

name	count
in0	1997
parameters	964
data	883
in1	672
jobid	465
accession	243
in2	216
in3	187
in4	140
in5	130
in6	126
in7	111
query	95
id	95
in8	93
params	90
in9	85
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in10	79
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in12	58
species	55
pathway_id	51
chid	47
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inputWrapper	41
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affyId	24
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email	16
in14	16
genelId	16
notificationDescriptor	16
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peg	15
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mol	14
genomeid	14
format	13
bg_color list	12
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nickname	12
object id list	12
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enzyme id	12
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mass	11
rxcul	11
range	11
array	10
CSID	10
rdf format	10
GetStatus	10
GetResult	10
eFetchRequest	10
start	10
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in15	9
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reaction id	9
orgName	9
quantity	9
field	9
composition	9
ids	8
rid	8
ihopid	8
data_uri	8
inDoc	8
sparql_construct_query	8
inchi	8
sparql_select_query	8
inchi key	8
str	8
chromosome	8
style	8
gene	8
resultNames	8
param1	7
in16	7
dbName	7
in17	7
tx_Name	7
orf	7
products	6
ticket	6
clone	6
location1	6
RunJob	6
org	6
in18	6
in19	6
context	6

name	count
in20	6
in21	6
alias	6
glycan_id	6
in22	6
compound_id	6
in23	6
key	6
in24	6
term	6
in25	6
in26	6
locus	6
element_list	6
idType	5
options	5
identifier	5
genes	5
db_names	5
alignment	5
in27	5
in28	5
ftid	5
in29	5
getKinLawIDs	4
getExpConditions	4
getCatalystsSpeciesIDs	4
getAllPathways	4
SeqDatabase	4
percentage	4
in30	4
in46	4
getKinLawIDsNotNull	4
getLocationID	4
outformat	4
getUnknownModifiersSpeciesIDs	4
returnType	4
getAllEnzymes	4
datatype	4
in31	4
in47	4
getKineticLaw	4
getLocationName	4
reportTypeInt	4
end	4
getCompoundIDFromSpeciesID	4
getAllReactionIDs	4
in32	4
in48	4
subject	4
getPubmed	4
getTissue	4
location2	4
getKinLawIDFromPubmed	4
getAllCompoundIDs	4
in33	4
datasources	4
in49	4
predicate	4
getParametersXML	4
getSBML	4
InternationalAccessionNumber	4
getReactionInstanceIDs	4
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name	count
CancelJob	4
in34	4
in50	4
ScorePairwiseRelations	4
object	4
getNormalizedParametersXML	4
getCompoundIDFromCHEBIID	4
inputData	4
getReactionIDsFromCompoundID	4
in35	4
in51	4
searchCompounds	4
getCompoundIDFromKEGGID	4
string	4
getKEGGReactionID	4
in36	4
in52	4
getReactionIDFromCompound	4
getMultipleCompoundIDs	4
getReactionIDByKEGG	4
in37	4
in53	4
searchEnzymesByName	4
CountryName	4
getSubstratesSpeciesIDs	4
getEnzymeProtein	4
in38	4
in54	4
searchEnzymesByECNumber	4
getProductsSpeciesIDs	4
queryPath	4
getEnzymeVariant	4
genename	4
in39	4
goid	4
text	4
getReactionIDFromEnzyme	4
ri	4
returnPath	4
getReactionIDFromEC	4
in40	4
collection	4
getOrganismFromKLID	4
getECByName	4
numberOfEsts	4
in41	4
xpath	4
getPathwayNames	4
getCompoundID	4
search	4
getCompoundName	4
in42	4
getReactionIDs	4
getKEGGID	4
stop	4
spectrum	4
getActivatorsSpeciesIDs	4
getAllUniProtIDs	4
in43	4
getReactionEquation	4
getCHEBIID	4
getInhibitorsSpeciesIDs	4
getAllUnits	4
order	4

