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ArrayOfProfileResult	1
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PdbSuperfamily2FuncatsResponse	1
getKabschSanderReturn	1
getModelNameByIdReturn	1
eSummaryResultMS	1
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GetChildHogenomResponse	1
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getStagesReturn	1
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getOrfsResponse	1
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getTigrscanReturn	1
UniprotAccArray	1
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Funcat2DomainIdsResponse	1
getPdbChainReturn	1
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connectResponse	1
eFetchResultMS	1
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getSymbolDefinitionsFromSymbolAndTaxIdResponse	1
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getOpenReadingFramesRepresentedByMoreThanAGivenNumberOfESTsReturn	1
getTranscriptsResponse	1
processSequencesInFastaReturn	1
cla_fetch_entryResponse	1
getOrthoMCLClustersWithProteinsOfAGivenGenomeReturn	1
getTranscriptsByGeneNameResponse	1
getInstancesByKinaseTextSearchResponse	1
cla_dump_entryResponse	1
getGenesofAGivenGenomeWithAGivenGeneOntologyAnnotationReturn	1
getSequencesFromESTReturn	1
getDisplayTermsReturn	1
getSequencesByTaxonNameResponse	1
default_setResponse	1
getOrthoMCLClustersContainingProteinsOfAGivenGenomeAndProteinsOfOnlyNonessentialYeastGenesReturn	1
GetPublicationResponse	1
readRegistryReturn	1
getStrengthReturn	1
getOligoReturn	1
whatGeneGivenRegionReturn	1
getAnnotationForProteinsThatAreInTheSameMCLClusterAsAGivenProteinReturn	1
RNAfoldSOAPResponse	1
getDomainsHierarchyResponse	1
BIVRecords	1
cronosWSResponse	1
Blast_Protein_HCResponse	1
GetRecordImageResponse	1
getOrganismListResponse	1
soap_apply_all_loopsResponse	1
SubmitTwoProteinSetsResponse	1
getPfamConservedDomainIdsByLocusLinkIdReturn	1
checkForUpdateReturn	1
extractRdfReturn	1
findPathwaysByTextResponse	1
addFileReturn	1
indexWithTCPReturn	1

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GetDFStreeHogenomResponse	1
startDefinedAnalysisReturn	1
getGeneSymbolReturn	1
seqSupNerReturn	1
seqAlignReturn	1
jobStatus	1
PsiBlastResultsResponse	1
queryPathwaysForReferenceIdentifiersReturn	1
getSwissProtReturn	1
score	1
contig_lnReturn	1
RetrieveDomainHitsResponse	1
getMappingTypesReturn	1
anovaReturn	1
getDBInfoReturn	1
reaction_to_roleReturn	1
ClustalWResponse	1
getFirstStructConfReturn	1
getTermsByAnnotationDataResponse	1
is_member_ofReturn	1
getProtResponse	1
getSnpInfoReturn	1
getTRNAReturn	1
whatTissueReturn	1
PdbSuperfamily2ECsResponse	1
runXmlQueryReturn	1
getModelsIdByChEBIIdReturn	1
disconnectResponse	1
eSpellResult	1
processSequencesStringReturn	1
getSymbolDefinitionsFromReferenceResponse	1
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getOpenReadingFramesRepresentedByMoreThanAGivenNumberOfESTsFromESTLibrariesThatAreAreNotRandomlySequencedReturn	1
getTranscriptsRangeResponse	1
getAttributesResponse	1
getScoringMatrixReturn	1
seq_fetch_propResponse	1
getOrthoMCLClustersWithProteinsOfAGroupOfGenomesReturn	1
getInstancesByBindingDomainTextSearchResponse	1
rpsblastReturn	1
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getRxNormVersionReturn	1
