

# Supplementary Information

## Self-assembly and regulation of protein cages from pre-organised coiled-coil modules

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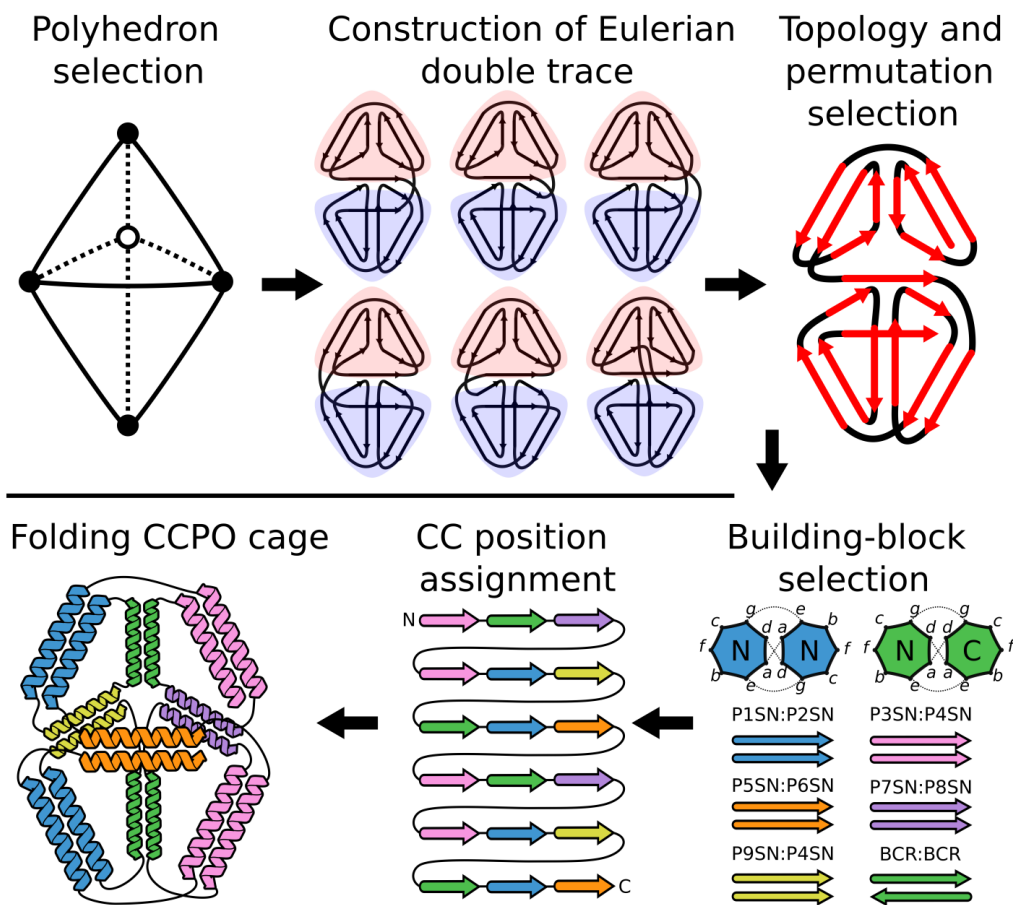
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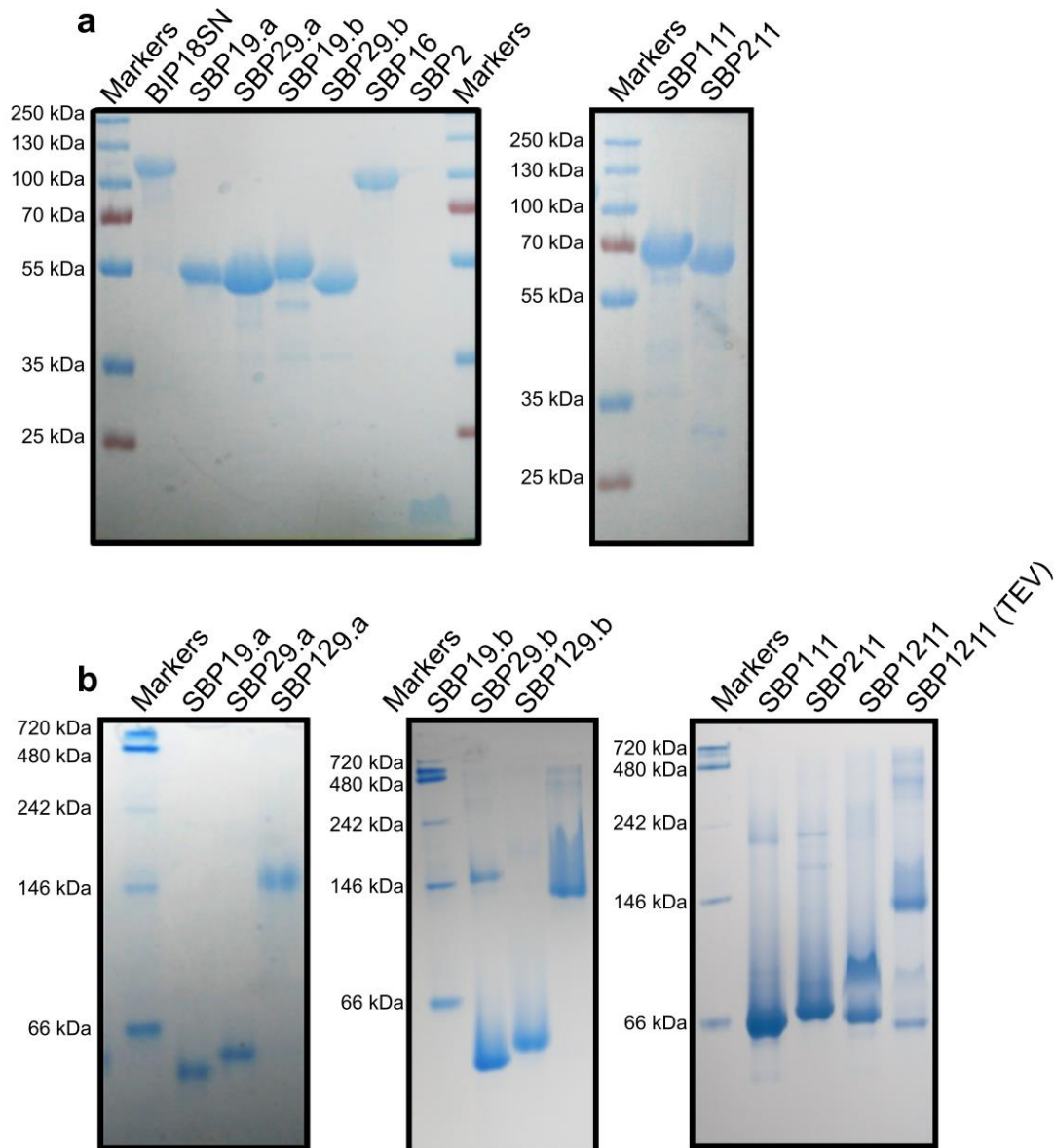
### This document includes:

- Supplementary Figures 1 to 10
- Supplementary Tables 1 to 3
- List of protein sequences
- List of DNA sequences

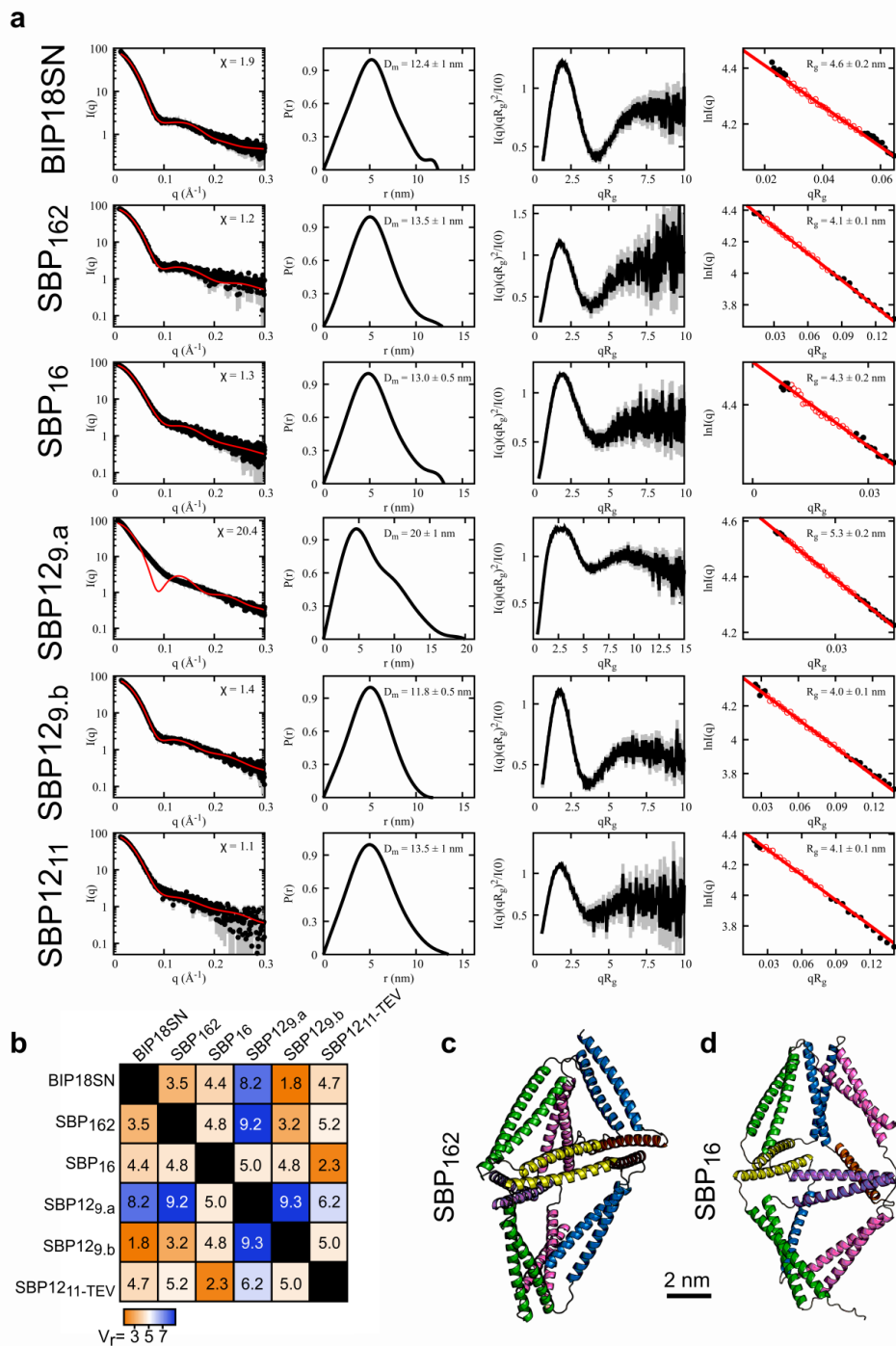
## Supplementary Figures



**Supplementary Figure 1: Design process for the modular trigonal bipyramid cage BIP18SN.** From left to right: i) the selection of a polyhedral shape was followed by ii) tracing a double Eulerian trail for different topological solution of two pseudo-symmetric tetrahedral halves. iii) The selection of the beginning and end of the linear chain was based on the selection of the lowest topological contact order (TCO) between the complementary edges of the polyhedron. iv) The CC building blocks were selected from a set of orthogonal CC dimers. v) The building blocks were assigned to different positions, prioritising stronger pairs at the termini and using the same pairs in each half as indicated by the colour. vi) Molecular models of the protein were built and used to fit experimental data.

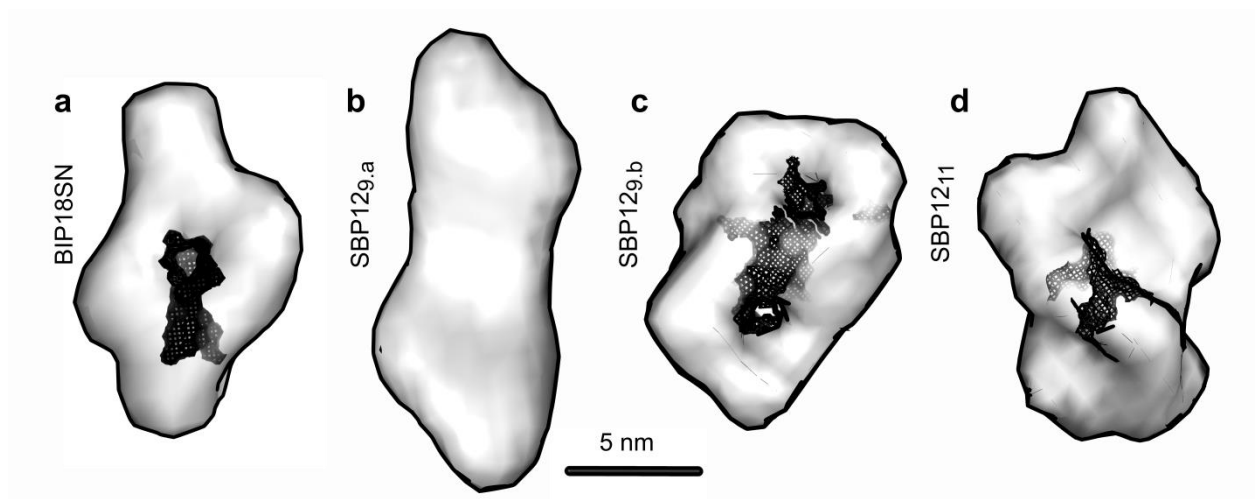


**Supplementary Figure 2: Electrophoretic analysis of purified proteins. a**, SDS-PAGE of purified proteins loaded next to molecular weight markers. Markers from bottom to top: 25 kDa, 35 kDa, 55 kDa, 70 kDa, 100 kDa, 130 kDa, 250 kDa. **b**, Native-PAGE of monomeric proteins and protein complexes before and after treatment with TEV protease at 37 °C loaded next to molecular weight markers. Markers from bottom to top: 66 kDa, 146 kDa, 242 kDa, 480 kDa, 720 kDa. The gels are representative of at least two repetitions of the same experiments. Source data are provided as a Source Data file.

