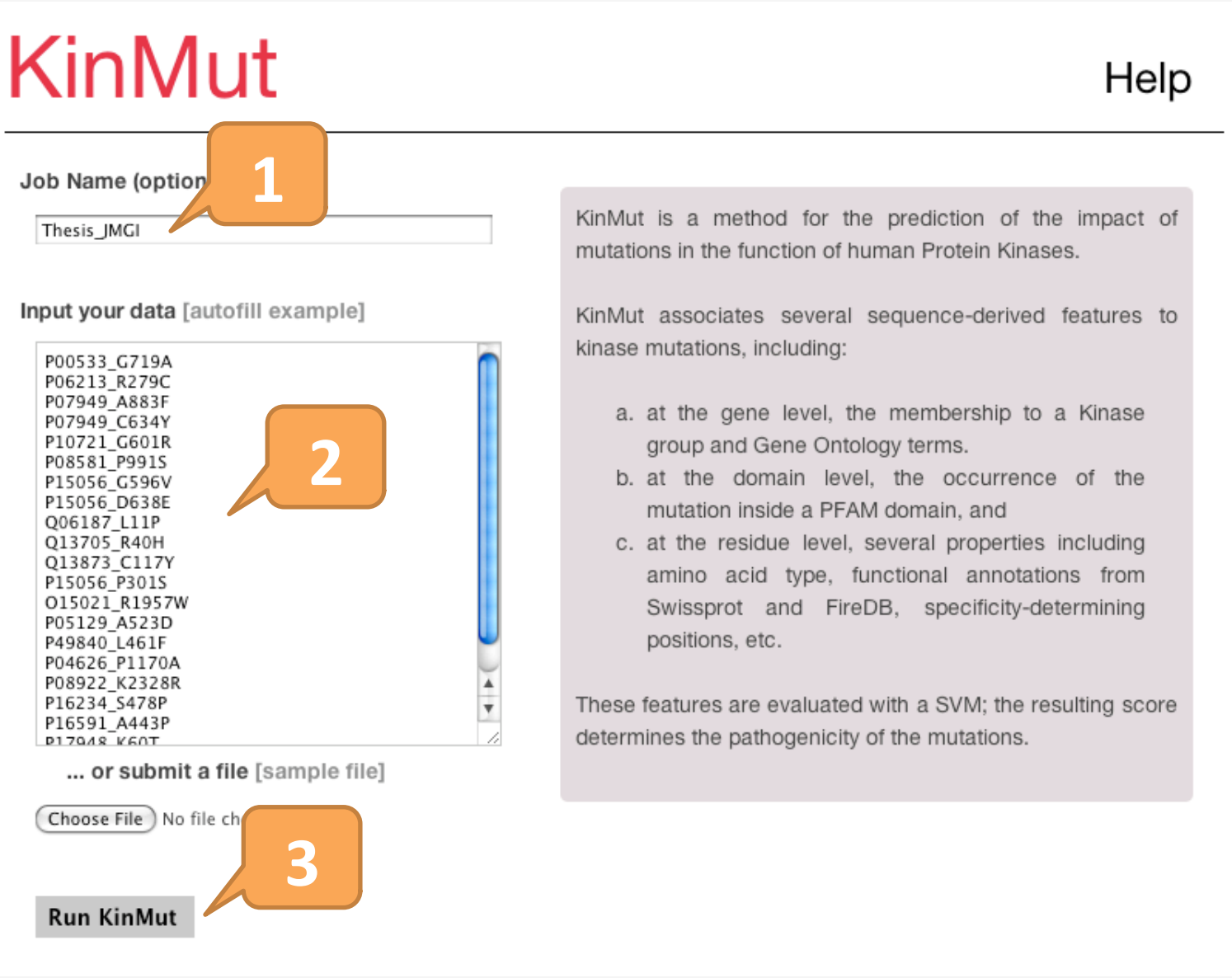
KinMut: Submitting a job



http://kinmut.bioinfo.cnio.es

KinMut: RET A883F mutation

KinMut Help

Job: Thesis [download results] [original input]

Protein	Mutation	Kinase Group	Score	Prediction*	Features
O15021	R1957W	AGC	-1.28	Neutral	details
P00533	G719A	TK	1.01	Damaging	details
P04626	P1170A	TK	-0.765	Neutral	
P05129	A523D	AGC	-0.93	Neutral	
P06213	R279C	TK	0.999	Damaging	de
P07949	A883F	TK	1.11	Damaging	details
P07949	C634Y	TK	0.999	Damaging	details
P08581	P991S	TK	0.69	Damaging	details
P08922	K2328R	TK	-1.27	Neutral	details
P10721	G601R	TK	0.642	Damaging	details
P15056	G596V	TKL	0.141	Damaging	details
P15056	D638E	TKL	0.077	Damaging	details

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KinMut report

Gene/Protein Features

Details for Protein: P07949, Mutation: A883F

Protein | Pfam Domains (1) | Residue | Other Databases (2) | Literature for Mutation (9) | IHOP Interactions (400)

