Figure S1

Helical regions predicted by JPred in p53 TAD

```
                        : 1---------11--------21--------31--------41--------51-------- :
OrigSeq                 : MEEPQSDPSVEPPLSQETFSDLWKLLPENNVLSPLPSQAMDDLMLSPDDIEQWFTEDPGP : OrigSeq

Jnet                    : -----------------HHHHHHH---------------H--------HHHHHH------ : Jnet
jhmm                    : ------------------HHHHH--------------HHH--------HHHHHH------ : jhmm
jpssm                   : ----------------HHHHHHHHH--------------HHH-------HHHHH------ : jpssm
```

```
Jnet            - Final secondary structure prediction for query
jhmm            - Jnet hmm profile prediction
jpssm           - Jnet PSIBLAST pssm profile prediction
```

Figure S2

p53 in complex with the nuclear coactivator binding domain of CBP
p53 structural data accession number 2l14 downloaded from PDB database are coloured accordingly to Figure 4.

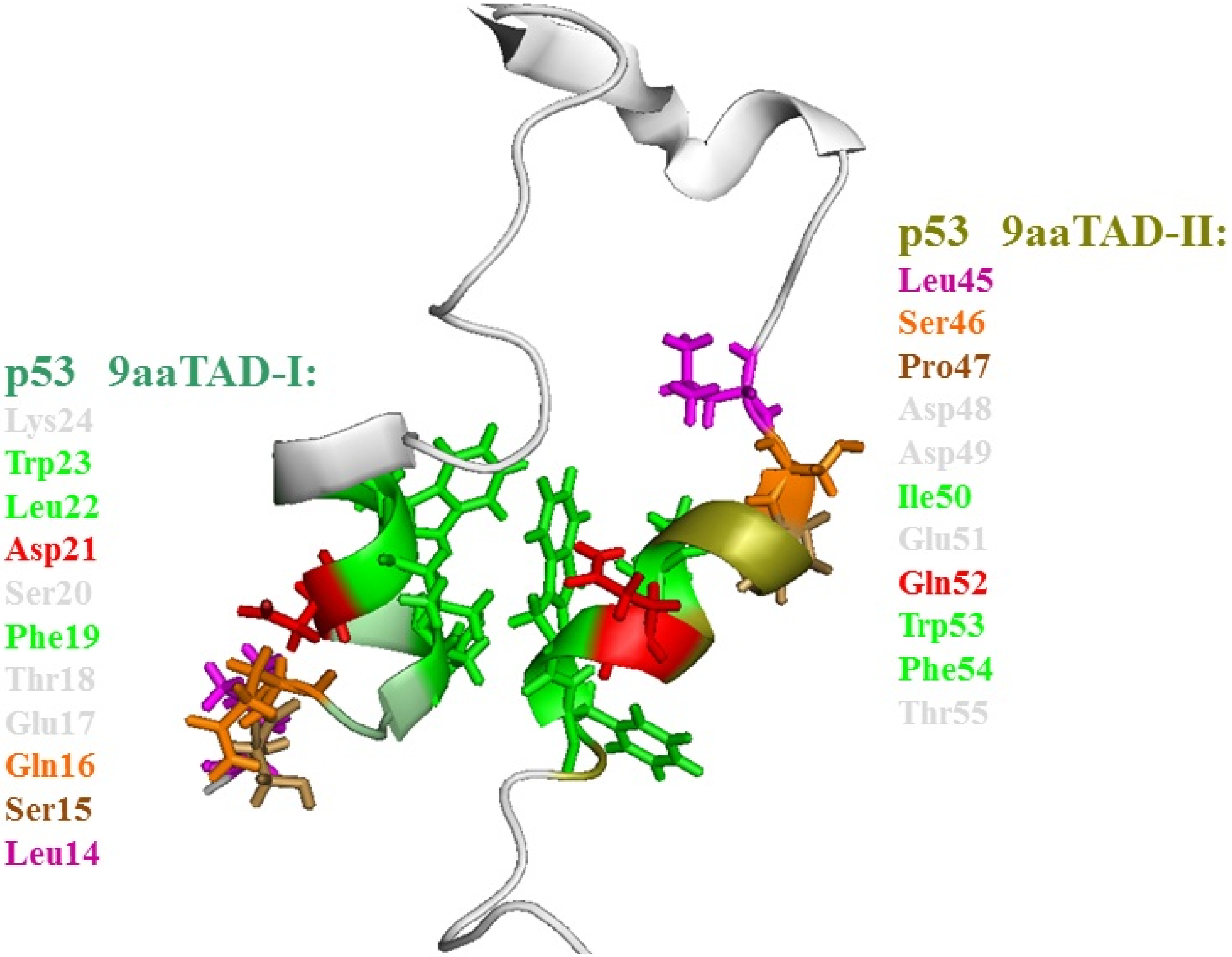


Figure S3

E2A family

```
        Leu -    9aaTAD
GTDK    EL   SD LL D FS MM   FPLP   TFE2_HUMAN
