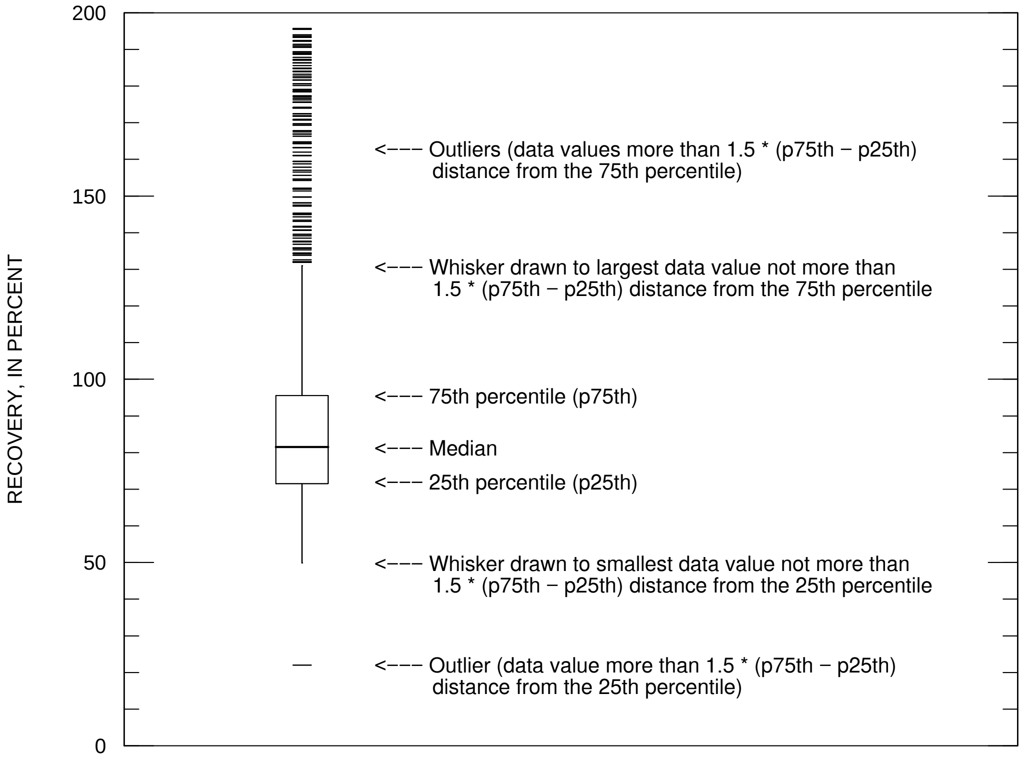
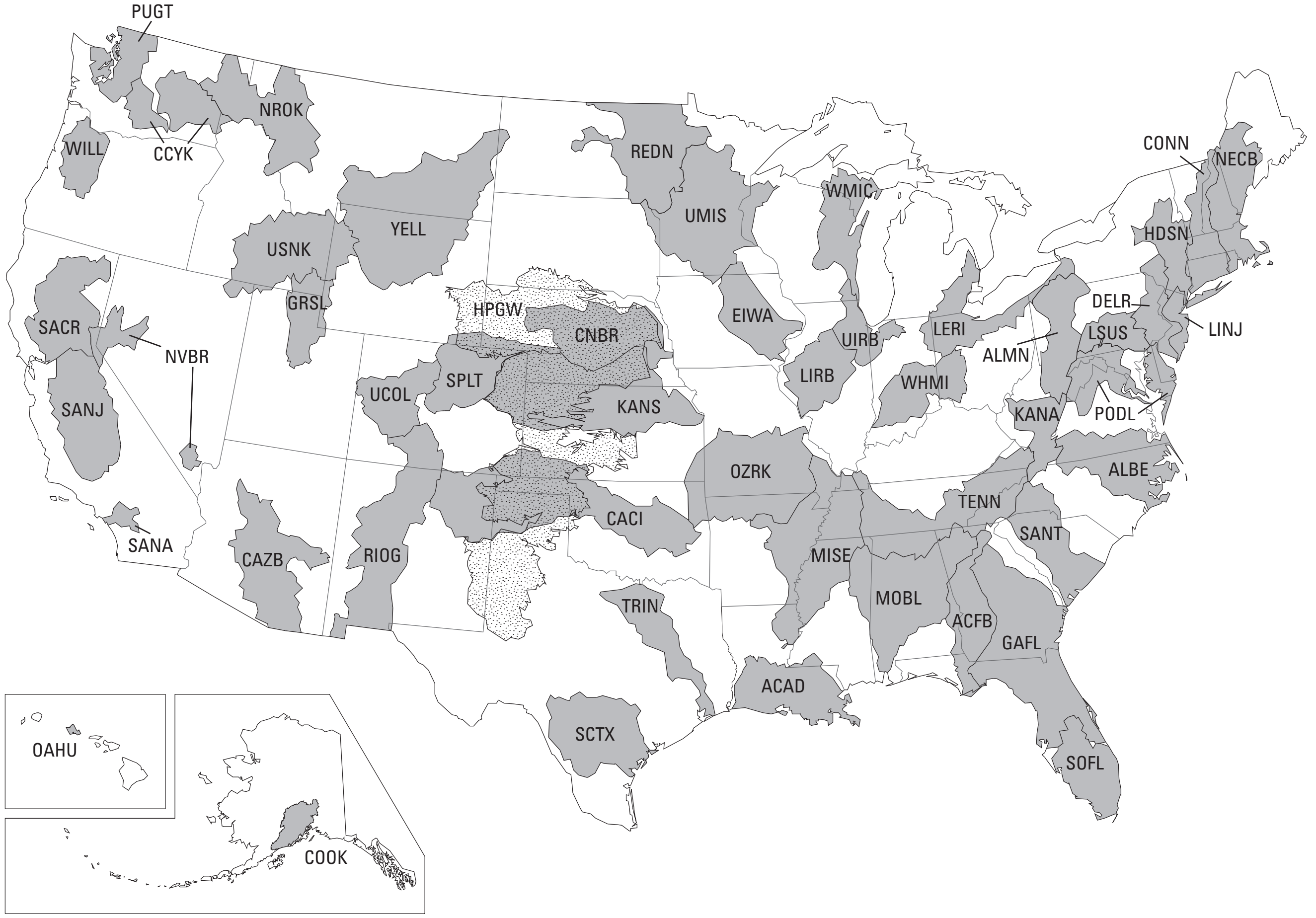
Appendix 7. Distribution of residual errors in modeled recovery for selected stream-water sites.



Explanation of boxplots used to depict distributions of recovery. In some figures, the number of measurements is shown at the top or bottom of the boxplot.



Study Units

ACAD	Acadian-Pontchartrain Drainages
ACFB	Apalachicola-Chattahoochee-Flint River Basin
ALBE	Albemarle-Pamlico Drainage Basin
ALMN	Allegheny and Monongahela River Basins
CACI	Canadian-Cimarron River Basins
CAZB	Central Arizona Basins
CCYK	Central Columbia Plateau - Yakima River Basin
CNBR	Central Nebraska Basins
CONN	Connecticut, Housatonic and Thames River Basins
COOK	Cook Inlet Basin
DELR	Delaware River Basin
EIWA	Eastern Iowa Basins
GAFL	Georgia-Florida Coastal Plain
GRSL	Great Salt Lake Basins
HDSN	Hudson River Basin
HPGW	High Plains Regional Ground Water Study
KANA	Kanawha - New River Basins
KANS	Kansas River Basin
LERI	Lake Erie - Lake Saint Clair Drainages
LINJ	Long Island - New Jersey Coastal Drainages
LIRB	Lower Illinois River Basin
LSUS	Lower Susquehanna River Basin
MISE	Mississippi Embayment
MOBL	Mobile River Basin
NECB	New England Coastal Basins
NROK	Northern Rockies Intermontane Basins
NVBR	Las Vegas Valley Area and the Carson and Truckee River Basins
OAHU	Island of Oahu
OZRK	Ozark Plateaus
PODL	Potomac River Basin and Delmarva Peninsula
PUGT	Puget Sound Basin
REDN	Red River of the North Basin
RIOG	Rio Grande Valley
SACR	Sacramento River Basin
SANA	Santa Ana Basin
SANJ	San Joaquin-Tulare Basins
SANT	Santee River Basin and Coastal Drainages
SCTX	South-Central Texas
SOFL	Southern Florida
SPLT	South Platte River Basin
TENN	Tennessee River Basin
TRIN	Trinity River Basin
UCOL	Upper Colorado River Basin
UIRB	Upper Illinois River Basin
UMIS	Upper Mississippi River Basin
USNK	Upper Snake River Basin
WHMI	White, Great and Little Miami River Basins
WILL	Willamette Basin
WMIC	Western Lake Michigan Drainages
YELL	Yellowstone River Basin

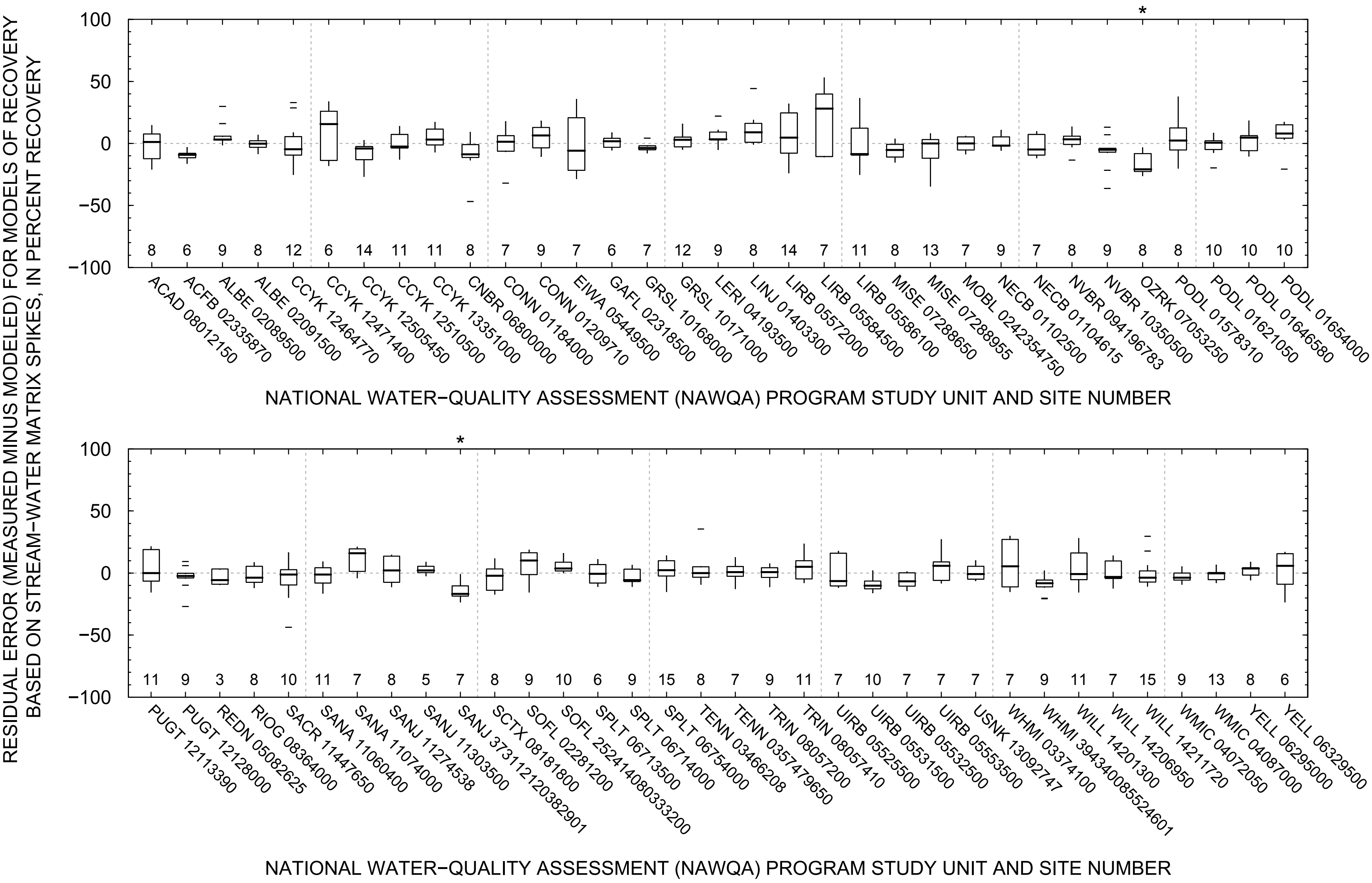


Figure A7−1. Distribution of residual errors in modeled recovery of acetochlor for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

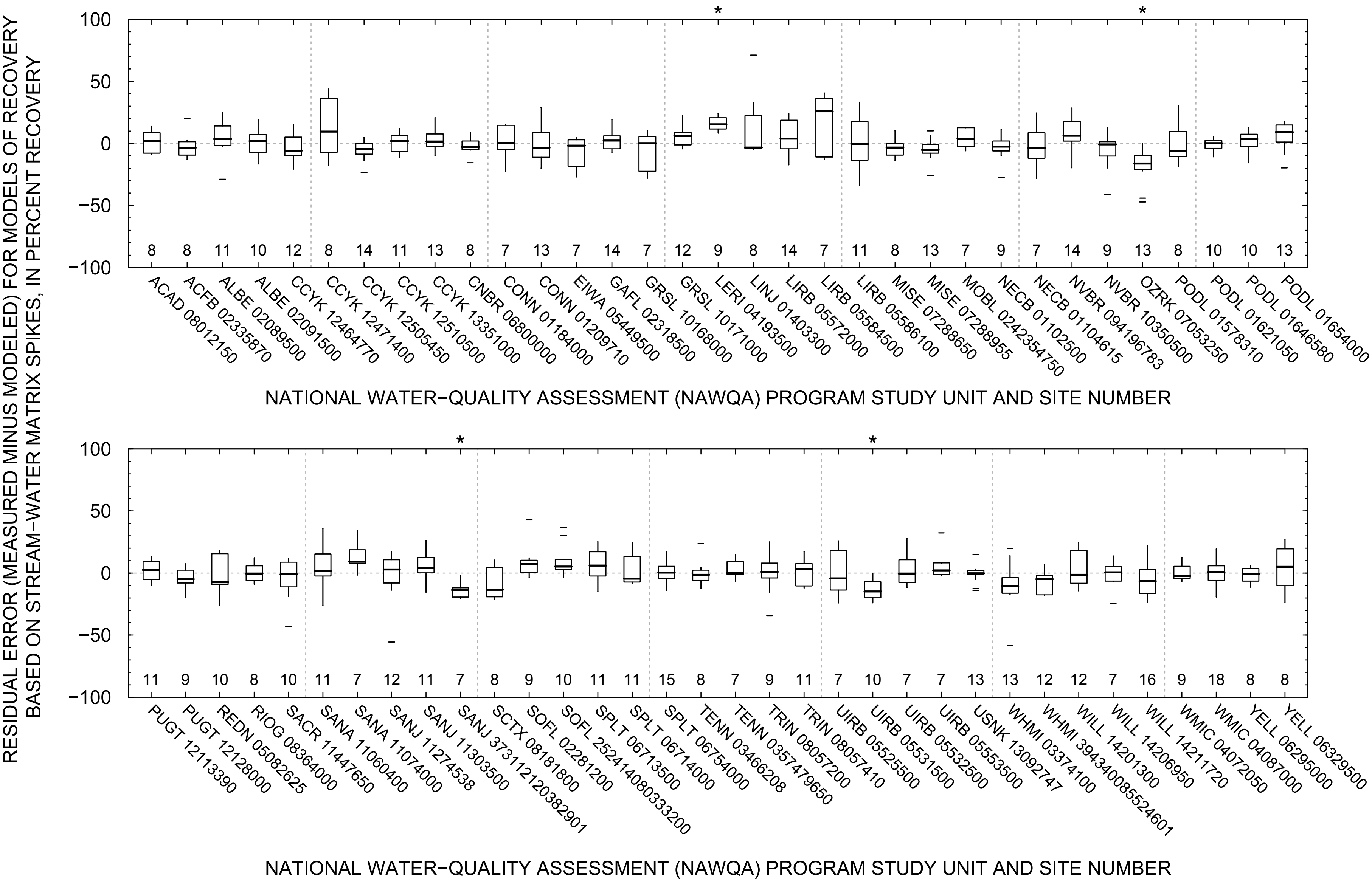


Figure A7−2. Distribution of residual errors in modeled recovery of alachlor for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is siginficantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

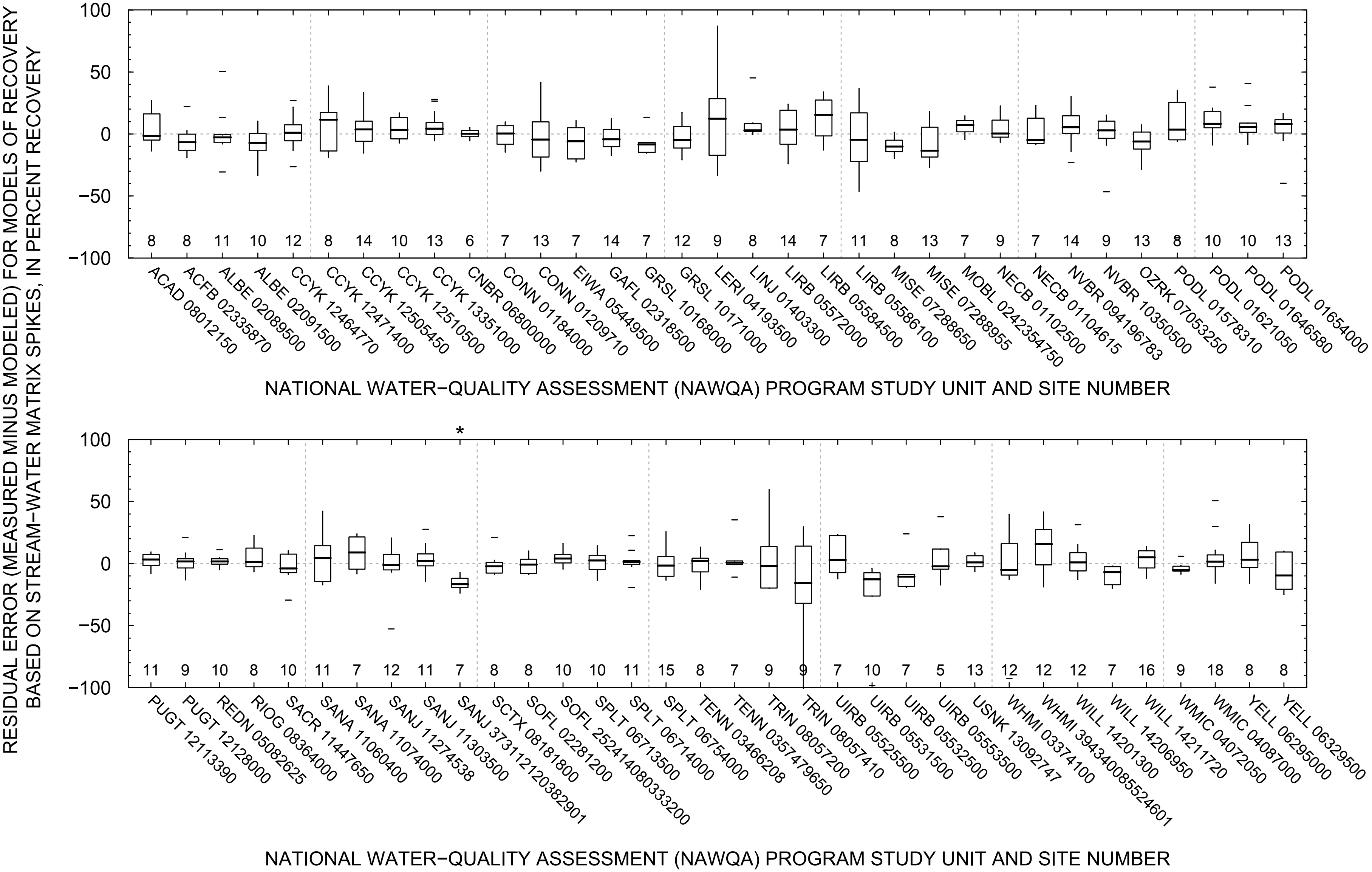


Figure A7−3. Distribution of residual errors in modeled recovery of atrazine for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

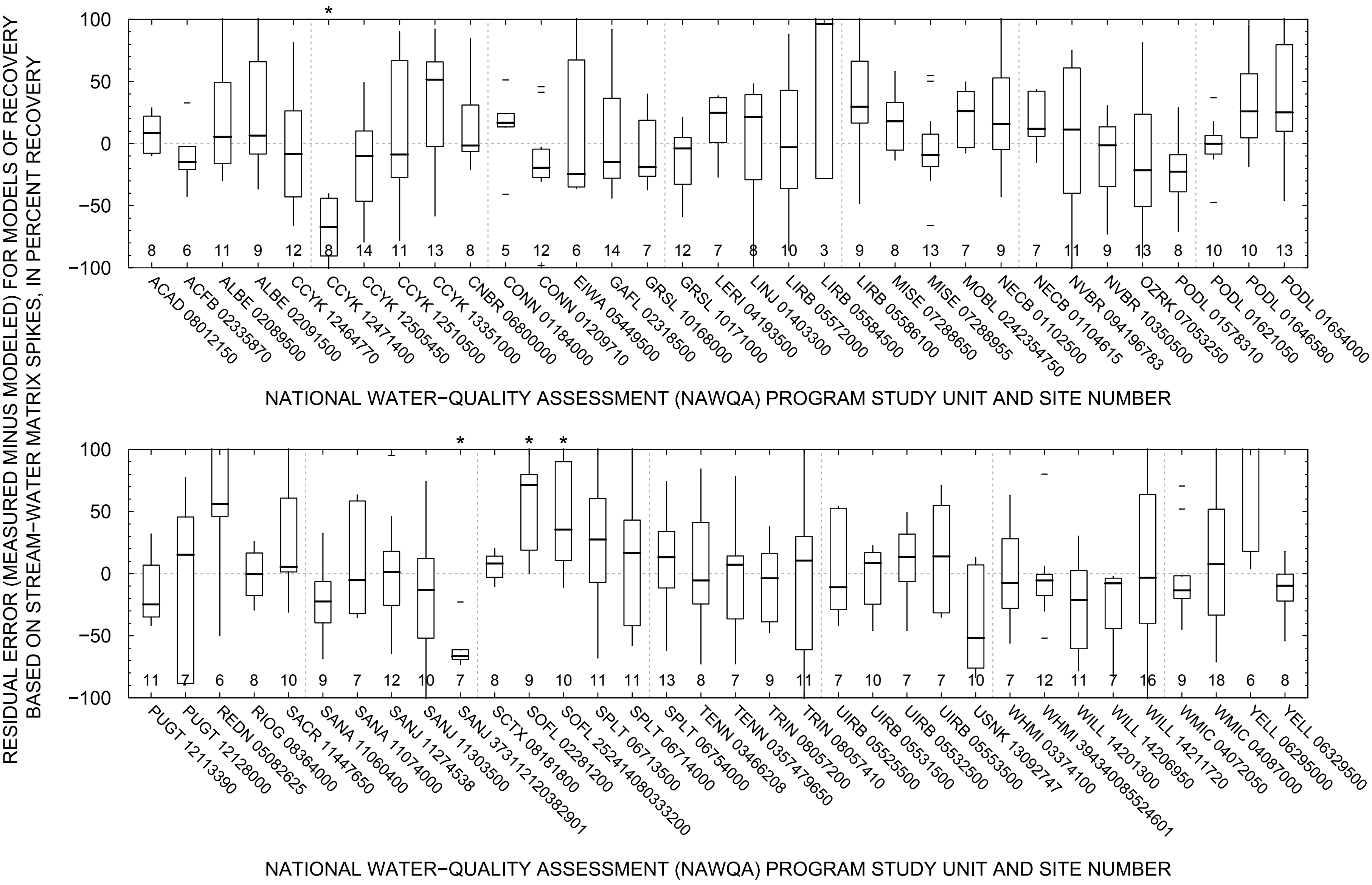


Figure A7−4. Distribution of residual errors in modeled recovery of azinphos−methyl for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

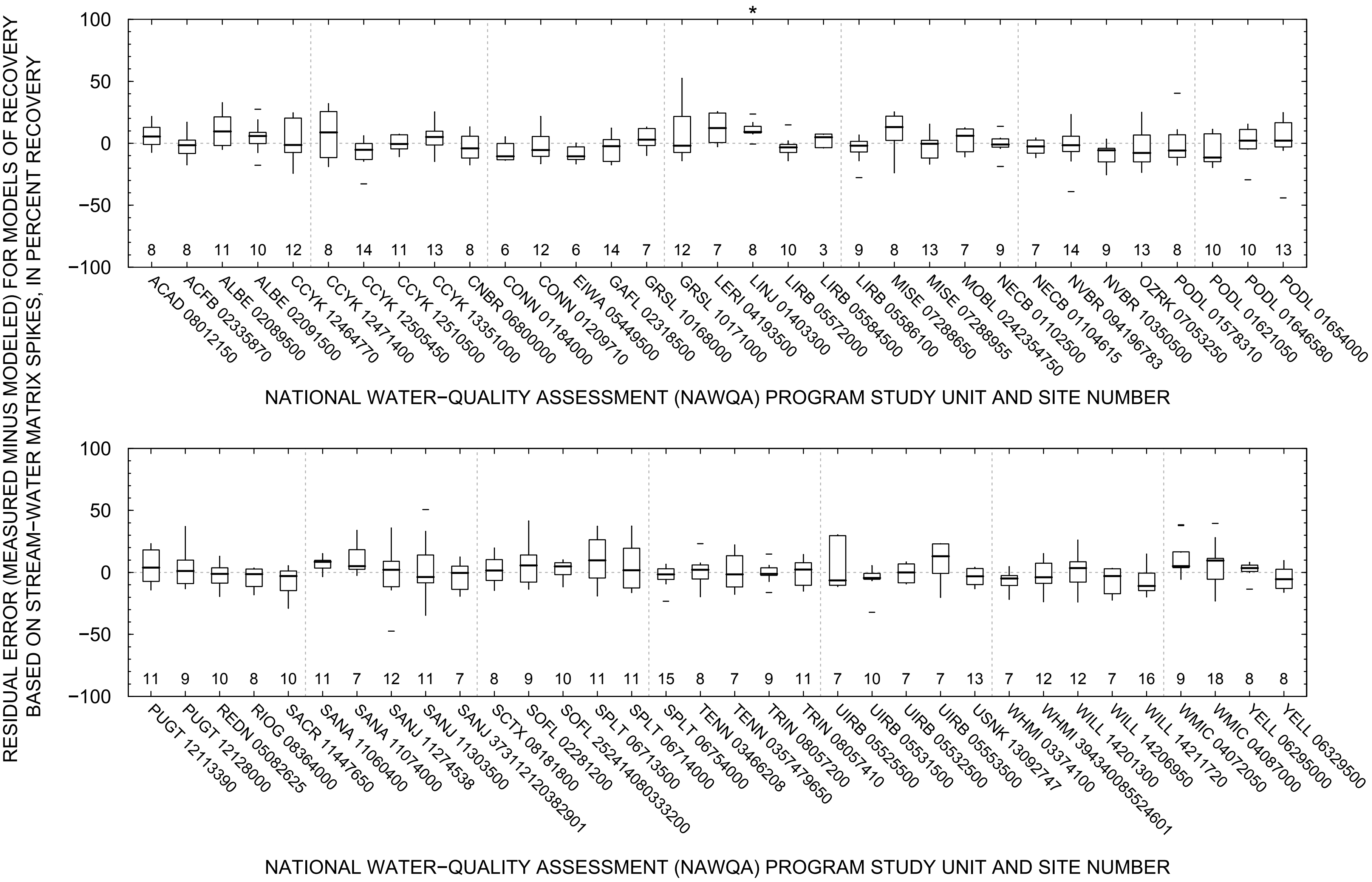


Figure A7−5. Distribution of residual errors in modeled recovery of benfluralin for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

