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getPIRSeedAlignmentByIDResponse	
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getESTLibrariesForAGivenGenomeReturn	1
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getProtResponse checkForUpdateReturn	-
RunBlastpJobResponse	$ \frac{1}{1}$
getObsoletePdbldsReturn	+ 1
getModelsIdByChEBIReturn	
whatEntryReturn	
PdbSuperfamily2ECsResponse	$\bar{1}$
getresultReturn	
getlalgorithmReturn	1
ecnumber	
getSymbolDefinitionsFromReferenceResponse	
getInstanceByldentifierResponse getTranscriptsResponse	$\frac{1}{4}$
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	count
getAttributesResponse	1
freq	
getTermMetadataResponse	
blseqReturn	
getTranscriptsAndInfoResponse	<u>_</u>
getTaxonByNameResponse getComponentFullDetailsReturn getSequencesFromESTReturn	
getComponentFullDetailSReturn	
getSequencesFromeStretum	
getDisplayTermsReturn doScoobyByIdResponse	
whatComponentExpressGeneReturn	
GetPublicationsResponse	- 1
readRegistryReturn	$-\bar{1}$
getStrengthReturn	1
getIdTypesReturn	1
seq_listResponse	1
identifyDatabasesReturn	1
RNAsuboptSOAPResponse	1
RNAsuboptSOAPResponse getReferencedEntriesFlatSetResponse	1
mot queryResponse getSignalPPredictionForAGivenProteinReturn	1
getSignalPPredictionForAGivenProteinReturn	1
getSignali Fredictioni Gradiveni rotelii Retarri getOrganismsByQueryTermResponse BlastofasResponse	1
BlastofasKesponse	
SimpleSearchResponse	<u>_</u>
mot fetch_propResponse	
getMCLClustersThatContainProteinsOfAGivenGenomeReturn	<u>_</u>
MOBYSHoundLocusIDFromConservedDomainDbIDReturn	
soap create modelResponse RetrievePairwiseScoresResponse	
mot dump propResponse	
mot_dump_propResponse getProteinsofAGivenGenomeWithAGivenPfamAnnotationReturn getAffyNormalizationMethodsReturn	 †
get 10temsonAdivendenomewithAdivem ramAnnotationNeturn netAffvNormalizationMethodsReturn	
runhogenomResponse	
runhogenomResponse removeRdfStatementWithContextReturn	一市
getPathwayAsResponse	$-\bar{1}$
getESTUnisequenceWithAGivenIdentifierReturn	$-\bar{1}$
queryDataByExpldReturn	1
getAnnotationDateReturn	1
indexWithSwAReturn	1
GetPresentFamiliesHogenomResponse	1
getNeuroBlast1Response	1
getAnnotationForProteinsOfAGivenGenomeThatAreInMCLClustersWithSecretoryOrNonsecretoryProteinsReturn	1
generatePathwayDiagramInSVGReturn	1
getSGDAccessionNumberReturn	1
availableReturn	1
SequenceSpaceResponse	
getMaxBatchSizeReturn	<u>_</u>
igandsmiles	
getBlocksReturn	
contig_InReturn runPconsDefaultResponse	<u>_</u>
getAllELMsResponse	
geralie Lindresponse fasta Query Return	
reaction to roleReturn	
runPdbResponse	<u>†</u>
getReleaseDatesReturn	1
getSimpleModelsByReactomeldsReturn	- i
s member ofReturn	- 1
queryGenomesResponse	1
RunBlastxJobResponse	1
getDomainFragmentsReturn	<u>1</u>
getDomainFragmentsReturn getModelsIdByUniprotIdReturn	ī
whatTissueReturn	1
EC2PdbSuperfamiliesResponse EC2PdbSuperfamiliesResponse	1

name	count
gashsupReturn	1
orocessSequencesStringReturn getSymbolDefinitionsFromIHOPResponse getInstancesWithPdbEntryAssignedResponse	
getSymbolDefinitionsFromIHOPResponse	<u> </u>
getInstancesWithPdbEntryAssignedResponse	<u> </u>
getTranscriptsRangeResponse	<u> </u>