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in44	4
getGeneralReactionEquation	4
getECFromReactionID	4
prefixText	4
getCofactorsSpeciesIDs	4
getReactionInstanceIDsFromProtein	4
variation_id	4
resource	4
in45	4
getEntryPoints	4
queryString	3
run	3
get_orthologs	3
random_seq	3
get_result	3
query_language	3
streamingConfig	3
param2	3
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genes_id_list	3
defaultField	3
gene_info	3
alter_graph	3
enzyme_id_list	3
parameter	3
kcf	3
supported_organisms	3
graph_cliques	3
reaction_id_list	3
option	3
bid	3
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pfamAacc	3
retrieve_seq	3
parse_psi_xml	3
GetResults	3
draw_heatmap	3
String 1	3
to db	3
collectionName	3
retrieve_seq_multigenome	3
roc_stats	3
compare_graphs	3
isObsolete	3
entry_id	3
convert_matrix	3
GetSimulatorStatus	3
drug_id_list	3
retrieve_ensembl_seq	3
xygraph	3
graph_node_degree	3
DeleteSimulationResource	3
psortPrediction	3
purge_seq	3
classfreq	3
graph_topology	3
wolfPsortPrediction	3
oligo_analysis	3
convert_seq	3
graph_cluster_membership	3

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getTermByld	3
compound_id_list	3
random	3
dyad_analysis	3
compare_classes	3
random_graph	3
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motif_id_list	3
glycan_id_list	3
reportType	3
affyIds	3
pattern_assembly	3
convert_classes	3
graph_get_clusters	3
ko_id	3
mol_text	3
dna_pattern	3
contingency_stats	3
graph_neighbours	3
convert_features	3
contingency_table	3
mcl	3
smile_string	3
pathway	3
signalPPrediction	3
feature_map	3
matrix_scan	3
rnc	3
filename	3
index	3
ecNumber	3
footprint_discovery	3
matrix_distrib	3
monitor	3
in78	2
indexName	2
sayHi	2
preseseq	2
searchOWL	2
HelloStringIn	2
min-sep	2
ColumnType	2
getEnzymeProteinList	2
CSIDs	2
population_id	2
in62	2
in79	2
searchPossibleCompletions	2
checkpoint	2
getStringTermByld	2
MiningModelName	2
maxHits	2
pathogenicity	2
getResultTypes	2
in63	2
in80	2
indexConfig	2
input_protein	2
getTree	2
param3	2
searchStringPossibleCompletions	2
NodeID	2
attachmentFormat	2
growthForm	2

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getParameterDetails	2
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in81	2
searchTermSynonyms	2
param4	2
SubmitQuery	2
getStringTree	2
array1	2
end	2
arg0	2
luceneQuery	2
getParameters	2
in65	2
defid	2
searchTermDetails	2
MonitorJob	2
searchStringTermSynonyms	2
array2	2
arg1	2
SMARTAnalysis	2
cannedQueryName	2
in66	2
searchTermMath	2
searchStringTermDetails	2
complete	2
position	2
arg2	2
tx_Clas	2
getGeneList	2
in67	2
searchTermName	2
searchStringTermMath	2
restrictions	2
arg3	2
runGenewiz	2
tx_Rank	2
in68	2
CityName	2
getTermsBylds	2
fields	2
searchStringTermName	2
domain	2
fasta	2
tx_Rmax	2
estUnisequenceld	2
in69	2
filter values	2
getTermByldOWL	2
getStringTermsBylds	2
ncbiTaxonIdentifier	2
oligomer	2
dbld	2
tx_Dcls	2
in70	2
datatype in	2
resultsRequest	2
searchPossibleCompletionsOWL	2
searchString	2
taxonName	2
result	2
RunSimulator	2
tx_Id	2
libraryId	2
in55	2