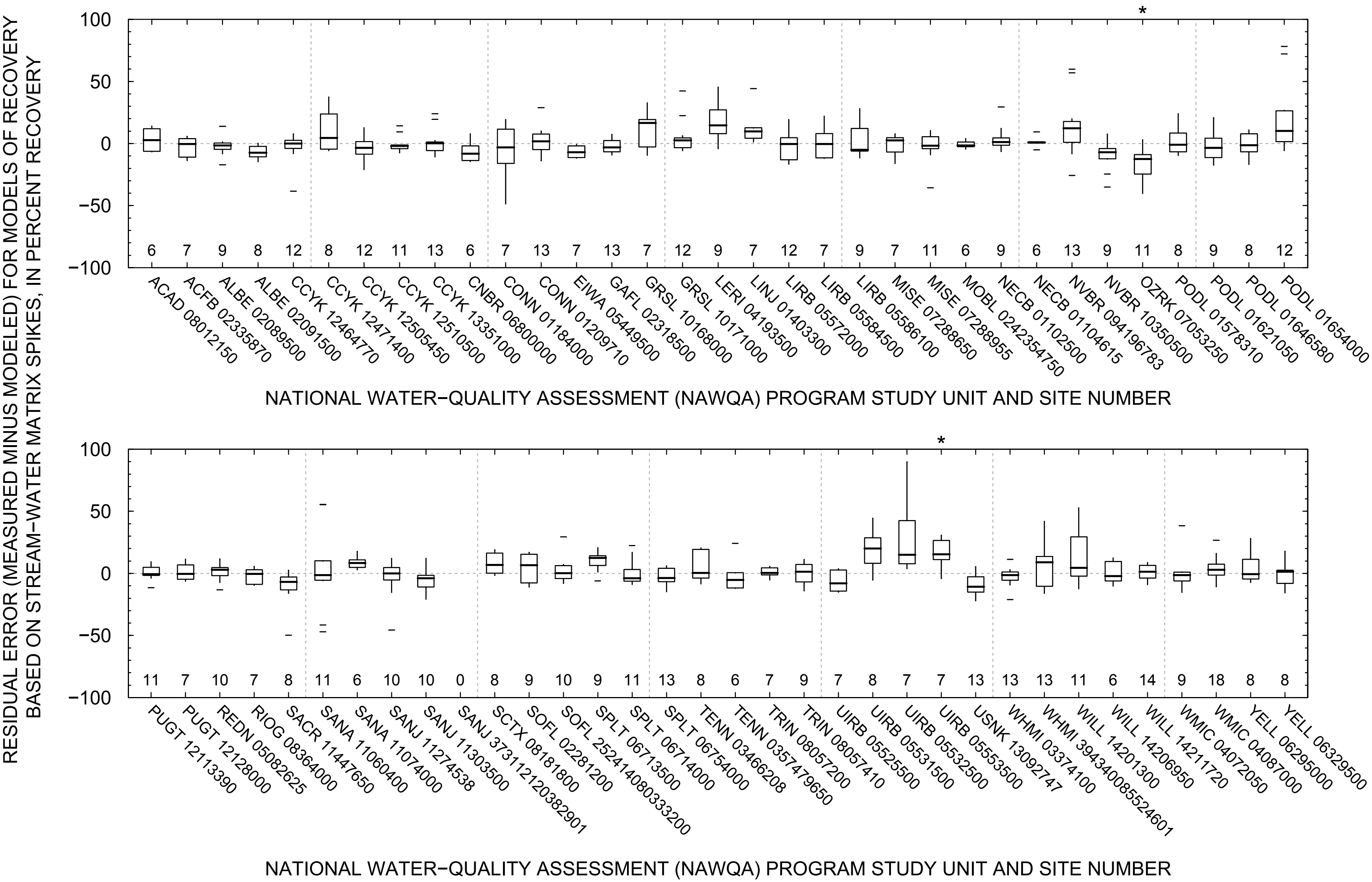


Figure A7−6. Distribution of residual errors in modeled recovery of butylate for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

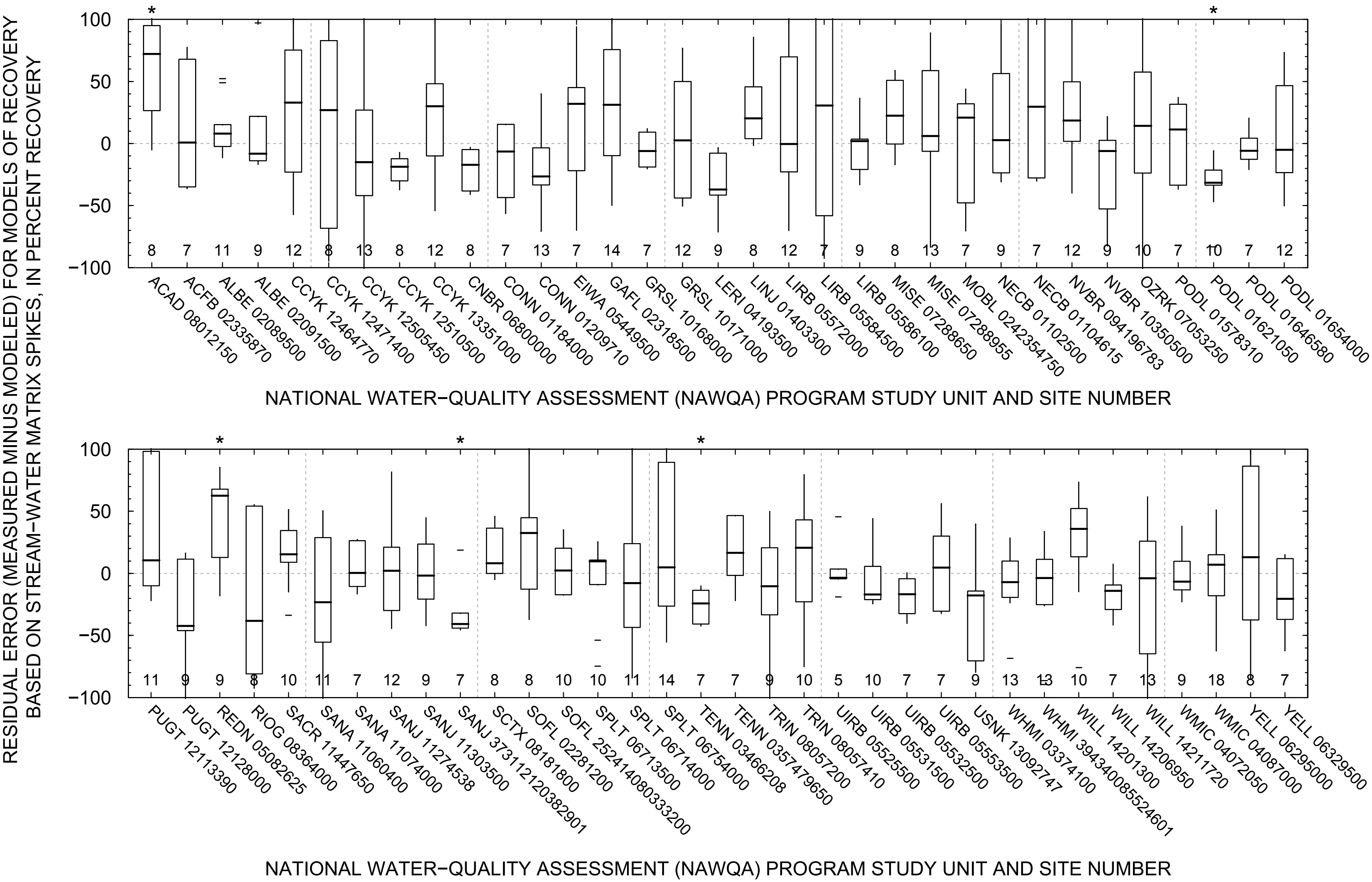


Figure A7−7. Distribution of residual errors in modeled recovery of carbaryl for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

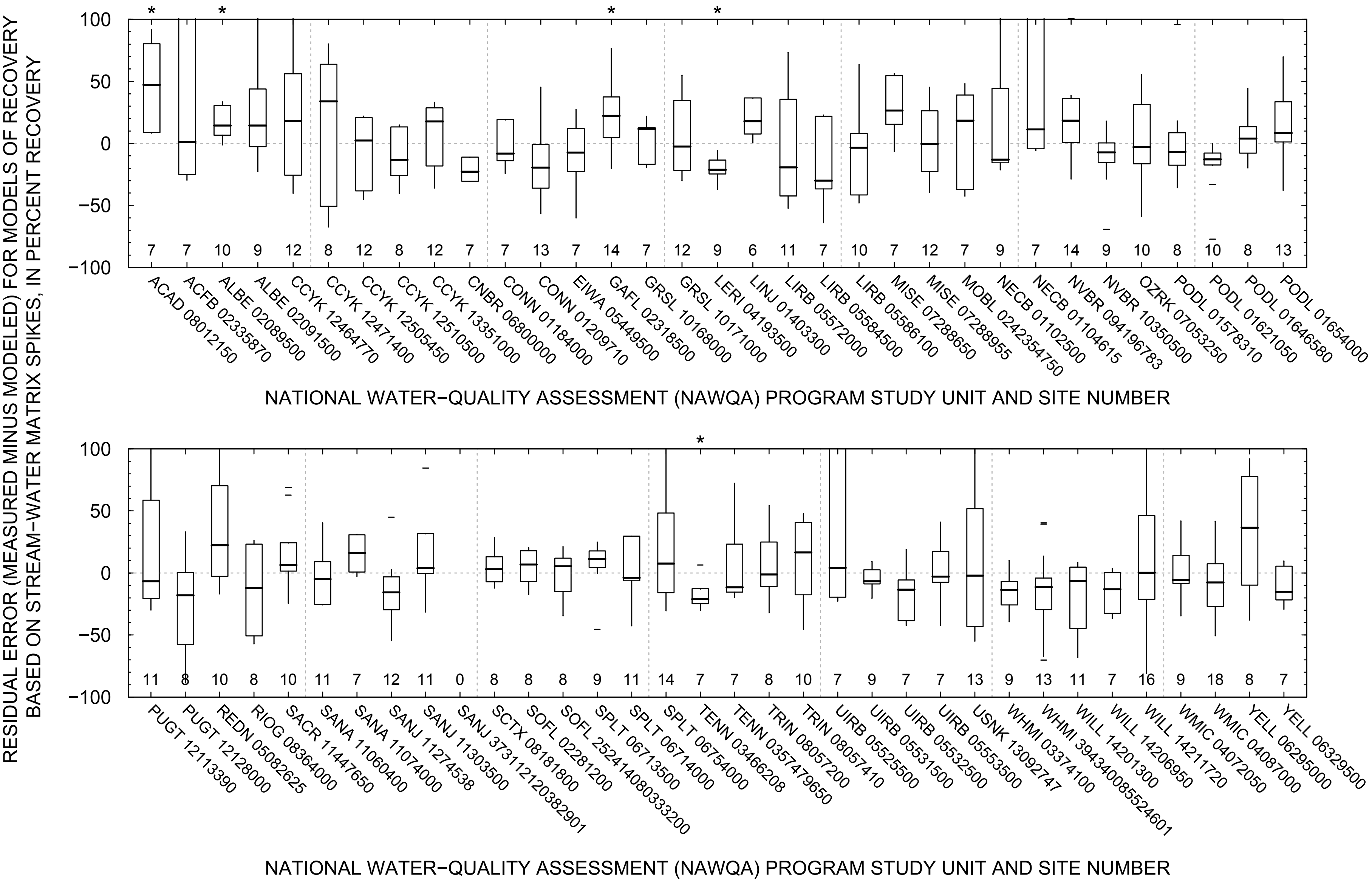


Figure A7−8. Distribution of residual errors in modeled recovery of carbofuran for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

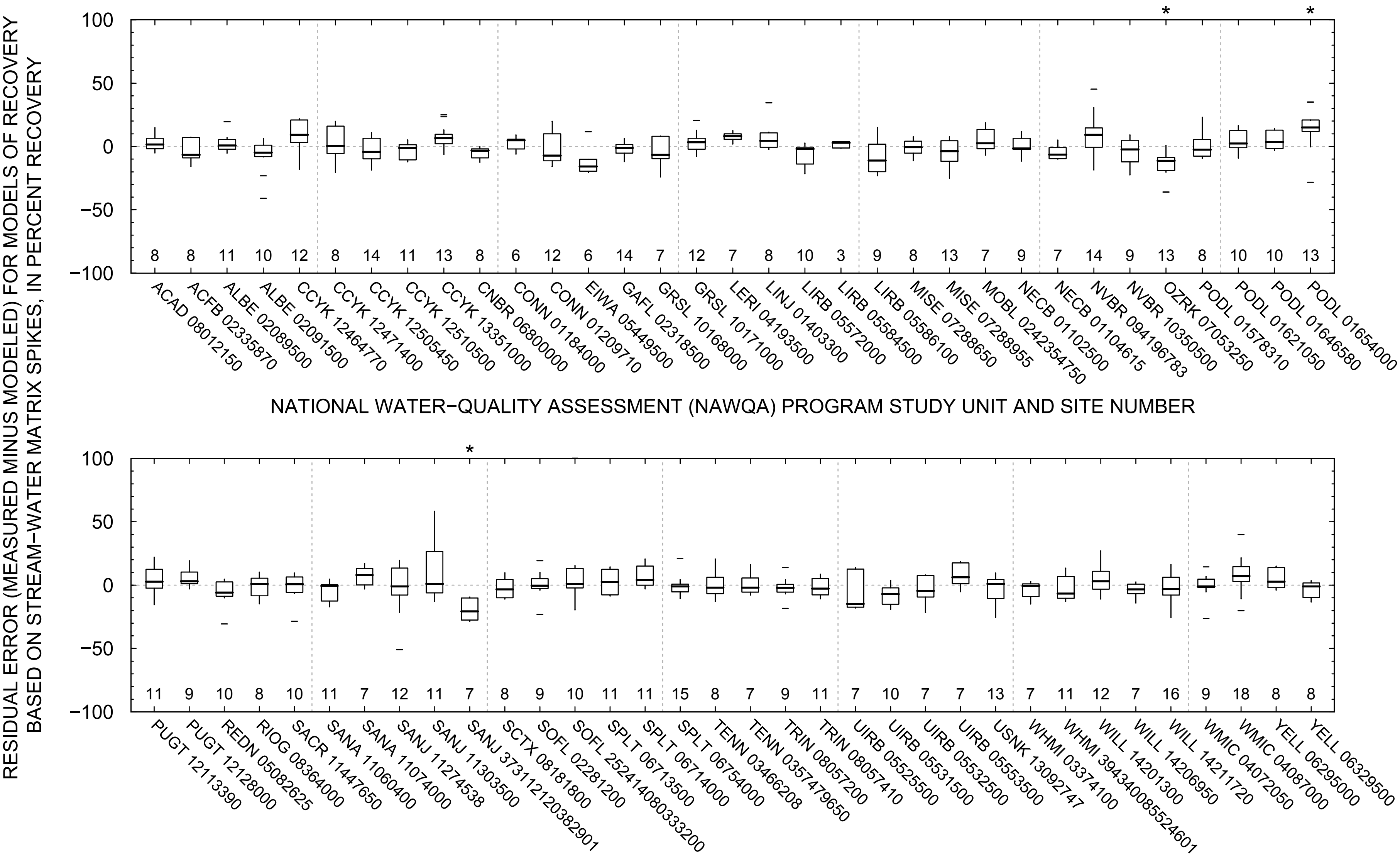


Figure A7−9. Distribution of residual errors in modeled recovery of chlorpyrifos for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

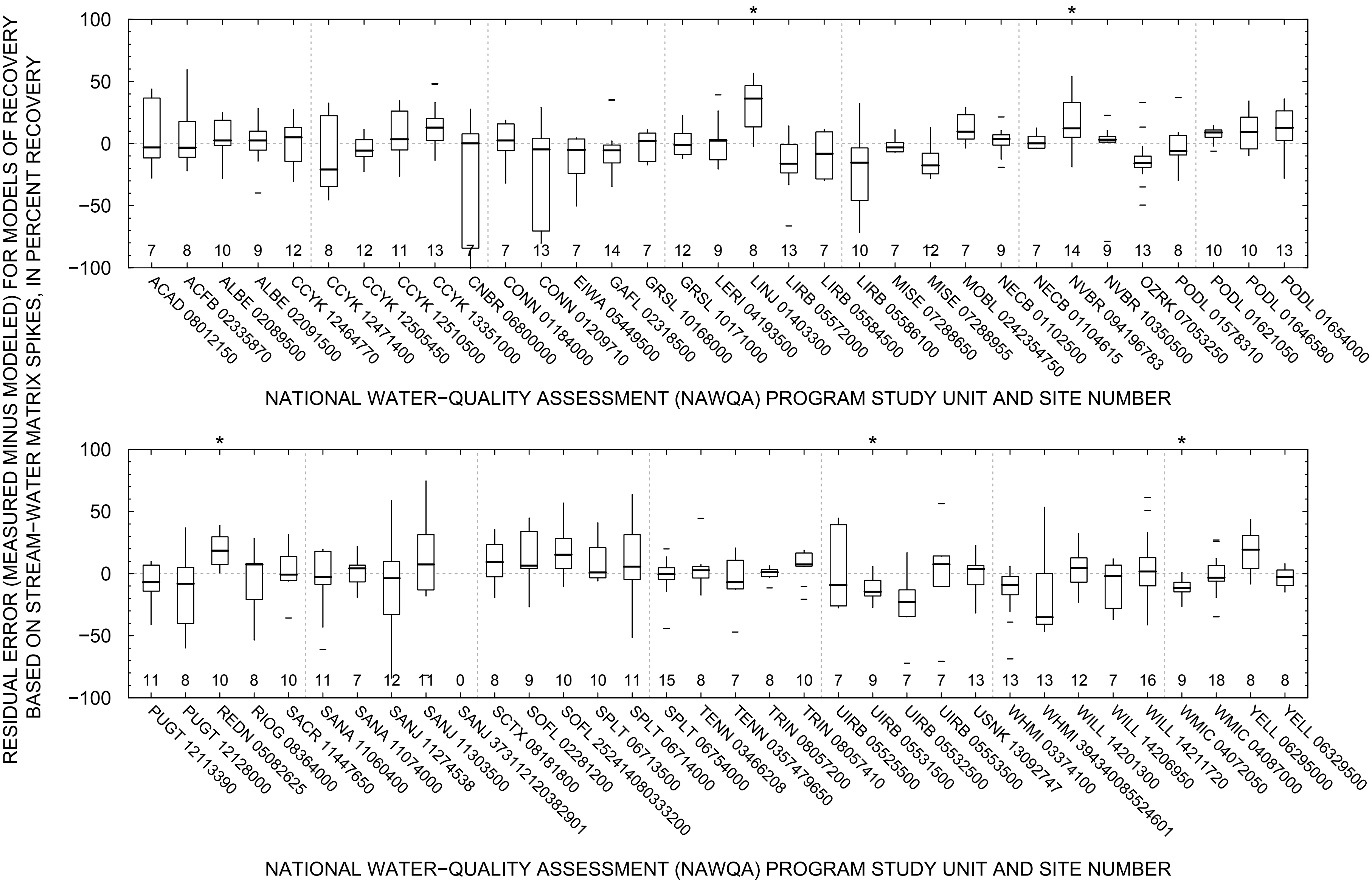


Figure A7−10. Distribution of residual errors in modeled recovery of cyanazine for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

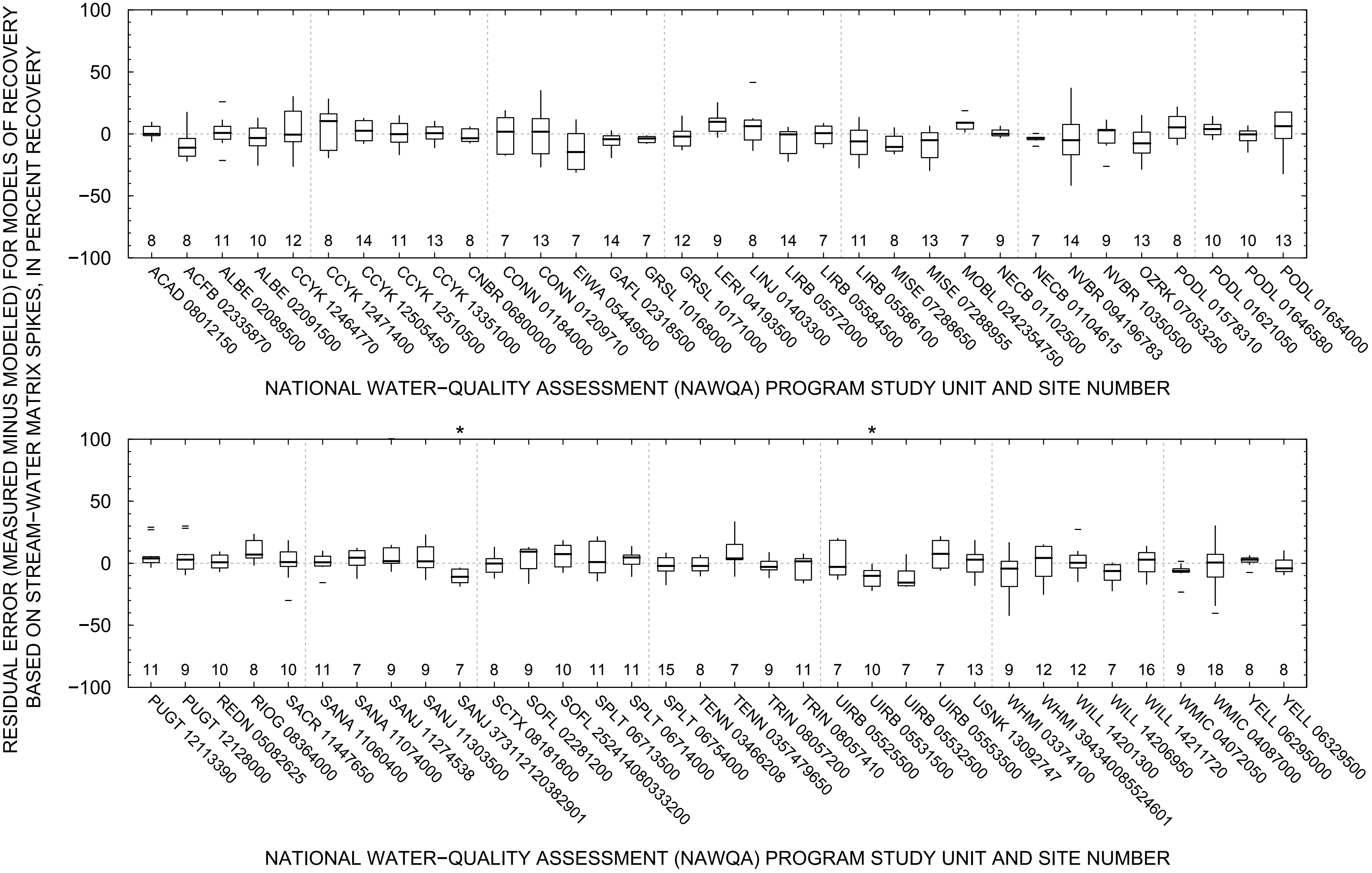


Figure A7−11. Distribution of residual errors in modeled recovery of dacthal for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