getFiltersResponse	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
score	+
getTermXrefsResponse blastn BasicReturn	+ + + + +
getTranscriptsByGeneNameResponse	+ +
retImageDetailsReturn	+
getImageDetailsReturn getAvailableTaxaResponse	+
getStagesReturn	
getSequencesFromESTVirtualReturn	
getRxNormVersionReturn	1
doScoobyBySeqResponse whatWholemountRegionExpressGeneReturn]
whatWhólemountRegionExpressGeneReturn	1
GetPublicationsBySearchResponse]
getXMLReturn	1
getEstGenomeMatchReturn	1
getRelaTypesReturn mot_listResponse	1
mot_listResponse	
dentifySimpleSearchesReturn bindndnaResponse	
oinananakesponse	<u> </u>
getNumberOfResultsResponse	<u> </u>
cla queryResponse	<u>_</u>
getTheNumberOfParalogsForAllMCLClustersContainingProteinsOfAGivenGenomeReturn	
getGeneldsByQueryTermResponse DecoderResponse	+
AsyncSimpleSearchResponse	+ + + + +
	+ + +
retΔIIMCI ClustersWithMoreThanΔGivenPercentageOfProteinsOfΔGivenGenomeReturn	+ + + + + + + + + + + + + + + + + + + +
cla fetch propResponse getAllMCLClustersWithMoreThanAGivenPercentageOfProteinsOfAGivenGenomeReturn getCogsConservedDomainIdsByLocusLinkIdReturn soap find classlesResponse	+ - †
soan find clashesResponse	+ 1
RetrieveCompleteScoresResponse	
cla_dump_propResponse	
getTheNumberOfGenomesInMCLClustersThatContainProteinsOfAGivenGenomeAndProteinsOfEssentialYeastGenesReturn	1
getTwoColorBackgroundCorrectionMethodsReturn	1
analyzeGenesReturn	1
removeRdfStatementReturn]]
getCurationTagHistoryResponse]
getESTsRepresentingÁGivenOpenReadingFrameReturn	1
queryDataByArrayIdReturn]
getSequenceTypeReturn	
transformReturn	1 1
GetInheritedFamiliesHogenomResponse	
getGeneList1Response	<u>_</u>
getAnnotationForProteinsOfAGivenGenomeThatAreInOrthoMCLClustersWithSecretoryOrNonsecretoryProteinsReturn	+
generatePathwayDiagramInSVGForIdReturn	
getGeneOntologyBiologicalProcessReturn	+
ali to segReturn runDSSPResponse	+
getDatabaseToFieldsMapReturn	+ + + + +
screeningsearchreturn	+ + + + + + + + + + + + + + + + + + + +
get dna seqReturn	+ + + + + + + + + + + + + + + + + + + +
runProqDefaultResponse	+ + +
getELMResponse	+
nomologyReductionOueryReturn	
coupled_toReturn	
runPfragDefaultResponse	+ j
runFetchDomResponse	
getEcNumsForStructuresReturn	
getSimpleModelsRelatedWithChEBIReturn	1 1
simsReturn]]

name	count
getFeaturesResponse	1
RunTblastnJobResponse	1
blastQueryXmlReturn	
getModelsIdByUniprotIdsReturn getAllAnnotatedTissueAccessionReturn UniProtId2DomainIdsResponse	
getaliannotated hssueaccessionketurn UniProtId2DomainIdcPosposo	+ +
retReportResponse	+
getReportResponse pickingResponse getSymbolInfoFromSymbolResponse getInstancesByPubMedIdResponse getchromNameResponse	 +
getSymbolInfoFromSymbolResponse	- †
getsymboliniorionsymbolicesponse	⊢ i
getchromNameResponse	$-\frac{1}{1}$
queryResponse	$\bar{1}$
since	1
getOntologyNamesResponse	1
blastp_BasicReturn	1
GetSpeciesListResponse	1
sliceChromosomeResponse	<u> </u>
getPBfromGOReturn	$\frac{1}{1}$
getDBInfoReturn	<u> </u>
getSequencesFromGenomeVirtualReturn	
getUMLSVersionReturn getSignalpPoturp	
getSignalpReturn whatVoxalPagionExpressGonoPoturn	
whatVoxelRegionExpressGeneReturn GetPublicationExperimentsResponse GetPublicationStrainsResponse	+
GetPublicationStrainsResponse	+