Gene Name
RET
Protein Long Name
c-ros oncogene 1 , receptor tyrosine kinase
Summary
This proto-oncogene, highly-expressed in a variety of tumor cell lines, belongs to the sevenless subfamily of tyrosine kinase insulin receptor genes. The protein encoded by this gene is a type I integral membrane protein with tyrosine kinase activity. The protein may function as a growth or differentiation factor receptor. [provided by RefSeq]
Kinase Group
TK: tyrosine protein kinase
Gene Ontology Log-Odds Ratio: 90.63

GOTerm	Sub-ontology	Name
GO:0000166	Molecular Function	nucleotide binding
GO:0001882	Molecular Function	nucleoside binding
GO:0001883	Molecular Function	purine nucleoside binding
GO:0003674	Molecular Function	molecular_function
GO:0003824	Molecular Function	catalytic activity
GO:0004672	Molecular Function	protein kinase activity
GO:0004713	Molecular Function	protein tyrosine kinase activity
GO:0004714	Molecular Function	transmembrane receptor protein tyrosine kinase activity
GO:0004871	Molecular Function	signal transducer activity
GO:0004872	Molecular Function	receptor activity

Domain Features

Protein | Pfam Domains (1) | Residue | Other Databases (2) | Literature for Mutation (9) | IHOP Interactions (400)

Protein tyrosine kinase (PF07714)

Residue Features

Kinase Family Subspecificity
Wild Type 0.00
Mutant 0.00
Difference 0.00

Kyte-Doolittle Hydrophobicity Change
1.00

SIFT Prediction (Score)
Neutral (0.0749)

FireDB	No
PhosphoELM	No
Transmembrane	No
Mutagenesis	No
Post Trans. Modification	No
Modified Residue	No
Signal Peptide	No
Catalytic Site	No
Disulfide Bond	No
Carbohyd	No
Active Site	No
Site	No
Nucleotide Binding	No
Metal Binding	No
Binding	No

Info in other Databases

Protein | Pfam Domains (1) | Residue | Other Databases (2) | Literature for Mutation (9) | IHOP Interactions (400)

Mutation	Description	Database
A883S	K00466 - Multiple endocrine neoplasia type II	kinmutbase
A883F	VARIANT	uniprot

iHop Interactions

Protein | Pfam Domains (1) | Residue | Other Databases (2) | Literature for Mutation (9) | IHOP Interactions (400)

[PMID: 11783847] Radiation-induced human papillary thyroid cancer (PTC) is associated with chromosomal inversions that involve the genetic loci H4 and RET on chromosome 10.

[PMID: 11783847] The predicted H4-RET dose-response has a linear-to-quadratic transition dose of approximately 7 Gy, suggesting the validity of linear risk extrapolations to very low doses for H4-RET mediated radiation-induced PTC.

[PMID: 11021799] The RET/PTC1 type of rearrangement is an inversion of chromosome 10 mediated by illegitimate recombination between the RET and the H4 genes, which are 30 megabases apart.

[PMID: 15761501] In papillary thyroid carcinomas (PTCs), rearrangements of the RET receptor (RET/PTC) and activating mutations in the BRAF or RAS oncogenes are mutually exclusive.

[PMID: 15761501] Here we show that the 3 proteins function along a linear oncogenic signaling cascade in which RET/PTC induces RAS-dependent BRAF activation and RAS- and BRAF-dependent ERK activation.

[PMID: 12907632] Surprisingly, we found that a large number of BRAF-mutated PTCs (8 of 21) also expressed RET, indicating that the RET proto-oncogene is rearranged in these BRAF-mutated PTCs.

[PMID: 16569669] Moreover, inhibition of SH2-Bbeta expression by RNA interference caused a significant decrease of GDNF-induced neuronal differentiation in PC12-GFRalpha1-RET cells.

[PMID: 16569669] Furthermore, functional analysis indicated that overexpression of SH2-Bbeta facilitated GDNF-induced neurite outgrowth in both PC12-GFRalpha1-RET cells and cultured mesencephalic neurons, whereas the mutant R555E inhibited the effect.

[PMID: 11932334] The expression of RET in all of the somatotropinomas and in 50% of the ACTH-producing tumors implies that GDNF and RET could be involved in the pathogenesis of pituitary tumors.

[PMID: 11973622] Consistently with the lack of genotype/phenotype correlation in human subjects, our results indicate absence of detectable alterations of mutant GDNF induced RET activation.