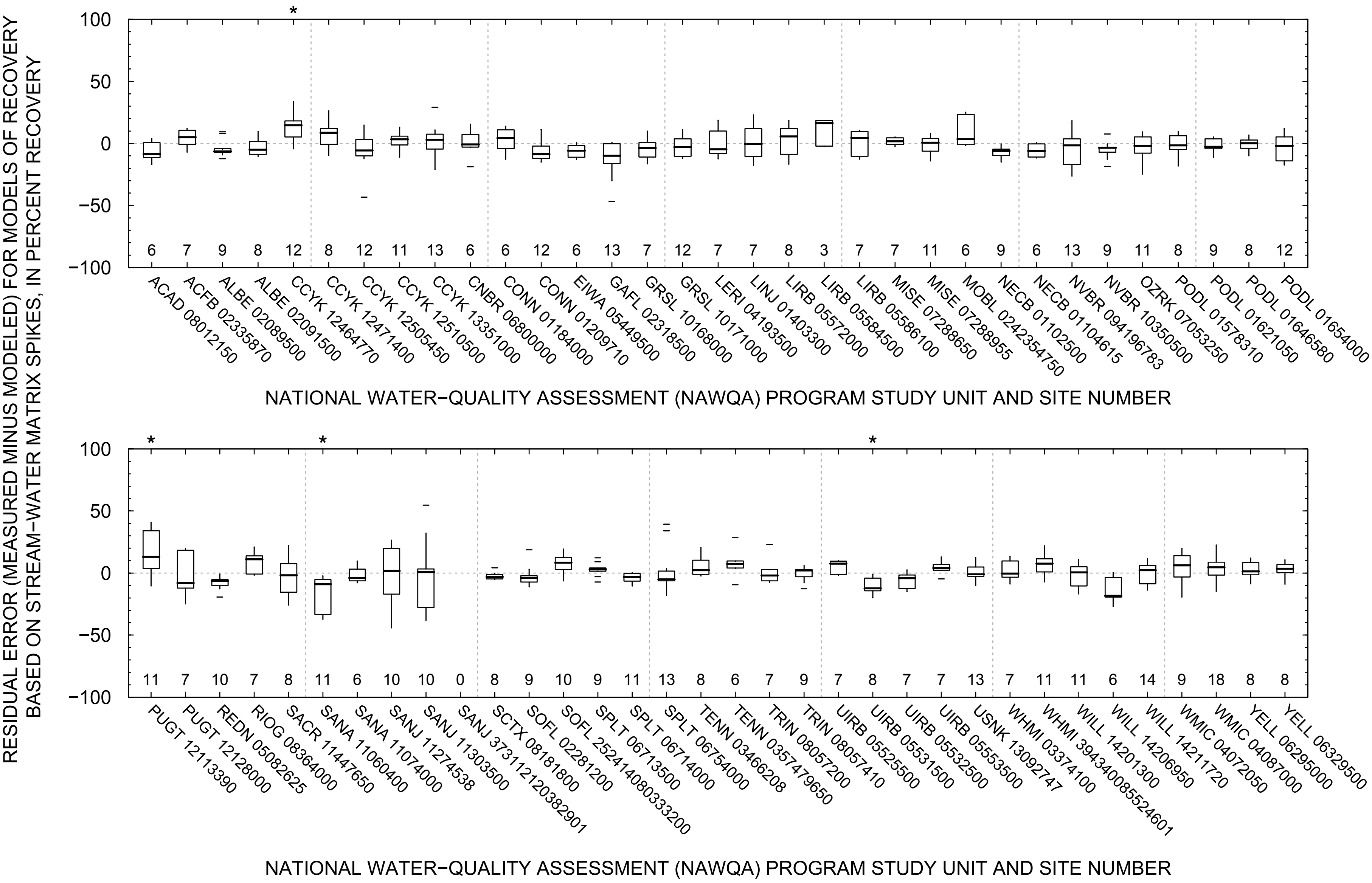


Figure A7−12. Distribution of residual errors in modeled recovery of p,p’−DDE for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

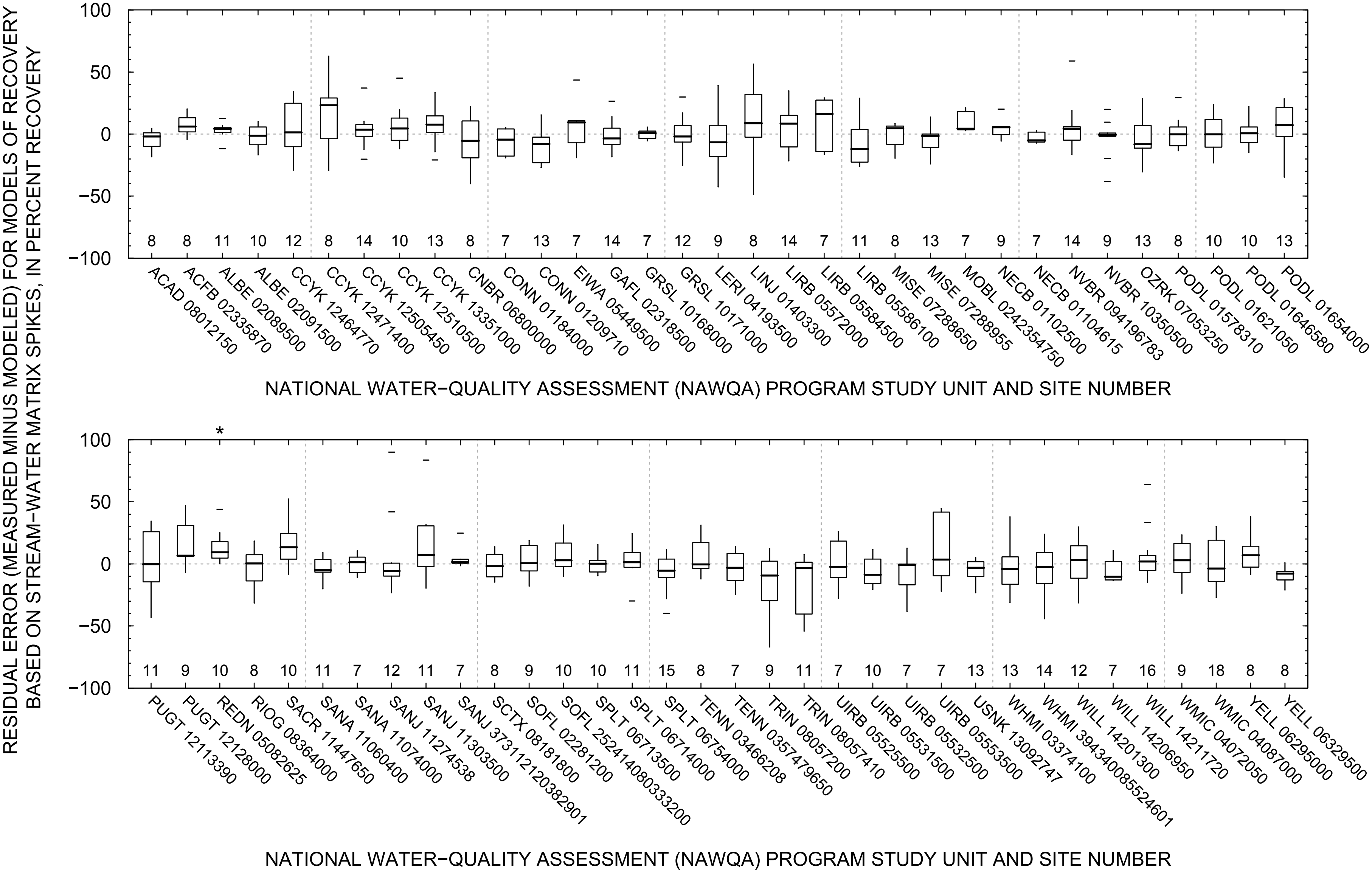


Figure A7−13. Distribution of residual errors in modeled recovery of deethylatrazine for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

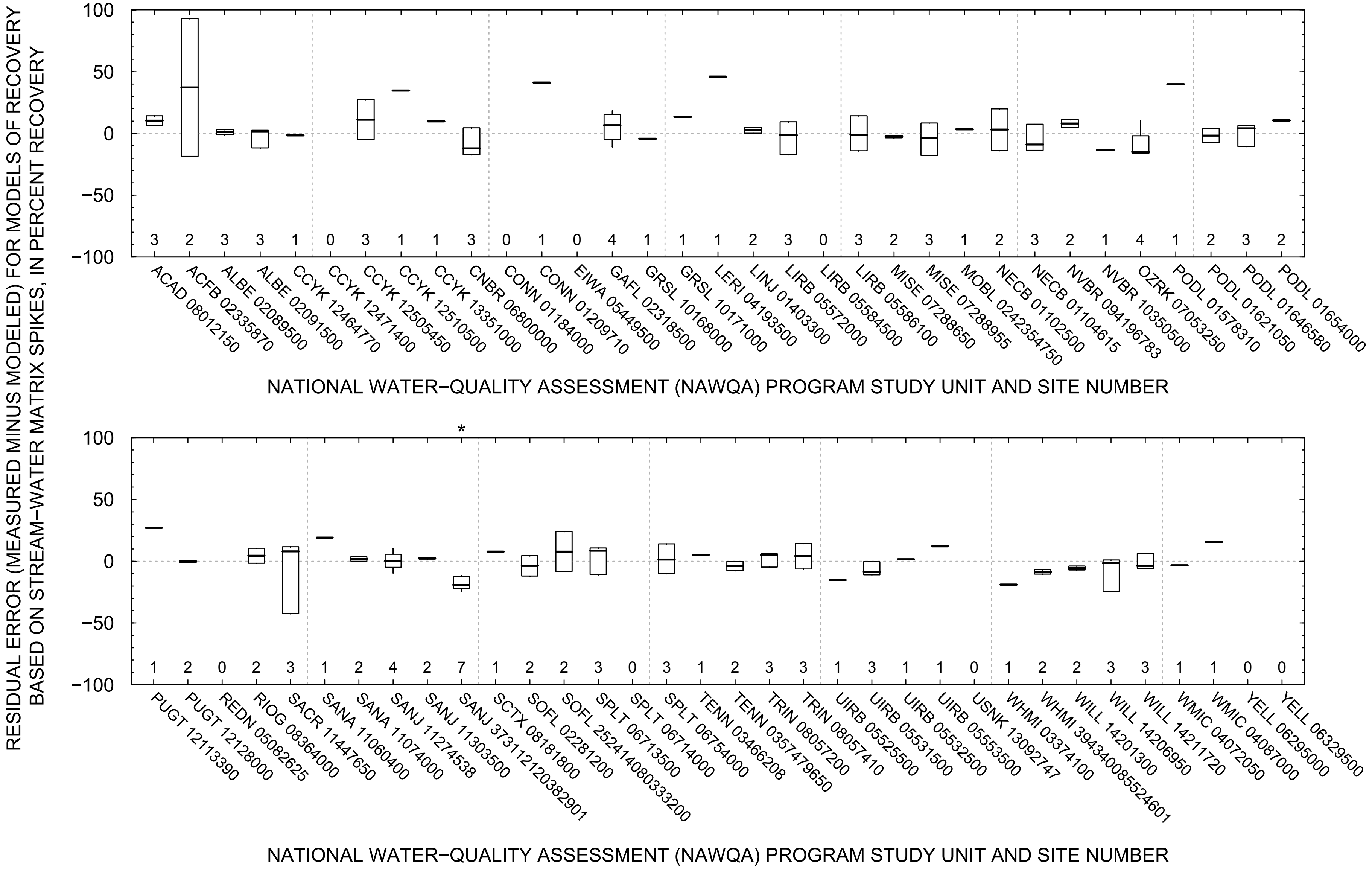


Figure A7−14. Distribution of residual errors in modeled recovery of desulfinylfipronil for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

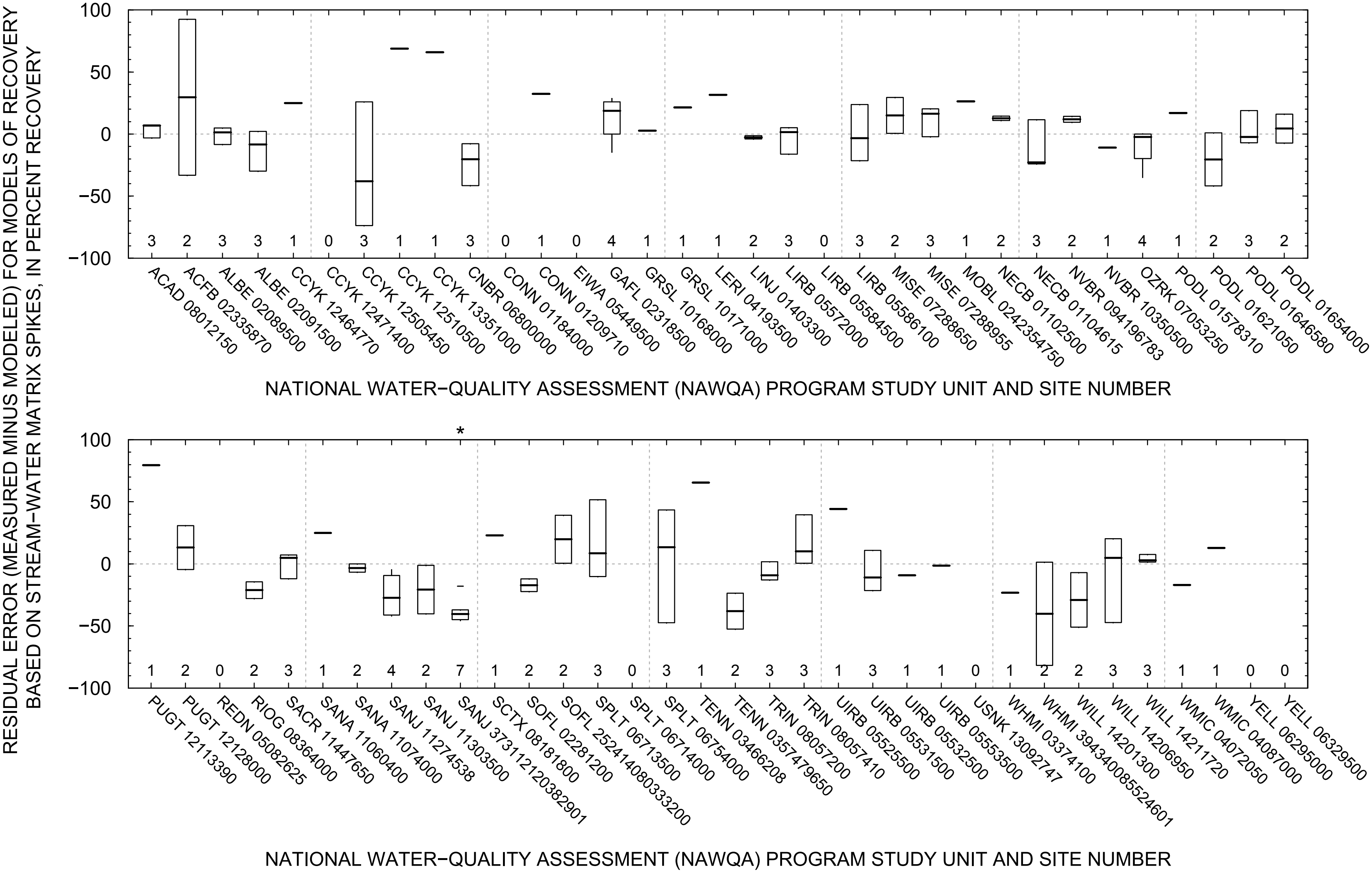


Figure A7−15. Distribution of residual errors in modeled recovery of desulfinylfipronil amide for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

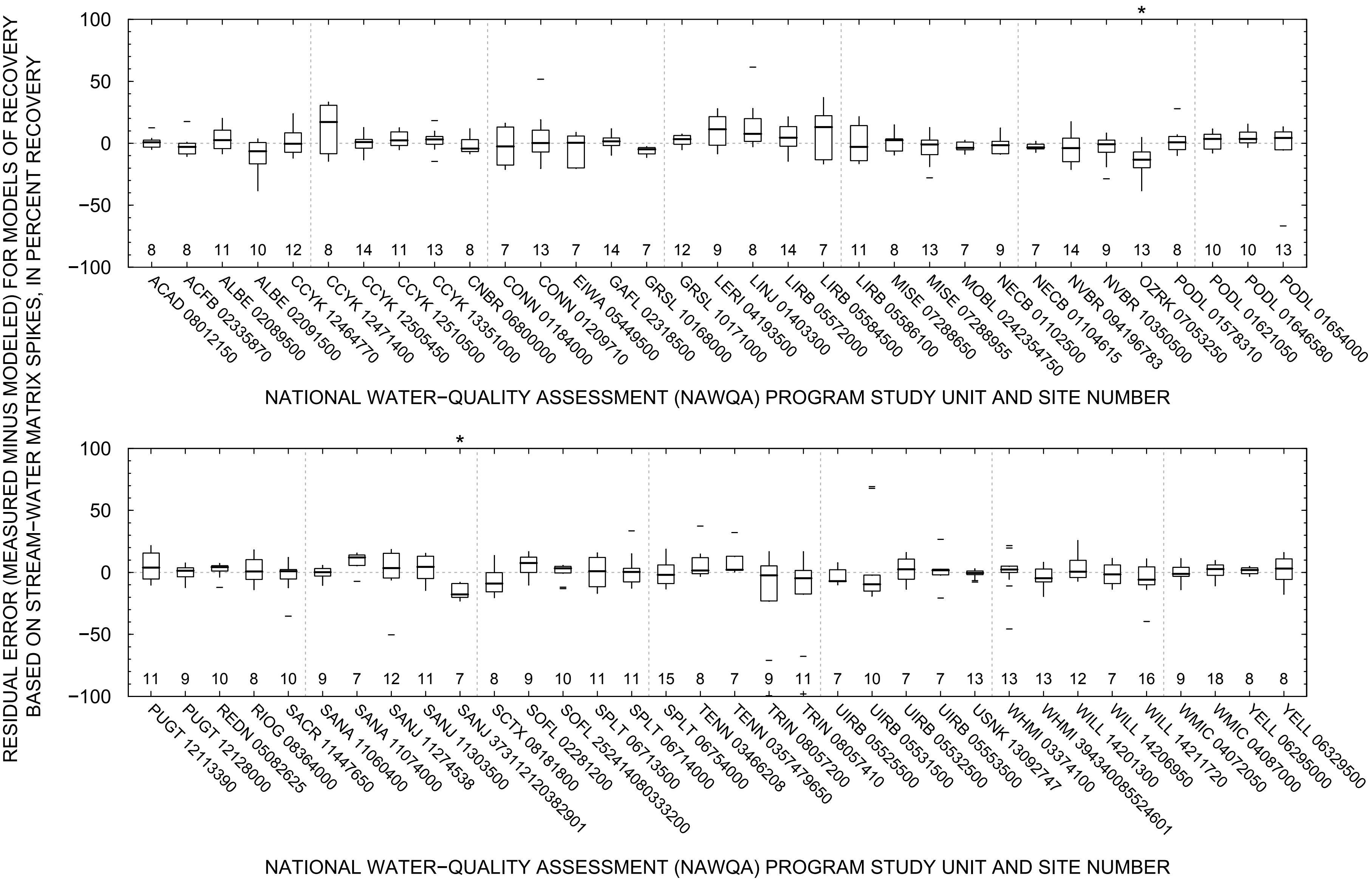


Figure A7−16. Distribution of residual errors in modeled recovery of diazinon for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

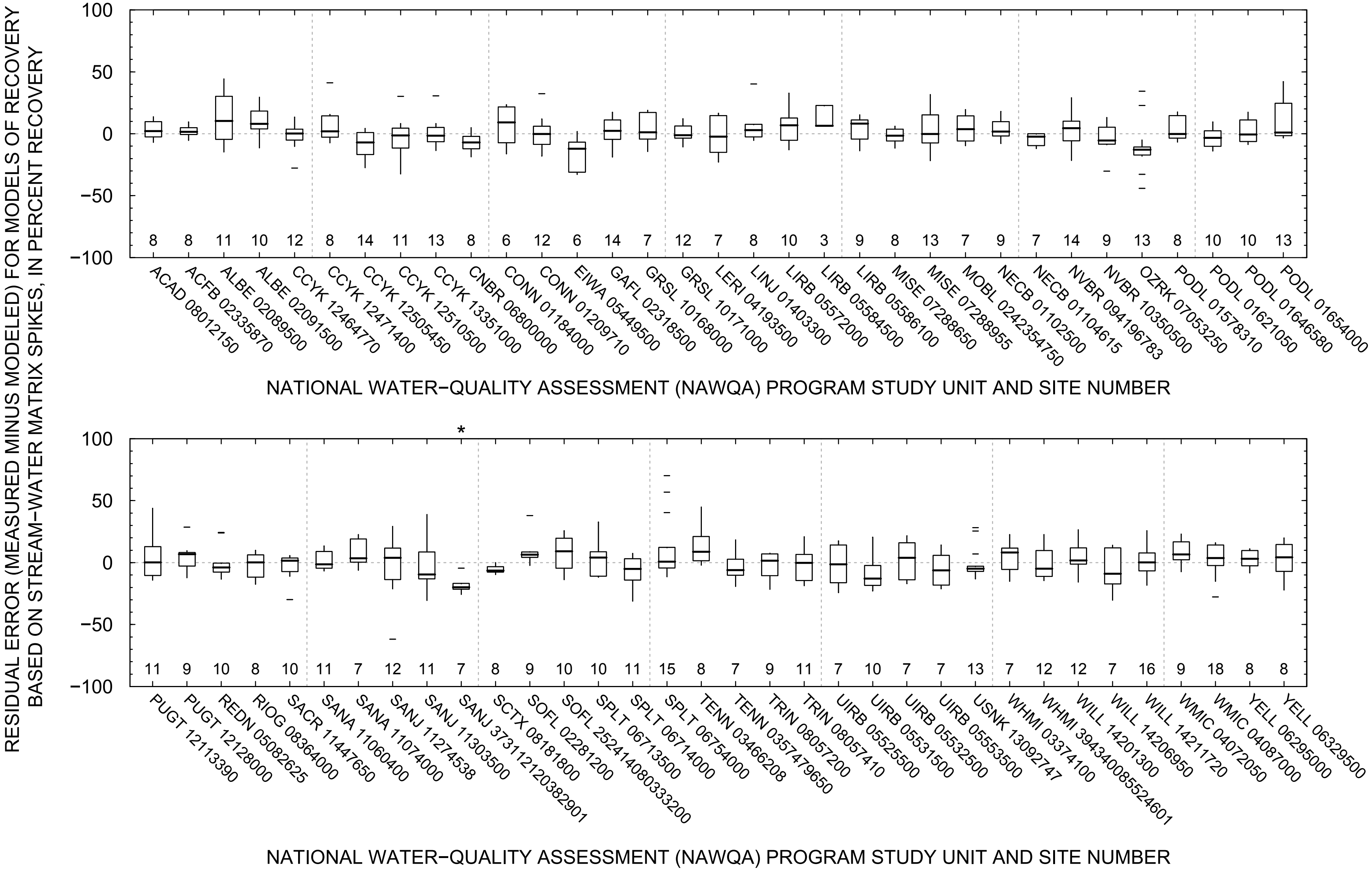


Figure A7−17. Distribution of residual errors in modeled recovery of dieldrin for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

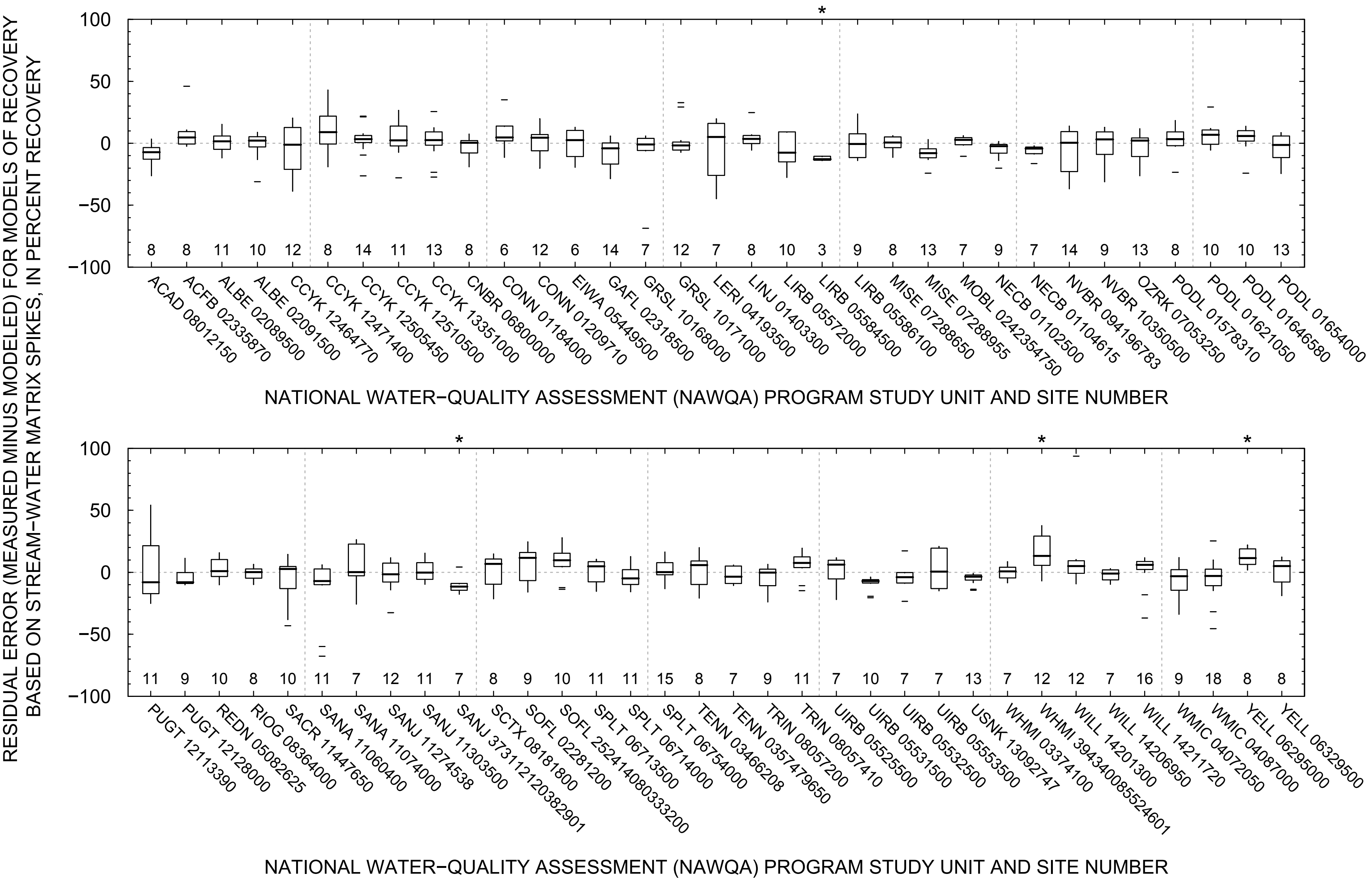


Figure A7−18. Distribution of residual errors in modeled recovery of 2,6−diethylaniline for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

