Section	Field	Type	Description
	codes	array	A list of codes used for this record, containing external identifiers, external classification designations, and external link-outs.
Codes	code	string	The literal code value.
Codes	code_system	string	The orginizational system which defines the code meaning (e.g. the originating database or classification system).
Codes	comments	string	Any comments regarding the relationship.
Codes	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
Codes	type	string	The type of the code (e.g. "PRIMARY" for a primary code, "SECONDARY" for a secondary code, and "SUPERSEDED" for a code which has been superseded by another code, etc).
Codes	url	string	The url to further information regarding this code.
Codes	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
	definition_level	string	The level of completeness and specificity of the definition (e.g. "complete", "incomplete", "representative").
	definition_type	string	The type of definition ("primary" or "alternative"). Primary definitions are the main descriptive form of the substance definition, while "alternative" definitions may be seen as definitional "synonyms" of some primary record.
	mixture	object	A container for the mixture information necesary to define a mixture substance. This includes the mixture components and an optioanl source material reference.

Mixture	components	array	A list of components found in the mixture. Each component has a type specifying whether it is a necessary/optional element of the mixture, as well as a reference to the substance it specifies. .
components	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
components	substance	object	A reference to the substance which is considered a component of the mixture.
substance	linking_id	string	The approvalID of the record if it exists, otherwise some compact and exchangable ID useful for linking to the referenced record (often the first 8 chars of its uuid).
substance	name	string	The literal string text of a name.
substance	ref_pname	string	The "Priority Name" (usually the display name) of the record being referenced.
substance	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
substance	refuuid	string	The UUID of the related record.
substance	substance_class	string	This value wall always be "reference" if it is intended as a real reference and "mention" if it is a place-holder. However, it can also specify a full substance class, in which case the whole record reference object is meant to be a full entire record rather than a reference.
substance	unii	string	The Unique Ingredient Identifier (UNII, aka "Approval ID") is a unique ID generated for each substance record.

substance	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
components	type	string	The component type relative to it's mixture ('may be present (any of)', 'must be present (all of)', etc.).
components	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
Mixture	parent_substance	object	A reference to the parent substance which this substance further qualifies. This tends to be null if this record is a "whole" structurally diverse record, and points back to the "whole" record if the part or other qualification is present.
parent_substance	linking_id	string	The approvalID of the record if it exists, otherwise some compact and exchangable ID useful for linking to the referenced record (often the first 8 chars of its uuid).
parent_substance	name	string	The literal string text of a name.
parent_substance	ref_pname	string	The "Priority Name" (usually the display name) of the record being referenced.
parent_substance	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
parent_substance	refuuid	string	The UUID of the related record.
parent_substance	substance_class	string	This value wall always be "reference" if it is intended as a real reference and "mention" if it is a place-holder. However, it can also specify a full substance class, in which case the whole record reference object is meant to be a full entire record rather than a reference.

parent_substance	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
parent_substance	unii	string	The Unique Ingredient Identifier (UNII, aka "Approval ID") is a unique ID generated for each substance record.
Mixture	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
Mixture	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
	modifications	object	A container for the set of physical, structural and agent modifications on the substance record.
Modifications	agent_modifications	array	A list of agent modifications applied to this substance. An agent modification is an "agent" (usually a substance) which specifically interacted with and permanently altered the original substance material under some specified conditions, forming a new substance.
agent_modification	agent_modification_process	string	The process used for the agent modification.
agent_modification	agent_modification_role	string	The role of the agent in the modification process.
agent_modification	agent_modification_type	string	The type of agent modification.
agent_modification	agent_substance	object	A reference to the substance which acts as an agent in the agent modification.
SubstanceReference	linking_id	string	The approvalID of the record if it exists, otherwise some compact and exchangable ID useful for linking to the referenced record (often the first 8 chars of its uuid).
SubstanceReference	name	string	The literal string text of a name.

SubstanceReference	ref_pname	string	The "Priority Name" (usually the display name) of the record being referenced.
SubstanceReference	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
SubstanceReference	refuuid	string	The UUID of the related record.
SubstanceReference	substance_class	string	This value wall always be "reference" if it is intended as a real reference and "mention" if it is a place-holder. However, it can also specify a full substance class, in which case the whole record reference object is meant to be a full entire record rather than a reference.
SubstanceReference	unii	string	The Unique Ingredient Identifier (UNII, aka "Approval ID") is a unique ID generated for each substance record.
SubstanceReference	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
agent_modification	amount	object	The amount of the agent which was used in the modification.
amount	average	float	The amount's numeric average if present.
amount	high	float	The highest numerical value likely for the average amount. (highest average).
amount	high_limit	float	The highest allowable numeric value usable for the amount. (highest limit).
amount	low	float	The lowest numerical value likely for the average amount. (lowest average).
amount	low_limit	float	The lowest allowable numeric value usable for the amount. (lowest limit).

amount	non_numeric_value	string	A textual description of a value which can not be quantified numerically. For example, "solubility" may be described quantitatively or it may be described with certain textual categories. Non-numeric values are meant to specify qualitative values and other values not easily described by numbers or ranges of numbers.
amount	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
amount	type	string	The type of the amount specified ('mol ratio'. 'degree of polymerization', 'weight ratio', etc.).
amount	units	string	The amount's unit of measurement.
amount	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
agent_modification	modification_group	string	A key specifying how this modification relates to other modifications. All modifications sharing a group key are considered to be occuring as part of a single process or event, or descriptive of the same change to the substance.
agent_modification	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
agent_modification	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).

