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ERequestStatus	2
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getArchaeaReturn	2
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getOrganellesReturn	2
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PhylotableResponse	1
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MOBYSHoundGiFromLocusIDReturn	1
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getBiologicalProcessGOTermByOrfReturn	1
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getSubstratesByNameSearchResponse	1
getSymbolInteractionsFromSymbolAndTaxIdResponse	1
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getFunctionalSiteResponse	1
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getCifChainLengthReturn	1
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FASTA	1
getRelatedSymbolsWithTaxIdResponse	1
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ArrayOfOperonResult	1
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GetExperimentsResponse	1
addDocumentReturn	1
getRelatedByTypeReturn	1
eSummaryResultMS	1
blastpgpout	1
AfoldSOAPResponse	1
getDomainsReferencedInDomainResponse	1
hit_infoResponse	1
getESTLibrariesThatAreAreNotRandomlySequencedReturn	1
getProteinResponse	1
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getReferencedEntriesResponse	1
seq_fetch_descResponse	1
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PsiBlast_ProteinResponse	1
seq_dump_descResponse	1
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listOrganismsResponse	1
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getSGDAccessionByOrfReturn	1
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getKeggCompoundsOnKeggPathwayReturn	1
getOrfsByGoldReturn	1
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getPIRSeedAlignmentByAccessionResponse	1
getAtomSiteReturn	1
boundaries_ofReturn	1
SuggestSearchTermsResponse	1
getFunctionalSitesByTextSearchResponse	1
getPubmedIdForStructureReturn	1
simple_searchReturn	1
DNApropertyFetchResultResponse	1
getMappedDatabaseNamesResponse	1
getKabschSanderReturn	1
getSimpleModelByIdReturn	1
getTimedNodeAccessionReturn	1
KeggPathway2DomainIdsResponse	1
bool	1
queueentry	1
getSymbolsFromReferenceResponse	1
getInstancesByProteinSequenceAccessionSearchWithLowThroughputDataOnlyResponse	1
getSynsetsReturn	1
getLatestSymbolInformationFromSymbolResponse	1
getXMLResultReturn	1
mathPlotResult	1

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GetRecordsSdfResponse	1
getTermChildrenResponse	1
tblastxReturn	1
getSliceReturn	1
getDatabaseVersionResponse	1
deleteResourceResults	1
ArrayOfRegulatorResult	1
getSubmissionAnnotationVoxelWlzReturn	1
GetExperimentsBySearchResponse	1
addDocumentDefaultDbReturn	1
getAllRelatedInfoReturn	1
eLinkResult	1
ContrafoldSOAPResponse	1
getReferencedEntriesSetResponse	1
hat infoResponse	1
getESTLibrariesWithMoreThanAGivenNumberOfESTsReturn	1
getTranscriptResponse	1
topconsResponse	1
mot fetch descResponse	1
getAllOrthoMCLClustersWithLessThanAGivenPercentageOfProteinsOfAGivenGenomeReturn	1
toDotBracketFastaReturn	1
PsiBlast Protein XMLResponse	1
mot dump descResponse	1
getTheExonsWithTheirPredictedTranscriptForAGivenGeneReturn	1
getFileReturn	1
addRdfFileReturn	1
getCurationTagsByNameResponse	1
query infoResponse	1
getOrthoMCLClustersContainingProteinsOfAGivenGenomeAndProteinsOfEssentialYeastGenesReturn	1