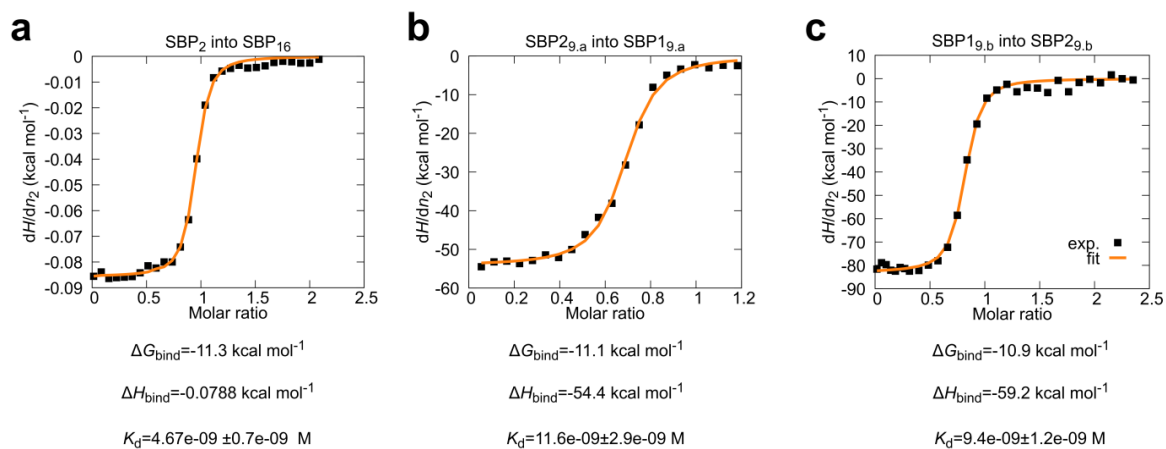


**Supplementary Figure 3: SAXS analysis of CCPO bipyramidal proteins. a**, SAXS analysis of main CCPO bipyramidal proteins. From left to right: SAXS scattering curve (black trace for experimental SAXS data and red trace for theoretical SAXS curve calculated from molecular model of the cage structure), pair distribution function; normalised Kratky plot and Guinier plot. Error bars in grey represent the standard deviation for each data point in black (mean). **b**, The bottom panel contains a similarity matrix with the volatility ratio for

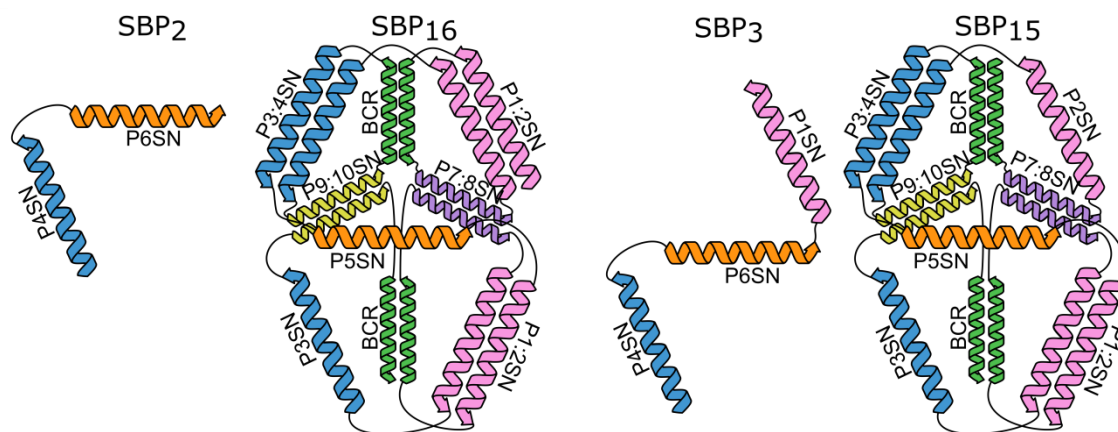
each protein calculated as described in the Methods section. **c**, Molecular model of SBP<sub>162</sub> used to fit experimental SAXS curve. **d**, Molecular model of SBP<sub>16</sub> used to fit SAXS results. Source data are provided as a Source Data file.



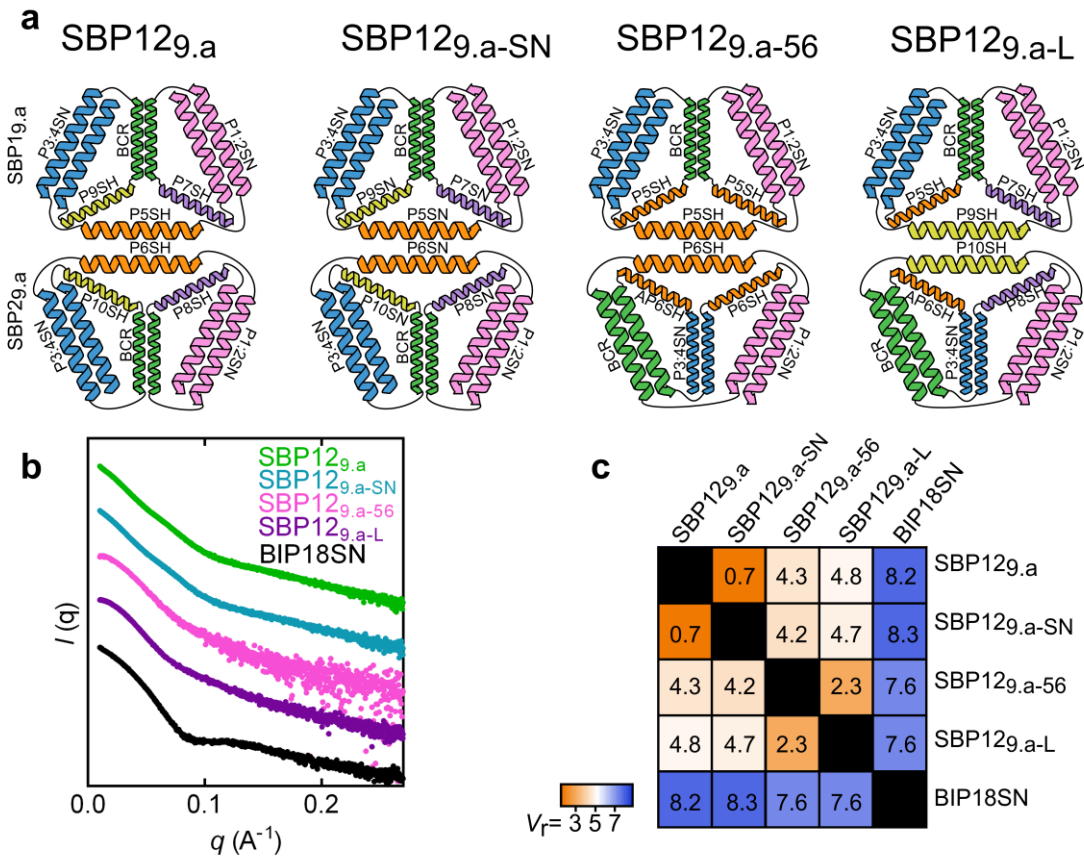
**Supplementary Figure 4: *Ab initio* reconstruction of the molecular shape based on SAXS data.** *Ab initio* SAXS reconstruction based on the pair distance distribution function for **a**, BIP18SN; **b**, SBP129,a; **c**, SBP129,b, **d**, SBP1211. The cavities are visible as black mesh surfaces.



**Supplementary Figure 5: Isothermal titration calorimetry of interactions between the CCPO modules.** ITC experiments were used to determine the  $K_d$  for the formation of the heterodimeric protein complexes **a**, SBP<sub>162</sub>, **b**, SBP<sub>129,a</sub>, **c**, SBP<sub>129,b</sub>. In each case, the experimental data was described with a 1:1 binding model to obtain the free energy and the enthalpy of binding. Source data are provided as a Source Data file.

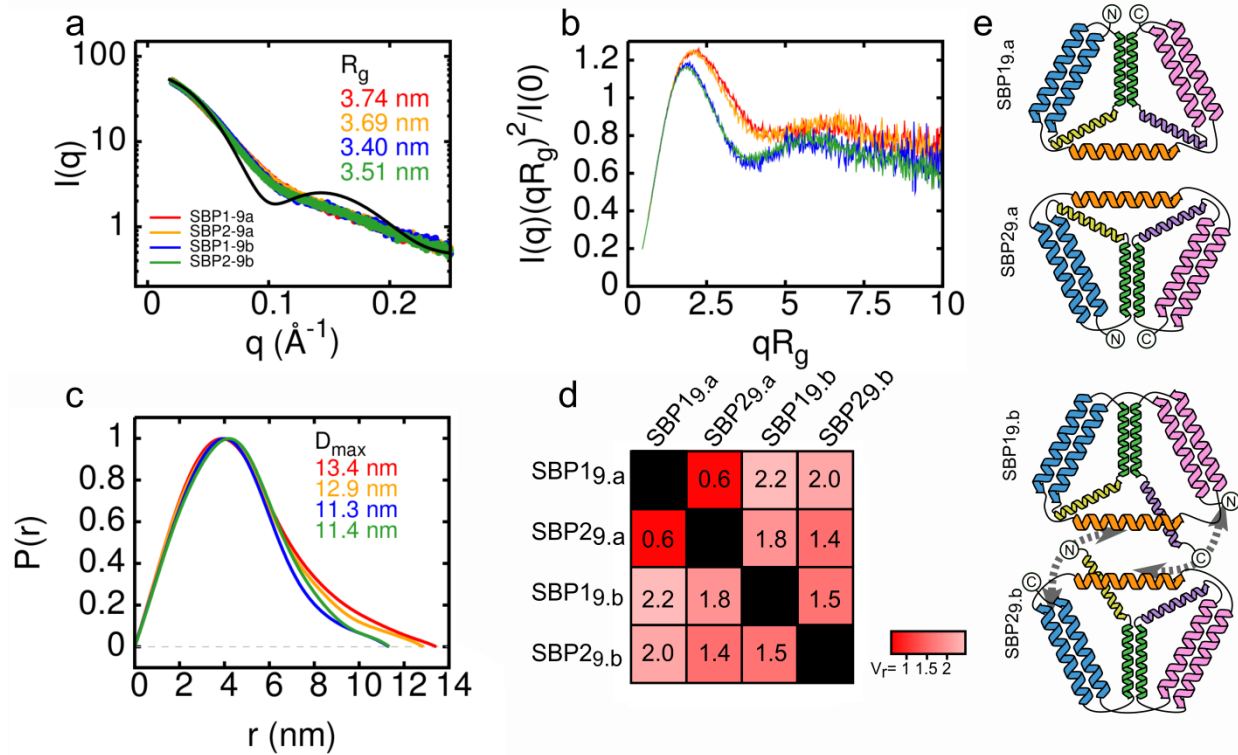


**Supplementary Figure 6: Topological schemes of the asymmetric assembly of SBP heterodimers.** The schemes represent different protein designs used for the asymmetric reconstruction of the heterodimeric bipyramid. While the complex SBP<sub>2</sub>:SBP<sub>16</sub> was fully characterised, the protein complex deriving from SBP<sub>15</sub> and SBP<sub>3</sub> was not characterised due to the low solubility of the subunit SBP<sub>15</sub>.

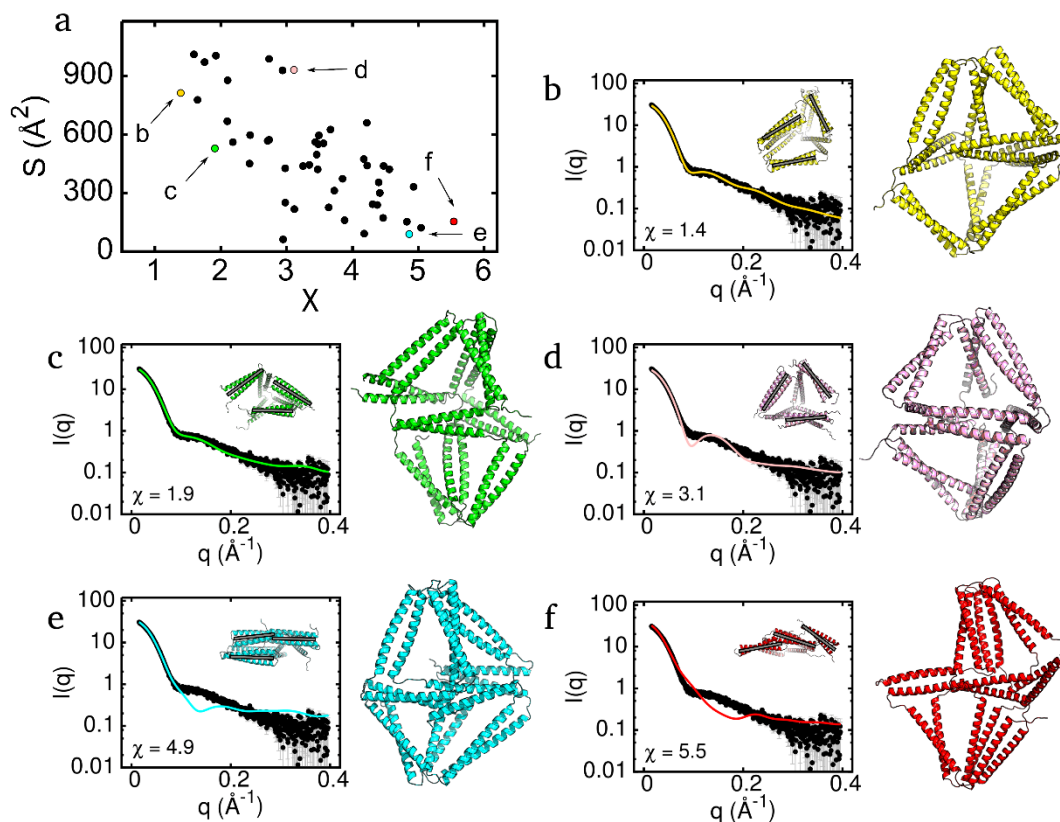


**Supplementary Figure 7: SAXS analysis of alternative SBP12<sub>9,a</sub> protein complexes. a,** Topological schemes of different variants of the protein complex SBP12<sub>9,a</sub>. Coiled-coil pairs are represented as coloured helices. The complex SBP12<sub>9,a</sub> is described in the main text. The complex SBP12<sub>9,a</sub>-SN is analogous to the former; however, CC segments with decreased helicity have been positioned at the interface (SN instead of SH). The complex SBP12<sub>9,a</sub>-56 has been designed employing a repetition the same CC segments P5SH:P6SH at interfacial positions. The complex SBP12<sub>9,a</sub>-L presents only a different arrangement of CC segments compared to the complex SBP12<sub>9,a</sub>. **b,** SAXS scattering curves of (from top to bottom) SBP12<sub>9,a</sub>, SBP12<sub>9,a</sub>-SN, SBP12<sub>9,a</sub>-56, SBP12<sub>9,a</sub>-L and BIP18SN. **c,**  $V_r$  matrix showing a comparison between experimental SAXS profiles obtained for different variants of the complex SBP12<sub>9,a</sub> and the single-chain protein BIP18SN. Source data are provided as a Source Data file.

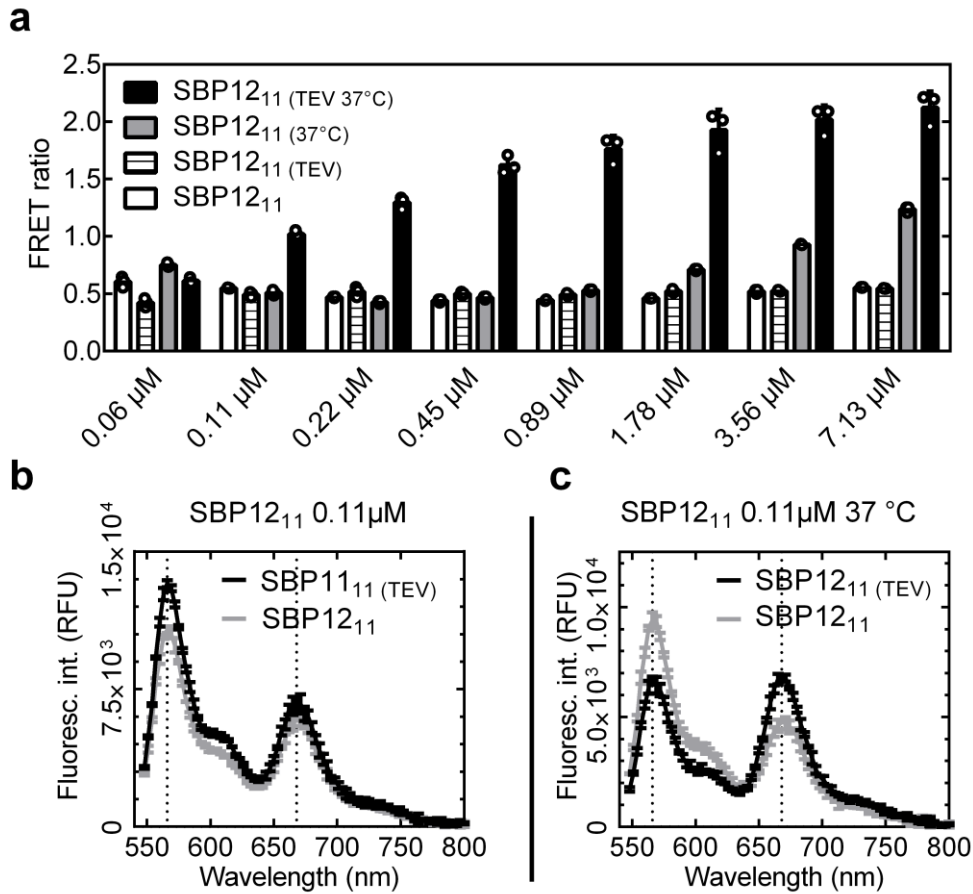




**Supplementary Figure 8: SAXS analysis of individual SBP<sub>9,a</sub>, SBP<sub>9,b</sub> subunits.** **a**, SAXS profiles of individual split-bipyramid subunits with  $R_g$  (black, red, yellow, blue and green traces for a theoretical bipyrmaid model, SBP1<sub>9,a</sub>, SBP2<sub>9,a</sub>, SBP1<sub>9,b</sub>, SBP2<sub>9,b</sub> respectively). **b**, Normalised Kratky plot of individual split-bipyramid subunits. **c**, SAXS pair distance distribution function for individual split-bipyramid subunits. **d**,  $V_r$  matrix showing the similarity of SAXS profiles measured for individual split-bipyramid subunits. **e**, Topological schemes of the subunits where coiled-coil pairs are represented as coloured helices. N- and C-termini are indicated with circled letters. Dashed arrows indicate the higher degree of freedom for the termini of the subunits SBP1<sub>9,b</sub> and SBP2<sub>9,b</sub> compared to SBP1<sub>9,a</sub> and SBP2<sub>9,a</sub>. Source data are provided as a Source Data file.