Modifications	physical_modifications	array	A list of physical modifications applied to this substance. A physical modification is a physical interaction (such as heating) where the result permanently alters the original source substance.
physical_modifications	modification_group	string	A key specifying how this modification relates to other modifications. All modifications sharing a group key are considered to be occuring as part of a single process or event, or descriptive of the same change to the substance.
physical_modifications	parameters	array	The list of paramaters needed to define the conditions, context or environment of applicability for the property value specified.
parameters	amount	object	The amount or value which qualifies the paramater describing the physical modification (e.g. the temperature used in a heating process).
amount	average	float	The amount's numeric average if present.
amount	high_limit	float	The highest allowable numeric value usable for the amount. (highest limit).
amount	low_limit	float	The lowest allowable numeric value usable for the amount. (lowest limit).
amount	non_numeric_value	string	A textual description of a value which can not be quantified numerically. For example, "solubility" may be described quantitatively or it may be described with certain textual categories. Non-numeric values are meant to specify qualitative values and other values not easily described by numbers or ranges of numbers.
amount	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
amount	type	string	The type of the amount specified ('mol ratio'. 'degree of polymerization', 'weight ratio', 'other' etc.).

amount	units	string	The amount's unit of measurement.
amount	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
parameters	parameter_name	string	The name of the paramater which qualifies / conditions the property's measurement or domain of applicability. .
parameters	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
parameters	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
physical_modifications	physical_modification_role	string	The role that the physical modification has in the process of the modification.
physical_modifications	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
physical_modifications	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
Modifications	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.

Modifications	structural_modifications	array	A list of structural modifications applied to this substance. A stuctural modification is a known and specific change to the original source substane described, where a description of the chemical structural change, location, and amount are feasible.
structural_modifications	extent	string	The type of extent for the structural modification. "Complete" if the extent is considered to have 100% occupancy / replacement, "partial" otherwise.
structural_modifications	extent_amount	object	An amount quantifying the extent of the structural modification.
extent_amount	average	float	The amount's numeric average if present.
extent_amount	high	float	The highest numerical value likely for the average amount. (highest average).
extent_amount	high_limit	float	The highest allowable numeric value usable for the amount. (highest limit).
extent_amount	low	float	The lowest numerical value likely for the average amount. (lowest average).
extent_amount	low_limit	float	The lowest allowable numeric value usable for the amount. (lowest limit).
extent_amount	non_numeric_value	string	A textual description of a value which can not be quantified numerically. For example, "solubility" may be described quantitatively or it may be described with certain textual categories. Non-numeric values are meant to specify qualitative values and other values not easily described by numbers or ranges of numbers.
extent_amount	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
extent_amount	type	string	The type of amount recorded for a modification of partial extent.

extent_amount	units	string	The amount's unit of measurement.
extent_amount	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
structural_modifications	location_type	string	The type of location specification for a residue modified in a structural modification. (e.g. "site-specific" or "residue-specific").
structural_modifications	modification_group	string	A key specifying how this modification relates to other modifications. All modifications sharing a group key are considered to be occuring as part of a single process or event, or descriptive of the same change to the substance.
structural_modifications	molecular_fragment	object	A reference to the substance which is substituting, binding or connecting to the main substance and thus modifying it. For proteins, this is most typically a full amino acid which is considered to replace an existing amino acid at a specific site. For nucleic acids, this is more commonly a full nucleotide which is also considered to replace the linkage, sugar and nucleobase at some specified site(s).
molecular_fragment	linking_id	string	The approvalID of the record if it exists, otherwise some compact and exchangable ID useful for linking to the referenced record (often the first 8 chars of its uuid).
molecular_fragment	name	string	The literal string text of a name.
molecular_fragment	ref_pname	string	The "Priority Name" (usually the display name) of the record being referenced.
molecular_fragment	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
molecular_fragment	refuuid	string	The UUID of the related record.

molecular_fragment	substance_class	string	This value wall always be "reference" if it is intended as a real reference and "mention" if it is a place-holder. However, it can also specify a full substance class, in which case the whole record reference object is meant to be a full entire record rather than a reference.
molecular_fragment	unii	string	The Unique Ingredient Identifier (UNII, aka "Approval ID") is a unique ID generated for each substance record.
molecular_fragment	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
structural_modifications	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
structural_modifications	residue_modified	string	The residue which was modified for the structural modification (necessary if the modification is residue specific instead of site-specific).
structural_modifications	sites	array	A list of explicit detailed sites where the linkage is applicable. A linkage site is always describing how the nucleoside connects to the NEXT nucleoside in the series. So a sequence of length 2 will have only 1 linkage, specified at the 1st site (not the second).
sites	residue_index	float	The index of the residue on that subunit being specified.
sites	subunit_index	float	The index of the subunit being specified.
structural_modifications	structural_modification_type	string	The type of structural modification.
structural_modifications	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).