uniquesubsReturn	 †
getTermTypesReturn	†
cla_listResponse	T T
identifySimpleSearchInnutParametersReturn	$\frac{1}{1}$
GetEMBLNucleotideSequence BsmlResponse bindnrnaResponse	$\bar{1}$
bindnrnaResponse	1
getEntriesFieldUrlsResponse	1
hit queryResponse	1
getTheNumberOfParalogsForAllOrthoMCLClustersContainingProteinsOfAGivenGenomeReturn	1
getGeneldsByProteomeldResponse	1
Domains 2 svgResponse	1
GetAsyncSearchStatusResponse	$\frac{1}{1}$
seq fetch fastaResponse	<u> </u>
getAllMCLClustersWithLessThanAGivenPercentageOfProteinsOfAGivenGenomeReturn	
getCddConservedDomainIdsByLocusLinkIdReturn	+
soap match alignment with modelResponse updatePathwayResponse	 +
seq_dump_fastaResponse	+ +
getTheNumberOfGenomesInMCLClustersThatContainProteinsOfAGivenGenomeAndProteinsOfOnlyEssentialYeastGenesReturn	+
getTwoColorWithinArrayNormalizationMethodsReturn	- †
getGOViewHTMLReturn	
addRdfReturn	T T
getCurationTagsResponse	$\frac{1}{1}$
getESTUnisequencesRepresentingAGivenOpenReadingFrameReturn	Ī
GetStpGraphListResponse	$ar{1}$
getSequenceSourceReturn	1
match summary	1
GetInnovatedFamiliesHogenomResponse	1
getRepresentativeImageSeriesResponse	1
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameMCLClustersAsProteinsWithAGivenPSortPredictionReturn	1
ToadPathwayForldReturn	1
getGeneOntologyMolecularFunctionReturn getGeneOntologyMolecularFunctionReturn	$+\frac{1}{2}$
adjacentReturn	$+\frac{1}{2}$
runDSSPByIDResponse	
getChipTypesReturn	
dockingscore	
is archaealReturn	1
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GetDatabankInfoResponse getELMByIdentifierResponse	1

name coun
seywordOuervReturn
abstract coupled toReturn
runPalignSeqSeqDefaultResponse runFetchProtResponse
getEcNumsReturn
getSimpleModelsByChEBIIdsReturn
uniprot acc runGlobPlotterResponse
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RunTblastxJobResponse plastStructureIdQueryXmlReturn getSimpleModelsByUniprotIdsReturn getAllModelsReturn
getSimpleModelsByUniprotIdsReturn
getAllModelsReturn Ode Cure of a mile 2 Uni Prot I de Pean ange
odbSuperfamily2UniProtldsResponse
mappingResponse getSymbolAndTaxIdResponse
request origResponse mappingInfoResponse GetDatabasesResponse
nappingInfoResponse
sources sources
getOntologyLoadDateResponse
ranslating Blast BasicReturn
ranslating Blast BasicReturn GetEnsIdsByRegionResponse
sliceChromosomeByGeneResponse
phyloML getGeneReturn
queryForExperimentReturn
getSpellingSuggestionsReturn getMsblastInfoReturn
getMsblastInfoReturn
getSubmissionAssayWlzReturn getStoreSizeResponse
GetStoresizeresponse GetPublicationModelTypesResponse
parsimonyReturn
getSplSetIdReturn
nit listResponse
evaluateSimpleSearchReturn GetEMBLNucleotideSeguence AGAVEResponse
disemblResponse
getDomainsReferencedInEntryResponse
nat_queryResponse
getEnzymesForAGivenProteinReturn getGeneldsByProteomeldAndQueryTermResponse
incoderResponse
GetAsyncSearchResultResponse
not fetch fastaResponse
getTheProteinsThatAreInTheSameMCLClusterAsAGivenProteinReturn
MOBYSHoundLocusIDFromOMIMReturn applyReturn
indPathwaysByXrefResponse
not dump fastaResponse
getTheNumberOfGenomesInMCLClustersThatContainProteinsOfAGivenGenomeAndProteinsOfOnlyNonessentialYeastGenesReturn