getGeneNameByOrfReturn	1
indexFromSRBReturn	1
getAnnotationForProteinsInAGivenMCLClusterReturn	1
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getChromosomalLocationReturn	1
getDescriptionReturn	1
GetPresentFamiliesProdomResponse	1
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameMCLClustersAsProteinsWithAGivenPfamAAnnotationReturn	1
getColoredKeggPathwayOfKeggIdsReturn	1
getGenenamesByGoldReturn	1
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getPIRSeedAlignmentByIdResponse	1
getAtomSitesReturn	1
getHitsReturn	1
pegs with md5Return	1
BlastResponse	1
getELMInstanceBySequenceMatchResponse	1
getSequenceForStructureAndChainReturn	1
all subsystem classificationsReturn	1
trnscanFetchResultResponse	1
getDisorderReturn	1
getModelNameByIdReturn	1
getAllStageNameReturn	1
DomainId2KeggPathwaysResponse	1
seqNeighborsReturn	1
processSequenceReturn	1
guessSymbolIdFromSymbolTextResponse	1
getInstancesByProteinSequenceAccessionSearchForAllRelatedSpeciesWithAllThroughputDataResponse	1
getUniprotIDReturn	1
getLatestSymbolInformationFromSymbolAndTaxIdResponse	1
Alignement	1
prismResult	1
GetExtendedCompoundInfoResponse	1
getTermRelationsResponse	1
getSequenceByACCResponse	1

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getWholemound2DInfoReturn	1
getSourceDatabaseVersionsResponse	1
searchResults	1
ArrayOfProfileParameterResult	1
existReturn	1
GetExperimentPhenoAssaysResponse	1
deleteDefaultDbReturn	1
getMultiIngredBrandReturn	1
eLinkResultMS	1
McQFoldSOAPResponse	1
listFieldsInformationResponse	1
hot_infoResponse	1
getESTLibrariesForAGivenGenomeReturn	1
getXrefResponse	1
Blast_NTResponse	1
cla_fetch_descResponse	1
getAllOrthoMCLClustersWithMoreThanAGivenPercentageOfProteinsOfAGivenGenomeReturn	1
fromDotBracketFastaReturn	1
cla_dump_descResponse	1
getGenesofAGivenGenomeWithTheSameGeneOntologyAnnotationAsAGivenGeneReturn	1
voidEvalReturn	1
addRdfStatementWithContextReturn	1
saveCurationTagResponse	1
query_statResponse	1
getOrthoMCLClustersContainingProteinsOfAGivenGenomeAndProteinsOfOnlyEssentialYeastGenesReturn	1
addStepTwoColorPreprocessingReturn	1
getAffyIdReturn	1
addToIndexReturn	1
NearestNodeHogenomResponse	1
getAnnotationForProteinsInAGivenOrthoMCLClusterReturn	1
queryByIdsReturn	1
getUnigeneClusterTypeReturn	1
resourcePathReturn	1
GetScenarioProdomResponse	1
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameOrhoMCLClustersAsProteinsWithAGivenPfamAAnnotationReturn	1
getKeggPathwaysByKeggIDReturn	1
getGoldsReturn	1
contigs_ofReturn	1
freeTextSearchResponse	1
runELMMatcherResponse	1
getFirstStructSheetRangeReturn	1
getIprscanReturn	1
pegs_with_md5_stringReturn	1
BlastJobStatusResponse	1
getELMInstanceBySequenceAccessionResponse	1
getPrimaryCitationTitleReturn	1
swanReturn	1
all_familiesReturn	1
aaUsageResponse	1
getDbRefIdsReturn	1
getModelIdByNameReturn	1
getStageNameReturn	1
PdbSuperfamily2FuncatsResponse	1
seqSupRmsdReturn	1
processSequencesReturn	1
guessSymbolIdFromSymbolTextAndTaxIdResponse	1
getInstancesByProteinSequenceAccessionSearchForAllRelatedSpeciesWithLowThroughputDataOnlyResponse	1
checkSyntaxResponse	1
getLatestSymbolInformationFromReferenceResponse	1
asyncResult	1
GetExtendedCompoundInfoArrayResponse	1
getChildrenFromRootResponse	1
getSequenceByGIResponse	1
getWholemound2DReturn	1

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getNamesResponse	1