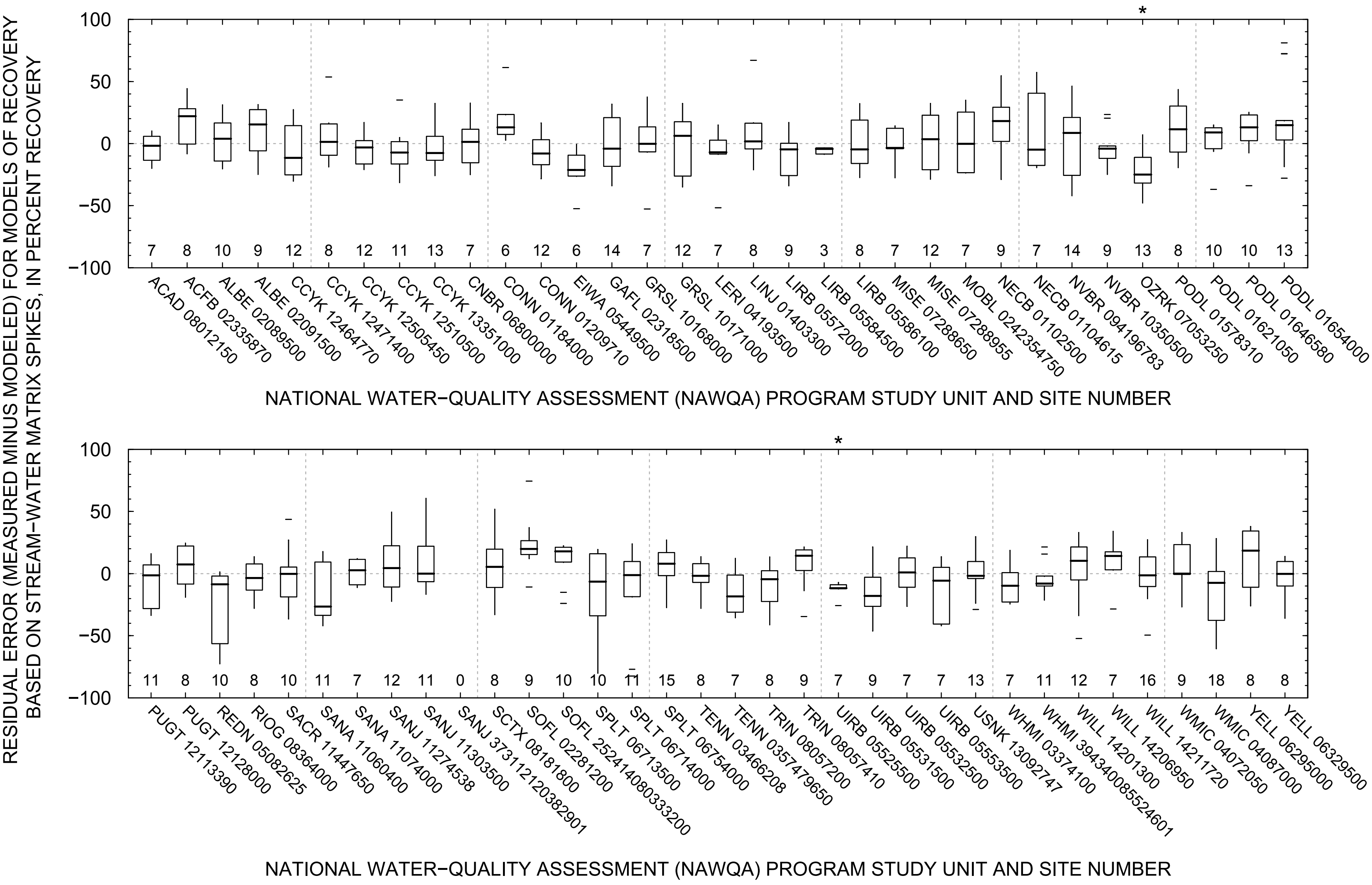


Figure A7−19. Distribution of residual errors in modeled recovery of disulfoton for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

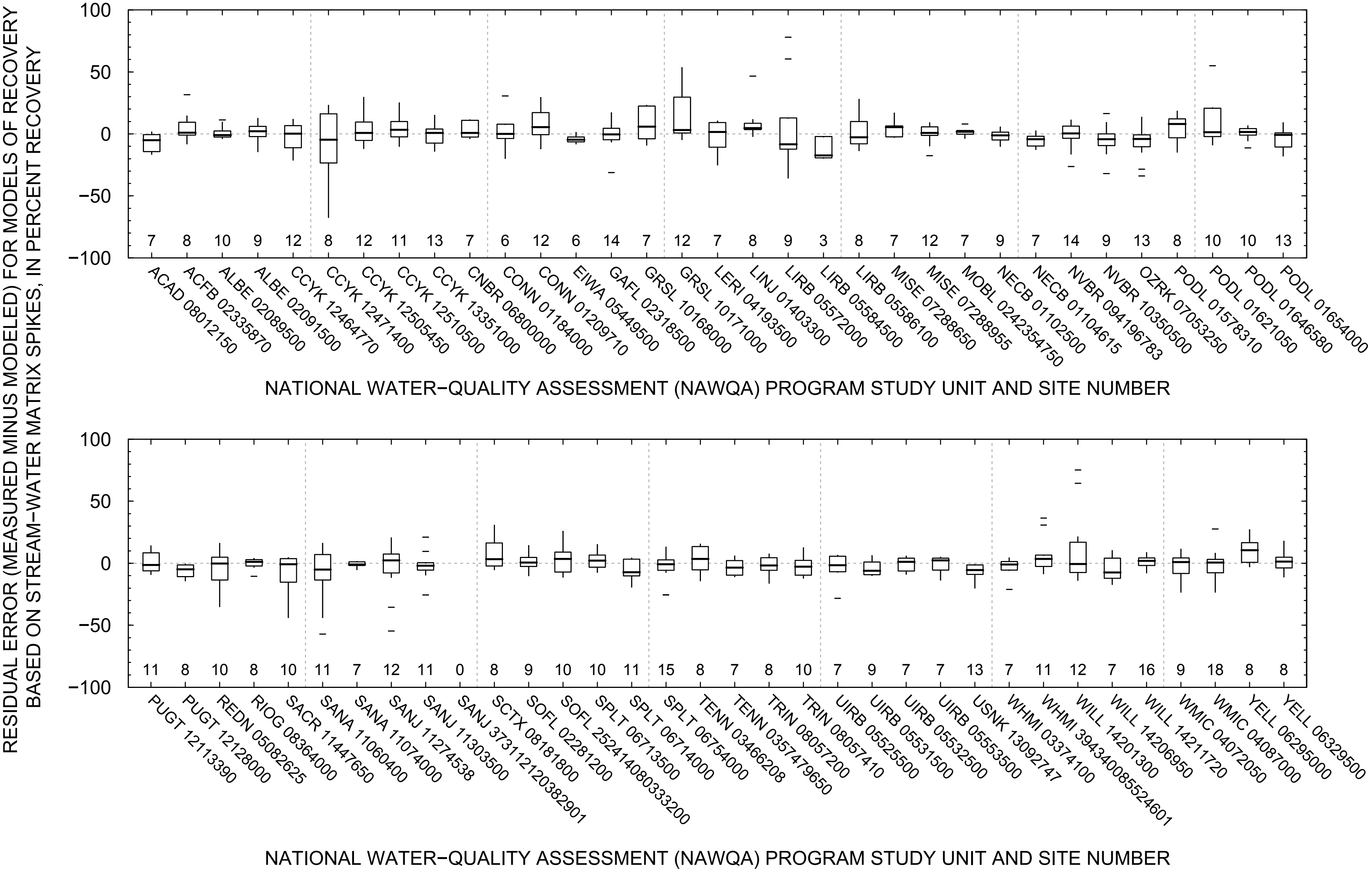


Figure A7−20. Distribution of residual errors in modeled recovery of EPTC for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

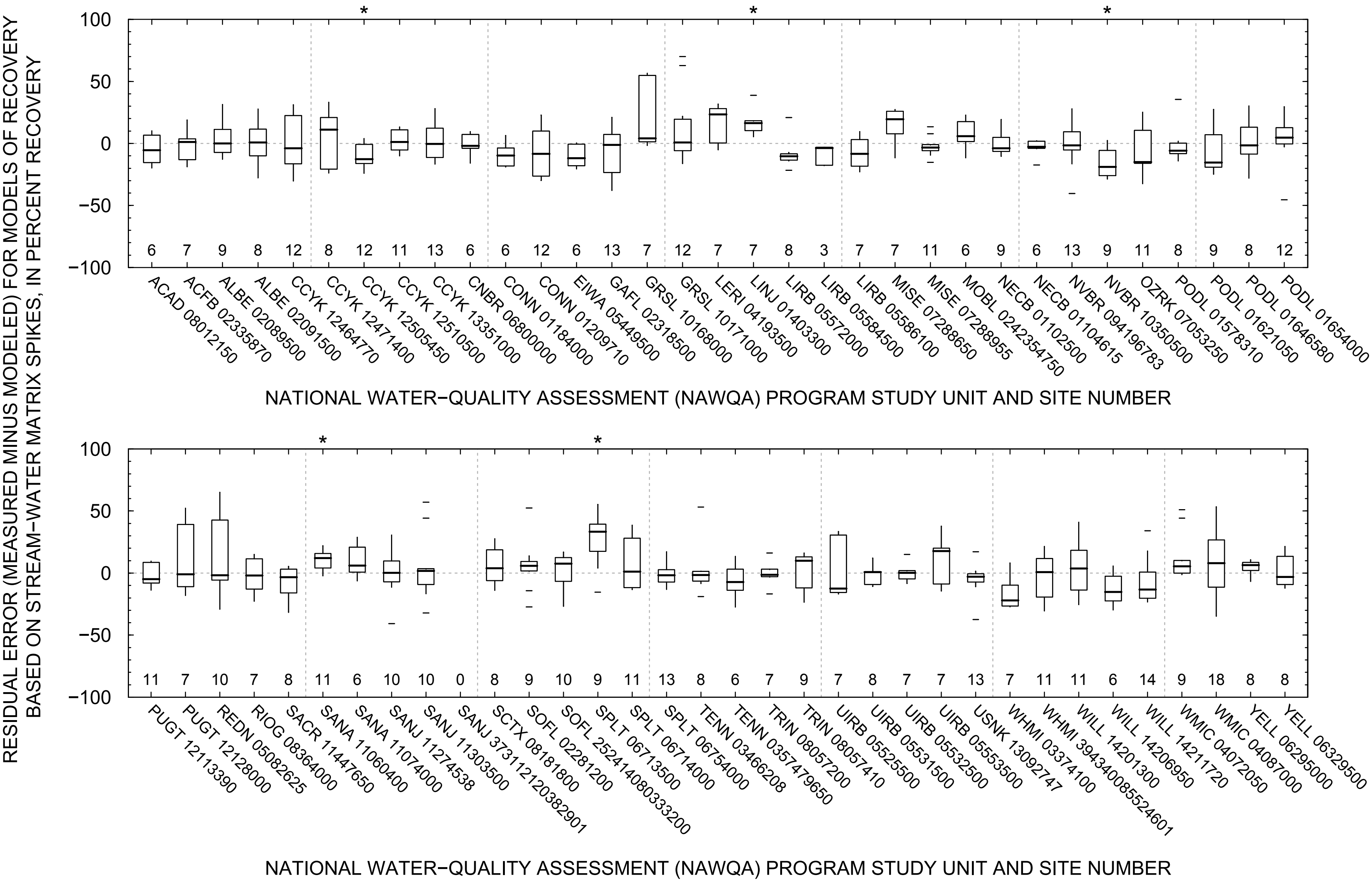


Figure A7−21. Distribution of residual errors in modeled recovery of ethalfluralin for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

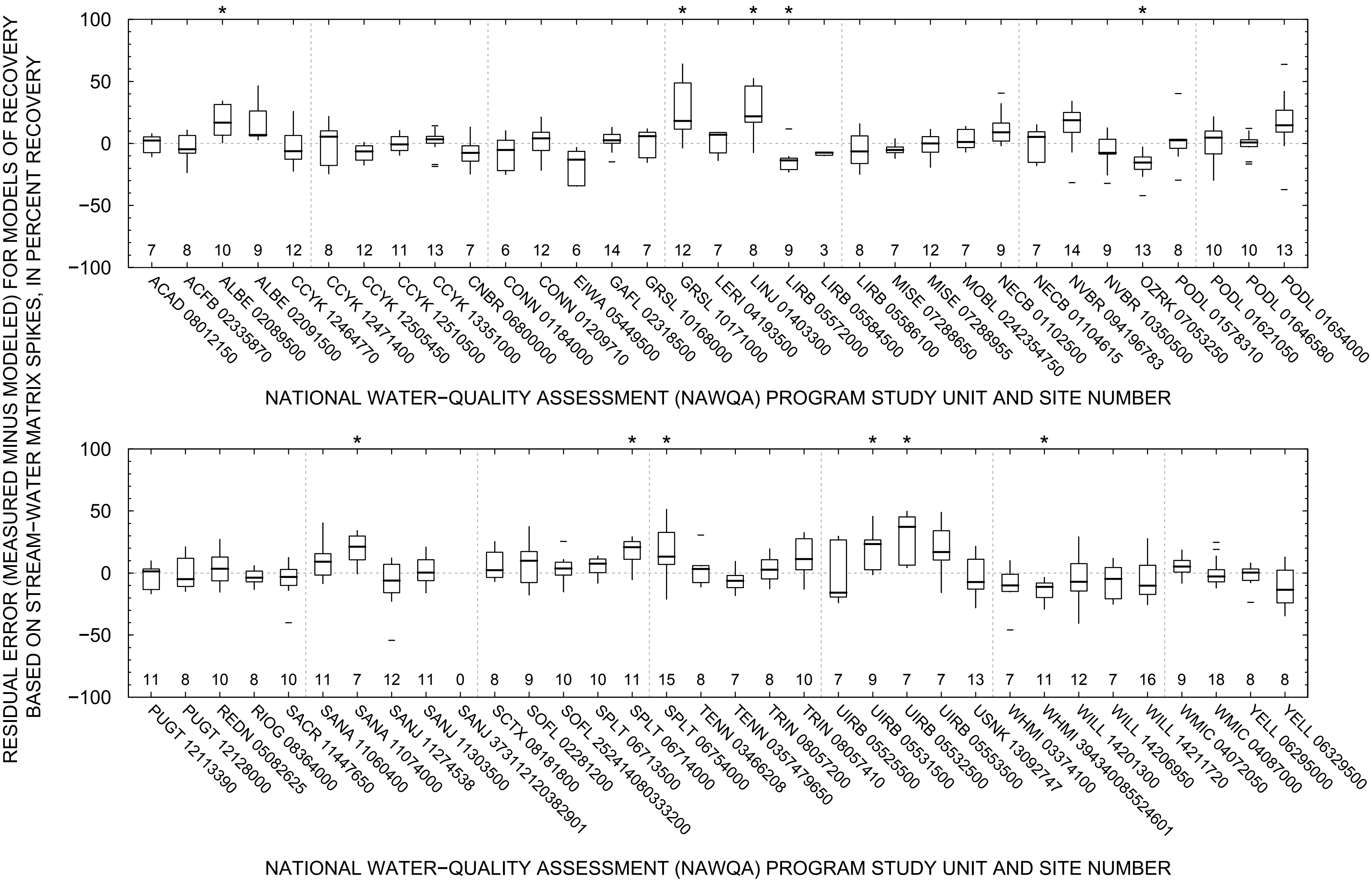


Figure A7−22. Distribution of residual errors in modeled recovery of ethoprophos for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

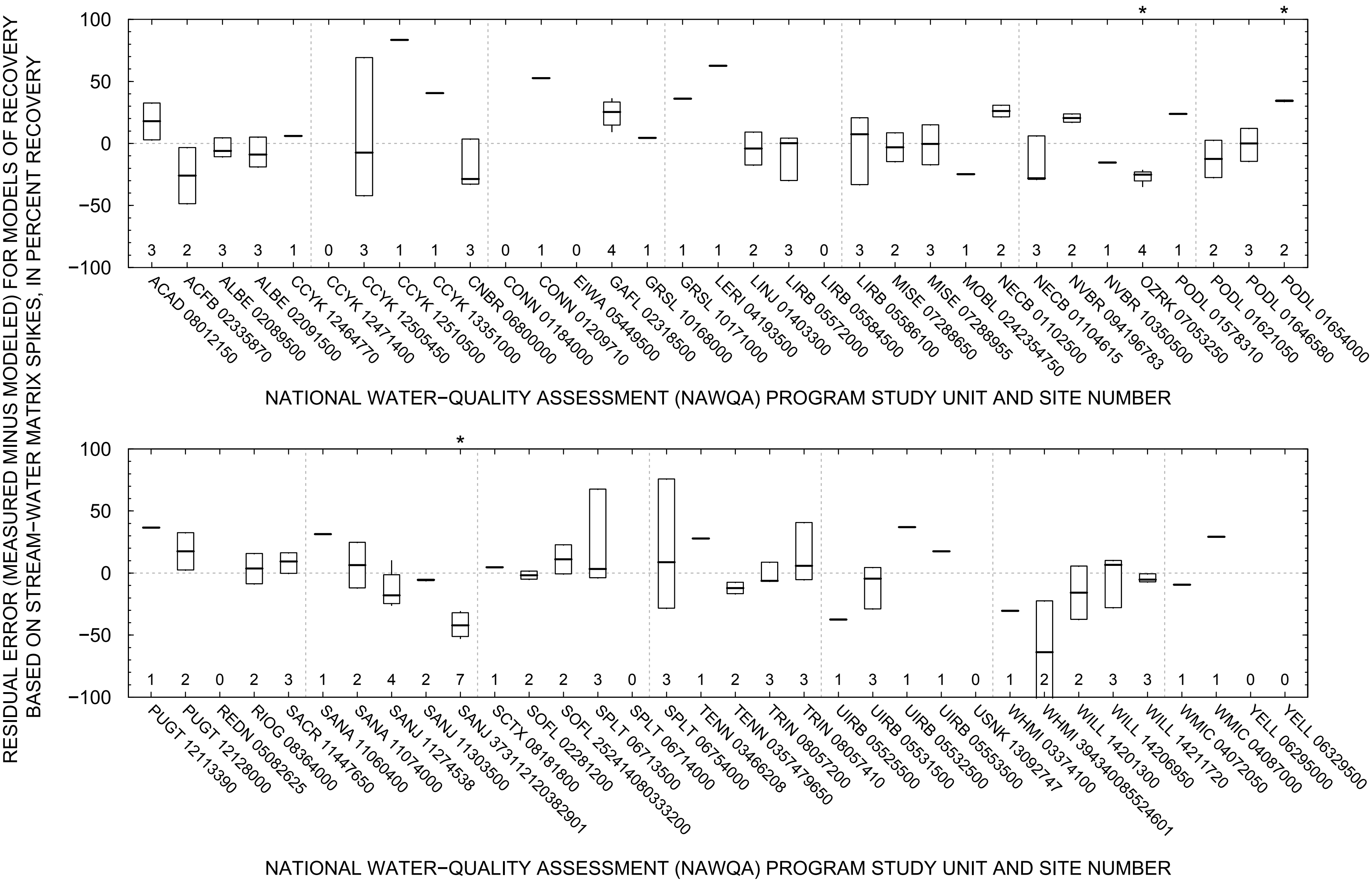


Figure A7−23. Distribution of residual errors in modeled recovery of fipronil for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

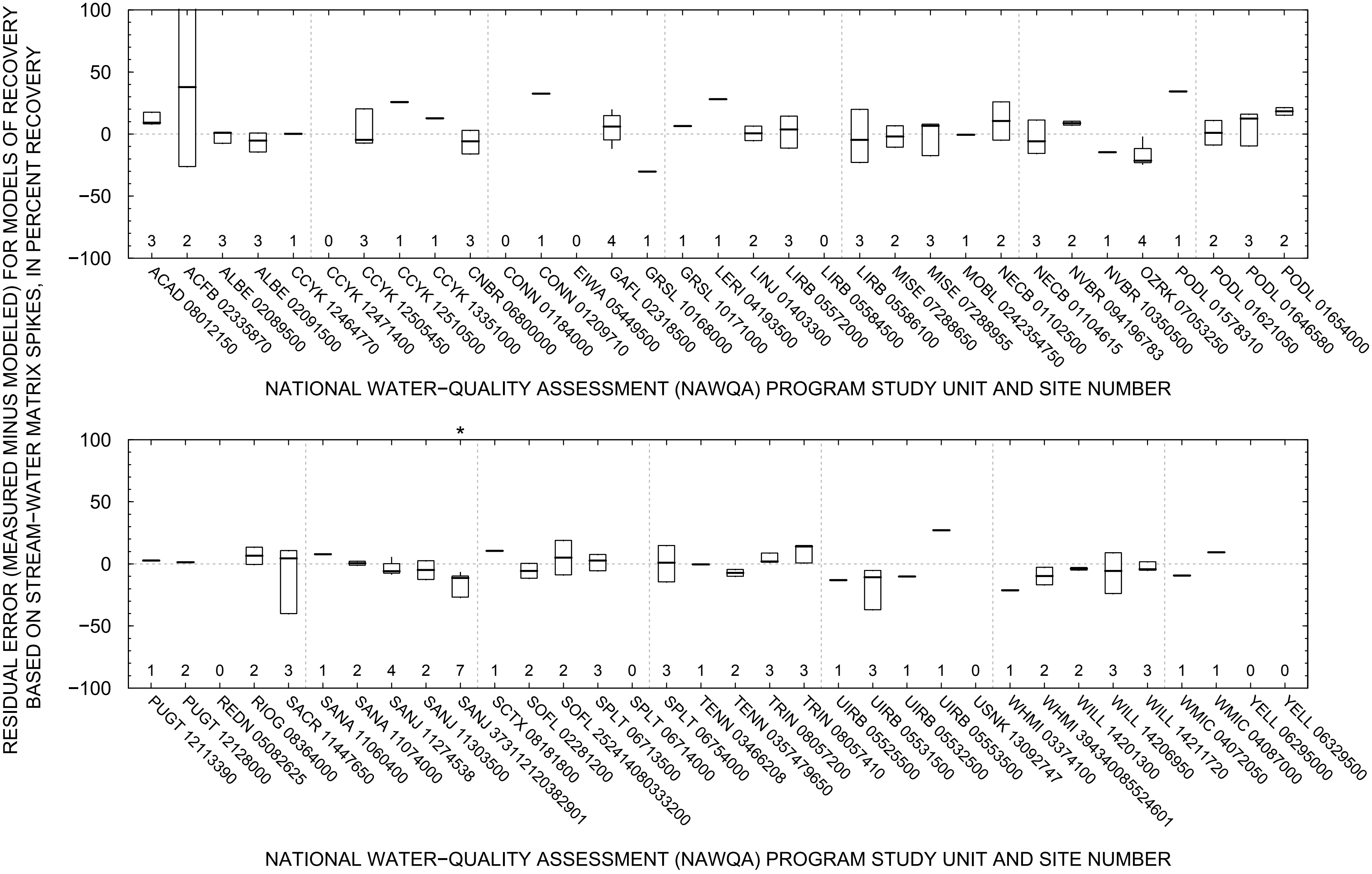


Figure A7−24. Distribution of residual errors in modeled recovery of fipronil sulfide for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

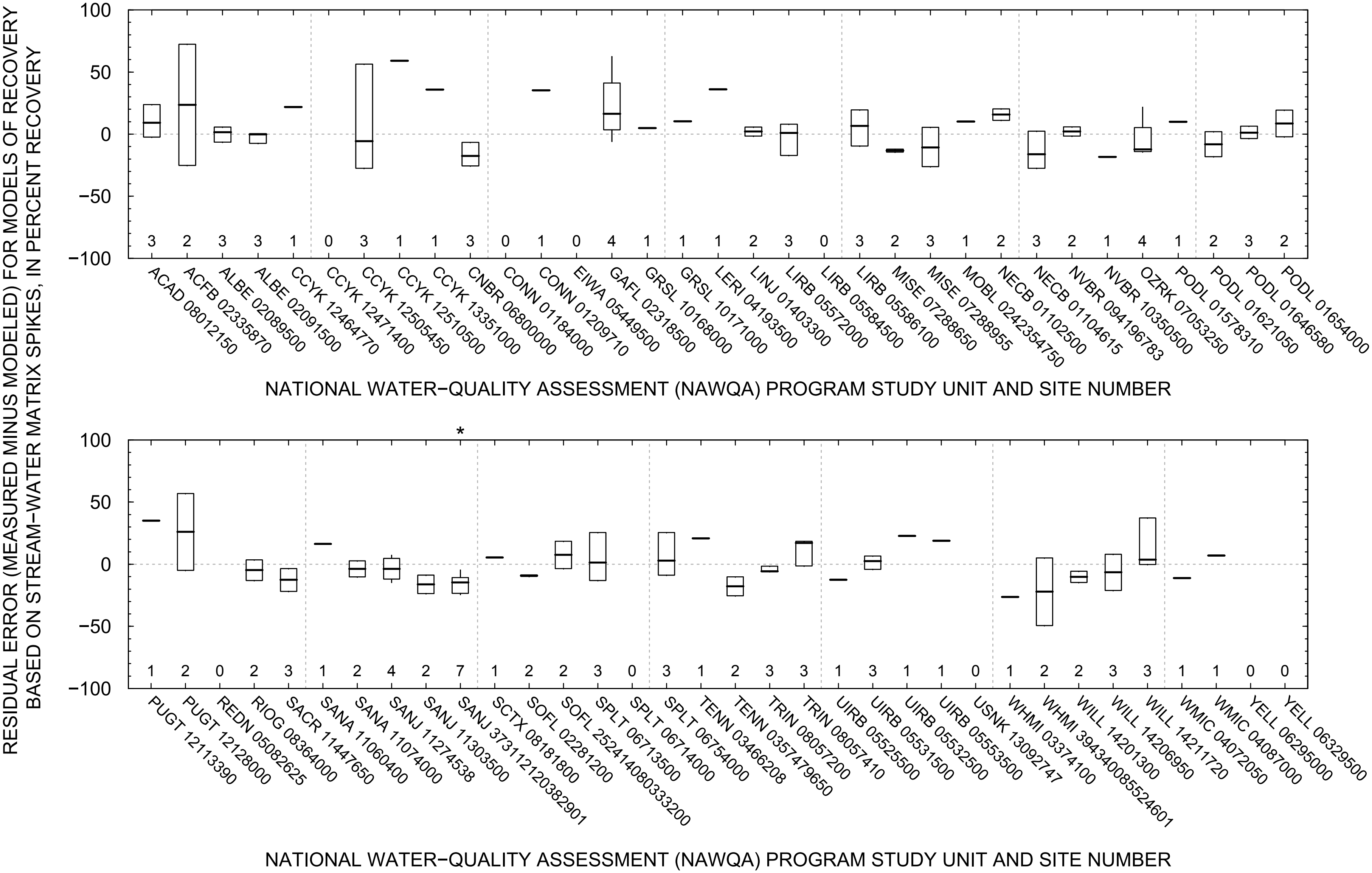


Figure A7−25. Distribution of residual errors in modeled recovery of fipronil sulfone for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

