METRIC	LABEL
	Biomass represented by individuals within the rotifer family Asplanchnidae (coarse and fine
ASPLAN_BIO	net samples combined)
	Density (indiv./L) of individuals within the rotifer family Asplanchnidae (coarse and fine net
ASPLAN_DEN	samples combined)
	Number of individuals within the rotifer family Asplanchnidae (coarse and fine net samples
ASPLAN_NIND	combined)
	Number of distinct taxa within the rotifer family Asplanchnidae (coarse and fine net samples
ASPLAN_NTAX	combined)
	Percent of biomass represented by individuals within the rotifer family Asplanchnidae (coarse
ASPLAN_PBIO	and fine net samples combined)
ACDI ANI DDENI	Percent of density (indiv./L) of individuals within the rotifer family Asplanchnidae (coarse and
ASPLAN_PDEN	fine net samples combined)  Percent of individuals within the rotifer family Asplanchnidae (coarse and fine net samples
ASPLAN_PIND	combined)
ASFLAN_FIND	Percent of distinct taxa within the rotifer family Asplanchnidae (coarse and fine net samples
ASPLAN_PTAX	combined)
7.01 27.11 _1 77.00	Biomass represented by individuals within the rotifer family Asplanchnidae in the 300-count
ASPLAN300_BIO	subsamples (coarse and fine net subsamples combined)
_	Number of individuals within the rotifer family Asplanchnidae in the 300-count subsamples
ASPLAN300_NIND	(coarse and fine net samples combined)
	Number of distinct taxa within the rotifer family Asplanchnidae in the 300-count subsamples
ASPLAN300_NTAX	(coarse and fine net samples combined)
	Boundard Charles and the Control of
ACDI ANIZOO DDIO	Percent of biomass represented by individuals within the rotifer family Asplanchnidae in the
ASPLAN300_PBIO	300-count subsamples (coarse and fine net samples combined)
	300-count subsamples (coarse and fine net samples combined) Percent of individuals within the rotifer family Asplanchnidae in the 300-count subsamples
ASPLAN300_PBIO ASPLAN300_PIND	300-count subsamples (coarse and fine net samples combined) Percent of individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined)
ASPLAN300_PIND	300-count subsamples (coarse and fine net samples combined) Percent of individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Percent of distinct taxa within the rotifer family Asplanchnidae in the 300-count subsamples
	300-count subsamples (coarse and fine net samples combined) Percent of individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Percent of distinct taxa within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined)
ASPLAN300_PIND ASPLAN300_PTAX	300-count subsamples (coarse and fine net samples combined) Percent of individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Percent of distinct taxa within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Biomass represented by individuals within the cladoceran family Bosminidae (coarse and fine
ASPLAN300_PIND	300-count subsamples (coarse and fine net samples combined) Percent of individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Percent of distinct taxa within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined)
ASPLAN300_PIND ASPLAN300_PTAX	300-count subsamples (coarse and fine net samples combined) Percent of individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Percent of distinct taxa within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Biomass represented by individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)
ASPLAN300_PIND ASPLAN300_PTAX BOSM_BIO	300-count subsamples (coarse and fine net samples combined) Percent of individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Percent of distinct taxa within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Biomass represented by individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Density (indiv./L) of individuals within the cladoceran family Bosminidae (coarse and fine net
ASPLAN300_PIND ASPLAN300_PTAX BOSM_BIO	300-count subsamples (coarse and fine net samples combined) Percent of individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Percent of distinct taxa within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Biomass represented by individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Density (indiv./L) of individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)
ASPLAN300_PIND ASPLAN300_PTAX BOSM_BIO BOSM_DEN	300-count subsamples (coarse and fine net samples combined) Percent of individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Percent of distinct taxa within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Biomass represented by individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Density (indiv./L) of individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Biomass represented by native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Density (indiv./L) of native individuals within the cladoceran family Bosminidae (coarse and
ASPLAN300_PIND ASPLAN300_PTAX BOSM_BIO BOSM_DEN	300-count subsamples (coarse and fine net samples combined) Percent of individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Percent of distinct taxa within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Biomass represented by individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Density (indiv./L) of individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Biomass represented by native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Density (indiv./L) of native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)
ASPLAN300_PIND  ASPLAN300_PTAX  BOSM_BIO  BOSM_DEN  BOSM_NAT_BIO	300-count subsamples (coarse and fine net samples combined) Percent of individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Percent of distinct taxa within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Biomass represented by individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Density (indiv./L) of individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Biomass represented by native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Density (indiv./L) of native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Number of native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)
ASPLAN300_PIND  ASPLAN300_PTAX  BOSM_BIO  BOSM_DEN  BOSM_NAT_BIO	300-count subsamples (coarse and fine net samples combined) Percent of individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Percent of distinct taxa within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Biomass represented by individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Density (indiv./L) of individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Biomass represented by native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Density (indiv./L) of native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Number of native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)
ASPLAN300_PIND  ASPLAN300_PTAX  BOSM_BIO  BOSM_DEN  BOSM_NAT_BIO  BOSM_NAT_DEN  BOSM_NAT_NIND	300-count subsamples (coarse and fine net samples combined) Percent of individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Percent of distinct taxa within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Biomass represented by individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Density (indiv./L) of individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Biomass represented by native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Density (indiv./L) of native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Number of native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Number of distinct native taxa within the cladoceran family Bosminidae (coarse and fine net
ASPLAN300_PIND  ASPLAN300_PTAX  BOSM_BIO  BOSM_DEN  BOSM_NAT_BIO  BOSM_NAT_DEN	300-count subsamples (coarse and fine net samples combined) Percent of individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Percent of distinct taxa within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Biomass represented by individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Density (indiv./L) of individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Biomass represented by native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Density (indiv./L) of native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Number of native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Number of distinct native taxa within the cladoceran family Bosminidae (coarse and fine net samples combined)
ASPLAN300_PIND  ASPLAN300_PTAX  BOSM_BIO  BOSM_DEN  BOSM_NAT_BIO  BOSM_NAT_DEN  BOSM_NAT_NIND  BOSM_NAT_NIND	Percent of individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined)  Percent of distinct taxa within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined)  Biomass represented by individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)  Density (indiv./L) of individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)  Biomass represented by native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)  Density (indiv./L) of native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)  Number of native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)  Number of distinct native taxa within the cladoceran family Bosminidae (coarse and fine net samples combined)  Percent of biomass represented by native individuals within the cladoceran family
ASPLAN300_PIND  ASPLAN300_PTAX  BOSM_BIO  BOSM_DEN  BOSM_NAT_BIO  BOSM_NAT_DEN  BOSM_NAT_NIND	300-count subsamples (coarse and fine net samples combined) Percent of individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Percent of distinct taxa within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined) Biomass represented by individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Density (indiv./L) of individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Biomass represented by native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Density (indiv./L) of native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Number of native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined) Number of distinct native taxa within the cladoceran family Bosminidae (coarse and fine net samples combined) Percent of biomass represented by native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)
ASPLAN300_PIND  ASPLAN300_PTAX  BOSM_BIO  BOSM_DEN  BOSM_NAT_BIO  BOSM_NAT_DEN  BOSM_NAT_NIND  BOSM_NAT_NIND	Percent of individuals within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined)  Percent of distinct taxa within the rotifer family Asplanchnidae in the 300-count subsamples (coarse and fine net samples combined)  Biomass represented by individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)  Density (indiv./L) of individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)  Biomass represented by native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)  Density (indiv./L) of native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)  Number of native individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)  Number of distinct native taxa within the cladoceran family Bosminidae (coarse and fine net samples combined)  Percent of biomass represented by native individuals within the cladoceran family

	Percent of native individuals within the cladoceran family Bosminidae (coarse and fine net
BOSM_NAT_PIND	samples combined)
BOSM_NAT_PTAX	Percent of distinct native taxa within the cladoceran family Bosminidae (coarse and fine net samples combined)
B0011_10/11_1 1/10	Number of individuals within the cladoceran family Bosminidae (coarse and fine net samples
BOSM_NIND	combined)
	Number of distinct taxa within the cladoceran family Bosminidae (coarse and fine net
BOSM_NTAX	samples combined)
BOSM_PBIO	Percent of biomass represented by individuals within the cladoceran family Bosminidae (coarse and fine net samples combined)
DOOM_I DIO	Percent of density (indiv./L) of individuals within the cladoceran family Bosminidae (coarse
BOSM_PDEN	and fine net samples combined)
	Percent of individuals within the cladoceran family Bosminidae (coarse and fine net samples
BOSM_PIND	combined)
DOCM DTAY	Percent of total distinct taxa that are within the cladoceran family Bosminidae (coarse and
BOSM_PTAX	fine net samples combined) Biomass represented by individuals within the cladoceran family Bosminidae in the 300-
BOSM300_BIO	count subsampless (coarse and fine net subsamples combined)
	, , , , , , , , , , , , , , , , , , , ,
	Biomass represented by native individuals within the cladoceran family Bosminidae in the 300-
BOSM300_NAT_BIO	count subsamples (coarse and fine net subsamples combined)
	Number of native individuals within the cladoceran family Bosminidae in the 300-count
BOSM300_NAT_NIND	subsamples (coarse and fine net samples combined)
DOCMOOD NAT NITAY	Number of distinct native taxa within the cladoceran family Bosminidae in the 300-count
BOSM300_NAT_NTAX	subsamples (coarse and fine net samples combined)
	Percent of biomass represented by native individuals within the cladoceran family
BOSM300_NAT_PBIO	Bosminidae in the 300-count subsamples (coarse and fine net samples combined)
	Percent of native individuals within the cladoceran family Bosminidae in the 300-count
BOSM300_NAT_PIND	subsamples (coarse and fine net samples combined)
	Percent of distinct native taxa within the cladoceran family Bosminidae in the 300-count
BOSM300_NAT_PTAX	subsamples (coarse and fine net samples combined)
DOCMOOD NIND	Number of individuals within the cladoceran family Bosminidae in the 300-coount
BOSM300_NIND	subsamples (coarse and fine net samples combined) Number of distinct taxa within the cladoceran family Bosminidae in the 300-count
BOSM300_NTAX	subsamples (coarse and fine net samples combined)
	Percent of biomass represented by individuals within the cladoceran family Bosminidae in the
BOSM300_PBIO	300-count subsamples (coarse and fine net samples combined)
	Percent of individuals within the cladoceran family Bosminidae in the 300-coount
BOSM300_PIND	subsamples (coarse and fine net samples combined)
DOGLAGOO DTAY	Percent of total distinct taxa that are within the cladoceran family Bosminidae in the 300-
BOSM300_PTAX	count subsamples (coarse and fine net samples combined) Biomass represented by individuals within the copepod order Calanoidea (coarse and fine net
CALAN_BIO	samples combined)
S/12/11/_DIO	
	Density (indiv./L) of individuals within the copepod order Calanoidea (coarse and fine net
CALAN_DEN	Density (indiv./L) of individuals within the copepod order Calanoidea (coarse and fine net samples combined)

