Supporting Information

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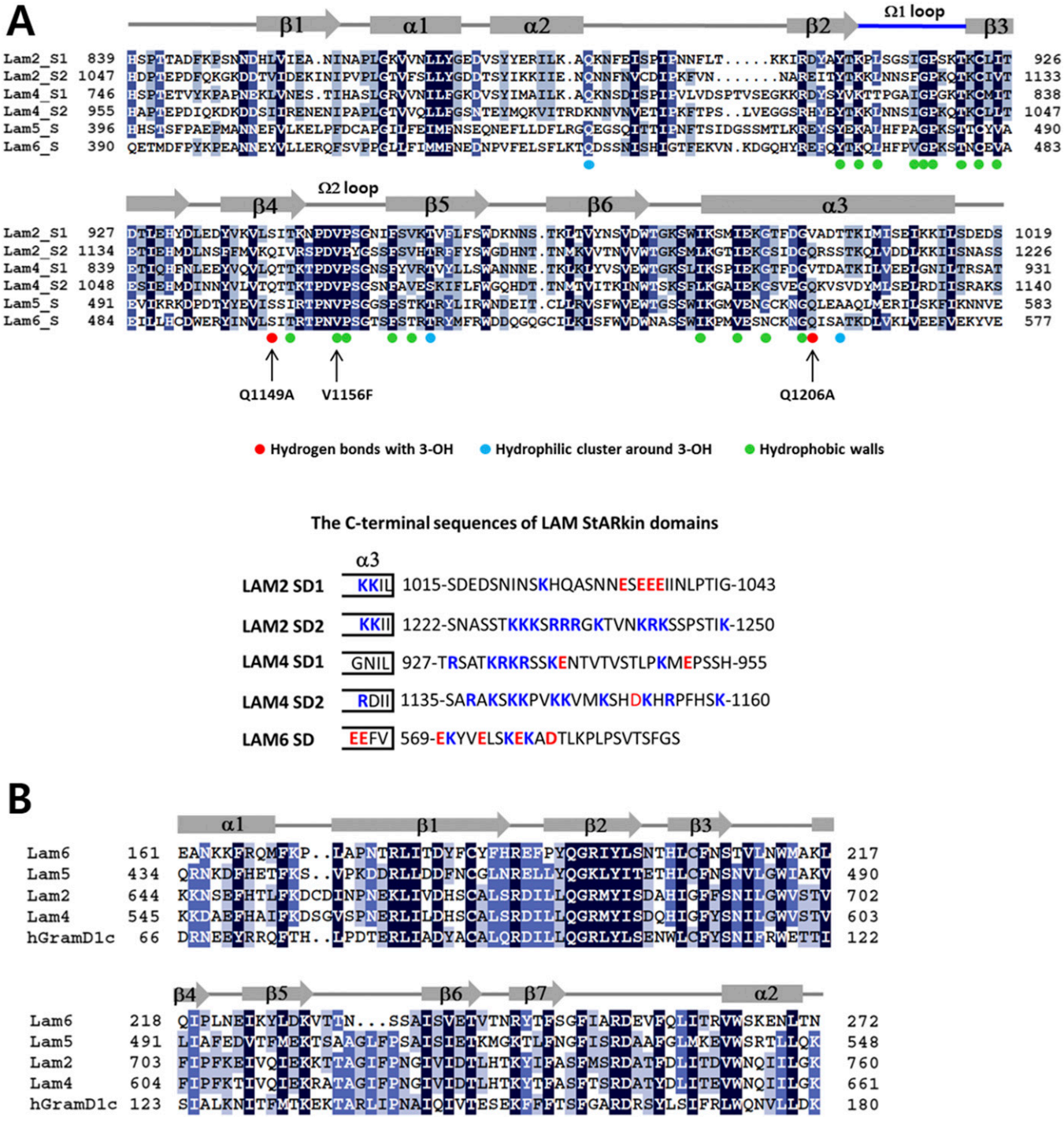

Fig. S1. Sequence alignments of yeast LAM SDs. (*A*) The sequences of the SDs of Lam2, Lam4, Lam5, and Lam6 from *Saccharomyces cerevisiae* were aligned. (*Top*) The secondary structure elements for the Lam2 SD2. (*Bottom*) Sequences of the C-terminal extensions of the LAM SDs. (*B*) The sequence alignments of the PH-like domains of Lam2, Lam4, Lam5, Lam6, and human GramD1c.