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GetPublicationsResponse	1
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getBdgfReturn	1
whatGeneGivenComponentReturn	1
geneSearch2Response	1
getAnnotationForProteinsThatAreInTheSameOrthoMCLClusterAsAGivenProteinReturn	1
RNAshapesSOAPResponse	1
getReferencedEntriesFlatSetResponse	1
pingReturn	1
isinRedListResponse	1
Blast_Protein_XMLResponse	1
GetRecordDetailsResponse	1
getGeneIdListResponse	1
soap_apply_missing_endsResponse	1
getSmartConservedDomainIdsByLocusLinkIdReturn	1
constructQueryReturn	1

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createPathwayResponse	1
getErrorMessageReturn	1
indexWithSOAPReturn	1
GetScenarioHogenomResponse	1
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getGeneChipArrayReturn	1
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queryPathwaysForEntitiesReturn	1
getRGDNameReturn	1
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get_dna_seqReturn	1
runPconsDefaultResponse	1
getAnatomyReturn	1
getGeneReturn	1
coupled_toReturn	1
runPdbResponse	1
getStructConfsReturn	1
getImageDetailsReturn	1
simsReturn	1
queryGenomesResponse	1
getLigandInfoReturn	1
getProbeReturn	1
getAllAnnotatedTissueAccessionReturn	1
EC2PdbSuperfamiliesResponse	1
getCurrentPdbIdsReturn	1
getModelsIdByChEBIReturn	1
seq_listResponse	1
eSpellResultMS	1
getSymbolDefinitionsFromIHOPResponse	1
mot_queryResponse	1
getOpenReadingFramesRepresentedByMoreThanAGivenNumberOfESTsFromESTLibrariesThatAreAreNotRandomlySequencedAndContainMoreThanAGivenNumberOfESTsReturn	1
getchromNameResponse	1
getFiltersResponse	1
processMutationListsReturn	1
mot_fetch_propResponse	1
getTheNumberOfProteinsForEachGenomeInAGivenOrthoMCLClusterReturn	1
getSubstrateByIdentifierResponse	1
sliceChromosomeResponse	1
blseqReturn	1
mot_dump_propResponse	1
getProteinsofAGivenGenomeWithTheSamePfamAnnotationAsAGivenProteinReturn	1
getSequencesFromGenomeVirtualReturn	1
getUMLSVersionReturn	1
getTaxonByNameResponse	1
getESTsThatAreInAGivenESTLibraryReturn	1
GetPublicationsBySearchResponse	1
getEstGenomeMatchReturn	1
getRelaTypesReturn	1
doScoobyByIdResponse	1
whatComponentExpressGeneReturn	1
getNeuroBlast1Response	1
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameMCLClustersAsProteinsWithAGivenGOAnnotationReturn	1
RNAsuboptSOAPResponse	1
getNumberOfResultsResponse	1
getMaxBatchSizeReturn	1
searchCitationsResponse	1
BlastofasResponse	1
SimpleSearchResponse	1
getOrganismsResponse	1
getAllELMsResponse	1
soap_create_modelResponse	1
RetrievePairwiseScoresResponse	1
MOBYSHoundLocusIDFromGiReturn	1

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removeRdfStatementWithContextReturn	1
getPathwayAsResponse	1
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RunBlastnJobResponse	1
indexWithSwAReturn	1
GetPresentFamiliesHogenomResponse	1
getSpeciesScientificNameReturn	1
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getSGDAccessionNumberReturn	1
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is_archaealReturn	1
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getMappingsReturn	1
getBlocksReturn	1
getAllGeneReturn	1
getTermMetadataResponse	1
abstract_coupled_toReturn	1
runPfragDefaultResponse	1
fastaStructureIdQueryReturn	1
getPBfromGOReturn	1
uniprot_acc	1
getFeaturesResponse	1
smilesQueryReturn	1
getSimpleModelsByReactomeIdsReturn	1