	Biomass represented by native individuals within the copepod order Calanoidea (coarse and
CALAN_NAT_BIO	fine net samples combined)
O/ (L/ (( \_   \ ( \ ( \   _   \ ( \ ( \   _   \ ( \ ( \   _   \ ( \ ( \   _   \ ( \ ( \ ( \   _   \ ( \ ( \ ( \ ( \ ( \ ( \ ( \ ( \ ( \	Density (indiv./L) of native individuals within the copepod order Calanoidea (coarse and fine
CALAN_NAT_DEN	net samples combined)
	Number of native individuals within the order Calanoidea (coarse and fine net samples
CALAN_NAT_NIND	combined)
	Number of distinct native taxa within the copepod order Calanoidea (coarse and fine net
CALAN_NAT_NTAX	samples combined)
	Percent of biomass represented by native individuals within the order Calanoidea (coarse and
CALAN_NAT_PBIO	fine net samples combined)
	Percent of density (indiv./L) of native individuals within the copepod order Calanoidea (coarse
CALAN_NAT_PDEN	and fine net samples combined)
	Percent of native individuals within the order Calanoidea (coarse and fine net samples
CALAN_NAT_PIND	combined)
	Percent of distinct native taxa within the order Calanoidea (coarse and fine net samples
CALAN_NAT_PTAX	combined)
CALAN_NIND	Number of individuals within the order Calanoidea (coarse and fine net samples combined)
CALAN_NIND	Number of distinct taxa within the copepod order Calanoidea (coarse and fine net samples
CALAN_NTAX	combined)
OALAN_INIAA	Percent of biomass represented by individuals within the order Calanoidea (coarse and fine
CALAN_PBIO	net samples combined)
	Percent of density (indiv./L) of individuals within the copepod order Calanoidea (coarse and
CALAN_PDEN	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)
	Biomass represented by individuals within the copepod order Calanoidea based on 300-
CALAN300_BIO	count subsampless (coarse and fine net subsamples combined)
	Diameter very very control by matics in dividuals within the several endow Colons idea in the 200
CALANDOO NAT DIO	Biomass represented by native individuals within the copepod order Calanoidea in the 300-
CALAN300_NAT_BIO	count subsamples (coarse and fine net subsamples combined)  Number of native individuals within the order Calanoidea in the 300-count subsamples
CALAN300_NAT_NIND	(coarse and fine net samples combined)
CALANGOO_NAI_NIND	Number of distinct native taxa within the copepod order Calanoidea in the 300-count
CALAN300_NAT_NTAX	subsamples (coarse and fine net samples combined)
	Percent of biomass represented by native individuals within the order Calanoidea in the 300-
CALAN300_NAT_PBIO	count subsamples (coarse and fine net samples combined)
	Percent of native individuals within the order Calanoidea in the 300-count subsamples
CALAN300_NAT_PIND	(coarse and fine net samples combined)
	Percent of distinct native taxa within the order Calanoidea in the 300-count subsamples
CALAN300_NAT_PTAX	(coarse and fine net samples combined)
	Number of individuals within the order Calanoidea in the 300-count subsamples (coarse and
CALAN300_NIND	fine net samples combined)

	Number of distinct taxa within the copepod order Calanoidea in the 300-count subsamples
CALAN300_NTAX	(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)
	Percent of individuals within the order Calanoidea in the 300-count subsamples (coarse and
CALAN300_PIND	fine net samples combined)  Percent of distinct taxa within the order Calanoidea in the 300-count subsamples (coarse and
CALAN300_PTAX	fine net samples combined)
OLAB BIO	Biomass represented by individuals within the suborder Cladocera (coarse and fine net
CLAD_BIO	samples combined)  Density (indiv./L) of individuals within the suborder Cladocera (coarse and fine net samples
CLAD_DEN	combined)
CLAD_HERB_BIO	Biomass represented by individuals within the suborder Cladocera that are herbivores
OLAD LIEDD DEN	Density (indiv./L) of individuals within the suborder Cladocera that are herbivores (coarse and
CLAD_HERB_DEN	fine net samples combined)  Number of individuals within the suborder Cladocera that are herbivores (coarse and fine net
CLAD_HERB_NIND	samples combined)
CLAD_HERB_NTAX	Number of distinct cladoceran taxa that are herbivores (coarse and fine net samples combined)
CLAD_IILND_IVIAX	Percent of biomass represented by individuals within the suborder Cladocera that are
CLAD_HERB_PBIO	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)
	Percent of individuals within the suborder Cladocera that are herbivores (coarse and fine net
CLAD_HERB_PIND	samples combined)  Percent of distinct taxa within the suborder Cladocera that are herbivores (coarse and fine net
CLAD_HERB_PTAX	samples combined)
	Diamaga rangagantad by individuals within the subsless Cladesare that are barbiyares in the
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)
	Number of individuals within the suborder Cladocera that are herbivores in the 300-count
CLAD_HERB300_NIND	subsamples (coarse and fine net samples combined)  Number of distinct cladoceran taxa that are herbivores in the 300-count subsamples (coarse
CLAD_HERB300_NTAX	and fine net samples combined)
	Percent of biomass represented by individuals within the suborder Cladocera that are
CLAD_HERB300_PBIO	herbivores in the 300-coount subsamples (coarse and fine net samples combined)
OLAR LIERROSS RIND	Percent of individuals within the suborder Cladocera that are herbivores in the 300-count
CLAD_HERB300_PIND	subsamples (coarse and fine net samples combined)  Percent of distinct taxa within the suborder Cladocera that are herbivores in the 300-count
CLAD_HERB300_PTAX	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)
31.10_10 N_DIO	Density (indiv./L) of native individuals within the suborder Cladocera (coarse and fine net
CLAD_NAT_DEN	samples combined)

	Number of native individuals within the suborder Cladocera (coarse and fine net samples
CLAD_NAT_NIND	combined)
OLAB MAT MTAY	Number of distinct native taxa within the subclass Cladocera (coarse and fine net samples
CLAD_NAT_NTAX	combined)
CLAD NAT DDIO	Percent of biomass represented by native individuals within the suborder Cladocera (coarse
CLAD_NAT_PBIO	and fine net samples combined)  Percent of density (indiv./L) of native individuals within the suborder Cladocera (coarse and
CLAD_NAT_PDEN	fine net samples combined)
CLAD_NAI_FDLN	Percent of native individuals within the suborder Cladocera (coarse and fine net samples
CLAD_NAT_PIND	combined)
02.02.1111_1.1110	comunica
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)
	Number of distinct taxa within the subclass Cladocera (coarse and fine net samples
CLAD_NTAX	combined)
CLAD_OMNI_BIO	Biomass represented by individuals within the suborder Cladocera that are omnivores
	Density (indiv./L) of individuals within the suborder Cladocera that are omnivores (coarse and
CLAD_OMNI_DEN	fine net samples combined)
OLAD OMALI MUND	Number of individuals within the suborder Cladocera that are omnivores (coarse and fine net
CLAD_OMNI_NIND	samples combined)
CLAD_OMNI_NTAX	Number of distinct cladoceran taxa that are omnivores (coarse and fine net samples combined)
CLAD_OMINI_INTAX	Percent of biomass represented by individuals within the suborder Cladocera that are
CLAD_OMNI_PBIO	omnivores (coarse and fine net samples combined)
01115_01 HN_1 510	Percent of density (indiv./L) of individuals within the suborder Cladocera that are omnivores
CLAD_OMNI_PDEN	(coarse and fine net samples combined)
	Percent of individuals within the suborder Cladocera that are omnivores (coarse and fine net
CLAD_OMNI_PIND	samples combined)
	Percent of distinct taxa within the suborder Cladocera that are omnivores (coarse and fine net
CLAD_OMNI_PTAX	samples combined)
0.15 0.000000	Biomass represented by individuals within the subclass Cladocera that are omnivores in the
CLAD_OMNI300_BIO	300-count subsamples (coarse and fine net samples combined)
OLAD OMNUOOO NUND	Number of individuals within the suborder Cladocera that are omnivores in the 300-count
CLAD_OMNI300_NIND	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_OMINISOO_INTAX	and the net samples combined)
	Percent of biomass represented by individuals within the suborder Cladocera that are
CLAD_OMNI300_PBIO	omnivores in the 300-coount subsamples (coarse and fine net samples combined)
	Percent of individuals within the suborder Cladocera that are omnivores in the 300-count
CLAD_OMNI300_PIND	subsamples (coarse and fine net samples combined)
	Percent of distinct taxa within the suborder Cladocera that are omnivores in the 300-count
CLAD_OMNI300_PTAX	subsamples (coarse and fine net samples combined)

	Percent of biomass represented by individuals within the suborder Cladocera (coarse and fine
CLAD_PBIO	net samples combined)
OLAD DDEN	Percent of density (indiv./L) of individuals within the suborder Cladocera (coarse and fine net
CLAD_PDEN	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
	Density (indiv.L) of individuals within the suborder Cladocera that are predators (coarse and
CLAD_PRED_DEN	fine net samples combined)
	Number of individuals within the suborder Cladocera that are predators (coarse and fine net
CLAD_PRED_NIND	samples combined)
	Number of distinct cladoceran taxa that are predators (coarse and fine net samples
CLAD_PRED_NTAX	combined)
CLAD DDED DDIO	Percent of biomass represented by individuals within the suborder Cladocera that are
CLAD_PRED_PBIO	predators (coarse and fine net samples combined)  Percent of density (indiv.L) of individuals within the suborder Cladocera that are predators
CLAD_PRED_PDEN	(coarse and fine net samples combined)
OLAD_I NED_I DEN	Percent of individuals within the suborder Cladocera that are predators (coarse and fine net
CLAD_PRED_PIND	samples combined)
	Percent of distinct taxa within the suborder Cladocera that are predators (coarse and fine net
CLAD_PRED_PTAX	samples combined)
	Biomass represented by individuals within the subclass Cladocera that are predators in the
CLAD_PRED300_BIO	300-count subsamples (coarse and fine net samples combined)
	Number of individuals within the suborder Cladocera that are predators in the 300-count
CLAD_PRED300_NIND	subsamples (coarse and fine net samples combined)
OLAD DDEDOOG NEAV	Number of distinct cladoceran taxa that are predators in the 300-count subsamples (coarse
CLAD_PRED300_NTAX	and fine net samples combined)
	Percent of biomass represented by individuals within the suborder Cladocera that are
CLAD_PRED300_PBIO	predators in the 300-coount subsamples (coarse and fine net samples combined)
OLAD_I NEDOGO_I DIO	Percent of individuals within the suborder Cladocera that are predators in the 300-count
CLAD_PRED300_PIND	subsamples (coarse and fine net samples combined)
	Percent of distinct taxa within the suborder Cladocera that are predators in the 300-count
CLAD_PRED300_PTAX	subsamples (coarse and fine net samples combined)
	Percent of distinct taxa within the suborder Cladocera (coarse and fine net samples
CLAD_PTAX	combined)
	Biomass represented by individuals within the suborder Cladocera in 300-count subsamples
CLAD300_BIO	(coarse and fine net subsamples combined)
0140000 1117 717	Biomass represented bynative individuals within the suborder Cladocera in the 300-count
CLAD300_NAT_BIO	subsamples (coarse and fine net subsamples combined)
CLADOOD NAT NIND	Number of native individuals within the suborder Cladocera in the 300-coount subsamples (coarse and fine net samples combined)
CLAD300_NAT_NIND	Number of distinct native taxa within the suborder Cladocera in the 300-count subsamples
CLAD300_NAT_NTAX	(coarse and fine net samples combined)
25/15000_14/11_141/1/C	(Source and into not earnpied combined)

