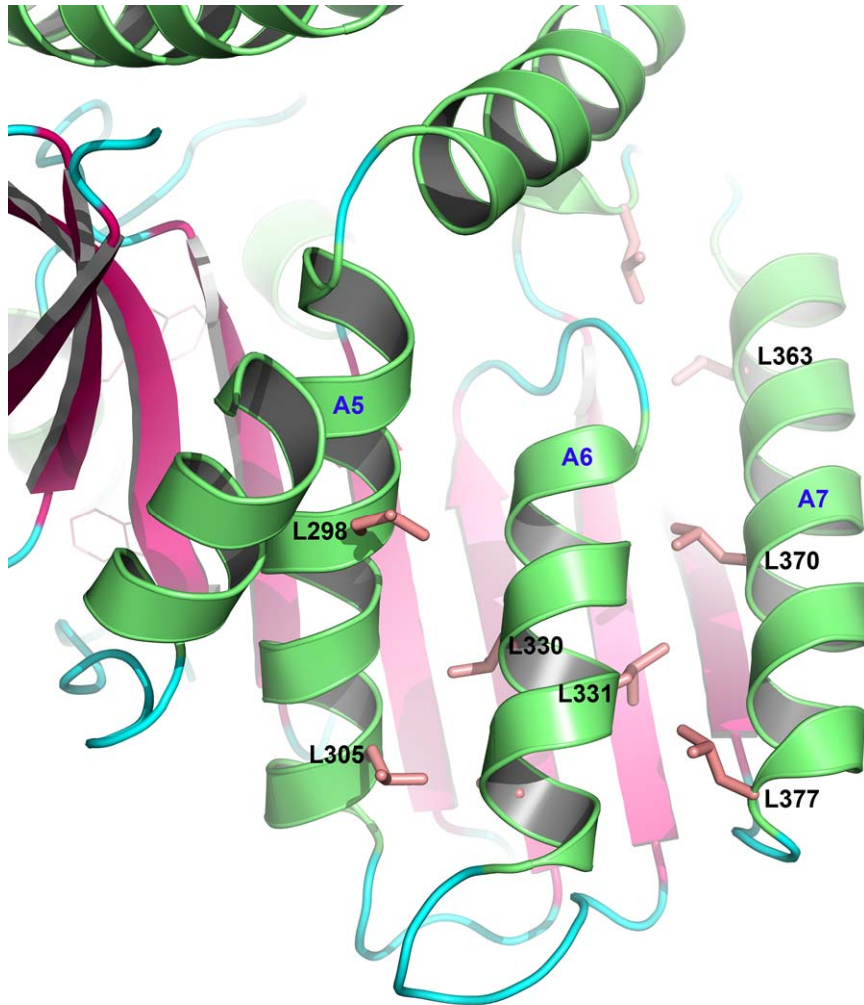
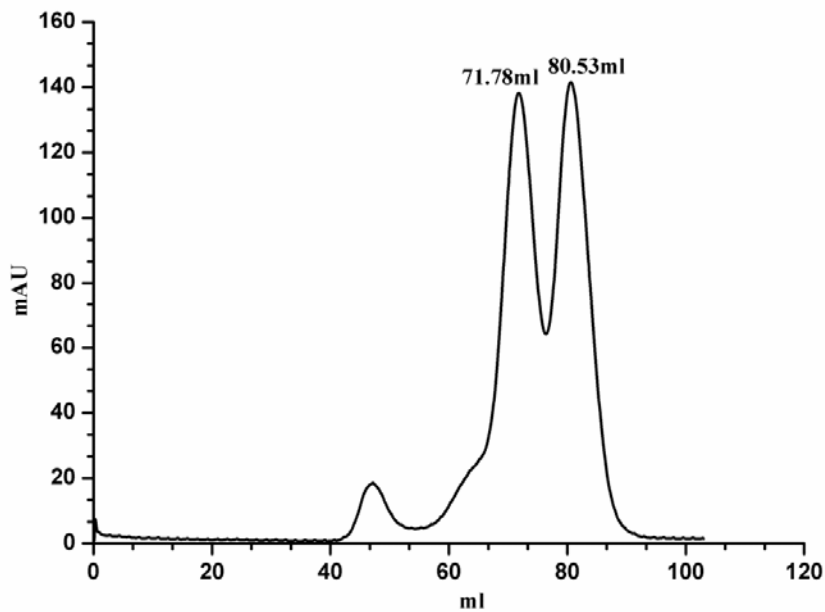


**Supplemental Figure 1. Sequence alignment of Os-SCL7 with other GRAS family members.** Alignment of Os-SCL7 and ten other GRAS proteins from different clades of GRAS family: Pe-SCL7 (KJ511863), Os-NSP2 (LOC\_Os03g15680), At-SCR (AT3G54220), Os-DLT (LOC\_Os06g03710), Os-GAI (LOC\_Os03g49990), At-PAT1 (AT5G48150), Os-NSP1 (LOC\_Os03g29480), At-LAS (AT1G55580), At-SCL14 (AT1G07530), At-SCL3 (AT1G50420), as performed by ClustalW and then drawn with Bioedit.

