

Label	Number of allowed labels	Allowed values and constraints	Content guidelines	Column from Chrissy	Display Name	Content
^PLATFORM	1	any, must be unique within local file	Provide an identifier for this entity. This identifier is used only as an internal reference within a given file. The identifier will not appear on final GEO records.	UNC_CE_Nimblegen2.1 _<DESIGNID> User entered		
!Platform_title	1	string of length 1-120 characters, must be unique within local file and over all previously submitted Platforms for that submitter	Provide a unique title that describes your Platform. We suggest that you use the system [institution/lab]-[species]-[number of features]-[version], e.g. "FHCRC Mouse 15K v1.0".	UNC_CE_Nimblegen2.1 _<DESIGNID> User entered		
!Platform_distribution	1	commercial, non-commercial, custom-commercial, or virtual	Microarrays are 'commercial', 'non-commercial', or 'custom-	Custom-commercial, Commercial	Custom-commercial, Commercial	Custom-commercial, Commercial

			commercial' in accordance with how the array was manufactured. Use 'virtual' only if creating a virtual definition for MS, MPSS, SARST, or RT-PCR data.	Non-commercial	Non-commercial	Non-commercial
!Platform_technology	1	spotted DNA/cDNA, spotted oligonucleotide, in situ oligonucleotide, antibody, tissue, SARST, RT-PCR, MS, or MPSS	Select the category that best describes the Platform technology.	in situ oligonucleotide	Spotted DNA/cDNA Spotted oligonucleotide In situ oligonucleotide	Spotted DNA/cDNA Spotted oligonucleotide In situ oligonucleotide
!Platform_organism	1 or more	use standard NCBI Taxonomy nomenclature	Identify the organism(s) from which the features on the Platform were designed or derived.	Caenorhabditis elegans, homo sapiens	Caenorhabditis elegans Homo sapiens	Caenorhabditis elegans Homo sapiens
!Platform_manufacturer	1	any	Provide the name of the company, facility or laboratory where the array was manufactured or produced.	Nimblegen Systems Inc.	Nimblegen Systems Inc.	Nimblegen Systems Inc.
!Platform_manufacturer	1	any	Describe the array	See nimblegen	PMID: 10504697	Singh-Gasson S,

acture_protocol			<p>manufacture protocol. Include as much detail as possible, e.g., clone/primer set identification and preparation, strandedness/length, arrayer hardware/software, spotting protocols. You can include as much text as you need to thoroughly describe the protocol; it is strongly recommended that complete protocol descriptions are provided within your submission.</p>	website		<p>Green RD, Yue Y, Nelson C, Blattner F, Sussman MR, Cerrina F. Maskless fabrication of light-directed oligonucleotide microarrays using a digital micromirror array. Nat Biotechnol. 1999 Oct;17(10):974-8. PMID: 10504697</p>
!Platform_catalog_number	0 or more	any	<p>Provide the manufacturer catalog number for commercially-available arrays.</p>			

!Platform_web_link	0 or more	valid URL	Specify a Web link that directs users to supplementary information about the array. Please restrict to Web sites that you know are stable.			
!Platform_support	0 or 1	any	Provide the surface type of the array, e.g., glass, nitrocellulose, nylon, silicon, unknown.	see nimblegen website	PMID: 10504697	
!Platform_coating	0 or 1	any	Provide the coating of the array, e.g., aminosilane, quartz, polysine, unknown.	see nimblegen website	PMID: 10504697	
!Platform_description	0 or more	any	Provide any additional descriptive information not captured in another field, e.g., array and/or feature physical dimensions, element grid system.	see nimblegen website	PMID: 10504697	
!Platform_contributor	0 or more	each value in the form 'firstname,middleinitial,la	List all people associated with this	see nimblegen website	PMID: 10504697	