	Percent of biomass represented by native individuals within the suborder Cladocera in the
CLAD300_NAT_PBIO	300-count subsamples (coarse and fine net samples combined)
CLAD300_NAT_FBIO	Percent of native individuals within the suborder Cladocera in the 300-coount subsamples
CLAD300_NAT_PIND	(coarse and fine net samples combined)
CLADSOO_NAT_FIND	Percent of native taxa within the suborder Cladocera in the 300-count subsamples (coarse
CLAD300_NAT_PTAX	and fine net samples combined)
CLADSUU_NAT_PTAX	
CLADSOO NIND	Number of individuals within the suborder Cladocera in the 300-count subsamples (coarse
CLAD300_NIND	and fine net samples combined)
OLADOOO NITAY	Number of distinct taxa within the suborder Cladocera in the 300-count subsamples (coarse
CLAD300_NTAX	and fine net samples combined)
OLABORA BRIO	Percent of biomass represented by individuals within the suborder Cladocera in the 300-
CLAD300_PBIO	count subsamples (coarse and fine net samples combined)
OLABORA BINIB	Percent of individuals within the suborder Cladocera in the 300-count subsamples (coarse
CLAD300_PIND	and fine net samples combined)
OLABORA BTAY	Percent of distinct taxa within the suborder Cladocera in the 300-count subsamples (coarse
CLAD300_PTAX	and fine net samples combined)
004805 810	Biomass represented by individuals of larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse
COARSE_BIO	and fine net samples combined)
004805 8511	Density (indiv./L) of individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse
COARSE_DEN	and fine net samples combined)
004005 NAT DIO	Biomass represented by individuals of native larger-sized taxa (NET_SIZECLS_NEW=COARSE;
COARSE_NAT_BIO	coarse and fine net samples combined)
	Density (indiv./L) of native individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE;
COARSE_NAT_DEN	coarse and fine net samples combined)
	Number of native individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse
COARSE_NAT_NIND	and fine net samples combined)
	Number of distinct larger-sized native taxa (NET_SIZECLS_NEW=COARSE; coarse and fine net
COARSE_NAT_NTAX	samples combined)
	Percent of biomass represented by native individuals of larger-sized taxa
COARSE_NAT_PBIO	(NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)
	Percent of density (indiv./L) of native individuals within larger-sized taxa
COARSE_NAT_PDEN	(NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)
	Percent of native individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse
COARSE_NAT_PIND	and fine net samples combined)
	Percent of distinct larger-sized native taxa (NET_SIZECLS_NEW=COARSE; coarse and fine net
COARSE_NAT_PTAX	samples combined)
	Number of individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse and fine
COARSE_NIND	net samples combined)
	Number of distinct larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse and fine net
COARSE_NTAX	samples combined)
	Percent of biomass represented by individuals of larger-sized taxa
COARSE_PBIO	(NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)
	Percent of density (indiv./L) of individuals within larger-sized taxa
COARSE_PDEN	(NET_SIZECLS_NEW=COARSE; coarse and fine net samples combined)
	Percent of individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE; coarse and fine
COARSE_PIND	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)  Number of distinct native larger-sized taxa (NET_SIZECLS_NEW=COARSE) in the 300-count
COARSE300_NAT_NTAX	subsamples (coarse and fine net samples combined) Percent of biomass represented by native individuals of larger-sized taxa
COARSE300_NAT_PBIO	(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)  Percent of distinct larger-sized native taxa (NET_SIZECLS_NEW=COARSE) in the 300-count
COARSE300_NAT_PTAX	subsamples (coarse and fine net samples combined)  Number of individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE) in the 300-
COARSE300_NIND	count subsamples (coarse and fine net samples combined)  Number of distinct larger-sized taxa (NET_SIZECLS_NEW=COARSE) in the 300-count
COARSE300_NTAX	subsamples (coarse and fine net samples combined)  Percent of biomass represented by individuals of larger-sized taxa  (NET_SIZECLS_NEW=COARSE) in the 300-count subsamples (coarse and fine net samples
COARSE300_PBIO	combined)  Percent of individuals within larger-sized taxa (NET_SIZECLS_NEW=COARSE) in the 300-count
COARSE300_PIND	subsamples (coarse and fine net samples combined)  Percent of distinct larger-sized taxa (NET_SIZECLS_NEW=COARSE) in the 300-count
COARSE300_PTAX	subsamples (coarse and fine net samples combined)  Biomass represented by individuals within the rotifer order Collothecaceae (coarse and fine
COLLO_BIO	net samples combined)  Density (indiv./L) of individuals within the rotifer order Collothecaceae (coarse and fine net
COLLO_DEN	samples combined)  Number of individuals within the rotifer order Collothecaceae (coarse and fine net samples
COLLO_NIND	combined)  Number of distinct taxa within the rotifer order Collothecaceae (coarse and fine net samples
COLLO_NTAX	combined)  Percent of biomass represented by individuals within the rotifer order Collothecaceae (coarse
COLLO_PBIO	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)

	Percent of distinct taxa within the rotifer order Collothecaceae (coarse and fine net samples
COLLO_PTAX	combined)
	Biomass represented by individuals within the rotifer order Collothecaceae in the 300-count
COLLO300_BIO	subsamples (coarse and fine net subsamples combined)
	Number of individuals within the rotifer order Collothecaceae in the 300-count subsamples
COLLO300_NIND	(coarse and fine net samples combined)
	Number of distinct taxa within the rotifer order Collothecaceae in the 300-count subsamples
COLLO300_NTAX	(coarse and fine net samples combined)
	Descent of hismage represented by individuals within the retifer order Callethoogogg in the
COLLO300_PBIO	Percent of biomass represented by individuals within the rotifer order Collothecaceae in the 300-count subsamples (coarse and fine net samples combined)
COLLO300_FBIO	Percent of individuals within the rotifer order Collothecaceae in the 300-count subsamples
COLLO300_PIND	(coarse and fine net samples combined)
GOLLOGOO_I IIVD	Percent of distinct taxa within the rotifer order Collothecaceae in the 300-count subsamples
COLLO300_PTAX	(coarse and fine net samples combined)
00110000	Biomass represented by individuals within the subclass Copepoda (coarse and fine net
COPE_BIO	samples combined)
	Density (indiv./L) of individuals within the subclass Copepoda (coarse and fine net samples
COPE_DEN	combined)
COPE_HERB_BIO	Biomass represented by individuals within the subclass Copepoda that are herbivores
	Density (indiv.L) of individuals within the subclass Copepoda that are herbivores (coarse and
COPE_HERB_DEN	fine net samples combined)
	Number of individuals within the subclass Copepoda that are herbivores (coarse and fine net
COPE_HERB_NIND	samples combined)
COPE_HERB_NTAX	Number of distinct copepod taxa that are herbivores (coarse and fine net samples combined)
COI L_IILIND_IVIAX	Percent of biomass represented by individuals within the subclass Copepoda that are
COPE_HERB_PBIO	herbivores (coarse and fine net samples combined)
001 = 1.12.115 = 1.510	Percent of density (indiv.L) of individuals within the subclass Copepoda that are herbivores
COPE_HERB_PDEN	(coarse and fine net samples combined)
	Percent of individuals within the subclass Copepoda that are herbivores (coarse and fine net
COPE_HERB_PIND	samples combined)
	Percent of distinct taxa within the subclass Copepoda that are herbivores (coarse and fine net
COPE_HERB_PTAX	samples combined)
	Biomass represented by individuals within the subclass Copepoda that are herbivores in the
COPE_HERB300_BIO	300-count subsamples (coarse and fine net samples combined)
	Number of individuals within the subclass Copepoda that are herbivores in the 300-count
COPE_HERB300_NIND	subsamples (coarse and fine net samples combined)
CODE LIERDOGO NITAV	Number of distinct copepod taxa that are herbivores in the 300-count subsamples (coarse
COPE_HERB300_NTAX	and fine net samples combined)
	Percent of biomass represented by individuals within the subclass Copepoda that are
COPE_HERB300_PBIO	herbivores in the 300-coount subsamples (coarse and fine net samples combined)
001 L_11L1\0000_1 b10	Percent of individuals within the subclass Copepoda that are herbivores in the 300-count
COPE_HERB300_PIND	subsamples (coarse and fine net samples combined)
501 E_11E11D000_1 111D	and anny too look to and the for an interest the formation

	Percent of distinct taxa within the subclass Copepoda that are herbivores in the 300-count
COPE_HERB300_PTAX	subsamples (coarse and fine net samples combined)
	Biomass represented by native individuals within the subclass Copepoda (coarse and fine net
COPE_NAT_BIO	samples combined)
	Density (indiv./L) of native individuals within the subclass Copepoda (coarse and fine net
COPE_NAT_DEN	samples combined)
	Number of native individuals within the subclass Copepoda (coarse and fine net samples
COPE_NAT_NIND	combined)
CODE MAT NEW	Number of distinct native taxa within the subclass Copepoda (coarse and fine net samples
COPE_NAT_NTAX	combined)
COPE_NAT_PBIO	Percent of biomass represented by native individuals within the subclass Copepoda (coarse and fine net samples combined)
COPE_INAI_PBIO	Percent of density (indiv./L) of native individuals within the subclass Copepoda (coarse and
COPE_NAT_PDEN	fine net samples combined)
001 = 11/11 = 1 DEIV	Percent of native individuals within the subclass Copepoda (coarse and fine net samples
COPE_NAT_PIND	combined)
	Percent of distinct native taxa within the subclass Copepoda (coarse and fine net samples
COPE_NAT_PTAX	combined)
COPE_NIND	Number of individuals within the subclass Copepoda (coarse and fine net samples combined)
	Number of distinct taxa within the subclass Copepoda (coarse and fine net samples
COPE_NTAX	combined)
COPE_OMNI_BIO	Biomass represented by individuals within the subclass Copepoda that are omnivores
CODE OMNII DENI	Density (indiv.L) of individuals within the subclass Copepoda that are omnivores (coarse and
COPE_OMNI_DEN	fine net samples combined)  Number of individuals within the subclass Copepoda that are omnivores (coarse and fine net
COPE_OMNI_NIND	samples combined)
OOI L_OI IIII IIIII	Samples combined)
COPE_OMNI_NTAX	Number of distinct copepod taxa that are omnivores (coarse and fine net samples combined)
	Percent of biomass represented by individuals within the subclass Copepoda that are
COPE_OMNI_PBIO	omnivores (coarse and fine net samples combined)
	Percent of density (indiv.L) of individuals within the subclass Copepoda that are omnivores
COPE_OMNI_PDEN	(coarse and fine net samples combined)
	Percent of individuals within the subclass Copepoda that are omnivores (coarse and fine net
COPE_OMNI_PIND	samples combined)
	Percent of distinct taxa within the subclass Copepoda that are omnivores (coarse and fine net
COPE_OMNI_PTAX	samples combined)
	Diamona represented by individuals within the substance Comment of the term and in the
CODE OMNISON BIO	Biomass represented by individuals within the subclass Copepoda that are omnivores in the
COPE_OMNI300_BIO	300-count subsamples (coarse and fine net samples combined)  Number of individuals within the subclass Copepoda that are omnivores in the 300-count
COPE_OMNI300_NIND	subsamples (coarse and fine net samples combined)
201 L_01 1141000_14114D	Number of distinct copepod taxa that are omnivores in the 300-count subsamples (coarse
COPE_OMNI300_NTAX	and fine net samples combined)

