Supplementary Table 1 Data collection, phasing and refinement statistics

	GA_4-GID1A-DELLA Native	GA_3-GID1A-DELLA Native	GA_3-GID1A-DELLA SeMet
Data collection			
Space group	$P4_32_12$	$P4_32_12$	$P4_32_12$
Cell dimensions			
a, *b*, *c* (Å)	81.8, 81.8, 129.9	82.0, 82.0, 130.1	82.1, 82.1, 129.8
			Peak
Wavelength (Å)	1.00000	0.99533	0.97938
Resolution (Å)	50-1.8 (1.86-1.80)*	50-1.8 (1.86-1.80)	20-2.0 (2.07-2.00)
R_{sym}	6.5 (6.8)	5.9 (12.9)	6.4 (11.9)
$I/\sigma I$	71.4 (58.8)	65.8 (28.6)	72.2 (39.7)
Completeness (%)	99.0 (98.2)	100 (98.4)	100 (100)
Redundancy	13.3 (11.2)	13.4 (14.4)	15.4 (15.3)
Refinement			
Resolution (Å)	50.0-1.8	50.0-1.8	
No. reflections	40,855	39,256	
R_{work}/ R_{free}	19.8/22.1	20.5/22.9	
No. atoms			
Protein	3,156	3,134	
Ligand/ion	24	25	
Water	267	216	
B-factors			
Protein	19.10	22.83	
Ligand/ion	11.04	17.75	
Water	24.32	27.28	
R.m.s deviations			
Bond lengths (Å)	0.005	0.005	
Bond angles (º)	1.21	1.18	

One crystal was used for each data set.

*Values in parenthesis are for highest resolution shell.

Supplementary Table 2 Lists of hydrogen bonds between GA and GID1A

		GA_3-GID1A-DELLA	**GA_4-GID1A-DELLA**
GA atom	GID1A residue/atom	distance for GA_3	distance for GA_4
O3-1	H_2O	2.80 Å	2.89 Å
O3-1	Y127/OH	2.83 Å	2.75 Å
O7-1	S116/N	3.01 Å	2.96 Å
O7-1	S116/Oγ	2.68 Å	2.71 Å
O7-1	S191/Oγ	3.28 Å	3.23 Å
O7-2	S191/Oγ	2.95 Å	3.17 Å
O7-2	H_2O	2.65 Å	2.71 Å
O19-1	G320/N	2.87 Å	2.90 Å
O13	F238/O	3.25 Å	- (GA_4 has no O13)
O13	H_2O	3.15 Å	- (GA_4 has no O13)

Figure S1 Structural comparison of the GA_3- and GA_4-GID1A-DELLA complexes.

a, Chemical structures of bioactive GA_1 and GA_7. The bioactive GA molecules conserve one 7-carboxylate, 3-hydroxyl and one lactone (a cyclic carboxylester) moiety. The 3-hydroxyl group is introduced by GA 3-oxidase at the final step to produce active GA derivatives.

b, Structural comparison of the GA_3- and GA_4-GID1A-DELLA complexes. The GA_3-GID1A-DELLA complex is superimposed on the GA_4-GID1A-DELLA complex (grey). The GA_3-GID1A-DELLA complex is colored in pink (GAI DELLA domain), light blue (GID1A) and green (GA_3). The GA_4-GID1A-DELLA complex is colored in light green (GAI DELLA domain), yellow-orange (GID1A) and magenta (GA_4). The overall mean rms deviation is extremely small, 0.18 Å, over all the C_α atom positions of aligned residues. The GID1A molecules superimpose with an averaged rms deviation of 0.14 Å over all the C_α atom positions and the DELLA domains superimpose with an averaged rms deviation of 0.25 Å.

c, Molecular surface of the GA_3-GID1A-DELLA complex with the GAI DELLA domain (pink), the GID1A N-terminal extension (cyan) and the GID1A α/β core domain (light blue).