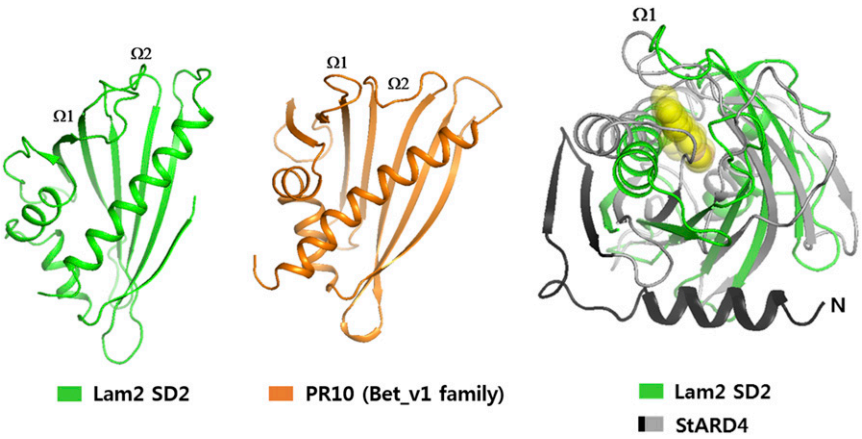

Fig. S2. Structural comparison of the LAM SD with a Bet_v1 family protein and STARD4. The ribbon structures of the Lam2 SD2 and PR10 of the Bet_v1 family are shown side by side. The PR10 (PDB id: 1IFV) was found to be structurally similar with the rmsd of 2.7 Å by DALI search in the Protein Data Bank. (*Right*) Structural superposition with a sterol-transfer protein, STARD4 (PDB id: 1JSS), of the StART family.

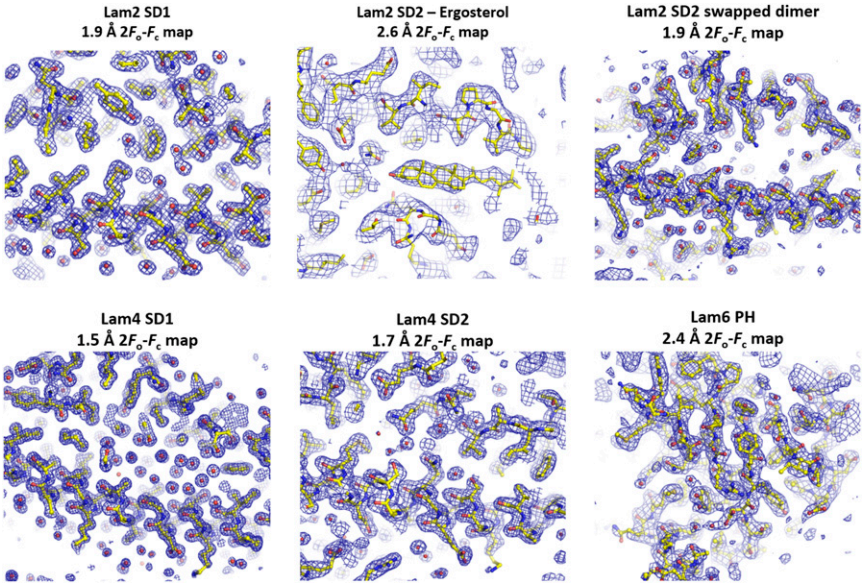

Fig. S3. The electron density maps. The $2F_o - F_c$ maps of the structures determined in this study are shown with the final models superimposed.