getAllModelsReturn	1
UniProtId2DomainIdsResponse	1
getObsoletePdbIdsReturn	1
getModelsIdByUniprotIdReturn	1
mot_listResponse	1
getSymbolInfoFromSymbolResponse	1
cla_queryResponse	1
getSecretoryOrNonsecretoryProteinsForAGivenGenomeReturn	1
mappingInfoResponse	1
queryResponse	1
getIalgorithmReturn	1
cla_fetch_propResponse	1
getTheProteinsThatAreInTheSameOrthoMCLClusterAsAGivenProteinReturn	1
GetSpeciesListResponse	1
getInstanceByIdentifierResponse	1
sliceChromosomeByGeneResponse	1
blastn_BasicReturn	1
cla_dump_propResponse	1
getPfamAAnnotationForAGivenProteinReturn	1
queryForExperimentReturn	1
getSpellingSuggestionsReturn	1
getAvailableTaxaResponse	1
getESTsWithAGivenESTUnisequenceReturn	1
GetPublicationExperimentsResponse	1
uniquesubsReturn	1
getTermTypesReturn	1
doScoobyBySeqResponse	1
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getGeneList1Response	1
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameOrthoMCLClustersAsProteinsWithAGivenGOAnnotationReturn	1
bindndnaResponse	1
getEntriesFieldUrlsResponse	1
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getOrganismsByQueryTermResponse	1

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getELMResponse	1
soap_find_clashesResponse	1
RetrieveCompleteScoresResponse	1
MOBYSHoundLocusIDFromConservedDomainDbIDReturn	1
removeRdfStatementReturn	1
getCurationTagHistoryResponse	1
performGOAnalysisReturn	1
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RunBlastpJobResponse	1
transformReturn	1
GetInheritedFamiliesHogenomResponse	1
selectMagemlReturn	1
getAnnotationDateReturn	1
gashsupReturn	1
cluster_by_bbhsReturn	1
runDSSPByIDResponse	1
generatePathwayDiagramInSVGReturn	1
getGeneOntologyBiologicalProcessReturn	1
is_bacterialReturn	1
GetDatabankInfoResponse	1
ligandsmiles	1
getSubmissionWithoutImageReturn	1
getTermXrefsResponse	1
pinned_region_dataReturn	1
runPalignSeqSeqDefaultResponse	1
fastaQueryReturn	1
getNodeAccessionReturn	1
runGlobPlotterResponse	1
getReleaseDatesReturn	1
getSimpleModelsRelatedWithChEBIReturn	1
response_treeReturn	1
PdbSuperfamily2UniProtIdsResponse	1
getDomainFragmentsReturn	1
getModelsIdByUniprotIdsReturn	1
cla_listResponse	1
identifyDatabasesReturn	1
RunDeterministicSimulatorResponse	1
getSymbolInfoFromSymbolAndTaxIdResponse	1
hit_queryResponse	1
getSignalPPredictionForAGivenProteinReturn	1
numberConversionResponse	1
GetDatabasesResponse	1
seq_fetch_fastaResponse	1
getMCLClustersThatContainProteinsOfAGivenGenomeReturn	1
GetEnsIdsByRegionResponse	1
getInstancesWithPdbEntryAssignedResponse	1
upLoadGenBankLocalFileResponse	1
blastp_BasicReturn	1
seq_dump_fastaResponse	1
getProteinsofAGivenGenomeWithAGivenPfamAnnotationReturn	1
queryForArraysReturn	1
getESTUnisequenceWithAGivenIdentifierReturn	1
GetPublicationStrainsResponse	1
parsimonyReturn	1
getSplSetIdReturn	1
getSignalpReturn	1
whatVoxelRegionExpressGeneReturn	1
getRepresentativeImageSeriesResponse	1
getAnnotationForProteinsOfAGivenGenomeThatAreInMCLClustersWithSecretoryOrNonsecretoryProteinsReturn	1
bindnrnaResponse	1
getDomainsReferencedInEntryResponse	1
getChipTypesReturn	1
Domains_2_svgResponse	1
GetAsyncSearchStatusResponse	1

name	count
getGeneIdsByQueryTermResponse	1
getELMByIdentifierResponse	1
soap_match_alignment_with_modelResponse	1
updatePathwayResponse	1
