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

	AtKAI2	AtD14	OsD14	OsD14/lactone
PDB code (*)	4IH1	4IH4	4IH9	4IHA
Data collection				
Beam line	21-ID-D APS	21-ID-D APS	BL17U-MX SSRF	BL17U-MX SSRF
Space group	P21	C2	P212121	P212121
Resolution, Å	30-1.55	30-3.5	40-1.55	40-1.55
Cell parameters, Å, °	a=51.3, b=56.0, c=53.5; α=90, β=116.1, γ=90	a=184.8, b=44.6, c=160.9; α=90, β=121.1, γ=90	a=48.2, b=88.5, c=121.2; α=β=γ=90	a=48.2, b=88.7, c=118.3; α=β=γ=90
Total/Unique reflections	281992/39492	51499/12471	503908/76211	509335/74350
Completeness, %	99.9 (99.6)	83.8 (85.6)	100.0 (100.0)	100.0 (100.0)
I/σ	22.5 (2.5)	5.3 (1.7)	22.1 (2.2)	21.8 (2.4)
Redundancy	7.1(5.8)	4.1(4.0)	6.6(6.5)	6.9(6.9)
Rsym	0.10 (0.62)	0.20 (0.55)	0.08 (0.73)	0.08 (0.79)
Structure determination				
Resolution, Å	30-1.55	30-3.5	30-1.55	30-1.55
No. reflections	32292	9439	76002	63304
NCS molecules	1	4	2	2
No. residues	268	1044	530	540
No. solvent molecules	114	0	374	425
No. of non-H atoms	2196	8164	4466	4578
Rcryst	17.8%	27.8%	17.9%	18.1%
Rfree	19.2%	33.6%	19.7%	20.1%
rmsd bonds, Å	0.013	0.010	0.011	0.015
rmsd angles, °	1.27	1.28	1.24	1.46
Average B factor, $Å^2$	19.4	37.3	12.1	15.6

Rmsd is for root-mean-square deviation from ideal geometry of protein.
(*): PDB code and structure factors will be available from RCSB data bank upon publication.