CoiledCoils	1
getSourcesResults	1
ArrayOfProfileResult	1
whatGeneInStageReturn	1
GetExperimentExpFactorsResponse	1
createDbReturn	1
getDrugsReturn	1
response_fastaReturn	1
eFetchResultMS	1
PknotsRGSOAPResponse	1
getAllResultsIdsResponse	1
seq_parse_nameResponse	1
getOpenReadingFramesRepresentedByMoreThanAGivenNumberOfESTsReturn	1
getStringListResponse	1
Blast_NT_XMLResponse	1
seq_fetch_entryResponse	1
getOrthoMCLClustersWithProteinsOfAGivenGenomeReturn	1
ec_number	1
soap_analyze_geometryResponse	1
seq_dump_entryResponse	1
getGenesofAGivenGenomeWithAGivenGeneOntologyAnnotationReturn	1
addFileReturn	1
addRdfStatementReturn	1
getPathwayHistoryResponse	1
query_resetResponse	1
getOrthoMCLClustersContainingProteinsOfAGivenGenomeAndProteinsOfOnlyNonessentialYeastGenesReturn	1
startDefinedAnalysisReturn	1
getRepresentativePublicIdReturn	1
addToIndexWithConfigReturn	1
GetParentHogenomResponse	1
getImageSeriesListResponse	1
getAnnotationForProteinsThatAreInTheSameMCLClusterAsAGivenProteinReturn	1
queryByObjectsReturn	1
getEnsemblReturn	1
getInputDescriptionReturn	1
BIVComplex	1
cronosWSResponse	1
getOrganismsReturn	1
getGoldsByGenenameReturn	1
dna_sequenceReturn	1
runInstanceMapperResponse	1
getStructSheetRangesReturn	1
aliases_ofReturn	1
BlastJobResultResponse	1
runLiftOverResponse	1
isStructureIdObsoleteReturn	1
tswnnReturn	1
all_families_with_funcsReturn	1
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getPdbChainReturn	1
getModelIdByPublicationReturn	1
getAllSubmissionReturn	1
Funcat2PdbSuperfamiliesResponse	1
seqSupNerReturn	1
processSequencesInFastaReturn	1
guessSymbolIdFromReferenceResponse	1
getInstancesByKinaseTextSearchResponse	1
chromAccessionResponse	1
getLatestSymbolInformationFromIHOPResponse	1
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sbml2PrismResult	1
SearchByMassAsyncResponse	1
getSequencesByTaxonIDResponse	1

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manovaReturn	1
getResourceTypesResults	1
ArrayOfExpressionFromGene	1
whatEntryGivenGeneReturn	1
GetExperimentsByModelTypeResponse	1
removeDbReturn	1
getNDCsReturn	1
response msfReturn	1
eSpellResult	1
RDfolderSOAPResponse	1
getResultsIdsResponse	1
mot_parse_nameResponse	1
getOpenReadingFramesRepresentedByMoreThanAGivenNumberOfESTsFromESTLibrariesThatAreAreNotRandomlySequencedReturn	1
getOrganismListResponse	1
Blast_ProteinResponse	1
SimpleSearch2IdListResponse	1
mot_fetch_entryResponse	1
getOrthoMCLClustersWithProteinsOfAGroupOfGenomesReturn	1
getPfamConservedDomainIdsByLocusLinkIdReturn	1
soap_apply_alignmentResponse	1
mot_dump_entryResponse	1
getGeneOntologyAnnotationForAGivenGeneReturn	1
getErrorMessageReturn	1
removeRdfFileReturn	1
getXrefListResponse	1
default_listResponse	1
getESTWithAGivenIdentifierReturn	1
queryMicroarrayDataReturn	1
getGeneSymbolReturn	1
streamContentReturn	1
GetChildHogenomResponse	1
getNeuroBlastResponse	1
getAnnotationForProteinsThatAreInTheSameOrthoMCLClusterAsAGivenProteinReturn	1
queryPathwaysForReferencIdentifiersReturn	1
getEntrezGeneReturn	1
getMethodExampleReturn	1
SequenceInfoResponse	1
BIVRecord	1
isinRedListResponse	1
getMappingTypesReturn	1
getSynonymsReturn	1
dna_seqReturn	1
RetrieveHitsResponse	1
getFirstStructConfReturn	1
BlastJobErrorResponse	1
getAvailableChainFilesResponse	1
getSnplInfoReturn	1
getTigrscanReturn	1
list_membersReturn	1
