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ValidateModelRequest	1
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getAllELMInstances	1
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odeSolverParams	1
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mot_fetch_entry	1
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mot_fetch_prop	1
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mot_dump_prop	1
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GetParentHogenom	1
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queryOptionSC	1
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Cooccurrence	1

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DomainId2KeggOrthologs	1
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ID_type	1
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getSymbolInteractionsFromSymbolAndTaxId	1
UploadStpGraph	1
proteinFASTAsequence	1
tissueId	1
getGeneName	1
ProteinAccString	1
getImage	1
sbml2PrismParams	1
seq_list	1
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cla_query	1
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cla_fetch_prop	1
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Blast_Protein	1
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soap_apply_all_loops	1
SequenceInfo	1
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SpellCheck	1
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DNApropertyRun	1
GetEMBLNucleotideSequence_Bsml	1
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PdbSuperfamily2KeggPathways	1
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cl	1
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main	1
getGeneAndTranscript	1
mot_list	1
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SimpleSearch2IdList	1
GetPublicationExperiments	1
seq_dump_fasta	1
SubmitTwoProteinSetsRequest	1
RNAfoldSOAP	1
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Blast_Protein_HC	1

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soap_apply_missing_ends	1
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RunTblastxJob	1
DNApropertyFetchResult	1
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n_sims	1
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position1	1
shortform	1
getTermParents	1
getRelatedSymbolsWithTaxId	1
seq_align_request	1
mpath	1
getSymbolInteractionsFromIHOP	1
clsName	1
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mappingType	1
getTranscriptsRange	1
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listAdditionalReferenceFieldsRequest	1
mot_fetch_fasta	1
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MonitorJobRequest	1
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soap_create_model	1
PsiBlastResults	1
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RetrieveHits	1
runLiftOver	1
runFetchFasta	1
Blast	1
tree	1
trnascanRun	1
sim_cutoff	1
KeggPathway2DomainIds	1
getGeneIdsByGenomeAc	1
position2	1
longform	1
getTermChildren	1
getSymbolsFromReference	1
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ma	1
getLatestSymbolInformationFromSymbol	1

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propertyName	1
pdbcode	1
getchromName	1
getBindingDomainList	1
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SearchByMass	1
hit_list	1
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proxyTicket	1
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seq_fetch_nr	1
GetRecordDetails	1
GetPublicationModelTypes	1
seq_dump_nr	1
CancelJobRequest	1
RNAsuboptSOAP	1
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createPathway	1
Blastofas	1
getImageSeriesList	1
eSearchRequestMS	1
GetPresentFamiliesHogenom	1
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soap_find_clashes	1
SequenceSpace	1
RetrieveChainHits	1
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getAvailableChainFiles	1
runFetchAlign	1
BlastJobStatus	1
trnascanFetchResult	1
getLocation	1
color_sim_cutoff	1
DomainId2KeggPathways	1
getGeneById	1
getTermRelations	1
guessSymbolIdFromSymbolText	1
LocusID	1
go	1
getLatestSymbolInformationFromSymbolAndTaxId	1
propertyValue	1
uppergi50	1
mappingInfo	1
getSubstratesByNameSearch	1
sliceChromosome	1
SearchByMass2	1
hat_list	1
submit_jobRequestSoapMsg5	1
runhogenom	1
rela_list	1
GetExpressionDatasets	1
mom_query	1
getReferencedEntriesFlatSetRequest	1
mot_fetch_nr	1
SimpleSearch	1
getCategories	1
mot_dump_nr	1
RetrievePairwiseScoresRequest	1
bindndna	1
countString	1
getPathwayAs	1
Decoder	1

name	count
getNeuroBlast	1
eSummaryRequest	1
GetInheritedFamiliesHogenom	1
modelName	1
soap_match_alignment_with_model	1
runDSSP	1
estId	1
RetrieveDomainHits	1
endPoint	1
recentVersion	1
runFetchKW	1
BlastJobResult	1
genbankAccession	1
seq1	1
GetAvailableDatabases	1
aaUsage	1
getGeneId	1
sort_by	1
PdbSuperfamily2Funcats	1
generateConceptsFromPubMedQuery	1
getChildrenFromRoot	1
guessSymbolIdFromSymbolTextAndTaxId	1
genotype_status	1
getLatestSymbolInformationFromReference	1
clsNames	1
param5	1
protein	1
numberConversion	1
getSubstratesByGeneNameSearch	1
sliceChromosomeByGene	1
SearchByFormula	1
hot_list	1
submit_jobRequestSoapMsg6	1
termType_list	1
GetPathwayList	1
seq_fetch_name	1
getNumberOfResultsRequest	1
seq_dump_name	1
abbr	1
AsyncSimpleSearch	1
getNonOboOntologies	1
hit_fetch_simple	1
RetrieveCompleteScoresRequest	1
bindnrna	1
operator	1
getCurationTagHistory	1
Domains_2_svg	1
eSummaryRequestMS	1
GetInnovatedFamiliesHogenom	1
publicationIdOrText	1
testFile	1
probes	1
filterName	1
runDSSPByID	1
runPconsDefault	1
method	1
runFetchKWscript	1
BlastJobError	1
genbankIdentifier	1
seq2	1
url	1
codonUsage	1
getGene	1
Funcat2PdbSuperfamilies	1

