

Supplemental Data

The Sec61/SecY complex is inherently deficient in translocating intrinsically disordered proteins

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Primary and secondary structure of proteins used in this study in FASTA-like format. α -helix: framed; β -strand: bold and labeled in grey; epitope tag: italic and light grey, asterisk: secondary structure based on Jpred 4 prediction.

Signal peptides:

PrP: MANLGYWLLALFVTMWTDVGLC

pelB: MKYLLPTAAAGLLLLAAQPMAM

dsbA: MKKIWLALAGLVLAFSASA

kre5p: MRLLALVLLLCAPLRA

Shadoo: MNWAPATCWALLLAAAFLCDSGAA

Primary and secondary structures of the constructs without signal peptide:

α :

α	α	α
GGLGGYMLGSAMSRPMIHFGN <u>D</u> E <u>D</u> R <u>Y</u> Y <u>R</u> E <u>N</u> M <u>Y</u> R <u>Y</u> P <u>N</u> Q <u>V</u> Y <u>R</u> P <u>V</u> D <u>Q</u> Y <u>S</u> N <u>Q</u> N <u>N</u> F <u>V</u> H <u>D</u> C <u>V</u> N <u>I</u> T <u>I</u> K <u>Q</u> H <u>T</u> V <u>T</u> T <u>T</u> K <u>G</u> E <u>N</u> F <u>T</u> E <u>T</u> D <u>V</u> K <u>M</u>		
<u>M</u> ER <u>V</u> V <u>E</u> Q <u>M</u> C <u>V</u> T <u>Q</u> Y <u>Q</u> K <u>E</u> S <u>Q</u> A <u>Y</u> Y <u>D</u> G <u>R</u> R <u>S</u> S <u>S</u> T <u>V</u> L <u>F</u> S <u>S</u> P <u>P</u> <u>V</u> I <u>L</u> I <u>S</u> F <u>L</u> I <u>F</u> L <u>I</u> <u>V</u> G		

α^*

α (PB):

α	α	α
KKRPKPGGWNTGGGLGGYMLGSAMSRPMIHFGN <u>D</u> E <u>D</u> R <u>Y</u> Y <u>R</u> E <u>N</u> M <u>Y</u> R <u>Y</u> P <u>N</u> Q <u>V</u> Y <u>R</u> P <u>V</u> D <u>Q</u> Y <u>S</u> N <u>Q</u> N <u>N</u> F <u>V</u> H <u>D</u> C <u>V</u> N <u>I</u> T <u>I</u> K <u>Q</u> H <u>T</u> V <u>T</u> T <u>T</u> K <u>G</u> E <u>N</u> F <u>T</u> E <u>T</u> D <u>V</u> K <u>M</u>		
<u>K</u> GEN <u>F</u> T <u>E</u> <u>T</u> D <u>V</u> K <u>M</u> ER <u>V</u> V <u>E</u> Q <u>M</u> C <u>V</u> T <u>Q</u> Y <u>Q</u> K <u>E</u> S <u>Q</u> A <u>Y</u> Y <u>D</u> G <u>R</u> R <u>S</u> S <u>S</u> T <u>V</u> L <u>F</u> S <u>S</u> P <u>P</u> <u>V</u> I <u>L</u> I <u>S</u> F <u>L</u> I <u>F</u> L <u>I</u> <u>V</u> G		

α^*

IDD114:

PGGNFTGGSRYPGQSPGGNRYPPQGGTWGQPHGGWGQPHGGSWQPHGGSWQPHGGWGQGGGTHNQWNKPSKPKNMKH
MAGA

IDD133:

KKRPK/AAAPA—PGGNFTGGSRYPGQSPGGNRYPPQGGTWGQPHGGWGQPHGGSWQPHGGSWQPHGGWGQGGGTHNQW
NKPSKPKNMKHMAGAAAAGAVVGGLGGYMLGSAM

IDD209:

KKRPK/AAAPA—PGGNFTGGSRYPGQSPGGNRYPPQGGTWGQPHGGWGQPHGGSWQPHGGSWQPHGGWGQGGGTHNQW
NKPSKPKNMKHMAGAAPRKRPKPGWNTGGSRYPGQSPGGNRYPPQGGTWGQPHGGWGQPHGGSWQPHGGSWQPHGG
WGQGGGTHNQWNKPSKPKNMKHMAGA

IDD α :

KKRPK/AAAPA—PGGWNTGGSRYPGQSPGGNRYPPQGGTWGQPHGGWGQPHGGSWQPHGGSWQPHGGWGQGGGTHNQW
 α
NKPSKPKNMKHMAGAQNNFVHDCVNITIKQHTVTTTKGENFTETDVKMERVVEQMCVTQYQKES

α •IDD:

α
QNNFVHDCVNITIKQHTVTTTKGENFTETDVKMERVVEQMCVTQYQKESKKRPK/AAAPA—PGGWNTGGSRYPGQSPGGNRYPPQGG
TYPPQGGTWGQPHGGWGQPHGGSWQPHGGSWQPHGGWGQGGGTHNQWNKPSKPKNMKHMAGA

α •IDD•IDD:

α
QNNFVHDCVNITIKQHTVTTTKGENFTETDVKMERVVEQMCVTQYQKESKKRPKPGGWNTGGSRYPQGSPGGNRYPPQGG
TWQPHGGWGQPHGGSWQPHGGSWQPHGGWGQGGGTHNQWNKPSKPKNMKHMAGAAPRKRPKPGGWNTGGSRYPQG
SPGGNRYPPQGGTWQPHGGWGQPHGGSWQPHGGSWQPHGGWGQGGGTHNQWNKPSKPKNMKHMAGA

