

METRIC	LABEL
ASPLAN_BIO	Biomass represented by individuals within the rotifer family Asplanchnidae (coarse and fine net samples combined)
ASPLAN_DEN	Density (indiv./L) of individuals within the rotifer family Asplanchnidae (coarse and fine net samples combined)
ASPLAN_NIND	Number of individuals within the rotifer family Asplanchnidae (coarse and fine net samples combined)
ASPLAN_NTAX	Number of distinct taxa within the rotifer family Asplanchnidae (coarse and fine net samples combined)
ASPLAN_PBIO	Percent of biomass represented by individuals within the rotifer family Asplanchnidae (coarse and fine net samples combined)
ASPLAN_PDEN	Percent of density (indiv./L) of individuals within the rotifer family Asplanchnidae (coarse and fine net samples combined)
ASPLAN_PIND	Percent of individuals within the rotifer family Asplanchnidae (coarse and fine net samples combined)
ASPLAN_PTAX	Percent of distinct taxa within the rotifer family Asplanchnidae (coarse and fine net samples combined)
ASPLAN300_BIO	Biomass represented by individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net subsamples combined)
ASPLAN300_NIND	Number of individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined)
ASPLAN300_NTAX	Number of distinct taxa within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined)
ASPLAN300_PBIO	Percent of biomass represented by individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined)
ASPLAN300_PIND	Percent of individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined)
ASPLAN300_PTAX	Percent of distinct taxa within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined)
BOSM_BIO	Biomass represented by individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)
BOSM_DEN	Density (indiv./L) of individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)
BOSM_NAT_BIO	Biomass represented by native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)
BOSM_NAT_DEN	Density (indiv./L) of native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)
BOSM_NAT_NIND	Number of native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)
BOSM_NAT_NTAX	Number of distinct native taxa within the cladoceran family Bosminidae (coarse and fine net samples combined)
BOSM_NAT_PBIO	Percent of biomass represented by native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)
BOSM_NAT_PDEN	Percent of density (indiv./L) of native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)

BOSM_NAT_PIND	Percent of native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)
BOSM_NAT_PTAX	Percent of distinct native taxa within the cladoceran family Bosminidae (coarse and fine net samples combined)
BOSM_NIND	Number of individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)
BOSM_NTAX	Number of distinct taxa within the cladoceran family Bosminidae (coarse and fine net samples combined)
BOSM_PBIO	Percent of biomass represented by individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)
BOSM_PDEN	Percent of density (indiv./L) of individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)
BOSM_PIND	Percent of individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)
BOSM_PTAX	Percent of total distinct taxa that are within the cladoceran family Bosminidae (coarse and fine net samples combined)
BOSM300_BIO	Biomass represented by individuals within the cladoceran family Bosminidae in the 300-count subsamples (coarse and fine net subsamples combined)
BOSM300_NAT_BIO	Biomass represented by native individuals within the cladoceran family Bosminidae in the 300-count subsamples (coarse and fine net subsamples combined)
BOSM300_NAT_NIND	Number of native individuals within the cladoceran family Bosminidae in the 300-count subsamples (coarse and fine net samples combined)
BOSM300_NAT_NTAX	Number of distinct native taxa within the cladoceran family Bosminidae in the 300-count subsamples (coarse and fine net samples combined)
BOSM300_NAT_PBIO	Percent of biomass represented by native individuals within the cladoceran family Bosminidae in the 300-count subsamples (coarse and fine net samples combined)
BOSM300_NAT_PIND	Percent of native individuals within the cladoceran family Bosminidae in the 300-count subsamples (coarse and fine net samples combined)
BOSM300_NAT_PTAX	Percent of distinct native taxa within the cladoceran family Bosminidae in the 300-count subsamples (coarse and fine net samples combined)
BOSM300_NIND	Number of individuals within the cladoceran family Bosminidae in the 300-count subsamples (coarse and fine net samples combined)
BOSM300_NTAX	Number of distinct taxa within the cladoceran family Bosminidae in the 300-count subsamples (coarse and fine net samples combined)
BOSM300_PBIO	Percent of biomass represented by individuals within the cladoceran family Bosminidae in the 300-count subsamples (coarse and fine net samples combined)
BOSM300_PIND	Percent of individuals within the cladoceran family Bosminidae in the 300-count subsamples (coarse and fine net samples combined)
BOSM300_PTAX	Percent of total distinct taxa that are within the cladoceran family Bosminidae in the 300-count subsamples (coarse and fine net samples combined)
CALAN_BIO	Biomass represented by individuals within the copepod order Calanoidea (coarse and fine net samples combined)
CALAN_DEN	Density (indiv./L) of individuals within the copepod order Calanoidea (coarse and fine net samples combined)

CALAN_NAT_BIO	Biomass represented by native individuals within the copepod order Calanoidea (coarse and fine net samples combined)
CALAN_NAT_DEN	Density (indiv./L) of native individuals within the copepod order Calanoidea (coarse and fine net samples combined)
CALAN_NAT_NIND	Number of native individuals within the order Calanoidea (coarse and fine net samples combined)
CALAN_NAT_NTAX	Number of distinct native taxa within the copepod order Calanoidea (coarse and fine net samples combined)
CALAN_NAT_PBIO	Percent of biomass represented by native individuals within the order Calanoidea (coarse and fine net samples combined)
CALAN_NAT_PDEN	Percent of density (indiv./L) of native individuals within the copepod order Calanoidea (coarse and fine net samples combined)
CALAN_NAT_PIND	Percent of native individuals within the order Calanoidea (coarse and fine net samples combined)
CALAN_NAT_PTAX	Percent of distinct native taxa within the order Calanoidea (coarse and fine net samples combined)
CALAN_NIND	Number of individuals within the order Calanoidea (coarse and fine net samples combined)
CALAN_NTAX	Number of distinct taxa within the copepod order Calanoidea (coarse and fine net samples combined)
CALAN_PBIO	Percent of biomass represented by individuals within the order Calanoidea (coarse and fine net samples combined)
CALAN_PDEN	Percent of density (indiv./L) of individuals within the copepod order Calanoidea (coarse and fine net samples combined)
CALAN_PIND	Percent of individuals within the order Calanoidea (coarse and fine net samples combined)
CALAN_PTAX	Percent of distinct taxa within the order Calanoidea (coarse and fine net samples combined)
CALAN300_BIO	Biomass represented by individuals within the copepod order Calanoidea based on 300-count subsamples (coarse and fine net subsamples combined)
CALAN300_NAT_BIO	Biomass represented by native individuals within the copepod order Calanoidea in the 300-count subsamples (coarse and fine net subsamples combined)
CALAN300_NAT_NIND	Number of native individuals within the order Calanoidea in the 300-count subsamples (coarse and fine net samples combined)
CALAN300_NAT_NTAX	Number of distinct native taxa within the copepod order Calanoidea in the 300-count subsamples (coarse and fine net samples combined)
CALAN300_NAT_PBIO	Percent of biomass represented by native individuals within the order Calanoidea in the 300-count subsamples (coarse and fine net samples combined)
CALAN300_NAT_PIND	Percent of native individuals within the order Calanoidea in the 300-count subsamples (coarse and fine net samples combined)
CALAN300_NAT_PTAX	Percent of distinct native taxa within the order Calanoidea in the 300-count subsamples (coarse and fine net samples combined)
CALAN300_NIND	Number of individuals within the order Calanoidea in the 300-count subsamples (coarse and fine net samples combined)

CALAN300_NTAX	Number of distinct taxa within the copepod order Calanoidea in the 300-count subsamples (coarse and fine net samples combined)
CALAN300_PBIO	Percent of biomass represented by individuals within the order Calanoidea in the 300-count subsamples (coarse and fine net samples combined)
CALAN300_PIND	Percent of individuals within the order Calanoidea in the 300-count subsamples (coarse and fine net samples combined)
CALAN300_PTAX	Percent of distinct taxa within the order Calanoidea in the 300-count subsamples (coarse and fine net samples combined)
CLAD_BIO	Biomass represented by individuals within the suborder Cladocera (coarse and fine net samples combined)
CLAD_DEN	Density (indiv./L) of individuals within the suborder Cladocera (coarse and fine net samples combined)
CLAD_HERB_BIO	Biomass represented by individuals within the suborder Cladocera that are herbivores
CLAD_HERB_DEN	Density (indiv./L) of individuals within the suborder Cladocera that are herbivores (coarse and fine net samples combined)
CLAD_HERB_NIND	Number of individuals within the suborder Cladocera that are herbivores (coarse and fine net samples combined)
CLAD_HERB_NTAX	Number of distinct cladoceran taxa that are herbivores (coarse and fine net samples combined)
CLAD_HERB_PBIO	Percent of biomass represented by individuals within the suborder Cladocera that are herbivores (coarse and fine net samples combined)
CLAD_HERB_PDEN	Percent of density (indiv./L) of individuals within the suborder Cladocera that are herbivores (coarse and fine net samples combined)
CLAD_HERB_PIND	Percent of individuals within the suborder Cladocera that are herbivores (coarse and fine net samples combined)
CLAD_HERB_PTAX	Percent of distinct taxa within the suborder Cladocera that are herbivores (coarse and fine net samples combined)
CLAD_HERB300_BIO	Biomass represented by individuals within the subclass Cladocera that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
CLAD_HERB300_NIND	Number of individuals within the suborder Cladocera that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
CLAD_HERB300_NTAX	Number of distinct cladoceran taxa that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
CLAD_HERB300_PBIO	Percent of biomass represented by individuals within the suborder Cladocera that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
CLAD_HERB300_PIND	Percent of individuals within the suborder Cladocera that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
CLAD_HERB300_PTAX	Percent of distinct taxa within the suborder Cladocera that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
CLAD_NAT_BIO	Biomass represented by native individuals within the suborder Cladocera (coarse and fine net samples combined)
CLAD_NAT_DEN	Density (indiv./L) of native individuals within the suborder Cladocera (coarse and fine net samples combined)