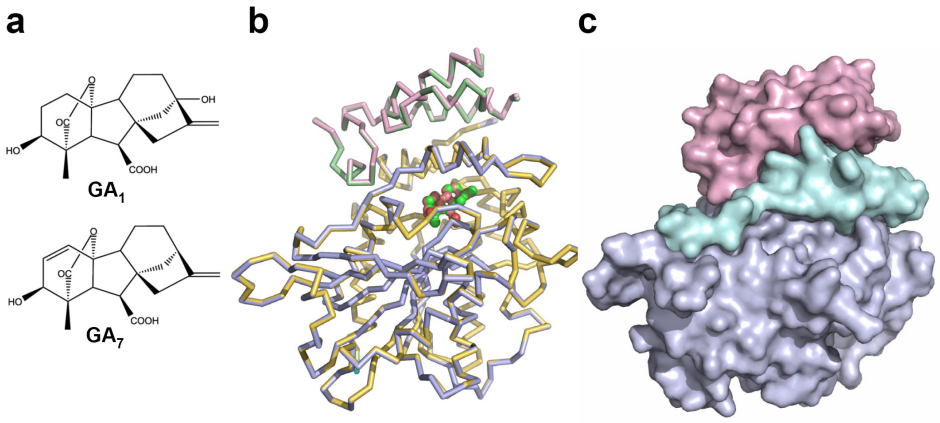

Figure S2 Structural comparison of GID1A and plant carboxylesterase CXE1. *Arabidopsis thaliana* GID1A is superimposed on *Actinidia eriantha* carboxylesterase CXE1 (from kiwifruits, PDB code 2O7V). The core domains superimpose well with an averaged rms deviation of 1.61 Å over the C_α atom positions of 148 out of 345 aligned residues without insertion and deletion segments. Tube diagrams of GID1A and CXE1 are shown in light blue and grey, respectively. Insertions in GID1A and CXE1 are highlighted in blue and red, respectively. Compared with CXE1, GID1A has 3 insertion and 4 deletion sites, where the N-terminal extension residues play a role in DELLA binding, although most of the other sites are located at the C-terminal edge of the β-sheet away from either the DELLA- or GA-binding sites. CXE1 lacks the corresponding helices found in the GID1A N-terminal extension, and instead contains a short pair of antiparallel strands that fail to completely cover the pocket.

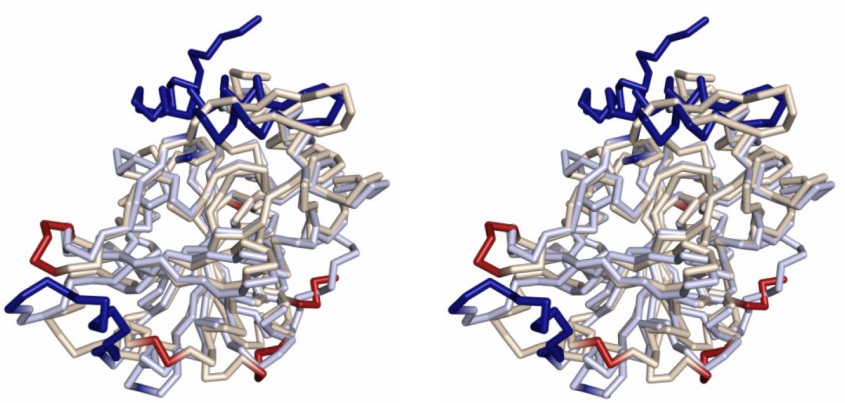

Figure S3 Sequence alignment of GID1s and a plant carboxylesterase. Structural-based sequence alignment of GID1 proteins, *A. thaliana* GID1A, B and C, *Oryza sativa*, (rice) GID1 (Os GID1), and *A. eriantha* (kiwifruit) carboxylesterase CXE1 (Ae CXE1, PDB code 2O7V). The secondary structures of GID1A are shown at the top with α-helices (yellow bars), 3_{10}-helices (orange bars), β-strands (green arrows) and disordered residues (dotted lines). The secondary structures of CXE1 are shown at the bottom. The N-terminal extension of GID1A comprises three helices, αa (residues 9-13), αb (18-34) and αc (43-49), followed by loop αc-β1 (residues 51-62). The GID1A core domain consists of a central eight-stranded mixed β-sheet (β1-β8) and seven α-helices (α1-α7) and two 3_{10} helices (η1 and η2). GID1A lacks three α-helices corresponding to α3, α5, and α8 (grey bars) of CXE1 and one 3_{10}-helix corresponding to η1 of CXE1. Instead of α3 of CXE1, GID1A has a 3_{10}-helix η1. Bold letters indicate important residues for GA_3 and GA_4 binding (blue circles), DELLA binding (black circles), and the catalytic triad and oxyanion hole found in carboxylesterase (red letters). The triad residues are Ser191 (loop β5-α3), Val319 (loop β8-α7) and Asp289 (at loop β7-α6). GA-interacting residues are highlighted in light green and boxed with bold lines. Identical residues to GID1A are highlighted in pale yellow. Accession numbers: GID1A, At3g05120; GID1B, At3g63010; GID1C, At5g27320; Os GID1, AB211399. GID1A and CXE1 share 22.5% sequence identity, whereas no homology at the N-terminal extension (62 residues) is detected. Among GID1 members, however, the N-terminal extensions are highly homologous, implying a specific function as the gibberellin receptor.