name	count
in71	2
datatype out	2
getTreeOWL	2
isDirectChildOf	2
pattern	2
StartSimulator	2
getDatasets	2
ranks	2
in56	2
in72	2
config	2
smiles	2
searchTermSynonymsOWL	2
isChildOf	2
feature	2
riWindow	2
doc	2
superkingdom	2
getMatrixByName	2
in57	2
in73	2
extension	2
uniprotIds	2
searchTermDetailsOWL	2
md5	2
AlkaneRetentionIndexGcColumnComposition	2
getCompoundIDsFromCHEBIID	2
length	2
pmid	2
aspect	2
getMatrixById	2
in58	2
in74	2
searchTermMathOWL	2
isRoot	2
getCompoundIDsFromKEGGID	2
orfID	2
ihoppmid	2
formula	2
searchByTag	2
txquery	2
in59	2
in75	2
filedata	2
searchTermNameOWL	2
GenomeParams	2
SpectrumID	2
getKEGGReactionIDs	2
kos_id_list	2
calc3d	2
getAllMatrices	2
schema	2
in60	2
in76	2
tanimoto coefficient	2
getTermsByIdsOWL	2
min-cov	2
getReactionIDsByKEGG	2
seq_sup_rmsd_request	2
pathwayId	2
requestID	2
eComp	2
getSIDD	2
in61	2

name	count
in77	2
cl	1
GetPresentFamiliesProdom	1
getPIRSeedAlignmentByAccession	1
n_pch_pins	1
FindSimilar	1
mot_list	1
runProdivtmhmmDefault	1
getTicketById	1
cla_query	1
KeggOrtholog2PdbSuperfamilies	1
getOrganismsByQueryTerm	1
cla_fetch_prop	1
GetHogenomFamDef	1
seq_neighbors_request	1
cla_dump_prop	1
getTranscripts	1
getSymbolInfoFromIHOP	1
GetStpGraph	1
getGeneAndTranscript	1
anatomyName	1
eGqueryRequest	1
mapping	1
stoplist	1
getInstancesByPubMedId	1
GetPublicationsBySearch	1
listFieldsInformationRequest	1
getELMInstanceBySequenceMatch	1
RDfolderSOAP	1
RunBlastpJob	1
Blast_Protein	1
soap_apply_all_loops	1
listOrganisms	1
getTermsByName	1
NearestNodeHogenom	1
mpath	1
GetScenarioProdom	1
getPIRSeedAlignmentById	1
n_sims	1
GetLinked	1
cla_list	1
position1	1
runProdivtmhmmParams	1
getTicketBySeq	1
hit_query	1
KeggOrtholog2DomainIds	1
getGeneldsByQueryTerm	1
seq_fetch_fasta	1
cell	1
getPubMedFromPMID	1
supid	1
seq_dump_fasta	1
getTranscriptsRange	1
getSymbolInteractionsFromSymbol	1
UploadStpGraph	1
proteinId	1
getTranscriptsAndInfo	1
GetDatabases	1
tissueId	1
eGqueryRequestMS	1
sources	1
GetSpeciesList	1
getImage	1
filter	1

name	count
submit_jobRequestSoapMsg1	1
runELMMatcher	1
GetPublicationExperiments	1
getResultsRequest	1
getELMInstanceBySequenceAccession	1
RNAfoldSOAP	1
RunBlastxJob	1
Blast Protein HC	1
soap_apply_missing_ends	1
getCurationTagsByName	1
shortform	1
getTermsByExactName	1
GetParentHogenom	1
ma	1
freeTextSearch	1
sim_cutoff	1
Cooccurrence	1
hit_list	1
position2	1
runTopcomp	1
GetEMBLNucleotideSequence_BsmI	1
hat_query	1
DomainId2KeggOrthologs	1
getGeneldsByProteomeld	1
mot_fetch_fasta	1
getPubMedFromIHOP	1
mot_dump_fasta	1
getchromName	1
getSymbolInteractionsFromSymbolAndTaxId	1
getCYGDAnnotations	1
getTranscriptsByGeneName	1
SearchByMass	1
targetAnatomyName	1
eInfoRequest	1
proxyTicket	1
GetEnslDsByRegion	1
main	1
submit_jobRequestSoapMsg2	1
runInstanceMapper	1
GetPublicationStrains	1
getAllResultsIdsRequest	1
runLiftOver	1
runFetchDom	1
RNAshapesSOAP	1
RunTblastnJob	1
Blast Protein XML	1
soap_create_model	1
saveCurationTag	1
longform	1
getPrefixedTermsByName	1
GetChildHogenom	1
go	1
dir	1
SequenceInfo	1
seq1	1
color sim_cutoff	1
SpellCheck	1
hat_list	1
DNApropertyRun	1
GetEMBLNucleotideSequence_AGAVE	1
hot_query	1
PdbSuperfamily2KeggPathways	1
getGeneldsByProteomeldAndQueryTerm	1
seq_fetch_nr	1