name	count
generateConceptsFromText	1
guessSymbolIdFromReference	1
genetic_manipulation	1
getLatestSymbolInformationFromIHOP	1
startIndex	1
RunDeterministicSimulator	1
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ligand	1
runMutalyzer	1
getInstancesByProteinSequenceAccessionSearchWithAllThroughputData	1
upLoadGenBankLocalFile	1
SearchByFormula2	1
seq_info	1
submit_jobRequestSoapMsg7	1
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mot_fetch_name	1
getEntriesFieldUrlsRequest	1
mot_dump_name	1
GetAsyncSearchStatus	1
getQualityCriteria	1
hat_fetch_simple	1
updatePathway	1
disembl	1
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Encoder	1
geneSearch2	1
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personName	1
modelFile	1
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userid	1
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getOrganism	1
getVersion	1
DomainId2Funcats	1
rnastructAlignmentML	1
array_seq	1
generateTerminology	1
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getSymbolDefinitionsFromSymbol	1
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designated_allele_name	1
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transcriptInfo	1
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GetRecordMol	1
mot_info	1
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Funcat2DomainIds	1
aligneddotbracketfasta	1
direction	1
getSymbolDefinitionsFromSymbolAndTaxId	1
strand	1
protein_acc	1
experimental_manipulation	1
searchCriteria	1
getInstancesByProteinSequenceAccessionSearchForAllRelatedSpeciesWithAllThroughputData	1
updateCollection	1
GetCompressedRecordsSdf	1
cla_info	1
submit_jobRequestSoapMsg9	1
AffyDEGFinder	1
seq_fetch_desc	1
getEntryRequest	1
GetExperiments	1
seq_dump_desc	1
GetCompoundThumbnail	1
getWSDLs	1
query_list	1
getColoredPathway	1
iupreds	1
getBetweenInteractors	1
login	1
Formatname	1
getGeneList1	1
eFetchRequestMS	1
GetTransferedFamiliesHogenom	1
tokenization	1
exactMatchGenbank	1
runZpredDefault	1
getELMByIdentifier	1
cronosWS	1
GetEntry	1
getMappedDatabaseNames	1
runPdb	1
sequenceCount	1

name	count
getProt	1
getTranscript	1
pattern1	1
getTermMetadata	1
PdbSuperfamily2ECs	1
microRNA	1
getSymbolDefinitionsFromReference	1
prior	1
category	1
description	1
getAttributes	1
objects	1
view	1
getInstancesByProteinSequenceAccessionSearchForAllRelatedSpeciesWithLowThroughputDataOnly	1
deleteCollection	1
GetRecordsSdf	1
hit_info	1
submit_jobRequestSoapMsg10	1
submit_jobRequestSoapMsg11	1
getDatabaseVersion	1
mot_fetch_desc	1
getDetailledNumberOfResultsRequest	1
GetExperimentsBySearch	1
mot_dump_desc	1
GetCompoundInfo	1
select	1
query_info	1
getPathwayInfo	1
pdisorder	1
getForInteractorlist	1
getRecentChanges	1
Phylotable	1
getRepresentativeImageSeries	1
eSpellRequest	1
NearestNodeProdom	1
uniprotId	1
ConvertCopasiMLToSBMLRequest	1
matchUnigeneSameCluster	1
getPRINTSRecordByAccession	1
getELMsByTextSearch	1
isinRedList	1
GetMetaData	1
runPfragDefault	1
contact	1
contig	1
queryGenomes	1
getXref	1
pattern2	1
getTermXrefs	1
EC2PdbSuperfamilies	1
rnastructML	1
keywords	1
blastprod	1
ImageNumber	1
getSymbolDefinitionsFromIHOP	1
mnt	1
UniProt_RefSeq_ID	1
tbase	1
getFilters	1
referenceIdentifiers	1
OperonParams	1
getInstancesByKinaseTextSearch	1
updateResource	1
GetExtendedCompoundInfo	1

name	count
hat_info	1
hot_info	1
submit_jobRequestSoapMsg12	1
getSourceDatabaseVersions	1
cla_fetch_desc	1
getEntryFieldUrlsRequest	1
GetExperimentPhenoAssays	1
cla_dump_desc	1
Mol2CSID	1
table	1
query_stat	1
listPathways	1
poodlel	1
getForInteractionDetectionMethod	1
getPathway	1
PsiBlast_NT	1
geneSearch1	1
eSpellRequestMS	1
GetParentProdom	1
ConvertSBMLToCopasiMLRequest	1
words	1
getPRINTSRecordByID	1
getELMsBySequenceMatch	1
searchCitations	1
GetIndices	1
runPalignSeqSeqDefault	1
getPipelinesStatus	1
featureid	1
getFeatures	1
getStringList	1
getOntologyNames	1
UniProtId2DomainIds	1
dotbracketfasta	1
getSymbolInfoFromSymbol	1
job	1
pubmed	1
entities	1
RegulatorParams	1
sequencesInFasta	1
addParams	1
getInstancesByBindingDomainTextSearch	1
appendResource	1
GetExtendedCompoundInfoArray	1