.206472
PSBP	ENDFPGVILR FLESVSYLLGK HQLIGATVGS DNK QAYSGETQSEGGFAPNR SGFVPYAGDGFALLPAK VSAASLLDVSTTTDKK YEDNFDAVNNLVIAQD TDKK	3.642855	1.052493
PSBQ	DLDLPQNV R EFIQAVEDLDFALR FDLNTLASTK GFDLIYEAR IDADLDVFIQK	2.291525	0.791265
PSBW	DLGDFEDADDGLKL	1.063709	0.164927
LHCB4	FADGLNNGK FPTPPGTQK GFDPLGLSKPSEFVVIGVDENDQNAAK KYQGDALWLPNTTRPEWLDGSLPGDR	1.086075	0.262131

Protein	Peptides	Ratio mean (¹⁴ N/ ¹⁵ N)	SD
LHCB4	LAPYSEVFGLAR NNKGSVEAIVQATPDEVSSNR	1.086075	0.262131
LHCB5	FDSSVFDGLDPLYGGPFDPLGLADDPEVLQELK GWLGGQGAADLDK GWLGGQGAADLDKWYGPRK HVADPFYNNLLTVLGAEER KLFLPSGLYDR LFLPSGLYDRSEIPEYLNAGELAGDYGYPDPLGLGKDPETVAK SEIPEYLNAGELAGDYGYPDPLGLGKDPETVAK YRENELLHAR	1.068557	0.212815
LHCBM1	ASTPDSFWYGPGR GPLQNLSDHLANPGTNNAFAYATK LYPGGSFDPLGLADDPDTFAELK PLFLGAFTEPPSYLTGEFPDYGWDTAGLSADPETFK	2.534266	0.755221
LHCBM3	GPIQNLDHLSNPTVNNAFAYATK QAPASSGIEFYGPNR SGTQFGEAVWFK	2.700815	0.916661
LHCBM4 and LHCBM6	GPVQNLDHLSNPTVNNAFAYATK	1.830968	0.522198
LHCBM2 and LHCBM7	ANGGPLGEGLDPLHPGAFDPLGLADDPDTFAELK FLGPFSEGDTPAYLTGEFPDYGWDTAGLSADPETFKR GPIQNLDHLSNPTAVNNAFAYATK NGIPFGEAVWFK	2.305643	0.655765
LHCBM5	AGWWSNGGNEK LHPGGQFFDPLGLAEDPDFAELK LSAFYGPDR NGTPIVEPVWFK	1.450154	0.345649
CP43	AAEYMTHAPLGLSLNSVGGVATEINAVNFVSPR AMYFGGVYDTWAPGGGDVDR DQETTGFVWWSGNAR GIDRFDEPVLSMRPLD GPWLEPLRGPNGLDLTK LGANVASAQGPTGLGK SPTGEIIFGGETMR VITNPTTNAAVIFGYLVK	0.913889	0.043640
CP47	DVFAGIDDDINDQVEFGK KAQLGEIFEFDR LAFYDYIGNNPAK RMPTFFETFPVLLLDKDGIVR QGMFVLPFMTR TGAMNSGDGIAGWLGHASFK	0.905514	0.120713

Protein	Peptides	Ratio mean (¹⁴ N/ ¹⁵ N)	SD
CP47	VQASLAEGASLSDAWSR YQWDQGGFFQQEIQK YSIEQVGVSVTFYGGELDGLTFTDPATVK	0.905514	0.120713
LHCSR3	DLGLPVTPLPDNLK EAILELDDIER	28.994430	10.385040
PSBR	VGLNSIEDPVVK YGANVDGYSPIYTPDLWTESGDSYTLGTK	1.891174	0.164706
α -CF1 "	AIESPAPGIVAR AMSGELLEFEFGTLGIALNLEANNVGAVLLGDGLK ASSVAQVLNTLK DLIEQYTPEVK EAYPGDVFYLHSR IAEIPVGEAYLGR LELAQFAELEAFSQFASDLLQATQNQLAR MVDFGIVFQVGDGIAR PTLIYDDLK QAINELYEEFK QPQSSPLSVEEQVASLYAGTNGYLDKLEVSQVR STLTFTPEAEGLVK SVYEPLATGLVAVDAMIPVGR SYLANSYPK TAIAVDTILNQK TPEELSNIKDLIEQYTPEVK VVDGLARPVDGK	1.238294	0.093626
β -CF1	AHGGVSVFAGVGER AVSMNPTEGLMR DGSITSIQAVYVPADDLTDPAPATTF AHLDATTVLSR DVNKQDVLFFIDNIFR FVQAGAEVSALLGR GIYPAVDPLESTSTMLQPWILGK GMEVVDTGKPLSVPVGK GQVPNIYNALTIR IFAGELDDLPEQAFYLVGNITEAISK IFNVLGEPVDNMGNVKVEETLPIHR LSIFETGIK MPSAVGYQPTLATEMGGQLER TAPAFVDLDTR TREGNDLYTEMK TVLIMELINNIK VALVYGMNEPPGAR VVDLLAPYR YKELQDIIAILGLDELSEEDRLIVAR	1.182675	0.129173