		<p>stname' or 'firstname,lastname': firstname must be at least one character and cannot contain spaces; middleinitial, if present, is one character; lastname is at least two characters and can contain spaces.</p>	array design.			
!Platform_pubmed_id	0 or more	an integer	Specify a valid PubMed identifier (PMID) that references a published article that describes the array.	PMID: 10504697		
!Platform_geo_accession	0 or 1	a valid Platform accession number (GPLxxx)	Only use for performing updates to existing GEO records.			
!Platform_table_begin	1	no content required	Indicates the start of the data table.	Derived from database		
!Platform_table_end	1	no content required	Indicates the end of the data table.	Derived from database		
^SAMPLE	1	any, must be unique	Provide an identifier for	USER ENTERS		

		within local file	this entity. This identifier is used only as an internal reference within a given file. The identifier will not appear on final GEO records.			
!Sample_title	1	string of length 1-120 characters, must be unique within local file and over all previously submitted Samples for that submitter	Provide a unique title that describes this Sample. We suggest that you use the system [biomaterial]-[condition(s)]-[replicate number], e.g., Muscle_exercised_60min_rep2.	USER ENTERS		
!Sample_supplementary_file	1 or more	name of supplementary file, or 'none'	Examples of supplementary file types include original Affymetrix CEL and EXP files, GenePix GPR files, and TIFF image files. Supplementary files should be zipped or tarred together with the	select from uploaded TIFF image files		

			SOFT file at time of submission. Provision of supplementary raw data files facilitates the unambiguous interpretation of data and potential verification of conclusions as set forth in the MIAME guidelines.			
!Sample_table	0 or 1	name of external file to be used as data table	At this time, the only allowed external sample table file type is Affymetrix CHP files. This field allows you to specify a native CHP file, rather than supply a tab-delimited data table in the ! Sample_table_begin section. Also, there is no need to specify the ! Sample_platform_id when CHP files are	n\\a		

			supplied. CHP files should be zipped or tarred together with the SOFT file at time of submission.			
!Sample_source_name_ch[n]	1 per channel	any	Briefly identify the biological material and the experimental variable(s), e.g., vastus lateralis muscle, exercised, 60 min.	N2 embryos, SS343 adults (glp-1(q224) III) at 25C	N2 embryos SS343 adults (glp-1(q224) III) at 25C	N2 embryos SS343 adults (glp-1(q224) III) at 25C
!Sample_organism_ch[n]	1 or more	use standard NCBI Taxonomy nomenclature	Identify the organism(s) from which the biological material was derived.	Caenorhabditis elegans, homo sapiens	Caenorhabditis elegans homo sapiens	Caenorhabditis elegans homo sapiens
!Sample_characteristics_ch[n]	1 or more	any	List all available characteristics of the biological source, including factors not necessarily under investigation, e.g., Strain: C57BL/6 Gender: female Age: 45 days	Strain: N2 embryos, Strain: SS343 adults at 25C	Strain: N2 embryos Strain: SS343 adults at 25C	Strain: N2 embryos Strain: SS343 adults at 25C

			<p>Tissue: bladder tumor Tumor stage: Ta You can provide as much text as you need to thoroughly describe your biological samples.</p>			
!Sample_biomaterial_provider_ch[n]	0 or more	any	<p>Specify the name of the company, laboratory or person that provided the biological material.</p>	<p>Caenorhabditis Genetics Center (http://www.cbs.umn.edu/CGC/), Susan Strome</p>	<p>Caenorhabditis Genetics Center Susan Strome</p>	<p>Caenorhabditis Genetics Center (http://www.cbs.umn.edu/CGC/) Susan Strome</p>
!Sample_treatment_protocol_ch[n]	0 or more	any	<p>Describe any treatments applied to the biological material prior to extract preparation. You can include as much text as you need to thoroughly describe the protocol; it is strongly recommended that complete protocol descriptions are provided within your</p>	<p>SAMPLE SUBMITTERS ENTERS</p>		

			submission.			
!Sample_growth_protocol_ch[n]	0 or more	any	Describe the conditions that were used to grow or maintain organisms or cells prior to extract preparation. You can include as much text as you need to thoroughly describe the protocol; it is strongly recommended that complete protocol descriptions are provided within your submission.	N2 embryos were grown using standard C.elegans liquid culture at 20C. , SS343 germline-less adults were grown using standard C.elegans liquid culture. L1's were shifted from 15C to 25C to obtain germline-less adults.	N2 embryos were grown SS343 germline-less adults were grown	N2 embryos were grown using standard C.elegans liquid culture at 20C. , SS343 germline-less adults were grown using standard C.elegans liquid culture. L1's were shifted from 15C to 25C to obtain germline-less adults.
!Sample_molecule_ch[n]	1 per channel	total RNA, polyA RNA, cytoplasmic RNA, nuclear RNA, genomic DNA, protein, or other	Specify the type of molecule that was extracted from the biological material.	genomic DNA, total RNA, polyA RNA>	genomic DNA total RNA polyA RNA	genomic DNA total RNA polyA RNA
!Sample_extract_protocol_ch[n]	1 or more	any	Describe the protocol used to isolate the extract material. You can include as much text	SAMPLE SUBMITTER ENTERS		