name	count
getRelatedSymbols	1
seq_align_request	1
seq_dump_nr	1
mappingInfo	1
getSymbolInteractionsFromReference	1
clsName	1
startString	1
sliceChromosome	1
SearchByMass2	1
mappingType	1
getImageSeriesList	1
eInfoRequestMS	1
rela_list	1
GetExpressionDatasets	1
getKinaseList	1
submit_jobRequestSoapMsg3	1
GetPublicationModelTypes	1
getResultIdsRequest	1
getAvailableChainFiles	1
runFetchProt	1
RNAsuboptSOAP	1
RunTblastxJob	1
Blastofas	1
soap_find_clashes	1
getPathwayHistory	1
getTermParents	1
getTermChildren	1
GetDFStreeHogenom	1
Reactomelds	1
genotype_status	1
endPoint	1
BlastResults	1
param5	1
seq2	1
sort_by	1
SuggestSearchTerms	1
tree	1
hot_list	1
DNApropertyFetchResult	1
mom_query	1
KeggPathway2PdbSuperfamilies	1
getGeneldsByGenomeAc	1
mot_fetch_nr	1
getRelatedSymbolsWithTaxId	1
gash_input	1
mot_dump_nr	1
numberConversion	1
getSymbolInteractionsFromIHOP	1
propertyName	1
countString	1
sliceChromosomeByGene	1
SearchByFormula	1
pdrcode	1
getNeuroBlast	1
eSearchRequest	1
termType_list	1
GetPathwayList	1
getBindingDomainList	1
submit_jobRequestSoapMsg4	1
getCategories	1
listAdditionalReferenceFieldsRequest	1
recentVersion	1
runFetchFasta	1
bindndna	1

name	count
SimpleSearch2IdList	1
Decoder	1
SubmitTwoProteinSetsRequest	1
soap_match_alignment_with_model	1
getXrefList	1
generateConceptsFromPubMedQuery	1
generateConceptsFromText	1
getTermRelations	1
GetScenarioHogenom	1
ChEBIIds	1
genetic_manipulation	1
method	1
PsiBlastResults	1
param6	1
runAndWaitFor	1
RetrieveHits	1
Blast	1
seq_info	1
trnscanRun	1
getLocation	1
seq_fetch_name	1
KeggPathway2DomainIds	1
getGeneById	1
seq_dump_name	1
RunDeterministicSimulator	1
getSymbolsFromReference	1
LocusID	1
hit_fetch_simple	1
runMutalyzer	1
getLatestSymbolInformationFromSymbol	1
propertyValue	1
operator	1
uploadGenBankLocalFile	1
SearchByFormula2	1
uppergi50	1
eSearchRequestMS	1
GetEnslDsByPathwayName	1
getSubstratesByNameSearch	1
probes	1
submit_jobRequestSoapMsg5	1
runhogenom	1
getNonOboOntologies	1
getDomainsHierarchyRequest	1
runFetchAlign	1
bindnrna	1
GetRecordImage	1
Domains_2_svg	1
MonitorJobRequest	1
testFile	1
findPathwaysByText	1
generateTerminology	1
getChildrenFromRoot	1
GetPresentFamiliesHogenom	1
modelName	1
designated_allele_name	1
generateContent	1
SequenceSpace	1
usa	1
pegs	1
RetrieveChainHits	1
BlastJobStatus	1
genbankAccession	1
mot_info	1
array_seq	1