COPE_OMNI300_PBIO	Percent of biomass represented by individuals within the subclass Copepoda that are omnivores in the 300-coount subsamples (coarse and fine net samples combined)
001 E_01 IN1000_1 BIO	Percent of individuals within the subclass Copepoda that are omnivores in the 300-count
COPE_OMNI300_PIND	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)
	Percent of biomass represented by individuals within the subclass Copepoda (coarse and fine
COPE_PBIO	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
CODE DRED DEN	Density (indiv.L) of individuals within the subclass Copepoda that are predators (coarse and
COPE_PRED_DEN	fine net samples combined)  Number of individuals within the subclass Copepoda that are predators (coarse and fine net
COPE_PRED_NIND	samples combined)
COPE_PRED_NTAX	Number of distinct copepod taxa that are predators (coarse and fine net samples combined)
001 L_1 NLD_141/4	Percent of biomass represented by individuals within the subclass Copepoda that are
COPE_PRED_PBIO	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)
001 L_1 NLD_1 DL1(	Percent of individuals within the subclass Copepoda that are predators (coarse and fine net
COPE_PRED_PIND	samples combined)
COPE_PRED_PTAX	Percent of distinct taxa within the subclass Copepoda that are predators (coarse and fine net samples combined)
00.122	
CODE DREDOM BIO	Biomass represented by individuals within the subclass Copepoda that are predators in the
COPE_PRED300_BIO	300-count subsamples (coarse and fine net samples combined)  Number of individuals within the subclass Copepoda that are predators in the 300-count
COPE_PRED300_NIND	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)
COFL_FREDS00_NTAX	ine net samples combined)
	Percent of biomass represented by individuals within the subclass Copepoda that are
COPE_PRED300_PBIO	predators in the 300-coount subsamples (coarse and fine net samples combined)  Percent of individuals within the subclass Copepoda that are predators in the 300-count
COPE_PRED300_PIND	subsamples (coarse and fine net samples combined)
CODE DDEDOGG DTAY	Percent of distinct taxa within the subclass Copepoda that are predators in the 300-count
COPE_PRED300_PTAX	subsamples (coarse and fine net samples combined)  Percent of distinct taxa within the subclass Copepoda (coarse and fine net samples
COPE_PTAX	combined)

COPE_RATIO_300_BIO	Ratio of Calanoid to (Cladoccera+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 (Cladoccera+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)  Ratio of Calanoid to (Cladoccera+Cyclopoids) based on biomass (coarse and fine net
COPE_RATIO_BIO	samples combined). Adapted from Kane et al. (2009) Lake Erie plankton IBI. Calculated as CALANOID_BIO/(CLAD_BIO+CYCLOPOID_BIO) Ratio of Calanoid to (Cladoccera+Cyclopoids) based on density (indiv./L; coarse and fine net
COPE_RATIO_DEN	samples combined). Adapted from Kane et al. (2009) Lake Erie plankton IBI. Calculated as CALANOID_DEN/(CLAD_DEN+CYCLOPOID_DEN)
	Ratio of Calanoid to (Cladoccera+Cyclopoids) based on the number of individuals (coarse and fine net samples combined). Adapted from Kane et al. (2009) Lake Erie plankton IBI.
COPE_RATIO_NIND	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)
	Biomass represented by native individuals within the subclass Copepoda in the 300-count
COPE300_NAT_BIO	subsamples (coarse and fine net subsamples combined)
	Number of native individuals within the subclass Copepoda in the 300-count subsamples
COPE300_NAT_NIND	(coarse and fine net samples combined)
	Number of distinct native taxa within the subclass Copepoda in the 300-count subsamples
COPE300_NAT_NTAX	(coarse and fine net samples combined)
	Percent of biomass represented by native individuals within the subclass Copepoda in the
COPE300_NAT_PBIO	300-count subsamples (coarse and fine net samples combined)
00. 2000 2.0	Percent of native individuals within the subclass Copepoda in the 300-count subsamples
COPE300_NAT_PIND	(coarse and fine net samples combined)
	Percent of distinct native taxa within the subclass Copepoda in the 300-count subsamples
COPE300_NAT_PTAX	(coarse and fine net samples combined)
	Number of individuals within the subclass Copepoda in the 300-count subsamples (coarse
COPE300_NIND	and fine net samples combined)
	Number of distinct taxa within the subclass Copepoda in the 300-count subsamples (coarse
COPE300_NTAX	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)
COPESUU_FBIO	Percent of individuals within the subclass Copepoda in the 300-count subsamples (coarse
COPE300_PIND	and fine net samples combined)
	Percent of distinct taxa within the subclass Copepoda in the 300-count subsamples (coarse
COPE300_PTAX	and fine net samples combined)
	Biomass represented by native individuals within the copepod order Cyclopoidea (coarse and
CYCLOP_BIO	fine net samples combined)
	Density (indiv./L) of native individuals within the copepod order Cyclopoidea (coarse and fine
CYCLOP_DEN	net samples combined)

CYCLOP_NIND	Number of individuals within the order Cyclopoidea (coarse and fine net samples combined) Number of distinct taxa within the copepod order Cyclopoidea (coarse and fine net samples
CYCLOP_NTAX	combined) Percent of biomass represented by individuals within the order Cyclopoidea (coarse and fine
CYCLOP_PBIO	net samples combined)  Percent of density (indiv./L) of native individuals within the copepod order Cyclopoidea
CYCLOP_PDEN	(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) Biomass represented by individuals within the copepod order Cyclopoidea in the 300-count
CYCLOP300_BIO	subsamples (coarse and fine net subsamples combined)  Number of individuals within the order Cyclopoidea in the 300-count subsamples (coarse and
CYCLOP300_NIND	fine net samples combined)  Number of distinct taxa within the copepod order Cyclopoidea in the 300-count subsamples
CYCLOP300_NTAX	(coarse and fine net samples combined)  Percent of biomass represented by individuals within the order Cyclopoidea in the 300-count
CYCLOP300_PBIO	subsamples (coarse and fine net samples combined)  Percent of individuals within the order Cyclopoidea in the 300-count subsamples (coarse and
CYCLOP300_PIND	fine net samples combined)  Percent of distinct taxa within the order Cyclopoidea in the 300-count subsamples (coarse
CYCLOP300_PTAX	and fine net samples combined)  Biomass represented by individuals within the family Daphiniidae (coarse and fine net
DAPHNIID_BIO	samples combined)  Density (indiv./L) of individuals within the cladoceran family Daphiniidae (coarse and fine net
DAPHNIID_DEN	samples combined)  Biomass represented by native individuals within the family Daphiniidae (coarse and fine net
DAPHNIID_NAT_BIO	samples combined)  Density (indiv./L) of native individuals within the cladoceran family Daphinidae (coarse and
DAPHNIID_NAT_DEN	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 Daphiniidae (coarse and fine net samples combined)
DAPHNIID_NAT_PBIO	Percent of biomass represented by native individuals within the cladoceran family  Daphiniidae (coarse and fine net samples combined)
DAPHNIID_NAT_PDEN	Percent of density (indiv./L) of native individuals within the cladoceran family Daphiniidae (coarse and fine net samples combined)  Percent of native individuals within the cladoceran family Daphniidae (coarse and fine net
DAPHNIID_NAT_PIND	samples combined)  Percent of distinct native taxa that are within the cladoceran family Daphiniidae (coarse and line net
DAPHNIID_NAT_PTAX	fine net samples combined0
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 Daphiniidae (coarse and fine net samples combined)
5/11 THATE_TATION	Percent of biomass represented by individuals within the cladoceran family Daphiniidae
DAPHNIID_PBIO	(coarse and fine net samples combined)  Percent of density (indiv./L) of individuals within the cladoceran family Daphiniidae (coarse
DAPHNIID_PDEN	and fine net samples combined)
DAPHNIID_PIND	Percent of individuals within the cladoceran family Daphniidae (coarse and fine net samples combined)
DAFHNIID_FIND	Percent of distinct taxa that are within the cladoceran family Daphiniidae (coarse and fine net
DAPHNIID_PTAX	samples combined)
DAPHNIID300_BIO	Biomass represented by individuals within the cladoceran family Daphiniidae in the 300-count subsamples (coarse and fine net subsamples combined)
DAPHNIID300_NAT_BIO	Biomass represented by native individuals within the cladoceran family Daphiniidae in the 300-count subsamples (coarse and fine net subsamples combined)
5/11 / II III 5000_ II II I	Number of native individuals within the cladoceran family Daphniidae in the 300-coount
DAPHNIID300_NAT_NIND	subsamples (coarse and fine net samples combined)
DAPHNIID300_NAT_NTAX	Number of distinct native taxa within the cladoceran family Daphiniidae in the 300-count subsamples (coarse and fine net samples combined)
DAFIINIID300_NAI_NIAX	subsamples (coarse and fine net samples combined)
	Percent of biomass represented by native individuals within the cladoceran family
DAPHNIID300_NAT_PBIO	Daphiniidae 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-coount subsamples (coarse and fine net samples combined)
DAI TIMIDOUO_NAT_TIMD	Percent of distinct native taxa that are within the cladoceran family Daphiniidae in the 300-
DAPHNIID300_NAT_PTAX	count subsamples (coarse and fine net samples combined0
	Number of individuals within the cladoceran family Daphniidae in the 300-count sabsamples
DAPHNIID300_NIND	(coarse and fine net samples combined)
DAPHNIID300_NTAX	Number of distinct taxa within the cladoceran family Daphiniidae in the 300-count subsamples (coarse and fine net samples combined)
DAFTINIID300_NTAX	subsamples (coarse and fine net samples combined)
	Percent of biomass represented by individuals within the cladoceran family Daphiniidae in the
DAPHNIID300_PBIO	300-count subsamples (coarse and fine net samples combined)  Percent of individuals within the cladoceran family Daphniidae in the 300-count sabsamples
DAPHNIID300_PIND	(coarse and fine net samples combined)
	Percent of distinct taxa that are within the cladoceran family Daphiniidae in the 300-count
DAPHNIID300_PTAX	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)
DOMI_SUO_CEAD_I BIO	Percent of individuals within the most abundant cladoceran taxon in the 300-count
DOM1_300_CLAD_PIND	subsamples (coarse and fine-mesh net samples combined)
	Percent of biomass within the most abundant copepod taxon in the 300-count subsamples
DOM1_300_COPE_PBIO	(coarse and fine-mesh net samples combined)  Percent of individuals within the most abundant copepod taxon in the 300-count subsamples
DOM1_300_COPE_PIND	(coarse and fine-mesh net samples combined)
	Percent of biomass within the most abundant taxon in the 300-count subsamples (coarse and
DOM1_300_PBIO	fine-mesh net samples combined)