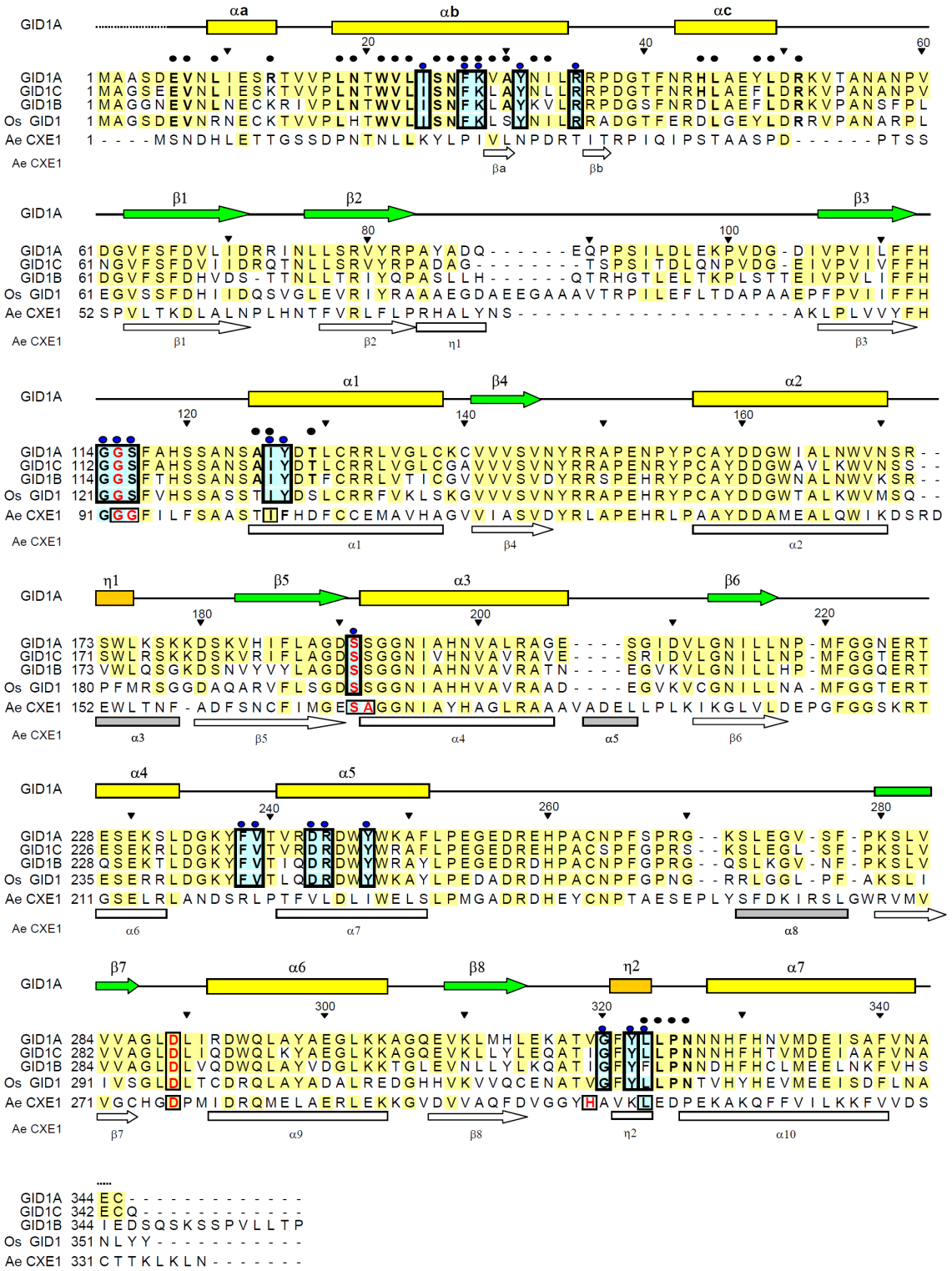
GID1A
αa
αb
αc
β1
β2
β3
α1
β4
α2
η1
β5
α3
β6
α4
α5
β7
α6
β8
η2
α7
GID1A
GID1C
GID1B
Os GID1
Ae CXE1
Ae CXE1

