Supplementary information, Table S1 Statistics of data collection and model refinement

	FERM/CTD	FERM/Lats1	FERM/Lats2
Data collection			
X-ray source	Photon Factory	SSRF	SSRF
Space group	$\boldsymbol{P}2_12_12_1$	$\boldsymbol{P}2_12_12_1$	$\boldsymbol{P}2_1$
Unit cell parameters (Å)	$\boldsymbol{a}$=67.9;$\boldsymbol{b}$=68.2;$\boldsymbol{c}$=82.3	$\boldsymbol{a}$=111.1;$\boldsymbol{b}$=110.8;$\boldsymbol{c}$=168.7	$\boldsymbol{a}$=63.0;$\boldsymbol{b}$=100.5;$\boldsymbol{c}$=65.0 $\boldsymbol{\beta}$=105.9
Resolution range (Å)	50-2.3(2.37-2.3)	50-2.3(2.38-2.3)	50-2.7(2.79-2.7)
No. of unique reflections	17,339(1,639)	89,074(8,835)	21,376(2,014)
Redundancy	7.2(6.6)	5.9(5.6)	3.8(3.5)
$\mathbf{I}/\boldsymbol{\sigma}$	26.3(7.3)	28.1(2.5)	20.4(2.2)
Completeness (%)	99.5(98.6)	99.4(99.8)	99.3(95.0)
$\boldsymbol{R}_{merge}$ (%)[a]	7.3(23.9)	6.1(77.5)	6.0(40.6)
Structure refinement			
Resolution (Å)	50-2.3(2.37-2.3)	50-2.3(2.34-2.3)	50-2.7(2.82-2.7)
$\boldsymbol{R}_{cryst}$ / $\boldsymbol{R}_{free}$ (%)[b]	19.3/24.8	24.7/27.9	22.9/27.0
r.m.s.d bonds (Å) / angles (°)	0.008/1.1	0.01/1.2	0.01/1.3
Average B factor	21.6	56.4	57.6
No. of atoms			
Protein atoms	3,045	10,271	4,972
Water molecules	107	33	3
Ramachandran plot[c]			
favored regions(%)	98.4	97.9	93.8
allowed regions(%)	1.3	1.9	6.0
outliners(%)	0.3	0.2	0.2

[a] $\boldsymbol{R}_{merge} = \sum|I_i - I_m|/\sum I_i$, where I_i is the intensity of the measured reflection and I_m is the mean intensity of all symmetry related reflections.

[b] $\boldsymbol{R}_{cryst} = \Sigma||F_{obs}| - |F_{calc}||/\Sigma|F_{obs}|$, where F_{obs} and F_{calc} are observed and calculated structure factors.

$\boldsymbol{R}_{free} = \Sigma_T||F_{obs}| - |F_{calc}||/\Sigma_T|F_{obs}|$, where T is a test data set of about 5-10% of the total reflections randomly chosen and set aside prior to refinement.

[c] Defined by MolProbity.

Numbers in parentheses represent the value for the highest resolution shell.