CLAD_NAT_NIND	Number of native individuals within the suborder Cladocera (coarse and fine net samples combined)
CLAD_NAT_NTAX	Number of distinct native taxa within the subclass Cladocera (coarse and fine net samples combined)
CLAD_NAT_PBIO	Percent of biomass represented by native individuals within the suborder Cladocera (coarse and fine net samples combined)
CLAD_NAT_PDEN	Percent of density (indiv./L) of native individuals within the suborder Cladocera (coarse and fine net samples combined)
CLAD_NAT_PIND	Percent of native individuals within the suborder Cladocera (coarse and fine net samples combined)
CLAD_NAT_PTAX	Percent of native taxa within the suborder Cladocera (coarse and fine net samples combined)
CLAD_NIND	Number of individuals within the suborder Cladocera (coarse and fine net samples combined)
CLAD_NTAX	Number of distinct taxa within the subclass Cladocera (coarse and fine net samples combined)
CLAD_OMNI_BIO	Biomass represented by individuals within the suborder Cladocera that are omnivores
CLAD_OMNI_DEN	Density (indiv./L) of individuals within the suborder Cladocera that are omnivores (coarse and fine net samples combined)
CLAD_OMNI_NIND	Number of individuals within the suborder Cladocera that are omnivores (coarse and fine net samples combined)
CLAD_OMNI_NTAX	Number of distinct cladoceran taxa that are omnivores (coarse and fine net samples combined)
CLAD_OMNI_PBIO	Percent of biomass represented by individuals within the suborder Cladocera that are omnivores (coarse and fine net samples combined)
CLAD_OMNI_PDEN	Percent of density (indiv./L) of individuals within the suborder Cladocera that are omnivores (coarse and fine net samples combined)
CLAD_OMNI_PIND	Percent of individuals within the suborder Cladocera that are omnivores (coarse and fine net samples combined)
CLAD_OMNI_PTAX	Percent of distinct taxa within the suborder Cladocera that are omnivores (coarse and fine net samples combined)
CLAD_OMNI300_BIO	Biomass represented by individuals within the subclass Cladocera that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
CLAD_OMNI300_NIND	Number of individuals within the suborder Cladocera that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
CLAD_OMNI300_NTAX	Number of distinct cladoceran taxa that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
CLAD_OMNI300_PBIO	Percent of biomass represented by individuals within the suborder Cladocera that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
CLAD_OMNI300_PIND	Percent of individuals within the suborder Cladocera that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
CLAD_OMNI300_PTAX	Percent of distinct taxa within the suborder Cladocera that are omnivores in the 300-count subsamples (coarse and fine net samples combined)

CLAD_PBIO	Percent of biomass represented by individuals within the suborder Cladocera (coarse and fine net samples combined)
CLAD_PDEN	Percent of density (indiv./L) of individuals within the suborder Cladocera (coarse and fine net samples combined)
CLAD_PIND	Percent of individuals within the suborder Cladocera (coarse and fine net samples combined)
CLAD_PRED_BIO	Biomass represented by individuals within the suborder Cladocera that are predators
CLAD_PRED_DEN	Density (indiv.L) of individuals within the suborder Cladocera that are predators (coarse and fine net samples combined)
CLAD_PRED_NIND	Number of individuals within the suborder Cladocera that are predators (coarse and fine net samples combined)
CLAD_PRED_NTAX	Number of distinct cladoceran taxa that are predators (coarse and fine net samples combined)
CLAD_PRED_PBIO	Percent of biomass represented by individuals within the suborder Cladocera that are predators (coarse and fine net samples combined)
CLAD_PRED_PDEN	Percent of density (indiv.L) of individuals within the suborder Cladocera that are predators (coarse and fine net samples combined)
CLAD_PRED_PIND	Percent of individuals within the suborder Cladocera that are predators (coarse and fine net samples combined)
CLAD_PRED_PTAX	Percent of distinct taxa within the suborder Cladocera that are predators (coarse and fine net samples combined)
CLAD_PRED300_BIO	Biomass represented by individuals within the subclass Cladocera that are predators in the 300-count subsamples (coarse and fine net samples combined)
CLAD_PRED300_NIND	Number of individuals within the suborder Cladocera that are predators in the 300-count subsamples (coarse and fine net samples combined)
CLAD_PRED300_NTAX	Number of distinct cladoceran taxa that are predators in the 300-count subsamples (coarse and fine net samples combined)
CLAD_PRED300_PBIO	Percent of biomass represented by individuals within the suborder Cladocera that are predators in the 300-count subsamples (coarse and fine net samples combined)
CLAD_PRED300_PIND	Percent of individuals within the suborder Cladocera that are predators in the 300-count subsamples (coarse and fine net samples combined)
CLAD_PRED300_PTAX	Percent of distinct taxa within the suborder Cladocera that are predators in the 300-count subsamples (coarse and fine net samples combined)
CLAD_PTAX	Percent of distinct taxa within the suborder Cladocera (coarse and fine net samples combined)
CLAD300_BIO	Biomass represented by individuals within the suborder Cladocera in 300-count subsamples (coarse and fine net subsamples combined)
CLAD300_NAT_BIO	Biomass represented by native individuals within the suborder Cladocera in the 300-count subsamples (coarse and fine net subsamples combined)
CLAD300_NAT_NIND	Number of native individuals within the suborder Cladocera in the 300-count subsamples (coarse and fine net samples combined)
CLAD300_NAT_NTAX	Number of distinct native taxa within the suborder Cladocera in the 300-count subsamples (coarse and fine net samples combined)

CLAD300_NAT_PBIO	Percent of biomass represented by native individuals within the suborder Cladocera in the 300-count subsamples (coarse and fine net samples combined)
CLAD300_NAT_PIND	Percent of native individuals within the suborder Cladocera in the 300-count subsamples (coarse and fine net samples combined)
CLAD300_NAT_PTAX	Percent of native taxa within the suborder Cladocera in the 300-count subsamples (coarse and fine net samples combined)
CLAD300_NIND	Number of individuals within the suborder Cladocera in the 300-count subsamples (coarse and fine net samples combined)
CLAD300_NTAX	Number of distinct taxa within the suborder Cladocera in the 300-count subsamples (coarse and fine net samples combined)
CLAD300_PBIO	Percent of biomass represented by individuals within the suborder Cladocera in the 300-count subsamples (coarse and fine net samples combined)
CLAD300_PIND	Percent of individuals within the suborder Cladocera in the 300-count subsamples (coarse and fine net samples combined)
CLAD300_PTAX	Percent of distinct taxa within the suborder Cladocera in the 300-count subsamples (coarse and fine net samples combined)
COARSE_BIO	Biomass represented by individuals of larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)
COARSE_DEN	Density (indiv./L) of individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)
COARSE_NAT_BIO	Biomass represented by individuals of native larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)
COARSE_NAT_DEN	Density (indiv./L) of native individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)
COARSE_NAT_NIND	Number of native individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)
COARSE_NAT_NTAX	Number of distinct larger-sized native taxa (NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)
COARSE_NAT_PBIO	Percent of biomass represented by native individuals of larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)
COARSE_NAT_PDEN	Percent of density (indiv./L) of native individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)
COARSE_NAT_PIND	Percent of native individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)
COARSE_NAT_PTAX	Percent of distinct larger-sized native taxa (NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)
COARSE_NIND	Number of individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)
COARSE_NTAX	Number of distinct larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)
COARSE_PBIO	Percent of biomass represented by individuals of larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)
COARSE_PDEN	Percent of density (indiv./L) of individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)
COARSE_PIND	Percent of individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)

COARSE_PTAX	Percent of distinct larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)
COARSE300_BIO	Biomass represented by individuals of larger-sized taxa (NET_SIZECLS_NEW=COARSE) in the 300-count subsamples (coarse and fine net subsamples combined)
COARSE300_NAT_BIO	Biomass represented by native individuals of larger-sized taxa (NET_SIZECLS_NEW=COARSE) in the 300-count subsamples (coarse and fine net subsamples combined)
COARSE300_NAT_NIND	Number of native individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE) in the 300-count subsamples (coarse and fine net samples combined)
COARSE300_NAT_NTAX	Number of distinct native larger-sized taxa (NET_SIZECLS_NEW=COARSE) in the 300-count subsamples (coarse and fine net samples combined)
COARSE300_NAT_PBIO	Percent of biomass represented by native individuals of larger-sized taxa (NET_SIZECLS_NEW=COARSE) in the 300-count subsamples (coarse and fine net samples combined)
COARSE300_NAT_PIND	Percent of native individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE) in the 300-count subsamples (coarse and fine net samples combined)
COARSE300_NAT_PTAX	Percent of distinct larger-sized native taxa (NET_SIZECLS_NEW=COARSE) in the 300-count subsamples (coarse and fine net samples combined)
COARSE300_NIND	Number of individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE) in the 300-count subsamples (coarse and fine net samples combined)
COARSE300_NTAX	Number of distinct larger-sized taxa (NET_SIZECLS_NEW=COARSE) in the 300-count subsamples (coarse and fine net samples combined)
COARSE300_PBIO	Percent of biomass represented by individuals of larger-sized taxa (NET_SIZECLS_NEW=COARSE) in the 300-count subsamples (coarse and fine net samples combined)
COARSE300_PIND	Percent of individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE) in the 300-count subsamples (coarse and fine net samples combined)
COARSE300_PTAX	Percent of distinct larger-sized taxa (NET_SIZECLS_NEW=COARSE) in the 300-count subsamples (coarse and fine net samples combined)
COLLO_BIO	Biomass represented by individuals within the rotifer order Collothecaceae (coarse and fine net samples combined)
COLLO_DEN	Density (indiv./L) of individuals within the rotifer order Collothecaceae (coarse and fine net samples combined)
COLLO_NIND	Number of individuals within the rotifer order Collothecaceae (coarse and fine net samples combined)
COLLO_NTAX	Number of distinct taxa within the rotifer order Collothecaceae (coarse and fine net samples combined)
COLLO_PBIO	Percent of biomass represented by individuals within the rotifer order Collothecaceae (coarse and fine net samples combined)
COLLO_PDEN	Percent of density (indiv./L) of individuals within the rotifer order Collothecaceae (coarse and fine net samples combined)
COLLO_PIND	Percent of individuals within the rotifer order Collothecaceae (coarse and fine net samples combined)



COLLO_PTAX	Percent of distinct taxa within the rotifer order Collotheceae (coarse and fine net samples combined)
COLLO300_BIO	Biomass represented by individuals within the rotifer order Collotheceae in the 300-count subsamples (coarse and fine net subsamples combined)
COLLO300_NIND	Number of individuals within the rotifer order Collotheceae in the 300-count subsamples (coarse and fine net samples combined)
COLLO300_NTAX	Number of distinct taxa within the rotifer order Collotheceae in the 300-count subsamples (coarse and fine net samples combined)
COLLO300_PBIO	Percent of biomass represented by individuals within the rotifer order Collotheceae in the 300-count subsamples (coarse and fine net samples combined)
COLLO300_PIND	Percent of individuals within the rotifer order Collotheceae in the 300-count subsamples (coarse and fine net samples combined)
COLLO300_PTAX	Percent of distinct taxa within the rotifer order Collotheceae in the 300-count subsamples (coarse and fine net samples combined)
COPE_BIO	Biomass represented by individuals within the subclass Copepoda (coarse and fine net samples combined)
COPE_DEN	Density (indiv./L) of individuals within the subclass Copepoda (coarse and fine net samples combined)
COPE_HERB_BIO	Biomass represented by individuals within the subclass Copepoda that are herbivores
COPE_HERB_DEN	Density (indiv.L) of individuals within the subclass Copepoda that are herbivores (coarse and fine net samples combined)
COPE_HERB_NIND	Number of individuals within the subclass Copepoda that are herbivores (coarse and fine net samples combined)
COPE_HERB_NTAX	Number of distinct copepod taxa that are herbivores (coarse and fine net samples combined)
COPE_HERB_PBIO	Percent of biomass represented by individuals within the subclass Copepoda that are herbivores (coarse and fine net samples combined)
COPE_HERB_PDEN	Percent of density (indiv.L) of individuals within the subclass Copepoda that are herbivores (coarse and fine net samples combined)
COPE_HERB_PIND	Percent of individuals within the subclass Copepoda that are herbivores (coarse and fine net samples combined)
COPE_HERB_PTAX	Percent of distinct taxa within the subclass Copepoda that are herbivores (coarse and fine net samples combined)
COPE_HERB300_BIO	Biomass represented by individuals within the subclass Copepoda that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
COPE_HERB300_NIND	Number of individuals within the subclass Copepoda that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
COPE_HERB300_NTAX	Number of distinct copepod taxa that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
COPE_HERB300_PBIO	Percent of biomass represented by individuals within the subclass Copepoda that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
COPE_HERB300_PIND	Percent of individuals within the subclass Copepoda that are herbivores in the 300-count subsamples (coarse and fine net samples combined)

