

A

M	motifType	peptideOr	motif Sequ	residue	moleculeMo	moleculeMo	mmod	aclass	asubClass	go	amod	moleculeTa	moleculeTarg	moleculeTarg	multi_subc	affinity	pdbid	maPubs	maAttrs	reviewer	
1	Lexicon	protein	PPPL	161	IVR	NP_057851	0	binds	general			APGEC3G	NP_001635		none	unknown			Required Modification none. Technique comm.	cpura, ip-e	
2	Lexicon	peptide	SKSKDKYK	188	Traf1D	NP_005278	0	modifies	methylated	-1-Lysine is	Se49	NP_085151	SET	none	34.0	2F69	16415881		Required Modification none. Technique x-ray	cpura, ip-e	
3	Consensus	unknown	IKRQASTKQ	unknown	unknown	unknown	0	modifies	methylated	-1-Lysine is	Se49	NP_085151	SET	none		2F69	16415881		Technique sequence based prediction. MI0101	cpura, ip-e	
4	Lexicon	peptide	LKSKKG	369	p53	BAC16799	0	modifies	methylated	-1-Lysine is	Se49	NP_085151	SET	none	17.0	1XG4	15525038		Technique nuclear magnetic resonance. MI007	cpura, ip-e	
5	Lexicon	peptide	ARTKQTAR	2	Histone H3	NP_003404	0	modifies	methylated	-1-Lysine is	Se49	NP_085151	SET	none	38.0	1MUJF, 1MT6	15240805		Technique assay. Technique Docking. MI0035	cpura, ip-e	
6	Lexicon	protein	SKSKDKA	2	TAF7	NP_005633	0	modifies	methylated	-1-Lysine is	Se49	NP_085151	SET	none		2F69	16415881		Required Modification none. Technique Docking	cpura, ip-e	
7	Lexicon	peptide	ARTKQT	2	Histone H3	NP_003404	0	binds	methyl-lysine			NLRIF	NP_872679	PHD finger	none		2F69, 2F5U, 2F5U	16729978		Activity Modification none. Technique nuclear m.	cpura, ip-e
8	Lexicon	peptide	ARTKQTAR	2	Histone H3	AAA37812	0	-1-Lysine m.	binds	methyl-lysine		ING2	NP_075992	PHD finger	none	1.5	2GQ0, 2JMU	16728977		Activity Modification none. Technique Docking	cpura, ip-e
9	Lexicon	peptide	ARTKQTAR	2	Histone H3	AAA37812	0	-1-Lysine m.	binds	methyl-lysine		ING1	NP_036049	PHD finger	none	3.3	2GQ0, 2JMU	16728977		Technique x-ray crystallography. MI0114. Activity	cpura, ip-e
10	Lexicon	peptide	ARTKQTAR	2	Histone H3	AAA37812	0	-1-Lysine m.	binds	methyl-lysine		ING3	NP_076116	PHD finger	none	6.9	2GQ0, 2JMU	16728977		Technique x-ray crystallography. MI0114. Activity	cpura, ip-e
11	Lexicon	peptide	ARTKQTAR	2	Histone H3	AAA37812	0	-1-Lysine m.	binds	methyl-lysine		ING4	NP_579923	PHD finger	none	7.9	2GQ0, 2JMU	16728977		Technique x-ray crystallography. MI0114. Activity	cpura, ip-e
12	Lexicon	peptide	ARTKQTAR	2	Histone H3	AAA37812	0	-1-Lysine m.	binds	methyl-lysine		ING5	NP_079730	PHD finger	none	2.4	2GQ0, 2JMU	16728977		Activity Modification none. Technique x-ray cryst.	cpura, ip-e
13	Lexicon	peptide	ARTKQTAR	2	Histone H3	AAA37812	0	-1-Lysine m.	binds	methyl-lysine		YH01	NP_014707	PHD finger	none	2.3	2GQ0, 2JMU	16728977		Technique x-ray crystallography. MI0114. Activity	cpura, ip-e
14	Lexicon	peptide	ARTKQTAR	2	Histone H3	AAA37812	0	-1-Lysine m.	binds	methyl-lysine		YH02	NP_011958	PHD finger	none	5.1	2GQ0, 2JMU	16728977		Technique x-ray crystallography. MI0114. Activity	cpura, ip-e
15	Lexicon	peptide	ARTKQTAR	2	Histone H3	AAA37812	0	-1-Lysine m.	binds	methyl-lysine		PHK023	NP_014302	PHD finger	none	4.5	2GQ0, 2JMU	16728977		Activity Modification none. Technique x-ray cryst.	cpura, ip-e
16	Lexicon	peptide	SYGRKRR	46	Tat	NP_057853	0	binds	acetylated	-1-Lysine is	PCAF	Q52831	Bromodomain	none	1.6	1J44	15724876		Required Modification none. Technique assay.	cpura, ip-e	
17	Lexicon	peptide	STSRHQL	376	p53	BAC16799	0	binds	acetylated	-1-Lysine is	CBP	Q52793	Bromodomain	none		1J5P	16428974		Technique assay. Technique Docking. MI0035	cpura, ip-e	
18	Lexicon	peptide	RKASSP	376	Tyrosine ty.	NP_033403	1	-1-second	binds	general		14-3-3	Unknown	14-3-3	1	unknown	8601312		Technique Docking. MI0035. Activity Modification	cpura, ip-e	
19	Lexicon	peptide	RSASEP	618	Raf1	NP_044956	1	-1-second	binds	general		14-3-3	Unknown	14-3-3	1	3CUB	8601312		Technique x-ray crystallography. MI0114. Techn.	cpura, ip-e	
20	Lexicon	peptide	RSASEP	763	Raf1	NP_047455	1	-1-second	binds	general		14-3-3	Unknown	14-3-3	1	unknown	8601312		Activity Modification none. Technique x-ray cryst.	cpura, ip-e	

B

Motif Data | Modifications | Attributes

id: 18

motifType: Lexicon

peptideOrProtein: Peptide

motifSequence: RHASSP

residuePosition: 316

moleculeMotifName: Tyrosine hydroxylase

moleculeMotifDbid: NP_033403

aclass: binds

asubClass: general

go:

moleculeTargetName: 14-3-3

moleculeTargetDbid: Unknown

moleculeTargetDomain: 14-3-3

multiDomain: 1

subcellularDomain:

affinity: null

maPubs: 8601312

pdbid: unknown

SaveAction | Clone Motif | Check Sequence

C

Motif Data | Modifications | Attributes

Modification Name:

Database ID:

Residue: R 316

Type: NULL

Add Modification

Modifications:

-1:second Ser must be phosphorylated:O-phospho-L-serine

Delete Modification

D

Motif Data | Modifications | Attributes

Attributes:

Technique = Docking_MI0035

Activity Modification = none

Technique = assay

Technique = Peptide mapping