**Supplementary Figure 9: SAXS fit to different SBP12<sub>9,b</sub> models.** **a**, The plot indicates the goodness of SAXS fit ( $\chi$ ) to molecular models in different conformations, which have a different surface area at the interface ( $S$ ). The graph shows a better fit for models having a larger surface area, which corresponds to a larger internal cavity. The data point colour corresponds to the models showed below in the figure. **b-f**, SAXS experimental curve for SBP12<sub>9,b</sub> (black trace) fitted to the theoretical scattering curve for models in different conformations. Error bars in grey represent the standard deviation for each data point in black (mean). In the plot is shown the fit between experimental data and theoretical scattering curve in addition to the  $\chi$  value for each conformation. In the top right of each plot is shown the molecular model missing one subunit from bottom view with segments at the interface labelled with bars. The models in different conformations are placed next to the corresponding graphs. Source data are provided as a Source Data file.



**Supplementary Figure 10: FRET ratio and fluorescence spectra of labelled proteins. a,** panel shows the FRET ratio at different concentration of the two labelled subunits SBP1<sub>11</sub> and SBP2<sub>11</sub> mixed in equimolar ratio (with and without addition of TEV protease and incubation at 37 °C). Error bars represent the standard deviation of three measurements of the same samples (n=3). **b,** Fluorescence spectra of the two subunits SBP1<sub>11</sub> and SBP2<sub>11</sub> mixed in equimolar ratio, in the presence or absence of TEV protease. **c,** Fluorescence spectra of the two subunits SBP1<sub>11</sub> and SBP2<sub>11</sub> mixed in equimolar ratio, in the presence or absence of TEV protease after incubation at 37 °C. Error bars represent the standard deviation of three measurements of the same samples (n=3). Fluorescence signal is reported in relative fluorescence units (RFU). Source data are provided as a Source Data file.

## Supplementary Tables

CC	Orientation	Sequence	Helicity
<i>Register</i>		<i>gabcdef gabcdef gabcdef gabcdef gab</i>	
P1SN	Parallel	SPED <b>E</b> IR <b>Q</b> LE <b>Q</b> <b>E</b> NS <b>Q</b> LE <b>R</b> <b>E</b> N <b>Q</b> RL <b>Q</b> <b>E</b> IQ <b>Q</b> LE <b>R</b>	16.18
P2SN	Parallel	SPED <b>K</b> IEEL <b>K</b> E <b>K</b> NS <b>Q</b> L <b>K</b> E <b>K</b> NEEL <b>K</b> Q <b>K</b> IYEL <b>K</b> E	6.82
P3SN	Parallel	SPED <b>E</b> IQ <b>Q</b> LE <b>E</b> <b>E</b> IS <b>Q</b> LE <b>Q</b> <b>K</b> NS <b>E</b> L <b>K</b> E <b>K</b> NQEL <b>K</b> Y	4.52
P4SN	Parallel	SPED <b>K</b> IS <b>Q</b> L <b>K</b> E <b>K</b> IQ <b>Q</b> L <b>K</b> Q <b>E</b> N <b>Q</b> QLE <b>E</b> <b>E</b> NS <b>Q</b> LE <b>Y</b>	3.84
P5SN	Parallel	SPED <b>E</b> NS <b>Q</b> LE <b>E</b> <b>K</b> IS <b>Q</b> L <b>K</b> Q <b>K</b> NS <b>E</b> L <b>K</b> E <b>E</b> IQ <b>Q</b> LE <b>Y</b>	3.51
P5SH	Parallel	SPED <b>E</b> NE <b>K</b> LE <b>E</b> <b>K</b> IWEL <b>K</b> R <b>K</b> NEEL <b>K</b> R <b>E</b> IK <b>E</b> LE <b>E</b>	44.47
P6SN	Parallel	SPED <b>K</b> NS <b>E</b> L <b>K</b> E <b>E</b> IQ <b>Q</b> LE <b>E</b> <b>E</b> N <b>Q</b> QLE <b>E</b> <b>K</b> IS <b>E</b> L <b>K</b> Y	2.53
P6SH	Parallel	SPED <b>K</b> NEEL <b>K</b> R <b>E</b> IK <b>E</b> LE <b>W</b> <b>E</b> NE <b>E</b> LE <b>R</b> <b>K</b> IEEL <b>K</b> R	30.73
P7SN	Parallel	SPED <b>E</b> IQ <b>Q</b> LE <b>E</b> <b>K</b> NS <b>Q</b> L <b>K</b> Q <b>E</b> IS <b>Q</b> LE <b>E</b> <b>K</b> NQEL <b>K</b> Y	3.54
P7SH	Parallel	SPED <b>E</b> IK <b>E</b> LE <b>W</b> <b>K</b> NEEL <b>K</b> R <b>E</b> IK <b>E</b> LE <b>E</b> <b>K</b> NEEL <b>K</b> R	40.02
P8SN	Parallel	SPED <b>K</b> IS <b>E</b> L <b>K</b> E <b>E</b> N <b>Q</b> QLE <b>Q</b> <b>K</b> IQ <b>Q</b> L <b>K</b> E <b>E</b> NS <b>Q</b> LE <b>Y</b>	4.28
P8SH	Parallel	SPED <b>K</b> IEEL <b>K</b> R <b>E</b> NE <b>E</b> LE <b>W</b> <b>K</b> IEEL <b>K</b> R <b>E</b> NE <b>E</b> LE <b>K</b>	28.09
P9SN	Parallel	SPED <b>E</b> N <b>Q</b> SLE <b>Q</b> <b>K</b> NS <b>Q</b> L <b>K</b> Q <b>E</b> IS <b>Q</b> LE <b>Q</b> <b>E</b> IQ <b>Q</b> LE <b>Y</b>	3.06
P9SH	Parallel	SPED <b>E</b> NE <b>K</b> LE <b>R</b> <b>K</b> NEEL <b>K</b> W <b>E</b> IK <b>K</b> LE <b>R</b> <b>E</b> IK <b>E</b> LE <b>R</b>	31.42
P10SN	Parallel	SPED <b>K</b> NS <b>Q</b> L <b>K</b> E <b>E</b> NS <b>Q</b> LE <b>E</b> <b>K</b> IE <b>Q</b> L <b>K</b> E <b>K</b> IQEL <b>K</b> Y	4.97
P10SH	Parallel	SPED <b>K</b> N <b>K</b> EL <b>K</b> E <b>E</b> N <b>K</b> ELE <b>W</b> <b>K</b> IEEL <b>K</b> E <b>K</b> IK <b>E</b> L <b>K</b> E	17.83
BCR	Antiparallel	DIEQ <b>E</b> LER <b>A</b> K <b>Q</b> <b>S</b> IEE <b>L</b> E <b>R</b> <b>E</b> VN <b>Q</b> E <b>R</b> S <b>R</b> M <b>Q</b> Y <b>L</b> Q <b>T</b> <b>R</b> L <b>S</b>	22.16
AP6SH	Antiparallel	SPED <b>K</b> LE <b>E</b> I <b>K</b> R <b>E</b> LE <b>E</b> NE <b>W</b> <b>E</b> LE <b>K</b> IE <b>R</b> <b>K</b> LE <b>E</b> N <b>K</b> R	29.10

**Supplementary Table 1: Coiled-coil building-blocks.** Orthogonal dimer-forming CC units used in bipyramidal CCPO cages. Polar amino acid residues in *e* and *g* position are coloured in red and blue. The helicity was calculated with AGADIR (ref. 56) for each individual sequence at pH 7, 5 °C and ionic strength 0.1 M.

### Data collection parameters

Radiation source	Petra III (DESY)		ALS
Beamline	EMBL P12		SIBYLS
Detector	Pilatus 6M		Pilatus3 2M
Beam geometry (mm)	200 $\mu$ m x 120 $\mu$ m		165 $\mu$ m x 130 $\mu$ m
Wavelength (nm)	0.124		0.103
Sample-detector distance (m)	3		1.5
Mode	Batch	SEC-SAXS	SEC-SAXS
Column (flow)	Superdex 200 increase (0.5 ml/min)		Superdex 200 increase (0.5 ml/min)
Exposure time (s)	1s (=20 x 0.05 s)	0.995	3
Temperature (K)	298		298

### Overall parameters

	BIP18SN	SBP162	SBP16	SBP12 <sub>9,a</sub>	SBP12 <sub>9,a-SN</sub>	SBP12 <sub>9,a-56</sub>	SBP12 <sub>9,a-L</sub>	SBP12 <sub>11</sub>	SBP12 <sub>9,b</sub>	SBP1 <sub>9,a</sub>	SBP2 <sub>9,a</sub>	SBP1 <sub>9,b</sub>	SBP2 <sub>9,b</sub>
$R_g$ from Guinier (nm)	4.61±0.02	4.07±0.03	4.26±0.01	5.37±0.02	5.41±0.01	4.36±0.02	4.53±0.01	4.13±0.04	4.04±0.03	3.74±0.02	3.69±0.02	3.4±0.02	3.5±0.01
$R_g$ from PDDF (nm)	4.6±0.2	4.1±0.1	4.3±0.2	5.3±0.2	5.7±0.1	4.4±0.1	4.6±0.1	4.2±0.1	4.0±0.1	3.7±0.1	3.7±0.1	3.4±0.1	3.5±0.1
$D_{max}$ (nm)	12.4±1.0	13.5±1.0	13.0±0.5	20.0±1.0	20.3±1.0	15.5±0.5	15.2±0.5	13.5±1.0	11.8±0.5	13.4±1.0	12.9±0.5	11.3	11.4
Porod Volume $V_P$ (nm <sup>3</sup> )	435	335	308	328	341	254	285	296	327	139	139	129	138
DAMMIF excluded volume (nm <sup>3</sup> )	357.7	-	-	423.5	-	-	-	295	305	-	-	-	-
Molecular weight from $V_P$ (kDa)	255.9	197.1	181.2	193.0	200.6	149.4	167.6	174.1	192.4	81.8	81.8	74.1	81.2
Molecular weight from excluded volume (kDa)	178.9	-	-	211.8	-	-	-	147.5	152.5	-	-	-	-
Molecular weight from sequence (kDa)	80.0	79.9	70.6	83.5	81.5	83.7	83.6	81.7	79.7	41.8	41.8	42.2	41.9
$V_r$ to BIP18SN	-	3.5	4.4	8.2	8.3	7.6	7.6	4.7	1.8	-	-	-	-

### Software employed

Primary data reduction	SASFLOW			
Data processing	PRIMUS			
<i>Ab initio</i> modelling	DAMMIF/DAMMIN			
Validation and averaging	DAMAVER			
Validation fitting to molecular models	PEPSI-SAXS			
Parameters of filtered <i>ab initio</i> model	Normalised Spatial Discrepancy	Standard deviation of NSD	Number of models excluded	Final $\chi^2$ after DAMMIN
BIP18SN	0.572	0.026	0	*
SBP12 <sub>9,a</sub>	0.729	0.031	0	*
SBP12 <sub>9,b</sub>	1.199	0.035	1	1.52
SBP12 <sub>11</sub>	1.195	0.035	1	0.95

**Supplementary Table 2: SAXS results.** The table indicates values resulting from SAXS analysis. The volatility ratio ( $V_r$ ) was calculated between the SAXS profile of BIP18SN, taken as reference, and the SAXS profile of the sample indicated in the table.\* *ab initio* models were generated with DAMMIF

**NAME SEQUENCE**

*Primers used for cloning constructs starting from the DNA of BIP18SN*

F-SBP <sub>16</sub>	GATCGTACCATATGAGCCCGGAGGACGAGATTCGCCAACTG
R-SBP <sub>16</sub>	ATGTCCTTCTCGAGACTTAAGCGGGTTGCAGGTATTGCATACGGCTACGCTC
F-SBP <sub>2</sub>	GATCGTACCATATGAGTCTGAGGATAAGATTAGCCAACTGAACAAG
R-SBP <sub>2</sub>	ATGTCCTTCTCGAGCTTCAGTTCGCTAATCTTTTCTCCAGTTGTTG
F-SBP <sub>15</sub>	CTTAAGAAGGAGATATACATATGGACATCGAGCAGGAATTAGAGCG
R-SBP <sub>15</sub>	CATATGTATATCTCCTTCTTAAAGTTAAACAAAATTATTTTC
R-SBP <sub>19,b</sub>	ACCACTTTGGAAATATAAGTTTTCCATATGGTGATGGTGGTGGTGGTGATGCCCCATGGT

*Primers used for cloning constructs starting from the DNA of SBP1<sub>11</sub> and SBP2<sub>11</sub>*

F-SBP <sub>19,b</sub>	CATCACCATATGGAAAACCTTATATTTCCAAAGTGGTTCGCGGTCTCCTGAGGATGAG
F-SBP <sub>29,b</sub>	CAGAGCGGTAGTGGGTCCTCGAGCACCACCATCACCACCATCACCCTAATGACCTAGG
R-SBP <sub>29,b</sub>	GATGGTGGTGCTCGAGTGACCCACTACCGCTCTGAAAATACAAATTCTCGCC
F-pETSBP <sub>19,b</sub>	CTGAAGGAAAAAATCAGGAGCTTAAGTATCTCGAGTAATGACCTAGGCTGCTAAACAAA
R-pETSBP <sub>19,b</sub>	GTTTTCTTCTTCAGTTCTTGTCTTGTCTCAGGAGACCCGGAACCACTTTGGAAAATA
F-SBP <sub>29,b</sub>	GACAAGAACAAGGAACTGAAGGAAGAAAACAAAGAGCTTGAATGG
R-SBP <sub>29,b</sub>	ATACTTAAGCTCCTGATTTTTTTCTTCAGCTCACTATTCTTTTG
F-pETstrep	CTGAAGGAAAAAATCAGGAGCTTAAGTATCTCGAGTAATGACCTAGGCTGCTAAACAAA
R-pETstrep	TCTCGAACTGTGGGTGAGACCAACCCATGGTGTATATCTCCTTCTTAAAGTTAAACAAA
F-strep	CTGCATGGTCTCACCCACAGTTCGAGAAATCTGCTTACCCGAGGACAAGAACAAGGAAC
R-strep	TTCTCGAACTGTGGGTGAGACCATGCAGAACCCATATGGGTGTATATCTCCTTCTTAAAG
F-SBP <sub>11Cys</sub>	GAACGCGAAATCAAAGAATTAGAACGCGGCTGCGGACCAGGGGACATTGAGCAAGAGC
R-SBP <sub>11Cys</sub>	GCTCTTGCTCAATGTCCCCTGGTCCGAGCCGCGTTCTAATTCTTTGATTTTCGCGTTC
F-SBP <sub>211Cys</sub>	GCAGTACCTTCAAACCCGCTTGTCAGGTTGTGGCCCAGGCTCTCCTGAAGACAAAATCG
R-SBP <sub>211Cys</sub>	CGATTTTGTCTTCAGGAGAGCCTGGGCCACAACCTGACAAGCGGGTTTGAAGGACTGC

**Supplementary Table 3: Primers used for cloning.** The table shows all the primers used in this study for cloning the constructs that were not purchased as synthetic genes.