Modifications	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
	moieties	array	A list of the important component chemical structures which comprise a chemical substance, as well as their relative ratios to each other (especially important in the case of non-stoichiometric chemical substances). These "moieties" are typically the unique set of disconnected covalent structures found in the substance.
Moieties	atropisomerism	string	Whether or not the record has atropisomerism, or has a chirality where a hindered rotation about a single bond as a resolt of steric or electronic constraints.
Moieties	charge	integer	The net charge of the structure.
Moieties	count	integer	The exact number of times that the structure is repeated.
Moieties	count_amount	object	The number of times that a structure is repeated in its referenced context, represented as an amount. This is particularly useful in defining ranges on amounts for moieties within non-stoichiometric chemicals.
count_amount	average	float	The amount's numeric average if present.
count_amount	high	float	The highest numerical value likely for the average amount. (highest average).
count_amount	low	float	The lowest numerical value likely for the average amount. (lowest average).
count_amount	non_numeric_value	string	A textual description of a value which can not be quantified numerically. For example, "solubility" may be described quantitatively or it may be described with certain textual categories. Non-numeric values are meant to specify qualitative values and other values not easily described by numbers or ranges of numbers.

count_amount	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
count_amount	type	string	The type of moiety count amount ('Mol ration', 'weight ratio', etc.)
count_amount	units	string	The amount's unit of measurement.
count_amount	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
Moieties	defined_stereo	integer	A count of defined stereocenters.
Moieties	digest	string	A hash of the raw structural information encoded.
Moieties	ez_centers	integer	A count of E/Z, or absolute double bond stereochemistry centers.
Moieties	formula	string	The chemical formula of the record.
Moieties	id	string	The identifier of the structural element itself (this is still a UUID).
Moieties	molecular_weight	float	The molecular weight of the structure.
Moieties	molfile	string	The chemical structure in MDL Molfile format (V2000).
Moieties	optical_activity	string	The optical activity or rotation of the material. "(+)" and "(-)" are used for optically active materials where activity is known and significantly useful for definition. "(+/-)" is used for racemic mixtures.
Moieties	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
Moieties	smiles	string	The chemical structure in SMILES format.
Moieties	stereo_centers	integer	A count of possible stereocenters.

Moieties	stereo_comments	string	Some textually descriptive information about specific stereochemistry that cannot adequately be captured elsewhere.
Moieties	stereochemistry	string	The structure's type of stereochemistry (absolute, achiral, racemic, etc.).
Moieties	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
	names	array	The list of names associated with a record. These include scientific, common, generic and brand names for substances and concepts. Name objects include both the name as a string, as well as other information.
Name	display_name	boolear	True if this is to be the displayed name for the substance.
Name	domains	array	The list of domains that this name is used in (e.g. "drug", "cosmetic", etc).
Name	languages	array	The list of languages that use that name as written (ISO 639-1 codes).
Name	name	string	The literal string text of a name.
Name	name_jurisdiction	array	The list of jurisdictions where that name is used.
Name	name_orgs	array	The list of naming organizations that have marked this name as official in some way.
name_orgs	deprecated_date	integer	A UNIX timestamp for when the naming organization deprecated the name's status (if it has been deprecated).
name_orgs	name_org	string	A string representing the naming organization which has designated the name as official in some regard. (e.g. "USAN", "INN").
name_orgs	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.

name_orgs	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
Name	preferred	boolean	True if this is a "preferred name" for the substance (each substance may have many).
Name	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
Name	type	string	The type of the name (e.g. "bn" for "brand name", "cn" for "common name", and "sys" for "systematic name", etc).
Name	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
	notes	array	A list of notes and general comments for the record.
Notes	note	string	The literal text of a note comment for a record. These is typically used to capture some orienting descriptive information, qualifications, or systematic notes on validation.
Notes	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
Notes	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).

	nucleic_acid	object	The definitional information of a nucleic acid substance. Contains information about the nucleic acid sequence as well as the sugars and linkages used.
Nucleic Acid	linkages	array	The list of linkages used to connect the nucleosides of the nucleic acid, as well as their sites of use.
linkages	linkage	string	The linkage itself which is used. This is a short-hand code for a defined structural linkage fragment found within the GSRS controlled vocabulary.
linkages	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
linkages	sites	array	A list of explicit detailed sites where the linkage is applicable. A linkage site is always describing how the nucleoside connects to the NEXT nucleoside in the series. So a sequence of length 2 will have only 1 linkage, specified at the 1st site (not the second).
sites	residue_index	integer	The index of the residue on that subunit being specified.
sites	subunit_index	integer	The index of the subunit being specified.
linkages	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
Nucleic Acid	nucleic_acid_sub_type	string	The sub-type of nucleic acid.
Nucleic Acid	nucleic_acid_type	string	The type of nucleic acid.
Nucleic Acid	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.