	Percent of individuals within the most abundant taxon in the 300-count subsamples (coarse
DOM1_300_PIND	and fine-mesh net samples combined)
DOTTI_000_1 111D	Percent of biomass within the most abundant rotifer taxon in the 300-count subsamples
DOM1_300_ROT_PBIO	(coarse and fine-mesh net samples combined)
B 0111_000_1101_1 B10	Percent of individuals within the most abundant rotifer taxon in the 300-count subsamples
DOM1_300_ROT_PIND	(coarse and fine-mesh net samples combined)
D 01112_000_1101_1 1111B	Percent of biomass within the most abundant cladoceran taxon (coarse and fine-mesh net
DOM1_CLAD_PBIO	samples combined)
5 0	Percent of density (indiv./L) within the most abundant cladoceran taxon (coarse and fine-
DOM1_CLAD_PDEN	mesh net samples combined)
	Percent of individuals within the most abundant cladoceran taxon (coarse and fine-mesh net
DOM1_CLAD_PIND	samples combined)
	Percent of biomass within the most abundant copepod taxon (coarse and fine-mesh net
DOM1_COPE_PBIO	samples combined)
	Percent of density (indiv./L) within the most abundant copepod taxon (coarse and fine-mesh
DOM1_COPE_PDEN	net samples combined)
	Percent of individuals within the most abundant copepod taxon (coarse and fine-mesh net
DOM1_COPE_PIND	samples combined)
	Percent of biomass within the most abundant taxon (coarse and fine-mesh net samples
DOM1_PBIO	combined)
	Percent of density (indiv./L) within the most abundant taxon (coarse and fine-mesh net
DOM1_PDEN	samples combined)
	Percent of individuals within the most abundant taxon (coarse and fine-mesh net samples
DOM1_PIND	combined)
	Percent of biomass within the most abundant rotifer taxon (coarse and fine-mesh net
DOM1_ROT_PBIO	samples combined)
	Percent of density (indiv./L) within the most abundant rotifer taxon (coarse and fine-mesh net
DOM1_ROT_PDEN	samples combined)
	Percent of individuals within the most abundant rotifer taxon (coarse and fine-mesh net
DOM1_ROT_PIND	samples combined)
	Percent of biomass within the 3 most abundant cladoceran taxa in the 300-count subsamples
DOM3_300_CLAD_PBIO	(coarse and fine-mesh net samples combined)
	Percent of individuals within the 3 most abundant cladoceran taxa in the 300-count
DOM3_300_CLAD_PIND	subsamples (coarse and fine-mesh net samples combined)
	Percent of biomass within the 3 most abundant copepod taxa in the 300-count subsamples
DOM3_300_COPE_PBIO	(coarse and fine-mesh net samples combined)
DOMO COO CODE DIND	Percent of individuals within the 3 most abundant copepod taxa in the 300-count subsamples
DOM3_300_COPE_PIND	(coarse and fine-mesh net samples combined)
DOMO 200 DDIO	Percent of biomass within the 3 most abundant taxa in the 300-count subsamples (coarse
DOM3_300_PBIO	and fine-mesh net samples combined)
DOM3_300_PIND	Percent of individuals within the 3 most abundant taxa in the 300-count subsamples (coarse
บบเมอ_งบบ_คแทบ	and fine-mesh net samples combined)  Percent of biomass within the 3 most abundant rotifer taxa in the 300-count subsamples
DOM3_300_ROT_PBIO	(coarse and fine-mesh net samples combined)
20110_000_NO1_1 blO	Percent of individuals within the 3 most abundant rotifer taxa in the 300-count subsamples
DOM3_300_ROT_PIND	(coarse and fine-mesh net samples combined)
DOMO_000_NOT_FIND	(vouloe and fine meeting confidence)

	Percent of biomass within the 3 most abundant cladoceran taxa (coarse and fine-mesh net
DOM3_CLAD_PBIO	samples combined)
	Percent of density (indiv./L) within the 3 most abundant cladoceran taxa (coarse and fine-
DOM3_CLAD_PDEN	mesh net samples combined)
	Percent of individuals within the 3 most abundant cladoceran taxa (coarse and fine-mesh net
DOM3_CLAD_PIND	samples combined)
	Percent of biomass within the 3 most abundant copepod taxa (coarse and fine-mesh net
DOM3_COPE_PBIO	samples combined)
DOMO CODE DDEN	Percent of density (indiv./L) within the 3 most abundant copepod taxa (coarse and fine-mesh
DOM3_COPE_PDEN	net samples combined)
DOM2 CODE DIND	Percent of individuals within the 3 most abundant copepod taxa (coarse and fine-mesh net
DOM3_COPE_PIND	samples combined) Percent of biomass within the 3 most abundant taxa (coarse and fine-mesh net samples
DOM3_PBIO	combined)
DOM3_F BIO	Percent of density (indiv./L) within the 3 most abundant taxa (coarse and fine-mesh net
DOM3_PDEN	samples combined)
DOI 10_1 DEN	Percent of individuals within the 3 most abundant taxa (coarse and fine-mesh net samples
DOM3_PIND	combined)
· · · · <u>-</u> · · · · ·	Percent of biomass within the 3 most abundant rotifer taxa (coarse and fine-mesh net
DOM3_ROT_PBIO	samples combined)
	Percent of density (indiv./L) within the 3 most abundant rotifer taxa (coarse and fine-mesh net
DOM3_ROT_PDEN	samples combined)
	Percent of individuals within the 3 most abundant rotifer taxa (coarse and fine-mesh net
DOM3_ROT_PIND	samples combined)
	Percent of biomass within the 5 most abundant cladoceran taxa in the 300-count subsamples
DOM5_300_CLAD_PBIO	(coarse and fine-mesh net samples combined)
	Percent of individuals within the 5 most abundant cladoceran taxa in the 300-count
DOM5_300_CLAD_PIND	subsamples (coarse and fine-mesh net samples combined)
	Percent of biomass within the 5 most abundant copepod taxa in the 300-count subsamples
DOM5_300_COPE_PBIO	(coarse and fine-mesh net samples combined)
	Percent of individuals within the 5 most abundant copepod taxa in the 300-count subsamples
DOM5_300_COPE_PIND	(coarse and fine-mesh net samples combined)
	Percent of biomass within the 5 most abundant taxa in the 300-count subsamples (coarse
DOM5_300_PBIO	and fine-mesh net samples combined)
DOME OOD DIND	Percent of individuals within the 5 most abundant taxa in the 300-count subsamples (coarse
DOM5_300_PIND	and fine-mesh net samples combined)  Percent of biomass within the 5 most abundant rotifer taxa in the 300-count subsamples
DOME 200 DOT DDIO	·
DOM5_300_ROT_PBIO	(coarse and fine-mesh net samples combined)  Percent of individuals within the 5 most abundant rotifer taxa in the 300-count subsamples
DOM5_300_ROT_PIND	(coarse and fine-mesh net samples combined)
DOMO_000_NOT_1 IND	Percent of biomass within the 5 most abundant cladoceran taxa (coarse and fine-mesh net
DOM5_CLAD_PBIO	samples combined)
	Percent of density (indiv./L) within the 5 most abundant cladoceran taxa (coarse and fine-
DOM5_CLAD_PDEN	mesh net samples combined)
- <b>-</b>	Percent of individuals within the 5 most abundant cladoceran taxa (coarse and fine-mesh net
DOM5_CLAD_PIND	samples combined)
<del>_</del>	

DOME CODE DDIO	Percent of biomass within the 5 most abundant copepod taxa (coarse and fine-mesh net
DOM5_COPE_PBIO	samples combined) Percent of density (indiv./L) within the 5 most abundant copepod taxa (coarse and fine-mesh
DOM5_COPE_PDEN	net samples combined)  Percent of individuals within the E-most shundant consend taxa (coarse and fine most not
DOM5_COPE_PIND	Percent of individuals within the 5 most abundant copepod taxa (coarse and fine-mesh net samples combined)
DOME DDIO	Percent of biomass within the 5 most abundant taxa (coarse and fine-mesh net samples
DOM5_PBIO	combined) Percent of density (indiv.L) within the 5 most abundant taxa (coarse and fine-mesh net
DOM5_PDEN	samples combined)
DOM5_PIND	Percent of individuals within the 5 most abundant taxa (coarse and fine-mesh net samples combined)
	Percent of biomass within the 5 most abundant rotifer taxa (coarse and fine-mesh net
DOM5_ROT_PBIO	samples combined) Percent of density (indiv./L) within the 5 most abundant rotifer taxa (coarse and fine-mesh net
DOM5_ROT_PDEN	samples combined)
DOM5_ROT_PIND	Percent of individuals within the 5 most abundant rotifer taxa (coarse and fine-mesh net samples combined)
DOMS_NOT_FIND	samples combined)
EVEN OLAD	Evenness based on the number of cladoceran individuals (coarse and fine net samples
EVEN_CLAD	combined). Calculated as HPRIME_ROT/Log(S) where Log is the natural logrithm 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
EVEN_CLAD300	natural logrithm
	Evenness based on the number of copepod individuals (coarse and fine net samples
EVEN_COPE	combined). Calculated as HPRIME_ROT/Log(S) where Log is the natural logrithm
	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
EVEN_COPE300	logrithm
EVEN NUND	Evenness based on the number of individuals (coarse and fine net samples combined).
EVEN_NIND	Calculated as HPRIME_ROT/Log(S) where Log is the natural logrithm
	Evenness based on the number of rotifer individuals (coarse and fine net samples combined).
EVEN_ROT	Calculated as HPRIME_ROT/Log(S) where Log is the natural logrithm  Eveness 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
EVEN_ROT300	logrithm
	Evenness based on the number of individuals in the 300-count subsamples (coarse and fine
EVEN300_NIND	net samples combined). Calculated as HPRIME_ROT/Log(S) where Log is the natural logrithm
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)  Number of native families represented in 300 count subsamples (coarse and fine net samples
FAM300_NAT_NTAX	combined)

	Number of families represented in 300 count subsamples (coarse and fine net samples
FAM300_NTAX	combined)
	Biomass represented by individuals of smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse
FINE_BIO	and fine net samples combined)
	Density (indiv./L) of individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse
FINE_DEN	and fine net samples combined)
	Biomass represented by native individuals of smaller-sized taxa (NET_SIZECLS_NEW=FINE;
FINE_NAT_BIO	coarse and fine net samples combined)
	Density (indiv./L) of native individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE;
FINE_NAT_DEN	coarse and fine net samples combined)
	Number of native individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and
FINE_NAT_NIND	fine net samples combined)
	Number of distinct smaller-sized native taxa (NET_SIZECLS_NEW=FINE; coarse and fine net
FINE_NAT_NTAX	samples combined)
	Percent of biomass represented by native individuals of smaller-sized taxa
FINE_NAT_PBIO	(NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
FINE MAT BREM	Percent of density (indiv./L) of native individuals within smaller-sized taxa
FINE_NAT_PDEN	(NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
FINE MAT DIND	Percent of native individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and
FINE_NAT_PIND	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_NAI_FIAX	Number of individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and fine
FINE_NIND	net samples combined)
TINE_MIND	Number of distinct smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and fine net samples
FINE_NTAX	combined)
· <u>-</u>	Percent of biomass represented by individuals of smaller-sized taxa
FINE_PBIO	(NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
_	Percent of density (indiv./L) of individuals within smaller-sized taxa
FINE_PDEN	(NET_SIZECLS_NEW=FINE; coarse and fine net samples combined)
	Percent of individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and fine
FINE_PIND	net samples combined)
	Percent of distinct smaller-sized taxa (NET_SIZECLS_NEW=FINE; coarse and fine net samples
FINE_PTAX	combined)
	Biomass represented by individuals of smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the
FINE300_BIO	300-count subsamples (coarse and fine net subsamples combined)
FINIFOGO NAT DIO	Biomass represented by native individuals of smaller-sized taxa (NET_SIZECLS_NEW=FINE) in
FINE300_NAT_BIO	the 300-count subsamples (coarse and fine net subsamples combined)
	Number of native individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-
FINE300_NAT_NIND	count subsamples (coarse and fine net samples combined)
I IINEOUU_INAT_INIINU	Number of distinct native smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-count
FINE300_NAT_NTAX	subsamples (coarse and fine net samples combined)