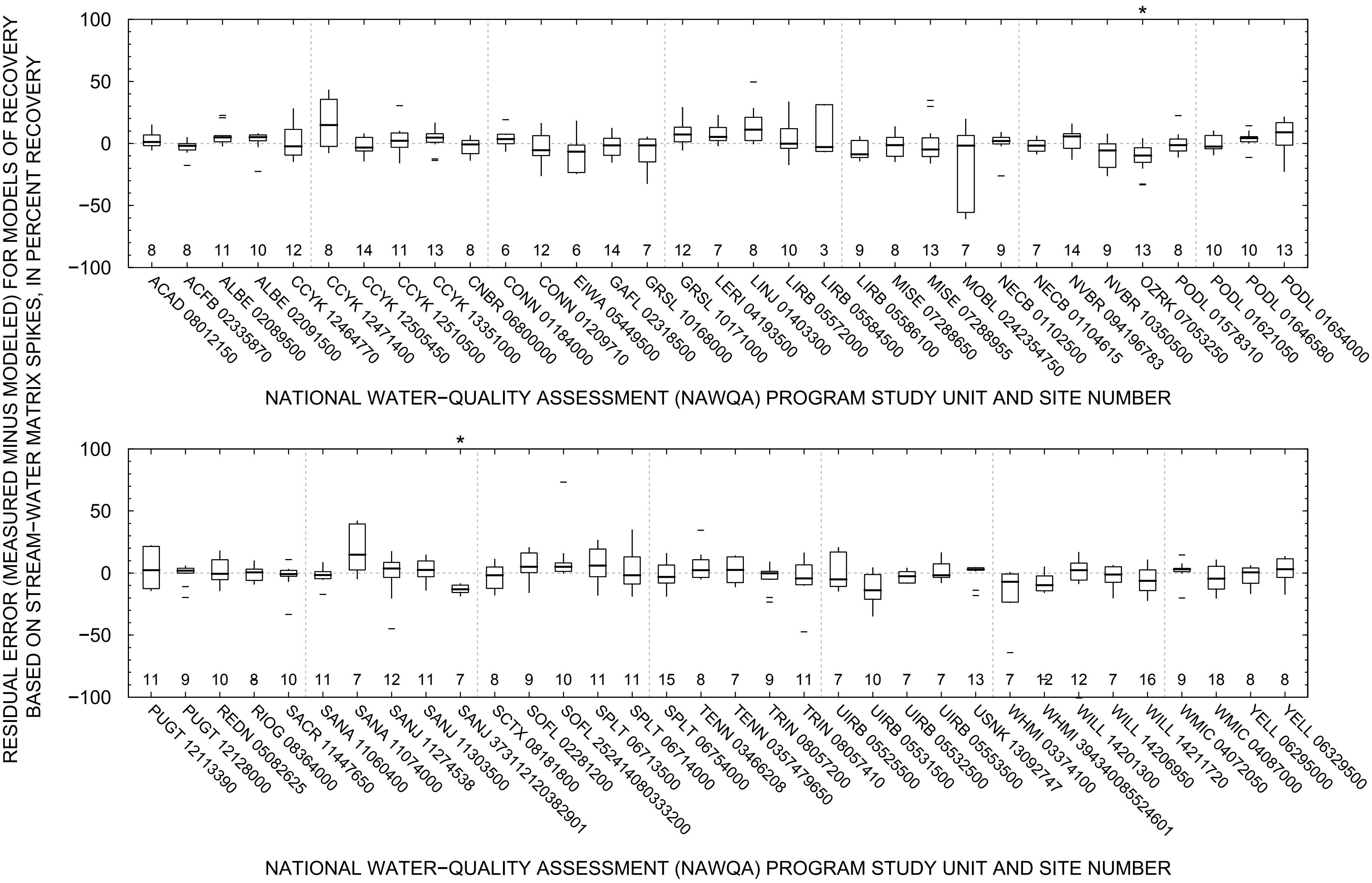


Figure A7−26. Distribution of residual errors in modeled recovery of fonofos for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

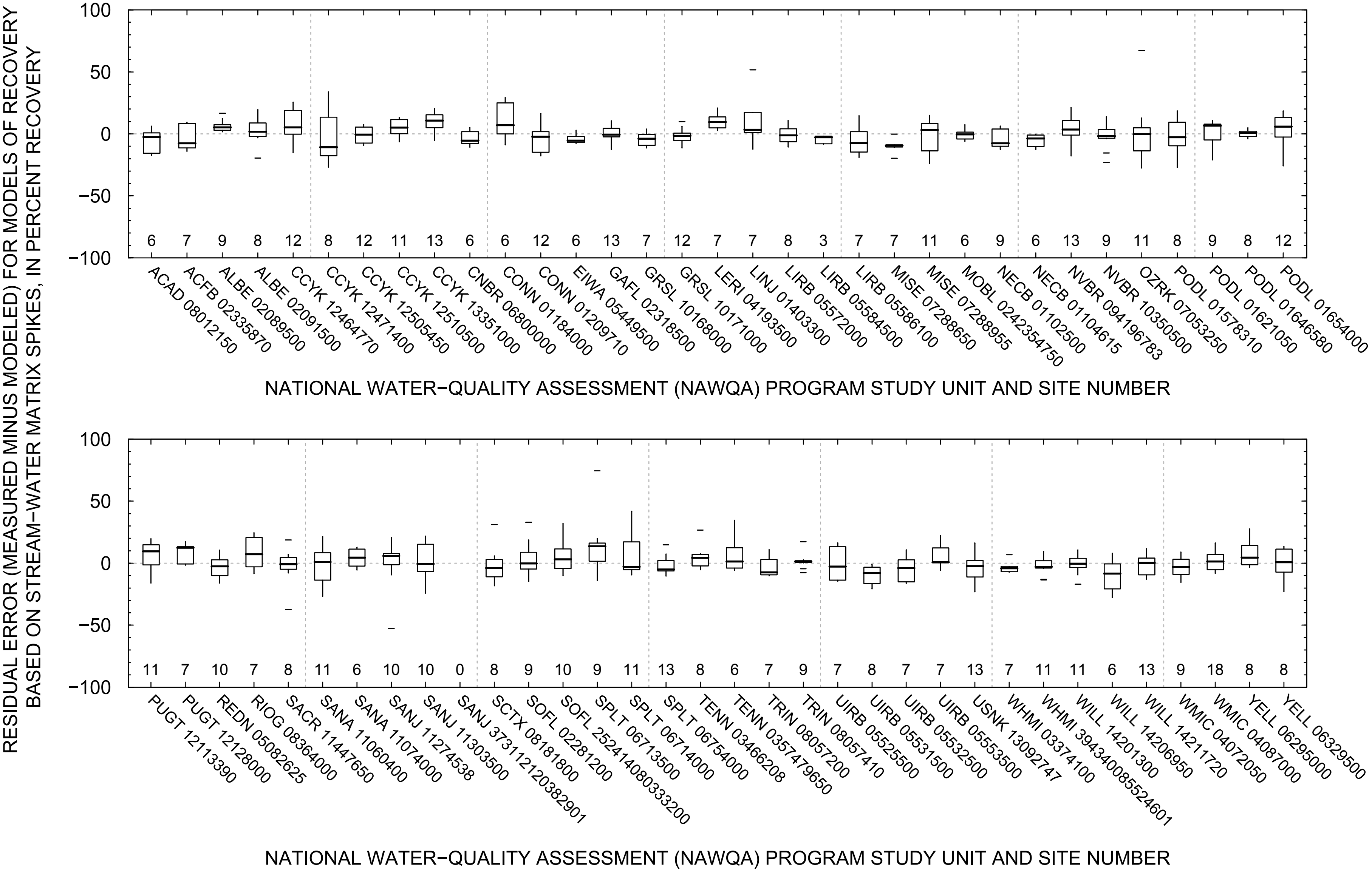


Figure A7−27. Distribution of residual errors in modeled recovery of alpha−HCH for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

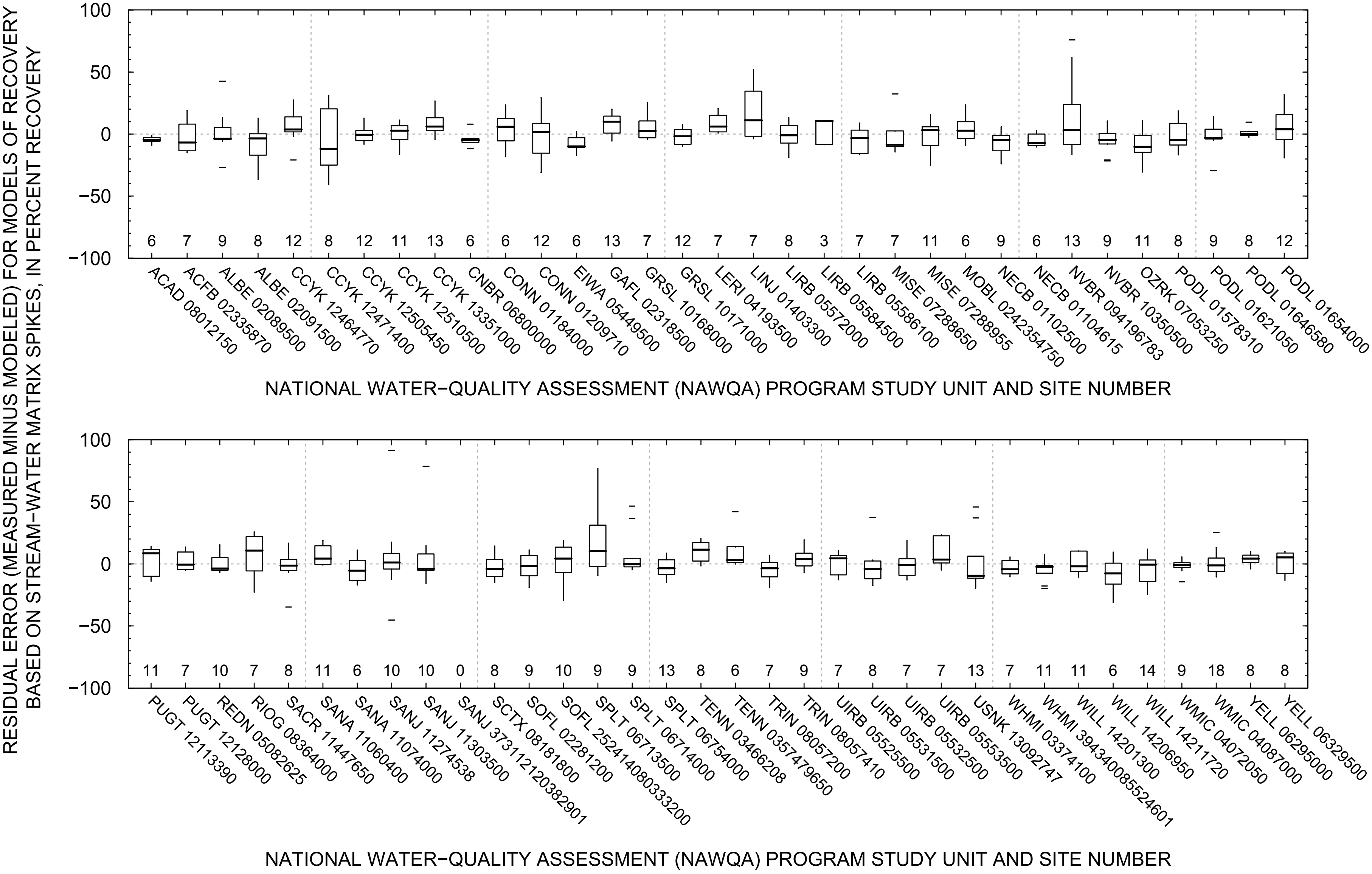


Figure A7−28. Distribution of residual errors in modeled recovery of gamma−HCH for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

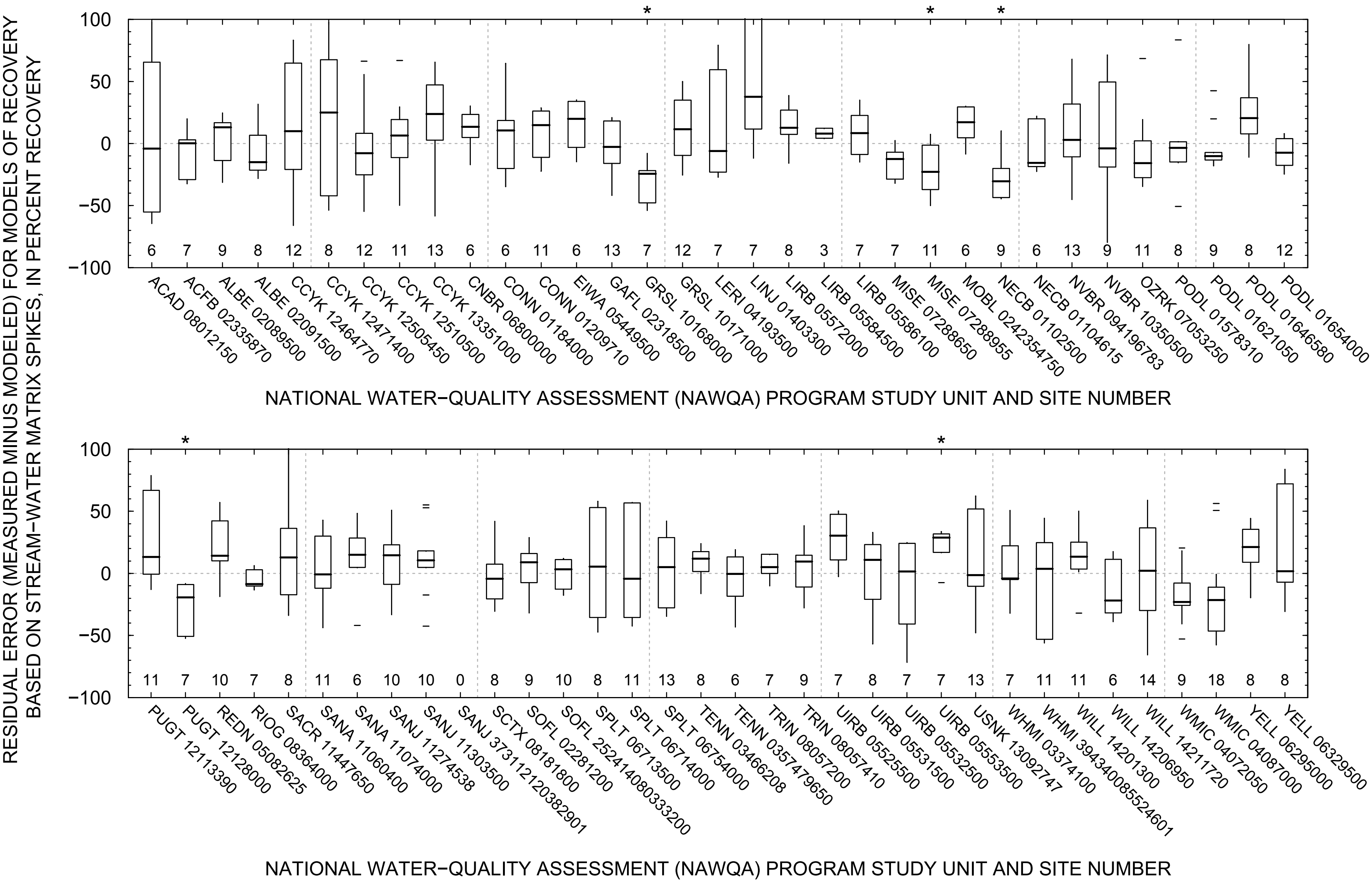


Figure A7−29. Distribution of residual errors in modeled recovery of linuron for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

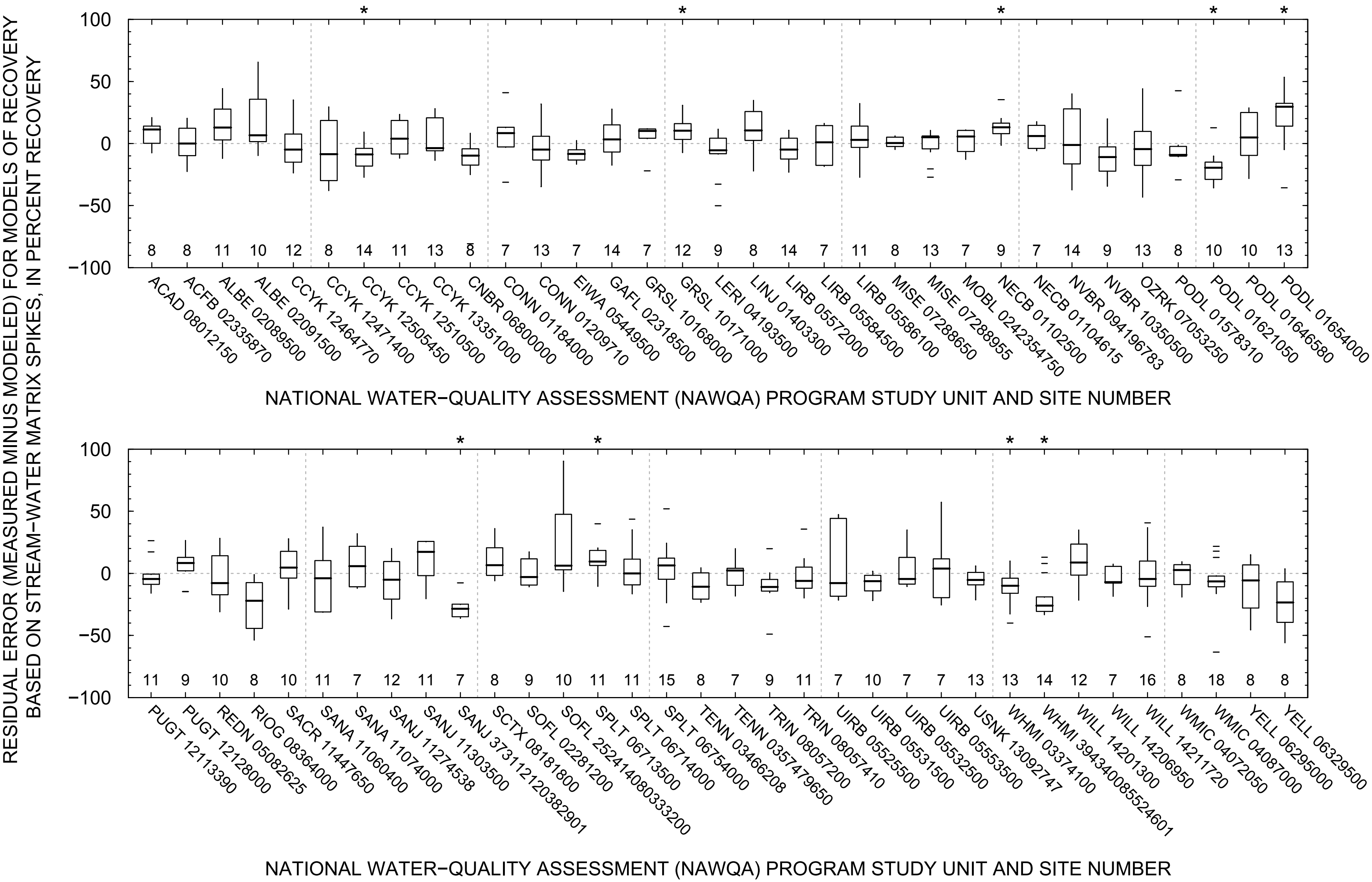


Figure A7−30. Distribution of residual errors in modeled recovery of malathion for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

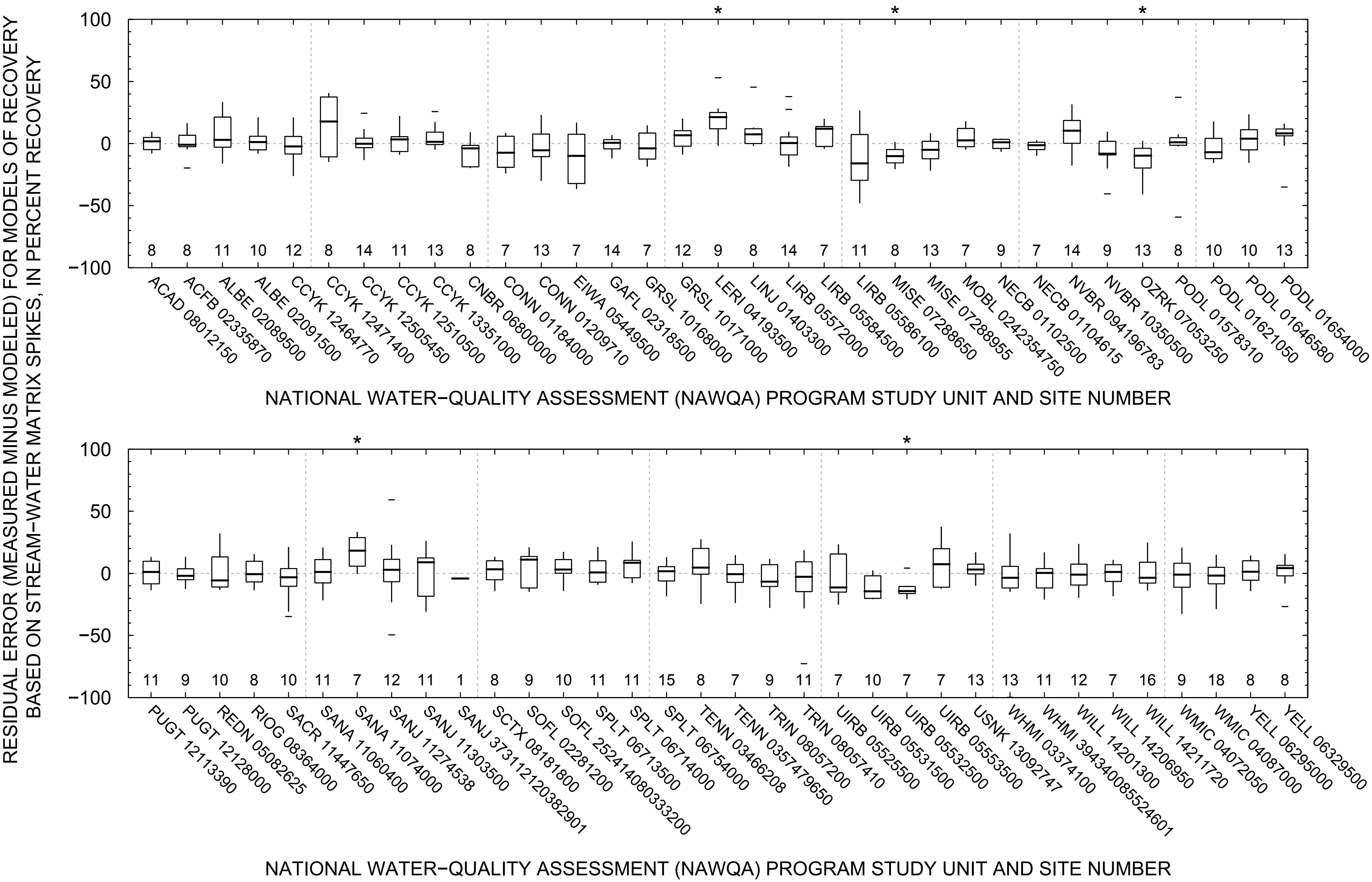


Figure A7−31. Distribution of residual errors in modeled recovery of metolachlor for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

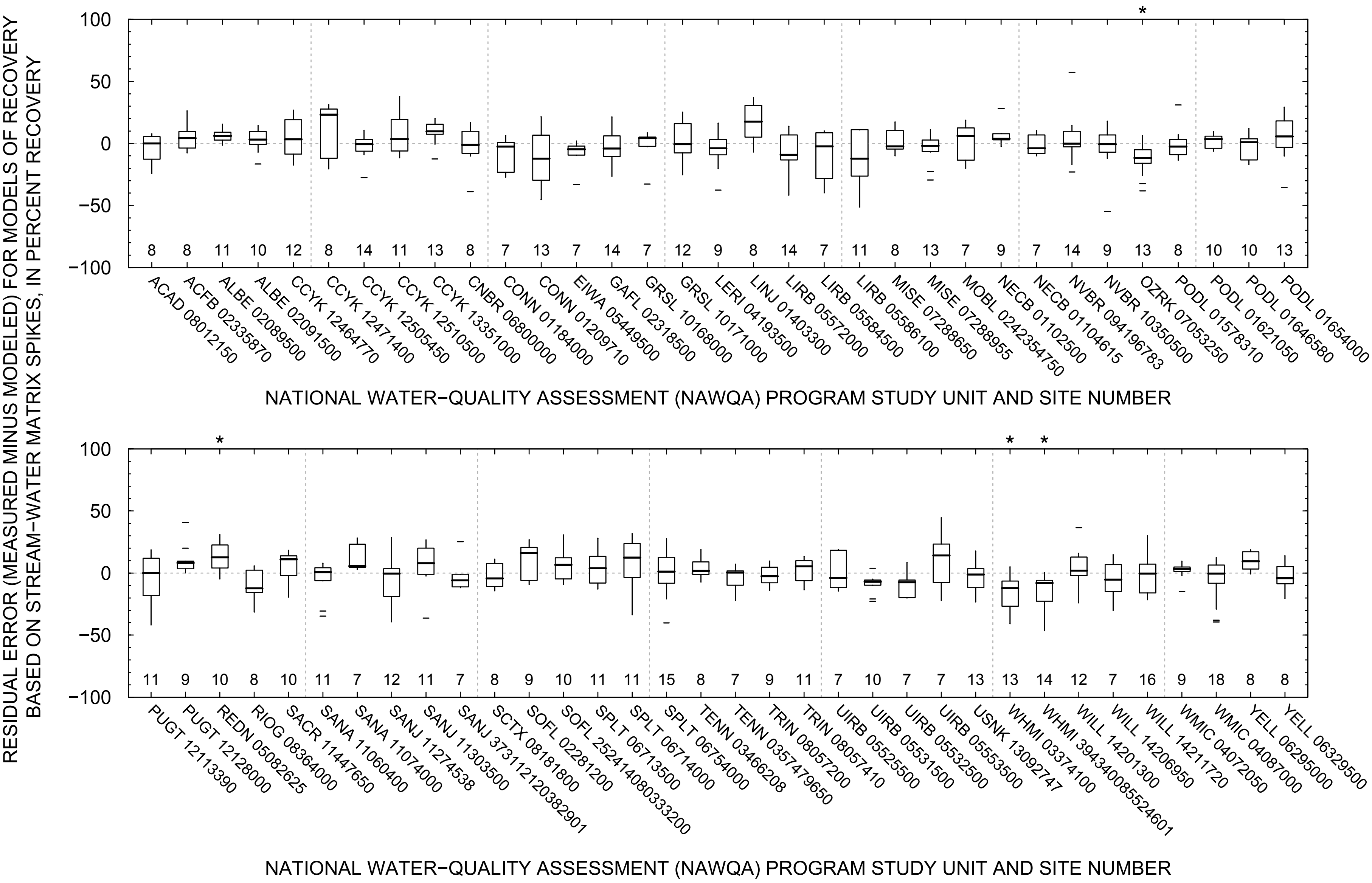


Figure A7−32. Distribution of residual errors in modeled recovery of metribuzin for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