name	count
trnascanFetchResult	1
getGeneld	1
mot fetch name	1
DomainId2KeggPathways	1
mot dump name	1
StartDeterministicSimulator	1
guessSymbolIdFromSymbolText	1
hat fetch simple	1
transcriptInfo	1
getLatestSymbolInformationFromSymbolAndTaxId	1
clsNames	1
getForInteractor	1
uploadGenBankRemoteFile	1
GetRecordMol	1
protein	1
geneSearch2	1
eSummaryRequest	1
GetEnslDsByExpression	1
getSubstratesByGeneNameSearch	1
queryFields	1
submit_jobRequestSoapMsg6	1
getAlIELMs	1
estId	1
getQualityCriteria	1
getReferencedEntriesFlatSetRequest	1
runFetchKW	1
disembl	1
GetRecordDetails	1
GetAvailableDatabases	1
Encoder	1
CancelJobRequest	1
modelFile	1
createPathway	1
select_output format	1
GetInheritedFamiliesHogenom	1
publicationIdOrText	1
experimental manipulation	1
runDSSP	1
RetrieveDomainHits	1
BlastJobResult	1
genbankIdentifier	1
cla info	1
direction	1
aaUsage	1
getGene	1
cla fetch name	1
protein acc	1
PdbSuperfamily2Funcats	1
cla_dump_name	1
abbr	1
guessSymbolIdFromSymbolTextAndTaxId	1
hot fetch simple	1
getLatestSymbolInformationFromReference	1
startIndex	1
getForInteractorLike	1
updateCollection	1
GetCompressedRecordsSdf	1
ligand	1
getNeuroBlast1	1
eSummaryRequestMS	1
GetExpressionByEnslDs	1
getInstancesByProteinSequenceAccessionSearchWithAllThroughputData	1
chipTypes	1
filterName	1

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GetExperiment	1
submit_jobRequestSoapMsg7	1
pvalue	1
getELM	1
getResourcesByCategory	1
getNumberOfResultsRequest	1
runFetchKWscript	1
iupredl	1
SimpleSearch	1
url	1
Fillseq	1
RetrievePairwiseScoresRequest	1
outputMode	1
getPathwayAs	1
getTermsByAnnotationData	1
GetInnovatedFamiliesHogenom	1
personName	1
description	1
runDSSPByID	1
view	1
runPconsDefault	1
pattern1	1
BlastJobError	1
hit_info	1
codonUsage	1
getOrganism	1
seq_fetch_desc	1
category	1
Funcat2PdbSuperfamilies	1
rnastructAlignmentML	1
seq_dump_desc	1
guessSymbolIdFromReference	1
bg	1
query_list	1
getLatestSymbolInformationFromIHOP	1
getBetweenInteractors	1
deleteCollection	1
GetRecordsSdf	1
box	1
getGeneList1	1
eLinkRequest	1
AffyDEGFinder	1
getInstancesByProteinSequenceAccessionSearchWithLowThroughputDataOnly	1
exactMatchGenbank	1
filterOperatorValues	1
GetExperiments	1
submit_jobRequestSoapMsg8	1
getELMByIdentifier	1
getWSDLs	1
getEntriesFieldUrlsRequest	1
getUPIForSequence	1
iupreds	1
AsyncSimpleSearch	1
userid	1
Formatname	1
RetrieveCompleteScoresRequest	1
getVersion	1
tokenization	1
getCurationTagHistory	1
blastprod	1
ImageNumber	1
GetLostFamiliesHogenom	1
ChEBId	1
tbase	1