COPE_HERB300_PTAX	Percent of distinct taxa within the subclass Copepoda that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
COPE_NAT_BIO	Biomass represented by native individuals within the subclass Copepoda (coarse and fine net samples combined)
COPE_NAT_DEN	Density (indiv./L) of native individuals within the subclass Copepoda (coarse and fine net samples combined)
COPE_NAT_NIND	Number of native individuals within the subclass Copepoda (coarse and fine net samples combined)
COPE_NAT_NTAX	Number of distinct native taxa within the subclass Copepoda (coarse and fine net samples combined)
COPE_NAT_PBIO	Percent of biomass represented by native individuals within the subclass Copepoda (coarse and fine net samples combined)
COPE_NAT_PDEN	Percent of density (indiv./L) of native individuals within the subclass Copepoda (coarse and fine net samples combined)
COPE_NAT_PIND	Percent of native individuals within the subclass Copepoda (coarse and fine net samples combined)
COPE_NAT_PTAX	Percent of distinct native taxa within the subclass Copepoda (coarse and fine net samples combined)
COPE_NIND	Number of individuals within the subclass Copepoda (coarse and fine net samples combined)
COPE_NTAX	Number of distinct taxa within the subclass Copepoda (coarse and fine net samples combined)
COPE_OMNI_BIO	Biomass represented by individuals within the subclass Copepoda that are omnivores
COPE_OMNI_DEN	Density (indiv.L) of individuals within the subclass Copepoda that are omnivores (coarse and fine net samples combined)
COPE_OMNI_NIND	Number of individuals within the subclass Copepoda that are omnivores (coarse and fine net samples combined)
COPE_OMNI_NTAX	Number of distinct copepod taxa that are omnivores (coarse and fine net samples combined)
COPE_OMNI_PBIO	Percent of biomass represented by individuals within the subclass Copepoda that are omnivores (coarse and fine net samples combined)
COPE_OMNI_PDEN	Percent of density (indiv.L) of individuals within the subclass Copepoda that are omnivores (coarse and fine net samples combined)
COPE_OMNI_PIND	Percent of individuals within the subclass Copepoda that are omnivores (coarse and fine net samples combined)
COPE_OMNI_PTAX	Percent of distinct taxa within the subclass Copepoda that are omnivores (coarse and fine net samples combined)
COPE_OMNI300_BIO	Biomass represented by individuals within the subclass Copepoda that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
COPE_OMNI300_NIND	Number of individuals within the subclass Copepoda that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
COPE_OMNI300_NTAX	Number of distinct copepod taxa that are omnivores in the 300-count subsamples (coarse and fine net samples combined)

COPE_OMNI300_PBIO	Percent of biomass represented by individuals within the subclass Copepoda that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
COPE_OMNI300_PIND	Percent of individuals within the subclass Copepoda that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
COPE_OMNI300_PTAX	Percent of distinct taxa within the subclass Copepoda that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
COPE_PBIO	Percent of biomass represented by individuals within the subclass Copepoda (coarse and fine net samples combined)
COPE_PDEN	Percent of density (indiv./L) of individuals within the subclass Copepoda (coarse and fine net samples combined)
COPE_PIND	Percent of individuals within the subclass Copepoda (coarse and fine net samples combined)
COPE_PRED_BIO	Biomass represented by individuals within the subclass Copepoda that are predators
COPE_PRED_DEN	Density (indiv.L) of individuals within the subclass Copepoda that are predators (coarse and fine net samples combined)
COPE_PRED_NIND	Number of individuals within the subclass Copepoda that are predators (coarse and fine net samples combined)
COPE_PRED_NTAX	Number of distinct copepod taxa that are predators (coarse and fine net samples combined)
COPE_PRED_PBIO	Percent of biomass represented by individuals within the subclass Copepoda that are predators (coarse and fine net samples combined)
COPE_PRED_PDEN	Percent of density (indiv.L) of individuals within the subclass Copepoda that are predators (coarse and fine net samples combined)
COPE_PRED_PIND	Percent of individuals within the subclass Copepoda that are predators (coarse and fine net samples combined)
COPE_PRED_PTAX	Percent of distinct taxa within the subclass Copepoda that are predators (coarse and fine net samples combined)
COPE_PRED300_BIO	Biomass represented by individuals within the subclass Copepoda that are predators in the 300-count subsamples (coarse and fine net samples combined)
COPE_PRED300_NIND	Number of individuals within the subclass Copepoda that are predators in the 300-count subsamples (coarse and fine net samples combined)
COPE_PRED300_NTAX	Number of distinct copepod taxa that are predators in the 300-count subsamples (coarse and fine net samples combined)
COPE_PRED300_PBIO	Percent of biomass represented by individuals within the subclass Copepoda that are predators in the 300-count subsamples (coarse and fine net samples combined)
COPE_PRED300_PIND	Percent of individuals within the subclass Copepoda that are predators in the 300-count subsamples (coarse and fine net samples combined)
COPE_PRED300_PTAX	Percent of distinct taxa within the subclass Copepoda that are predators in the 300-count subsamples (coarse and fine net samples combined)
COPE_PTAX	Percent of distinct taxa within the subclass Copepoda (coarse and fine net samples combined)

COPE_RATIO_300_BIO	Ratio of Calanoid to (Cladocera+Cyclopoids) based on biomass in 300-count subsamples (coarse and fine net samples combined). Adapted from Kane et al. (2009) Lake Erie plankton IBI. Calculated as $CALANOID\_BIO / (CLAD\_BIO + CYCLOPOID\_BIO)$
COPE_RATIO_300_NIND	Ratio of Calanoid to (Cladocera+Cyclopoids) based on the number of individuals in 300-count subsamples (coarse and fine net samples combined). Adapted from Kane et al. (2009) Lake Erie plankton IBI. Calculated as $CALANOID\_NIND / (CLAD\_NIND + CYCLOPOID\_NIND)$
COPE_RATIO_BIO	Ratio of Calanoid to (Cladocera+Cyclopoids) based on biomass (coarse and fine net samples combined). Adapted from Kane et al. (2009) Lake Erie plankton IBI. Calculated as $CALANOID\_BIO / (CLAD\_BIO + CYCLOPOID\_BIO)$
COPE_RATIO_DEN	Ratio of Calanoid to (Cladocera+Cyclopoids) based on density (indiv./L; coarse and fine net samples combined). Adapted from Kane et al. (2009) Lake Erie plankton IBI. Calculated as $CALANOID\_DEN / (CLAD\_DEN + CYCLOPOID\_DEN)$
COPE_RATIO_NIND	Ratio of Calanoid to (Cladocera+Cyclopoids) based on the number of individuals (coarse and fine net samples combined). Adapted from Kane et al. (2009) Lake Erie plankton IBI. Calculated as $CALANOID\_NIND / (CLAD\_NIND + CYCLOPOID\_NIND)$
COPE300_BIO	Biomass represented by individuals within the subclass Copepoda in the 300-count subsamples (coarse and fine net subsamples combined)
COPE300_NAT_BIO	Biomass represented by native individuals within the subclass Copepoda in the 300-count subsamples (coarse and fine net subsamples combined)
COPE300_NAT_NIND	Number of native individuals within the subclass Copepoda in the 300-count subsamples (coarse and fine net samples combined)
COPE300_NAT_NTAX	Number of distinct native taxa within the subclass Copepoda in the 300-count subsamples (coarse and fine net samples combined)
COPE300_NAT_PBIO	Percent of biomass represented by native individuals within the subclass Copepoda in the 300-count subsamples (coarse and fine net samples combined)
COPE300_NAT_PIND	Percent of native individuals within the subclass Copepoda in the 300-count subsamples (coarse and fine net samples combined)
COPE300_NAT_PTAX	Percent of distinct native taxa within the subclass Copepoda in the 300-count subsamples (coarse and fine net samples combined)
COPE300_NIND	Number of individuals within the subclass Copepoda in the 300-count subsamples (coarse and fine net samples combined)
COPE300_NTAX	Number of distinct taxa within the subclass Copepoda in the 300-count subsamples (coarse and fine net samples combined)
COPE300_PBIO	Percent of biomass represented by individuals within the subclass Copepoda in the 300-count subsamples (coarse and fine net samples combined)
COPE300_PIND	Percent of individuals within the subclass Copepoda in the 300-count subsamples (coarse and fine net samples combined)
COPE300_PTAX	Percent of distinct taxa within the subclass Copepoda in the 300-count subsamples (coarse and fine net samples combined)
CYCLOP_BIO	Biomass represented by native individuals within the copepod order Cyclopoidea (coarse and fine net samples combined)
CYCLOP_DEN	Density (indiv./L) of native individuals within the copepod order Cyclopoidea (coarse and fine net samples combined)

CYCLOP_NIND	Number of individuals within the order Cyclopoidea (coarse and fine net samples combined)
CYCLOP_NTAX	Number of distinct taxa within the copepod order Cyclopoidea (coarse and fine net samples combined)
CYCLOP_PBIO	Percent of biomass represented by individuals within the order Cyclopoidea (coarse and fine net samples combined)
CYCLOP_PDEN	Percent of density (indiv./L) of native individuals within the copepod order Cyclopoidea (coarse and fine net samples combined)
CYCLOP_PIND	Percent of individuals within the order Cyclopoidea (coarse and fine net samples combined)
CYCLOP_PTAX	Percent of distinct taxa within the order Cyclopoidea (coarse and fine net samples combined)
CYCLOP300_BIO	Biomass represented by individuals within the copepod order Cyclopoidea in the 300-count subsamples (coarse and fine net subsamples combined)
CYCLOP300_NIND	Number of individuals within the order Cyclopoidea in the 300-count subsamples (coarse and fine net samples combined)
CYCLOP300_NTAX	Number of distinct taxa within the copepod order Cyclopoidea in the 300-count subsamples (coarse and fine net samples combined)
CYCLOP300_PBIO	Percent of biomass represented by individuals within the order Cyclopoidea in the 300-count subsamples (coarse and fine net samples combined)
CYCLOP300_PIND	Percent of individuals within the order Cyclopoidea in the 300-count subsamples (coarse and fine net samples combined)
CYCLOP300_PTAX	Percent of distinct taxa within the order Cyclopoidea in the 300-count subsamples (coarse and fine net samples combined)
DAPHNIID_BIO	Biomass represented by individuals within the family Daphniidae (coarse and fine net samples combined)
DAPHNIID_DEN	Density (indiv./L) of individuals within the cladoceran family Daphniidae (coarse and fine net samples combined)
DAPHNIID_NAT_BIO	Biomass represented by native individuals within the family Daphniidae (coarse and fine net samples combined)
DAPHNIID_NAT_DEN	Density (indiv./L) of native individuals within the cladoceran family Daphniidae (coarse and fine net samples combined)
DAPHNIID_NAT_NIND	Number of native individuals within the cladoceran family Daphniidae (coarse and fine net samples combined)
DAPHNIID_NAT_NTAX	Number of distinct native taxa within the cladoceran family Daphniidae (coarse and fine net samples combined)
DAPHNIID_NAT_PBIO	Percent of biomass represented by native individuals within the cladoceran family Daphniidae (coarse and fine net samples combined)
DAPHNIID_NAT_PDEN	Percent of density (indiv./L) of native individuals within the cladoceran family Daphniidae (coarse and fine net samples combined)
DAPHNIID_NAT_PIND	Percent of native individuals within the cladoceran family Daphniidae (coarse and fine net samples combined)
DAPHNIID_NAT_PTAX	Percent of distinct native taxa that are within the cladoceran family Daphniidae (coarse and fine net samples combined)
DAPHNIID_NIND	Number of individuals within the cladoceran family Daphniidae (coarse and fine net samples combined)