getCogsConservedDomainIdsByLocusLinkIdReturn	1
addRdfReturn	1
getCurationTagsResponse	1
getAffyNormalizationMethodsReturn	1
analyzeGenesReturn	1
RunBlastxJobResponse	1
match_summary	1
GetInnovatedFamiliesHogenomResponse	1
queryDataByExpIdReturn	1
getSequenceTypeReturn	1
getReportResponse	1
cluster_by_simReturn	1
runMkDomResponse	1
generatePathwayDiagramInSVGForIdReturn	1
getGeneOntologyMolecularFunctionReturn	1
is_eukaryoticReturn	1
GetMetaDataResponse	1
screeningsearchreturn	1
getAllSubmissionsReturn	1
getOntologyNamesResponse	1
all_genomesReturn	1
runPalignSeqSeqResponse	1
homologyReductionQueryReturn	1
TFmodellerReturn	1
getNodeInfoReturn	1
PdbSuperfamily2KeggOrthologsResponse	1
getEcNumsForStructuresReturn	1
getSimpleModelsByChEBIIdsReturn	1
response_alignmentReturn	1
GetHogenomFamCompResponse	1
blastQueryXmlReturn	1
getSimpleModelsByUniprotIdsReturn	1
hit_listResponse	1
identifySimpleSearchesReturn	1
StartDeterministicSimulatorResponse	1
getSymbolInfoFromReferenceResponse	1
hat_queryResponse	1
getTheNumberOfParalogsForAllMCLClustersContainingProteinsOfAGivenGenomeReturn	1
runMutalyzerResponse	1
SearchByMassResponse	1
pickingResponse	1
mot_fetch_fastaResponse	1
getAllMCLClustersWithMoreThanAGivenPercentageOfProteinsOfAGivenGenomeReturn	1
GetExpressionDatasetsResponse	1
getInstancesByPubMedIdResponse	1
upLoadGenBankRemoteFileResponse	1
translating_Blast_BasicReturn	1
mot_dump_fastaResponse	1
getTheNumberOfGenomesInMCLClustersThatContainProteinsOfAGivenGenomeAndProteinsOfEssentialYeastGenesReturn	1
deleteReturn	1
getProprietaryInformationReturn	1
phyloML	1
getESTsRepresentingAGivenOpenReadingFrameReturn	1
GetPublicationModelTypesResponse	1
maximumlikelihoodReturn	1
findRemappedReturn	1
getMsblastInfoReturn	1
getSubmissionAssayWlzReturn	1
geneSearch1Response	1
getAnnotationForProteinsOfAGivenGenomeThatAreInOrthoMCLClustersWithSecretoryOrNonsecretoryProteinsReturn	1

name	count
disemblResponse	1
GetEMBLNucleotideSequence_BsmlResponse	1
getDatabasesWithDetailsReturn	1
EncoderResponse	1
GetAsyncSearchResultResponse	1
getGeneIdsByProteomeIdResponse	1
getELMsByTextSearchResponse	1
applyReturn	1
findPathwaysByXrefResponse	1
getCddConservedDomainIdsByLocusLinkIdReturn	1
runFetchDomResponse	1
removeRdfReturn	1
findInteractionsResponse	1
getTwoColorBackgroundCorrectionMethodsReturn	1
getGOViewHTMLReturn	1
RunTblastnJobResponse	1
search_summary	1
GetLostFamiliesHogenomResponse	1
queryDataByArrayIdReturn	1
getSequenceSourceReturn	1
external_callsReturn	1
runZpredDefaultResponse	1
loadPathwayForIdReturn	1
getGeneOntologyCellularComponentReturn	1
is_prokaryoticReturn	1
GetIndicesResponse	1
dockingscore	1
getSubmissionAssayImageReturn	1
getOntologyLoadDateResponse	1
genomesReturn	1
runPalignSeqSeqSSDefaultResponse	1
keywordQueryReturn	1
outseq	1
getNodeStageReturn	1
KeggOrtholog2PdbSuperfamiliesResponse	1
getEcNumsReturn	1
helloBioModelsReturn	1
response_sequencesReturn	1
GetHogenomFamDefResponse	1
blastStructureIdQueryXmlReturn	1
getModelsIdByUniprotReturn	1
hat_listResponse	1
identifySimpleSearchInputParametersReturn	1
getSymbolInfoFromIHOPResponse	1
hot_queryResponse	1
getTheNumberOfParalogsForAllOrthoMCLClustersContainingProteinsOfAGivenGenomeReturn	1
transcriptInfoResponse	1
SearchByMass2Response	1
mappingResponse	1
seq_fetch_nrResponse	1