	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
FINE300_NAT_PBIO	combined)
	Percent of native individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-
FINE300_NAT_PIND	count subsamples (coarse and fine net samples combined)
	Percent of distinct native smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-count
FINE300_NAT_PTAX	subsamples (coarse and fine net samples combined)
	Number of individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-count
FINE300_NIND	subsamples (coarse and fine net samples combined)
	Number of distinct smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-count
FINE300_NTAX	subsamples (coarse and fine net samples combined)
	Percent of biomass represented by individuals of smaller-sized taxa
	(NET_SIZECLS_NEW=FINE) in the 300-count subsamples (coarse and fine net samples
FINE300_PBIO	combined)
	Percent of individuals within smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-count
FINE300_PIND	subsamples (coarse and fine net samples combined)
	Percent of distinct smaller-sized taxa (NET_SIZECLS_NEW=FINE) in the 300-count
FINE300_PTAX	subsamples (coarse and fine net samples combined)
	Biomass represented by individuals within the rotifer order Flosculariaceae (coarse and fine
FLOS_BIO	net samples combined)
	Density (indiv./L) of individuals within the rotifer order Flosculariaceae (coarse and fine net
FLOS_DEN	samples combined)
	Number of individuals within the rotifer order Flosculariaceae (coarse and fine net samples
FLOS_NIND	combined)
	Number of distinct taxa within the rotifer order Flosculariaceae (coarse and fine net samples
FLOS_NTAX	combined)
	Percent of biomass represented by individuals within the rotifer order Flosculariaceae (coarse
FLOS_PBIO	and fine net samples combined)
	Percent of density (indiv./L) of individuals within the rotifer order Flosculariaceae (coarse and
FLOS_PDEN	fine net samples combined)
	Percent of individuals within the rotifer order Flosculariaceae (coarse and fine net samples
FLOS_PIND	combined)
	Percent of distinct taxa within the rotifer order Flosculariaceae (coarse and fine net samples
FLOS_PTAX	combined)
	Biomass represented by individuals within the rotifer order Flosculariaceae in the 300-count
FLOS300_BIO	subsamples (coarse and fine net subsamples combined)
	Number of individuals within the rotifer order Flosculariaceae in the 300-count subsamples
FLOS300_NIND	(coarse and fine net samples combined)
FLOCOCO NITAV	Number of distinct taxa within the rotifer order Flosculariaceae in the 300-count subsamples
FLOS300_NTAX	(coarse and fine net samples combined)
	Develop of his many control by individual quithing the matifest and at Classical and a second at the
ELOCODO DDIO	Percent of biomass represented by individuals within the rotifer order Flosculariaceae in the
FLOS300_PBIO	300-coount subsamples (coarse and fine net samples combined)
ELOCADO DINID	Percent of individuals within the rotifer order Flosculariaceae in the 300-count subsamples
FLOS300_PIND	(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 GEN300_NAT_NTAX	Number of genera represented by distinct taxa (coarse and fine net samples combined)  Number of native genera represented in the 300 count subsamples (coarse and fine net samples combined)
GENSOO_NAT_NTAX	Number of genera represented in the 300 count subsamples (coarse and fine net samples
GEN300_NTAX	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)
HEDD DDIO	Percent of biomass represented by individuals that are herbivores (coarse and fine net
HERB_PBIO	samples combined) Percent of density (indiv.L) of individuals that are herbivores (coarse and fine net samples
HERB_PDEN	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) Biomass represented by individuals that are herbivores in the 300-count subsamples (coarse
HERB300_BIO	and fine net samples combined)
HERB300_NIND	Number of individuals that are herbivores in the 300-count subsamples (coarse and fine net samples combined)
LIEDDOOG NITAV	Number of distinct herbivore taxa in the 300-count subsamples (coarse and fine net samples
HERB300_NTAX	combined)  Percent of biomass represented by individuals that are herbivores in the 300-coount
HERB300_PBIO	subsamples (coarse and fine net samples combined)
LIEDDOGG DINID	Percent of individuals that are herbivores in the 300-count subsamples (coarse and fine net
HERB300_PIND	samples combined)  Percent of distinct taxa that are herbivores in the 300-count subsamples (coarse and fine net
HERB300_PTAX	samples combined)
	Shannon Diversity based on the biomass of individuals (coarse and fine net samples combined). Calculated as SUM{p(i)*Log[p(i)]}, where p(i) is proportion of biomass of taxon i,
HPRIME_BIO	and Log= natural logrithm.
	Shannon Diversity based on the number of cladoceran individuals (coarse and fine net
	samples combined). Calculated as $SUM\{p(i)*Log[p(i)]\}$ , where $p(i)$ is proportion of individuals
HPRIME_CLAD	of taxon i , and Log= natural logrithm.
	Shannon Diversity based on the number of cladoceran individuals in the 300-count
	subsamples (coarse and fine net samples combined). Calculated as $SUM\{p(i)*Log[p(i)]\}$ ,
HPRIME_CLAD300	where p(i) is proportion of individuals of taxon i , and Log= natural logrithm.

HPRIME_COPE	Shannon Diversity based on the number of copepod individuals (coarse and fine net samples combined). Calculated as $SUM\{p(i)*Log[p(i)]\}$ , where $p(i)$ is proportion of individuals of taxon $i$ , and $Log=$ natural logrithm.
HPRIME_COPE300	Shannon Diversity based on the number of copepod individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as SUM{p(i)*Log[p(i)]}, where p(i) is proportion of individuals of taxon i, and Log= natural logrithm.  Shannon Diversity based on the density (indiv./L) of individuals (coarse and fine net samples
HPRIME_DEN	combined). Calculated as $SUM\{p(i)*Log[p(i)]\}$ , where $p(i)$ is proportion of density of taxon $i$ , and $Log=$ natural logrithm. Shannon Diversity based on the total number of individuals (coarse and fine net samples
HPRIME_NIND	combined). Calculated as $SUM\{p(i)*Log[p(i)]\}$ , where $p(i)$ is proportion of individuals of taxon $i$ , and $Log=$ natural logrithm. Shannon Diversity based on the number of rotifer individuals (coarse and fine net samples
HPRIME_ROT	combined). Calculated as $SUM\{p(i)*Log[p(i)]\}$ , where $p(i)$ is proportion of individuals of taxon $i$ , and $Log=$ natural logrithm.
HPRIME_ROT300	Shannon Diversity based on the number of rotifer individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as $SUM\{p(i)*Log[p(i)]\}$ , where $p(i)$ is proportion of individuals of taxon $i$ , and $Log=$ natural logrithm.
HPRIME300_BIO	Shannon Diversity based on the biomass of individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as $SUM\{p(i)*Log[p(i)]\}$ , where $p(i)$ is proportion of biomass of taxon $i$ , and $Log=$ natural logrithm.
HPRIME300_NIND LGCLAD_BIO	Shannon Diversity based on the total number of individuals in the 300-count subsamples (coarse and fine net samples combined). Calculated as SUM{p(i)*Log[p(i)]}, where p(i) is proportion of individuals of taxon i, and Log= natural logrithm.  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 CLADOCERAN_SIZE=LARGE; coarse and fine net samples combined)
LGCLAD_NAT_PIND	Percent of native individuals within large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=LARGE; coarse and fine net samples combined)  Percent of distinct native large cladoceran taxa (SUBORDER=CLADOCERA and
LGCLAD_NAT_PTAX	CLADOCERAN_SIZE=LARGE; coarse and fine net samples combined)  Number of individuals within large cladoceran taxa (SUBORDER=CLADOCERA and
LGCLAD_NIND	CLADOCERAN_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)  Percent of biomass represented by individuals within large cladoceran taxa  (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE; coarse and fine net samples
LGCLAD_PBIO	combined) Percent of density (indiv./L) of individuals within large cladoceran taxa
LGCLAD_PDEN	(SUBORDER=CLADOCERA and CLADOCERAN_SIZE=LARGE; coarse and fine net samples combined)
LGCLAD_PIND	Percent of individuals within large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=LARGE; coarse and fine net samples combined)
LGCLAD_PTAX	Percent of distinct large cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=LARGE; coarse and fine net samples combined) Biomass represented by large cladoceran individuals (SUBORDER=CLADOCERA and
LGCLAD300_BIO	CLADOCEAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net subsamples combined) Biomass represented by native large cladoceran individuals (SUBORDER=CLADOCERA and
LGCLAD300_NAT_BIO	CLADOCEAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net subsamples combined)  Number of native individuals within large cladoceran taxa (SUBORDER=CLADOCERA and
LGCLAD300_NAT_NIND	CLADOCERAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net samples combined)  Number of distinct taxa represented by native large cladocerans (SUBORDER=CLADOCERA
LGCLAD300_NAT_NTAX	and CLADOCEAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net samples combined)  Percent of biomass represented by native large cladoceran individuals
LGCLAD300_NAT_PBIO	(SUBORDER=CLADOCERA and CLADOCEAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net samples combined)  Percent of native individuals within large cladoceran taxa (SUBORDER=CLADOCERA and
LGCLAD300_NAT_PIND	CLADOCERAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net samples combined)  Percent of distinct native large cladoceran taxa (SUBORDER=CLADOCERA and
LGCLAD300_NAT_PTAX	CLADOCERAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net samples combined)

	Number of individuals within large cladoceran taxa (SUBORDER=CLADOCERA and
	CLADOCERAN_SIZE=LARGE) in the 300-coount subsamples (coarse and fine net samples
LGCLAD300_NIND	combined)
	Number of distinct taxa represented by large cladocerans (SUBORDER=CLADOCERA and
	CLADOCEAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net samples
LGCLAD300_NTAX	combined)
	Percent of biomass represented by large cladoceran individuals (SUBORDER=CLADOCERA
	and CLADOCEAN_SIZE=LARGE) in the 300-coount subsamples (coarse and fine net samples
LGCLAD300_PBIO	combined)
LOOLADOUO_I DIO	Percent of individuals within large cladoceran taxa (SUBORDER=CLADOCERA and
	CLADOCERAN_SIZE=LARGE) in the 300-coount subsamples (coarse and fine net samples
LCCLAD200 DINID	
LGCLAD300_PIND	combined)
	Percent of distinct large cladoceran taxa (SUBORDER=CLADOCERA and
	CLADOCERAN_SIZE=LARGE) in the 300-count subsamples (coarse and fine net samples
LGCLAD300_PTAX	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)
	Percent of biomass represented by individuals that are omnivores (coarse and fine net
OMNI_PBIO	samples combined)
	Percent of density (indiv.L) of individuals that are omnivores (coarse and fine net samples
OMNI_PDEN	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)
	Biomass represented by individuals that are omnivores in the 300-count subsamples (coarse
OMNI300_BIO	and fine net samples combined)
	Number of individuals that are omnivores in the 300-count subsamples (coarse and fine net
OMNI300_NIND	samples combined)
	Number of distinct omnivore taxa in the 300-count subsamples (coarse and fine net samples
OMNI300_NTAX	combined)
	Percent of biomass represented by individuals that are omnivores in the 300-coount
OMNI300_PBIO	subsamples (coarse and fine net samples combined)
	Percent of individuals that are omnivores in the 300-count subsamples (coarse and fine net
OMNI300_PIND	samples combined)
	Percent of distinct taxa that are omnivores in the 300-count subsamples (coarse and fine net
OMNI300_PTAX	samples combined)
_	
	Hurlburts Probability of Insterspecific 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 proportin of taxon I in the sample, N is the total number of indiviual in the
PIE_CLAD	sample, and n(i) is the number of individuals of taxon i in the sample.
L_ <i>3L</i>	sample, and man to hamber of maintains of taken in the sample.