getTwoColorBetweenArrayNormalizationMethodsReturn getGOViewPDFReturn
getGOVIewPDFReturn removeRdfReturn
indInteractionsResponse
getESTUniseguencesForAGivenGenomeReturn
GetStpGraphResponse
getTranscriptIdReturn search summary
GetLostFamiliesHogenomResponse
geneSearch1Response
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameOrthoMCLClustersAsProteinsWithAGivenPSortPredictionReturn
oadPathwayForObjectReturn
getGeneOntologyCellularComponentReturn cluster by bbhsReturn

name	count
runMkDomResponse	1
getDatabasesWithDetailsReturn	1
getSnpsBySwissProtIdReturn is_bacterialReturn	1
GetMetaDataResponse	1
getELMsByTextSearchResponse	
pubmedAbstractQueryReturn	$\overline{1}$
pinned region dataReturn	1
runPalignSegSegResponse	1
runFetchFastaResponse	1
getCifChainReturn	1
helloBioModelsReturn	1
getNodeAccessionReturn PdbSuporfamily2KoggOrthologsPospopso	1
PdbSuperfamily2KeggOrthologsResponse getSNPIdsReturn getModelsIdByUniprotReturn	+
getSM lasketam	1
response treeReturn	$\overline{1}$
GetHogenomFamCompResponse	$\bar{1}$
getImageResponse	1
RunDeterministicSimulatorResponse	1
getSymbolInfoFromReferenceResponse	1
PhysicoChemProfile	1
numberConversionResponse	<u>_</u>
SearchByMassResponse getAllTermsFromOntologyResponse	1
blastn AdvancedReturn	1
Get Expression Datasets Response	1
GetExpressionDatasetsResponse upLoadGenBankLocalFileResponse TFmodellerReturn	<u> </u>
TFmodellerReturn	$\overline{1}$
getAllGeneReturn	$\overline{1}$
queryForArraysReturn ResultMS	1
ResultMS	1
getMsTagInfoReturn	1
eInfoResult	<u> </u>
getMsFitInfoReturn generateConceptsFromPubMedQueryResponse	1
getCategoriesResponse	1
maximumlikelihoodReturn	1
	$\overline{1}$
findRemappedReturn hat_listResponse	$\bar{1}$
identifyAdvancedSearchCollectionsReturn	1
iupredĺResponse	1
hot_queryResponse	1
getProteinsofAGivenGenomeWithAGivenEnzymeAnnotationReturn	$\frac{1}{1}$
getGeneldsByGenomeAcResponse	<u> </u>
FillseqResponse GetCompoundThumbnailResponse	1
seq fetch nrResponse	1
getTheNumberOfProteinsForEachGenomeInAGivenMCLClusterReturn	1
MOBYSHoundGOIDFromLocusIDReturn	$\overline{1}$
ConvertCopasiMLToSBMLResponse	1
getColoredPathwayResponse	1
seq_dump_nrResponse getTheNumberOfGenomesInOrthoMCLClustersThatContainProteinsOfAGivenGenomeAndProteinsOfEssentialYeastGenesReturn	1
getTheNumberOtGenomesInOrthoMCLClustersThatContainProteinsOfAGivenGenomeAndProteinsOfEssentialYeastGenesReturn	1
analyseGenesPDFOutputReturn	1
selectQuerySerializedReturn	<u></u>
loginResponse getESTsForAGivenGenomeReturn	1
UploadStpGraphResponse	1
getTargetDescriptionReturn	1
filter file	<u>†</u>
GetRegainedFamiliesHogenomResponse	1
geneSearchResponse	$\overline{1}$
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameMCLClustersAsProteinsWithAGivenWolfPSortPredictionReturn	1

listPathwayParticipantsPaturn	COL
stPathwayParticipantsReturn etAffyIdByOrfReturn luster_by_simReturn	
etanyiobyonketum Justor by simPoturn	
uster_by_simketum inZpredDefaultResponse	
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etLinksReturn	
etCogldReturn	
eukaryoticReturn	
etIndicesResponse	
etELMsBySequenceMatchResponse	
etSpaceGroupForStructureReturn Il genomesReturn	
II_genomesReturn	
unPalignSeqSeqSSDefaultResponse	