getSeqResponse	1
runXmlQueryReturn	1
getModelIdByPersonReturn	1
getAllSubmissionAccessionReturn	1
DomainId2FuncatsResponse	1
seqAlignReturn	1
getScoringMatrixReturn	1
getSymbolDefinitionsFromSymbolResponse	1
getInstancesByBindingDomainTextSearchResponse	1
chromosomeNameResponse	1
getRegistryResponse	1
sf	1
getGeneAndTranscriptResponse	1

name	count
SearchByFormulaAsyncResponse	1
getTermsByAnnotationDataResponse	1
getSequencesByTaxonNameResponse	1
getRegionGivenComponentReturn	1
ORApathwaysResponse	1
loginReturn	1
startSessionResults	1
getOligoReturn	1
whatGeneGivenRegionReturn	1
GetExperimentsStrainsResponse	1
createDefaultDbReturn	1
getQuantityReturn	1
connectResponse	1
eSpellResultMS	1
RNAfoldSOAPResponse	1
listAdditionalReferenceFieldsResponse	1
cla_parse_nameResponse	1
getOpenReadingFramesRepresentedByMoreThanAGivenNumberOfESTsFromESTLibrariesThatAreAreNotRandomlySequencedAndContainMoreThanAGivenNumberOfESTsReturn	1
getGenelDListResponse	1
Blast Protein HCResponse	1
GetRecordImageResponse	1
cla_fetch_entryResponse	1
getTheNumberOfProteinsForEachGenomeInAGivenOrthoMCLClusterReturn	1
getSmartConservedDomainIdsByLocusLinkIdReturn	1
soap_apply_all_loopsResponse	1
SubmitTwoProteinSetsResponse	1
cla_dump_entryResponse	1
getProteinsofAGivenGenomeWithTheSamePfamAnnotationAsAGivenProteinReturn	1
generateIDReturn	1
extractRdfReturn	1
findPathwaysByTextResponse	1
default_setResponse	1
getESTsThatAreInAGivenESTLibraryReturn	1
getGeneChipArrayReturn	1
indexWithTCPReturn	1
GetDFStreeHogenomResponse	1
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameMCLClustersAsProteinsWithAGivenGOAnnotationReturn	1
queryPathwaysForEntitiesReturn	1
getSwissProtReturn	1
getInputExampleReturn	1
BlastResultsResponse	1
BIVRecords	1
searchCitationsResponse	1
getAnatomyReturn	1
anovaReturn	1
pegs_ofReturn	1
RetrieveChainHitsResponse	1
getStructConfsReturn	1
alias2figReturn	1
runTopconsDefaultResponse	1
getLigandInfoReturn	1
getTRNAReturn	1
CDS_dataReturn	1
getOrfsResponse	1
RunBlastnJobResponse	1
getCurrentPdbIdsReturn	1
getModelIdByChEBIIDReturn	1
getTextExpressionOfSubmissionReturn	1
Funcat2DomainIdsResponse	1
processMutationListsReturn	1
getSymbolDefinitionsFromSymbolAndTaxIdResponse	1
getSubstrateByIdentifierResponse	1
getGeneNameResponse	1
If	1

name	count
rpsblastReturn	1
getTaxonByIdResponse	1
getSpeciesInfoReturn	1
getSequencesFromGenomeReturn	1
endSessionResults	1
UniprotAccArray	1
getBdgfReturn	1
whatGeneGivenComponentReturn	1
GetPublicationResponse	1
removeDefaultDbReturn	1
getUNIIReturn	1
disconnectResponse	1
RNAshapesSOAPResponse	1
getDomainsHierarchyResponse	1
seq_queryResponse	1
getSecretoryOrNonsecretoryProteinsForAGivenGenomeReturn	1
getOrganismsResponse	1
Blast_Protein_XMLResponse	1
GetRecordDetailsResponse	1
seq_fetch_propResponse	1
getTheProteinsThatAreInTheSameOrthoMCLClusterAsAGivenProteinReturn	1
MOBYSHoundLocusIDFromGiReturn	1
soap_apply_missing_endsResponse	1
seq_dump_propResponse	1
getPfamAAnnotationForAGivenProteinReturn	1
performGOAnalysisReturn	1
constructQueryReturn	1
createPathwayResponse	1
stickerResponse	1
getESTsWithAGivenESTUnisequenceReturn	1
selectMagemlReturn	1
getSpeciesScientificNameReturn	1
indexWithSOAPReturn	1
GetScenarioHogenomResponse	1
geneSearch2Response	1
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameOrthoMCLClustersAsProteinsWithAGivenGOAnnotationReturn	1