getAllMCLClustersWithLessThanAGivenPercentageOfProteinsOfAGivenGenomeReturn	1
GetPathwayListResponse	1
request_origResponse	1
updateCollectionResults	1
blastn_AdvancedReturn	1
seq_dump_nrResponse	1
getTheNumberOfGenomesInMCLClustersThatContainProteinsOfAGivenGenomeAndProteinsOfOnlyEssentialYeastGenesReturn	1
runQueryDefaultDbReturn	1
getESTUnisequencesRepresentingAGivenOpenReadingFrameReturn	1
getCategoriesResponse	1
distanceReturn	1
getSourceTypesReturn	1
getMsTagInfoReturn	1
getStoreSizeResponse	1

name	count
geneSearchResponse	1
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameMCLClustersAsProteinsWithAGivenPSortPredictionReturn	1
iupredlResponse	1
getDetailledNumberOfResultsResponse	1
GetEMBLNucleotideSequence_AGAVEResponse	1
getLinksReturn	1
FillseqResponse	1
GetCompoundThumbnailResponse	1
getGeneIdsByProteomeIdAndQueryTermResponse	1
getELMsBySequenceMatchResponse	1
ConvertCopasiMLToSBMLResponse	1
getColoredPathwayResponse	1
MOBYSHoundLocusIDFromOMIMReturn	1
runFetchProtResponse	1
selectQuerySerializedReturn	1
loginResponse	1
getTwoColorWithinArrayNormalizationMethodsReturn	1
getGOViewPDFReturn	1
RunTblastxJobResponse	1
filter_file	1
GetRegainedFamiliesHogenomResponse	1
GetStpGraphListResponse	1
getTranscriptIdReturn	1
function_ofReturn	1
getPRINTSRecordByAccessionResponse	1
loadPathwayForObjectReturn	1
getAffyIdByOrfReturn	1
getTimedNodesReturn	1
translation_ofReturn	1
getSnpsBySwissProtIdReturn	1
getCogIdReturn	1
getAllTermsFromOntologyResponse	1
replacesReturn	1
runProdivtmhmmDefaultResponse	1
pubmedAbstractQueryReturn	1
getRootAccessionReturn	1
KeggOrtholog2DomainIdsResponse	1
getCifChainReturn	1
getAllModelsIdReturn	1
ResultMS	1
getPubMedFromPMIDResponse	1
getSNPIdsReturn	1
getModelsIdByGOIdReturn	1
hot_listResponse	1
evaluateSimpleSearchReturn	1
getSymbolInteractionsFromSymbolResponse	1
mom_queryResponse	1
getEnzymesForAGivenProteinReturn	1
SearchByFormulaResponse	1
getImageResponse	1
mot_fetch_nrResponse	1
getTheProteinsThatAreInTheSameMCLClusterAsAGivenProteinReturn	1
GetEnsIdsByPathwayNameResponse	1
PhysicoChemProfile	1
deleteCollectionResults	1
blastp_AdvancedReturn	1
mot_dump_nrResponse	1
getTheNumberOfGenomesInMCLClustersThatContainProteinsOfAGivenGenomeAndProteinsOfOnlyNonessentialYeastGenesReturn	1
retriveDocReturn	1
getRxConceptPropertiesReturn	1
sequenceML	1
getESTUnisequencesForAGivenGenomeReturn	1
getNonOboOntologiesResponse	1
helpResponseSoapMsg	1

name	count
getMsFitInfoReturn	1
generateConceptsFromPubMedQueryResponse	1
getGeneList2Response	1
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameOrthoMCLClustersAsProteinsWithAGivenPSortPredictionReturn	1
iupredsResponse	1
getEntryFieldUrlsResponse	1
getField2TableAndColumnMapReturn	1
FormatnameResponse	1
GetCompoundInfoResponse	1
getGeneIdsByGenomeAcResponse	1
getAllELMInstancesResponse	1
ConvertSBMLToCopasiMLResponse	1
getPathwayInfoResponse	1
MOBYSHoundGOIDFromLocusIDReturn	1
runFetchFastaResponse	1
addRdfWithContextReturn	1
getRecentChangesResponse	1
getTwoColorBetweenArrayNormalizationMethodsReturn	1
analyseGenesPDFOutputReturn	1
GetTransferedFamiliesHogenomResponse	1
GetStpGraphResponse	1
getTargetDescriptionReturn	1
genomes_ofReturn	1
getPRINTSRecordByIDResponse	1
listPathwayParticipantsReturn	1
getInterproByOrfReturn	1
getAbstractNodesReturn	1
get_translationReturn	1