Nucleic Acid	sequence_origin	string	The original source of the amino acid sequence. This is a general category which, for organisms, typically specifies a useful general abstract taxonic level with increasing granularity as it approaches humans (e.g. "bacteria","mouse", "mouse chimeric", "human").
Nucleic Acid	sequence_type	string	The type of sequence being specified (e.g. "incomplete", "complete").
Nucleic Acid	subunits	array	The list of Subunits found in this nucleic acid. Each subunit is described by a sequence of nucleobases. Double stranded nucleic acids should typically be represented by 2 subunits, while single-stranded nucleic acids will more typically be represented with 1.
subunits	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
subunits	sequence	string	The amino acid sequence as a string of 1-letter amino acids, from N-term to C-term. Lower-case letters represent D-amino acids, while upper-case are the standard L-amino acids.
subunits	subunit_index	integer	The index of the subunit being specified.
subunits	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
Nucleic Acid	sugars	array	The list of sugars (e.g. ribose, deoxyribose, morphilino) which the nucleobases connect to, as well as their sites of use within the sequence.

sugars	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
sugars	sites	array	A list of explicit detailed sites where the linkage is applicable. A linkage site is always describing how the nucleoside connects to the NEXT nucleoside in the series. So a sequence of length 2 will have only 1 linkage, specified at the 1st site (not the second).
sites	residue_index	integer	The index of the residue on that subunit being specified.
sites	subunit_index	integer	The index of the subunit being specified.
sugars	sugar	string	The sugar itself which is used. This is a short-hand code for a defined structural sugar fragment found within the GSRS controlled vocabulary.
sugars	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
Nucleic Acid	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
	polymer	object	The definitional information of a polymer substance. Contains information about the monomers, structural repeat units, amounts, connectivity and idealized structural form of the polymer.
Polymer	classification	object	A container for classification properties of a polymer.
classification	parent_substance	object	A reference to the parent substance which this substance further qualifies. This tends to be null if this record is a "whole" structurally diverse record, and points back to the "whole" record if the part or other qualification is present.

parent_substance	linking_id	string	The approvalID of the record if it exists, otherwise some compact and exchangable ID useful for linking to the referenced record (often the first 8 chars of its uuid).
parent_substance	name	string	The literal string text of a name.
parent_substance	ref_pname	string	The "Priority Name" (usually the display name) of the record being referenced.
parent_substance	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
parent_substance	refuuid	string	The UUID of the related record.
parent_substance	substance_class	string	This value wall always be "reference" if it is intended as a real reference and "mention" if it is a place-holder. However, it can also specify a full substance class, in which case the whole record reference object is meant to be a full entire record rather than a reference.
parent_substance	unii	string	The Unique Ingredient Identifier (UNII, aka "Approval ID") is a unique ID generated for each substance record.
parent_substance	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
classification	polymer_class	string	A general classication of the polymer type (e.g. "homopolymer", "copolymer").
classification	polymer_geometry	string	A general classification of the polymer geometry (e.g. "linear", "branch", "network").
classification	polymer_subclass	array	The set of subclasses describing the polymer (e.g. "cross-link", "graft").

classification	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
classification	source_type	string	The type of material used as the source for the polymer. If from a biological or natural source, further reference to the source material will be needed.
classification	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
Polymer	display_structure	object	A form of the structure which is meant for displaying a simplified form of the polymer. This display structure is not meant to be trusted as canonical for the polymer definition, but is meant to be useful for communicating a "conceptual" diagram of the polymer.
display_structure	charge	integer	The net charge of the structure.
display_structure	count	integer	The exact number of times that the structure is repeated.
display_structure	defined_stereo	integer	A count of defined stereocenters.
display_structure	ez_centers	integer	A count of E/Z, or absolute double bond stereochemistry centers.
display_structure	id	string	The identifier of the structural element itself (this is still a UUID).
display_structure	molecular_weight	float	The molecular weight of the structure.
display_structure	molfile	string	The chemical structure in MDL Molfile format (V2000).
display_structure	optical_activity	string	The optical activity or rotation of the material. "(+)" and "(-)" are used for optically active materials where activity is known and significantly useful for definition. "(+/-)" is used for racemic mixtures.

display_structure	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
display_structure	stereo_centers	integer	A count of possible stereocenters.
display_structure	stereochemistry	string	The structure's type of stereochemistry (absolute, achiral, racemic, etc.).
Polymer	idealized_structure	object	A form of the structure which is meant for communicating a more accurate, but sometimes less intuitive view of the polymeric structure. This form of the polymer definition is also not meant to be an exhaustive cannonical form, but is meant to be the most compatible aranagement possible for unerstanding the structural units.
idealized_structure	charge	integer	The net charge of the structure.
idealized_structure	count	integer	The exact number of times that the structure is repeated.
idealized_structure	defined_Stereo	integer	A count of defined stereocenters.
idealized_structure	ez_centers	integer	A count of E/Z, or absolute double bond stereochemistry centers.
idealized_structure	id	string	The identifier of the structural element itself (this is still a UUID).
idealized_structure	molecular_weight	float	The molecular weight of the structure.
idealized_structure	molfile	string	The chemical structure in MDL Molfile format (V2000).
idealized_structure	optical_activity	string	The optical activity or rotation of the material. "(+)" and "(-)" are used for optically active materials where activity is known and significantly useful for definition. "(+/-)" is used for racemic mixtures.
idealized_structure	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
idealized_structure	stereo_centers	integer	A count of possible stereocenters.