listPathwaysForEntityIdsReturn	1
getRGDNameReturn	1
CSTfinderReturn	1
PsiBlastResultsResponse	1
pingReturn	1
doc2locResponse	1
getMappingsReturn	1
rnas_ofReturn	1
RetrieveDomainHitsResponse	1
fastaStructureIdQueryReturn	1
ec_nameReturn	1
ClustalWResponse	1
smilesQueryReturn	1
getProbeReturn	1
CDS_sequencesReturn	1
getProtResponse	1
checkForUpdateReturn	1
RunBlastpJobResponse	1
getObsoletePdbIdsReturn	1
getModelIdByChEBIReturn	1
whatEntryReturn	1
PdbSuperfamily2ECsResponse	1
getResultReturn	1
getAlgorithmReturn	1
ecnumber	1
getSymbolDefinitionsFromReferenceResponse	1
getInstanceByIdentifierResponse	1
getTranscriptsResponse	1

name	count
getAttributesResponse	1
freq	1
getTermMetadataResponse	1
blseqReturn	1
getTranscriptsAndInfoResponse	1
getTaxonByNameResponse	1
getComponentFullDetailsReturn	1
getSequencesFromESTReturn	1
getDisplayTermsReturn	1
doScoobyByIdResponse	1
whatComponentExpressGeneReturn	1
GetPublicationsResponse	1
readRegistryReturn	1
getStrengthReturn	1
getIdTypesReturn	1
seq_listResponse	1
identifyDatabasesReturn	1
RNASuboptSOAPResponse	1
getReferencedEntriesFlatSetResponse	1
mot_queryResponse	1
getSignalPPredictionForAGivenProteinReturn	1
getOrganismsByQueryTermResponse	1
BlastofasResponse	1
SimpleSearchResponse	1
mot_fetch_propResponse	1
getMCLClustersThatContainProteinsOfAGivenGenomeReturn	1
MOBYSHoundLocusIDFromConservedDomainDbIDReturn	1
soap_create_modelResponse	1
RetrievePairwiseScoresResponse	1
mot_dump_propResponse	1
getProteinsOfAGivenGenomeWithAGivenPfamAnnotationReturn	1
getAffyNormalizationMethodsReturn	1
runhogenomResponse	1
removeRdfStatementWithContextReturn	1
getPathwayAsResponse	1
getESTUnisequenceWithAGivenIdentifierReturn	1
queryDataByExpldReturn	1
getAnnotationDateReturn	1
indexWithSwAReturn	1
GetPresentFamiliesHogenomResponse	1
getNeuroBlast1Response	1
getAnnotationForProteinsOfAGivenGenomeThatAreInMCLClustersWithSecretoryOrNonsecretoryProteinsReturn	1
generatePathwayDiagramInSVGReturn	1
getSGDAccessionNumberReturn	1
availableReturn	1
SequenceSpaceResponse	1
getMaxBatchSizeReturn	1
ligandsmiles	1
getBlocksReturn	1
contig_inReturn	1
runPconsDefaultResponse	1
getAllELMsResponse	1
fastaQueryReturn	1
reaction_to_roleReturn	1
runPdbResponse	1
getReleaseDatesReturn	1
getSimpleModelsByReactomeldsReturn	1
is_member_ofReturn	1
queryGenomesResponse	1
RunBlastxJobResponse	1
getDomainFragmentsReturn	1
getModelByIdByUniprotIdReturn	1
whatTissueReturn	1
EC2PdbSuperfamiliesResponse	1

name	count
gashsupReturn	1
processSequencesStringReturn	1
getSymbolDefinitionsFromIHOPResponse	1
getInstancesWithPdbEntryAssignedResponse	1
getTranscriptsRangeResponse	1
getFiltersResponse	1
score	1
getTermXrefsResponse	1
blastn_BasicReturn	1
getTranscriptsByGeneNameResponse	1
getImageDetailsReturn	1
getAvailableTaxaResponse	1
getStagesReturn	1
getSequencesFromESTVirtualReturn	1
getRxNormVersionReturn	1
doScoobyBySeqResponse	1
whatWholemoundRegionExpressGeneReturn	1
GetPublicationsBySearchResponse	1
getXMLReturn	1
getEstGenomeMatchReturn	1
getRelaTypesReturn	1
mot_listResponse	1
identifySimpleSearchesReturn	1
bindndnaResponse	1
getNumberOfResultsResponse	1
cla_queryResponse	1
getTheNumberOfParalogsForAllMCLClustersContainingProteinsOfAGivenGenomeReturn	1
getGeneldsByQueryTermResponse	1
DecoderResponse	1
AsyncSimpleSearchResponse	1
cla_fetch_propResponse	1