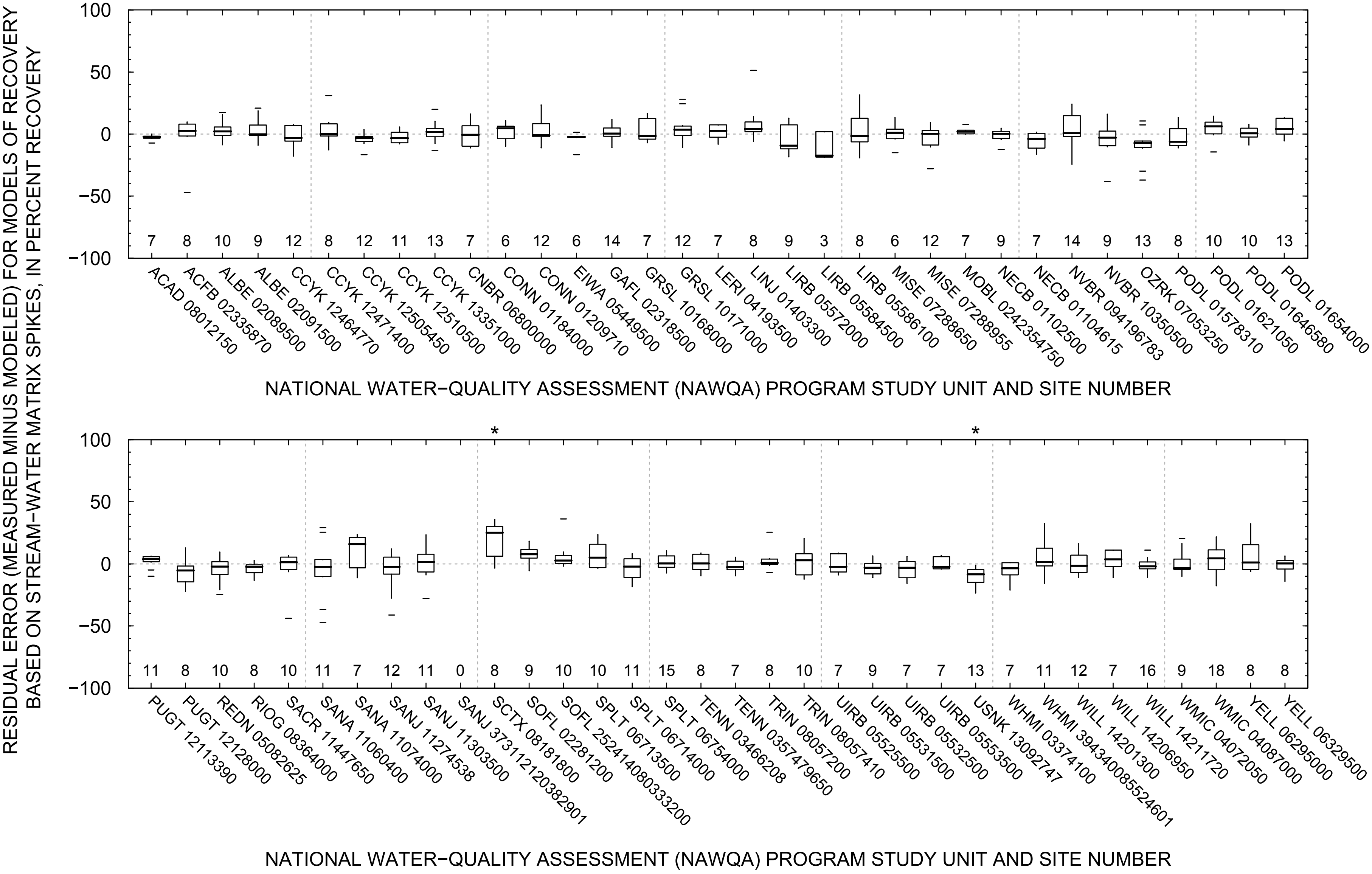


Figure A7−33. Distribution of residual errors in modeled recovery of molinate for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

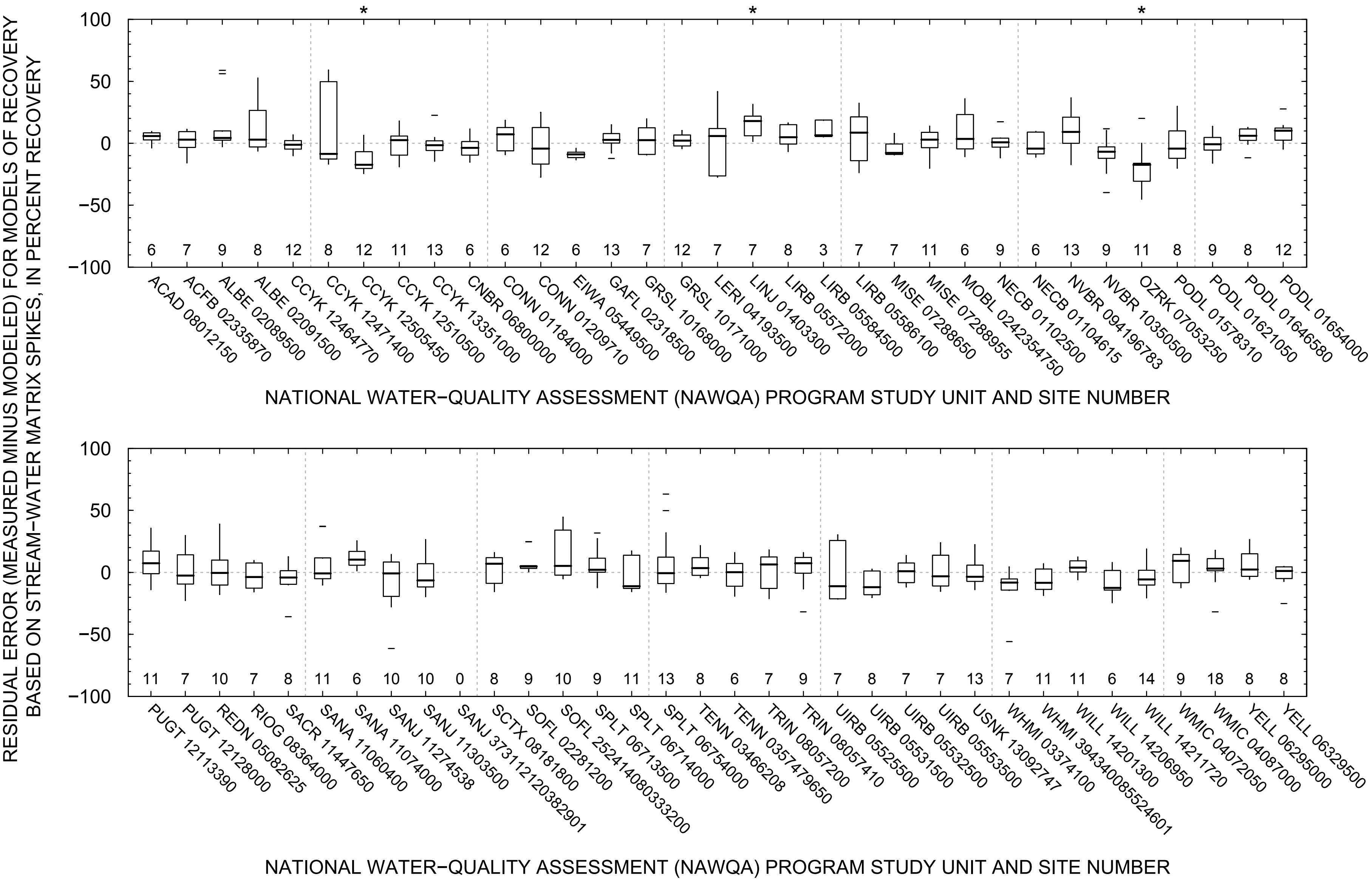


Figure A7−34. Distribution of residual errors in modeled recovery of napropamide for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

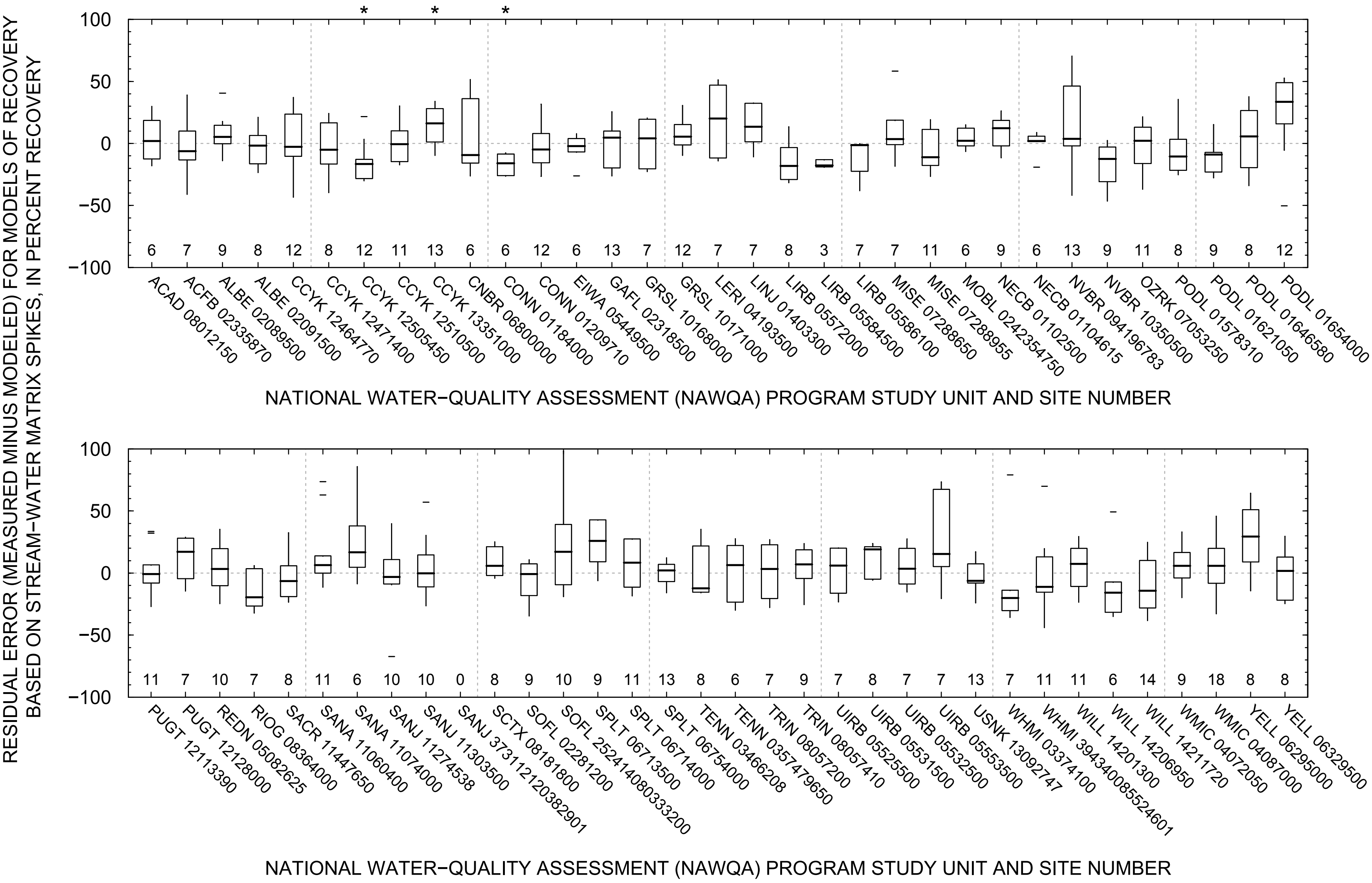


Figure A7−35. Distribution of residual errors in modeled recovery of parathion for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

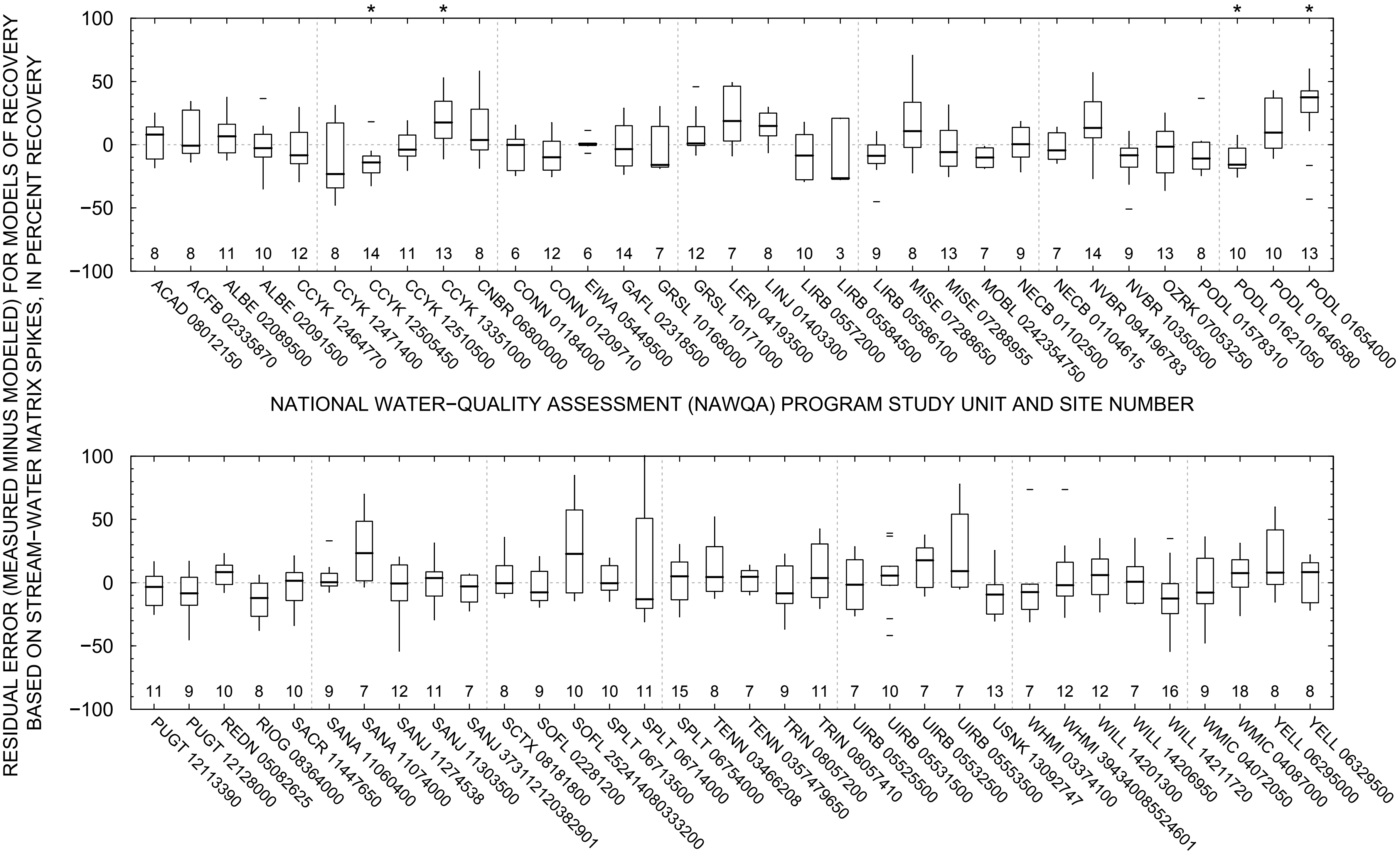


Figure A7−36. Distribution of residual errors in modeled recovery of parathion−methyl for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

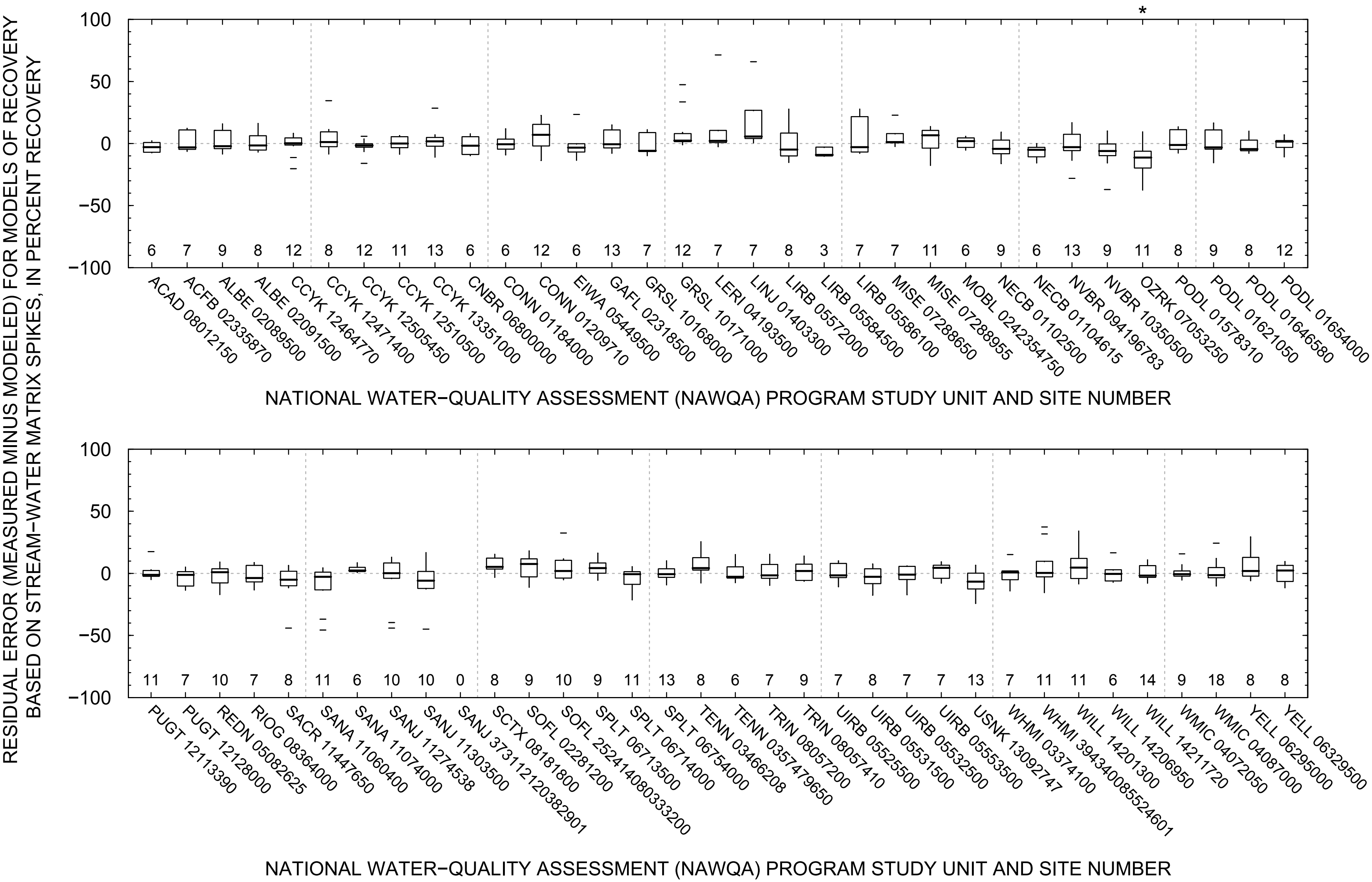


Figure A7−37. Distribution of residual errors in modeled recovery of pebulate for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

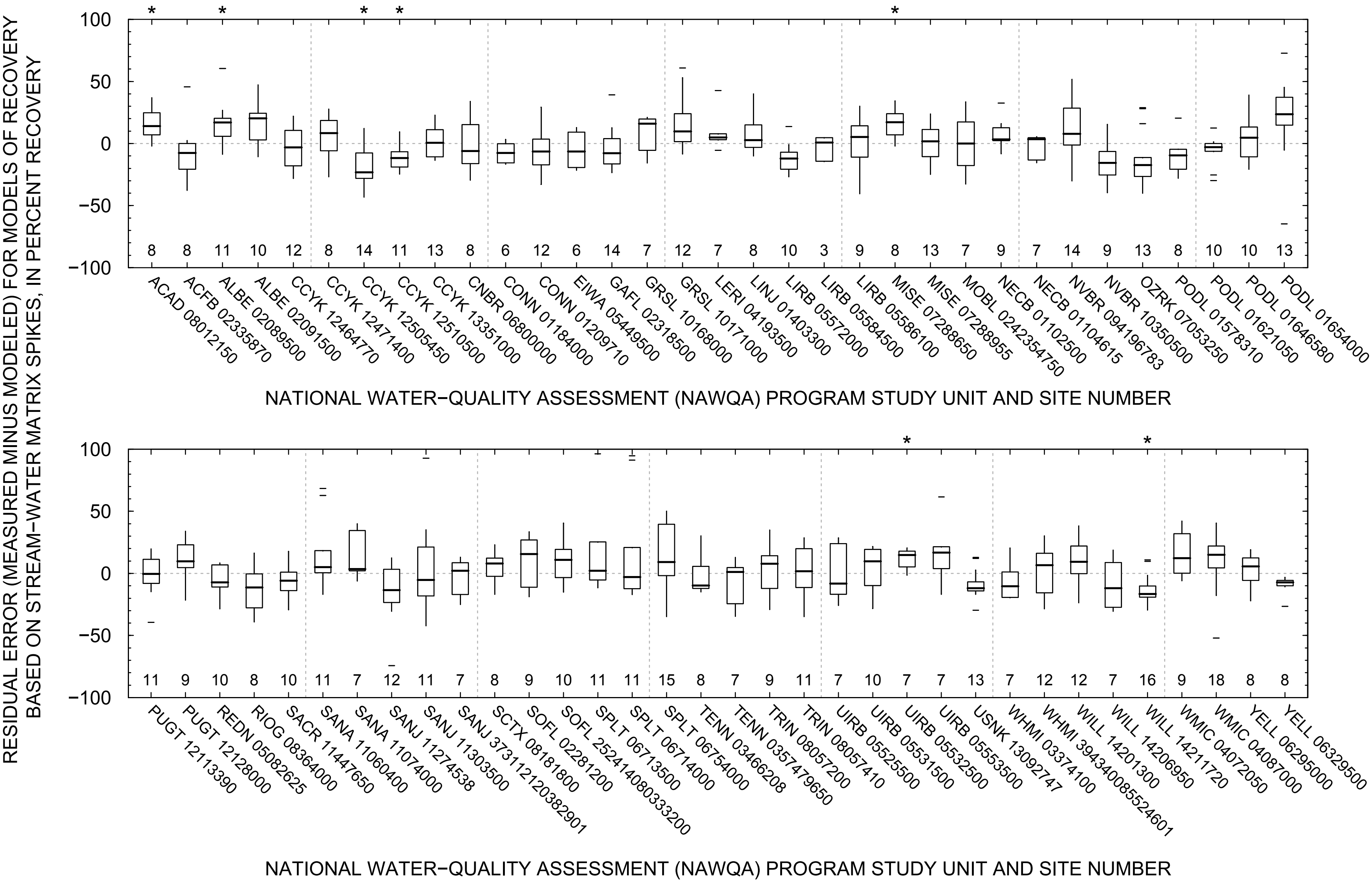


Figure A7−38. Distribution of residual errors in modeled recovery of pendimethalin for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

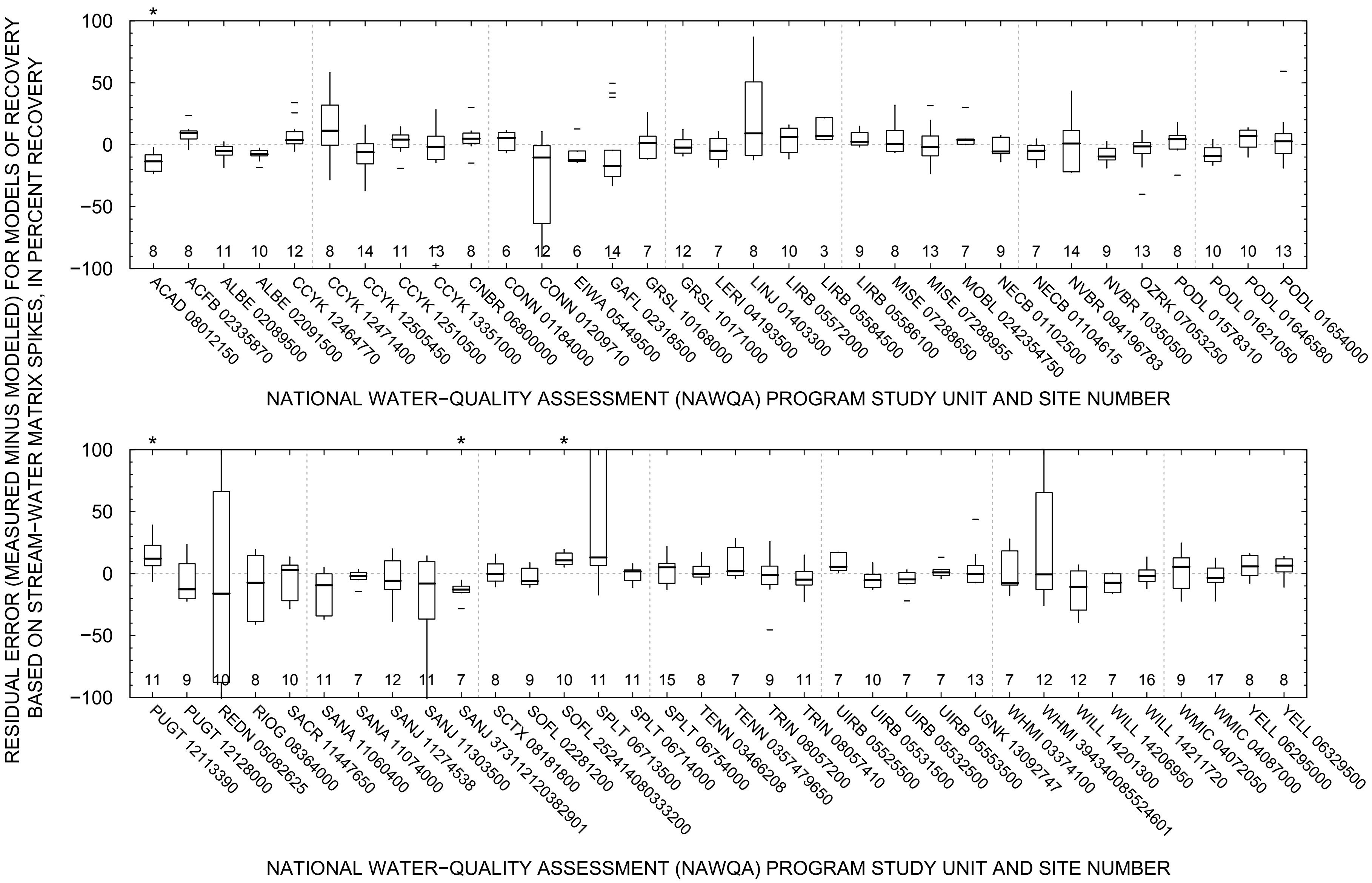


Figure A7−39. Distribution of residual errors in modeled recovery of cis−permethrin for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