idealized_structure	stereochemistry	string	The structure's type of stereochemistry (absolute, achiral, racemic, etc.).
Polymer	monomers	array	A list of starting materials and/or conceptual "monomers" that either were used in the synthesis of the polymer, or "could have been used" in its synthesis. Each "monomer" has a type, an extent (or amount) and a reference to another substance record. It is important to note, despite the name, that catalysts and non-monomer starting materials may be captured here as well.
monomers	amount	object	The amount of the monomer / starting material which was used, often as a ratio to other monomers and starting materials.
amount	average	float	The amount's numeric average if present.
amount	high	float	The highest numerical value likely for the average amount. (highest average).
amount	high_limit	float	The highest allowable numeric value usable for the amount. (highest limit).
amount	low	float	The lowest numerical value likely for the average amount. (lowest average).
amount	low_limit	float	The lowest allowable numeric value usable for the amount. (lowest limit).
amount	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
amount	non_numeric_value	string	A textual description of a value which can not be quantified numerically. For example, "solubility" may be described quantitatively or it may be described with certain textual categories. Non-numeric values are meant to specify qualitative values and other values not easily described by numbers or ranges of numbers.

amount	type	string	The type of the amount specified ('mol ratio'. 'degree of polymerization', 'weight ratio', etc.).
amount	units	string	The amount's unit of measurement.
amount	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
monomers	defining	boolean	A flag for whether or not the monomer / starting material is considered canonically defining for the polymer.
monomers	monomer_substance	object	A reference to the substance which is used as a starting material or monomer.
monomer_substance	linking_id	string	The approvalID of the record if it exists, otherwise some compact and exchangable ID useful for linking to the referenced record (often the first 8 chars of its uuid).
monomer_substance	name	string	The literal string text of a name.
monomer_substance	ref_pname	string	The "Priority Name" (usually the display name) of the record being referenced.
monomer_substance	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
monomer_substance	refuuid	string	The UUID of the related record.
monomer_substance	substance_class	string	This value wall always be "reference" if it is intended as a real reference and "mention" if it is a place-holder. However, it can also specify a full substance class, in which case the whole record reference object is meant to be a full entire record rather than a reference.
monomer_substance	unii	string	The Unique Ingredient Identifier (UNII, aka "Approval ID") is a unique ID generated for each substance record.

monomer_substance	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
monomers	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
monomers	type	string	The chemical's type or role in polymerization ('initiator', 'monomer', 'starting material', etc.).
monomers	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
Polymer	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
Polymer	structural_units	array	A list of SRUs (Structural Repeating Units) as well as non-repeating structural units which comprise the polymer. Each unit present has a chemical structure, a label, an extent/amount, a type and information about how the unit can connect to other units and/or itself. This can be seen as the set of "pieces" which can be combined together to make the polymer in question.
structural_units	amount	object	The amount of the monomer / starting material which was used, often as a ratio to other monomers and starting materials.
amount	average	float	The amount's numeric average if present.
amount	high	float	The highest numerical value likely for the average amount. (highest average).

amount	high_limit	float	The highest allowable numeric value usable for the amount. (highest limit).
amount	low	float	The lowest numerical value likely for the average amount. (lowest average).
amount	low_limit	float	The lowest allowable numeric value usable for the amount. (lowest limit).
amount	non_numeric_value	string	A textual description of a value which can not be quantified numerically. For example, "solubility" may be described quantitatively or it may be described with certain textual categories. Non-numeric values are meant to specify qualitative values and other values not easily described by numbers or ranges of numbers.
amount	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
amount	type	string	The type of the amount specified ('mol ratio'. 'degree of polymerization', 'weight ratio', etc.)
amount	units	string	The amount's unit of measurement.
amount	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
structural_units	attachment_count	float	A count of the attachment points allowed for the given structural unit
structural_units	attachment_map	object	A map detailing the allowed connections between each connection point in the structural unit (specified by using R-Group aliases) and the set of allowed other connection points where they can connect
structural_units	label	string	A label for the structural unit, typically a sequential capital letter starting with "A" ("A","B","C", etc)

structural_units	structure	string	The molfile-format structure of the structural unit
structural_units	type	string	The type of structural unit specified, describing whether it is an end group, SRU, or fragment.
Polymer	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
	properties	array	A list of physical, chemical or other properties of the record.
Property	defining	boolean	A flag for whether or not the property is considered canonically defining for the substance definition.
Property	name	string	The literal string text of a name.
Property	parameters	array	The list of paramaters needed to define the conditions, context or environment of applicability for the property value specified.
parameters	name	string	The literal string text of a name.
parameters	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
parameters	type	string	The type of parameter specified, (e.g. 'CHEMICAL', ''PHYSICAL', 'ENZYMATIC', or other).
parameters	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
parameters	value	object	The value of the property.
value	average	float	The amount's numeric average if present.
value	high	float	The highest numerical value likely for the average amount. (highest average).
value	low	float	The lowest numerical value likely for the average amount. (lowest average).