getAllMCLClustersWithMoreThanAGivenPercentageOfProteinsOfAGivenGenomeReturn	1
getCogsConservedDomainIdsByLocusLinkIdReturn	1
soap_find_clashesResponse	1
RetrieveCompleteScoresResponse	1
cla_dump_propResponse	1
getTheNumberOfGenomesInMCLClustersThatContainProteinsOfAGivenGenomeAndProteinsOfEssentialYeastGenesReturn	1
getTwoColorBackgroundCorrectionMethodsReturn	1
analyzeGenesReturn	1
removeRdfStatementReturn	1
getCurationTagHistoryResponse	1
getESTsRepresentingAGivenOpenReadingFrameReturn	1
queryDataByArrayIdReturn	1
getSequenceTypeReturn	1
transformReturn	1
GetInheritedFamiliesHogenomResponse	1
getGeneList1Response	1
getAnnotationForProteinsOfAGivenGenomeThatAreInOrthoMCLClustersWithSecretoryOrNonsecretoryProteinsReturn	1
generatePathwayDiagramInSVGForIdReturn	1
getGeneOntologyBiologicalProcessReturn	1
ali_to_seqReturn	1
runDSSPResponse	1
getDatabaseToFieldsMapReturn	1
screeningsearchreturn	1
get_dna_seqReturn	1
runProqDefaultResponse	1
getELMResponse	1
homologyReductionQueryReturn	1
coupled_toReturn	1
runPfragDefaultResponse	1
runFetchDomResponse	1
getEcNumsForStructuresReturn	1
getSimpleModelsRelatedWithChEBIReturn	1
simsReturn	1

name	count
getFeaturesResponse	1
RunTblastnJobResponse	1
blastQueryXmlReturn	1
getModelSIdByUniprotIdsReturn	1
getAllAnnotatedTissueAccessionReturn	1
UniProtId2DomainIdsResponse	1
getReportResponse	1
pickingResponse	1
getSymbolInfoFromSymbolResponse	1
getInstancesByPubMedIdResponse	1
getchromNameResponse	1
queryResponse	1
since	1
getOntologyNamesResponse	1
blastp_BasicReturn	1
GetSpeciesListResponse	1
sliceChromosomeResponse	1
getPBfromGOReturn	1
getDBInfoReturn	1
getSequencesFromGenomeVirtualReturn	1
getUMLSVersionReturn	1
getSignalpReturn	1
whatVoxelRegionExpressGeneReturn	1
GetPublicationExperimentsResponse	1
GetPublicationStrainsResponse	1
uniquesubsReturn	1
getTermTypesReturn	1
cla_listResponse	1
IdentifySimpleSearchInputParametersReturn	1
GetEMBLNucleotideSequence_BsmlResponse	1
bindnrnaResponse	1
getEntriesFieldUrlsResponse	1
hit_queryResponse	1
getTheNumberOfParalogsForAllOrthoMCLClustersContainingProteinsOfAGivenGenomeReturn	1
getGeneldsByProteomeldResponse	1
Domains_2_svgResponse	1
GetAsyncSearchStatusResponse	1
seq_fetch_fastaResponse	1
getAllMCLClustersWithLessThanAGivenPercentageOfProteinsOfAGivenGenomeReturn	1
getCddConservedDomainIdsByLocusLinkIdReturn	1
soap_match_alignment_with_modelResponse	1
updatePathwayResponse	1
seq_dump_fastaResponse	1
getTheNumberOfGenomesInMCLClustersThatContainProteinsOfAGivenGenomeAndProteinsOfOnlyEssentialYeastGenesReturn	1
getTwoColorWithinArrayNormalizationMethodsReturn	1
getGOViewHTMLReturn	1
addRdfReturn	1
getCurationTagsResponse	1
getESTUnisequencesRepresentingAGivenOpenReadingFrameReturn	1
GetStpGraphListResponse	1
getSequenceSourceReturn	1
match_summary	1
GetInnovatedFamiliesHogenomResponse	1
getRepresentativeImageSeriesResponse	1
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameMCLClustersAsProteinsWithAGivenPSortPredictionReturn	1
loadPathwayForIdReturn	1
getGeneOntologyMolecularFunctionReturn	1
adjacentReturn	1
runDSSPByIdResponse	1
getChipTypesReturn	1
dockingscore	1
is_archaealReturn	1
GetDatabankInfoResponse	1
getELMByIdentifierResponse	1

name	count
keywordQueryReturn	1
abstract coupled toReturn	1
runPalignSeqSeqDefaultResponse	1
runFetchProtResponse	1
getEcNumsReturn	1
getSimpleModelsByChEBIIdsReturn	1