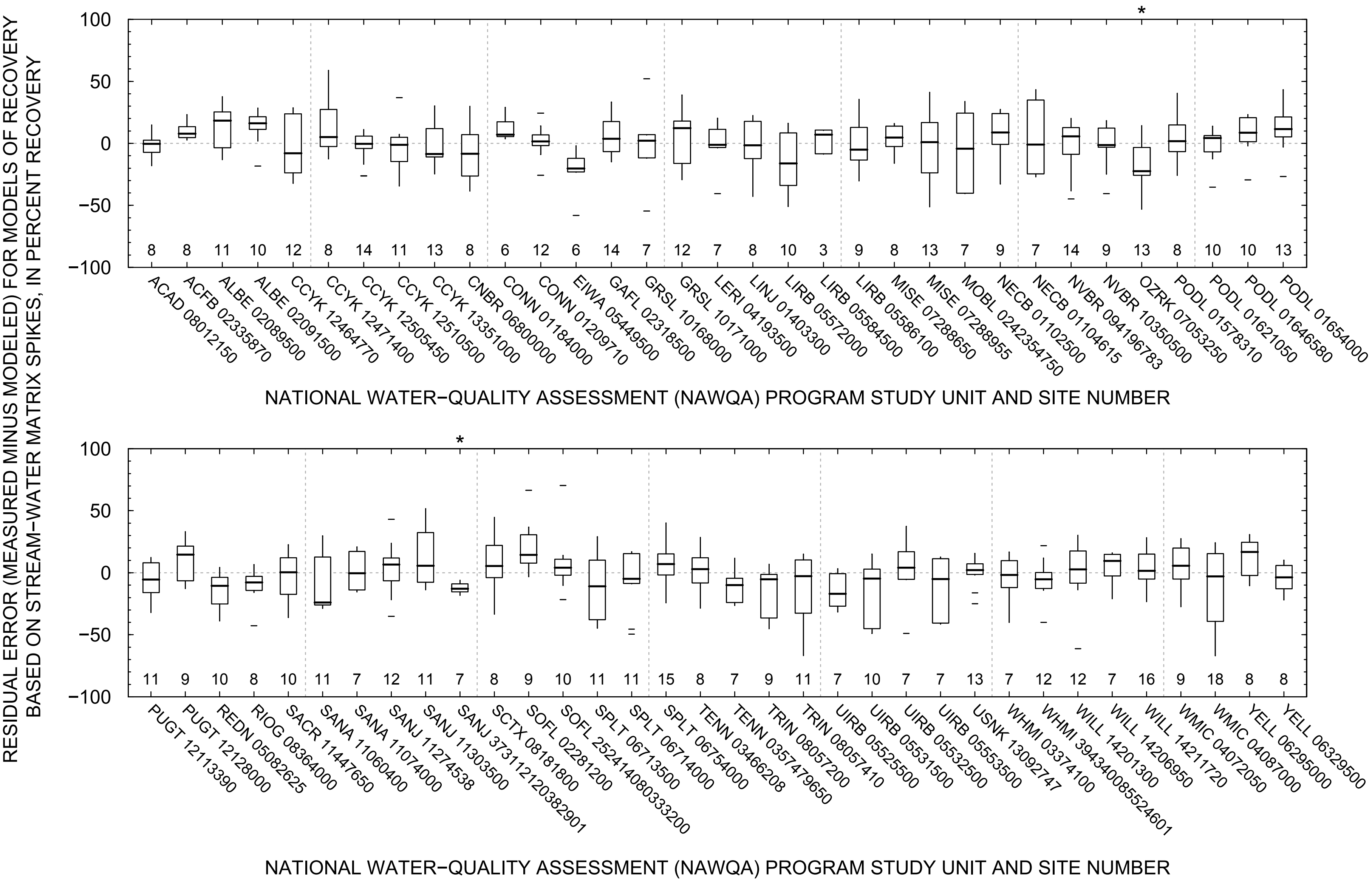


Figure A7−40. Distribution of residual errors in modeled recovery of phorate for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

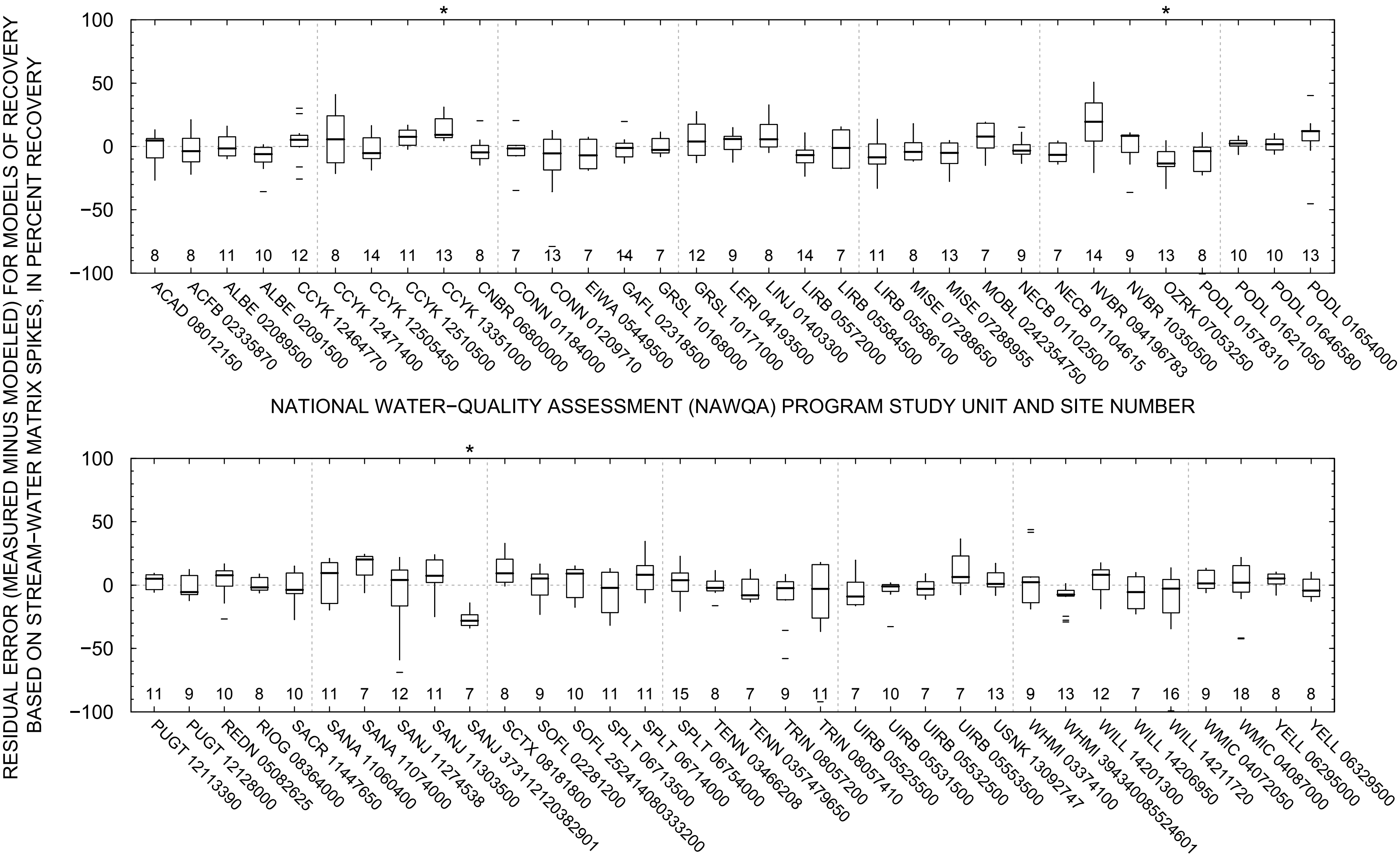


Figure A7−41. Distribution of residual errors in modeled recovery of prometon for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

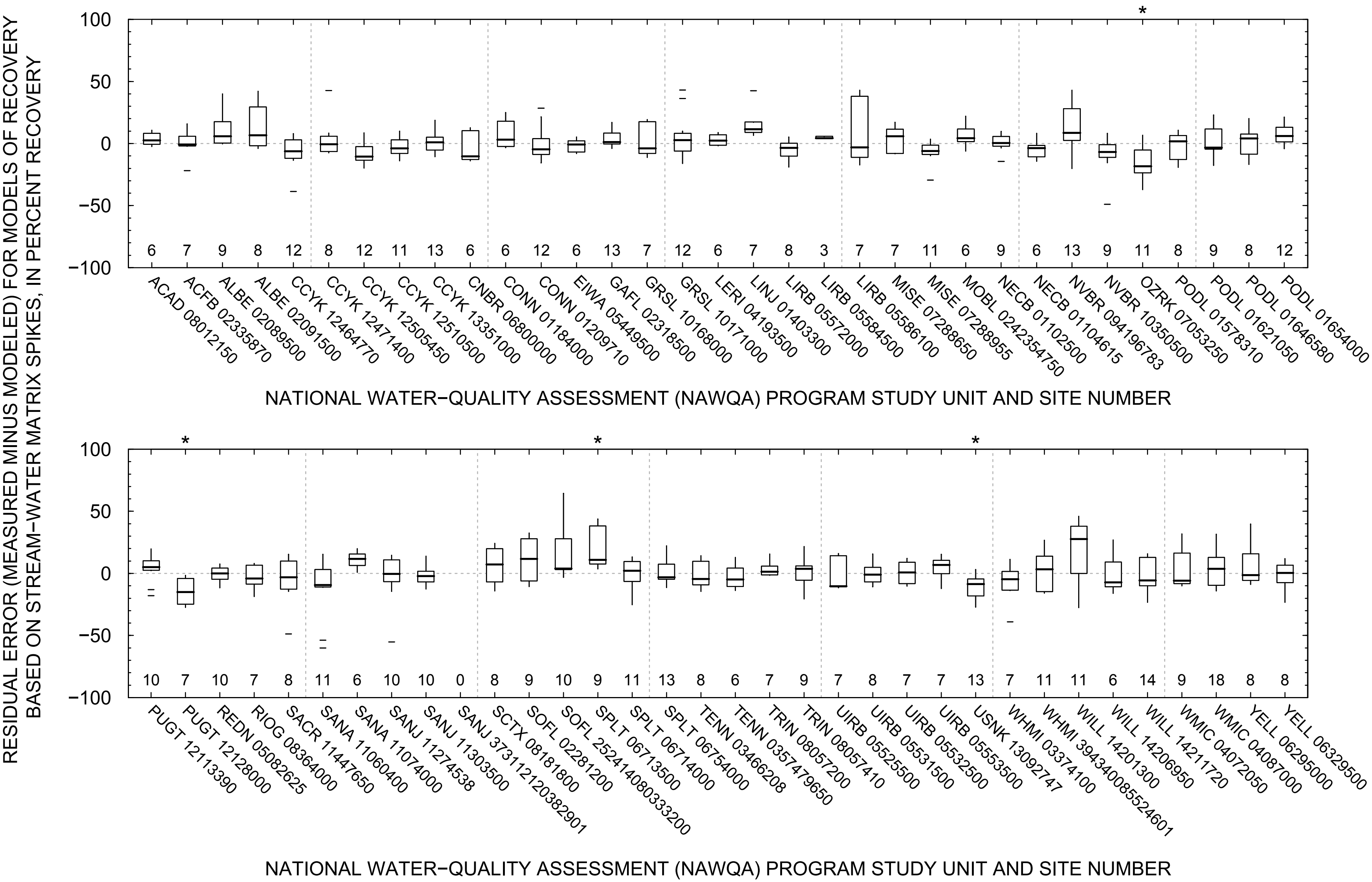


Figure A7−42. Distribution of residual errors in modeled recovery of propachlor for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

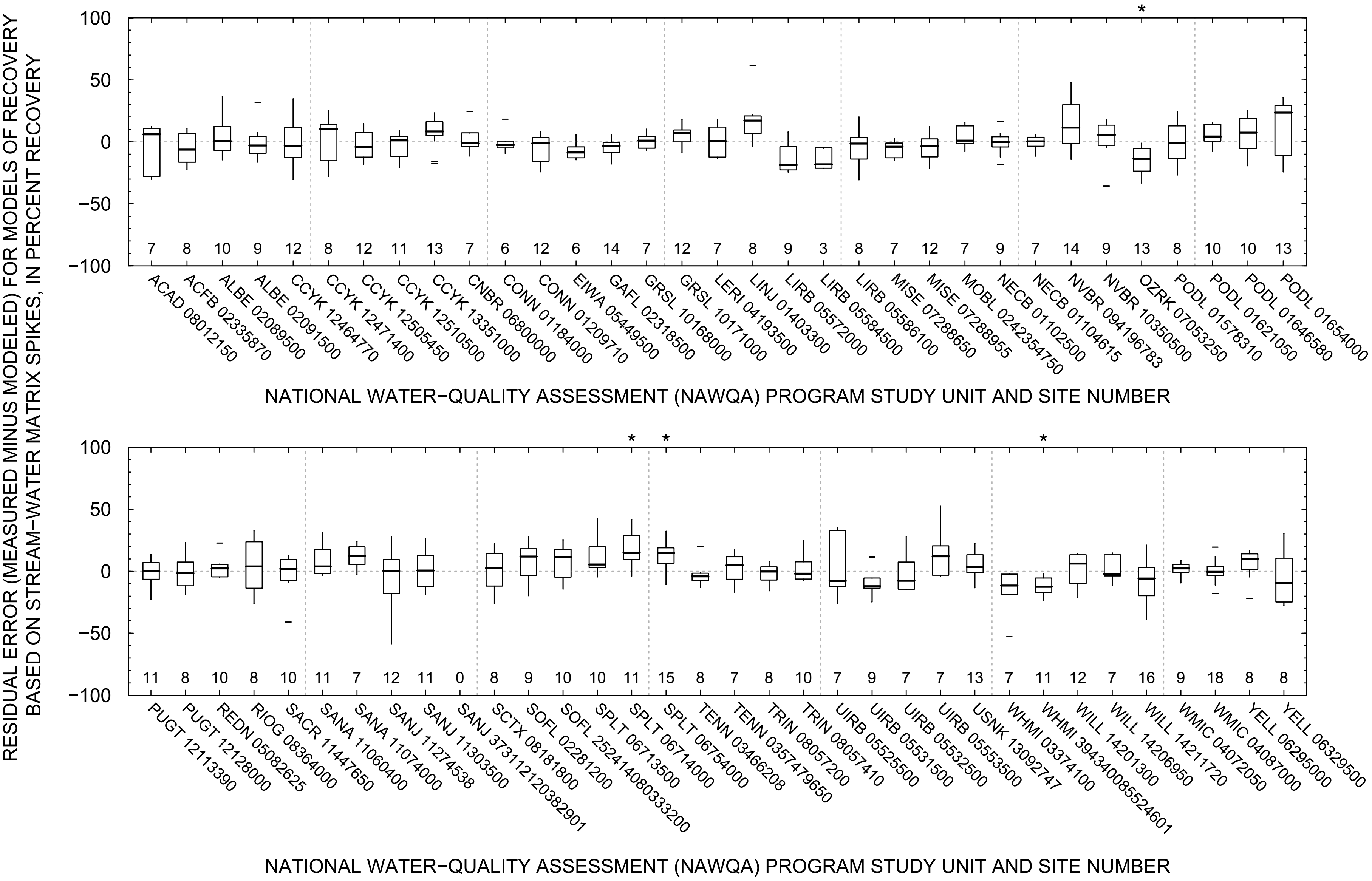


Figure A7−43. Distribution of residual errors in modeled recovery of propanil for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

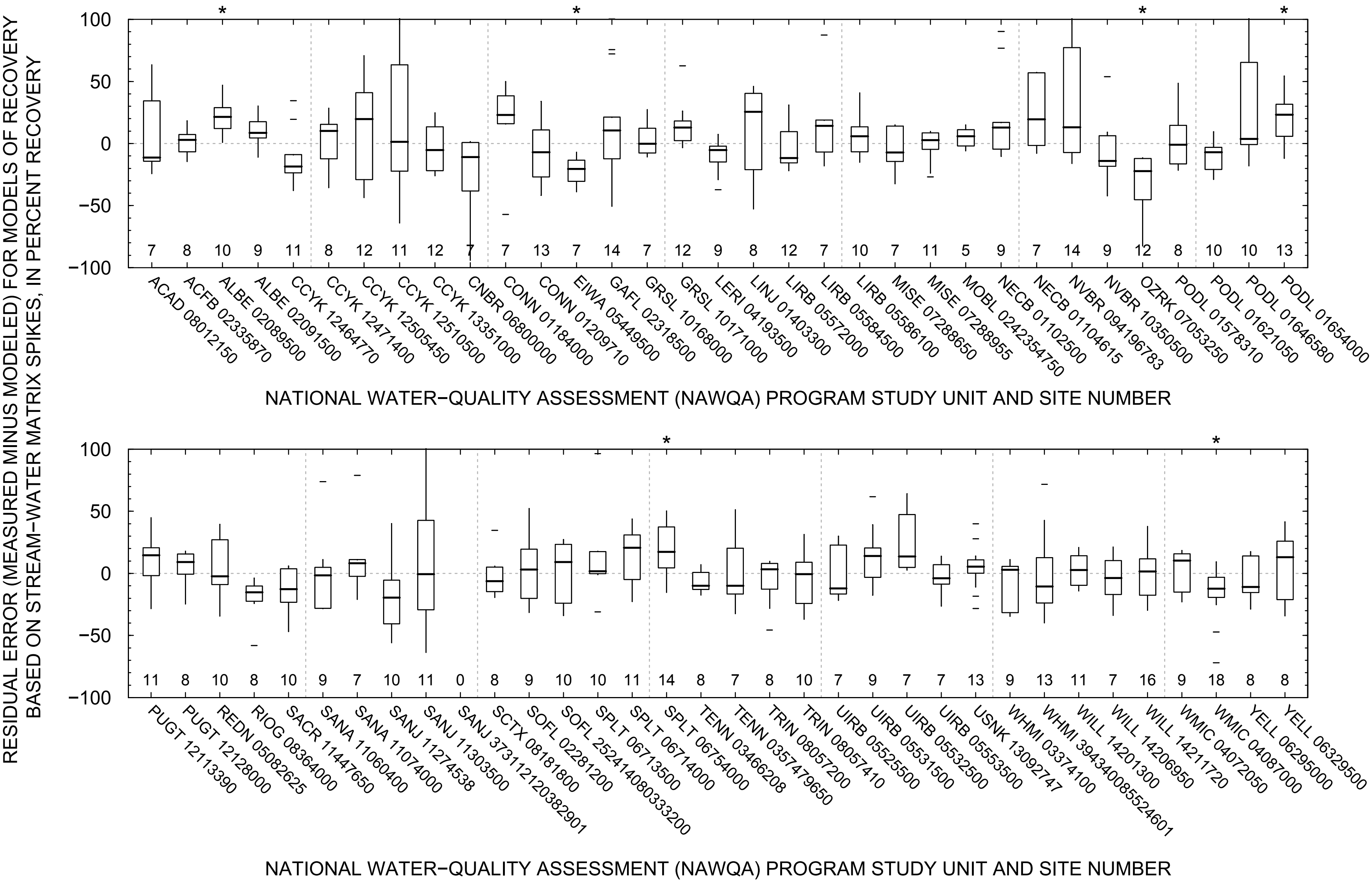


Figure A7−44. Distribution of residual errors in modeled recovery of propargite for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

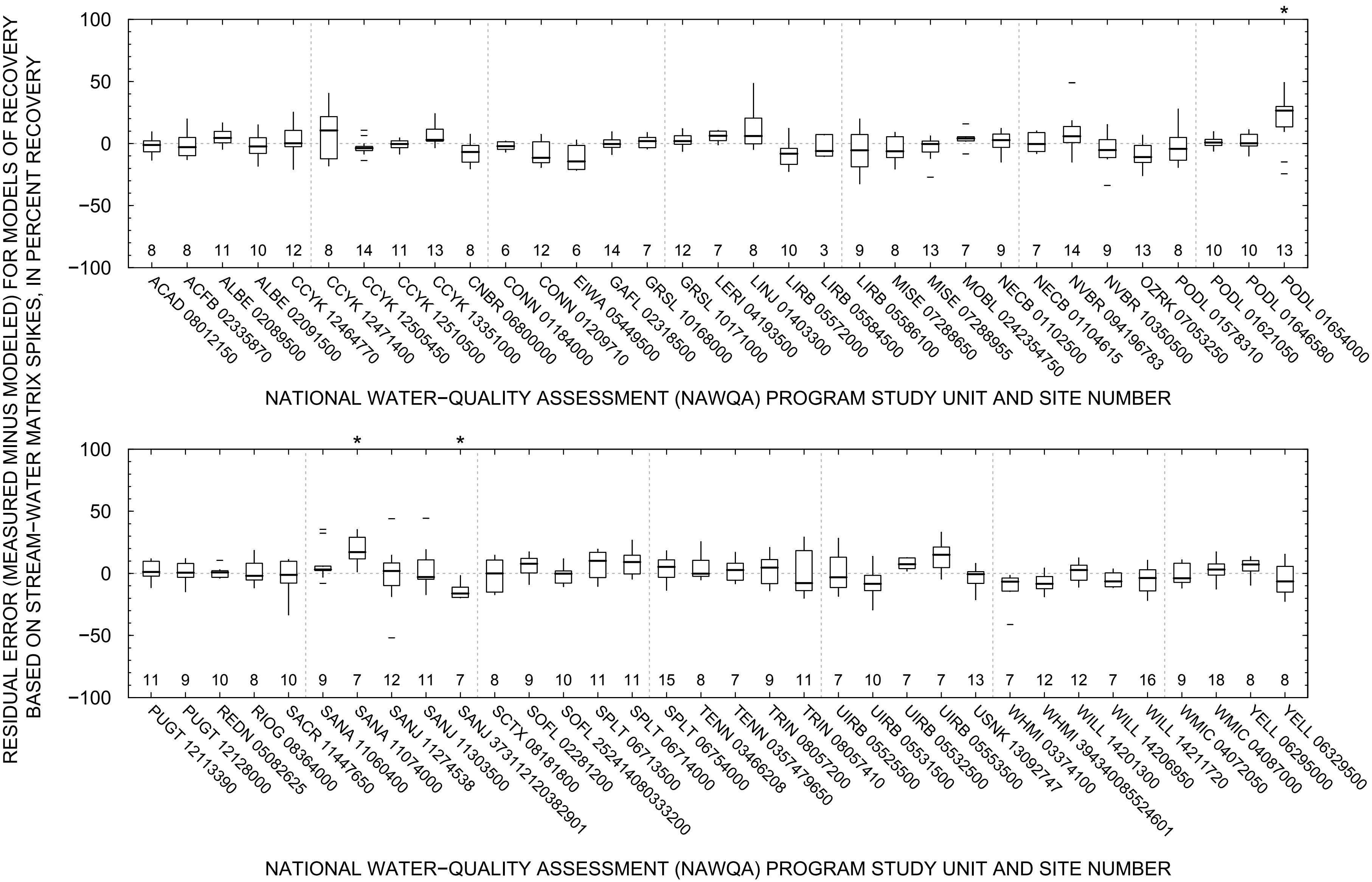


Figure A7−45. Distribution of residual errors in modeled recovery of propyzamide for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