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<u>letCifResidueReturn</u>	
letAllModelsIdReturn	
jetNodeInfoReturn	
KeggOrtholog2PdbSuperfamiliesResponse JetUniProtSNPsReturn	
etUniProtSNPsReturn	
etModelsIdByGOldReturn esponse alignmentReturn	
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GetHogenomFamDetResponse	
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SetPathwayListResponse	
pLoadGenBankRemoteFileResponse	
putseq	
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petSubmissionWithoutImageReturn	
leleteReturn	
jetProprietaryInformationReturn	
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InfoResultMS	
etTicketByldResponse	
enerateConceptsFromTextResponse	
etNonOboOntologiesResponse	
istanceReturn	
etSourceTypesReturn	
ot_listResponse	
dentifyAdvancedSearchFiltersReturn	
etLocationResponse	
ıpredsResponse	
etDetailledNumberOfResultsResponse	
nom queryResponse	
nom_queryResponse etProteinsofAGivenGenomeWithTheSameEnzymeAnnotationAsAGivenProteinReturn	
etGeneByldResponse	
ormatnameResponse	
etCompoundInfoResponse	
ot fetch nrResponse	
etASummarvOfTheMCLClusterAnalysisForAGivenGenomeReturn	
OBYSHoundLocusIDFromGOIDAndECodeReturn	
onvertSBMLToCopasiMLResponse	
etPathwayInfoResponse	
ot_dump_nrResponse	
etTheNumberOfGenomesInOrthoMCLClustersThatContainProteinsOfAGivenGenomeAndProteinsOfOnlyEssentialYeastGenesReturn	
erformJustAffyNormalizationReturn	
otCN/iowlmageReturn	
etGOViewImageReturn ddRdfWithContextReturn	
etRecentChangesResponse	
etRecentChangesResponse etCellularLocalisationPredictionPSortWolfPSortForAGivenProteinReturn	
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name	coun
CYGDAnnotations	
getArchivalUniGeneClusterReturn	
GetTransferedFamiliesHogenomResponse	
getGeneList2Response	
getAnnotationForProteinsOfAGivenGenomeThatAreInTheSameOrhoMCLClustersAsProteinsWithAGivenWolfPSortPredictionReturn	
listPathwayParticinantsForldReturn	
getInterproBvOrfReturn	
getInterproByOrfReturn external_callsReturn	
getPRINTSRecordByAccessionResponse getField2TableAndColumnMapReturn getAnnotationsReturn	
getField2TableAndColumnMapReturn	-
get Annotations Return	-
is prokaryoticReturn	
getAllELMInstancesResponse getPubmedIdForAllStructuresReturn	
netPuhmedIdForAllStructuresReturn	
genomesReturn	
genomesketam gunProdivtmhmmDefaultResnonse	
runProdivtmhmmDefaultResponse runFetchKWResponse	
getChainsReturn	
getChamsReturn getAllCuratedModelsIdReturn	
getNodeStageReturn	
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KeggOrtholog2DomainIdsResponse GetAvailableDatabasesResponse	
getNCBIdbSNPDescriptorReturn	
getNCDIQDSNPDesCriptorReturn	
getNodelsIdByGOReturn	
response sequencesReturn getPubMedFromPMIDResponse getBindingDomainListResponse getSymbolInteractionsFromSymbolResponse	
<u>JetPubMedFromPMIDResponse</u>	
<u>JetBindingDomainListResponse</u>	
getSymbolinteractionsFromSymbolResponse	
ČI2	
transcriptInfoResponse	
SearchByFormulaResponse	
getTermsByNameResponse	
translating Blast AdvancedReturn GetEnsIdsByPathwayNameResponse	
GetEnsIdsByPathwayNameResponse	
updateCollectionResults	
getSupportedLibsReturn	
contactResponse	
getAllSubmissionsReturn	
runQueryDefaultDbReturn	