DAPHNIID_NTAX	Number of distinct taxa within the cladoceran family Daphniidae (coarse and fine net samples combined)
DAPHNIID_PBIO	Percent of biomass represented by individuals within the cladoceran family Daphniidae (coarse and fine net samples combined)
DAPHNIID_PDEN	Percent of density (indiv./L) of individuals within the cladoceran family Daphniidae (coarse and fine net samples combined)
DAPHNIID_PIND	Percent of individuals within the cladoceran family Daphniidae (coarse and fine net samples combined)
DAPHNIID_PTAX	Percent of distinct taxa that are within the cladoceran family Daphniidae (coarse and fine net samples combined)
DAPHNIID300_BIO	Biomass represented by individuals within the cladoceran family Daphniidae in the 300-count subsamples (coarse and fine net subsamples combined)
DAPHNIID300_NAT_BIO	Biomass represented by native individuals within the cladoceran family Daphniidae in the 300-count subsamples (coarse and fine net subsamples combined)
DAPHNIID300_NAT_NIND	Number of native individuals within the cladoceran family Daphniidae in the 300-count subsamples (coarse and fine net samples combined)
DAPHNIID300_NAT_NTAX	Number of distinct native taxa within the cladoceran family Daphniidae in the 300-count subsamples (coarse and fine net samples combined)
DAPHNIID300_NAT_PBIO	Percent of biomass represented by native individuals within the cladoceran family Daphniidae in the 300-count subsamples (coarse and fine net samples combined)
DAPHNIID300_NAT_PIND	Percent of native individuals within the cladoceran family Daphniidae in the 300-count subsamples (coarse and fine net samples combined)
DAPHNIID300_NAT_PTAX	Percent of distinct native taxa that are within the cladoceran family Daphniidae in the 300-count subsamples (coarse and fine net samples combined)
DAPHNIID300_NIND	Number of individuals within the cladoceran family Daphniidae in the 300-count subsamples (coarse and fine net samples combined)
DAPHNIID300_NTAX	Number of distinct taxa within the cladoceran family Daphniidae in the 300-count subsamples (coarse and fine net samples combined)
DAPHNIID300_PBIO	Percent of biomass represented by individuals within the cladoceran family Daphniidae in the 300-count subsamples (coarse and fine net samples combined)
DAPHNIID300_PIND	Percent of individuals within the cladoceran family Daphniidae in the 300-count subsamples (coarse and fine net samples combined)
DAPHNIID300_PTAX	Percent of distinct taxa that are within the cladoceran family Daphniidae in the 300-count subsamples (coarse and fine net samples combined)
DOM1_300_CLAD_PBIO	Percent of biomass within the most abundant cladoceran taxon in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM1_300_CLAD_PIND	Percent of individuals within the most abundant cladoceran taxon in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM1_300_COPE_PBIO	Percent of biomass within the most abundant copepod taxon in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM1_300_COPE_PIND	Percent of individuals within the most abundant copepod taxon in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM1_300_PBIO	Percent of biomass within the most abundant taxon in the 300-count subsamples (coarse and fine-mesh net samples combined)

DOM1_300_PIND	Percent of individuals within the most abundant taxon in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM1_300_ROT_PBIO	Percent of biomass within the most abundant rotifer taxon in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM1_300_ROT_PIND	Percent of individuals within the most abundant rotifer taxon in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM1_CLAD_PBIO	Percent of biomass within the most abundant cladoceran taxon (coarse and fine-mesh net samples combined)
DOM1_CLAD_PDEN	Percent of density (indiv./L) within the most abundant cladoceran taxon (coarse and fine-mesh net samples combined)
DOM1_CLAD_PIND	Percent of individuals within the most abundant cladoceran taxon (coarse and fine-mesh net samples combined)
DOM1_COPE_PBIO	Percent of biomass within the most abundant copepod taxon (coarse and fine-mesh net samples combined)
DOM1_COPE_PDEN	Percent of density (indiv./L) within the most abundant copepod taxon (coarse and fine-mesh net samples combined)
DOM1_COPE_PIND	Percent of individuals within the most abundant copepod taxon (coarse and fine-mesh net samples combined)
DOM1_PBIO	Percent of biomass within the most abundant taxon (coarse and fine-mesh net samples combined)
DOM1_PDEN	Percent of density (indiv./L) within the most abundant taxon (coarse and fine-mesh net samples combined)
DOM1_PIND	Percent of individuals within the most abundant taxon (coarse and fine-mesh net samples combined)
DOM1_ROT_PBIO	Percent of biomass within the most abundant rotifer taxon (coarse and fine-mesh net samples combined)
DOM1_ROT_PDEN	Percent of density (indiv./L) within the most abundant rotifer taxon (coarse and fine-mesh net samples combined)
DOM1_ROT_PIND	Percent of individuals within the most abundant rotifer taxon (coarse and fine-mesh net samples combined)
DOM3_300_CLAD_PBIO	Percent of biomass within the 3 most abundant cladoceran taxa in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM3_300_CLAD_PIND	Percent of individuals within the 3 most abundant cladoceran taxa in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM3_300_COPE_PBIO	Percent of biomass within the 3 most abundant copepod taxa in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM3_300_COPE_PIND	Percent of individuals within the 3 most abundant copepod taxa in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM3_300_PBIO	Percent of biomass within the 3 most abundant taxa in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM3_300_PIND	Percent of individuals within the 3 most abundant taxa in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM3_300_ROT_PBIO	Percent of biomass within the 3 most abundant rotifer taxa in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM3_300_ROT_PIND	Percent of individuals within the 3 most abundant rotifer taxa in the 300-count subsamples (coarse and fine-mesh net samples combined)

DOM3_CLAD_PBIO	Percent of biomass within the 3 most abundant cladoceran taxa (coarse and fine-mesh net samples combined)
DOM3_CLAD_PDEN	Percent of density (indiv./L) within the 3 most abundant cladoceran taxa (coarse and fine-mesh net samples combined)
DOM3_CLAD_PIND	Percent of individuals within the 3 most abundant cladoceran taxa (coarse and fine-mesh net samples combined)
DOM3_COPE_PBIO	Percent of biomass within the 3 most abundant copepod taxa (coarse and fine-mesh net samples combined)
DOM3_COPE_PDEN	Percent of density (indiv./L) within the 3 most abundant copepod taxa (coarse and fine-mesh net samples combined)
DOM3_COPE_PIND	Percent of individuals within the 3 most abundant copepod taxa (coarse and fine-mesh net samples combined)
DOM3_PBIO	Percent of biomass within the 3 most abundant taxa (coarse and fine-mesh net samples combined)
DOM3_PDEN	Percent of density (indiv./L) within the 3 most abundant taxa (coarse and fine-mesh net samples combined)
DOM3_PIND	Percent of individuals within the 3 most abundant taxa (coarse and fine-mesh net samples combined)
DOM3_ROT_PBIO	Percent of biomass within the 3 most abundant rotifer taxa (coarse and fine-mesh net samples combined)
DOM3_ROT_PDEN	Percent of density (indiv./L) within the 3 most abundant rotifer taxa (coarse and fine-mesh net samples combined)
DOM3_ROT_PIND	Percent of individuals within the 3 most abundant rotifer taxa (coarse and fine-mesh net samples combined)
DOM5_300_CLAD_PBIO	Percent of biomass within the 5 most abundant cladoceran taxa in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM5_300_CLAD_PIND	Percent of individuals within the 5 most abundant cladoceran taxa in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM5_300_COPE_PBIO	Percent of biomass within the 5 most abundant copepod taxa in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM5_300_COPE_PIND	Percent of individuals within the 5 most abundant copepod taxa in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM5_300_PBIO	Percent of biomass within the 5 most abundant taxa in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM5_300_PIND	Percent of individuals within the 5 most abundant taxa in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM5_300_ROT_PBIO	Percent of biomass within the 5 most abundant rotifer taxa in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM5_300_ROT_PIND	Percent of individuals within the 5 most abundant rotifer taxa in the 300-count subsamples (coarse and fine-mesh net samples combined)
DOM5_CLAD_PBIO	Percent of biomass within the 5 most abundant cladoceran taxa (coarse and fine-mesh net samples combined)
DOM5_CLAD_PDEN	Percent of density (indiv./L) within the 5 most abundant cladoceran taxa (coarse and fine-mesh net samples combined)
DOM5_CLAD_PIND	Percent of individuals within the 5 most abundant cladoceran taxa (coarse and fine-mesh net samples combined)



