

Table S3

Table S3. LC-MS/MS parameters for PRM analyses. *, Single Ion Monitoring (SIM) data was acquired in parallel to PRM data, but was excluded from further analyses.

LHCSR3 phosphosite mutants*		High light kinetics		LC parameters				
Trypsin digested samples	LysC digested samples	200 µmol photons m ⁻² s ⁻¹	500 µmol photons m ⁻² s ⁻¹					
Eluent compositions		Peptide trapping: 0.05% trifluoroacetic acid (TFA) in ultrapure water (A1), 0.05% TFA in 80% acetonitrile (B1) Peptide separation: 0.1% formic acid (FA) in ultrapure water (A2), 0.1% FA in 80% acetonitrile (B2)						
Trap Column		C18 PepMap 100, 300 µM x 5 mm, 5 µm particle size, 100 Å pore size; Thermo Scientific						
Peptide trapping (eluents A1+B1)	2.5% B1 at 10 µl/min for 10 min	2.5% B1 at 10 µl/min for 5 min		MS settings (PRM)				
Separation Column	Acclaim PepMap C18, 75 µm x 50 cm, 2 µm particle size, 100 Å pore size; Thermo Scientific	Acclaim PepMap C18, 75 µm x 15 cm, 2 µm particle size, 100 Å pore size; Thermo Scientific	Acclaim PepMap C18, 75 µm x 50 cm, 2 µm particle size, 100 Å pore size; Thermo Scientific					
Gradient for peptide separation (eluents A2+B2)	2.5-30% B2 over 240 min, 30-50% B2 over 60 min, 50%-99% B2 over 5 min 99% B2 over 15 min	2.5-15% B2 over 47 min, 15%-34% B2 over 33 min, 34%-99% B2 over 5 min, 99% B over 5 min	2.5-18% B2 over 65 min, 18%-35% B2 over 40 min, 35%-99% B2 over 5 min, 99% B2 over 20 min					
Flow rate	300 nl/min							
Chromatographic peak width	15 s							
Resolution (FWHM) at m/z 200	70,000	35,000	35,000					
AGC target	1e5		5e4					
Maximum injection time	480 ms	240 ms	240 ms					
Isolation window	2 m/z	3 m/z	2 m/z					
Isolation offset	0 m/z	1 m/z	0.5 m/z					
Normalized collision energy (NCE)	27							