IDD•α•IDD:

KKRKP_αPGGNTGGSRYPQGSPGGNRYP_αPQGGTWGQPHGGWGQPHGGSGWQPHGGSWQPHGGWGQGGGTHNQWNKPSKPK
 TNMKHMAGAQ_αNFVHDCVNITIKQHTVTTTKGENFTE_αTDVKMMERVVEQMCVTQYQKESKKRP_αPGGNTGGSRYPQGSPG
 GNRYPPQGGTWGQPHGGWGQPHGGSGWQPHGGSWQPHGGWGQGGGTHNQWNKPSKPKTNMKHMAGA

IDD•IDD•α:

KKRKP_αPGGNTGGSRYPQGSPGGNRYP_αPQGGTWGQPHGGWGQPHGGSGWQPHGGSWQPHGGWGQGGGTHNQWNKPSKPK
 TNMKHMAGAAPRK_αRKPKPGGNTGGSRYPQGSPGGNRYP_αPQGGTWGQPHGGWGQPHGGSGWQPHGGSWQPHGGWGQGGG
 THNQWNKPSKPKTNMKHMAGAQ_αNFVHDCVNITIKQHTVTTTKGENFTE_αTDVKMMERVVEQMCVTQYQKES

IDD•β:

KKRKP_αPGGNFTGGSRYPQGSPGGNRYP_αPQGGTWGQPHGGWGQPHGGSGWQPHGGSWQPHGGWGQGGGTHNQWNKPSKPK
 TNMKHMAGAY_βQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYN_βYNSHN_βVIMADKQ_βKNGIKVN_βF
 KIRHNIEDGSVQLADHYQ_βQNTPIGDGPVLLPDNHYLSTQSA_βSKDPNEKRDHMVLLEFVTAAGITLGMDELYK

α•β (HA):

_αQN_αNFVHDCVNITIKQHTVTTTKGENFTE_αTDVKMMERVVEQMCVTQYQKESY_βQERTIFFKDDGNYKTRAEVKFEGDTLVNRI_β
 ELKGIDFKEDGNILGHKLEYN_βYNSHN_βVIMADKQ_βKNGIKVN_βF_βKIRHNIEDGSVQLADHYQ_βQNTPIGDGPVLLPDNHYLSTQSA_β
 LSKDPNEKRDHMVLLEFVTAAGITLGMDELYK_{HA}AAAYPYDVPDYA

β (HA):

KKRPK/AAAPA-PGGNFTGGSRYG_βYQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEY_β YN_βSHN_β
 VYIMADKQ_βKNGIKVN_βF_βKIRHNIEDGSVQLADHYQ_βQNTPIGDGPVLLPDNHYLSTQSA_βSKDPNEKRDHMVLLEFVTAAGITLG_β
 MDELYK_{HA}AAAYPYDVPDYA

Prion protein:

KKRPK/AAAPA-PGGWNTGGSRYPQGSPGGNRYP_αPQGGTWGQPHGGWGQPHGGSGWQPHGGSWQPHGGWGQGGGTHNQW_α
 NKPSKPKTNMKHMAGAAAAGAVVGG_αGYMLGSAMSRPMI_αHFGND_αWEDRYYREN_αMYRYPNQVYYRPVDQYSNQ_αNFVHDCVN_αI
 TIKQHTVTTTKGENFTE_αTDVKMMERVVEQMCVTQYQKESQAYDGRSSSTVLFSSPP_{α*}VILLISFLIFLIVG

Shadoo (V5):

MKGGRGGARGSARGGVRG_{V5}GARGASRV_{V5}RPAQR_{V5}YGA_{V5}P_{V5}GSSLRVAAAGAAAGAAAGAAAGLAAGSGWRRAAGPGERGLEDEEDG_{α*}
 VP_{V5}GGNGTGP_{V5}GIYSYRAWT_{V5}GKPIPNPL_{V5}L_{V5}LD_{V5}STSGAGPTRG_{V5}PRLCLV_{V5}LGGALGALGLLRP

IDD114•Syn:

KKRKP_αGGNFTGGSRYPQGSPGGNRYP_αPQGGTWGQPHGGWGQPHGGSGWQPHGGSWQPHGGWGQGGGTHNQWNKPSKPK
 TNMKHMAGADVFMKGLSKAKEGV_αAAEAKT_αKQGV_αAEAAGKTKEGVLYVGSKTKEGV_αVHG_αVATVAEKTKEQ_αVTNVGGAVVTGVT
 AVA_αQKTVEGAGSIAAATGFVKKDQLGKNEEGAPQEGILEDMPVDPDNEAYEMPSEEGYQDYEPEA

IDD114•Tau:

KKRKP_αGGNFTGGSRYPQGSPGGNRYP_αPQGGTWGQPHGGWGQPHGGSGWQPHGGSWQPHGGWGQGGGTHNQWNKPSKPK
 TNMKHMAGAAEAEAGNGDTPSLEDEAAGHVTQARMVS_αSKDGTGSDDKKAKGADGKT_αIA_αPRGAAPPQKGQANATRIPAKTP
 PAPKTP_αSSGEPPKSGDRSGY