GTDK    EL   SD LL D FS KM   FPLP   G1QMU8_NOMLE
GTDK    EL   SD LL D LS MM   FPLP   G3UGS9_LOXAF
ATDK    EL   SD LL D FS VM   FPLP   W5KGK3_ASTMX
GTDK    EL   SD LL D FS AV    RYP   F7BGG6_XENTR
GTDK    DL   SD LL D FS AM   FSPP   F6Y2I2_CANFA
GTDM    EL   ND LL D FS IM   FPHP   Q90491_DANRE
ETDK    EL   ND LL D FT AM   FELP   H2T6R8_TAKRU
NQTK    VL   QE TL D FS LV   TPTP   RTG3_YEAST
SQTK    IL   QE TL D FS LV     TP   J4TS14_SACK1
```

9aaTAD pattern of the E2A family:
`[SNQ][DE][LT]LD[FL][ST][MKVAIL][MV]`

MLL family

```
       Leu  -    9aaTAD
GN      LP   SD IM D FV LK  NTP     KMT2A_HUMAN (MLL)
GN      LP   SD IM D FV LN  TPS     H3BFF4_LATCH
GN      LP   SD IM E FV LN  TPS     A8VKP8_DANRE
GN      IP   SD IM E FV LN  TPS     M4A2U4_XIPMA
ED      LP   SE IV D FV LK  NLG     KMT2B_HUMAN (MLL2)
ED      LP   SE IV D FV LK  NLG     J9NZ02_CANFA
SH      IP   SE IV E FV LK  NTG     B0JZH9_XENTR
SH      IP   SE IV E FV LK  NTG     F6XZK4_XENTR
SH      IP   SE IV E FV LK  NTA     F6YNY3_XENTR
```

