Supplementary Table 1 Super-helical parameters of building block modules

LRR type	Rise (Å)	Radius (Å)	Rotation angle (radian)	Number of repeat units used for fitting	Fitted RMSD (Å)
L22	2.34	18.67	0.24	8	0.09
L24	1.41	24.62	0.20	9	0.13
{L28→L29}	0.82	16.52	0.31	10	0.17

The L22, L24 and {L28→L29} repeats form unique solenoid shapes which can be described by three super-helical parameters (**radius**: distance to the helical axis, **rise**: projected distance along the helical axis between adjacent units, and **rotation angle**: rotation angle about the helical axis between units). The global helical shapes and parameters are estimated by fitting the three parameters to the repeat protein structures. For the parameter fitting, one of the highly conserved positions, the second Leu in LxxLxLxxN/C motif, is used as a representative for each repeat module. The Cα coordinates of the representative positions are obtained from the crystal structures of DLRR_A (L22) and DLRR_B (L24), and from the model structure of DLRR_C ({L28→L29}). Eight to ten Cα coordinates are used to fit the same number of coordinates arbitrary generated from the three helical parameters. RMSD between the two coordinate sets is minimized by using non-linear optimization algorithm (*constrOptim.nl*) in *alabama* R package[3,4]. Initial helical parameters, the input of the optimization procedure, are inferred from the transformation matrix between the first two modules of the building block structures. After performing the optimization procedure, the parameter of the lowest RMSD is used to represent the global helical shape of the idealized building block structures (Supplementary Fig. 1b).

Supplementary Table 2 Module organization and module origins of the multiple fusion designs in Figure 4c.

Design name	Module organization	Individual modules	Original design
DLRR_I	Ncap–L24^{2}–JN$_{L24\rightarrow L32\rightarrow L24}$–JN$_{L24\rightarrow L32\rightarrow L24}$–L24^{2}	Ncap–L24^{2}	DLRR_B
		JN$_{L24\rightarrow L32\rightarrow L24}$	DLRR_H1
		JN$_{L24\rightarrow L32\rightarrow L24}$	DLRR_H1
		L24^{2}	DLRR_B
DLRR_J	Ncap–L22^{4}→L24^{2}–JN$_{L24\rightarrow L28}$→L29→[L28→L29]^{2}	Ncap–L22^{4}	DLRR_A
		L24^{2}	DLRR_B
		JN$_{L24\rightarrow L28}$	DLRR_G3
		L29	DLRR_G3
		[L28→L29]^{2}	DLRR_G3
DLRR_K	Ncap–L24^{2}–JN$_{L24\rightarrow L32\rightarrow L24}$–L24^{3}–JN$_{L24\rightarrow L28}$→L29→[L28→L29]^{2}	Ncap–L24^{2}	DLRR_B
		JN$_{L24\rightarrow L32\rightarrow L24}$	DLRR_H2
		L24^{3}	DLRR_B
		JN$_{L24\rightarrow L28}$	DLRR_G6
		L29	DLRR_G6
		[L28→L29]^{2}	DLRR_G6
DLRR_L	Ncap–L22^{3}→L24^{3}–JN$_{L24\rightarrow L32\rightarrow L24}$–L24^{3}–JN$_{L24\rightarrow L28}$→L29→[L28→L29]^{2}	Ncap–L22^{3}	DLRR_A
		L24^{3}	DLRR_B
		JN$_{L24\rightarrow L32\rightarrow L24}$	DLRR_H2
		L24^{3}	DLRR_B
		JN$_{L24\rightarrow L28}$	DLRR_G6
		L29	DLRR_G6
		[L28→L29]^{2}	DLRR_G6

Supplementary Table 3 Number of possible fusion LRR structures with respect to the number of repeat units.

Number of repeat units	Number of possible LRR structures	Fold change (i) → (i+1)
5	64	
6	145	2.266
7	327	2.255
8	736	2.251
9	1,655	2.249
10	3,720	1.976
11	8,360	2.247
12	18,786	2.247
13	42,213	2.247
14	94,853	2.247
15	213,134	2.247
16	478,909	2.247
17	1,076,100	2.247
18	2,417,996	2.247
19	5,433,237	2.247

LRR structures are generated by recursively following the edges of the network in Figure 4a. The general module assembly starts from Ncap-L22 or Ncap-L24 in the network except $\{L28 \rightarrow L29\}^n$ and each assembly (transition in the network) adds one repeat unit to the structure. The number of repeat units in the table only considers the internal repeat units excluding N-terminal capping domain.

Supplementary Table 4 Crystallization conditions

Design names	Crystallization conditions
DLRR_A	22% PEG3350 w/v, 0.1 M MES pH 6.0, 0.2 M NaCl
DLRR_E	20% PEG 1000 v/v, 0.1 M Na/K phosphate pH 6.2
DLRR_G3	2 M ammonium sulfate, 0.1 M Bis-Tris Ph 5.5
DLRR_H2	22% PEG 3350 w/v, 300 mM Ammonium sulfate, unbuffered
DLRR_I	24% PEG 3350 w/v, 0.2 M ammonium sulfate, 0.1 M HEPES pH 7.5, 0.1 M proline
DLRR_K	20% PEG-3000, 0.1 M Tris pH 7.0, 0.2 M Ca(OAc)2

Supplementary Table 5 Designed sequences

> DLRR_A

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>DLRR_B

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>DLRR_C

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LHELHLSNNNIGEEGKAWLEEARRHPGSTLETgshhhhhh

*C-terminal linkers and 6x His tags are shown in lower case.

*AS or TS in the regular repeat sequences are for inserting the restriction sites (NheI and SpeI).

Supplementary References

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