CountResponse	1
getRootTermsResponse	1
taxonomy_ofReturn	1
runProdivtmhmmParamsResponse	1
getSpaceGroupForStructureReturn	1
srs-result	1
getOntologyReturn	1
DomainId2KeggOrthologsResponse	1
getCifResidueReturn	1
getAllCuratedModelsIdReturn	1
eInfoResult	1
UniProt_ID	1
getPubMedFromIHOPResponse	1
getUniProtSNPsReturn	1
getModelsIdByGOReturn	1
seq_infoResponse	1
identifyAdvancedSearchCollectionsReturn	1
getSymbolInteractionsFromSymbolAndTaxIdResponse	1
seq_fetch_nameResponse	1
getProteinsofAGivenGenomeWithAGivenEnzymeAnnotationReturn	1
addResult	1
SearchByFormula2Response	1
getKinaseListResponse	1
seq_dump_nameResponse	1
getTheNumberOfProteinsForEachGenomeInAGivenMCLClusterReturn	1
GetEnsIdsByExpressionResponse	1
Clu	1
updateResourceResults	1
translating_Blast_AdvancedReturn	1
hit_fetch_simpleResponse	1
getTheNumberOfGenomesInOrthoMCLClustersThatContainProteinsOfAGivenGenomeAndProteinsOfEssentialYeastGenesReturn	1
retriveDocDefaultDbReturn	1
getRelatedByRelationshipReturn	1
contactResponse	1
geneSearchReturn	1
getESTsForAGivenGenomeReturn	1

name	count
getQualityCriteriaResponse	1
submit_jobResponseSoapMsg	1
getTicketByIdResponse	1
generateConceptsFromTextResponse	1
runAtlasResponse	1
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameMCLClustersAsProteinsWithAGivenWolfPSortPredictionReturn	1
pdisorderResponse	1
listFieldsResponse	1
getLocationResponse	1
annotateProbesReturn	1
PhylotableResponse	1
Mol2CSIDResponse	1
getGeneByIdResponse	1
getELMInstanceResponse	1
ValidateModelResponse	1
listPathwaysResponse	1
MOBYSHoundLocusIDFromGOIDAndECodeReturn	1
runFetchAlignResponse	1
addRdfFileWithContextReturn	1
getPathwayResponse	1
getGOViewImageReturn	1
getDescriptionReturn	1
NearestNodeProdomResponse	1
UploadStpGraphResponse	1
getArchivalUniGeneClusterReturn	1
genus_speciesReturn	1
getSeedAlignmentByAccessionResponse	1
listPathwayParticipantsForIdReturn	1
batchGetGeneSymbolReturn	1
getSliceReturn	1
feature_locationReturn	1
CooccurrenceResponse	1
getAnnotationsReturn	1
getTermsByNameResponse	1
search_and_grepReturn	1
runTopcompResponse	1
getPubmedIdForAllStructuresReturn	1
getPcaAnalysisReturn	1
getSupportedLibsReturn	1
getOntologyTermReturn	1
PdbSuperfamily2KeggPathwaysResponse	1
getChainsReturn	1
getAllNonCuratedModelsIdReturn	1
eInfoResultMS	1
FASTA	1
getRelatedSymbolsResponse	1
getNCBIdbSNPDescriptorReturn	1
getModelsIdByTaxonomyIdReturn	1
mot_infoResponse	1
identifyAdvancedSearchFiltersReturn	1
getSymbolInteractionsFromReferenceResponse	1
mot_fetch_nameResponse	1
getProteinsofAGivenGenomeWithTheSameEnzymeAnnotationAsAGivenProteinReturn	1
odeSolverResult	1
GetRecordMolResponse	1
getBindingDomainListResponse	1
mot_dump_nameResponse	1
getASummaryOfTheMCLClusterAnalysisForAGivenGenomeReturn	1
GetExpressionByEnsIdsResponse	1
Cl2	1
appendResourceResults	1
getTagIdentInfoReturn	1
hat_fetch_simpleResponse	1
getTheNumberOfGenomesInOrthoMCLClustersThatContainProteinsOfAGivenGenomeAndProteinsOfOnlyEssentialYeastGenesReturn	1

name	count
GetExperimentResponse	1
addDocumentReturn	1
getRelatedByTypeReturn	1
getPipelinesStatusResponse	1
searchReturn	1
getCellularLocalisationPredictionPSortWolfPSortForAGivenProteinReturn	1
getResourcesByCategoryResponse	1
listDomainsResponse	1
getTicketBySeqResponse	1
generateTerminologyResponse	1
fetchAtlasResultResponse	1