			as you need to thoroughly describe the protocol; it is strongly recommended that complete protocol descriptions are provided within your submission.			
!Sample_label_ch[n]	1 per channel	any	Specify the compound used to label the extract e.g., biotin, Cy3, Cy5, 33P.	<Cy3, Cy5>	Cy3 Cy5	Cy3 Cy5
!Sample_label_protocol_ch[n]	1 or more	any	Describe the protocol used to label the extract. You can include as much text as you need to thoroughly describe the protocol; it is strongly recommended that complete protocol descriptions are provided within your submission.	Samples were labeled by Nimblegen Systems, Inc. www.nimblegen.com	Samples were labeled by Nimblegen Systems, Inc.	Samples were labeled by Nimblegen Systems, Inc. www.nimblegen.com
!Sample_hyb_pr	1 or	any	Describe the protocols	Hybridization was	Hybridization was	Hybridization was

<p>otocol</p>	<p>more</p>		<p>used for hybridization, blocking and washing, and any post-processing steps such as staining. You can include as much text as you need to thoroughly describe the protocol; it is strongly recommended that complete protocol descriptions are provided within your submission.</p>	<p>performed by Nimblegen Systems, Inc. www.nimblegen.com</p>	<p>performed by Nimblegen Systems, Inc.</p>	<p>performed by Nimblegen Systems, Inc. www.nimblegen.com</p>
<p>!Sample_scan_protocol</p>	<p>1 or more</p>	<p>any</p>	<p>Describe the scanning and image acquisition protocols, hardware, and software. You can include as much text as you need to thoroughly describe the protocol; it is strongly recommended that complete protocol descriptions are provided within your</p>	<p>Arrays were scanned on an Axon 4000B scanner per manufacturer's protocol (http://www.nimblegen.com/products/lit/lit.html).</p>	<p>Arrays were scanned on an Axon 4000B scanner</p>	<p>Arrays were scanned on an Axon 4000B scanner per manufacturer's protocol (http://www.nimblegen.com/products/lit/lit.html).</p>

			submission.			
!Sample_data_processing	1	any	Provide details of how data in the VALUE column of your table were generated and calculated, i.e., normalization method, data selection procedures and parameters, transformation algorithm (e.g., MAS5.0), and scaling parameters. You can include as much text as you need to thoroughly describe the processing procedures.	Geo submitter enters		
!Sample_description	1 or more	any	Include any additional information not provided in the other fields, or paste in broad descriptions that cannot be easily dissected into	Geo submitter enters <multi-line>		

			the other fields.			
!Sample_platform_id	1	a valid Platform identifier	Reference the Platform upon which this hybridization was performed. Reference the Platform accession number (GPLxxx) if the Platform already exists in GEO, or reference the ^Platform identifier if the Platform record is being batch submitted within the same SOFT file. To identify the accession number of an existing commercial Platform in GEO, use the FIND PLATFORM tool.	Geo submitter enters		
!Sample_geo_accession	0 or 1	a valid Sample accession number (GSMxxx)	Only use for performing updates to existing GEO records.	Geo submitter enters		
!Sample_anchor	1	SAGE enzyme anchor, usually NlaIII or Sau3A	Use for SAGE submissions only.	n/a		