name	count
OperonParams	1
contig	1
runProqDefault	1
pattern2	1
runTopconsDefault	1
hat info	1
keywords	1
getSeq	1
getProtein	1
mot fetch desc	1
UniProt RefSeq ID	1
DomainId2Funcats	1
alignddotbracketfasta	1
mot dump desc	1
getSymbolDefinitionsFromSymbol	1
strand	1
query info	1
getRegistry	1
searchCriteria	1
getForInteractorlist	1
updateResource	1
GetExtendedCompoundInfo	1
getRepresentativeImageSeries	1
eLinkRequestMS	1
getDatabaseVersion	1
getInstancesByProteinSequenceAccessionSearchForAllRelatedSpeciesWithAllThroughputData	1
matchUnigeneSameCluster	1
GetExperimentsBySearch	1
submit_jobRequestSoapMsg9	1
getELMsByTextSearch	1
select	1
getDomainsReferencedInEntryRequest	1
getUPIForAccession	1
pdisorder	1
GetAsyncSearchStatus	1
Phylotable	1
updatePathway	1
ConvertCopasiMLToSBMLRequest	1
getCurationTags	1
GetRegainedFamiliesHogenom	1
pubmed	1
runMkDom	1
RegulatorParams	1
featureid	1
GetDatabankInfo	1
ClustalW	1
sequenceCount	1
hot info	1
getOrfs	1
getTranscript	1
cla fetch desc	1
job	1
Funcat2DomainIds	1
microRNA	1
cla dump desc	1
getSymbolDefinitionsFromSymbolAndTaxId	1
prior	1
query stat	1
addParams	1
objects	1
getForInteractionDetectionMethod	1
appendResource	1
GetExtendedCompoundInfoArray	1
geneSearch1	1

name	count
eFetchRequestMS	1
getSourceDatabaseVersions	1
getInstancesByProteinSequenceAccessionSearchForAllRelatedSpeciesWithLowThroughputDataOnly	1
words	1
GetExperimentPhenoAssays	1
submit_jobRequestSoapMsg10	1
getELMsBySequenceMatch	1
cronosWS	1
table	1
getEntryRequest	1
getMappedDatabaseNames	1
poodlel	1
GetAsyncSearchResult	1
PsiBlast NT	1
findPathwaysByXref	1
getTermMetadata	1
ConvertSBMLToCopasiMLRequest	1
findInteractions	1
bank	1
magnification	1
GetTransferredFamiliesHogenom	1
uniprotId	1
series_number	1
runZpredDefault	1
ProfileParameterParams	1
locations	1
GetEntry	1
inputSequences	1
runPdb	1
contact	1
seq_parse_name	1
getProt	1
getXref	1
seq_fetch_entry	1
PdbSuperfamily2ECs	1
rnastructML	1
seq_dump_entry	1
getSymbolDefinitionsFromReference	1
mnt	1
query_reset	1
odeSolverParams	1
getAttributes	1
referenceIdentifiers	1
getForOrganism	1
deleteResource	1
SearchByMassAsync	1
geneSearch	1
eSpellRequest	1
getNames	1
getInstancesByKinaseTextSearch	1
kwSrc	1
GetExperimentExpFactors	1
submit_jobRequestSoapMsg11	1
getAllELMInstances	1
isinRedList	1
subsection	1
getDetailedNumberOfResultsRequest	1
rnabindr	1
GetCompoundThumbnail	1
PsiBlast NT XML	1
getColorPathway	1
getTermXrefs	1
ValidateModelRequest	1
login	1