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameOrhoMCLClustersAsProteinsWithAGivenWolfPSortPredictionReturn	1
poodlelResponse	1
getEntriesResponse	1
getGeneIdResponse	1
idsToProbesReturn	1
PsiBlast_NTResponse	1
CSID2ExtRefsResponse	1
getAllFunctionalSitesResponse	1
clearReturn	1
findPathwaysByLiteratureResponse	1
MOBYSHoundGiFromLocusIDReturn	1
runFetchKWResponse	1
removeRdfWithContextReturn	1
MUSCLEAlignment	1
performJustAffyNormalizationReturn	1
getBiologicalProcessGOTermByOrfReturn	1
GetAvailableDatabasesResponse	1
resourcePathReturn	1
GetParentProdomResponse	1
CYGDAnnotations	1
getUniGeneIdReturn	1
fid2dnaReturn	1
getSeedAlignmentByIDResponse	1
maxSizeInListObjects	1
batchGetTranscriptIdReturn	1
getWholemount2DInfoReturn	1
rnastructAlignmentML	1
boundaries_ofReturn	1
SpellCheckResponse	1
getEntitiesReturn	1
getSeqIdReturn	1
getTermsByExactNameResponse	1
simple_searchReturn	1
getStructureGenomicsPdbIdsReturn	1
rsomReturn	1
ArrayOfOperonResult	1
getTimedNodeAccessionReturn	1
KeggPathway2PdbSuperfamiliesResponse	1
getCifChainsReturn	1
getModelByIdReturn	1
eSearchResult	1
queueentry	1
getRelatedSymbolsWithTaxIdResponse	1
getModelsIdByTaxonomyReturn	1
cla_infoResponse	1
identifyAdvancedSearchFilterOperatorsReturn	1
getSynsetsReturn	1
getSymbolInteractionsFromIHOPResponse	1
cla_fetch_nameResponse	1
getProteinsofAGivenGenomeInAGivenPathwayReturn	1
mathPlotResult	1
GetCompressedRecordsSdfResponse	1
getSubstratesByNameSearchResponse	1

name	count
info	1
cla_dump_nameResponse	1
getMCLClustersThatContainProteinsOfAGroupOfGenomesReturn	1
AffyDEGFinderResponse	1
Msf	1
deleteResourceResults	1
blastxReturn	1
hot_fetch_simpleResponse	1
getTheNumberOfGenomesInOrthoMCLClustersThatContainProteinsOfAGivenGenomeAndProteinsOfOnlyNonessentialYeastGenesReturn	1
GetExperimentsResponse	1
addDocumentDefaultDbReturn	1
getAllRelatedInfoReturn	1
queryPmidResponse	1
getSubmissionAnnotationTextReturn	1
searchJasonReturn	1
getProteinsofAGivenGenomeWithAGivenCellularLocalisationAsPredictedByPSortReturn	1
getWSDLsResponse	1
getDomainsReferencedInDomainResponse	1
pronetQueryReturn	1
blastprodResponse	1
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameMCLClustersAsProteinsWithAGivenEnzymeAnnotationReturn	1
rnabindrResponse	1
getReferencedEntriesResponse	1
getGeneResponse	1
keywordsToProbesReturn	1
PsiBlast_NT_XMLResponse	1
getFunctionalSiteResponse	1
getRepositoriesReturn	1
removeCurationTagResponse	1
MOBYSHoundLocusIDFromGiListReturn	1
runFetchKWscriptResponse	1
removeRdfFileWithcontextReturn	1
voidCallSweaveReturn	1
getGeneDescriptionByOrfReturn	1
getInputDescriptionReturn	1
GetChildProdomResponse	1
listByQueryReturn	1
getGenomeVersionReturn	1
fids2dnaReturn	1
getPIRSeedAlignmentByAccessionResponse	1
getKeggPathwayAsGifReturn	1
batchGetTargetDescriptionReturn	1
getWholemount2DReturn	1
getPSFilesReturn	1
pegs_with_md5Return	1
SuggestSearchTermsResponse	1
getGlimmersReturn	1
getPrefixedTermsByNameResponse	1
all_subsystem_classificationsReturn	1
DNApropertyFetchResultResponse	1
getSwissProtIdsReturn	1
ArrayOfRegulatorResult	1
getAllStageNameReturn	1
KeggPathway2DomainIdsResponse	1
getChainLengthReturn	1
getModelSBMLByIdReturn	1
eSearchResultMS	1
getSymbolsFromReferenceResponse	1
getSubModelSBMLReturn	1
hit_infoResponse	1
evaluateAdvancedSearchReturn	1