SNP2L Literature

Protein | Pfam Domains (1) | Residue | Other Databases (2) | Literature for Mutation (9) | IHOP Interactions (400)

Mutation	PMID	Content	Comments
A883F	10076558	Most patients with MEN 2B carry a germline mutation (M918T) of the RET proto-oncogene, while a few carry	
A883F	10076558	We examined a patient with MEN 2B, but without M918T or A883F, and her	
A883F	10445857	We introduced seven mutations (glutamic acid 768-->aspartic acid (E768D), valine 804-->leucine (V804L), alanine 883-->phenylalanine (A883F), serine 891-->alanine (S891A), methionine 918-->threonine (M918T), alanine 919-->proline (A919P) and E768D/A919P) into the short and long isoforms of RET cDNA and transfected the mutant cDNAs into NIH3T3	
A883F	10445857	Based on the levels of the transforming activity, these mutant RET genes were classified into two groups; a group with high transforming activity (A883F, M918T and E768D/A919P) and a group with low transforming activity (E768D, V804L, S891A and A919P) (designated high group and low	
A883F	10445857	Interestingly, the level of transforming activity correlated with clinical phenotypes; high group Ret with the A883F or M918T mutation and low group Ret with the E768D, V804L or S891A mutation were associated with the development of MEN 2B and FMTC,	

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KinMut: Protein/Gene level info

Gene/Protein Features

Details for Protein: P07949, Mutation: A883F

Protein | Pfam Domains (1) | Residue | Other Databases (2) | Literature for Mutation (9) | IHOP Interactions (400)

Gene Name
RET

Protein Long Name
c-ros oncogene 1 , receptor tyrosine kinase

Summary
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TK: tyrosine protein kinase

Gene Ontology Log-Odds Ratio: 90.63

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KinMut: Domain and Residue info

Domain Features

Protein | Pfam Domains (1) | Residue | Other Databases (2) | Literature for Mutation (9) | IHOP Interactions (400)

Protein tyrosine kinase (PF07714)

Residue Features

Kinase Family Subspecificity

Wild Type	0.00
Mutant	0.00
Difference	0.00

Kyte-Doolittle Hydrophobicity Change

1.00

SIFT Prediction (Score)

Neutral (0.0749)

FireDB	No
PhosphoELM	No
Transmembrane	No
Mutagenesis	No
Post Trans. Modification	No
Modified Residue	No
Signal Peptide	No
Catalytic Site	No
Disulfide Bond	No
Carbohyd	No
Active Site	No
Site	No
Nucleotide Binding	No
Metal Binding	No
Binding	No

KinMut: The mutation in other DBs

Info in other Databases

Protein | Pfam Domains (1) | Residue | Other Databases (2) | Literature for Mutation (9) | IHOP Interactions (400)

Mutation	Description	Database
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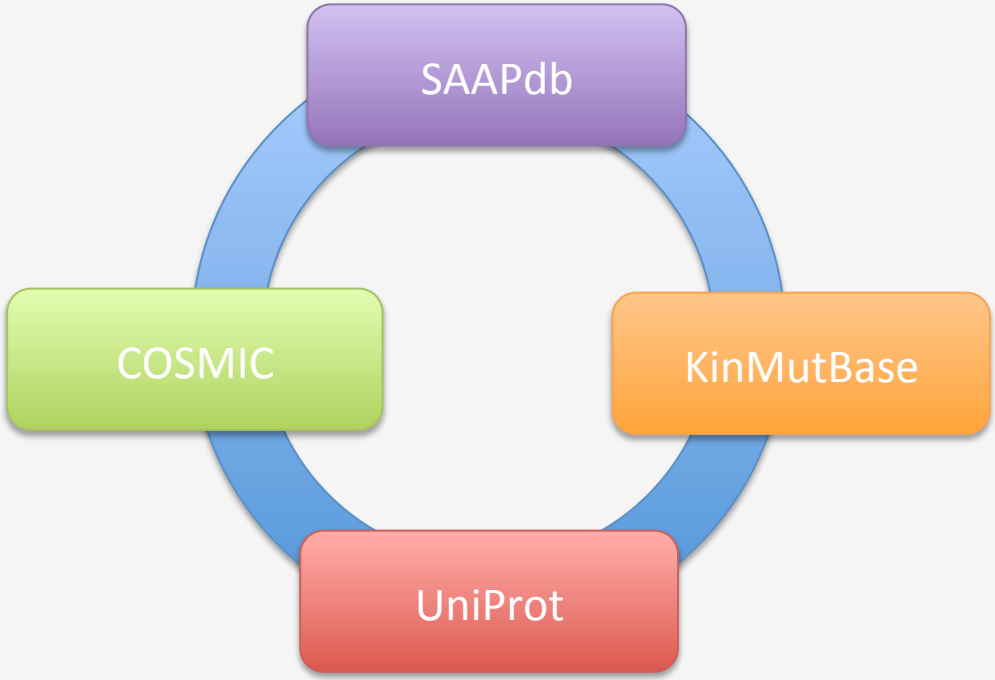

KinMut: The mutation in the literature

SNP2L Literature

Protein | Pfam Domains (1) | Residue | Other Databases (2) | Literature for Mutation (9) | IHOP Interactions (400)

Mutation	PMID	Content	Comments
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KinMut: Interactions from the literature

iHop Interactions

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