value	non_numeric_value	string	A textual description of a value which can not be quantified numerically. For example, "solubility" may be described quantitatively or it may be described with certain textual categories. Non-numeric values are meant to specify qualitative values and other values not easily described by numbers or ranges of numbers.
value	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
value	type	string	The type of the property parameter (e.g. 'CHEMICAL', ''PHYSICAL', 'ENZYMATIC', or other).
value	units	string	The amount's unit of measurement.
value	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
Property	property_type	string	The type of property: chemical, enzymatic, physical, or other.
Property	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
Property	type	string	The type of the name (e.g. "bn" for "brand name", "cn" for "common name", and "sys" for "systematic name", etc).
Property	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
Property	value	object	The value of the property.
value	average	float	The amount's numeric average if present.

value	high	float	The highest numerical value likely for the average amount. (highest average).
value	high_limit	float	The highest allowable numeric value usable for the amount. (highest limit).
value	low	float	The lowest numerical value likely for the average amount. (lowest average).
value	low_limit	float	The lowest allowable numeric value usable for the amount. (lowest limit).
value	non_numeric_value	string	A textual description of a value which can not be quantified numerically. For example, "solubility" may be described quantitatively or it may be described with certain textual categories. Non-numeric values are meant to specify qualitative values and other values not easily described by numbers or ranges of numbers.
value	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
value	type	string	The type of property specified, (e.g. 'CHEMICAL', ''PHYSICAL', 'ENZYMATIC', or other).
value	units	string	The amount's unit of measurement.
value	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
	protein	object	The definitional information of a protein substance. Contains information about the amino acid sequence, gylcosylation, classification, disulfide links and other links.
Protein	disulfide_links	array	The set of disulfide links that connect different cysteine residues to each other via a sulfur-sulfur covalent bond.

disulfide_links	sites	array	A list of explicit detailed sites where the linkage is applicable. A linkage site is always describing how the nucleoside connects to the NEXT nucleoside in the series. So a sequence of length 2 will have only 1 linkage, specified at the 1st site (not the second).
sites	residue_index	integer	The index of the residue on that subunit being specified.
sites	subunit_index	integer	The index of the subunit being specified.
Protein	glycosylation	object	Stores information on glycosylation sites and glycosylation type for the protein.
glycosylation	c_glycosylation_sites	array	The set of sites where the protein is c-glycosylated.
sites	residue_index	integer	The index of the residue on that subunit being specified.
sites	subunit_index	integer	The index of the subunit being specified.
glycosylation	glycosylation_type	string	The type of glycosylation pattern found on the protein. Here, this is a very general term meant to capture the organism-level pattern that the glycosylation roughly corresponds to. (e.g. "mouse", "human", "porcine").
glycosylation	n_glycosylation_sites	array	The set of sites where the protein is n-glycosylated.
sites	residue_index	integer	The index of the residue on that subunit being specified.
sites	subunit_index	integer	The index of the subunit being specified.
glycosylation	o_glycosylation_sites	array	The set of sites where the protein is c-glycosylated.
sites	residue_index	integer	The index of the residue on that subunit being specified.
sites	subunit_index	integer	The index of the subunit being specified.
glycosylation	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
glycosylation	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).

Protein	other_links	array	The set of links, other than disulfide links, which connect different amino acid residues found within the protein.
other_links	linkage_type	string	The type of linkage which connects the residues in a protein.
other_links	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
other_links	sites	array	A list of explicit detailed sites where the linkage is applicable. A linkage site is always describing how the nucleoside connects to the NEXT nucleoside in the series. So a sequence of length 2 will have only 1 linkage, specified at the 1st site (not the second).
sites	residue_index	integer	The index of the residue on that subunit being specified.
sites	subunit_index	integer	The index of the subunit being specified.
other_links	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
Protein	protein_sub_type	string	A comma-separated set of subtypes descriptive of the protein.
Protein	protein_type	string	A general typing of the protein.
Protein	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
Protein	sequence_origin	string	The original source of the amino acid sequence. This is a general category which, for organisms, typically specifies a useful general abstract taxonic level with increasing granularity as it approaches humans (e.g. "bacteria","mouse", "mouse chimeric", "human").

Protein	sequence_type	string	The type of sequence being specified (e.g. "incomplete", "complete").
Protein	subunits	array	The list of Subunits found in this nucleic acid. Each subunit is described by a sequence of nucleobases. Double stranded nucleic acids should typically be represented by 2 subunits, while single-stranded nucleic acids will more typically be represented with 1.
subunits	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
subunits	sequence	string	The amino acid sequence as a string of 1-letter amino acids, from N-term to C-term. Lower-case letters represent D-amino acids, while upper-case are the standard L-amino acids.
subunits	subunit_index	integer	The index of the subunit being specified.
subunits	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
Protein	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
Reference	citation	string	The reference text or citation.
Reference	doc_type	string	The type of reference or document represented (e.g. "INN", "Journal Article", etc).