Figure S3

Figure S4 Schematic representation of the interactions. Summary of intermolecular interactions between GID1A and GA_3 in the GA_3-GID1A-DELLA complex. Van der Waals contacts (dotted lines), hydrogen bonds (arrows) and a salt bridge (an arrow with a dotted line) are shown. Residue side chains that participate in the interactions are indicated by boxes with bold lines. The N-terminal extension residues of GID1A are highlighted (cyan). All the interactions are conserved in those with GA_4 in the GA_4-GID1A-DELLA complex. Basically, contacts between hydrogen donor and acceptor atoms are nominated for hydrogen bonds with the typical distances (for example, 2.9 Å for H-bond between N-H and O) plus/minus 0.2 Å and the angles (for example, C-N---O and N---O-C) larger than 90°.

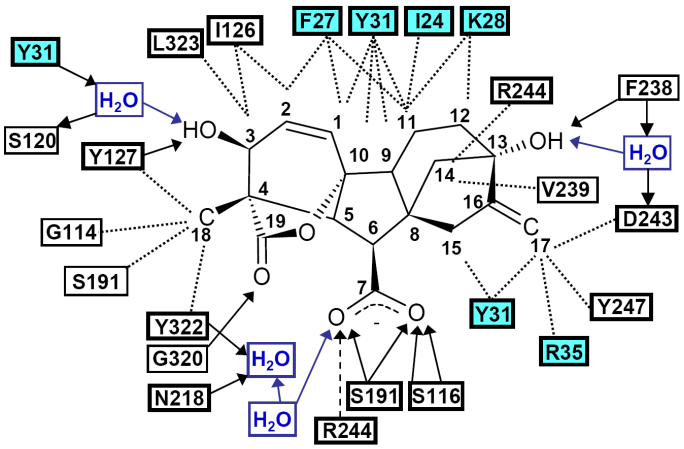

Figure S5 A stereo-view of GA perception in the GA_4-GID1A-DELLA complex. GID1A residues that contact GA_4 are highlighted in yellow (the core domain) or cyan (the N-terminal extension) and shown as stick models with van der Waals surfaces represented by dots. Water molecules are shown as blue spheres. Hydrogen bonds are indicated with dotted lines. Atom codes are oxygen in red and nitrogen in blue.

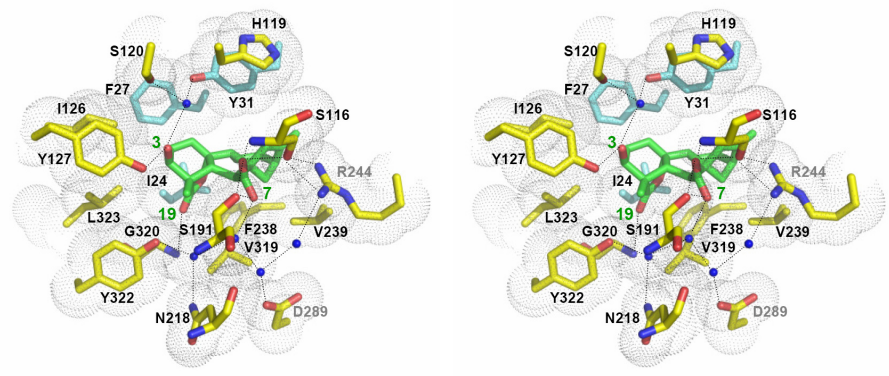

Figure S6 Sequence alignment of DELLA domains. The N-terminal DELLA domains from *A. thaliana* and *O. sativa* DELLA proteins are aligned. The secondary structures of GAI are shown at the top with α-helices (yellow bars), loops (solid lines) and disordered residues (dotted lines). GID1A-binding residues (purple circles) are indicated with bold letters. Identical residues to GAI are highlighted in pale yellow. Accession numbers: GAI, At1g14920; RGA, At2g01570; RGL1, At1g66350; RGL2, At3g03450; RGL3, At5g17490; SLR1, AB262980. GID1A-interacting residues are highlighted in light green and boxed with bold lines. Identical residues to GID1A are highlighted in pale yellow.