DOM5_COPE_PBIO	Percent of biomass within the 5 most abundant copepod taxa (coarse and fine-mesh net samples combined)
DOM5_COPE_PDEN	Percent of density (indiv./L) within the 5 most abundant copepod taxa (coarse and fine-mesh net samples combined)
DOM5_COPE_PIND	Percent of individuals within the 5 most abundant copepod taxa (coarse and fine-mesh net samples combined)
DOM5_PBIO	Percent of biomass within the 5 most abundant taxa (coarse and fine-mesh net samples combined)
DOM5_PDEN	Percent of density (indiv./L) within the 5 most abundant taxa (coarse and fine-mesh net samples combined)
DOM5_PIND	Percent of individuals within the 5 most abundant taxa (coarse and fine-mesh net samples combined)
DOM5_ROT_PBIO	Percent of biomass within the 5 most abundant rotifer taxa (coarse and fine-mesh net samples combined)
DOM5_ROT_PDEN	Percent of density (indiv./L) within the 5 most abundant rotifer taxa (coarse and fine-mesh net samples combined)
DOM5_ROT_PIND	Percent of individuals within the 5 most abundant rotifer taxa (coarse and fine-mesh net samples combined)
EVEN_CLAD	Evenness based on the number of cladoceran individuals (coarse and fine net samples combined). Calculated as $HPRIME\_ROT/Log(S)$ where Log is the natural logarithm
EVEN_CLAD300	Evenness based on the number of cladoceran individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as $HPRIME\_ROT/Log(S)$ where Log is the natural logarithm
EVEN_COPE	Evenness based on the number of copepod individuals (coarse and fine net samples combined). Calculated as $HPRIME\_ROT/Log(S)$ where Log is the natural logarithm
EVEN_COPE300	Evenness based on the number of copepod individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as $HPRIME\_ROT/Log(S)$ where Log is the natural logarithm
EVEN_NIND	Evenness based on the number of individuals (coarse and fine net samples combined). Calculated as $HPRIME\_ROT/Log(S)$ where Log is the natural logarithm
EVEN_ROT	Evenness based on the number of rotifer individuals (coarse and fine net samples combined). Calculated as $HPRIME\_ROT/Log(S)$ where Log is the natural logarithm
EVEN_ROT300	Evenness based on the number of rotifer individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as $HPRIME\_ROT/Log(S)$ where Log is the natural logarithm
EVEN300_NIND	Evenness based on the number of individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as $HPRIME\_ROT/Log(S)$ where Log is the natural logarithm
FAM_NAT_NTAX	Number of families represented by distinct native taxa (coarse and fine net samples combined)
FAM_NTAX	Number of families represented by distinct taxa (coarse and fine net samples combined)
FAM300_NAT_NTAX	Number of native families represented in 300 count subsamples (coarse and fine net samples combined)

FAM300_NTAX	Number of families represented in 300 count subsamples (coarse and fine net samples combined)
FINE_BIO	Biomass represented by individuals of smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
FINE_DEN	Density (indiv./L) of individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
FINE_NAT_BIO	Biomass represented by native individuals of smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
FINE_NAT_DEN	Density (indiv./L) of native individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
FINE_NAT_NIND	Number of native individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
FINE_NAT_NTAX	Number of distinct smaller-sized native taxa (NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
FINE_NAT_PBIO	Percent of biomass represented by native individuals of smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
FINE_NAT_PDEN	Percent of density (indiv./L) of native individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
FINE_NAT_PIND	Percent of native individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
FINE_NAT_PTAX	Percent of distinct native smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
FINE_NIND	Number of individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
FINE_NTAX	Number of distinct smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
FINE_PBIO	Percent of biomass represented by individuals of smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
FINE_PDEN	Percent of density (indiv./L) of individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
FINE_PIND	Percent of individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
FINE_PTAX	Percent of distinct smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
FINE300_BIO	Biomass represented by individuals of smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-count subsamples (coarse and fine net subsamples combined)
FINE300_NAT_BIO	Biomass represented by native individuals of smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-count subsamples (coarse and fine net subsamples combined)
FINE300_NAT_NIND	Number of native individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-count subsamples (coarse and fine net samples combined)
FINE300_NAT_NTAX	Number of distinct native smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-count subsamples (coarse and fine net samples combined)

FINE300_NAT_PBIO	Percent of biomass represented by native individuals of smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-count subsamples (coarse and fine net samples combined)
FINE300_NAT_PIND	Percent of native individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-count subsamples (coarse and fine net samples combined)
FINE300_NAT_PTAX	Percent of distinct native smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-count subsamples (coarse and fine net samples combined)
FINE300_NIND	Number of individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-count subsamples (coarse and fine net samples combined)
FINE300_NTAX	Number of distinct smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-count subsamples (coarse and fine net samples combined)
FINE300_PBIO	Percent of biomass represented by individuals of smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-count subsamples (coarse and fine net samples combined)
FINE300_PIND	Percent of individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-count subsamples (coarse and fine net samples combined)
FINE300_PTAX	Percent of distinct smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-count subsamples (coarse and fine net samples combined)
FLOS_BIO	Biomass represented by individuals within the rotifer order Flosculariaceae (coarse and fine net samples combined)
FLOS_DEN	Density (indiv./L) of individuals within the rotifer order Flosculariaceae (coarse and fine net samples combined)
FLOS_NIND	Number of individuals within the rotifer order Flosculariaceae (coarse and fine net samples combined)
FLOS_NTAX	Number of distinct taxa within the rotifer order Flosculariaceae (coarse and fine net samples combined)
FLOS_PBIO	Percent of biomass represented by individuals within the rotifer order Flosculariaceae (coarse and fine net samples combined)
FLOS_PDEN	Percent of density (indiv./L) of individuals within the rotifer order Flosculariaceae (coarse and fine net samples combined)
FLOS_PIND	Percent of individuals within the rotifer order Flosculariaceae (coarse and fine net samples combined)
FLOS_PTAX	Percent of distinct taxa within the rotifer order Flosculariaceae (coarse and fine net samples combined)
FLOS300_BIO	Biomass represented by individuals within the rotifer order Flosculariaceae in the 300-count subsamples (coarse and fine net subsamples combined)
FLOS300_NIND	Number of individuals within the rotifer order Flosculariaceae in the 300-count subsamples (coarse and fine net samples combined)
FLOS300_NTAX	Number of distinct taxa within the rotifer order Flosculariaceae in the 300-count subsamples (coarse and fine net samples combined)
FLOS300_PBIO	Percent of biomass represented by individuals within the rotifer order Flosculariaceae in the 300-count subsamples (coarse and fine net samples combined)
FLOS300_PIND	Percent of individuals within the rotifer order Flosculariaceae in the 300-count subsamples (coarse and fine net samples combined)

FLOS300_PTAX	Percent of distinct taxa within the rotifer order Flosculariaceae in the 300-count subsamples (coarse and fine net samples combined)
GEN_NAT_NTAX	Number of genera represented by distinct native taxa (coarse and fine net samples combined)
GEN_NTAX	Number of genera represented by distinct taxa (coarse and fine net samples combined)
GEN300_NAT_NTAX	Number of native genera represented in the 300 count subsamples (coarse and fine net samples combined)
GEN300_NTAX	Number of genera represented in the 300 count subsamples (coarse and fine net samples combined)
HERB_BIO	Biomass represented by individuals that are herbivores
HERB_DEN	Density (indiv.L) of individuals that are herbivores (coarse and fine net samples combined)
HERB_NIND	Number of individuals that are herbivores (coarse and fine net samples combined)
HERB_NTAX	Number of distinct herbivore taxa (coarse and fine net samples combined)
HERB_PBio	Percent of biomass represented by individuals that are herbivores (coarse and fine net samples combined)
HERB_PDEN	Percent of density (indiv.L) of individuals that are herbivores (coarse and fine net samples combined)
HERB_PIND	Percent of individuals that are herbivores (coarse and fine net samples combined)
HERB_PTAX	Percent of distinct taxa that are herbivores (coarse and fine net samples combined)
HERB300_BIO	Biomass represented by individuals that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
HERB300_NIND	Number of individuals that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
HERB300_NTAX	Number of distinct herbivore taxa in the 300-count subsamples (coarse and fine net samples combined)
HERB300_PBio	Percent of biomass represented by individuals that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
HERB300_PIND	Percent of individuals that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
HERB300_PTAX	Percent of distinct taxa that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
HPRIME_BIO	Shannon Diversity based on the biomass of individuals (coarse and fine net samples combined). Calculated as $\text{SUM}\{p(i) \cdot \text{Log}[p(i)]\}$ , where $p(i)$ is proportion of biomass of taxon $i$ , and $\text{Log}$ = natural logarithm.
HPRIME_CLAD	Shannon Diversity based on the number of cladoceran individuals (coarse and fine net samples combined). Calculated as $\text{SUM}\{p(i) \cdot \text{Log}[p(i)]\}$ , where $p(i)$ is proportion of individuals of taxon $i$ , and $\text{Log}$ = natural logarithm.
HPRIME_CLAD300	Shannon Diversity based on the number of cladoceran individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as $\text{SUM}\{p(i) \cdot \text{Log}[p(i)]\}$ , where $p(i)$ is proportion of individuals of taxon $i$ , and $\text{Log}$ = natural logarithm.

HPRIME_COPE	Shannon Diversity based on the number of copepod individuals (coarse and fine net samples combined). Calculated as $\text{SUM}\{p(i) \cdot \text{Log}[p(i)]\}$ , where $p(i)$ is proportion of individuals of taxon $i$ , and $\text{Log}$ = natural logarithm.
HPRIME_COPE300	Shannon Diversity based on the number of copepod individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as $\text{SUM}\{p(i) \cdot \text{Log}[p(i)]\}$ , where $p(i)$ is proportion of individuals of taxon $i$ , and $\text{Log}$ = natural logarithm.
HPRIME_DEN	Shannon Diversity based on the density (indiv./L) of individuals (coarse and fine net samples combined). Calculated as $\text{SUM}\{p(i) \cdot \text{Log}[p(i)]\}$ , where $p(i)$ is proportion of density of taxon $i$ , and $\text{Log}$ = natural logarithm.
HPRIME_NIND	Shannon Diversity based on the total number of individuals (coarse and fine net samples combined). Calculated as $\text{SUM}\{p(i) \cdot \text{Log}[p(i)]\}$ , where $p(i)$ is proportion of individuals of taxon $i$ , and $\text{Log}$ = natural logarithm.
HPRIME_ROT	Shannon Diversity based on the number of rotifer individuals (coarse and fine net samples combined). Calculated as $\text{SUM}\{p(i) \cdot \text{Log}[p(i)]\}$ , where $p(i)$ is proportion of individuals of taxon $i$ , and $\text{Log}$ = natural logarithm.
HPRIME_ROT300	Shannon Diversity based on the number of rotifer individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as $\text{SUM}\{p(i) \cdot \text{Log}[p(i)]\}$ , where $p(i)$ is proportion of individuals of taxon $i$ , and $\text{Log}$ = natural logarithm.
HPRIME300_BIO	Shannon Diversity based on the biomass of individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as $\text{SUM}\{p(i) \cdot \text{Log}[p(i)]\}$ , where $p(i)$ is proportion of biomass of taxon $i$ , and $\text{Log}$ = natural logarithm.
HPRIME300_NIND	Shannon Diversity based on the total number of individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as $\text{SUM}\{p(i) \cdot \text{Log}[p(i)]\}$ , where $p(i)$ is proportion of individuals of taxon $i$ , and $\text{Log}$ = natural logarithm.
LGCLAD_BIO	Biomass represented by large cladoceran individuals (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE; coarse and fine net samples combined)
LGCLAD_DEN	Density (indiv./L) of individuals within large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=LARGE; coarse and fine net samples combined)
LGCLAD_NAT_BIO	Biomass represented by native large cladoceran individuals (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE; coarse and fine net samples combined)
LGCLAD_NAT_DEN	Density (indiv./L) of native individuals within large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=LARGE; coarse and fine net samples combined)
LGCLAD_NAT_NIND	Number of native individuals within large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=LARGE; coarse and fine net samples combined)
LGCLAD_NAT_NTAX	Number of distinct taxa represented by native large cladocerans (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE; coarse and fine net samples combined)