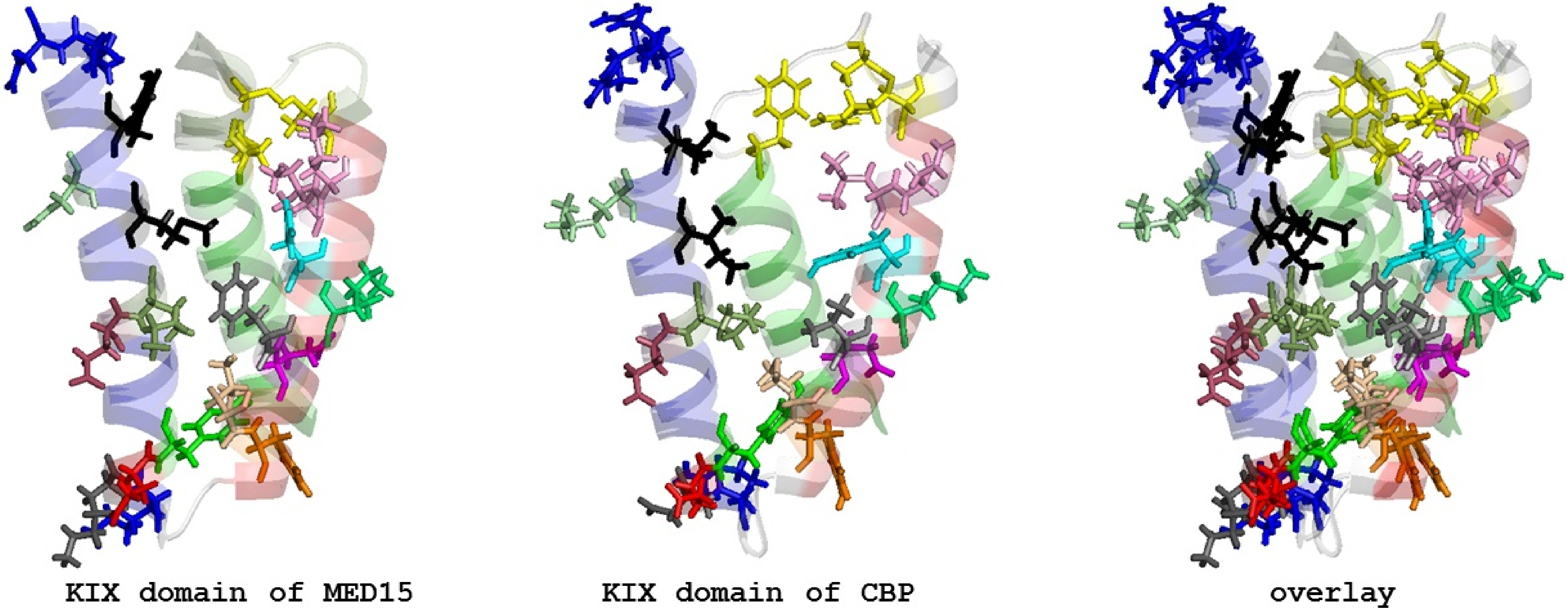
9aaTAD pattern of the MLL family:
`[SNQ][DE][LTI][LMV][DE][FL][STV][MKVAIL][MVKN]`