getUniprotIDReturn	1
getLatestSymbolInformationFromSymbolResponse	1
seq_fetch_descResponse	1

name	count
getProteinsofAGivenGenomeThatAreInTheSamePathwayAsAGivenProteinReturn	1
prismResult	1
GetRecordsSdfResponse	1
getSubstratesByGeneNameSearchResponse	1
seq_dump_descResponse	1
getTheGeneForAGivenGeneSymbolReturn	1
getDatabaseVersionResponse	1
CoiledCoils	1
searchResults	1
tblastnReturn	1
query_listResponse	1
getMCLClustersContainingProteinsOfAGivenGenomeAndProteinsOfEssentialYeastGenesReturn	1
GetExperimentsBySearchResponse	1
deleteDefaultDbReturn	1
getMultiIngredBrandReturn	1
getSubmissionAnnotationWholemountWlzReturn	1
searchMFqueryReturn	1
getProteinsofAGivenGenomeWithAGivenCellularLocalisationAsPredictedByWolfPSortReturn	1
AfoldSOAPResponse	1
getReferencedEntriesSetResponse	1
blastprodout	1
isServiceAliveReturn	1
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameOrthoMCLClustersAsProteinsWithAGivenEnzymeAnnotationReturn	1
say_helloResponse	1
getOrganismResponse	1
PsiBlast_ProteinResponse	1
toAlignedDotBracketFastaReturn	1
getFunctionalSitesByTextSearchResponse	1
selectQueryReturn	1
listOrganismsResponse	1
MOBYSHoundGiFromLocusIDListReturn	1
getUPIForSequenceResponse	1
indexFromRemoteReturn	1
addStepAffyNormalizationReturn	1
getOrfByGenenameReturn	1
getMethodExampleReturn	1
GetDFStreeProdomResponse	1
listObjectsReturn	1
getAlignmentsReturn	1
contigs_ofReturn	1
getPIRSeedAlignmentByIDResponse	1
getKeggIdsByKeggPathwayReturn	1
getOrfsByGoIdReturn	1
getStagesWithReconstructionReturn	1
getDotFileReturn	1
pegs_with_md5_stringReturn	1
BlastResponse	1
getIdStatusReturn	1
getTermParentsResponse	1
all_familiesReturn	1
trnascanFetchResultResponse	1
getGenomeDetailsReturn	1
ArrayOfProfileParameterResult	1
getStageNameReturn	1
DomainId2KeggPathwaysResponse	1
getCifChainLengthReturn	1
getSimpleModelByIdReturn	1
eSummaryResult	1
guessSymbolIdFromSymbolTextResponse	1
hat_infoResponse	1
getESTLibraryWithAGivenIdentifierReturn	1
checkSyntaxResponse	1
getLatestSymbolInformationFromSymbolAndTaxIdResponse	1
mot_fetch_descResponse	1

name	count
getPathwaysForAGivenProteinReturn	1
asyncResult	1
GetExtendedCompoundInfoResponse	1
getInstancesByProteinSequenceAccessionSearchWithAllThroughputDataResponse	1
mot_dump_descResponse	1
getTheProteinsForAGivenGeneReturn	1
getSourceDatabaseVersionsResponse	1
manovaReturn	1
getSourcesResults	1
tblastxReturn	1
query_infoResponse	1
getMCLClustersContainingProteinsOfAGivenGenomeAndProteinsOfOnlyEssentialYeastGenesReturn	1
GetExperimentPhenoAssaysResponse	1
createDbReturn	1
getDrugsReturn	1
getSubmissionAnnotationVoxelWlzReturn	1
getProteinsofAGivenGenomeWithTheSamePredictedPSortCellularLocalisationAsAGivenProteinReturn	1
ContrafoldSOAPResponse	1
listFieldsInformationResponse	1
blastpgpout	1
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameMCLClustersAsProteinsInAGivenPathwayReturn	1
topconsResponse	1
getProteinResponse	1
PsiBlast_Protein_XMLResponse	1
fromAlignedDotBracketFastaReturn	1
getELMInstanceBySequenceMatchResponse	1
addRdfFileReturn	1
getCurationTagsByNameResponse	1
listFilesReturn	1
getUPIForAccessionResponse	1
indexFromSRBReturn	1
performJustTwoColorPreprocessingReturn	1
getSGDAccessionByOrfReturn	1
getInputExampleReturn	1
GetPresentFamiliesProdomResponse	1
listTopLevelPathwaysReturn	1
getGeneTitleReturn	1