Reference	document_date	float	The date that the document or reference was obtained / accessed.
Reference	id	string	The identifier of the structural element itself (this is still a UUID).
Reference	public_domain	boolean	A marking of whether the reference itself is known to be publicly accessible.
Reference	tags	array	A collection of strings which mark the reference as having specific properties (nomenclature, spectra, definition, etc).
Reference	url	string	The url to further information regarding this code.
Reference	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
	relationships	array	A list of related records which share some known relationship with this record (e.g. salt forms, metabolites, impurities, etc).
Relationship	amount	object	The value or amount that describes the relationship between the two records. An amount is not always present, but sometimes quantifies the interaction between two records in some context (e.g. "the IC50 for an inhibitor").
amount	average	float	The amount's numeric average if present.
amount	high	float	The highest numerical value likely for the average amount. (highest average).
amount	high_limit	float	The highest allowable numeric value usable for the amount. (highest limit).
amount	low	float	The lowest numerical value likely for the average amount. (lowest average).
amount	low_limit	float	The lowest allowable numeric value usable for the amount. (lowest limit).

amount	non_numeric_value	string	A textual description of a value which can not be quantified numerically. For example, "solubility" may be described quantitatively or it may be described with certain textual categories. Non-numeric values are meant to specify qualitative values and other values not easily described by numbers or ranges of numbers.
amount	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
amount	type	string	The type of the amount specified ('mol ratio'. 'degree of polymerization', 'weight ratio', etc.).
amount	units	string	The amount's unit of measurement.
amount	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
Relationship	comments	string	Any comments regarding the relationship.
Relationship	interaction_type	string	The type of interaction which occurs between the two specified substance records, if applicable.
Relationship	mediator_substance	object	A reference to the substance which is considered to be mediating the relationship or interaction between the two substance records. For example, in a metabolism relationship the mediator will typically be the metabolizing enzyme.
mediator_substance	linking_id	string	The approvalID of the record if it exists, otherwise some compact and exchangable ID useful for linking to the referenced record (often the first 8 chars of its uuid).
mediator_substance	name	string	The literal string text of a name.
related_substance	ref_pname	string	The "Priority Name" (usually the display name) of the record being referenced.

mediator_substance	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
mediator_substance	refuuid	string	The UUID of the related record.
mediator_substance	substance_Class	string	This value wall always be "reference" if it is intended as a real reference and "mention" if it is a place-holder. However, it can also specify a full substance class, in which case the whole record reference object is meant to be a full entire record rather than a reference.
mediator_substance	unii	string	The Unique Ingredient Identifier (UNII, aka "Approval ID") is a unique ID generated for each substance record.
mediator_substance	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
Relationship	qualification	string	Any qualifier needed to describe the relationship / interaction between the two records.
Relationship	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
Relationship	related_substance	object	A reference to the related substance (or concept) record.
related_substance	linking_id	string	The approvalID of the record if it exists, otherwise some compact and exchangable ID useful for linking to the referenced record (often the first 8 chars of its uuid).
related_substance	name	string	The literal string text of a name.
related_substance	ref_pname	string	The "Priority Name" (usually the display name) of the record being referenced.

related_substance	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
related_substance	refuuid	string	The UUID of the related record.
related_substance	substance_class	string	This value wall always be "reference" if it is intended as a real reference and "mention" if it is a place-holder. However, it can also specify a full substance class, in which case the whole record reference object is meant to be a full entire record rather than a reference.
related_substance	unii	string	The Unique Ingredient Identifier (UNII, aka "Approval ID") is a unique ID generated for each substance record.
related_substance	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
Relationship	type	string	The type of relationship (e.g. 'parent -> salt solvate', 'active moiety', 'inhibitor -> 'target', 'toxin -> conjugate' etc.).
Relationship	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
	structurally_diverse	object	The definitional information of a structurally diverse substance. This includes informaiton about the source of the material (e.g. taxonomy for organisms) as well as the state, form and part of the source material used.
Structurally Diverse	developmental_stage	string	The developmental stage of the organism, when necessary to describe the material. (e.g. "adult", "larva", etc).
Structurally Diverse	fraction_material_type	string	A general material type of the fraction which is isolated in a structurally diverse substance (e.g. "oils", "cells", etc).

Structurally Diverse	fraction_name	string	A specific name for the fraction which is isolated in a structirally diverse substance (e.g. "low molecular weight oils").
Structurally Diverse	hybrid_species_maternal_organism	object	The scientific name of the species which provided the ovum for a hybrid. Sometimes the left hand side of the "x" in hybrid nomenclature.
hybrid_species_maternal_organism	linking_id	string	The approvalID of the record if it exists, otherwise some compact and exchangable ID useful for linking to the referenced record (often the first 8 chars of its uuid).
hybrid_species_maternal_organism	name	string	The literal string text of a name.
hybrid_species_maternal_organism	ref_pname	string	The "Priority Name" (usually the display name) of the record being referenced.
hybrid_species_maternal_organism	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
hybrid_species_maternal_organism	refuuid	string	The UUID of the related record.
hybrid_species_maternal_organism	substance_class	string	This value wall always be "reference" if it is intended as a real reference and "mention" if it is a place-holder. However, it can also specify a full substance class, in which case the whole record reference object is meant to be a full entire record rather than a reference.
hybrid_species_maternal_organism	unii	string	The Unique Ingredient Identifier (UNII, aka "Approval ID") is a unique ID generated for each substance record.
hybrid_species_maternal_organism	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
Structurally Diverse	hybrid_species_paternal_organism	object	The scientific name of the species which provided the sperm for a hybrid. Sometimes the right hand side of the "x" in hybrid nomenclature.