This journal is © The Royal Society of Chemistry 2014

Figure S4

MED15 LSNAERAKNVNGLLQVL MDINTLNGGSSDT ADKIRIHARNFEAALFAK SSS KKEYMDSMNEKVAVMRNTYNTKRN

CBP VTQDLRSHLVHKLVQAI FPTPDPAALKDRR MENLVAYAKKVEGDMYES ANS RDEYYHLLAEKIYKIQKELEEKRR



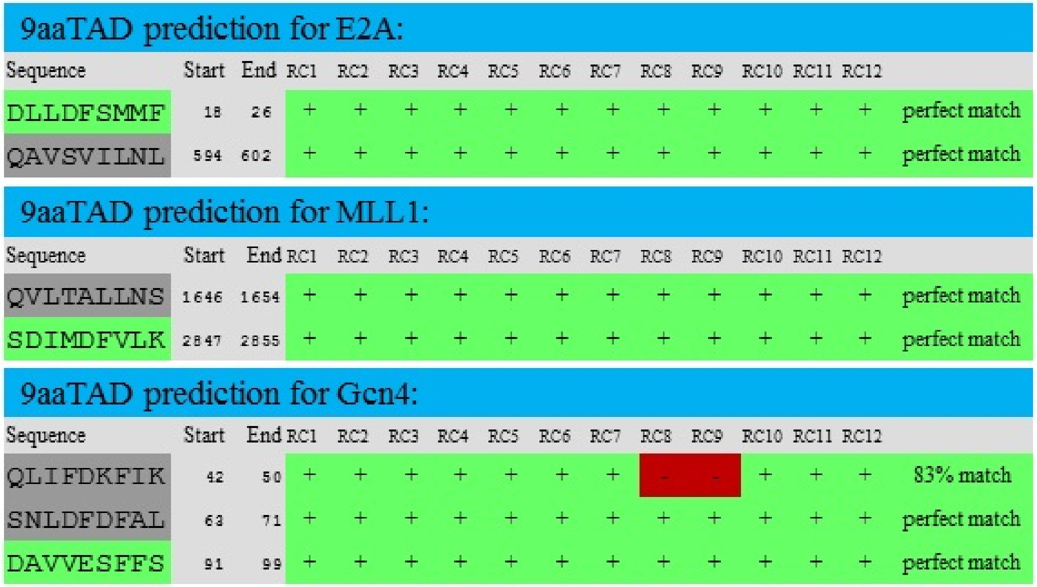
KIX domain of MED15

KIX domain of CBP

overlay

The KIX domain of MED15 and KIX domain of CBP overlay. The structure coordinates accession number 2K0N for MED15 and 2AGH for CBP KIX domain were downloaded from PDB. Molecular graphics were generated using PyMOL.

Figure S5



9aaTAD prediction for E2A:

Sequence	Start	End	RC1	RC2	RC3	RC4	RC5	RC6	RC7	RC8	RC9	RC10	RC11	RC12	
DLLDFSMMF	18	26	+	+	+	+	+	+	+	+	+	+	+	+	perfect match
QAVSVILNL	594	602	+	+	+	+	+	+	+	+	+	+	+	+	perfect match

9aaTAD prediction for MLL1:

Sequence	Start	End	RC1	RC2	RC3	RC4	RC5	RC6	RC7	RC8	RC9	RC10	RC11	RC12	
QVLTALLNS	1646	1654	+	+	+	+	+	+	+	+	+	+	+	+	perfect match
SDIMDFVLK	2847	2855	+	+	+	+	+	+	+	+	+	+	+	+	perfect match

9aaTAD prediction for Gcn4:

Sequence	Start	End	RC1	RC2	RC3	RC4	RC5	RC6	RC7	RC8	RC9	RC10	RC11	RC12	
QLIFDKFIK	42	50	+	+	+	+	+	+	+	-	-	+	+	+	83% match
SNLDFDFAL	63	71	+	+	+	+	+	+	+	+	+	+	+	+	perfect match
DAVVESFFS	91	99	+	+	+	+	+	+	+	+	+	+	+	+	perfect match