Supplemental Table S4. Quantitative proteomics data of Figure 7D

Protein	Peptides	Ratio mean (¹⁴ N/ ¹⁵ N)	SD
PSBA	ANLGMEVMHER	1.317301	0.207086
	ETTENESANEGYR		
	FGQEEETYNIVAAHGYFGR		
	VLNTWADIINR		
PSBD	AAEDPEFETFYTK	1.420160	0.064670
	AFNPTQAEETYSMVTANR		
	AWMAAQDQIPHER		
	AYDFVSQEIR		
	LVFPPEVLPR		
	NILLNEGIR		
	TWFDDADDWLR		
PSBH	VNSDFQEPGLVTPGLTLLR	1.760052	0.307073
	VNSDFQEPGLVTPGLTLLRPLNSEAGK		
PSBO	ADAEELLKENVK	1.821720	0.483510
	EDDGIDYAATTVQLPgger		
	GDFLVPSYR		
	GGSTGYDNAVALPAR		
	GSAVFSVAK		
	GSSFDPK		
	LTYTLDAMSGSFK		
	VAFLETK		
	VDPVTGEIAGVFESIQPSDTDLGAKPPK		
	VGSDGSAELKEDDGIDYAATTVQLPgger		
	VTGLWYAQLK		
PSBP	ENDFPGVILR	3.642855	1.152493
	FLESVSYLLGK		
	HQLIGATVGSNDK		
	QAYSGETQSEGGFAPNR		
	SGFVPYAGDGFALLPAK		
	VSAASLLDVSTTTDKK		
	YEDNFDVNNLVVIAQDTDK		
PSBQ	AKLDSVLA AVL	2.357266	1.072902
	DLDPQNR		
	EFIQAVEDLDFALR		
	FDLNLTASTK		
	GFDLIYEAR		
	IDADLDVFIQK		
PSBW	DLGDFEDADDGLKL	1.063709	0.164927
LHCB4	FPTPPGTQK	1.265684	0.430443
	GSVEAIVQATPDEVSSNR		

Protein	Peptides	Ratio mean (¹⁴ N/ ¹⁵ N)	SD
LHCB4	FRECELIHGR KYQGDALWLPNTRPEWLDGSLPGDR LAPYSEVFGLAR PSEFVVIGVDENDQNAAK GFDPLGLSKPSEFVVIGVDENDQNAAK	1.265684	0.430443
LHCB5	FDSSVFDGLDPLYPGGPFDPGLLADDP EVLQELK GWLGGQGAADLDKWYGPDR HVADPFGYNLLTVLGAEER KFLPSGLYDR NGTGPAGYSPGIGK SEIPEYLNAGELAGDYGYD YRENELLHAR	1.068557	0.212814
LHCBM1	ASTPDSFWYGPGR GPLQNLSHDHLANPGTNNAFAYATK LYPGGSFDPLGLADDPDTFAELK PLFLGAFTGEPPSYLTGEFPGDYGWDTAGLSADVNGGP LGEGLDK	3.538052	0.702943
LHCBM4 and LHCBM6	GPVQNDDHLANPTVNNAFAFATK	2.845682	0.681379
LHCBM2 and LHCBM7	ANGGPLGEGLDPLHPGGAFDPLGLADDPDTFAELK FLGPFSEGDTPAYLTGEFPGDYGWDTAGLSADP ETFKR GPIQNDDHLANPTAVNAFAYATK NGIPFGEAVWFK	2.342341	0.656609
LHCBM3	GPIQNDDHLSNPTVNNAFAFATK QAPASSGIEFYGPNR SGTQFGEAVWFK	2.832832	0.824732
LHCBM5	AGWWSNGGNEK LHPGGQFFDPLGLAEDPDFAELK LSAFYGPDR NGTPIVEPVWFK	1.450154	0.345649
CP43	AAEYMTAPLGLSLNSVGGVATEINAVNFVSPR AMYFGGVYDTWAPGGGDVR DQETTGFVWWSGNAR FDEPVLSMRPLD GIDRFDEPVLSMR GPWLEPLR LGANVASAQGPTGLGK LKNDIQPWQER VITNPTTNAAVIFGYLVK	1.307824	0.143116