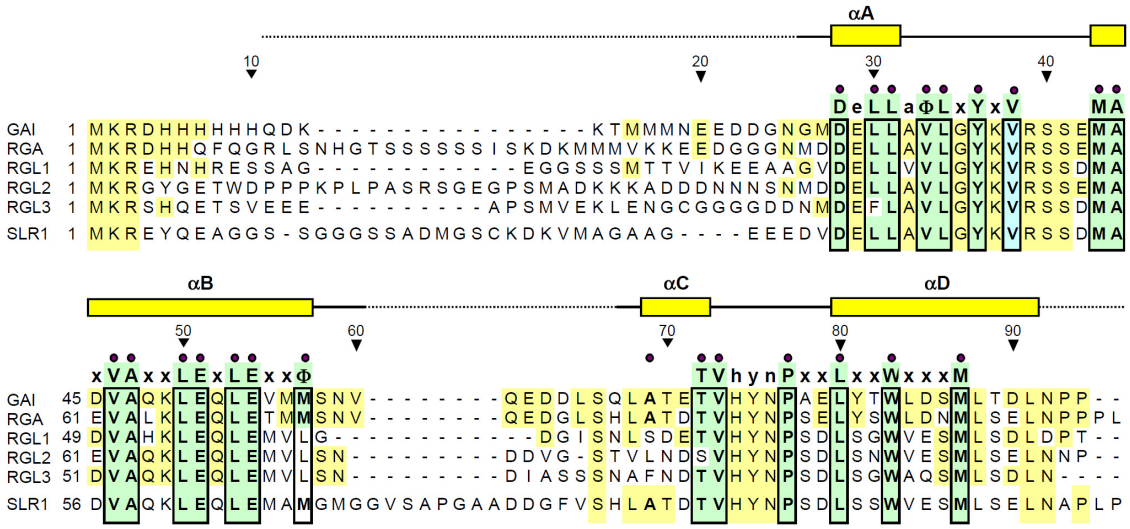

Figure S7 Effects of mutation of the DELLA domain on GID1A binding. Pull-down binding assays of mutated DELLA domains of GAI with GA_3-bound GID1A were performed with single mutations of the DELLA (Leu31, Tyr36 and Val38) and the LExLE (Met43, Glu51 and Glu54) motifs, and double mutations of Leu31 and Val38, Tyr36 and Met43, Glu51 and Glu54. Eluted samples analyzed by SDS-PAGE.

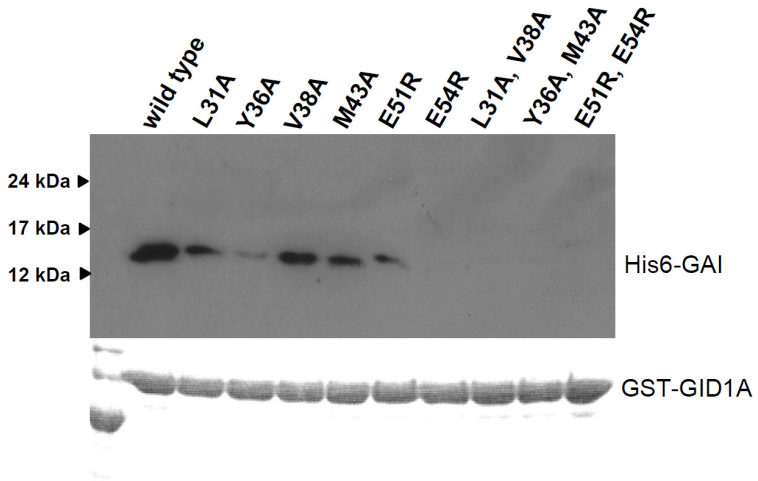

Figure S8 Conformational flexibility of the GID1A and the DELLA domain of GAI.

a, Conformational flexibility of the GID1 N-terminal extension. Proteolysis of GID1A in the free, GA_3-bound and DELLA-bound states. GID1A (residues 14-345) produced by trypsin-treatment of GST-GID1A was degraded rapidly within 10 min in the GA-unbound state, whereas resistant over 20-30 min in the GA-bound and DELLA-bound states.

b, Conformational flexibility of the DELLA domain of GAI. CD spectra of the DELLA domain. No significant changes were observed in the spectra at 20, 37, 50 and 70°C. Secondary structure estimations suggest a 100% random coil structure.