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  $SUM\{p(i)*[N-n(i)/N-1]\}$  where p(i) is the proportin of taxon I in the sample, N is the total number of indiviual in the sample, and n(i) is the number of individuals of taxon i in PIE\_CLAD300 the sample. Hurlburts Probability of Insterspecific Encounter (PIE) based on the number of copepod individuals (coarse and fine net samples combined). Calculated as SUM{p(i)\*[N-n(i)/N-1]} where p(i) is the proportin of taxon I in the sample, N is the total number of indiviual in the PIE COPE sample, and n(i) is the number of individuals of taxon i in the sample. 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 SUM{p(i)\*[N-n(i)/N-1]} where p(i) is the proportin of taxon I in the sample, N is the total number of indiviual in the sample, and n(i) is the number of individuals of taxon i in PIE\_COPE300 the sample. Hurlburts Probability of Insterspecific Encounter (PIE) based on the total number of individuals (coarse and fine net samples combined). Calculated as SUM{p(i)\*[N-n(i)/N-1]} where p(i) is the proportin of taxon I in the sample, N is the total number of indiviual in the PIE\_NIND sample, and n(i) is the number of individuals of taxon i in the sample. Hurlburts Probability of Insterspecific Encounter (PIE) based on the number of rotifer individuals (coarse and fine net samples combined). Calculated as SUM{p(i)\*[N-n(i)/N-1]} where p(i) is the proportin of taxon I in the sample, N is the total number of indiviual in the PIE\_ROT sample, and n(i) is the number of individuals of taxon i in the sample. 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 SUM{p(i)\*[N-n(i)/N-1]} where p(i) is the proportin of taxon I in the sample, N is the total number of indiviual in the sample, and n(i) is the number of individuals of taxon i in PIE\_ROT300 the sample. 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 SUM{p(i)\*[N-n(i)/N-1]} where p(i) is the proportin of taxon I in the sample, N is the total number of indiviual in the sample, and n(i) is the number of individuals of taxon i in PIE300\_NIND the sample. Biomass represented by individuals within the rotifer order Ploima (coarse and fine net PLOIMA BIO samples combined) Density (indiv./L) of individuals within the rotifer order Ploima (coarse and fine net samples combined) PLOIMA DEN PLOIMA\_NIND Number of individuals within the rotifer order Ploima (coarse and fine net samples combined) Number of distinct taxa within the rotifer order Ploima (coarse and fine net samples PLOIMA\_NTAX combined) Percent of biomass represented by individuals within the rotifer order Ploima (coarse and fine PLOIMA\_PBIO net samples combined) Percent of density (indiv./L) of individuals within the rotifer order Ploima (coarse and fine net

PLOIMA PDEN

samples combined)

PLOIMA_PTAX combined) Biomass represented by individuals within the rotifer order Ploima in the 300-count  PLOIMA300_BIO subsamples (coarse and fine net subsamples combined) Number of individuals within the rotifer order Ploima in the 300-count subsamples (coarse
Biomass represented by individuals within the rotifer order Ploima in the 300-count subsamples (coarse and fine net subsamples combined)
PLOIMA300_BIO subsamples (coarse and fine net subsamples combined)
Number of individuals within the rother order i tolling in the 500-count subscillptes (coalse
PLOIMA300_NIND and fine net samples combined)
Number of distinct taxa within the rotifer order Ploima in the 300-count subsamples (coarse
PLOIMA300_NTAX and fine net samples combined)
Percent of biomass represented by individuals within the rotifer order Ploima in the 300- PLOIMA300_PBIO count subsamples (coarse and fine net samples combined)
Percent of individuals within the rotifer order Ploima in the 300-count subsamples (coarse
PLOIMA300_PIND and fine net samples combined)
Percent of distinct taxa within the rotifer order Ploima in the 300-count subsamples (coarse
PLOIMA300_PTAX 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)
Percent of biomass represented by individuals that are predators (coarse and fine net PRED_PBIO samples combined)
Percent of density (indiv.L) of individuals that are predators (coarse and fine net samples
PRED_PDEN 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)
Biomass represented by individuals that are predators in the 300-count subsamples (coarse
PRED300_BIO and fine net samples combined)
Number of individuals that are predators in the 300-count subsamples (coarse and fine net
PRED300_NIND samples combined)
Number of distinct predator taxa in the 300-count subsamples (coarse and fine net samples
PRED300_NTAX combined)
Percent of biomass represented by individuals that are predators in the 300-coount PRED300_PBIO subsamples (coarse and fine net samples combined)
Percent of individuals that are predators in the 300-count subsamples (coarse and fine net
PRED300_PIND samples combined)
Percent of distinct taxa that are predators in the 300-count subsamples (coarse and fine net
PRED300_PTAX samples combined)
ROT_BIO Biomass represented by individuals within the phylum Rotifera
Density (indiv./L) of native individuals within the phylum Rotifera (coarse and fine net samples
ROT_DEN combined)
ROT_HERB_BIO Biomass represented by individuals within the phylum Rotifera that are herbivores

ROT_HERB_DEN  ROT_HERB_NIND	Density (indiv.L) of individuals within the phylum Rotifera that are herbivores (coarse and fine net samples combined)  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)  Percent of biomass represented by individuals within the phylum Rotifera that are herbivores
ROT_HERB_PBIO	(coarse and fine net samples combined)  Percent of density (indiv.L) of individuals within the phylum Rotifera that are herbivores
ROT_HERB_PDEN	(coarse and fine net samples combined)  Percent of individuals within the phylum Rotifera that are herbivores (coarse and fine net
ROT_HERB_PIND	samples combined) Percent of distinct taxa within the phylum Rotifera that are herbivores (coarse and fine net
ROT_HERB_PTAX	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)  Number of individuals within the phylum Rotifera that are herbivores in the 300-count
ROT_HERB300_NIND	subsamples (coarse and fine net samples combined)  Number of distinct rotifer taxa that are herbivores in the 300-count subsamples (coarse and
ROT_HERB300_NTAX	fine net samples combined)
ROT_HERB300_PBIO	Percent of biomass represented by individuals within the phylum Rotifera that are herbivores in the 300-coount subsamples (coarse and fine net samples combined)  Percent of individuals within the phylum Rotifera that are herbivores in the 300-count
ROT_HERB300_PIND	subsamples (coarse and fine net samples combined)  Percent of distinct taxa within the phylum Rotifera that are herbivores in the 300-count
ROT_HERB300_PTAX	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  Density (indiv.L) of individuals within the phylum Rotifera that are omnivores (coarse and fine
ROT_OMNI_DEN	net samples combined) Number of individuals within the phylum Rotifera that are omnivores (coarse and fine net
ROT_OMNI_NIND	samples combined)
ROT_OMNI_NTAX	Number of distinct rotifer taxa that are omnivores (coarse and fine net samples combined)  Percent of biomass represented by individuals within the phylum Rotifera that are omnivores
ROT_OMNI_PBIO	(coarse and fine net samples combined)  Percent of density (indiv.L) of individuals within the phylum Rotifera that are omnivores
ROT_OMNI_PDEN	(coarse and fine net samples combined)  Percent of individuals within the phylum Rotifera that are omnivores (coarse and fine net
ROT_OMNI_PIND	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)  Number of individuals within the phylum Rotifera that are omnivores in the 300-count
ROT_OMNI300_NIND	subsamples (coarse and fine net samples combined) Number of distinct rotifer taxa that are omnivores in the 300-count subsamples (coarse and
ROT_OMNI300_NTAX	fine net samples combined)
ROT_OMNI300_PBIO	Percent of biomass represented by individuals within the phylum Rotifera that are omnivores in the 300-coount subsamples (coarse and fine net samples combined)  Percent of individuals within the phylum Rotifera that are omnivores in the 300-count
ROT_OMNI300_PIND	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)
<del>-</del>	Percent of density (indiv./L) of native individuals within the phylum Rotifera (coarse and fine
ROT_PDEN	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  Density (indiv.L) of individuals within the phylum Rotifera that are predators (coarse and fine
ROT_PRED_DEN	net samples combined) Number of individuals within the phylum Rotifera that are predators (coarse and fine net
ROT_PRED_NIND	samples combined)
	Samples combined)
ROT_PRED_NTAX	Number of distinct rotifer taxa that are predators (coarse and fine net samples combined)  Percent of biomass represented by individuals within the phylum Rotifera that are predators
	Number of distinct rotifer taxa that are predators (coarse and fine net samples combined)  Percent of biomass represented by 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) Percent of biomass represented by individuals within the phylum Rotifera that are predators (coarse and fine net samples combined) Percent of density (indiv.L) of individuals within the phylum Rotifera that are predators (coarse and fine net samples combined)
ROT_PRED_NTAX ROT_PRED_PBIO	Number of distinct rotifer taxa that are predators (coarse and fine net samples combined) Percent of biomass represented by individuals within the phylum Rotifera that are predators (coarse and fine net samples combined) Percent of density (indiv.L) of individuals within the phylum Rotifera that are predators (coarse
ROT_PRED_NTAX ROT_PRED_PBIO ROT_PRED_PDEN ROT_PRED_PIND	Number of distinct rotifer taxa that are predators (coarse and fine net samples combined) Percent of biomass represented by individuals within the phylum Rotifera that are predators (coarse and fine net samples combined) Percent of density (indiv.L) of individuals within the phylum Rotifera that are predators (coarse and fine net samples combined) Percent of individuals within the phylum Rotifera that are predators (coarse and fine net samples combined) Percent of distinct taxa within the phylum Rotifera that are predators (coarse and fine net
ROT_PRED_NTAX  ROT_PRED_PBIO  ROT_PRED_PDEN	Number of distinct rotifer taxa that are predators (coarse and fine net samples combined)  Percent of biomass represented by individuals within the phylum Rotifera that are predators (coarse and fine net samples combined)  Percent of density (indiv.L) of individuals within the phylum Rotifera that are predators (coarse and fine net samples combined)  Percent of individuals within the phylum Rotifera that are predators (coarse and fine net samples combined)  Percent of distinct taxa within the phylum Rotifera that are predators (coarse and fine net samples combined)
ROT_PRED_NTAX ROT_PRED_PBIO ROT_PRED_PDEN ROT_PRED_PIND	Number of distinct rotifer taxa that are predators (coarse and fine net samples combined) Percent of biomass represented by individuals within the phylum Rotifera that are predators (coarse and fine net samples combined) Percent of density (indiv.L) of individuals within the phylum Rotifera that are predators (coarse and fine net samples combined) Percent of individuals within the phylum Rotifera that are predators (coarse and fine net samples combined) Percent of distinct taxa within the phylum Rotifera that are predators (coarse and fine net
ROT_PRED_NTAX  ROT_PRED_PBIO  ROT_PRED_PDEN  ROT_PRED_PIND  ROT_PRED_PTAX	Number of distinct rotifer taxa that are predators (coarse and fine net samples combined)  Percent of biomass represented by individuals within the phylum Rotifera that are predators (coarse and fine net samples combined)  Percent of density (indiv.L) of individuals within the phylum Rotifera that are predators (coarse and fine net samples combined)  Percent of individuals within the phylum Rotifera that are predators (coarse and fine net samples combined)  Percent of distinct taxa within the phylum Rotifera that are predators (coarse and fine net samples combined)  Biomass represented by individuals within the phylum Rotifera that are predators in the 300-count subsamples (coarse and fine net samples combined)