## List of protein sequences

### Name: BIP18SN

Order of segments: P1SN-BCR-P7SN-P2SN- P3SN-P9SN-BCR-P4SN-P5SN-P1SN-BCR-P8SN-P2SN-P3SN-P10SN-BCR-P4SN-P6SN

Amino acid sequence:

MGHHHHHHHHENLYFQGSPED<sup>E</sup>IRQL<sup>E</sup>QENS<sup>Q</sup>L<sup>E</sup>REN<sup>Q</sup>RLE<sup>Q</sup>EI<sup>Y</sup>QL<sup>E</sup>RGS<sup>G</sup>PG<sup>D</sup>IE<sup>Q</sup>EL<sup>E</sup>RA<sup>K</sup>Q<sup>S</sup>I  
EEL<sup>E</sup>RE<sup>V</sup>N<sup>Q</sup>ER<sup>S</sup>RM<sup>Q</sup>YL<sup>Q</sup>TR<sup>L</sup>SG<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>EIQ<sup>L</sup>E<sup>E</sup>K<sup>N</sup>S<sup>Q</sup>L<sup>K</sup>Q<sup>E</sup>IS<sup>Q</sup>L<sup>E</sup>E<sup>K</sup>N<sup>Q</sup>EL<sup>K</sup>YGS<sup>G</sup>PG<sup>S</sup>PE<sup>D</sup>  
KIE<sup>E</sup>L<sup>K</sup>E<sup>K</sup>N<sup>S</sup>Q<sup>L</sup>K<sup>E</sup>K<sup>N</sup>E<sup>E</sup>L<sup>K</sup>Q<sup>K</sup>I<sup>Y</sup>EL<sup>K</sup>E<sup>G</sup>SG<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>EIQ<sup>L</sup>EE<sup>E</sup>IS<sup>Q</sup>L<sup>E</sup>Q<sup>K</sup>N<sup>S</sup>EL<sup>K</sup>E<sup>K</sup>N<sup>Q</sup>EL<sup>K</sup>YGS<sup>G</sup>  
PG<sup>S</sup>PE<sup>D</sup>EN<sup>Q</sup>S<sup>L</sup>E<sup>Q</sup>K<sup>N</sup>S<sup>Q</sup>L<sup>K</sup>Q<sup>E</sup>IS<sup>Q</sup>L<sup>E</sup>Q<sup>E</sup>I<sup>Q</sup>Q<sup>L</sup>E<sup>Y</sup>GS<sup>S</sup>PG<sup>D</sup>IE<sup>Q</sup>EL<sup>E</sup>RA<sup>K</sup>Q<sup>S</sup>IE<sup>E</sup>L<sup>E</sup>RE<sup>V</sup>N<sup>Q</sup>ER<sup>S</sup>RM<sup>Q</sup>  
YL<sup>Q</sup>TR<sup>L</sup>SG<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>KIS<sup>Q</sup>L<sup>K</sup>E<sup>K</sup>I<sup>Q</sup>Q<sup>L</sup>K<sup>Q</sup>EN<sup>Q</sup>Q<sup>L</sup>EE<sup>E</sup>NS<sup>Q</sup>L<sup>E</sup>YGS<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>ENS<sup>Q</sup>L<sup>E</sup>E<sup>K</sup>IS<sup>Q</sup>L<sup>K</sup>Q<sup>K</sup>N  
SEL<sup>K</sup>EEI<sup>Q</sup>Q<sup>L</sup>E<sup>Y</sup>GS<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>IRQL<sup>E</sup>QENS<sup>Q</sup>L<sup>E</sup>REN<sup>Q</sup>RLE<sup>Q</sup>EI<sup>Y</sup>QL<sup>E</sup>RGS<sup>G</sup>PG<sup>D</sup>IE<sup>Q</sup>EL<sup>E</sup>RA<sup>K</sup>Q<sup>S</sup>IE<sup>E</sup>  
L<sup>E</sup>RE<sup>V</sup>N<sup>Q</sup>ER<sup>S</sup>RM<sup>Q</sup>YL<sup>Q</sup>TR<sup>L</sup>SG<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>KISEL<sup>K</sup>EEN<sup>Q</sup>Q<sup>L</sup>E<sup>Q</sup>KI<sup>Q</sup>Q<sup>L</sup>K<sup>E</sup>ENS<sup>Q</sup>L<sup>E</sup>YGS<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>KIE  
EL<sup>K</sup>E<sup>K</sup>N<sup>S</sup>Q<sup>L</sup>K<sup>E</sup>K<sup>N</sup>E<sup>E</sup>L<sup>K</sup>Q<sup>K</sup>I<sup>Y</sup>EL<sup>K</sup>E<sup>G</sup>SG<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>EIQ<sup>L</sup>EE<sup>E</sup>IS<sup>Q</sup>L<sup>E</sup>Q<sup>K</sup>N<sup>S</sup>EL<sup>K</sup>E<sup>K</sup>N<sup>Q</sup>EL<sup>K</sup>YGS<sup>S</sup>PG<sup>S</sup>  
PED<sup>K</sup>N<sup>S</sup>Q<sup>L</sup>K<sup>E</sup>ENS<sup>Q</sup>L<sup>E</sup>E<sup>K</sup>IE<sup>Q</sup>L<sup>K</sup>E<sup>K</sup>I<sup>Q</sup>EL<sup>K</sup>YGS<sup>S</sup>PG<sup>D</sup>IE<sup>Q</sup>EL<sup>E</sup>RA<sup>K</sup>Q<sup>S</sup>IE<sup>E</sup>L<sup>E</sup>RE<sup>V</sup>N<sup>Q</sup>ER<sup>S</sup>RM<sup>Q</sup>YL<sup>Q</sup>  
TR<sup>L</sup>SG<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>KIS<sup>Q</sup>L<sup>K</sup>E<sup>K</sup>I<sup>Q</sup>Q<sup>L</sup>K<sup>Q</sup>EN<sup>Q</sup>Q<sup>L</sup>EE<sup>E</sup>NS<sup>Q</sup>L<sup>E</sup>YGS<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>KNSEL<sup>K</sup>EEI<sup>Q</sup>Q<sup>L</sup>EE<sup>E</sup>N<sup>Q</sup>L  
E<sup>E</sup>KISEL<sup>K</sup>YLE

### Name: SBP<sub>16</sub>

Order of segments: P1SN-BCR-P7SN-P2SN- P3SN-P9SN-BCR-P4SN-P5SN-P1SN-BCR-P8SN-P2SN-P3SN-P10SN-BCR

Amino acid sequence:

MSPED<sup>E</sup>IRQL<sup>E</sup>QENS<sup>Q</sup>L<sup>E</sup>REN<sup>Q</sup>RLE<sup>Q</sup>EI<sup>Y</sup>QL<sup>E</sup>RGS<sup>G</sup>PG<sup>D</sup>IE<sup>Q</sup>EL<sup>E</sup>RA<sup>K</sup>Q<sup>S</sup>IE<sup>E</sup>L<sup>E</sup>RE<sup>V</sup>N<sup>Q</sup>ER<sup>S</sup>RM<sup>Q</sup>YL  
Q<sup>T</sup>R<sup>L</sup>SG<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>EIQ<sup>L</sup>E<sup>E</sup>K<sup>N</sup>S<sup>Q</sup>L<sup>K</sup>Q<sup>E</sup>IS<sup>Q</sup>L<sup>E</sup>E<sup>K</sup>N<sup>Q</sup>EL<sup>K</sup>YGS<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>KIE<sup>E</sup>L<sup>K</sup>E<sup>K</sup>N<sup>S</sup>Q<sup>L</sup>K<sup>E</sup>K<sup>N</sup>E  
EL<sup>K</sup>Q<sup>K</sup>I<sup>Y</sup>EL<sup>K</sup>E<sup>G</sup>SG<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>EIQ<sup>L</sup>EE<sup>E</sup>IS<sup>Q</sup>L<sup>E</sup>Q<sup>K</sup>N<sup>S</sup>EL<sup>K</sup>E<sup>K</sup>N<sup>Q</sup>EL<sup>K</sup>YGS<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>EN<sup>Q</sup>S<sup>L</sup>E<sup>Q</sup>K<sup>N</sup>S<sup>Q</sup>  
L<sup>K</sup>Q<sup>E</sup>IS<sup>Q</sup>L<sup>E</sup>Q<sup>E</sup>I<sup>Q</sup>Q<sup>L</sup>E<sup>Y</sup>GS<sup>S</sup>PG<sup>D</sup>IE<sup>Q</sup>EL<sup>E</sup>RA<sup>K</sup>Q<sup>S</sup>IE<sup>E</sup>L<sup>E</sup>RE<sup>V</sup>N<sup>Q</sup>ER<sup>S</sup>RM<sup>Q</sup>YL<sup>Q</sup>TR<sup>L</sup>SG<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>KIS  
Q<sup>L</sup>K<sup>E</sup>KI<sup>Q</sup>Q<sup>L</sup>K<sup>Q</sup>EN<sup>Q</sup>Q<sup>L</sup>EE<sup>E</sup>NS<sup>Q</sup>L<sup>E</sup>YGS<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>ENS<sup>Q</sup>L<sup>E</sup>E<sup>K</sup>IS<sup>Q</sup>L<sup>K</sup>Q<sup>K</sup>N<sup>S</sup>EL<sup>K</sup>EEI<sup>Q</sup>Q<sup>L</sup>E<sup>Y</sup>GS<sup>S</sup>PG<sup>S</sup>  
PE<sup>D</sup>EIRQL<sup>E</sup>QENS<sup>Q</sup>L<sup>E</sup>REN<sup>Q</sup>RLE<sup>Q</sup>EI<sup>Y</sup>QL<sup>E</sup>RGS<sup>G</sup>PG<sup>D</sup>IE<sup>Q</sup>EL<sup>E</sup>RA<sup>K</sup>Q<sup>S</sup>IE<sup>E</sup>L<sup>E</sup>RE<sup>V</sup>N<sup>Q</sup>ER<sup>S</sup>RM<sup>Q</sup>YL<sup>Q</sup>  
TR<sup>L</sup>SG<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>KISEL<sup>K</sup>EEN<sup>Q</sup>Q<sup>L</sup>E<sup>Q</sup>KI<sup>Q</sup>Q<sup>L</sup>K<sup>E</sup>ENS<sup>Q</sup>L<sup>E</sup>YGS<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>KIE<sup>E</sup>L<sup>K</sup>E<sup>K</sup>N<sup>S</sup>Q<sup>L</sup>K<sup>E</sup>K<sup>N</sup>E<sup>E</sup>L  
K<sup>Q</sup>K<sup>I</sup>Y<sup>E</sup>L<sup>K</sup>E<sup>G</sup>SG<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>EIQ<sup>L</sup>EE<sup>E</sup>IS<sup>Q</sup>L<sup>E</sup>Q<sup>K</sup>N<sup>S</sup>EL<sup>K</sup>E<sup>K</sup>N<sup>Q</sup>EL<sup>K</sup>YGS<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>KNS<sup>Q</sup>L<sup>K</sup>E<sup>E</sup>NS<sup>Q</sup>L  
EKIE<sup>Q</sup>L<sup>K</sup>E<sup>K</sup>I<sup>Q</sup>EL<sup>K</sup>YGS<sup>S</sup>PG<sup>D</sup>IE<sup>Q</sup>EL<sup>E</sup>RA<sup>K</sup>Q<sup>S</sup>IE<sup>E</sup>L<sup>E</sup>RE<sup>V</sup>N<sup>Q</sup>ER<sup>S</sup>RM<sup>Q</sup>YL<sup>Q</sup>TR<sup>L</sup>SLHHHHHHHH

### Name: SBP<sub>2</sub>

Order of segments: P4SN-P6SN

Amino acid sequence:

MSPED<sup>K</sup>IS<sup>Q</sup>L<sup>K</sup>E<sup>K</sup>I<sup>Q</sup>Q<sup>L</sup>K<sup>Q</sup>EN<sup>Q</sup>Q<sup>L</sup>EE<sup>E</sup>NS<sup>Q</sup>L<sup>E</sup>YGS<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>KNSEL<sup>K</sup>EEI<sup>Q</sup>Q<sup>L</sup>EE<sup>E</sup>N<sup>Q</sup>L<sup>E</sup>E<sup>K</sup>ISEL  
KLEHHHHHHHH

### Name: SBP<sub>15</sub>

Order of segments: BCR-P7SN-P2SN- P3SN-P9SN-BCR-P4SN-P5SN-P1SN-BCR-P8SN-P2SN-P3SN-P10SN-BCR

Amino acid sequence:

MDIE<sup>Q</sup>EL<sup>E</sup>RA<sup>K</sup>Q<sup>S</sup>IE<sup>E</sup>L<sup>E</sup>RE<sup>V</sup>N<sup>Q</sup>ER<sup>S</sup>RM<sup>Q</sup>YL<sup>Q</sup>TR<sup>L</sup>SG<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>EIQ<sup>L</sup>E<sup>E</sup>K<sup>N</sup>S<sup>Q</sup>L<sup>K</sup>Q<sup>E</sup>IS<sup>Q</sup>L<sup>E</sup>E<sup>K</sup>N  
Q<sup>L</sup>EL<sup>K</sup>YGS<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>KIE<sup>E</sup>L<sup>K</sup>E<sup>K</sup>N<sup>S</sup>Q<sup>L</sup>K<sup>E</sup>K<sup>N</sup>E<sup>E</sup>L<sup>K</sup>Q<sup>K</sup>I<sup>Y</sup>EL<sup>K</sup>E<sup>G</sup>SG<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>EIQ<sup>L</sup>EE<sup>E</sup>IS<sup>Q</sup>L<sup>E</sup>Q<sup>K</sup>N<sup>S</sup>  
L<sup>K</sup>E<sup>K</sup>N<sup>Q</sup>EL<sup>K</sup>YGS<sup>S</sup>PG<sup>S</sup>PE<sup>D</sup>EN<sup>Q</sup>S<sup>L</sup>E<sup>Q</sup>K<sup>N</sup>S<sup>Q</sup>L<sup>K</sup>Q<sup>E</sup>IS<sup>Q</sup>L<sup>E</sup>Q<sup>E</sup>I<sup>Q</sup>Q<sup>L</sup>E<sup>Y</sup>GS<sup>S</sup>PG<sup>D</sup>IE<sup>Q</sup>EL<sup>E</sup>RA<sup>K</sup>Q<sup>S</sup>IE<sup>E</sup>L