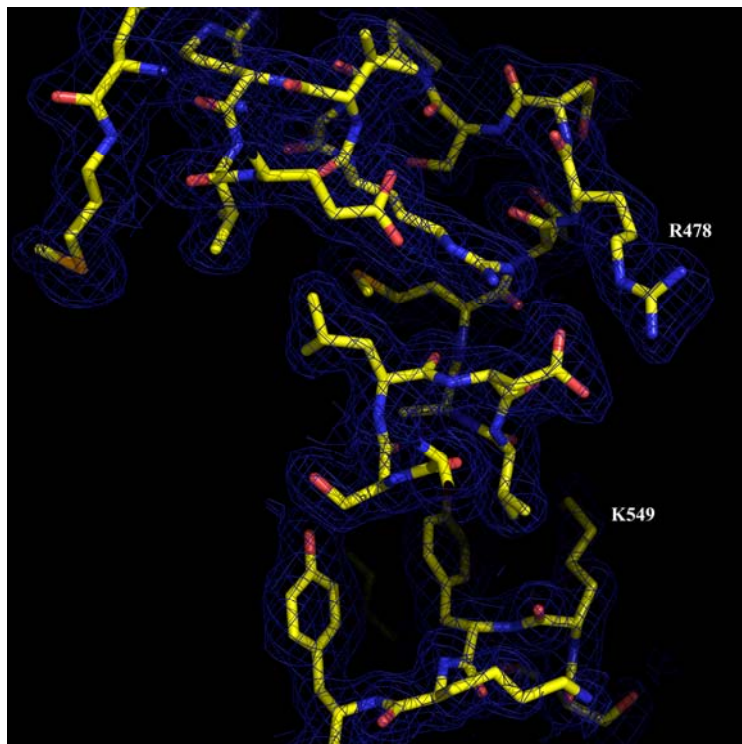


**Supplemental Figure 2. Structure of leucine heptad repeat region of Os-SCL7.** Ribbon diagram of the leucine heptad repeat region of Os-SCL7 GRAS domain structure, with  $\alpha$ -helices labelled and featured leucine residues in ball-and-stick representation and labelled.





**Supplemental Figure 3. Size exclusive chromatography for Os-SCL7 protein.** The two marked peaks eluted from HiLoad 16/600 superdex200 column match the molecular weight of about 80kD and 40kD, corresponding to a size of dimer and monomer of Os-SCL7 protein, respectively.



**Supplemental Figure 4.** The 2Fo-Fc electron-density map by Pymol of DNA binding-relevant site of Os-SCL7 protein.

**Supplemental Table 1. List of primers used in this study.**

<b>Primer Name</b>	<b>Sequence</b>
<b>Plasmid construct</b>	
Os-SCL7-BamHI	CGG <b>ATCCTG</b> CTCCGCTCCCATCCTCCAG
Os-SCL7-HindIII	CCCA <b>AAGCTT</b> TTTACCTCCAAGCAGACACAGTAAGCAATG
<b>Mutagenesis</b>	
K284A-Forward	AGCTCACGCTCTGCTACGCGACGCTCAACGACGCCTG
K284A-Reverse	CAGGCGTCGTTGAGCGTCGCGTAGCAGAGCGTGAGCT
K284E-Forward	GCTCACGCTCTGCTACGAGACGCTCAACGACGCC
K284E-Reverse	GGCGTCGTTGAGCGTCTCGTAGCAGAGCGTGAGC
R478A-Forward	GATGTGGCAATGACCGCGGACTCACCGGAGAG
R478A-Reverse	CTCTCCGGTGAGTCCGCGGTCATTGCCACATC
R485A-Forward	TCACCGGAGAGGGTGGCGGTGGAGCGTTGGATG
R485A-Reverse	CATCCAACGCTCCACCGCCACCCTCTCCGGTGA
K549A-Forward	CTGGA <sup>A</sup> ACTATGATTCCGCGTACAAGTATTC <sup>A</sup> CTTG
K549A-Reverse	CAAGTGA <sup>A</sup> ACTTGTACGCGGAATCATAGTTCCAG
K549E-Forward	CTGGA <sup>A</sup> ACTATGATTCCGAGTACAAGTATTC <sup>A</sup> C
K549E-Reverse	GTGA <sup>A</sup> ACTTGTACTCGGAATCATAGTTCCAG
K551A-Forward	ACTATGATTCCAAGTACGCGTATTC <sup>A</sup> CTTGTTGAGTT
K551A-Reverse	AACTCAACAAGTGAATACGCGTACTTGG <sup>A</sup> AATCATAGT