Table S1. Data collection and refinement statistics

Crystal	Lam2 SD1	Lam2 SD2 Swap dimer	Lam2 SD2-ergosterol complex	Lam4 SD1 Se-Met	Lam4 SD1	Lam4 SD2	Lam6 PH
Construct	Residue 850–1,016	Residue 1,060–1,223	Residue 1,060–1,223	Residue 749–929	Residue 749–929	Residue 953–1,137	T4L – Residue 161–272
Beamline	PLS-7A	PLS-7A	PLS-7A	PLS-7A	PLS-7A	PLS-7A	PLS-7A
Wavelength, Å	0.97950	0.97950	0.97950	0.97931	0.97950	0.97950	0.97950
Space group	$P2_12_12_1$	$P1$	$C2$	$P2_1$	$P2_1$	$I222$	$P2_12_12_1$
Unit-cell parameters a, b, c (Å), α, β, γ (°)	33.4, 59.5, 84.3	33.9, 52.1, 53.0, $\alpha = 107.8$, $\beta = 90.2$, $\gamma = 105.1$	189.7, 70.3, 41.5, $\beta = 103.1$	38.9, 55.0, 119.4, $\beta = 94.9$	38.8, 55.0, 119.5, $\beta = 95.1$	68.3, 89.1, 111.3	59.5, 60.1, 105.6
Rotation range, Å	50–1.6 (1.63–1.60)	50–1.9 (1.93–1.90)	50–2.6 (2.64–2.60)	50–2.0 (2.03–2.00)	50–1.5 (1.50–1.53)	50–1.7 (1.73–1.70)	50–2.4 (2.44–2.40)
No. of reflections	128,373	64,364	80,718	135,971	327,744	333,245	123,116
No. of unique reflections	22,632 (1,117)	25,976 (1,273)	16,717 (845)	33,700 (1,718)	80,061 (3,964)	37,918 (1,880)	15,204 (727)
Multiplicity	5.7 (5.8)	2.5 (2.5)	4.8 (4.8)	4.0 (4.2)	4.1 (4.1)	8.8 (8.9)	8.1 (9.4)
Mean I/σ(I)	45.5 (5.3)	32.3 (5.5)	48.9 (6.9)	40.1 (15.2)	31.6 (4.8)	51.7 (8.2)	48.3 (9.7)
Completeness, %	98.6 (100)	97.4 (96.6)	99.0 (99.8)	98.5 (99.0)	99.6 (99.0)	99.6 (100)	99.0 (100.0)
R_{merge}, %	6.0 (42.7)	4.5 (27.9)	3.9 (33.1)	13.9 (42.8)	6.2 (37.1)	7.1 (38.3)	9.8 (41.2)
Wilson B factor, Å	22.7	28.0	63.5	18.4	14.3	21.7	41.7
Refinement							
R_{work}, %	20.6 (22.3)	19.4 (22.0)	24.4 (31.4)	17.9 (26.2)	15.8 (18.6)	20.2 (25.6)	23.5 (28.1)
R_{free}, %	24.6 (24.6)	24.2 (28.7)	29.3 (37.7)	19.3 (30.7)	21.1 (27.8)	24.2 (31.6)	27.0 (35.8)
rmsd bond lengths, Å	0.006	0.006	0.010	0.008	0.005	0.007	0.008
rmsd bond angles, °	0.746	0.862	1.165	0.890	0.731	0.923	1.092
B factor, Å^2							
Molecule A (B, C)	25.4	33.2 (32.5)	66.6 (68.7, 87.0)		20.9 (20.8, 21.4)	24.8 (29.3)	57.9
Ligands	—	—	77.4 (74.9)	—	—	—	65.5 (PEG)
Water	32.0	37.2	61.8	—	34.1	33.0	53.9
No. of non-H atoms							
Protein	1,328	2,537	3,775	—	4,131	2,920	2,199
Ligand	—	—	58 (ergosterol)	—	—	—	—
Solvent	119	223	23	—	837	352	32
Ramachandran statistics							
Favored, %	97.53	96.13	88.21		96.65	98.09	91.76
Disallowed, %	0	0.32	1.75		0	0	2.62
PDB entry	5YQI	5YQQ	5YS0		5YQJ	5YQP	5YQR

Values in parentheses indicate the highest-resolution shell.