Protein	Peptides	Ratio mean (¹⁴ N/ ¹⁵ N)	SD
CP43	SPTGEIIFGGETMR	1.307824	0.143116
CP47	DVFAGIDDDINDQVEFGK KAQLGEIFEFDR LAFYDYIGNNPAK MPTFFETFPVLLLDKDGIVR QGMFVLPFMTR STLQSDGVFR TGAMNSGDGIAGVWLGHASFK VHTVVINDPGR VQASLAEGASLSDAWSR YQWDQGGFFQQEIQK YSIEQVGVSVTFYGGELDGLTFTDPATVK	1.740408	0.194429
LHCSR3	DLGLPVTPLPDNLK EAILELDDIER	28.994430	8.385042
PSBR	VGLNSIEDPVVK YGANVDGYSPIYTPDLWTESGDSYTLGTK	2.507445	0.190226
α-CF1 "	AIESPAPGIVAR AMSGELLEFDGTLGIALNLEANNVGAVLLGDGLK ASSVAQVLNTLK DLIEQYTPEVK EAYPGDVFYLHSR IAEIPVGEAYLGR LELAQFAELEAFSQFASDLQATQNQLAR MVDFGIVFQVGDGIAR PTLTIYDDLK QAINLEYLEEFK QPQSSPLSVEEQVASLYAGTNGYLDKLEVSQVR STLTFTPEAEGLVK SVYEPLATGLVAVDAMIPVGR SYLANSYPK TAIAVDTILNQK TPEELSNLIKDLIEQYTPEVK VVDGLARPVDGK	0.874402	0.078655
β-CF1	AHGGVSVFAGVGER AVSMNPTEGLMR DGSITSIQAVYVPADDLTDPAATTFAHLDATTVLSR DVNKQDVLFFIDNIFR FVQAGAEVSALLGR GIYPAVDPLESTSTMLQPWILGEK GMEVVDTGKPLSVPVGK GQVPNIYNALTIR IFAGELDDLPEQAFYLVGNITEAISK	0.801150	0.077406

Protein	Peptides	Ratio mean (¹⁴ N/ ¹⁵ N)	SD
β-CF1	IFNVLGEPVDNMGNVKVEETLPIHR LSIFETGIK MPSAVGYQPTLATEMGGGLQER TAPAFVDLDTR TREGNDLYTEMK TVLIMELINNIK VALVYQMNEPPGAR VVDLLAPYR YKELQDIHAILGLDELSEEDRLIVAR YVSLAETIEGFGK	0.801150	0.077406

Supplemental Table S5. Proteomics analysis of polypeptides of PSII-LHCII supercomplex from WT and FUD39

The 100µl PSII-LHCII supercomplex fractions from 24h HL SDGs of WT and FUD 39 were digested with trypsin in 30k filter devices (Millipore) as FASP methods described in the literature (Wiśniewski et al. 2009). Peptides were collected by centrifugation of the filter units and analyzed with by electrospray liquid chromatography–tandem MS (LC-MS/MS) using a linear ion trap–orbitrap instrument (LTQ).

PSII-LHCII supercomplex Protein	WT		FUD39	
	Spectral count	Number of peptides	Spectral count	Number of peptides
CP47	57	13	60	11
CP43	62	15	22	11
PSBA	38	5	12	5
PSBD	55	7	15	8
PSBO	24	9	12	8
PSBP	4	3		
PSBQ	2	1		
PSBR	7	1	2	2
PSBH	9	2	3	1
LHCB4	23	8	14	9
LHCB5	31	11	12	8
LHCBM1	1	1	8	4
LHCBM3	1	1	3	2
LHCBM3/6	1	1	2	2
LHCBM4/6	1	1	5	3
LHCBM2/7	1	1	3	3
LHCBM5	2	1	1	1
LHCBM3/4/9	1	1	1	1
Cytochrome b559 alpha subunit	1	1	1	1
Cytochrome b559 beta subunit	1	1	1	1