EREVNQERSRMQYLQTRLSGSGPGSPEDKISQLKEKIQQLKQENQQLEEENSQLEYGSGPGSPEDEN  
SQLEEKISQLKQKNSSELKEEIQQLEYGSGPGSPEDEIRQLEQENSQLERENQRLEQEIYQLERGSGPGD  
IEQELERAKQSIEELEREVNQERSRMQYLQTRLSGSGPGSPEDKISELKEENQQLEQKIQQLKEENSQ  
LEYGSGPGSPEDKIEELKEKNSQLKEKNEELKQKIYELKEGSGPGSPEDEIQLEEEISQLEQKNSSELK  
EKNQELKYGSGPGSPEDKNSQLKEENSQLEEKIEQLKEKIQELKYGSGPGDIEQELERAKQSIEELER  
EVNQERSRMQYLQTRLSLEHHHHHHH

**Name: SBP<sub>3</sub>**

Order of segments: P4SN-P6SN-P1SN

Amino acid sequence:

MSPEDKISQLKEKIQQLKQENQQLEEENSQLEYGSGPGSPEDKNSSELKEEIQQLEENQQLEEKISEL  
KYGSGPGSPEDEIRQLEQENSQLERENQRLEQEIYQLERLEHHHHHHH

**Name: SBP<sub>19,a</sub>**

Order of segments: P3SN-P9SH-BCR-P4SN-P5SH-P1SN-BCR-P7SH-P2SN

Amino acid sequence:

MHHHHHHHHENLYFQGHMSPEDEIQLEEEISQLEQKNSSELKEKNQELKYGSGPGSPEDENEKLER  
KNEELKWEIKKLEREIKELERGSGPGDIEQELERAKQSIEELEREVNQERSRMQYLQTRLSGSGPGSP  
EDKISQLKEKIQQLKQENQQLEEENSQLEYGSGPGSPEDENEKLEEKIWELKRKNEELKREIKELEEG  
SGPGSPEDEIRQLEQENSQLERENQRLEQEIYQLERGSGPGDIEQELERAKQSIEELEREVNQERSRMQ  
YLQTRLSGSGPGSPEDEIKLEWKNNEELKREIKELEEKNEELKRGSGPGSPEDKIEELKEKNSQLKEK  
NEELKQKIYELKELE

**Name: SBP<sub>29,a</sub>**

Order of segments: P3SN-P10SH-BCR-P4SN-P6SH-P1SN-BCR-P8SH-P2SN

Amino acid sequence:

MHHHHHHHHENLYFQGHMSPEDEIQLEEEISQLEQKNSSELKEKNQELKYGSGPGSPEDKNKELKE  
ENKELEWKIEELKEKIKELKEGSGPGDIEQELERAKQSIEELEREVNQERSRMQYLQTRLSGSGPGSP  
EDKISQLKEKIQQLKQENQQLEEENSQLEYGSGPGSPEDKNEELKREIKELEWENEELERKIEELKRG  
SGPGSPEDEIRQLEQENSQLERENQRLEQEIYQLERGSGPGDIEQELERAKQSIEELEREVNQERSRMQ  
YLQTRLSGSGPGSPEDKIEELKRENELEWKIEELKRENEELEKSGSGPGSPEDKIEELKEKNSQLKEK  
NEELKQKIYELKELE

**Name: SBP<sub>19,a-SN</sub>**

Order of segments: P3SN-P9SN-BCR-P4SN-P5SN-P1SN-BCR-P7SN-P2SN

Amino acid sequence:

MHHHHHHHHENLYFQGSPEDEIQLEEEISQLEQKNSSELKEKNQELKYGSGPGSPEDENQSLEQKNS  
QLKQEISQLEQEIYQLEYGSGPGDIEQELERAKQSIEELEREVNQERSRMQYLQTRLSGSGPGSPEDKI  
SQLKEKIQQLKQENQQLEEENSQLEYGSGPGSPEDENSQLEEKISQLKQKNSSELKEEIQQLEYGSGPG  
SPEDEIRQLEQENSQLERENQRLEQEIYQLERGSGPGDIEQELERAKQSIEELEREVNQERSRMQYLQ  
TRLSGSGPGSPEDEIQLEEKNSQLKQEISQLEEKQELKYGSGPGSPEDKIEELKEKNSQLKEKNEEL  
KQKIYELKE

**Name: SBP<sub>29,a-SN</sub>**

Order of segments: P3SN-P10SN-BCR-P4SN-P6SN-P1SN-BCR-P8SN-P2SN



Amino acid sequence:

MHHHHHHHHENLYFQGSPEDEIQLEEEISQLEQKNSSELKEKNQELKYGSGPGSPEDKNSQLKEENS  
QLEEKIEQLKEKIQELKYGSGPGDIEQELERAKQSIEELEREVNQERSRMQYLQTRLSGSGPGSPEDKI  
SQLKEKIQQLKQENQQLLEEENSQLEYGSGPGSPEDKNSSELKEEIQLEENQQLLEEKISELKYGSGPG  
SPEDEIRQLEQENSQLERENQRLEQEIYQLERGSGPGDIEQELERAKQSIEELEREVNQERSRMQYLQ  
TRLSGSGPGSPEDKISELKEENQQLQKIQQLKEENSQLEYGSGPGSPEDKIEELKEKNSQLKEKNEEL  
KQKIYELKE

**Name: SBP1<sub>9,a-56</sub>**

Order of segments: P3SN-P5SH-BCR-P4SN-P5SH-P1SN-BCR-P5SH-P2SN

Amino acid sequence:

MHHHHHHHHENLYFQGHMSPEDEIQLEEEISQLEQKNSSELKEKNQELKYGSGPGSPEDENEKLEE  
KIWELKRKNEELKREIKELEE GSGPGDIEQELERAKQSIEELEREVNQERSRMQYLQTRLSGSGPGSP  
EDKISQLKEKIQQLKQENQQLLEEENSQLEYGSGPGSPEDENEKLEEKIWELKRKNEELKREIKELEE G  
SGPGSPEDEIRQLEQENSQLERENQRLEQEIYQLERGSGPGDIEQELERAKQSIEELEREVNQERSRMQ  
YLQTRLSGSGPGSPEDENEKLEEKIWELKRKNEELKREIKELEE GSGPGSPEDKIEELKEKNSQLKEK  
NEELKQKIYELKELE

**Name: SBP2<sub>9,a-56</sub>**

Order of segments: P3SN-AP6SH-BCR-P4SN-P6SH-P1SN-BCR-P6SH-P2SN

Amino acid sequence:

MHHHHHHHHENLYFQGHMSPEDEIQLEEEISQLEQKNSSELKEKNQELKYGSGPGSPEDKLEEKRE  
LEENEWELEKIERKLEENKR GSGPGDIEQELERAKQSIEELEREVNQERSRMQYLQTRLSGSGPGSPE  
DKISQLKEKIQQLKQENQQLLEEENSQLEYGSGPGSPEDKNEELKREIKELEWENEELERKIEELKRGS  
GPGSPEDEIRQLEQENSQLERENQRLEQEIYQLERGSGPGDIEQELERAKQSIEELEREVNQERSRMQ  
YLQTRLSGSGPGSPEDKNEELKREIKELEWENEELERKIEELKR GSGPGSPEDKIEELKEKNSQLKEK  
NEELKQKIYELKELE

**Name: SBP1<sub>9,a-L</sub>**

Order of segments: P3SN-P5SH-BCR-P4SN-P9SH-P1SN-BCR-P7SH-P2SN

Amino acid sequence:

MHHHHHHHHENLYFQGHMSPEDEIQLEEEISQLEQKNSSELKEKNQELKYGSGPGSPEDENEKLEE  
KIWELKRKNEELKREIKELEE GSGPGDIEQELERAKQSIEELEREVNQERSRMQYLQTRLSGSGPGSP  
EDKISQLKEKIQQLKQENQQLLEEENSQLEYGSGPGSPEDENEKLERKNEELKWEIKKLEREIKELER G  
SGPGSPEDEIRQLEQENSQLERENQRLEQEIYQLERGSGPGDIEQELERAKQSIEELEREVNQERSRMQ  
YLQTRLSGSGPGSPEDEIKELEWKNEELKREIKELEEKNEELKR GSGPGSPEDKIEELKEKNSQLKEK  
NEELKQKIYELKELE

**Name: SBP2<sub>9,a-L</sub>**

Order of segments P3SN-AP6SH-BCR-P4SN-P8SH-P1SN-BCR-P10SH-P2SN

Amino acid sequence:

MHHHHHHHHENLYFQGHMSPEDEIQLEEEISQLEQKNSSELKEKNQELKYGSGPGSPEDKLEEKRE  
LEENEWELEKIERKLEENKR GSGPGDIEQELERAKQSIEELEREVNQERSRMQYLQTRLSGSGPGSPE  
DKISQLKEKIQQLKQENQQLLEEENSQLEYGSGPGSPEDKIEELKRENEELEWKIEELKRENEELEKGS  
GPGSPEDEIRQLEQENSQLERENQRLEQEIYQLERGSGPGDIEQELERAKQSIEELEREVNQERSRMQ  
YLQTRLSGSGPGSPEDKNKELKEENKELEWKIEELKEKIKELKE GSGPGSPEDKIEELKEKNSQLKEK

NEELKQKIYELKELE

**Name: SBP1<sub>9,b</sub>**

Order of segments: P1SN-P3SN-P9SH-BCR-P4SN-P5SH-P2SN-BCR-P7SH

Amino acid sequence:

MGHHHHHHHHHMENLYFQSGSGSPEDAIRQLEQENSLERENQRLEQEIYQLERGSGPGSPEDAIQQL  
EEEISQLEQKNSSELKEKNQELKYGSGPGSPEDENEKLERKNEELKWEIKKLEREIKELERGSGPGDIE  
QELERAKQSIEELEREVNQERSRMQYLQTRLSGSGPGSPEDKISQLKEKIQQLKQENQQLEEENSQLE  
YSGSGPGSPEDENEKLEEKIWELKRKNEELKREIKELEEESGSGPGSPEDKIEELKEKNSQLKEKNEELKQ  
KIYELKEGSGPGDIEQELERAKQSIEELEREVNQERSRMQYLQTRLSGSGPGSPEDAIKELEWKNEEL  
KREIKELEEKNEELKRLELE

**Name: SBP2<sub>9,b</sub>**

Order of segments: P10SH-BCR-P4SN-P6SH-P2SN-BCR-P8SH-P1SN-P3SN

Amino acid sequence:

MGHHHHHHHHHMENLYFQSGSGSPEDKNKELKEENKELEWKIEELKEKIKELKEGSGPGDIEQELER  
AKQSIEELEREVNQERSRMQYLQTRLSGSGPGSPEDKISQLKEKIQQLKQENQQLEEENSQLEYGSGP  
GSPEDKNEELKREIKELEWENEELERKIEELKRGSGPGSPEDKIEELKEKNSQLKEKNEELKQKIYEL  
KEGSGPGDIEQELERAKQSIEELEREVNQERSRMQYLQTRLSGSGPGSPEDKIEELKRENEELEWKIE  
ELKRENEELEKSGSGPGSPEDAIRQLEQENSLERENQRLEQEIYQLERGSGPGSPEDAIQQLEEEISQLE  
QKNSSELKEKNQELKYLE

**Name: SBP1<sub>11</sub>**

Order of segments: P10SH-P8SH-TEVs-P1SN-P3SN-P9SH-Cys-BCR-P4SN-P5SH-P2SN-  
BCR-P7SH

Amino acid sequence:

MGHHHHHHHHHMSPEDKNKELKEENKELEWKIEELKEKIKELKEGSGPGSPEDKIEELKRENEELEW  
KIEELKRENEELEKSGGENLYFQSGSGSPEDAIRQLEQENSLERENQRLEQEIYQLERGSGPGSPED  
IQLEEEEISQLEQKNSSELKEKNQELKYGSGPGSPEDENEKLERKNEELKWEIKKLEREIKELERGCGP  
GDIEQELERAKQSIEELEREVNQERSRMQYLQTRLSGSGPGSPEDKISQLKEKIQQLKQENQQLEEN  
SQLEYGSGPGSPEDENEKLEEKIWELKRKNEELKREIKELEEESGSGPGSPEDKIEELKEKNSQLKEKNE  
ELKQKIYELKEGSGPGDIEQELERAKQSIEELEREVNQERSRMQYLQTRLSGSGPGSPEDAIKELEWK  
NEELKREIKELEEKNEELKRLELE

**Name: SBP2<sub>11</sub>**

Order of segments: P10SH-BCR-P4SN-P6SH-P2SN-BCR-Cys-P8SH-P1SN-P3SN-TEVs-  
P9SH-P7SH

Amino acid sequence:

MGSAWSHPOFEKSASPEDKNKELKEENKELEWKIEELKEKIKELKEGSGPGDIEQELERAKQSIEELE  
REVNQERSRMQYLQTRLSGSGPGSPEDKISQLKEKIQQLKQENQQLEEENSQLEYGSGPGSPEDKNE  
ELKREIKELEWENEELERKIEELKRGSGPGSPEDKIEELKEKNSQLKEKNEELKQKIYELKEGSGPGDI  
EQELERAKQSIEELEREVNQERSRMQYLQTRLSGCGPGSPEDKIEELKRENEELEWKIEELKRENEEL  
EKSGSGPGSPEDAIRQLEQENSLERENQRLEQEIYQLERGSGPGSPEDAIQQLEEEISQLEQKNSSELKE  
KNQELKYSGGENLYFQSGSGSPEDENEKLERKNEELKWEIKKLEREIKELERGSGPGSPEDAIKELEW  
KNEELKREIKELEEKNEELKRLEHHHHHHHHH

**Name: TEV protease**

Amino acid sequence:

MGHHHHHHHHGESLFKGRDYNPISSTICHLTNE SDGHTTSLYGIGFGPFIITNKHLFRRNNGTLLVQ  
SLHGVFKVKNTTTLQHLIDGRDMIIRMPKDFPPFPQKLFREPQREERICLVTTNFQTKSMSSMVS  
DTSCTFPSSDGIFWKHWIQTKDGQCGSPLVSTRDGFIVGIHSASNFTNTNNYFTSVPKNFMELLTNQE  
AQQWVSGWRLNADSVLWGGHKVFMSKPEEPFQPVKEATQLMSELVYSQ