uniprot acc	1
runGlobPlotterResponse	1
RunTblastxJobResponse	1
blastStructureIdQueryXmlReturn	1
getSimpleModelsByUniprotIdsReturn	1
getAllModelsReturn	1
PdbSuperfamily2UniProtIdsResponse	1
mappingResponse	1
getSymbolInfoFromSymbolAndTaxIdResponse	1
request_origResponse	1
mappingInfoResponse	1
GetDatabasesResponse	1
sources	1
getOntologyLoadDateResponse	1
translating Blast BasicReturn	1
GetEnslDsByRegionResponse	1
sliceChromosomeByGeneResponse	1
phyloML	1
getGeneReturn	1
queryForExperimentReturn	1
getSpellingSuggestionsReturn	1
getMsblastInfoReturn	1
getSubmissionAssayWlzReturn	1
getStoreSizeResponse	1
GetPublicationModelTypesResponse	1
parsimonyReturn	1
getSpISetIdReturn	1
hit_listResponse	1
evaluateSimpleSearchReturn	1
GetEMBLNucleotideSequence_AGAVEResponse	1
disemblResponse	1
getDomainsReferencedInEntryResponse	1
hat_queryResponse	1
getEnzymesForAGivenProteinReturn	1
getGeneldsByProteomeldAndQueryTermResponse	1
EncoderResponse	1
GetAsyncSearchResultResponse	1
mot_fetch_fastaResponse	1
getTheProteinsThatAreInTheSameMCLClusterAsAGivenProteinReturn	1
MOBYSHoundLocusIDFromOMIMReturn	1
applyReturn	1
findPathwaysByXrefResponse	1
mot_dump_fastaResponse	1
getTheNumberOfGenomesInMCLClustersThatContainProteinsOfAGivenGenomeAndProteinsOfOnlyNonessentialYeastGenesReturn	1
getTwoColorBetweenArrayNormalizationMethodsReturn	1
getGOViewPDFReturn	1
removeRdfReturn	1
findInteractionsResponse	1
getESTUnisequencesForAGivenGenomeReturn	1
GetStpGraphResponse	1
getTranscriptIdReturn	1
search_summary	1
GetLostFamiliesHogenomResponse	1
geneSearch1Response	1
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameOrthoMCLClustersAsProteinsWithAGivenPSortPredictionReturn	1
loadPathwayForObjectReturn	1
getGeneOntologyCellularComponentReturn	1
cluster by bbhsReturn	1

name	count
runMkDomResponse	1
getDatabasesWithDetailsReturn	1
getSnpsBySwissProtIdReturn	1
is_bacterialReturn	1
GetMetaDataResponse	1
getELMsByTextSearchResponse	1
pubmedAbstractQueryReturn	1
pinned_region_dataReturn	1
runPalignSeqSeqResponse	1
runFetchFastaResponse	1
getCifChainReturn	1
helloBioModelsReturn	1
getNodeAccessionReturn	1
PdbSuperfamily2KeggOrthologsResponse	1
getSNPIdsReturn	1
getModelIdByUniprotReturn	1
response_treeReturn	1
GetHogenomFamCompResponse	1
getImageResponse	1
RunDeterministicSimulatorResponse	1
getSymbolInfoFromReferenceResponse	1
PhysicoChemProfile	1
numberConversionResponse	1
SearchByMassResponse	1
getAllTermsFromOntologyResponse	1
blastn_AdvancedReturn	1
GetExpressionDatasetsResponse	1
upLoadGenBankLocalFileResponse	1
TFmodellerReturn	1
getAllGeneReturn	1
queryForArraysReturn	1
ResultMS	1
getMsTagInfoReturn	1
eInfoResult	1
getMsFitInfoReturn	1
generateConceptsFromPubMedQueryResponse	1
getCategoriesResponse	1
maximumlikelihoodReturn	1
findRemappedReturn	1
hat_listResponse	1
identifyAdvancedSearchCollectionsReturn	1
iupredIResponse	1
hot_queryResponse	1
getProteinsOfAGivenGenomeWithAGivenEnzymeAnnotationReturn	1
getGeneldsByGenomeAcResponse	1
FillseqResponse	1
GetCompoundThumbnailResponse	1
seq_fetch_nrResponse	1
getTheNumberOfProteinsForEachGenomeInAGivenMCLClusterReturn	1
MOBYSHoundGOIDFromLocusIDReturn	1
ConvertCopasiMLToSBMLResponse	1
getColorPathwayResponse	1
seq_dump_nrResponse	1
getTheNumberOfGenomesInOrthoMCLClustersThatContainProteinsOfAGivenGenomeAndProteinsOfEssentialYeastGenesReturn	1
analyseGenesPDFOutputReturn	1