!Sample_type	1	SAGE	Use for SAGE submissions only.	n\a		
!Sample_tag_count	1	sum of tags quantified in SAGE library	Use for SAGE submissions only.	n\a		
!Sample_tag_length	1	base pair length of the SAGE tags, excluding anchor sequence	Use for SAGE submissions only.	n\a		
!Sample_table_begin	1	no content required	Indicates the start of the data table.	Derived from database		
!Sample_table_end	1	no content required	Indicates the end of the data table.	Derived from database		
^SERIES	1	any, must be unique within local file	Provide an identifier for this entity. This identifier is used only as an internal reference within a given file. The identifier will not appear on final GEO records.	Geo submitter enters		
!Series_title	1	string of length 1-120 characters, must be unique within local file and over all previously submitted Series for that	Provide a unique title that describes the overall study.	Geo submitter enters		

		submitter				
!Series_summary	1 or more	any	Summarize the goals and objectives of this study. The abstract from the associated publication may be suitable. You can include as much text as you need to thoroughly describe the study.	Geo submitter enters		
!Series_type	1	any	Enter keyword(s) that generally describe the type of study. Examples include: time course, dose response, comparative genomic hybridization, ChIP-chip, cell type comparison, disease state analysis, stress response, genetic modification, etc.	Time course, chip-chip, cell type comparison		
!Series_overall_design	1	any	Provide a description of the experimental design.	Geo submitter enters		

			Indicate how many Samples are analyzed, if replicates are included, are there control and/or reference Samples, dye-swaps, etc.	<multi-line>		
!Series_pubmed_id	0 or more	an integer	Specify a valid PubMed identifier (PMID) that references a published article describing this study. Most commonly, this information is not available at the time of submission - it can be added later once the data are published.	Geo submitter enters		
!Series_web_link	0 or more	valid URL	Specify a Web link that directs users to supplementary information about the study. Please restrict to Web sites that you know are stable.	Geo submitter enters		
!Series_contribut	0 or	each value in the form	List all people	Geo submitter		

or	more	'firstname,middleinitial,lastname' or 'firstname,lastname': firstname must be at least one character and cannot contain spaces; middleinitial, if present, is one character; lastname is at least two characters and can contain spaces.	associated with this study.	enters <multi-line>		
!Series_variable _[n]	0 or more	dose, time, tissue, strain, gender, cell line, development stage, age, agent, cell type, infection, isolate, metabolism, shock, stress, temperature, specimen, disease state, protocol, growth protocol, genotype/variation, species, individual, or other	Indicate the variable type(s) investigated in this study, e.g., !Series_variable_1 = age !Series_variable_2 = age NOTE - this information is optional and does not appear in Series records or downloads, but will be used to assemble corresponding GEO DataSet records.	Geo submitter enters <multi-line>		

!Series_variable_description_[n]	0 or more	any	Describe each variable, e.g., !Series_variable_description_1 = 2 months !Series_variable_description_2 = 12 months NOTE - this information is optional and does not appear in Series records or downloads, but will be used to assemble corresponding GEO DataSet records.	Geo submitter enters <multi-line>		
!Series_variable_sample_list_[n]	0 or more	each value a valid reference to a ^SAMPLE identifier, or all	List which Samples belong to each group, e.g., !Series_variable_sample_list_1 = samA, samB !Series_variable_sample_list_2 = samC, samD NOTE - this information is optional and does not appear in Series records or downloads, but will be used to assemble	Geo submitter enters <multi-line>		

			corresponding GEO DataSet records.			
!Series_repeats_ [n]	0 or more	biological replicate, technical replicate - extract, or technical replicate - labeled-extract	Indicate the repeat type(s), e.g., !Series_repeats_1 = biological replicate !Series_repeats_2 = biological replicate NOTE - this information is optional and does not appear in Series records or downloads, but will be used to assemble corresponding GEO DataSet records.	Geo submitter enters <multi-line>		
!Series_repeats_ sample_list_[n]	0 or more	each value a valid reference to a ^SAMPLE identifier, or all	List which Samples belong to each group, e.g., !Series_repeats_sample_list_1 = samA, samB !Series_repeats_sample_list_2 = samC, samD NOTE - this information is optional and does not	Geo submitter enters <multi-line>		

			appear in Series records or downloads, but will be used to assemble corresponding GEO DataSet records.			
!Series_sample_id	1 or more	valid Sample identifiers	Reference the Samples that make up this experiment. Reference the Sample accession numbers (GSMxxx) if the Samples already exists in GEO, or reference the ^Sample identifiers if they are being submitted in the same file.			
!Series_geo_accession	0 or 1	a valid Series accession number (GSExxx)	Only use for performing updates to existing GEO records.			