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stain	1
NearestNodeProdom	1
submitter_id	1
inputFormat	1
getPRINTSRecordByAccession	1
ProfileAcc	1
GetMetaData	1
input_params	1
maxN	1
runPfragDefault	1
getPipelinesStatus	1
mot_parse_name	1
queryGenomes	1
getStringList	1
mot_fetch_entry	1
EC2PdbSuperfamilies	1
dotbracketfasta	1
mot_dump_entry	1
checkSyntax	1
getSymbolDefinitionsFromIHOP	1
default_list	1
mathPlotParams	1
getFilters	1
entities	1
getSources	1
SearchByFormulaAsync	1
sequencesInFasta	1
getGeneList2	1
eSpellRequestMS	1
getDBrefs	1
getInstancesByBindingDomainTextSearch	1
arrayTypeID	1
GetExperimentsByModelType	1
submit_jobRequestSoapMsg12	1
getELMInstance	1
searchCitations	1
AfoldSOAP	1
getEntryFieldUrlsRequest	1
say_hello	1
GetCompoundInfo	1
PsiBlast Protein	1
getPathwayInfo	1
getOntologyNames	1
getRecentChanges	1
sex	1
fromPath	1
GetParentProdom	1
taxonomyId	1
source_reliability	1
outputFormat	1
getPRINTSRecordByID	1
ExpressionFromGeneParams	1
EC_number	1
GetIndices	1
connect	1
maxP	1
runPalignSeqSeqDefault	1
queryPmid	1
cla_parse_name	1
getFeatures	1
getOrganismList	1
cla_fetch_entry	1
UniProtId2DomainIds	1
cla_dump_entry	1

name	count
ko id list	1
chromAccession	1
getSymbolInfoFromSymbol	1
overlap	1
default set	1
prismParamsCompact	1
entityIds	1
getResourceTypes	1
mutationsList	1
runAtlas	1
src	1
ORApayloads	1
getSubstrateByIdentifier	1
allWords	1
numberOfEstsInLibrary	1
GetExperimentsStrains	1
listDomainsRequest	1
getAllFunctionalSites	1
doc2loc	1
ContrafoldSOAP	1
listFieldsRequest	1
topcons	1
Mol2CSID	1
PsiBlast Protein XML	1
listPathways	1
getOntologyLoadDate	1
getPathway	1
strain	1
GetChildProdom	1
modelId	1
searchParameters	1
getSeedAlignmentByAccession	1
Reaction number	1
Find	1
tool	1
disconnect	1
Gene ID	1
runPalignSeqSeq	1
doScoobyById	1
seq query	1
runGlobPlotter	1
getGenelIdList	1
seq fetch_prop	1
PdbSuperfamily2UniProtIds	1
seq dump_prop	1
chromosomeName	1
getSymbolInfoFromSymbolAndTaxId	1
runs	1
sticker	1
asyncPrismParamsCompact	1
startSession	1
ialgorithm	1
fetchAtlasResult	1
input format	1
getInstanceByIdentifier	1
queryOptionGB	1
GetPublication	1
getDomainsReferencedInDomainRequest	1
getFunctionalSite	1
McQFoldSOAP	1
getEntriesRequest	1
Blast NT	1
CSID2ExtRefs	1
soap analyze geometry	1

name	count
findPathwaysByLiterature	1
getAllTermsFromOntology	1
runMUSCLE	1
emap	1
GetDFSTreeProdom	1
elementsIds	1
proteinFASTAsequence	1
getSeedAlignmentByID	1
ProteinAccString	1
peg_id	1
FindBoolean	1
seq_list	1
ID_type	1
runPalignSeqSeqSSDefault	1
doScoobyBySeq	1
mot_query	1
PdbSuperfamily2KeggOrthologs	1
getOrganisms	1
mot_fetch_prop	1
GetHogenomFamComp	1
mot_dump_prop	1
getGeneName	1
getSymbolInfoFromReference	1
GetStpGraphList	1
sbml2PrismParams	1
endSession	1
picking	1
output_format	1
getInstancesWithPdbEntryAssigned	1
queryOptionSC	1
GetPublications	1
getReferencedEntriesSetRequest	1
getFunctionalSitesByTextSearch	1
PknotsRGSOAP	1
getReferencedEntriesRequest	1
RunBlastnJob	1
Blast_NT_XML	1
getReport	1
soap_apply_alignment	1
removeCurationTag	1
getRootTerms	1
read_write	1