Affinity tags are underlined

# List of DNA sequences

## Name: BIP18SN

### DNA sequence:

CATATGGGCCACCACCATCATCACCATCACCACGAAAATCTGTACTTTCAAGGCAGCCCAGGAGACGAGATTCGCCAACTG  
GAGCAGGAGAACAGTCAACTGGAAACGTGAAAACCAGCGTCTGGAACAAGAAATTTATCAGCTGGAACGCGGTAGCGGCC  
CTGGTGACATCGAGCAAGAAATAGAGCGCGCAAAAACAGAGTATCGAAGAGCTGGAGCGGAGGTGAACCAAGAACGCAG  
TCGTATGCAATACCTGCAGACACGCTTAAAGCGGTAGCGGTCCGGGTAGCCCGGAAGACGAAATCAACAACCTGGAGGAAA  
AGAATAGTCAGCTGAAAGCAGGAGATTAGTCAACTGGAAGAGAAAAATCAAGAGCTGAAATATGGCAGTGGTCCGGGCAGC  
CCGGAAGATAAAATCGAGGAGCTGAAGGAGAAAAATAGCCAGCTGAAAAGAAAAGAATGAAGAACTGAAACAGAAGATTT  
ACGAGCTGAAGGAAGGCAGTGGCCCGGCAGCCCGGAGGACGAGATCCAGCAGCTGGAAGAGGAGATTAGCCAGCTGG  
AGCAGAAAGAACTAGCGAGCTGAAGGAGAAGAACCAAGAGTTAAAGTATGGCAGCGGTCCGGGTAGCCCGGAAGATGAAAA  
TCAGAGCCTGGAGCAAAAAGAACAGCCAACCTGAAGCAGGAAATTAGCCAATTAGAGCAGGAGATCCAACTGGAGTAT  
GGCAGTGGCCCGGGCGACATTGAGCAAGAACTGGAACGCGCCAAGCAGAGCATTGAAGAGCTGGAACGCGAAGTGAATC  
AGGAGCGCAGCCGCATGCAGTATCTGCAGACCCGCTGAGCGGTAGTGGCCCGGCAGCCCGGAGGACAAGATCAGCCA  
ACTGAAGGAGAAGATCCAGCAGCTGAAACAAGAAAACAGCAACTGGAGGAAGAAAATAGCCAACCTGGAATATGGTAGC  
GGTCCGGGTAGCCCGGAAGATGAAAATAGTCAAGTTAGAGGAAAAAATTAGCCAATTAACAGAAAAATAGCGAACTGAA  
GGAAGAAATTCAACAGCTGGAATACGGCAGTGGTCTGGTAGTCCGGAGGACGAAAATTCGTCAGCTGGAACAGGAAAAAC  
AGCCAGCTGGAACGTGAGAACAGCGCCTGGAGCAAGAGATTTACCAGCTGGAACGTGGCAGCGGTCTGGTGACATTG  
AACAGAACTGGAGCGCGCCAAACAGAGCATCGAGGAGCTGGAGCGGAGGTGAACCAGGAGCGTAGCCGCATGCAATA  
TCTGCAGACCCGCTGAGTGGTAGTGGTCCGGGCAGCCTGAAGACAAAATCAGCGAACTGAAAAGAAAACCAGCAA  
CTGGAGCAAAAAATCCAGCAGCTGAAAGAAGAAAATAGTCAACTGGAGTACGGTAGCGGTCCGGGCAGTCCGGAAGACA  
AGATCGAGGAGCTGAAAGAGAAAAATAGCCAACCTGAAAGAGAAAAACGAAGAACTGAAGCAGAAAATTTATGAGCTGAA  
AGAAGGTAGCGGCCCTGGTAGTCCGGAGGATGAGATTCAGCAACTGGAAGAGGAGATTAGCCAATTAGCAAGAAAAATA  
GTAACTGAAGGAAAAGAAATCAGGAATTAATAACGCGCAGCGGTCCGGGCAGTCTGAAGATAAAAAACAGTCAACTGAA  
GGAAGAGAACAGCCAGCTGGAAGAGAAGATCGAGCAACTGAAAGAGAAGATCCAGGAGCTGAAGTATGGTAGCGCCCC  
GGCGATATTGAACAGGAACTGGAACGCGCAAAGCAGAGCATGAAAGAGCTGGAACGCGAAGTGAACCAAGAGCGTAGCC  
GTATGCAATACCTGCAACCCGCTTAAAGTGGTAGCGGTCCGGGCAGTCTGAGGATAAGATTAGCCAACCTGAAAAGAAAAG  
ATTCAGCAACTGAAACAAGAGAATCAACAGCTGGAGGAAGAGAATAGCCAGCTGGAGTACGGTAGCGGCCCGGGTAGCC  
CGGAGGATAAGAACAGTGAGCTGAAGGAAGAAATCCAGCAACTGGAAGAAGAAAATCAACAACCTGGAAGAAAAGATTAG  
CGAACTGAAGTATTAATGACTCGAG

## Name: SBP16

### DNA sequence:

GATCGTACCATATGACCCCGGAGGACGAGATTCGCCAACTGGAGCAGGAGAACAGTCAACTGGAACGTGAAAACCAGCGT  
CTGGAACAAGAAATTTATCAGCTGGAACGCGGTAGCGGCCCTGGTGACATCGAGCAGGAATTAGAGCGCGCAAAAACAGAG  
TATCGAAGAGCTGGAGCGGAGGTGAACCAAGAACGCAGTCTGTATGCAATACCTGCAGACACGCTTAAAGCGGTAGCGGT  
CGGGTAGCCCGGAAGACGAAATTAACAACCTGGAGGAAAAGAATAGTCAAGTGAAGCAGGAGATTAGTCAACTGGAAGA  
GAAAAATCAAGAGCTGAAATATGGCAGTGGTCCGGGCAGCCCGGAAGATAAAAATCGAGGAGCTGAAGGAGAAAAATAGC  
CAGCTGAAAAGAAAAGAATGAAGAACTGAAACAGAAGATTTACGAGCTGAAGGAAGGCAGTGGCCCGGCAGCCCGGAG  
GACGAGATCCAGCAGCTGGAAGAGGAGATTAGCCAGCTGGAGCAGAAGAATAGCGAGCTGAAGGAGAAGAACCAAGAG  
TAAAAGTATGGCAGCGGTCCGGGTAGCCCGGAAGATGAAAATCAGAGCCTGGAGCAAAAAGAACAGCCAACCTGAAGCAGG  
AAATTAGCCAATTAGAGCAGGAGATCCAACAACCTGGAGTATGGCAGTGGCCCGGGCGACATTGAGCAAGAACTGGAACGC  
GCCAAGCAGAGCATTGAAGAGCTGGAACGCGAAGTGAATCAGGAGCGCAGCCGCATGCAGTATCTGCAGACCCGCTGAG  
CGGTAGTGGCCCGGCAGCCCGGAGGACAAGATCAGCCAACCTGAAGGAGAAGATCCAGCAGCTGAAAACAAGAAAACCA  
GCAACTGGAGGAAGAAAATAGCCAACCTGGAATATGGTAGCGGTCCGGGTAGCCCGGAAGATGAAAATAGTCAAGTTAGAGG  
AAAAAATTAGCCAATTAACAGAAAAATAGCGAACTGAAAGGAAGAAATTAACAGCTGGAATACGGCAGTGGTCTGGT  
AGTCCGGAGGACGAAATTCGTCAGCTGGAACAGGAAAACAGCCAGCTGGAACGTGAGAACAGCGCCTGGAGCAAGAG  
ATTTACCAGCTGGAACGTGGCAGCGGTCTGGTGACATTGAACAGGAACTGGAGCGCGCCAAACAGAGCATCGAGGAGCT  
GGAGCGGAGGTGAACCAGGAGCGTAGCCGCATGCAATATCTGCAGACCCGCTGAGTGGTAGTGGTCCGGGCAGCCCTG  
AAGACAAAATCAGCGAACTGAAAAGAAGAAAACCAGCAACTGGAGCAAAAAATCCAGCAGCTGAAAAGAAAATAGTCA  
AACTGGAGTACGGTAGCGGTCCGGGCAGTCCGGAAGACAAGATCGAGGAGCTGAAAGAGAAAATAGCCAACCTGAAAGA  
GAAAAACGAAGAAGAACTGAAGCAGAAAAATTTATGAGCTGAAAAGAAGGTAGCGGCCCTGGTAGTCCGGAGGATGAGATTCA  
CAACTGGAAGAGGAGATTAGCCAATTAGAACAGAAAAATAGTGAACCTGAAGGAAAAGAATCAGGAATTAATAACGGCAG  
CGGTCCGGGCAGTCTGAAGATAAAAAACAGTCAACTGAAGGAAGAGAACAGCCAGCTGGAAGAGAAGATCGAGCAACTG  
AAAGAGAAGATCCAGGAGCTGAAGTATGGTAGCGGCCCGGGCGATATTGAACAGGAACTGGAACGCGCAAAGCAGAGCA

TCGAAGAGCTGGAACGCGAAGTGAACCAAGAGCGTAGCCGTATGCAATACCTGCAAACCCGCTTAAGTCTCGAGAAGGAC  
AT

**Name: SBP<sub>2</sub>**

**DNA sequence:**

GATCGTACCATATGAGTCTCTGAGGATAAGATTAGCCAACTGAAAGAAAAGATTTCAGCAACTGAAACAAGAGAATCAACAG  
CTGGAGGAAGAGAATAGCCAGCTGGAGTACGGTAGCGGCCCGGGTAGCCCGGAGGATAAGAACAGTGAAGGAAG  
AAATCCAGCAACTGGAAGAAGAAAATCAACAACTGGAAGAAAAGATTAGCGAACTGAAGCTCGAGAAGGACAT

**Name: SBP<sub>15</sub>**

**DNA sequence:**

GAAGGAGATATACATATGGACATCGAGCAGGAATTAGAGCGCGCAAAAACAGAGTATCGAAGAGCTGGAGCGGAGGTGAA  
CCAAGAACGCAGTCGTATGCAATACCTGCAGACACGCTTAAGCGGTAGCGGTCCGGGTAGCCCGGAAGACGAAATTCAAC  
AACTGGAGGAAAAGAATAGTCAGCTGAAGCAGGAGATTAGTCAACTGGAAGAGAAAAATCAAGAGCTGAAATATGGCAG  
TGGTCCGGGCAGCCCGGAAGATAAAATCGAGGAGCTGAAGGAGAAAAATAGCCAGCTGAAAGAAAAAGAATGAAGAAGT  
AAACAGAAGATTTACGAGCTGAAGGAAGGCAGTGGCCCGGCAGCCCGGAGGACGAGATCCAGCAGCTGGAAGAGGAG  
ATTAGCCAGCTGGAGCAGAAGAATAGCAGCTGAAGGAGAAGAACCAAGAGTTAAAGTATGGCAGCGGTCCGGGTAGCC  
CGGAAGATGAAAATCAGAGCCTGGAGCAAAAAGAACAGCCAACTGAAGCAGGAAATTAGCCAATTAGAGCAGGAGATCCA  
ACAACTGGAGTATGGCAGTGGCCCGGGCGACATTGAGCAAGAACTGGAACGCGCCAAGCAGAGCATTGAAGAGCTGGAA  
CGCGAAGTGAATCAGGAGCGCAGCCGATGCAGTATCTGCAGACCCGCTGAGCGGTAGTGGCCCGGCAGCCCGGAGGA  
CAAGATCAGCCAACTGAAGGAGAAGATCCAGCAGCTGAAACAAGAAAAACCAGCAACTGGAGGAAGAAAAATAGCCAACTG  
GAATATGGTAGCGGTCCGGGTAGCCCGGAAGATGAAAATAGTCAGTTAGAGGAAAAAATTAGCCAATTAACAGAAAAA  
TAGCGAACTGAAGGAAGAAATCAACAGCTGGAATACGGCAGTGGTCTGGTAGTCCGGAGGACGAAATTCGTCAGCTGG  
AACAGGAAAAACAGCCAGCTGGAACGTGAGAACCAGCGCTGGAGCAAGAGATTTACCAGCTGGAACGTGGCAGCGGTCC  
TGGTGACATTGAACAGGAACTGGAGCGCGCAAAAACAGAGCATCGAGGAGCTGGAGCGGAGGTGAACCAGGAGCGTAGC  
CGCATGCAATATCTGCAGACCCGCTGAGTGGTAGTGGTCCGGGCAGCCCTGAAGACAAAATCAGCGAACTGAAAGAAGA  
AAACAGCAACTGGAGCAAAAAATCCAGCAGCTGAAAGAAGAAAAATAGTCAACTGGAGTACGGTAGCGGTCCGGGCAGT  
CCGGAAGACAAGATCGAGGAGCTGAAAGAGAAAAATAGCCAACTGAAAGAGAAAAACGAAGAAGTGAAGCAGAAAAATT  
TATGAGCTGAAAGAAGGTAGCGGCCCTGGTAGTCCGGAGGATGAGATTCAGCAACTGGAAGAGGAGATTAGCCAATTAGA  
ACAGAAAAATAGTGAAGTGAAGGAAAAGAATCAGGAATTAATAACGGCAGCGGTCCGGGCAGTCTGAAGATAAAAAAC  
AGTCAACTGAAGGAAGAGAACAGCCAGCTGGAAGAGAAGATCGAGCAACTGAAAGAGAAGATCCAGGAGCTGAAGTAT  
GGTAGCGGCCCGGGCGATATTGAACAGGAACTGGAACGCGCAAAAGCAGAGCATCGAAGAGCTGGAACGCGAAGTGAACC  
AAGAGCGTAGCCGTATGCAATACCTGCAAACCCGCTTAAGTCTCGAGCACCACCACCACCACCACCACCACCTAATTGATTA  
ATACCTAGG

**Name: SBP<sub>3</sub>**

**DNA sequence:**

TCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACATATGTCCCCAGAGGATAAAAATCAGTCAGTTAAAGGAGAAGA  
TCCAGCAATTAACAAGAAAACCAACAGCTTGAAGAGGAAAAACAGCCAGCTGGAATATGGTTCTGGTCCCGCTCCCC  
GAAGCAAAAACTCGGAATTAAGGAAGAAATCCAGCAGCTGGAAGAGGAGAATCAGCAACTGGAAGAAAAAATTTCCG  
AATTGAAGTATGGAAGCGGACCAGGCTCACCTGAAGACGAAATTCGCCAGCTTGAACAAGAGAACAGCCAATTAGAACGC  
GAAAATCAACGTCTGGAGCAGGAGATCTACCAGTTGGAGCGTCTCGAGCACCACCACCACCACCACCACCTAATTGATT  
AATACCTAGG

**Name: SBP<sub>19,a</sub>**

**DNA sequence:**

TCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACATATGCACCATCACCATCATCACCATCAGGAGAATCTTTACTT  
CCAAGGCCATATGAGTCCCGAAGATGAAATTCACAACTGGAGGAAGAGATTTCTCAACTTGAGCAGAAAACTCAGAAT  
TAAAAGAAAAAACAAGAGCTGAAGTACGGTAGTGGCCCGGGTTCACCTGAAGACGAGAATGAAAAATTTGGAGCGCAA  
GAACGAGGAATTAAGTGGGAAATCAAGAAGCTGGAACGTGAAATCAAGGAATTGGAGCGTGGGAGTGGACCGGGGAC  
ATCGAAACAAGAATTGGAACGCGCAAGCAGTCGATTGAGGAACTGAAACGCGAAGTTAATCAGGAGCGTTCACGTATGCA  
GTATCTTCAAACGCGCTTGTGCGGGTTCGGGGCCAGGTAGTCTTGAAGACAAGATCTCCAGTTAAAGGAAAAAATTCAC  
AATTGAAGCAGGAAAATCAGCAGTTGGAAGAGGAAAATTTCTAGTTAGAGTACGGGAGCGGACCAGGGTCCCCTGAGGA  
CGAAAACGAGAAATAGAAGAGAAGATCTGGGAGTTAAAACGTAAAGAATGAAGAGTTAAAGCGCGAGATCAAGGAGCTG  
GAAGAAGGTTCCGGCCCCGGAAGTCTGAGGACGAGATTCCAGCTGGAGCAGGAGAACTCTCAGCTGGAGCGTGAGA

ACCAGCGTTTAGAACAAAGAGATTTACCAGTTAGAGCGTGGCTCTGGTCTGGGGACATTGAACAGGAACTGGAGCGCGCC  
AAGCAATCCATTGAAGAAGCTGGAGCGTGAGGTGAATCAAGAACGCAGCCGTATGCAGTATTTGCAGACGCGTTTTAAGCGG  
AAGTGGACCAGGATCACCCGAGGACGAGATTAAGAGTTGGAGTGGAAAAATGAAGAAGCTTAAGCGCGAAATTAAGAG  
CTGGAGGAAAAAACGAGGAATTGAAACGCGGGTCAAGACCCGGTTCACCAGAAGACAAGATTGAAGAAGCTGAAGGAA  
AAAAACAGTCAATTAAGAAAAAGAAATGAGGAGCTGAAGCAGAAGATCTACGAACTGAAAGAGCTCGAGTAATGACCTA  
GG