Figure S6

Gcn4 family

	Leu -	9aaTAD						
PIP	ELD	AA	VV	E	SF	FS	SSTDSTP	A6ZQT9_YEAS7
PLN	ELD	SN	VV	D	AF	FS	SSTDSTP	G0VJK4_NAUCC
NNN	ELD	SA	VV	D	AF	FS	STSDSTP	G0W5D3_NAUDC
ASP	EVS	AA	LV	D	AF	FS	SSADSTP	J7RCV7_KAZNA
AYQ	EID	SA	IV	D	AF	FS	SSTENTP	G8BZU6_TETPH
NYN	ELD	SA	VV	D	AF	FS	SSADSTP	A7TQ76_VANPO
DNN	DID	AA	VV	D	AF	FS	SSTDSTP	Q6FLL6_CANGA
TAA	DAE	SL	VA	D	HF	LA	SSADSTP	C5DLF6_LACTC
STT	ELN	AS	IV	E	TF	FD	AASSTDSTP	Q6CQU7_KLULA
SAT	ELS	AS	IV	D	NF	FD	PSSSTDSTP	W0TBM9_KLUMA
RST	DL	DS	AV	E	NF	FG	SSSDSTP	R9XE39_ASHAC
KSST	DL	DS	AV	E	NF	FG	SSSDSTP	M9N3K0_ASHG1
NTV	ELS	SH	VV	E	SF	FE	SSSDSTP	G8JU33_ERECY
GYE	DID	SA	TV	D	AF	FS	SSTDSTP	I2GUU6_TETBL
NST	ELD	AD	LV	E	TF	FS	SSVDSTP	H2B208_KAZAF
SVP	ELD	QA	VV	D	EF	FV	NDDAP	W0VM48_ZYGBA
EAP	FVH	SS	VL	D	SV	FS	SNLDEADP	G8YPT9_PICSO
SSL	AFH	SE	VL	D	SV	FS	NDEAVDHT	G3B807_CANTC
PL	QLH	SS	IV	E	SI	FS	PSLVESTP	A0A061AP43_CYBFA
PL	QLH	SS	VV	E	SI	FD	PIMENQSP	K0KP45_WICCF
PL	HVQ	SS	VL	D	SV	FS	TTLEG	A5DEW1_PICGU
PL	EIH	TS	VL	D	SV	LS	TDFTDAD	C4QY58_PICPG
PI	IVH	SE	VL	D	SV	FS	TNLDDN	C4YB11_CLAL4
PF	NIH	SS	VL	D	SV	FS	STMDEN	Q6BW79_DEBHA
PF	EIH	SS	VI	D	SI	FE	DPDAQAAP	W1QLF0_OGAPD
PF	NIH	SA	VL	D	SV	FS	NVLDEHD	A3LU14_PICST
PM	PIH	SS	VL	D	SV	FS	CTMDELEN	G3AMH4_SPAPN
PF	QIH	SS	VL	E	SV	FS	TNLDGVN	C4YKR0_CANAW
PF	EIH	SD	VL	D	SI	FS	TNLDGTN	C5M582_CANTT
PL	EIH	AS	TI	D	SV	FD	SALMPDEAP	W6MGB6_9ASCO
PF	QIH	SS	VL	E	SV	FS	TNLDGVN	Q9UV12_CANAX
PG	CLG	AE	IA	D	SF	FL	EDEQA	C5DVT1_ZYGRC
PF	QIH	SS	VL	D	SV	FS	SNMDGSN	M3K219_CANMX
PF	QIH	SS	VL	E	SG	FS	TNLDGVN	Q59YG8_CANAL
PF	QIH	SS	VL	E	SV	FS	TNLHGVN	B9WCQ8_CANDC
PF	QIH	SS	VL	E	SV	FS	TNLDGKD	H8X2T6_CANO9
PF	QIH	SS	VL	D	SV	FS	TTNLDGK	A5DYV6_LODEL

9aaTAD pattern of the Gcn4 family:
[ASTDQ] [ALSDENH] [LIVAT] [LIVA] [DE] [STEAHN] [FIVG] [FL] [SALVDEG]

Oaf1 family

	Leu	-		9aaTAD				
GG	L		DL	FD	Y	DF	LF	OAF1_YEAST
GS	L		DF	FD	Y	DL	LF	PIP2_YEAST
GG	L		DL	FD	Y	EF	LF	H2AZK4_KAZAF
DN	L		DF	LD	Y	DL	FF	H2ASY9_KAZAF
GN	L		DI	FN	Y	DF	FF	J7S6A9_KAZNA
GR	L		DL	FN	Y	DF	LF	I2H429_TETBL
GG	L		DL	FD	Y	DF	LF	G8C0X6_TETPH
AT	L		GV	LD	F	EF	LL	Q6FP27_CANGA
GG	L		DI	FD	F	LF	GN	W0VT70_ZYGBA
GG	L		NL	FD	Y	DF	LF	C5DSJ9_ZYGRC
SS	L		GV	SE	F	DL	LF	G0VJL5_NAUCC
QS	L		GI	SD	F	DG	FL	G0W5E4_NAUDC
DD	L		DL	LD	Y	EF	LF	R9XEX1_ASHAC
DI	L		DF	FD	T	FS	MN	W0TI53_KLUMA
HG	V		SV	LN	D	YF	KQ	Q6CY39_KLULA
	LA	G	VS	AD	F	DI	VF	W0TA41_KLUMA
	LA	G	LS	AN	F	DF	VF	Q6CY40_KLULA
	FL	G	DI	FD	R	LM	GT	K0KVI9_WICCF
	LN	G	DF	FN	S	AI	IE	K0KRW3_WICCF