LGCLAD_NAT_PBIO	Percent of biomass represented by native individuals within large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE; coarse and fine net samples combined)
LGCLAD_NAT_PDEN	Percent of density (indiv./L) of native individuals within large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE; coarse and fine net samples combined)
LGCLAD_NAT_PIND	Percent of native individuals within large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE; coarse and fine net samples combined)
LGCLAD_NAT_PTAX	Percent of distinct native large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE; coarse and fine net samples combined)
LGCLAD_NIND	Number of individuals within large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE; coarse and fine net samples combined)
LGCLAD_NTAX	Number of distinct taxa represented by large cladocerans (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE; coarse and fine net samples combined)
LGCLAD_PBIO	Percent of biomass represented by individuals within large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE; coarse and fine net samples combined)
LGCLAD_PDEN	Percent of density (indiv./L) of individuals within large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE; coarse and fine net samples combined)
LGCLAD_PIND	Percent of individuals within large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE; coarse and fine net samples combined)
LGCLAD_PTAX	Percent of distinct large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE; coarse and fine net samples combined)
LGCLAD300_BIO	Biomass represented by large cladoceran individuals (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net subsamples combined)
LGCLAD300_NAT_BIO	Biomass represented by native large cladoceran individuals (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net subsamples combined)
LGCLAD300_NAT_NIND	Number of native individuals within large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net samples combined)
LGCLAD300_NAT_NTAX	Number of distinct taxa represented by native large cladocerans (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net samples combined)
LGCLAD300_NAT_PBIO	Percent of biomass represented by native large cladoceran individuals (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net samples combined)
LGCLAD300_NAT_PIND	Percent of native individuals within large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net samples combined)
LGCLAD300_NAT_PTAX	Percent of distinct native large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net samples combined)

LGCLAD300_NIND	Number of individuals within large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net samples combined)
LGCLAD300_NTAX	Number of distinct taxa represented by large cladocerans (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net samples combined)
LGCLAD300_PBio	Percent of biomass represented by large cladoceran individuals (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net samples combined)
LGCLAD300_PIND	Percent of individuals within large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net samples combined)
LGCLAD300_PTAX	Percent of distinct large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net samples combined)
OMNI_BIO	Biomass represented by individuals that are omnivores
OMNI_DEN	Density (indiv.L) of individuals that are omnivores (coarse and fine net samples combined)
OMNI_NIND	Number of individuals that are omnivores (coarse and fine net samples combined)
OMNI_NTAX	Number of distinct omnivore taxa (coarse and fine net samples combined)
OMNI_PBio	Percent of biomass represented by individuals that are omnivores (coarse and fine net samples combined)
OMNI_PDEN	Percent of density (indiv.L) of individuals that are omnivores (coarse and fine net samples combined)
OMNI_PIND	Percent of individuals that are omnivores (coarse and fine net samples combined)
OMNI_PTAX	Percent of distinct taxa that are omnivores (coarse and fine net samples combined)
OMNI300_BIO	Biomass represented by individuals that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
OMNI300_NIND	Number of individuals that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
OMNI300_NTAX	Number of distinct omnivore taxa in the 300-count subsamples (coarse and fine net samples combined)
OMNI300_PBio	Percent of biomass represented by individuals that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
OMNI300_PIND	Percent of individuals that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
OMNI300_PTAX	Percent of distinct taxa that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
PIE_CLAD	Hurlburts Probability of Interspecific Encounter (PIE) based on the number of cladoceran individuals (coarse and fine net samples combined). Calculated as $\sum \{p(i) * [N - n(i) / N - 1]\}$ where $p(i)$ is the proportion of taxon $i$ in the sample, $N$ is the total number of individual in the sample, and $n(i)$ is the number of individuals of taxon $i$ in the sample.

PIE_CLAD300	<p>Hurlburts Probability of Insterspecific Encounter (PIE) based on the number of cladoceran individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as <math>\sum\{p(i) \cdot [N-n(i)/N-1]\}</math> where <math>p(i)</math> is the proportion of taxon <math>i</math> in the sample, <math>N</math> is the total number of individual in the sample, and <math>n(i)</math> is the number of individuals of taxon <math>i</math> in the sample.</p>
PIE_COPE	<p>Hurlburts Probability of Insterspecific Encounter (PIE) based on the number of copepod individuals (coarse and fine net samples combined). Calculated as <math>\sum\{p(i) \cdot [N-n(i)/N-1]\}</math> where <math>p(i)</math> is the proportion of taxon <math>i</math> in the sample, <math>N</math> is the total number of individual in the sample, and <math>n(i)</math> is the number of individuals of taxon <math>i</math> in the sample.</p>
PIE_COPE300	<p>Hurlburts Probability of Insterspecific Encounter (PIE) based on the number of copepod individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as <math>\sum\{p(i) \cdot [N-n(i)/N-1]\}</math> where <math>p(i)</math> is the proportion of taxon <math>i</math> in the sample, <math>N</math> is the total number of individual in the sample, and <math>n(i)</math> is the number of individuals of taxon <math>i</math> in the sample.</p>
PIE_NIND	<p>Hurlburts Probability of Insterspecific Encounter (PIE) based on the total number of individuals (coarse and fine net samples combined). Calculated as <math>\sum\{p(i) \cdot [N-n(i)/N-1]\}</math> where <math>p(i)</math> is the proportion of taxon <math>i</math> in the sample, <math>N</math> is the total number of individual in the sample, and <math>n(i)</math> is the number of individuals of taxon <math>i</math> in the sample.</p>
PIE_ROT	<p>Hurlburts Probability of Insterspecific Encounter (PIE) based on the number of rotifer individuals (coarse and fine net samples combined). Calculated as <math>\sum\{p(i) \cdot [N-n(i)/N-1]\}</math> where <math>p(i)</math> is the proportion of taxon <math>i</math> in the sample, <math>N</math> is the total number of individual in the sample, and <math>n(i)</math> is the number of individuals of taxon <math>i</math> in the sample.</p>
PIE_ROT300	<p>Hurlburts Probability of Interspecific Encounter (PIE) based on the number of rotifer individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as <math>\sum\{p(i) \cdot [N-n(i)/N-1]\}</math> where <math>p(i)</math> is the proportion of taxon <math>i</math> in the sample, <math>N</math> is the total number of individual in the sample, and <math>n(i)</math> is the number of individuals of taxon <math>i</math> in the sample.</p>
PIE300_NIND	<p>Hurlburts Probability of Insterspecific Encounter (PIE) based on the total number of individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as <math>\sum\{p(i) \cdot [N-n(i)/N-1]\}</math> where <math>p(i)</math> is the proportion of taxon <math>i</math> in the sample, <math>N</math> is the total number of individual in the sample, and <math>n(i)</math> is the number of individuals of taxon <math>i</math> in the sample.</p>
PLOIMA_BIO	<p>Biomass represented by individuals within the rotifer order Ploima (coarse and fine net samples combined)</p>
PLOIMA_DEN	<p>Density (indiv./L) of individuals within the rotifer order Ploima (coarse and fine net samples combined)</p>
PLOIMA_NIND	<p>Number of individuals within the rotifer order Ploima (coarse and fine net samples combined)</p>
PLOIMA_NTAX	<p>Number of distinct taxa within the rotifer order Ploima (coarse and fine net samples combined)</p>
PLOIMA_PBio	<p>Percent of biomass represented by individuals within the rotifer order Ploima (coarse and fine net samples combined)</p>
PLOIMA_PDEN	<p>Percent of density (indiv./L) of individuals within the rotifer order Ploima (coarse and fine net samples combined)</p>



PLOIMA_PIND	Percent of individuals within the rotifer order Ploima (coarse and fine net samples combined)
PLOIMA_PTAX	Percent of distinct taxa within the rotifer order Ploima (coarse and fine net samples combined)
PLOIMA300_BIO	Biomass represented by individuals within the rotifer order Ploima in the 300-count subsamples (coarse and fine net subsamples combined)
PLOIMA300_NIND	Number of individuals within the rotifer order Ploima in the 300-count subsamples (coarse and fine net samples combined)
PLOIMA300_NTAX	Number of distinct taxa within the rotifer order Ploima in the 300-count subsamples (coarse and fine net samples combined)
PLOIMA300_PBIO	Percent of biomass represented by individuals within the rotifer order Ploima in the 300-count subsamples (coarse and fine net samples combined)
PLOIMA300_PIND	Percent of individuals within the rotifer order Ploima in the 300-count subsamples (coarse and fine net samples combined)
PLOIMA300_PTAX	Percent of distinct taxa within the rotifer order Ploima in the 300-count subsamples (coarse and fine net samples combined)
PRED_BIO	Biomass represented by individuals that are predators
PRED_DEN	Density (indiv./L) of individuals that are predators (coarse and fine net samples combined)
PRED_NIND	Number of individuals that are predators (coarse and fine net samples combined)
PRED_NTAX	Number of distinct predator taxa (coarse and fine net samples combined)
PRED_PBIO	Percent of biomass represented by individuals that are predators (coarse and fine net samples combined)
PRED_PDEN	Percent of density (indiv./L) of individuals that are predators (coarse and fine net samples combined)
PRED_PIND	Percent of individuals that are predators (coarse and fine net samples combined)
PRED_PTAX	Percent of distinct taxa that are predators (coarse and fine net samples combined)
PRED300_BIO	Biomass represented by individuals that are predators in the 300-count subsamples (coarse and fine net samples combined)
PRED300_NIND	Number of individuals that are predators in the 300-count subsamples (coarse and fine net samples combined)
PRED300_NTAX	Number of distinct predator taxa in the 300-count subsamples (coarse and fine net samples combined)
PRED300_PBIO	Percent of biomass represented by individuals that are predators in the 300-count subsamples (coarse and fine net samples combined)
PRED300_PIND	Percent of individuals that are predators in the 300-count subsamples (coarse and fine net samples combined)
PRED300_PTAX	Percent of distinct taxa that are predators in the 300-count subsamples (coarse and fine net samples combined)
ROT_BIO	Biomass represented by individuals within the phylum Rotifera
ROT_DEN	Density (indiv./L) of native individuals within the phylum Rotifera (coarse and fine net samples combined)
ROT_HERB_BIO	Biomass represented by individuals within the phylum Rotifera that are herbivores