**Name: SBP2<sub>9.a</sub>**

**DNA sequence:**

TCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACACATGCATCACCACCACCACCATCACCATGAAAACCTATATTT  
TCAGGGACATATGAGTCTTGAGGACGAAATACAGCAGCTTGAGGAAGAAATTCACAACCTTGAGCAGAAGAATTCTGAAT  
TGAAGGAAAAGAATCAAGAACTTAAATATGGTTCAGGACCTGGCTCGCCCGAGGATAAGAACAAGAGTTAAAAAGAGGA  
AAACAAAGAGCTAGAGTGGAAAATAGAGGAGTTGAAGGAGAAAATCAAAGAATTGAAGGAAGGATCTGGCCCTGGAGAC  
ATAGAGCAAGAGTTGGAGAGAGCCAAACAATCGATCGAAGAATTAGAGAGAGAGGTAAATCAAGAGAGATCACGTATGCA  
ATACCTGCAAACCAGACTTTCTGGGAGTGGACCTGGATCTCCCGAGGACAAGATATCTCAGTTAAAAGAGAAAATCCAGCA  
ATTAAAACAAGAGAACCAGCAGCTGGAAGAAGAGAATTCGACAGCTTGAGTACGGCTCAGGACCAGTTCCCCCGAGGATA  
AGAATGAAGAGCTGAAACGTGAGATTAAGAGCTGGAGTGGGAAAACGAGGAACTAGAGAGAAAAGATAGAAGAGCTGA  
AACGAGGGTCTGGTCCCGAAGTCTGAGGACGAGATACGACAGTTGGAACAGGAAAACCTCTCAACTAGAACGTGAGAA  
CCAGAGGTTGGAACAGGAAATCTATCAATTGGAGCGTGGATCTGGACCTGGGGACATCGAGCAGGAACTTGAGAGAGCAA  
AGCAATCCATAGAGGAATTAGAAAAGGGAAGTTAACCAAGAGAGGTCGCAATGCAATATTTGCAGACCCGACTTTCTGGCT  
CAGGCCCTGGCTCACAGAGGATAAGATCGAGGAACTAAAACGAGAGAACCAGGAGCTAGAGTGAAGATTGAGGAACT  
GAAGAGGAAAAATGAGGAGCTTGAGAAGGGAAGCGGTCCAGGCTCTCCAGAGGACAAAATAGAAGAGCTCAAGGAAAA  
GAATAGCCAATTGAAGGAGAAGAACGAAGAGTTAAAGCAGAAAATCTACGAGTTGAAGGAACTCGAGTAATGACCTAGG

**Name: SBP1<sub>9.a-SN</sub>**

**DNA sequence:**

CATATGCATCACCACCATCACCATCATCAGGAACTGTACTTCCAGGGTAGTCTGAAGATGAGATTACGACGCTGGAAG  
AAGAAATCAGTCAGCTGGAACAAAAGAATAGCGAGCTGAAAGAGAAAAATCAGGAACTGAAATACGGTAGTGGCCCGGG  
TAGCCCGGAGGACGAGAATCAGAGCCTGGAGCAAAAAGAATAGTCAACTGAAACAAGAGATTAGCCAACTGGAGCAGGAA  
ATCAACAGCTGGAATACGGCAGCGCCCGGGTACATCGAGCAAGAGCTGGAGCGCGCAAAAACAGAGCATTGAAGAGC  
TGGAACGCGAGGTGAACCAAGAACGTAGCCGTATGCAGTACCTGCAGACCCGTCTGAGCGGCAGCGGCCCGGGTAGCCCG  
GAGGACAAAATCAGCCAGCTGAAGGAGAAGATTAGCAACTGAAGCAAGAAAATCAACAGCTGGAAGAAGAAAACAGC  
CAGCTGGAGTATGGTAGTGGCCCGGGTAGTCCGGAGGATGAGAATAGCCAACCTGGAGGAAAAGATCAGCCAACTGAAGCA  
GAAGAACAGCGAACTGAAGGAAGAGATTAGCAACTGGAATATGGCAGCGGTCCGGGTAGCCCGGAGGACGAAATTCGC  
CAACTGGAGCAAGAGAACAGCCAACTGGAGCGGAGAATCAGCGTCTGGAACAGGAGATTACCAACTGGAGCGCGGTA  
GCGGTCCGGGTGACATTGAACAGGAACTGGAGCGCGCAAAGCAGAGCATCGAAGAAGCTGGAGCGTGAAGTGAATCAGGA  
ACGCAGCCGATGCAATATCTGCAGACACGTTAAGTGGCAGCGGTCTGGTAGTCTCTGAGGACGAGATCCAACAGCTGG  
AGGAAAAGAAATAGCCAGCTGAAGCAGGAAATAGCCAGCTGGAGGAGAAGAACCAGGAGCTGAAGTACGGCAGCGGTCC  
GGGTAGCCCGGAAGATAAAAATCGAGGAGCTGAAAGAGAAAAATAGTCAACTGAAGGAGAAAAATGAAGAAGCTGAAGCAG  
AAAATTTATGAATTAAGAAATAATGACTCGAG

**Name: SBP2<sub>9.a-SN</sub>**

**DNA sequence:**

GATATACCATGGGCCATCACCATCATCACCATCATGAGAACCTGTATTTTCAAGGCCATATGAGTCTGAAGATGAGATT  
CAGCAGCTGGAGGAAGAAATAGCCAACTGGAACAGAAAAACAGCGAACTGAAGGAGAAAAATCAGGAACTGAAATATG  
GCAGCGCCCGGGTAGCCCGGAGGACAAAACAGTCAACTGAAAGAAGAGAACAGCCAGCTGGAAGAGAAAATTTAAC  
AGTTAAAGGAAAAAATCCAGGAGTTAAAATATGGTAGCGGCCCGGGCATATTGAACAAGAGCTGGAACGCGCCAAGCAG  
AGCATCGAAGAGCTGGAACGCGAAGTGAATCAGGAACGTAGCCGCATGCAATACCTGCAGACCCGCCTGAGTGGCAGCGG  
TCCGGGTAGTCCGGAGGACAAAATCAGCCAGCTGAAGGAAAAAATTCAGCAGCTGAAACAGGAAAAATCAAACCTGGAA  
GAAGAAAATAGCCAGCTGGAATATGGCAGTGGTCCGGGCAGTCCGGAAGATAAAAATAGCGAGCTGAAAGAAGAAATCCA  
GCAACTGGAGGAAGAGAATCAGCAGCTGGAGGAAAAGATCAGCGAGCTGAAGTATGGCAGCGGCCCGGGTAGCCCGGAG  
GACGAAATTCGCCAGCTGGAGCAGGAAAATAGCCAGCTGGAGCGGAAAATCAGCGCCTGGAACAAAGAAATCTACCAGC  
TGGAGCGCGGTAGTGGCCCGGGTATATTGAGCAGGAACTGGAGCGTGCCAAAACAAAGCATTGAGGAACTGGAGCGCGA  
GGTGAACCAGGAACGCAGCCGCATGCAATATCTGCAGACACGTTAAGTGGTAGCGGTCCGGGTAGTCCGGAGGATAAGA  
TCAGTGAAGTTAAAAGAAGAAAACCAACAGCTGGAACAGAAGATTCAACAACCTGAAAGAAGAAAATAGCCAACTGGAATA  
CGGCAGTGGCCCGGGCAGCCCGAAGACAAAATCGAGGAACTGAAAGAGAAGAACAGCCAGCTGAAAGAGAAAAATGA  
AGAACTGAAGCAGAAAATCTATGAACTGAAGGAGTAATAGCTCGAGTACCTAGGCTG

**Name: SBP1<sub>9.a-56</sub>**

**DNA sequence:**

TCTAGAAACAACCTTTGTGTAATTATGAGAGGGGGACATTCACATGCATCATCATCATCACCATCACCACGAGAACTTATATTT  
TCAGGGGCATATGTCTCCAGAAGACGAGATCCAGCAACTTGAAGAAGAGATCAGTCAGTTAGAGCAGAAAAATCCGAAC  
TGAAGGAGAAAAATCAAGAGTTAAAGTACGGCTCCGGTCCAGGTTACCTGAGGATGAAAACGAGAAATTAGAAGAGAA  
GATCTGGGAGTTAAAAACGCAAAAATGAAGAGTTGAAGCGTGAGATCAAGGAACTTGAGGAAGGTTCCGGTCCGGGAGAT  
ATCGAACAGGAATTAGAGCGCGCAAAGCAATCTATCGAAGAGCTTGAACGTGAGGTAAATCAAGAACGCTCCCGCATGCA  
GTACTTGCAAACGCGTTTGTCTGGAAGCGGCCCGGGTAGTCTGAGGATAAGATTAGTCAATTAAGAAGAAAAATCCAGCA  
ATTAAAGCAAGAGAACCAACAATTGGAAGAAGAAAATCCAGCTTGTAGTACGGGTCAGGCCTGGGAGCCCAGAGGAC  
GAGAATGAAAAATTGGAGGAAAAAGATTGGGAATTGAAACGCAAAAATGAGGAGTTGAAACGTGAGATCAAGGAATTAG  
AAGAAGTAGTGGACCGGGAGTCTGAGGACGAAATTCGCCAGCTGGAGCAAGAAAACAGTCAACTGGAGCGCGAAA  
ATCAGCGTCTGGAACAGGAGATTTACCAGTTGGAGCGCGGCTCCGGACCGGGTGATATCGAGCAGGAGTTGGAGCGTGCG  
AAACAATCGATCGAGAACTTAGAACCGGAGGTGAACCGAAGAACGCTCTCGCATGCAGTATTACAGACCCGTTTGTGAGG  
AGTGACCAAGCTCACAGAAAGACGAGAACGAAAAAGTTGGAAGAGAAAATCTGGGAACCTTAAACGTAAGAATGAAGAAT  
TAAAGCGTGAGATTAAAGAATTAGAGGAGGGATCAGGACCAGGCAGTCTGAAGACAAGATCGAAGAACTTAAAGAGAA  
GAACAGTCAGCTGAAGGAAAAAACGAAGAGCTGAAACAGAAATTTATGAACCTGAAAGAACTCGAGTAATGACCTAGG

**Name: SBP2<sub>9.a-56</sub>**

**DNA sequence:**

TCTAGAAACAACCTTTGTCTAACTGTAAGAGGGTGATATTCACATGCATCATCATCATCACCATCATGAAAATTTGACTT  
CCAAGGACATATGTCTCCGAGGATGAGATCCAGCAGTTGGAAGAGGAGATCTCACAGTTGGAACAAAAGAACTCTGAGT  
TAAAAAGAAAAAACCAAGAATTGAAATATGGCTCTGGCCCGGGTTCTCCAGAAGACAAATGGAAGAAATTAACGCGAG  
TTGGAAGAGAATGAATGGGAGTTGGAAAAATCGAGCGTAAAGCTGAAGAAAATAAGCGCGGGAGCGGTCCCGGCGACA  
TTGAACAGGAGCTGGAACGTGCAAAGCAATCTATCGAGGAATTAGAGCGGAAGTGAATCAAGAGCGTAGCCGCATGCAG  
TACCTGCAGACAGTTTAAGTGGGTCTGGTCTCGTTCGCCGAAGACAAAATTTGCAGTTAAAGGAAAAGATCCAACA  
ACTGAAGCAGGAGAATCAACAGCTGGAGGAAGAGAACAGTCAAGTTGGAGTATGGGAGCGGGCCAGGAAGTCCAGAGGA  
CAAAAATGAGGAGTTGAAGCGTGAGATCAAAAGAAATTGGAGTGGGAAAATGAGGAGTTAGAACGTAAGATCGAAGAAGT  
AAGCGCGGGTCAGGTCCAGGCTCCCTGAAGATGAGATCCGTCAGCTTGAACAAGAAAATTCGCAGTTGGAGCGCGAGA  
ACCAACGCTTAGAGCAAGAGATTTACCAACTTGAACGTGGATCAGGACCTGGGGACATCGAGCAAGAGCTTGAACGCGCG  
AAACAGTCAATTGAGGAATTAGAACCGGAGGTAAACCAAGAACGCTCCCGTATGCAGTACTTGCAGACGCGCCTTTCCGG  
TAGCGGACCCGGTTCCCGAGAAGATAAAAATGAAGAGCTTAAACGCGAAAATTAAGAAGCTTGAAGTGGGAGAACGAGGAAT  
TAGAGCGCAAGATTGAGGAGCTGAAACGTGGTTCGGGGCCCGGACGCCGGAAGATAAAAATTAAGAAGCTGAAAGAGAA  
AACTCTCAACTGAAGGAGAAGAACGAGGAGTTGAAACAAAAATCTATGAGTTGAAGGAACTCGAGTAATGACCTAGG

**Name: SBP1<sub>9.a-L</sub>**

**DNA sequence:**

TCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACACATGCATCACCATCACCACCATCACCATGAAAACCTCTATTT  
TCAGGGTCATATGTGCGCTGAGGATGAAATACAGCAGTTGGAAGAGGAGATCTCCAGCTTGAGCAAAAAGAAATAGCGAAC  
TGAAGAGAAAGAACAGGAACTGAAATATGGCAGTGGTCCAGGTTCCCCGAGGACGAGAATGAGAAACTCGAAGAGAA  
AATTTGGAACTTAAACGTAAGAATGAGGAGCTAAAACGTGAAATAAAGGAGTTGGAAGAGGGAAGTGGACCAGGCGAC  
ATCGAACAGGAGCTGGAAGAGCTAAGCAGTCTATTGAGGAAGTGGAGCGGAGAAGTTAATCAGGAACGAAGCAGAATGC  
AATACTTACAGACTAGGCTTCCGGTTCAGGTCAGGTCACCTGAGGATAAGATCTCGCAGCTGAAAGAGAAAAATCCAGC  
AGCTGAAAACAGGAAAACCAACAGCTTGAAGGAAGAGAATAGTCAACTGGAATATGGATCAGGTCCCGGAAGTCCGGAAGA  
CGAAAATGAGAAATTTGAACGTAAGAACGAAGAGCTTAAATGGGAAATCAAGAAGCTAGAGAGGGAGATAAAAGAGTTA  
GAAAGAGGAAGCGGTCTGGCTCCCGGAAGACGAGATACGACAGTTGGAACAGGAGAATTTCGAGCTGGAGCGTGAAA  
ACCAAAGACTAGAGCAAGAGATTTACCAATTGGAAGAGGCTCGGGCCCGGTGATATCGAACAGGAATTGGAACGTGCT  
AAACAATCCATCGAGGAGTTGGAAGGGAAGTCAATCAAGAAAGGTCTCGTATGCAATATTTACAAACTAGACTATCCGGA  
TCGGGGCCTGGTAGCCCCGAGGATGAAATTAAGGAAGCTCGAATGGAAGAATGAGGAACCTTAAAGAGAAATCAAGGAACT  
TGAGGAAAAAGAACGAAGAGTTAAAACGAGGCTCAGGACCTGGCTCTCTGAAGACAAAATGAGGAAGTGAAGGAGAA  
GAACCTCAGATTGAAGGAAAAAGAACGAAGAGTTGAAGCAGAAAATTTATGAGTTGAAGGAACTCGAGTAATGACCTAGG