hybrid_species_paternal_organism	linking_id	string	The Unique Ingredient Identifier (UNII, aka "Approval ID") is a unique ID generated for each substance record.
hybrid_species_paternal_organism	name	string	The literal string text of a name.
hybrid_species_paternal_organism	ref_pname	string	The "Priority Name" (usually the display name) of the record being referenced.
hybrid_species_paternal_organism	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
hybrid_species_paternal_organism	refuuid	string	The UUID of the related record.
hybrid_species_paternal_organism	substance_class	string	This value wall always be "reference" if it is intended as a real reference and "mention" if it is a place-holder. However, it can also specify a full substance class, in which case the whole record reference object is meant to be a full entire record rather than a reference.
hybrid_species_paternal_organism	unii	string	The Unique Ingredient Identifier (UNII, aka "Approval ID") is a unique ID generated for each substance record.
hybrid_species_paternal_organism	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
Structurally Diverse	infra_specific_name	string	The part of the organisms name that is more specific than the species rank.
Structurally Diverse	infra_specific_type	string	The type of rank of the infra specific name such as variety, subspecies, or forma. .
Structurally Diverse	organism_author	string	The author of the organism's scientific name.
Structurally Diverse	organism_family	string	The organism's taxonomic family.
Structurally Diverse	organism_genus	string	The organism's taxonomic genus.
Structurally Diverse	organism_Species	string	The organism's species scientific name excluding the genus, known as the specific epithet.

Structurally Diverse	parent_substance	object	A reference to the parent substance which this substance further qualifies. This tends to be null if this record is a "whole" structurally diverse record, and points back to the "whole" record if the part or other qualification is present.
parent_substance	linking_id	string	The approvalID of the record if it exists, otherwise some compact and exchangable ID useful for linking to the referenced record (often the first 8 chars of its uuid).
parent_substance	name	string	The literal string text of a name.
parent_substance	ref_pname	string	The "Priority Name" (usually the display name) of the record being referenced.
parent_substance	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
parent_substance	refuuid	string	The UUID of the related record.
parent_substance	substance_class	string	This value wall always be "reference" if it is intended as a real reference and "mention" if it is a place-holder. However, it can also specify a full substance class, in which case the whole record reference object is meant to be a full entire record rather than a reference.
parent_substance	unii	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
parent_substance	uuid	string	The approvalID of the record if it exists, otherwise some compact and exchangable ID useful for linking to the referenced record (often the first 8 chars of its uuid).
Structurally Diverse	part	array	The contiguous physical part(s) of the source material that are isolated in this substance (e.g. "flower", "fruit", "stem", "bone"). Full organisms receive the part of "Whole".

Structurally Diverse	part_location	string	The location of the part(s), if necessary to explain the context of the part.
Structurally Diverse	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
Structurally Diverse	source_material_class	string	The class of source material (e.g. "organism" or "mineral").
Structurally Diverse	source_material_state	string	A textual catagorization of what state the material is in, if needed (e.g. "live", "killed").
Structurally Diverse	source_material_type	string	The type of source material. This is a general category which, for organisms, typically specifies a useful general abstract taxonic level with increasing granularity as it approaches humans (e.g. "plant", "fungus", "mammal", "primate", "human").
Structurally Diverse	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
	structure	object	Chemical Structure of a chemical substance.
Structure	atropisomerism	string	Whether or not the record has atropisomerism, or has a chirality where a hindered rotation about a single bond as a resolt of steric or electronic constraints.
Structure	charge	integer	The net charge of the structure.
Structure	count	integer	The exact number of times that the structure is repeated.
Structure	defined_stereo	integer	A count of defined stereocenters.
Structure	ez_centers	integer	A count of E/Z, or absolute double bond stereochemistry centers.
Structure	formula	string	The chemical formula of the record.
Structure	id	string	The identifier of the structural element itself (this is still a UUID).
Structure	mwt	float	The molecular weight of the structure.

Structure	molfile	string	The chemical structure in MDL Molfile format (V2000).
Structure	optical_activity	string	The optical activity or rotation of the material. "(+)" and "(-)" are used for optically active materials where activity is known and significantly useful for definition. "(+/-)" is used for racemic mixtures.
Structure	references	array	A list of reference uuids, which refer back to the root record's references, essentially acting as footnotes. The included references are considered to be the supporting origins of the data element in question.
Structure	smiles	string	The chemical structure in SMILES format.
Structure	stereo_centers	integer	A count of possible stereocenters.
Structure	stereo_comments	string	Some textually descriptive information about specific stereochemistry that cannot adequately be captured elsewhere.
Structure	stereochemistry	string	The structure's type of stereochemistry (absolute, achiral, racemic, etc.).
	substance_class	string	This value wall always be "reference" if it is intended as a real reference and "mention" if it is a place-holder. However, it can also specify a full substance class, in which case the whole record reference object is meant to be a full entire record rather than a reference.
	tags	array	A collection of strings which mark the reference as having specific properties (nomenclature, spectra, definition, etc).
	unii	string	The Unique Ingredient Identifier (UNII, aka "Approval ID") is a unique ID generated for each substance record.
	uuid	string	A Universally Unique Identifier (also sometimes called a GUID) for the element. Most GSRS elements have a uuid to be used for tracking, processing and referencing a record (and any element of that record).
	version	string	The version of the substance being viewed. Increments with every saved edit.