ROT_HERB_DEN	Density (indiv.L) of individuals within the phylum Rotifera that are herbivores (coarse and fine net samples combined)
ROT_HERB_NIND	Number of individuals within the phylum Rotifera that are herbivores (coarse and fine net samples combined)
ROT_HERB_NTAX	Number of distinct rotifer taxa that are herbivores (coarse and fine net samples combined)
ROT_HERB_PBIO	Percent of biomass represented by individuals within the phylum Rotifera that are herbivores (coarse and fine net samples combined)
ROT_HERB_PDEN	Percent of density (indiv.L) of individuals within the phylum Rotifera that are herbivores (coarse and fine net samples combined)
ROT_HERB_PIND	Percent of individuals within the phylum Rotifera that are herbivores (coarse and fine net samples combined)
ROT_HERB_PTAX	Percent of distinct taxa within the phylum Rotifera that are herbivores (coarse and fine net samples combined)
ROT_HERB300_BIO	Biomass represented by individuals within the phylum Rotifera that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
ROT_HERB300_NIND	Number of individuals within the phylum Rotifera that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
ROT_HERB300_NTAX	Number of distinct rotifer taxa that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
ROT_HERB300_PBIO	Percent of biomass represented by individuals within the phylum Rotifera that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
ROT_HERB300_PIND	Percent of individuals within the phylum Rotifera that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
ROT_HERB300_PTAX	Percent of distinct taxa within the phylum Rotifera that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
ROT_NIND	Number of individuals within the phylum Rotifera (coarse and fine net samples combined)
ROT_NTAX	Number of distinct taxa within the phylum Rotifera (coarse and fine net samples combined)
ROT_OMNI_BIO	Biomass represented by individuals within the phylum Rotifera that are omnivores
ROT_OMNI_DEN	Density (indiv.L) of individuals within the phylum Rotifera that are omnivores (coarse and fine net samples combined)
ROT_OMNI_NIND	Number of individuals within the phylum Rotifera that are omnivores (coarse and fine net samples combined)
ROT_OMNI_NTAX	Number of distinct rotifer taxa that are omnivores (coarse and fine net samples combined)
ROT_OMNI_PBIO	Percent of biomass represented by individuals within the phylum Rotifera that are omnivores (coarse and fine net samples combined)
ROT_OMNI_PDEN	Percent of density (indiv.L) of individuals within the phylum Rotifera that are omnivores (coarse and fine net samples combined)
ROT_OMNI_PIND	Percent of individuals within the phylum Rotifera that are omnivores (coarse and fine net samples combined)

ROT_OMNI_PTAX	Percent of distinct taxa within the phylum Rotifera that are omnivores (coarse and fine net samples combined)
ROT_OMNI300_BIO	Biomass represented by individuals within the phylum Rotifera that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
ROT_OMNI300_NIND	Number of individuals within the phylum Rotifera that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
ROT_OMNI300_NTAX	Number of distinct rotifer taxa that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
ROT_OMNI300_PBIO	Percent of biomass represented by individuals within the phylum Rotifera that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
ROT_OMNI300_PIND	Percent of individuals within the phylum Rotifera that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
ROT_OMNI300_PTAX	Percent of distinct taxa within the phylum Rotifera that are omnivores in the 300-count subsamples (coarse and fine net samples combined)
ROT_PBIO	Percent of biomass represented by individuals within the phylum Rotifera (coarse and fine net samples combined)
ROT_PDEN	Percent of density (indiv./L) of native individuals within the phylum Rotifera (coarse and fine net samples combined)
ROT_PIND	Percent of individuals within the phylum Rotifera (coarse and fine net samples combined)
ROT_PRED_BIO	Biomass represented by individuals within the phylum Rotifera that are predators
ROT_PRED_DEN	Density (indiv.L) of individuals within the phylum Rotifera that are predators (coarse and fine net samples combined)
ROT_PRED_NIND	Number of individuals within the phylum Rotifera that are predators (coarse and fine net samples combined)
ROT_PRED_NTAX	Number of distinct rotifer taxa that are predators (coarse and fine net samples combined)
ROT_PRED_PBIO	Percent of biomass represented by individuals within the phylum Rotifera that are predators (coarse and fine net samples combined)
ROT_PRED_PDEN	Percent of density (indiv.L) of individuals within the phylum Rotifera that are predators (coarse and fine net samples combined)
ROT_PRED_PIND	Percent of individuals within the phylum Rotifera that are predators (coarse and fine net samples combined)
ROT_PRED_PTAX	Percent of distinct taxa within the phylum Rotifera that are predators (coarse and fine net samples combined)
ROT_PRED300_BIO	Biomass represented by individuals within the phylum Rotifera that are predators in the 300-count subsamples (coarse and fine net samples combined)
ROT_PRED300_NIND	Number of individuals within the phylum Rotifera that are predators in the 300-count subsamples (coarse and fine net samples combined)
ROT_PRED300_NTAX	Number of distinct rotifer taxa that are predators in the 300-count subsamples (coarse and fine net samples combined)

ROT_PRED300_P BIO	Percent of biomass represented by individuals within the phylum Rotifera that are predators in the 300-count subsamples (coarse and fine net samples combined)
ROT_PRED300_P IND	Percent of individuals within the phylum Rotifera that are predators in the 300-count subsamples (coarse and fine net samples combined)
ROT_PRED300_P TAX	Percent of distinct taxa within the phylum Rotifera that are predators in the 300-count subsamples (coarse and fine net samples combined)
ROT_P TAX	Percent of distinct taxa within the phylum Rotifera (coarse and fine net samples combined)
ROT300_B IO	Biomass represented by individuals within the phylum Rotifera in the 300-count subsamples (coarse and fine net subsamples combined)
ROT300_N IND	Number of individuals within the phylum Rotifera in the 300-count subsamples (coarse and fine net samples combined)
ROT300_N TAX	Number of distinct taxa within the phylum Rotifera in the 300-count subsamples (coarse and fine net samples combined)
ROT300_P BIO	Percent of biomass represented by individuals within the phylum Rotifera in the 300-count subsamples (coarse and fine net samples combined)
ROT300_P IND	Percent of individuals within the phylum Rotifera in the 300-count subsamples (coarse and fine net samples combined)
ROT300_P TAX	Percent of distinct taxa within the phylum Rotifera in the 300-count subsamples (coarse and fine net samples combined)
SIDID_B IO	Biomass represented by individuals within the cladoceran family Sididae (coarse and fine net samples combined)
SIDID_D EN	Density (indiv./L) of individuals within the cladoceran family Sididae (coarse and fine net samples combined)
SIDID_N IND	Number of individuals within the cladoceran family Sididae (coarse and fine net samples combined)
SIDID_N TAX	Number of distinct taxa within the cladoceran family Sididae (coarse and fine net samples combined)
SIDID_P BIO	Percent of biomass represented by individuals within the cladoceran family Sididae (coarse and fine net samples combined)
SIDID_P DEN	Percent of density (indiv./L) of individuals within the cladoceran family Sididae (coarse and fine net samples combined)
SIDID_P IND	Percent of individuals within the cladoceran family Sididae (coarse and fine net samples combined)
SIDID_P TAX	Percent of total distinct taxa that are within the cladoceran family Sididae (coarse and fine net samples combined)
SIDID300_B IO	Biomass represented by individuals within the cladoceran family Sididae in the 300-count subsamples (coarse and fine net subsamples combined)
SIDID300_N IND	Number of individuals within the cladoceran family Sididae in the 300-count subsamples (coarse and fine net samples combined)
SIDID300_N TAX	Number of distinct taxa within the cladoceran family Sididae in the 300-count subsamples (coarse and fine net samples combined)
SIDID300_P BIO	Percent of biomass represented by individuals within the cladoceran family Sididae in the 300-count subsamples (coarse and fine net samples combined)
SIDID300_P IND	Percent of individuals within the cladoceran family Sididae in the 300-count subsamples (coarse and fine net samples combined)

SIDID300_PTAX	Percent of total distinct taxa that are within the cladoceran family Sididae in the 300-count subsamples (coarse and fine net samples combined)
SIMPSON_BIO	Simpson Diversity based on the biomass of individuals (coarse and fine net samples combined). Calculated as $\sum \{p(i) * p(i)\}$ where $p(i)$ is the proportion of biomass of taxon I in the sample.
SIMPSON_CLAD	Simpson Diversity based on the number of cladoceran individuals (coarse and fine net samples combined). Calculated as $\sum \{p(i) * p(i)\}$ where $p(i)$ is the proportion of taxon I in the sample.
SIMPSON_CLAD300	Simpson Diversity based on the number of cladoceran individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as $\sum \{p(i) * p(i)\}$ where $p(i)$ is the proportion of taxon I in the sample.
SIMPSON_COPE	Simpson Diversity based on the number of copepod individuals (coarse and fine net samples combined). Calculated as $\sum \{p(i) * p(i)\}$ where $p(i)$ is the proportion of taxon I in the sample.
SIMPSON_COPE300	Simpson Diversity based on the number of copepod individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as $\sum \{p(i) * p(i)\}$ where $p(i)$ is the proportion of taxon I in the sample.
SIMPSON_DEN	Simpson Diversity based on the density (indiv./L) of individuals (coarse and fine net samples combined). Calculated as $\sum \{p(i) * p(i)\}$ where $p(i)$ is the proportion of density of taxon I in the sample.
SIMPSON_NIND	Simpson Diversity based on the total number of individuals (coarse and fine net samples combined). Calculated as $\sum \{p(i) * p(i)\}$ where $p(i)$ is the proportion of taxon I in the sample.
SIMPSON_ROT	Simpson Diversity based on the number of rotifer individuals (coarse and fine net samples combined). Calculated as $\sum \{p(i) * p(i)\}$ where $p(i)$ is the proportion of taxon I in the sample.
SIMPSON_ROT300	Simpson Diversity based on the number of rotifer individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as $\sum \{p(i) * p(i)\}$ where $p(i)$ is the proportion of taxon I in the sample.
SIMPSON300_BIO	Simpson Diversity based on the biomass of individuals (coarse and fine net samples combined). Calculated as $\sum \{p(i) * p(i)\}$ where $p(i)$ is the proportion of biomass of taxon I in the sample.
SIMPSON300_NIND	Simpson Diversity based on the total number of individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as $\sum \{p(i) * p(i)\}$ where $p(i)$ is the proportion of taxon I in the sample.
SMCLAD_BIO	Biomass represented by small cladoceran individuals (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=SMALL; coarse and fine net samples combined)
SMCLAD_DEN	Density (indiv./L) of individuals within small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=SMALL; coarse and fine net samples combined)
SMCLAD_NAT_BIO	Biomass represented by native small cladoceran individuals (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=SMALL; coarse and fine net samples combined)
SMCLAD_NAT_DEN	Density (indiv./L) of native individuals within small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=SMALL; coarse and fine net samples combined)