9aaTAD pattern of the Oaf1 family:

[DNGSLV] [LIVFS] [LFSA] [DN] [YFTDRS] [DELFA] [FILMGS] [LIFVMGK] [FLNQ TE]

Pdr1 family

	Leu -	9aaTAD					
GD	L	ED	LY	S	IL	WS	PDR1_YEAST
GD	L	TD	LY	H	TL	WN	PDR3_YEAST
TT	M	DD	VY	N	YL	FD	GAL4_YEAST*
TD	M	ND	LY	N	VL	WS	G0V5I5_NAUCC
TD	L	SD	LY	N	VL	WS	G0WA57_NAUDC
AD	I	DD	LY	N	VL	WG	G0WA58_NAUDC
GD	L	ND	LY	S	TL	WS	W0VXU5_ZYGBA
GD	L	ND	LY	T	TL	WS	C5E070_ZYGRC
GD	L	NE	LY	N	SL	WG	Q1PSH2_CANGB
SD	M	TD	LC	N	IL	WS	H2AX37_KAZAF
GD	L	ND	LC	N	TL	WS	G8ZWQ0_TORDC
TD	L	ND	LY	S	VL	WN	G0V626_NAUCC
GD	L	TE	LY	H	TL	WN	J4TTH2_SACK1
GD	L	ND	LY	S	TL	WS	W0VXU5_ZYGBA
TD	M	ND	LF	K	TL	WN	H2AP04_KAZAF
AD	I	DD	LY	N	VL	WG	G0WA58_NAUDC
TD	M	ND	LY	N	VL	WS	G0V5I5_NAUCC
TD	L	ND	LY	S	VL	WN	G0V626_NAUCC
GD	L	ND	LY	T	TL	WS	C5E070_ZYGRC
SD	M	TD	LC	N	IL	WS	H2AX37_KAZAF
TD	L	ND	LY	D	QL	WS	G0V625_NAUCC
GD	L	ND	LC	N	TL	WS	G8ZWQ0_TORDC
TD	L	SD	LY	N	VL	WS	G0WA57_NAUDC
GD	L	NE	LY	N	SL	WG	Q1PSH2_CANGB

9aaTAD pattern of the Pdr1 family:

[DENST][DE]L[YCF][STHKND][ISTVQ]LW[SNG]

* Pdr1 clostes homolog Gal4 was aligned

Gal4 family

	Leu -	9aaTAD					
TT	M	DD	VY	N	YL	FD	GAL4_YEAST
TT	M	DD	VY	D	YL	FD	J8PVU2_SACAR
TT	M	DD	VY	S	YL	FD	G0VHW3_NAUCC
TT	M	DD	VY	N	FL	FD	C5E4R9_ZYGRC
TT	M	DD	IF	N	YV	FN	C5E274_LACTC
TT	M	DD	VY	N	YI	FD	LAC9_KLULA
TT	M	DD	VY	N	YI	FD	M4YCE1_KLUMA
TT	L	DD	VY	T	YL	FN	G0WFT2_NAUDC
TT	I	DD	VY	N	YL	FD	G0VEK9_NAUCC
EL	L	ND	IY	S	ML	FD	W1QGS8_OGAPD
EW	M	TD	IY	S	LF	FN	A0A060T6Y5_BLAAD
EF	V	ND	FY	S	LI	FN	K0KTZ9_WICCF
TP	Q	ED	FY	S	MM	FS	A0A061AR74_CYBFA

9aaTAD pattern of the Gal4 family:

[DENT]D[IFV][YF][STND][YMLF][MLIV]F[DNS]

p53 family

```
             Leu -    9aaTAD-I                            Leu -     9aaTAD-II
MEEPQSDPSVEPPLSQ  ET FS D LW KL  LPENNVLSPLPSQA    MD D LMLSP   DD IE Q WF TE  DPGP    P53_HUMAN
MEEPQSDPSIEPPLSQ  ET FS D LW KL  LPENNVLSPLPSQA    VD D LMLSP   DD LA Q WL TE  DPGP    P53_MACMU
MEEAQSDLSIEPPLSQ  ET FS D LW NL  LPENNVLSPVLSPP    MD D LLLSS   ED VE N WF DK  GP      P53_MARMO
MEEPHSDLSIEPPLSQ  ET FS D LW KL  LPENNVLSDSLSPP    MD H LLLSP   EE VA S WL GE  NP      P53_CAVPO
MEESQSDLSLEPPLSQ  ET FS D LW KL  LPENNLLTTSLNPP    VD D  LLSA   ED VA N WL NE  DP      P53_RABIT
MEEPQSDLSIELPLSQ  ET FS D LW KL  LPPNNVLSTLPSSDS   IE E  LFLS   EN VA G WL ED  PG      P53_MESAU
MEESQSELGVEPPLSQ  ET FS D LW KL  LPENNLLSSELSLAA   VN D   LLL   SP VT N WL DE  NP      P53_PIG
MEEPQSDLSIELPLSQ  ET FS D LW KL  LPPNNVLSTLPSSDS   IE E  LFLS   EN VT G WL ED  SG      P53_CRIGR
MEESQAELGVEPPLSQ  ET FS D LW NL  LPENNLLSSELSAP    VD D  LLPYS  ED VV T WL DE  CP      P53_SHEEP
MQEPPLELTIEPPLSQ  ET FS E LW NL  LPENNVLSSELSSA    MN E LPLS    ED VA N WL DE  AP      P53_FELCA
MEESQSELNIDPPLSQ  ET FS E LW NL  LPENNVLSSELCPA    VD E  LLLP   ES VV N WL DE  DS      P53_CANFA
MEESQAELNVEPPLSQ  ET FS D LW NL  LPENNLLSSELSAP    VD D  LLPY   TD VA T WL DE  CP      P53_BOVIN
MEESQSDISLELPLSQ  ET FS G LW KL  LPPEDILPSPHC      MD D  LLLP   QD VE E FF EG  PS      P53_MOUSE
MEDSQSDMSIELPLSQ  ET FS C LW KL  LPPDDILPTTATGSPNS ME D  LFLP   QD VA E LL EG  PE      P53_RAT
MEPSSETGMD PPLSQ  ET FE D LW SL  LPDPLQTVTCR                                           P53_XENLA
MEEADLT    LPLSQ  DT FH D LW NN  VFLSTENESLAPP                                         P53_XIPHE
MEEADLT    LPLSQ  DT FH D LW NN  VFLSTENESLPPP                                         P53_XIPMA
MADLAENVS  LPLSQ  ES FE D LW KM  NLNLVAVQPPETES                                        P53_ONCMY
MEEENIS    LPLSQ  DT FQ D LW DN  VSAPPISTIQTAAL                                        P53_TETMU
MAEEMEP     LLEPT EV FM D LW SM  LPYSMQQLPLPEDH                                        P53_CHICK
```

9aaTAD pattern of the p53 family:

p53TAD-I	**[DE][TSV]F[SEHQM][DE]LW[KNSD][LMN]**
p53TAD-II	**[DESTQ][DESNP][ILV][ETA][QNGSTE][WFL][FL][DETG][DEGK]**
p53TADs	**[DESTQ][DETSNVP][FILV][ESTAMQH][QNGSTDE][WFL][WFL][DESTGKN][DEGLMNK]**