ROT_PRED300_PBIO	Percent of biomass represented by individuals within the phylum Rotifera that are predators in the 300-coount subsamples (coarse and fine net samples combined)
ROT_PRED300_PIND	Percent of individuals within the phylum Rotifera that are predators in the 300-count subsamples (coarse and fine net samples combined)  Percent of distinct taxa within the phylum Rotifera that are predators in the 300-count
ROT_PRED300_PTAX	subsamples (coarse and fine net samples combined)
ROT_PTAX	Percent of distinct taxa within the phylum Rotifera (coarse and fine net samples combined) Biomass represented by individuals within the phylum Rotifera in the 300-count subsamples
ROT300_BIO	(coarse and fine net subsamples combined) Number of individuals within the phylum Rotifera in the 300-count subsamples (coarse and
ROT300_NIND	fine net samples combined)  Number of distinct taxa within the phylum Rotifera in the 300-count subsamples (coarse and
ROT300_NTAX	fine net samples combined)
ROT300_PBIO	Percent of biomass represented by individuals within the phylum Rotifera in the 300-count subsamples (coarse and fine net samples combined)
ROT300_PIND	Percent of individuals within the phylum Rotifera in the 300-count subsamples (coarse and fine net samples combined)
ROT300_PTAX	Percent of distinct taxa within the phylum Rotifera in the 300-count subsamples (coarse and fine net samples combined)
	Biomass represented by individuals within the cladoceran family Sididae (coarse and fine net
SIDID_BIO	samples combined)  Density (indiv./L) of individuals within the cladoceran family Sididae (coarse and fine net
SIDID_DEN	samples combined) Number of individuals within the cladoceran family Sididae (coarse and fine net samples
SIDID_NIND	combined) Number of distinct taxa within the cladoceran family Sididae (coarse and fine net samples
SIDID_NTAX	combined)
SIDID_PBIO	Percent of biomass represented by individuals within the cladoceran family Sididae (coarse and fine net samples combined)
SIDID_PDEN	Percent of density (indiv./L) of individuals within the cladoceran family Sididae (coarse and fine net samples combined)
SIDID_PIND	Percent of individuals within the cladoceran family Sididae (coarse and fine net samples combined)
	Percent of total distinct taxa that are within the cladoceran family Sididae (coarse and fine net
SIDID_PTAX	samples combined) Biomass represented by individuals within the cladoceran family Sididae in the 300-count
SIDID300_BIO	subsamples (coarse and fine net subsamples combined) Number of individuals within the cladoceran family Sididae in the 300-count subsamples
SIDID300_NIND	(coarse and fine net samples combined) Number of distinct taxa within the cladoceran family Sididae in the 300-count subsamples
SIDID300_NTAX	(coarse and fine net samples combined)
SIDID300_PBIO	Percent of biomass represented by individuals within the cladoceran family Sididae in the 300-count subsamples (coarse and fine net samples combined)
SIDID300_PIND	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 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
SIMPSON_BIO	the sample. Simpson Diversity based on the number of cladoceran individuals (coarse and fine net
SIMPSON_CLAD	samples combined). Calculated as SUM{p(i)*p(i)} where p(i) is the proportion of taxon I in the sample.  Simpson Diversity based on the number of cladoceran individuals in the 300-count
SIMPSON_CLAD300	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 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
SIMPSON_COPE300	proportion of taxon I in the sample.  Simpson Diversity based on the density (indiv./L) of individuals (coarse and fine net samples
SIMPSON_DEN	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 Diversity based on the number of rotifer individuals in the 300-count subsampless (coarse and fine net samples combined). Calculated as $SUM\{p(i)*p(i)\}$ where $p(i)$ is the
SIMPSON_ROT300	proportion of taxon I in the sample.  Simpson Diversity based on the biomass of individuals (coarse and fine net samples
SIMPSON300_BIO	combined). Calculated as $SUM\{p(i)*p(i)\}$ where $p(i)$ is the proportion of biomass of taxon I in the sample.
	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
SIMPSON300_NIND	proportion of taxon I in the sample. Biomass represented by small cladoceran individuals (SUBORDER=CLADOCERA and
SMCLAD_BIO	CLADOCEAN_SIZE=SMALL; coarse and fine net samples combined)
SMCLAD_DEN	Density (indiv./L) of individuals within small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL; coarse and fine net samples combined)
SMCLAD_NAT_BIO	Biomass represented by native small cladoceran individuals (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL; coarse and fine net samples combined)
SMCLAD_NAT_DEN	Density (indiv./L) of native individuals within small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_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)  Percent of biomass represented by native individuals within small cladoceran taxa
SMCLAD_NAT_PBIO	(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_PBIO	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)
	Percent of distinct small cladoceran taxa (SUBORDER=CLADOCERA and
SMCLAD_PTAX	CLADOCERAN_SIZE=SMALL; coarse and fine net samples combined) Biomass represented by small cladoceran individuals (SUBORDER=CLADOCERA and CLADOCEAN_SIZE=SMALL) in the 300-count subsamples (coarse and fine net subsamples
SMCLAD300_BIO	combined) Biomass represented by native small cladoceran individuals (SUBORDER=CLADOCERA and
SMCLAD300_NAT_BIO	CLADOCEAN_SIZE=SMALL) in the 300-count subsamples (coarse and fine net subsamples combined)
CMCI AD200 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_NIND	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
SMCLAD300_NAT_NTAX	combined) Percent of biomass represented by native small cladoceran individuals
SMCLAD300_NAT_PBIO	(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)
0.1.02/18000_1VII_1 1118	Percent of distinct native small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL) in the 300-count subsamples (coarse and fine net samples
SMCLAD300_NAT_PTAX	combined)
	Number of individuals within small cladoceran taxa (SUBORDER=CLADOCERA and
SMCLAD300_NIND	CLADOCERAN_SIZE=SMALL) in the 300-count subsamples (coarse and fine net samples combined)
	Number of distinct taxa represented by small cladocerans (SUBORDER=CLADOCERA and
CMCI AD200 NTAV	CLADOCEAN_SIZE=SMALL) in the 300-count subsamples (coarse and fine net samples
SMCLAD300_NTAX	combined)  Percent of biomass represented by small cladoceran individuals (SUBORDER=CLADOCERA
	and CLADOCEAN_SIZE=SMALL) in the 300-coount subsamples (coarse and fine net samples
SMCLAD300_PBIO	combined) Percent of individuals within small cladoceran taxa (SUBORDER=CLADOCERA and
	CLADOCERAN_SIZE=SMALL) in the 300-count subsamples (coarse and fine net samples
SMCLAD300_PIND	combined)
	Percent of distinct small cladoceran taxa (SUBORDER=CLADOCERA and CLADOCERAN_SIZE=SMALL) in the 300-count subsamples (coarse and fine net samples
SMCLAD300_PTAX	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 TOTL_NTAX	Total number of individuals counted across ZOCN and ZOFN samples  Total number of distinct taxa (coarse and fine net samples combined)
TOTE_WINK	Total biomass of individuals in 300-count subsamples (coarse and fine net subsamples
TOTL300_BIO	combined)
TOTL300_NAT_BIO	Total biomass of native individuals in 300-count subsamples (coarse and fine net subsamples combined)
1012300_tt/tt_blo	Number of native individuals in the 300-count subsamples (coarse and fine net samples
TOTL300_NAT_NIND	combined) Total number of distinct native taxa in the 300-count subsamples (coarse and fine net
TOTL300_NAT_NTAX	samples combined)
	Percent of biomass represented by individuals in the 300-count subsamples (coarse and fine
TOTL300_NAT_PBIO	net samples combined)

	Percent of native individuals in the 300-count subsamples (coarse and fine net samples
TOTL300_NAT_PIND	combined)
	Percent of distinct native taxa in the 300-count subsamples (coarse and fine net samples
TOTL300_NAT_PTAX	combined)
TOTI COO NIND	Total number of individuals in random (300 organisms from ZOCN and 300 from ZOFN
TOTL300_NIND	sample)
TOTL300_NTAX	Total number of distinct taxa in the 300-count subsamples (coarse and fine net samples combined)
ZOCN_BIO	Biomass represented by individuals in the coarse-mesh net sample (150-um)
ZOCN_DEN	Density (indiv./L) of individuals in the coarse mesh net sample (150-um)
20011_52.11	Number of families represented by distinct native taxa in the coarse-mesh net sample (150
ZOCN_FAM_NAT_NTAX	um)
ZOCN_FAM_NTAX	Number of families represented by distinct taxa in the coarse-mesh net sample (150 um)
	Number of genera represented by distinct native taxa in the coarse-mesh net sample (150
ZOCN_GEN_NAT_NTAX	um)
ZOCN_GEN_NTAX	Number of genera represented by distinct taxa in the coarse-mesh net sample (150 um)
ZOON NAT DIO	Diamaga yang agamtad bu nativa individuala in the agama ash nat agama (450 um)
ZOCN_NAT_BIO	Biomass represented by native individuals in the coarse-esh net sample (150-um)
ZOCN_NAT_DEN ZOCN_NAT_NIND	Density (indiv./L) of native individuals in the coarse-mesh net sample (150-um)  Number of native individuals in the coarse-mesh net sample (150-um)
ZOCN_NAT_NTAX	Number of distinct native taxa in the coarse-mesh net sample (150-um)
ZOON_NAT_NTAX	Percent of biomass represented by native individuals in the coarse-mesh net sample (150-
ZOCN_NAT_PBIO	um)
ZOCN_NAT_PDEN	Percent of density (indiv./L) of native individuals in the coarse-mesh net sample (150-um)
ZOCN_NAT_PIND	Percent of native individuals in the coarse-mesh net sample (150-um)
	Percent of distinct taxa represented by native individuals in coarse-mesh net sample (150-
ZOCN_NAT_PTAX	um)
ZOCN_NIND	Number of individuals counted in ZOCN sample
ZOCN_NTAX	Number of distinct taxa in the coarse-mesh net sample (150-um)
ZOCN300_BIO	Biomass of individuals in the 300-count subsample of the coarse-mesh net sample (150 um)
ZOONOOO FAM NAT NITAY	Number of families represented by distinct native taxa in the coarse-mesh net sample (150
ZOCN300_FAM_NAT_NTAX	Number of families represented by distinct taxa in the 300-count subsample from the coarse-
ZOCN300_FAM_NTAX	mesh net sample (150 um)
200N000_1 AM_N1AX	Number of genera represented by distinct native taxa in the 300-count subsample from the
7OCN300 GEN NAT NTAX	( coarse-mesh net sample (150 um)
	Number of genera represented by distinct taxa in the 300-count subsample from the coarse-
ZOCN300_GEN_NTAX	mesh net sample (150 um)
_ <del>_</del>	Biomass of native individuals in the 300-count subsample of the coarse-mesh net sample
ZOCN300_NAT_BIO	(150 um)
	Number of native individuals in the 300-count subsamples from the coarse-mesh net sample
ZOCN300_NAT_NIND	(150-um)

ZOCN300_NAT_NTAX	Number of distinct native taxa in the 300-count subsample from the coarse-mesh net sample (150-um)
ZOONOOU_NAT_NTAX	Percent of biomass represented by native individuals in the 300-count subsample from the
ZOCN300_NAT_PBIO	coarse-mesh net sample (150-um)  Percent of native individuals in the 300-count subsamples from the coarse-mesh net sample
ZOCN300_NAT_PIND	(150-um)
ZOCN300_NAT_PTAX	Percent of distinct taxa represented by native individuals in the 300-couont subsample from the coarse-mesh net sample (150-um)
ZOCN300_NIND	Number of individuals in 300 organism random subsample from ZOCN sample
20011000_111110	Number of distinct taxa in the 300-count subsample from the coarse-mesh net sample (150-
ZOCN300_NTAX	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)
	Number of genera represented by distinct native taxa in the fine-mesh net sample (50-um
ZOFN_GEN_NAT_NTAX	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)  Number of families represented by distinct taxa in the 300-count subsample from the fine-
ZOFN300_FAM_NTAX	mesh net sample (50 um)  Number of genera represented by distinct native taxa in the 300-count subsample from the
ZOFN300_GEN_NAT_NTAX	fine-mesh net sample (50 um)  Number of genera represented by distinct taxa in the 300-count subsample from the fine-
ZOFN300_GEN_NTAX	mesh net sample (50 um)  Biomass of native individuals in the 300-count subsample of the fine-mesh net sample (50
ZOFN300_NAT_BIO	um)  Number of native individuals in the 300-count subsample from the fine-mesh net sample (50-
ZOFN300_NAT_NIND	um)

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