**Name: SBP2<sub>9.a-L</sub>**

**DNA sequence:**

TCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACACATGCATCACCATCACCACCATCACCATGAAAACCTGATTT  
TCAGGGTCATATGTGCGCTGAAAGATGAGATCCAACAACCTTGAAGGAAGAGATTAGTCAAGTTAGAGCAGAAAGAAATCTGAGTT

AAAAGAGAAGAATCAGGAGCTTAAATATGGTTCAGGCCCGGTTCTCCAGAAGATAAACTTGAGGAAATTAAGAGAGAAC  
TTGAGGAGAATGAGTGGGAGCTGGAGAAAATTGAGAGAAAACCTTGAGGAAAATAAACGTGGTTCCTGGACCAGGTGACAT  
TGAGCAGGAGCTGGAAAGGGCTAAGCAATCTATTGAGGAGCTGGAAAGGGAAGTGAATCAAGAACGATCCCGTATGCAAT  
ACTTGCAGACGCGTTTGGAGCGGTCTGGACCTGGTAGTCCGGAAGACAAAATTTCTCAGCTTAAAGAGAAGATTCAACAA  
CTGAAACAGGAGAATCAACAGCTGGAAGAGGAGAACTCTCAATTGGAGTACGGAAGTGGTCCGGGCTCTCCAGAGGACA  
AAATAGAAGAACTCAAACGTGAGAACGAAGAGCTGGAATGGAAAATTGAAGAGCTTAAAAAGAGAAAACGAGGAGCTGG  
AAAAGGGTTCGGGCCGGGATCTCCTGAGGATGAAATCAGGCAGTTGGAGCAGGAAAATTCACAATTGGAAAGAGAGAA  
CCAAAGGCTTGAGCAGGAGATTTACCAGTTGGAACGTGGGTCTGGCCCAGGAGACATAGAGCAGGAACTAGAACGAGCA  
AAGCAGAGTATAGAGGAATTAGAACGTGAAGTCAATCAAGAACGATCTCGTATGCAATACCTGCAAACACGACTGTCAGG  
AAGTGGCCAGGATCTCCCGAGGATAAGAAACAAAGAACTCAAAGAGGAAAATAAAGAATTAGAATGGAAGATTGAGGAA  
CTGAAGGAGAAAATTAAGAAGCTGAAAGAGGGTTCCGGTCCCGGTTCTCCCGAGGATAAGATTGAGGAACTTAAAGAGAA  
GAACTCACAGCTGAAGGAGAAGAACGAGGAGTTAAAGCAGAAGATCTATGAACTGAAAGAGCTCGAGTAATGACCTAGG

**Name: SBP1<sub>9,b</sub>**

**DNA sequence:**

TCTAGATAATTTTGTTTAACTTAAAGAAGGAGATATACACCATGGGGCATCACCACCACCACCATCACCATATGGAAAACTTA  
TATTTCCAAAAGTGGTTCGGGTCTCCTGAGGATGAGATCCGCCAGCTGGAGCAGGAAAACAGTCAGCTTGAACGCGAAAA  
TCAGCGCCTTGAACAAGAGATCTACCAATTAGAGCGGTTCCGGCCCCGGGAGCCCGGAAGATGAAATTAACAGCTTG  
AGGAGGAAATCTCTCAGCTGGAACAAAAAATTCCGAACGAAAAGAAAAAATCAGGAGCTTAAATACGGTTCGGCCCC  
GGATCCCCAGAGGACGAAAATGAGAAGTTAGAACGCAAGAATGAGGAGTTGAAGTGGGAGATTAAGAAGCTTGAACGCG  
AAATCAAAGAATTAGAACGCGGCAGCGGACCAGGGGACATTGAGCAAGAGCTTGAGCGCGCAAAGCAGTCCATTGAAGA  
GTTGGAGCGCAGGTTAAACAAAGAAGTCTCGCATGCAATATCTTCAAACCCGTTTGTCTGGGAGTGGACCGGGAAGCC  
CTGAAGATAAGATTCGCAATTGAAGGAAAAGATCCAACAACGAAACAAGAGAATCAGCAACTTGAGGAGGAAAACCTC  
ACAACCTTGAGTATGGTAGCGGGCCCGGCTCTCCTGAGGACGAGAACGAGAAAATTAGAAGAGAAAATCTGGGAGCTTAAGC  
GTAAAAATGAGGAGTTAAAGCGTGAAATCAAGGAATTAGAGGAAGGGTCCGGTCCAGGCAGTCCGGAGGATAAAATTGAA  
GAATTAAGGAGAAAAACAGTCAGTTGAAAGAAAAAACGAGGAATTGAAACAAAAAATCTATGAGTTAAAGGAGGGCT  
CTGCCCCAGGTGATATTGAACAGGAGTTGGAACGTGCCAAACAATCAATTGAAGAGCTGGAACGTGAGGTCAACCAGGAA  
CGCAGCCGATGCAGTATTACAGACTCGTTAAGCGGGTCCGGCCCCGGATCGCCTGAGGACGAAAATCAAAGAGCTGGA  
ATGAAAAACGAGGAGCTGAAACGTGAAATTAAGAATTGGAGGAGAAAAATGAAGAATTAACGCCTTGAACCTCGAG  
TAATGACCTAGG

**Name: SBP2<sub>9,b</sub>**

**DNA sequence:**

TCTAGAATAATTTGTTTAACTTAAAGAAGGAGATATACACCATGGGGCATCACCACCACCACCATCACCATATGGAAAACTT  
ATATTTCCAAAAGTGGTTCGGGTCTCCTGAGGACAAGAACAAGAACTGAAGGAAGAAAACAAAGAGCTTGAATGGAAA  
ATCGAGGAATTGAAAGAGAAGATTAAGAACTGAAAGAAGGGTCTGGGCCAGGGGATATTGAGCAAGAGCTTGAGCGTG  
CCAAGACTCAATCGAAGAGCTTGAACGTGAAGTGAACAGGAGCGCTCCCGTATGCAATATTGACAGACGCGTCTGTCTG  
GCAGTGGGCCCGGTTCTCCAGAGGACAAAATTCGCAATTGAAAGAAAAAATCCAGCAGCTGAAAACAAGAGAACCAACA  
GTTAGAGGAGGAGAATTCCCAATTGGAATACGGGTCTGGTCCCGGTTCCGCCGAGGACAAAAACGAAGAATTAAGCGCG  
AGATCAAGGAGTTAGAGTGGGAGAACGAGAACTGGAGCGCAAAAATTGAAGAGCTGAAGCGTGATCTGGGCCAGGGAG  
TCCTGAAGATAAGATTGAAGAATTAAGGAGAAAAACTCGCAGCTTAAGGAGAAAAATGAAGAACTGAAGCAGAAAAATT  
ACGAACTGAAGGAGGGCTCGGGCCCGGTGATATTGAGCAAGAACTGGAACGCGCTAAGCAATCTATTGAGGAACTTGAG  
CGTGAGGTTAACCGAAGCGCTCTCGTATGCAGTACCTTCAAACCCGTTGTCAGGTTCCGGGCCAGGCTCTCTGAAGAC  
AAAATCGAAGAACTTAAGCGCGAAAACGAGGAACTGGAGTGGAAAGATCGAGGAATTGAAACGTGAGAATGAAGAATTGG  
AGAAGGCTCAGGGCCCGATCCCTGAAGATGAGATCCGCCAGTTAGAGCAGGAAAATAGCCAACCTGGAGCGTGAGAAT  
CAGCGCTTGAGCAGGAGATTTACCAGTTGGAGCGCGAAGCGGCCAGGATCTCCAGAAGATGAAATTCAGCAACTTGA  
GGAAGAGATCTCACAGTTAGAACAAAAGAATAGTGAGCTGAAGGAAAAAATCAGGAGCTTAAAGTATCTCGAGTAATGAC  
CTAGG

**Name: SBP1<sub>11</sub>**

**DNA sequence:**

TCTAGAAATAATTTTGTTTAACTTAAAGAAGGAGATATACACCATGGGGCATCACCACCACCACCATCACCATATGCCCCAG  
AAGACAAAAATAAAGAGCTGAAGGAGGAAAACAAGGAGTTAGAGTGGAAAATCGAGGAATTAAGGAAAAAATTAAGG  
AACTGAAGGAGGGTAGTGGACCGGGAAGTCCAGAAGATAAGATCGAGGAACTTAAACGCGAGAATGAAGAATTGAGTG  
GAAGATTGAGGAATTAAGCGCGAAAATGAAGAGCTTGAGAAAAGTTCCGGCGAAAACCTTATATTTCCAAAAGTGGTTCG



GGTCTCTGAGGATGAGATCCGCCAGCTGGAGCAGGAAAACAGTCAGCTTGAACGCGAAAATCAGCGCCTTGAACAAGA  
GATCTACCAATTAGAGCGCGGTTCCGGGCCCGGGAGCCCGGAAGATGAAATTC AACAGCTTGAGGAGGAAATCTCTCAGC  
TGGAACAAAAAATTCGAACTGAAAGAAAAAATCAGGAGCTTAAATACGGTTCCGGCCCGGGATCCCCAGAGGACGA  
AAATGAGAAGTTAGAACGCAAGAATGAGGAGTTGAAGTGGGAGATTAAGAAGCTTGAACGCGAAAATCAAAGAATTAGAA  
CGCGGTGCGGACCAGGGGACATTGAGCAAGAGCTTGAGCGCGCAAAGCAGTCCATTGAAGAGTTGGAGCGCGAGGTAA  
ACCAAGAACGTTCTCGCATGCAATATCTTCAAACCCGTTTGTCTGGGAGTGGACCGGGAAGCCCTGAAGATAAGATTCGC  
AATTGAAGGAAAAGATCCAACAAGTGAACAAGAGAATCAGCAACTTGAGGAGGAAAACCTCACAACCTGAGTATGGTAG  
CGGGCCCGGCTCTCTGAGGACGAGAACGAGAAAATTAGAAGAGAAAATCTGGGAGCTTAAAGCGTAAAAATGAGGAGTTA  
AAGCGTGAAATCAAGGAATTAGAGGAAGGTCCGGTCCAGGCAGTCCGGAGGATAAAAATTGAAGAATTAAGGAGAAAA  
ACAGTCAGTTGAAAGAAAAAACGAGGAATTGAAACAAAAAATCTATGAGTTAAAGGAGGGCTCTGGCCAGGTGATATT  
GAACAGGAGTTGGAACGTGCCAAAACAATCAATTGAAGAGCTGGAACGTGAGGTCAACCAGGAACGCAGCCGCATGCAGT  
ATTTACAGACTCGTTTAAAGCGGCTCCGGCCCCGATCGCTGAGGACGAAATCAAAGAGCTGGAATGAAAAACGAGGAG  
CTGAAACGTGAAATTAAGAATTGGAGGAGAAAAATGAAGAATTAACGCCTTGAACTCGAGTAATGACCTAGG

**Name: SBP2<sub>11</sub>**

**DNA sequence:**

TCTAGAAATAATTTTGTAACTTAAAGAAGGAGATATACACCATGGGTTGGTCTCACCCACAGTTCGAGAAAATCTGCTTCA  
CCCGAGGACAAGAACAAGGAACTGAAGGAAGAAAACAAAGAGCTTGAATGGAAAATCGAGGAATTGAAAAGAGAAGATT  
AAGGAACTGAAAGAAGGGTCTGGGCCAGGGGATATTGAGCAAGAGCTTGAGCGTGCCAAGCAGTCAATCGAAGAGCTTG  
AACGTGAAGTGAACCAGGAGCGCTCCCGTATGCAATATTTGCAGACGCGTCTGTCTGGCAGTGGGCCCGGTTCTCCAGAG  
GACAAAATTTCCGAATTGAAAGAAAAATCCAGCAGCTGAAACAAGAGAACCAACAGTTAGAGGAGGAGAAATCCCAATT  
GGAATACGGGTCTGGTCCCGTTTCGCCGAGGACAAAAACGAAGAATTAAGCGCGAGATCAAGGAGTTAGAGTGGGAG  
AACGAGAACTGGAGCGCAAAATTGAAGAGCTGAAGCGTGGATCTGGGCCAGGGAGTCTTGAAGATAAGATTGAAGAAT  
TAAAGGAGAAAAACTCGCAGCTTAAAGGAGAAAAATGAAGAAGTGAAGCAGAAAATTTACGAACTGAAGGAGGGCTCGGG  
CCCGGTGATATTGAGCAAGAACTGGAACGCGCTAAGCAATCTATTGAGGAACTTGAGCGTGAGGTTAACCAAGGAACGCT  
CTCGTATGCAGTACCTTCAAACCCGCTTGTCTAGGTTGTGGCCAGGCTCTCTGAAGACAAAATCGAAGAACCTAAGCGCG  
AAAACGAGGAACTGGAGTGGAAAGATCGAGGAATTGAAACGTGAGAATGAAGAATTGGAGAAGGGCTCAGGGCCCGGATC  
CCCTGAAGATGAGATCCGCCAGTTAGAGCAGGAAAATAGCCAACCTGGAGCGTGAGAATCAGCGCTTGGAGCAGGAGATTT  
ACCAAGTTGGAGCGCGAAAGCGGCCAGGATCTCCAGAAGATGAAATTCAGCAACTTGAGGAAGAGATCTCACAGTTAGAA  
CAAAAGAATAGTGAGCTGAAGGAAAAAATCAGGAGCTTAAAGTATGGCTCAGGCGAGAATTTGATTTTCAGAGCGGTAGT  
GGGTCACCTGAAGATGAGAACGAAAAACTTGAACGTAAGAATGAGGAATTAATAAGGAAATTAAGGTTAGAACCGGA  
GATTAAGAGTTGGAACGTGGTCTGGCCCCGTTCTCCGGAAGATGAGATTAAGAATTAAGAATGAAAAATGAGGAACT  
GAAACGCGAGATCAAGGAATTAGAAGAAAAGAACGAGGAACTGAAGAGTCTCGAGCACCAACCATCACCAACCATCACCA  
TAATGACCTAGG

**Name: TEV protease**

**DNA sequence:**

TAACCTTAAAGAAGGAGATATACATATGGGCCATCACCATCATCATCACCATCATGGAGAAAGCTTGTAAAGGGACCACGTG  
ATTACAACCCGATATCGAGCACCATTTGTCACTTGACGAATGAATCTGATGGGCACACAACATCGTTGTATGGTATTGGATTT  
GGTCCCTTATCATTACAAAACAAGCACTTGTTTAGAAGAAATAATGGAACACTGTTGGTCCAATCACTACATGGTGTATTCA  
AGGTCAAGAACACCACGACTTTGCAACAACACCTCATTGATGGGAGGGACATGATAATTATTCGCATGCCTAAGGATTTCCC  
ACCATTTCTCAAAGCTGAAATTTAGAGAGCCACAAAGGGAAGAGCGCATATGTCTTGTGACAACCAACTTCAAACATAA  
GAGCATGTCTAGCATGGTGTACAGACACAGTTGCACATTCCTTCATCTGATGGCATATTCTGGAAGCATTGGATTCAAACC  
AAGGATGGGCAGTGTGGCAGTCCATTAGTATCAACTAGAGATGGGTTTATTGTTGGTATACACTCAGCATCGAATTTACCA  
ACACAAAACAAATTATTTACAAGCGTGCCGAAAAACTTCATGGAATTGTTGACAAATCAGGAGGCGCAGCAGTGGGTTAGT  
GGTTGGCGATTAATGCTGACTCAGTATTGTGGGGGGGCCATAAAGTTTTTCATGAGCAAACCTGAAGAGCCTTTTCAGCCA  
GTTAAGGAAGCGACTCAACTCATGAGTGAATTGGTGTACTCGCAATAATAGCTCGAGTACCTAGGCTGCTAAACAAAGCCC  
GAA