Supplemental Table S6. Quantitative proteomics data of Figure 9A

Protein	Peptides	Ratio mean (¹⁴ N/ ¹⁵ N)	SD
PSBA	ANLGMEVMHER	2.171896	0.278818
	ENSSLWAR		
	ETTENESANEGYR		
	EWELSFR		
	RENSSLWAR		
	FGQEEETYNIVAAHGYFGR		
	VLNTWADIINR		
	VNSDFQEPGLVTPGLTLLR		
	VNSDFQEPGLVTPGLTLLRPLNSEAGK		
	VNSDFQEPGLVTPGLTLLRPLNSEAGK		
PSBD	AAEDPEFETFYTK	2.056777	0.289577
	AFNPTQAEETYSMVTANR		
	AWMAAQDQIPHER		
	AYDFVSQEIR		
	LVFPPEVLPR		
	NILLNEGIR		
	TIAIGTYQEK		
	TWFDDADDWLR		
PSBH	VNSDFQEPGLVTPGLTLLR	2.157495	0.0481684
	VNSDFQEPGLVTPGLTLLRPLNSEAGK		
PSBO	ADAEELLK	2.858039	0.455611
	ADAEELLKENVK		
	EDDGIDYAATTVQLPGER		
	GDFLVPSYR		
	GGSTGYDNAVALPAR		
	GSAVFSVAK		
	GSSFLDPK		
	LYTLDAMSGSFK		
	VAFLETK		
	VDPVTGEIAGVFESIQPSDTDLGAKPPK		
	VGSDGSAELKEDDGIDYAATTVQLPGER		
	VTGLWYAQLK		
LHCB4	FADGLNNGK	2.038196	0.146513
	FPTPPGTQK		
	GFDPLGLSKPSEFVVIGVDENDQNAAK		
	GSVEAIVQATPDEVSSNR		
	KYQGDALWLPNTRPEWLDGSLPGDR		
	LAPYSEVFLAR		
	NNKGSVEAIVQATPDEVSSNR		
	PSEFVVIGVDENDQNAAK		
	YQGDALWLPNTRPEWLDGSLPGDR		
	YQGDALWLPNTRPEWLDGSLPGDR		

Protein	Peptides	Ratio mean (¹⁴ N/ ¹⁵ N)	SD
LHCBS	ENELLHAR FDSSVFDGLDPLYGGPFDPGLGLADDPEVLQELK GWLGGQGAADLDK GWLGGQGAADLDKWYGPDR HVADPFGYNLLTVLGAER KLFLPSGLYDR LFLPSGLYDR NGTGPAGYSPGIGK SEIPEYLNAGELAGDYGYDPLGLGK SEIPEYLNAGELAGDYGYDPLGLGKDPETVAK WYGPDRK YRENELLHAR	2.029510	0.171230
LHCBM1	ASTPDSFWYGPGR GPLQNLSDHLANPGTNNAFAYATK LYPGGSFDPLGLADDPDTFAELK VNGGPLGEGLDK	0.9293594	0.045767
LHCBM3	GPIQNLDHLSNPTVNNAFATK QAPASSGIEFYGPNR SGTQFGEAVWFK	1.375893	0.051150
LHCBM4/6/8	SSGVEFYGPNR	1.129030	0.250721
LHCBM2 and LHCBM7	ANGGPLGEGLDPLHPGGAFDPLGLADDPDTFAELK FLGPFSEGDTPAYLTGEFPGDYGWDTAGLSADPETFKR GPIQNLDHLSNPTAVNAFAYATK NGIPFGEAVWFK	1.262367	0.252905
LHCBM5	VNGGPAGEGLDK LHPGGQFFDPLGLAEDPDFAELK LSAFYGPDR	0.755537	0.194373
CP43	AAEYMTHAPLGLSLNSVGGVATEINAVNFVSPR AMYFGGVYDTWAPGGGDVDR DQETTGFVWWSGNAR FDEPVLSMRPLD GIDRFDEPVLSMRPLD GPNGLDLNK GPWLEPLR GPWLEPLRGPNGLDLNK LGANVASAQGPTGLGK LKNDIQPWQER NDIQPWQER SPTGEIIFGGETMR VITNPTTNAAVIFGYLVK	2.051706	0.240605
CP47	ADVPRK AQLGEIFEFDR	1.292974	0.247392

Protein	Peptides	Ratio mean (¹⁴ N/ ¹⁵ N)	SD
CP47	DVFAGIDDDINDQVEFGK KAQLGEIFEFDK KLGDTSSLR LAFYDYIGNNPAK LGD TSSLR LGD TSSLREAF MPTFFETFPVLLLDK QGMFVLPFMTR STLQSDGVFR TGAMNSGDGIAVGWLGHASFK VHTVVINDPGR VQASLAEGASLSDAWSR YQWDQGFFQQEIQK	1.292974	0.247392
LHCSR3	EAILLEDDIER TTAAEPQTAAPVAAEDVFAYTK	2.636894	0.119513
PSBR	VGLNSIEDPVVK YGANVDGYSPIYTPDLWTESGDSYTLGTK	2.744204	0.341450
α -CF1 "	AIESPAPGIVAR DLIEQYTPVVK EMSLLLR IAEIPVGEAYLGR LEVSQVR QAINELYEEFK SVYEPLATGLVAVDAMIPVGR TAIAVDTILNQK TPEELSNLIK	3.717900	0.585734
β -CF1	DGSITSIQAVYVPADDLTPAPATTF AHL DATTVLSR ELQDIIAILGLDELSEEDR FVQAGAEVSALLGR GMEVVD TGKPLSVPV GK IFNVLGEPVDNMGNVK QDVLFFIDNIFR TAPAFVDLDTR VALTALTMAEYFR VALVYGQMNEPPGAR VEETLPIHR VVDLLAPYR	3.566088	0.487106