selectQuerySerializedReturn	1
loginResponse	1
getESTsForAGivenGenomeReturn	1
UploadStpGraphResponse	1
getTargetDescriptionReturn	1
filter_file	1
GetRegainedFamiliesHogenomResponse	1
geneSearchResponse	1
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameMCLClustersAsProteinsWithAGivenWolfPSortPredictionReturn	1

name	count
listPathwayParticipantsReturn	1
getAffyIdByOrfReturn	1
cluster by simReturn	1
runZpredDefaultResponse	1
getLinksReturn	1
getCogIdReturn	1
is eukaryoticReturn	1
GetIndicesResponse	1
getELMsBySequenceMatchResponse	1
getSpaceGroupForStructureReturn	1
all genomesReturn	1
runPalignSeqSeqSSDefaultResponse	1
runFetchAlignResponse	1
getCifResidueReturn	1
getAllModelsIdReturn	1
getNodeInfoReturn	1
KeggOrtholog2PdbSuperfamiliesResponse	1
getUniProtSNPsReturn	1
getModelIdByGOIdReturn	1
response alignmentReturn	1
GetHogenomFamDefResponse	1
getKinaseListResponse	1
StartDeterministicSimulatorResponse	1
getSymbolInfoFromIHOPResponse	1
Clu	1
runMutalyzerResponse	1
SearchByMass2Response	1
getRootTermsResponse	1
blastp_AdvancedReturn	1
GetPathwayListResponse	1
uploadGenBankRemoteFileResponse	1
outseq	1
sequenceML	1
getSubmissionWithoutImageReturn	1
deleteReturn	1
getProprietaryInformationReturn	1
eInfoResultMS	1
getTicketByIdResponse	1
generateConceptsFromTextResponse	1
getNonOboOntologiesResponse	1
distanceReturn	1
getSourceTypesReturn	1
hot_listResponse	1
identifyAdvancedSearchFiltersReturn	1
getLocationResponse	1
iupredsResponse	1
getDetailedNumberOfResultsResponse	1
mom_queryResponse	1
getProteinsOfAGivenGenomeWithTheSameEnzymeAnnotationAsAGivenProteinReturn	1
getGeneByIdResponse	1
FormatnameResponse	1
GetCompoundInfoResponse	1
mot_fetch_nrResponse	1
getASummaryOfTheMCLClusterAnalysisForAGivenGenomeReturn	1
MOBYSHoundLocusIDFromGOIDAndECodeReturn	1
ConvertSBMLToCopasiMLResponse	1
getPathwayInfoResponse	1
mot_dump_nrResponse	1
getTheNumberOfGenomesInOrthoMCLClustersThatContainProteinsOfAGivenGenomeAndProteinsOfOnlyEssentialYeastGenesReturn	1
performJustAffyNormalizationReturn	1
getGOViewImageReturn	1
addRdfWithContextReturn	1
getRecentChangesResponse	1
getCellularLocalisationPredictionPSortWolfPSortForAGivenProteinReturn	1

name	count
CYGDAnnotations	1
getArchivalUniGeneClusterReturn	1
GetTransferredFamiliesHogenomResponse	1
getGeneList2Response	1
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameOrhoMCLClustersAsProteinsWithAGivenWolfPSortPredictionReturn	1
listPathwayParticipantsForIdReturn	1
getInterproByOrfReturn	1
external_callsReturn	1
getPRINTSRecordByAccessionResponse	1
getField2TableAndColumnMapReturn	1
getAnnotationsReturn	1
is_prokaryoticReturn	1
getAlIELMInstancesResponse	1
getPubmedIdForAllStructuresReturn	1
genomesReturn	1
runProdivtmhmmDefaultResponse	1
runFetchKWRResponse	1
getChainsReturn	1
getAllCuratedModelsIdReturn	1
getNodeStageReturn	1
KeggOrtholog2DomainIdsResponse	1
GetAvailableDatabasesResponse	1
getNCBIdbSNPDescriptorReturn	1
getModelIdByGOReturn	1
response_sequencesReturn	1
getPubMedFromPMIDResponse	1
getBindingDomainListResponse	1
getSymbolInteractionsFromSymbolResponse	1
CI2	1
transcriptInfoResponse	1
SearchByFormulaResponse	1
getTermsByNameResponse	1
translating_Blast_AdvancedReturn	1
GetEnslIdsByPathwayNameResponse	1
updateCollectionResults	1
getSupportedLibsReturn	1
contactResponse	1
getAllSubmissionsReturn	1
runQueryDefaultDbReturn	1