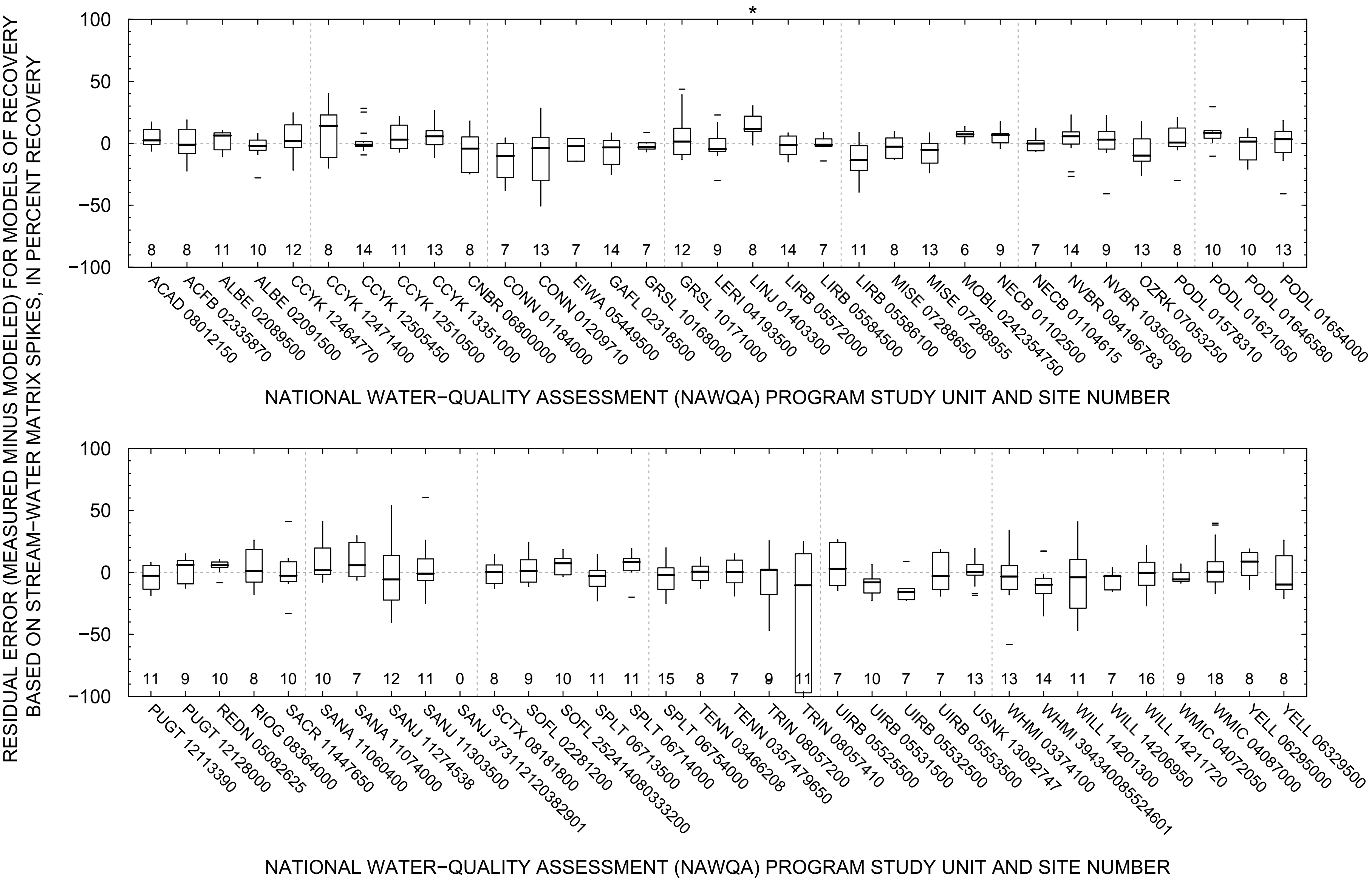


Figure A7−46. Distribution of residual errors in modeled recovery of simazine for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

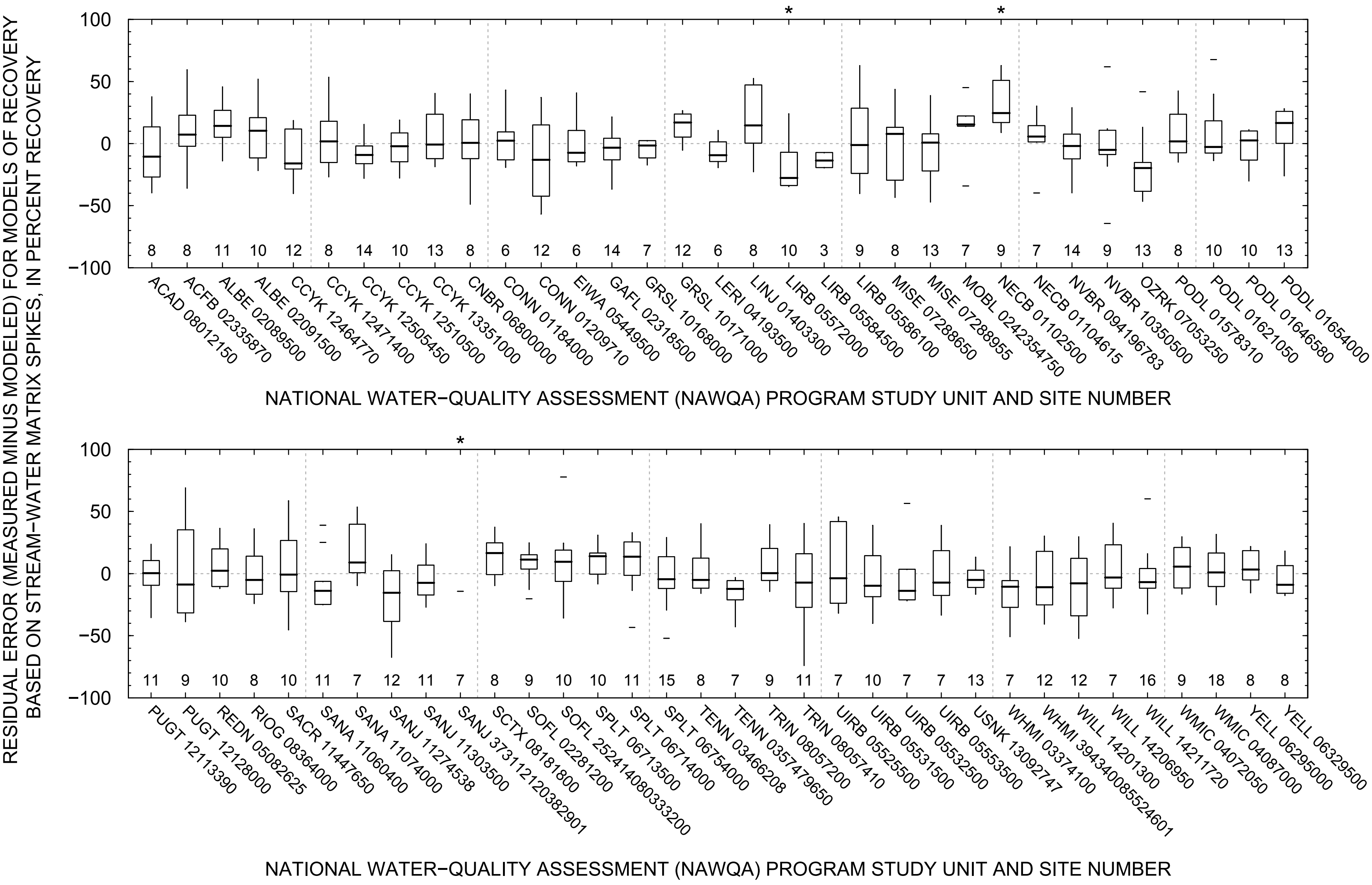


Figure A7−47. Distribution of residual errors in modeled recovery of tebuthiuron for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

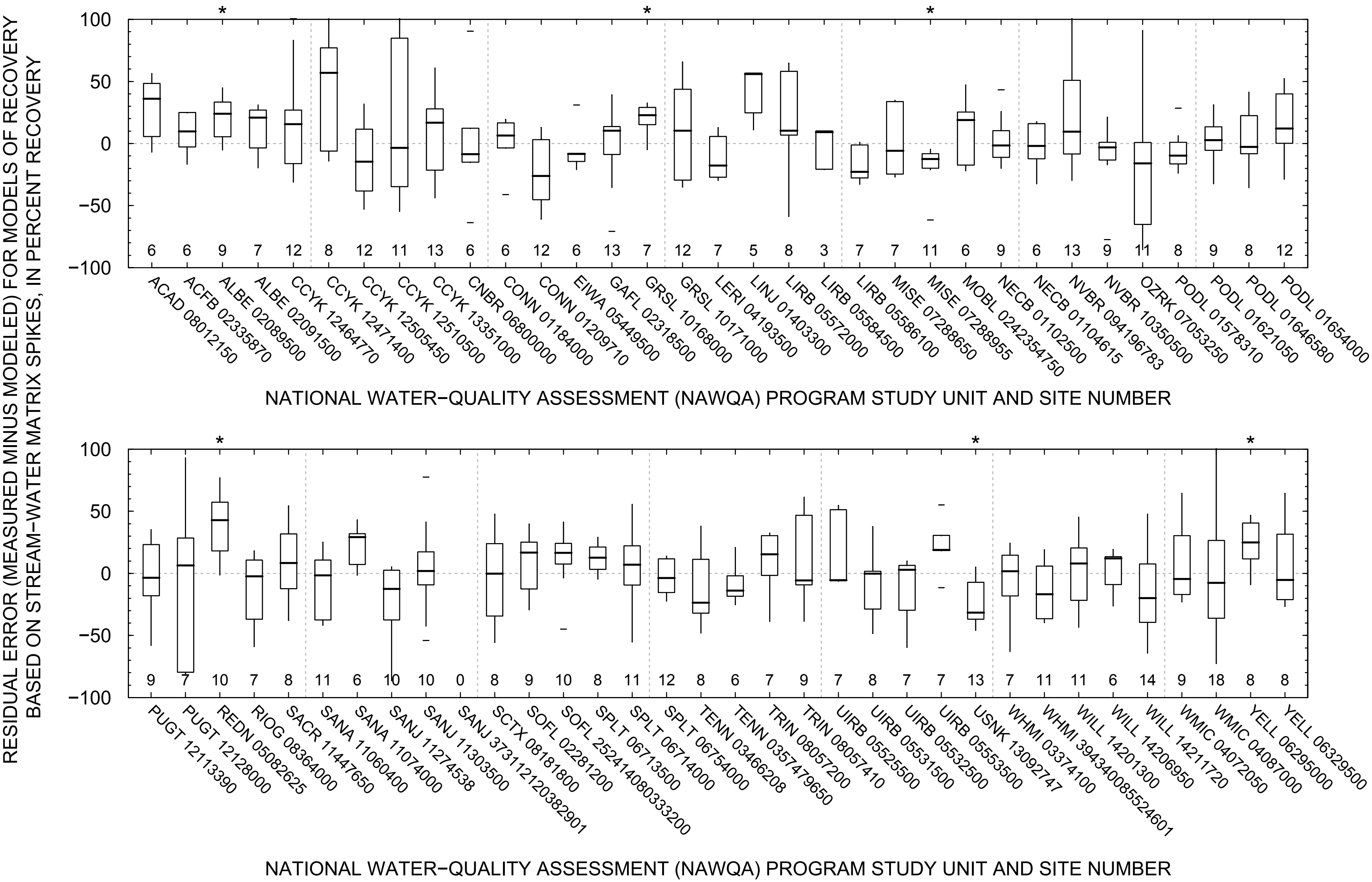


Figure A7−48. Distribution of residual errors in modeled recovery of terbacil for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

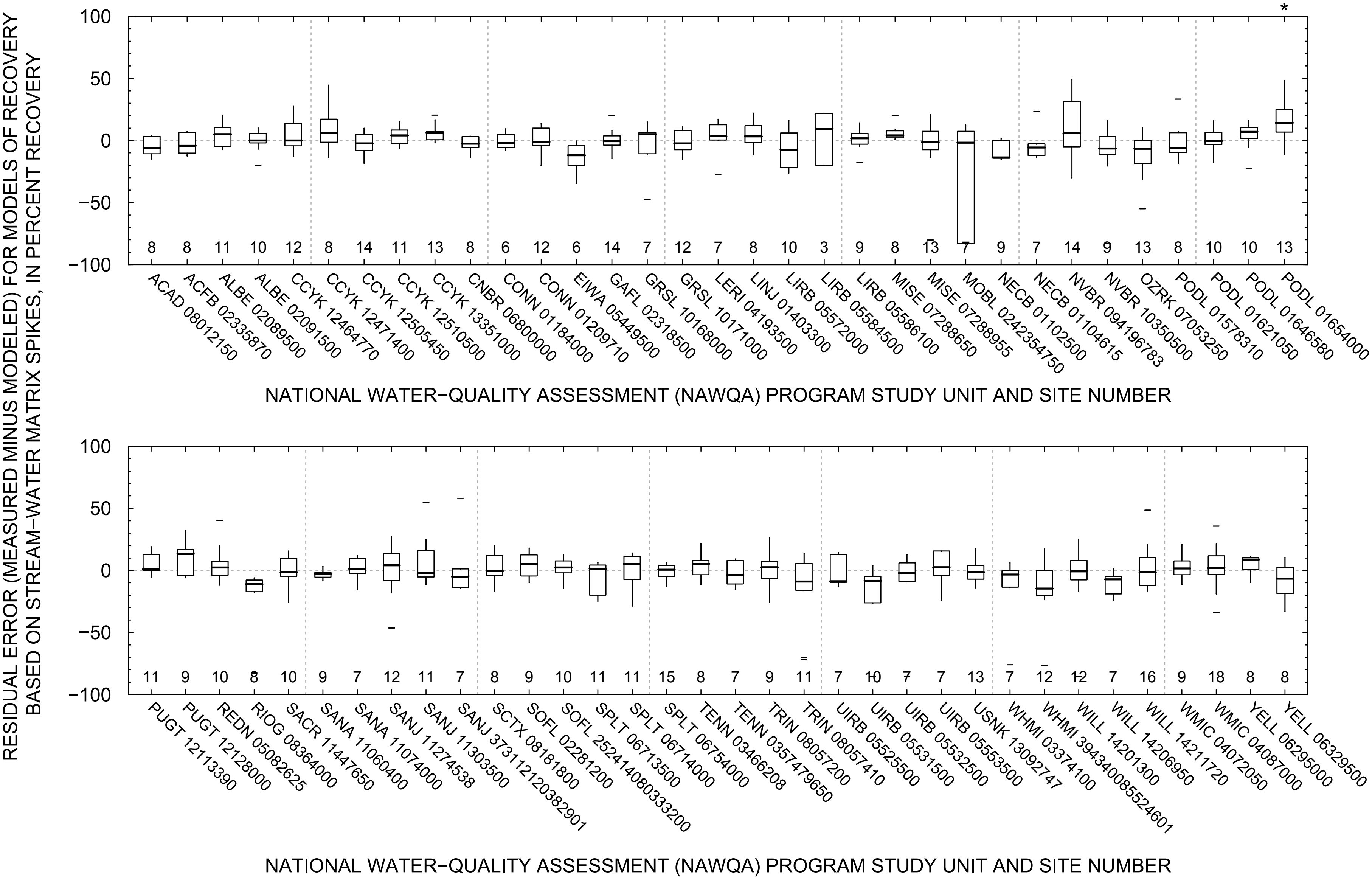


Figure A7−49. Distribution of residual errors in modeled recovery of terbufos for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

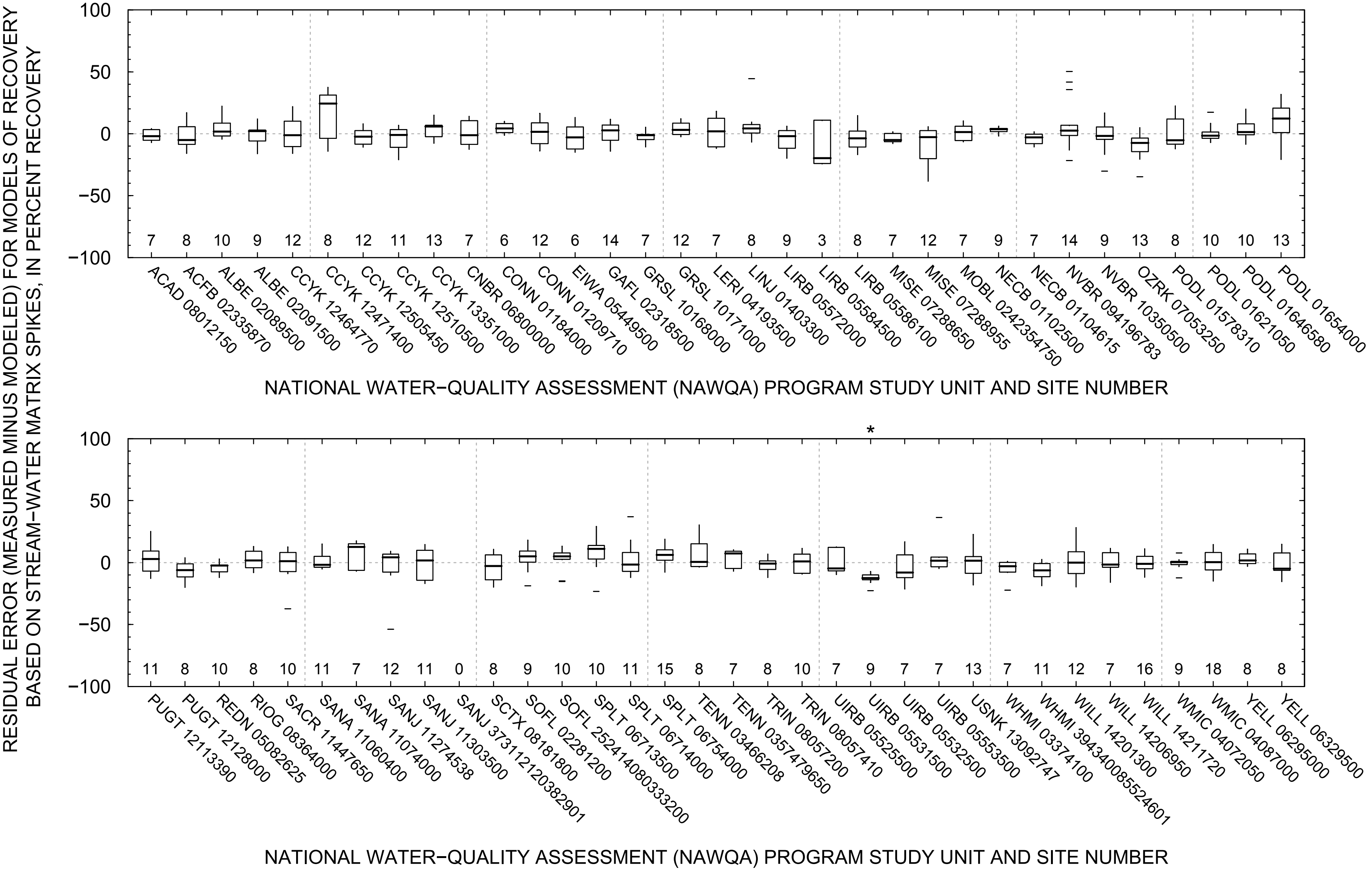


Figure A7−50. Distribution of residual errors in modeled recovery of thiobencarb for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

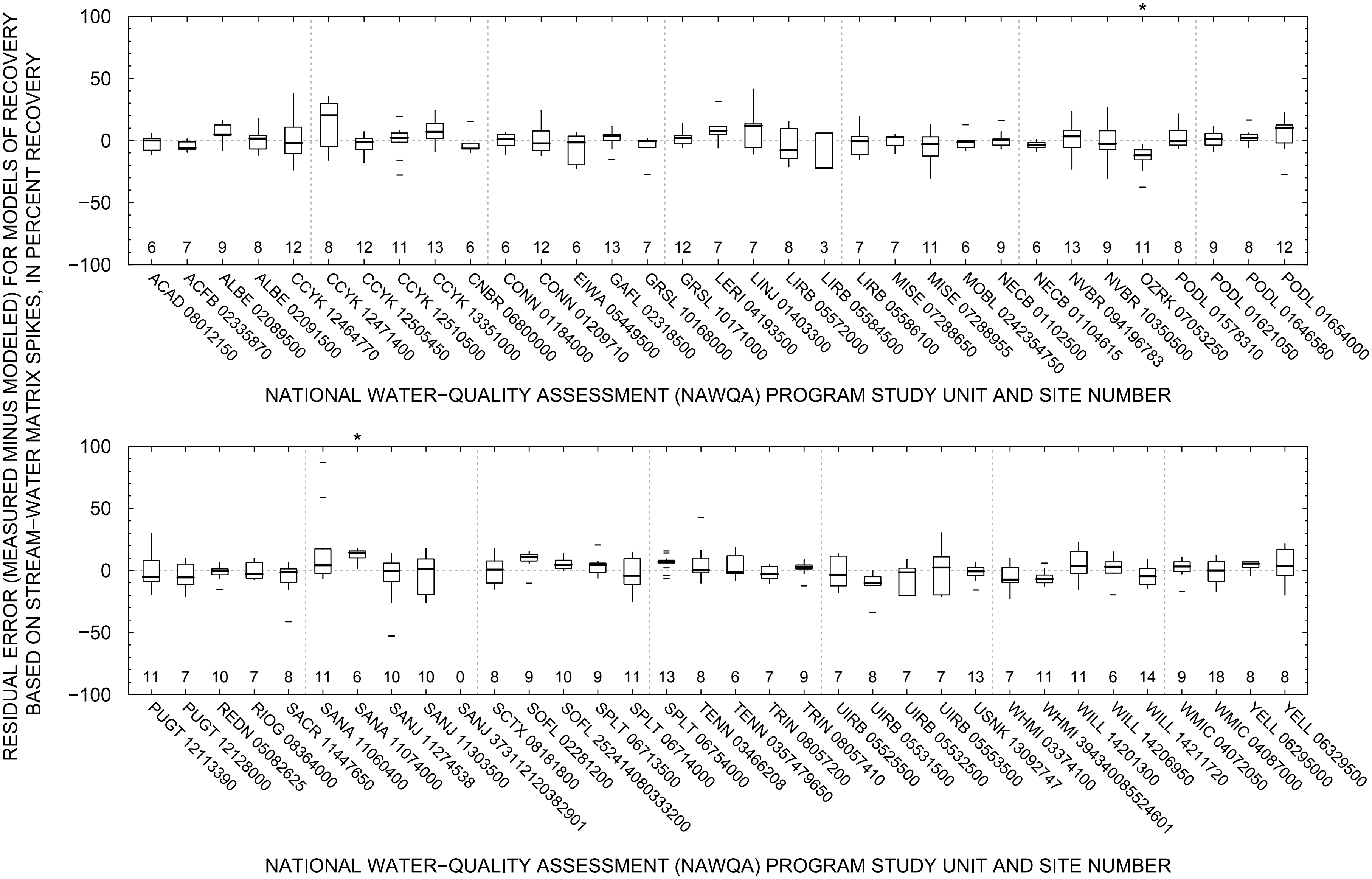


Figure A7−51. Distribution of residual errors in modeled recovery of triallate for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 ($p<0.01$) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).

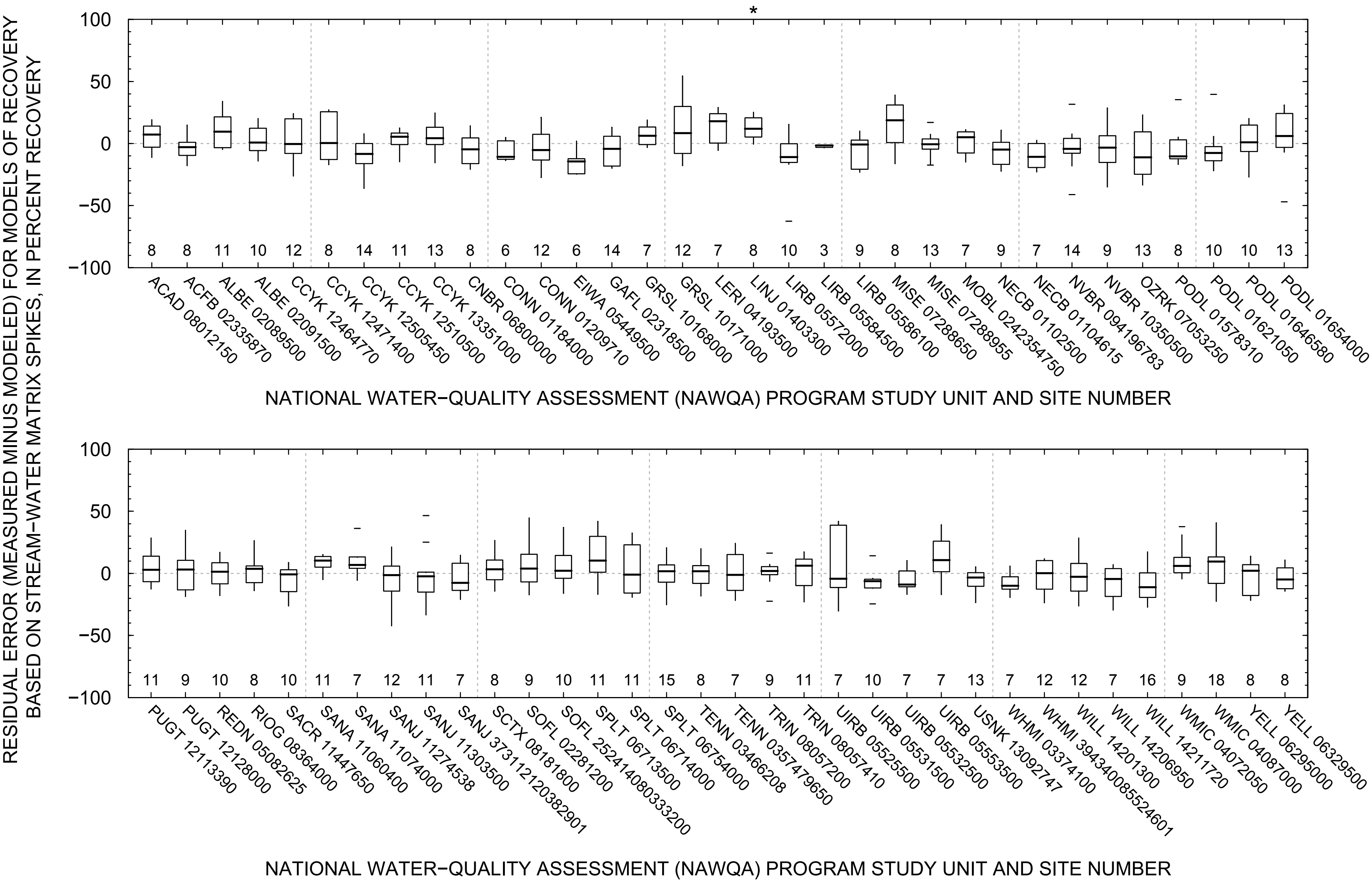


Figure A7−52. Distribution of residual errors in modeled recovery of trifluralin for selected stream−water sites. The number of matrix spikes is shown at the bottom of the boxplot. An asterisk at the top of the boxplot indicates sites where mean residual error (1) is significantly different from 0 (p<0.01) and (2) differs from 0 by more than 10 percent. Study Units are identified in figure 7. Boxplots are explained in figure 1. (Residual errors greater than 100 percent or less than −100 percent are not shown).