SMCLAD_NAT_NIND	Number of native individuals within small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL; coarse and fine net samples combined)
SMCLAD_NAT_NTAX	Number of distinct taxa represented by native small cladocerans (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=SMALL; coarse and fine net samples combined)
SMCLAD_NAT_PPIO	Percent of biomass represented by native individuals within small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=SMALL; coarse and fine net samples combined)
SMCLAD_NAT_PDEN	Percent of density (indiv./L) of native individuals within large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL; coarse and fine net samples combined)
SMCLAD_NAT_PIND	Percent of native individuals within small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL; coarse and fine net samples combined)
SMCLAD_NAT_PTAX	Percent of distinct native small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL; coarse and fine net samples combined)
SMCLAD_NIND	Number of individuals within small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL; coarse and fine net samples combined)
SMCLAD_NTAX	Number of distinct taxa represented by small cladocerans (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=SMALL; coarse and fine net samples combined)
SMCLAD_PPIO	Percent of biomass represented by individuals within small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=SMALL; coarse and fine net samples combined)
SMCLAD_PDEN	Percent of density (indiv./L) of individuals within small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL; coarse and fine net samples combined)
SMCLAD_PIND	Percent of individuals within small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL; coarse and fine net samples combined)
SMCLAD_PTAX	Percent of distinct small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL; coarse and fine net samples combined)
SMCLAD300_BIO	Biomass represented by small cladoceran individuals (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=SMALL) in the 300-count subsamples (coarse and fine net subsamples combined)
SMCLAD300_NAT_BIO	Biomass represented by native small cladoceran individuals (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=SMALL) in the 300-count subsamples (coarse and fine net subsamples combined)
SMCLAD300_NAT_NIND	Number of native individuals within small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL) in the 300-count subsamples (coarse and fine net samples combined)
SMCLAD300_NAT_NTAX	Number of distinct taxa represented by native small cladocerans (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=SMALL) in the 300-count subsamples (coarse and fine net samples combined)
SMCLAD300_NAT_PPIO	Percent of biomass represented by native small cladoceran individuals (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=SMALL) in the 300-count subsamples (coarse and fine net samples combined)

SMCLAD300_NAT_PIND	Percent of native individuals within small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL) in the 300-count subsamples (coarse and fine net samples combined)
SMCLAD300_NAT_PTAX	Percent of distinct native small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL) in the 300-count subsamples (coarse and fine net samples combined)
SMCLAD300_NIND	Number of individuals within small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL) in the 300-count subsamples (coarse and fine net samples combined)
SMCLAD300_NTAX	Number of distinct taxa represented by small cladocerans (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL) in the 300-count subsamples (coarse and fine net samples combined)
SMCLAD300_PBIO	Percent of biomass represented by small cladoceran individuals (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL) in the 300-count subsamples (coarse and fine net samples combined)
SMCLAD300_PIND	Percent of individuals within small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL) in the 300-count subsamples (coarse and fine net samples combined)
SMCLAD300_PTAX	Percent of distinct small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL) in the 300-count subsamples (coarse and fine net samples combined)
TOTL_BIO	Total biomass of individuals (coarse and fine net samples combined)
TOTL_DEN	Total density (Indiv./L) based on all individuals (coarse and fine net samples combined)
TOTL_NAT_BIO	Total biomass of native individuals (coarse and fine net samples combined)
TOTL_NAT_DEN	Total density (Indiv./L) of native individuals (coarse and fine net samples combined)
TOTL_NAT_NIND	Number of native individuals (coarse and fine net samples combined)
TOTL_NAT_NTAX	Total number of distinct native taxa (coarse and fine net samples combined)
TOTL_NAT_PBIO	Percent of biomass represented by native individuals (coarse and fine net samples combined)
TOTL_NAT_PDEN	Percent of density (Indiv./L) of native individuals (coarse and fine net samples combined)
TOTL_NAT_PIND	Percent of native individuals (coarse and fine net samples combined)
TOTL_NAT_PTAX	Percent of distinct native taxa (coarse and fine net samples combined)
TOTL_NIND	Total number of individuals counted across ZOCN and ZOFN samples
TOTL_NTAX	Total number of distinct taxa (coarse and fine net samples combined)
TOTL300_BIO	Total biomass of individuals in 300-count subsamples (coarse and fine net subsamples combined)
TOTL300_NAT_BIO	Total biomass of native individuals in 300-count subsamples (coarse and fine net subsamples combined)
TOTL300_NAT_NIND	Number of native individuals in the 300-count subsamples (coarse and fine net samples combined)
TOTL300_NAT_NTAX	Total number of distinct native taxa in the 300-count subsamples (coarse and fine net samples combined)
TOTL300_NAT_PBIO	Percent of biomass represented by individuals in the 300-count subsamples (coarse and fine net samples combined)

TOTL300_NAT_PIND	Percent of native individuals in the 300-count subsamples (coarse and fine net samples combined)
TOTL300_NAT_PTAX	Percent of distinct native taxa in the 300-count subsamples (coarse and fine net samples combined)
TOTL300_NIND	Total number of individuals in random (300 organisms from ZOEN and 300 from ZOEN sample)
TOTL300_NTAX	Total number of distinct taxa in the 300-count subsamples (coarse and fine net samples combined)
ZOEN_BIO	Biomass represented by individuals in the coarse-mesh net sample (150-um)
ZOEN_DEN	Density (indiv./L) of individuals in the coarse mesh net sample (150-um)
ZOEN_FAM_NAT_NTAX	Number of families represented by distinct native taxa in the coarse-mesh net sample (150 um)
ZOEN_FAM_NTAX	Number of families represented by distinct taxa in the coarse-mesh net sample (150 um)
ZOEN_GEN_NAT_NTAX	Number of genera represented by distinct native taxa in the coarse-mesh net sample (150 um)
ZOEN_GEN_NTAX	Number of genera represented by distinct taxa in the coarse-mesh net sample (150 um)
ZOEN_NAT_BIO	Biomass represented by native individuals in the coarse-mesh net sample (150-um)
ZOEN_NAT_DEN	Density (indiv./L) of native individuals in the coarse-mesh net sample (150-um)
ZOEN_NAT_NIND	Number of native individuals in the coarse-mesh net sample (150-um)
ZOEN_NAT_NTAX	Number of distinct native taxa in the coarse-mesh net sample (150-um)
ZOEN_NAT_PBIO	Percent of biomass represented by native individuals in the coarse-mesh net sample (150-um)
ZOEN_NAT_PDEN	Percent of density (indiv./L) of native individuals in the coarse-mesh net sample (150-um)
ZOEN_NAT_PIND	Percent of native individuals in the coarse-mesh net sample (150-um)
ZOEN_NAT_PTAX	Percent of distinct taxa represented by native individuals in coarse-mesh net sample (150-um)
ZOEN_NIND	Number of individuals counted in ZOEN sample
ZOEN_NTAX	Number of distinct taxa in the coarse-mesh net sample (150-um)
ZOEN300_BIO	Biomass of individuals in the 300-count subsample of the coarse-mesh net sample (150 um)
ZOEN300_FAM_NAT_NTAX	Number of families represented by distinct native taxa in the coarse-mesh net sample (150 um)
ZOEN300_FAM_NTAX	Number of families represented by distinct taxa in the 300-count subsample from the coarse-mesh net sample (150 um)
ZOEN300_GEN_NAT_NTAX	Number of genera represented by distinct native taxa in the 300-count subsample from the coarse-mesh net sample (150 um)
ZOEN300_GEN_NTAX	Number of genera represented by distinct taxa in the 300-count subsample from the coarse-mesh net sample (150 um)
ZOEN300_NAT_BIO	Biomass of native individuals in the 300-count subsample of the coarse-mesh net sample (150 um)
ZOEN300_NAT_NIND	Number of native individuals in the 300-count subsamples from the coarse-mesh net sample (150-um)



ZOCN300_NAT_NTAX	Number of distinct native taxa in the 300-count subsample from the coarse-mesh net sample (150-um)
ZOCN300_NAT_PBIO	Percent of biomass represented by native individuals in the 300-count subsample from the coarse-mesh net sample (150-um)
ZOCN300_NAT_PIND	Percent of native individuals in the 300-count subsamples from the coarse-mesh net sample (150-um)
ZOCN300_NAT_PTAX	Percent of distinct taxa represented by native individuals in the 300-count subsample from the coarse-mesh net sample (150-um)
ZOCN300_NIND	Number of individuals in 300 organism random subsample from ZOCN sample
ZOCN300_NTAX	Number of distinct taxa in the 300-count subsample from the coarse-mesh net sample (150-um)
ZOFN_BIO	Biomass represented by individuals in the fine-mesh net sample (50-um)
ZOFN_DEN	Density (indiv./L) of individuals in the fine-mesh net sample (50-um)
ZOFN_FAM_NAT_NTAX	Number of families represented by distinct native taxa in the fine-mesh net sample (50-um)
ZOFN_FAM_NTAX	Number of families represented by distinct taxa in the fine-mesh net sample (50-um)
ZOFN_GEN_NAT_NTAX	Number of genera represented by distinct native taxa in the fine-mesh net sample (50-um mesh)
ZOFN_GEN_NTAX	Number of genera represented by distinct taxa in fine-mesh net sample (50-um)
ZOFN_NAT_BIO	Biomass represented by native individuals in the fine-mesh net sample (50-um)
ZOFN_NAT_DEN	Density (indiv./L) of individuals in the fine-mesh net sample (50-um)
ZOFN_NAT_NIND	Number of native individuals in the fine-mesh net sample (50-um)
ZOFN_NAT_NTAX	Number of distinct native taxa in the fine-mesh net sample (50-um mesh)
ZOFN_NAT_PBIO	Percent of biomass represented by native individuals in the fine-mesh net sample (50-um)
ZOFN_NAT_PDEN	Percent of density (indiv./L) of native individuals in the fine-mesh net sample (50-um)
ZOFN_NAT_PIND	Percent of native individuals in the fine-mesh net sample (50-um)
ZOFN_NAT_PTAX	Percent of distinct taxa represented by native individuals in the fine-mesh net sample (50-um)
ZOFN_NIND	Number of individuals counted in ZOFN sample
ZOFN_NTAX	Number of distinct taxa in the fine-mesh net sample (50-um)
ZOFN300_BIO	Biomass of individuals in the 300-count subsample of the fine-mesh net sample (50 um)
ZOFN300_FAM_NAT_NTAX	Number of families represented by distinct native taxa in the fine-mesh net sample (50 um)
ZOFN300_FAM_NTAX	Number of families represented by distinct taxa in the 300-count subsample from the fine-mesh net sample (50 um)
ZOFN300_GEN_NAT_NTAX	Number of genera represented by distinct native taxa in the 300-count subsample from the fine-mesh net sample (50 um)
ZOFN300_GEN_NTAX	Number of genera represented by distinct taxa in the 300-count subsample from the fine-mesh net sample (50 um)
ZOFN300_NAT_BIO	Biomass of native individuals in the 300-count subsample of the fine-mesh net sample (50 um)
ZOFN300_NAT_NIND	Number of native individuals in the 300-count subsample from the fine-mesh net sample (50-um)

ZOFN300_NAT_NTAX	Number of distinct native taxa in the 300-count subsample from the fine-mesh net sample (50-um)
ZOFN300_NAT_PBIO	Percent of biomass represented by native individuals in the 300-count subsample from the fine-mesh net sample (50-um)
ZOFN300_NAT_PIND	Percent of native individuals in the 300-count subsample from the fine-mesh net sample (50-um)
ZOFN300_NAT_PTAX	Percent of distinct taxa represented by native individuals in the 300-count subsample from the fine-mesh net sample (50-um)
ZOFN300_NIND	Number of individuals in 300 organism random subsample from ZOFN sample
ZOFN300_NTAX	Number of distinct taxa in the 300-count subsample from the fine-mesh net sample (50-um)