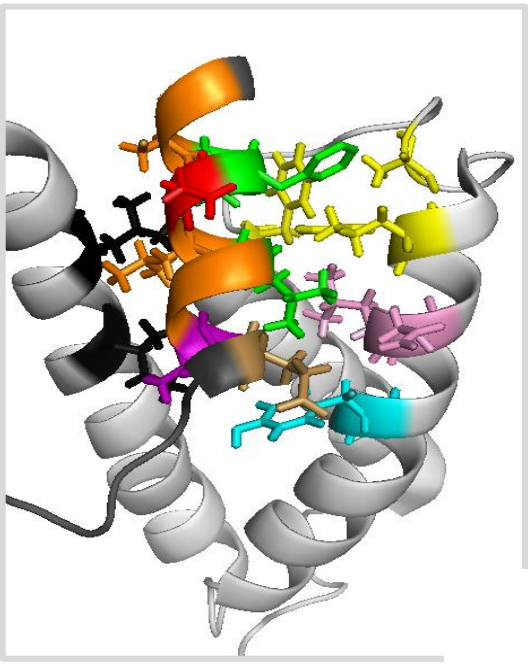
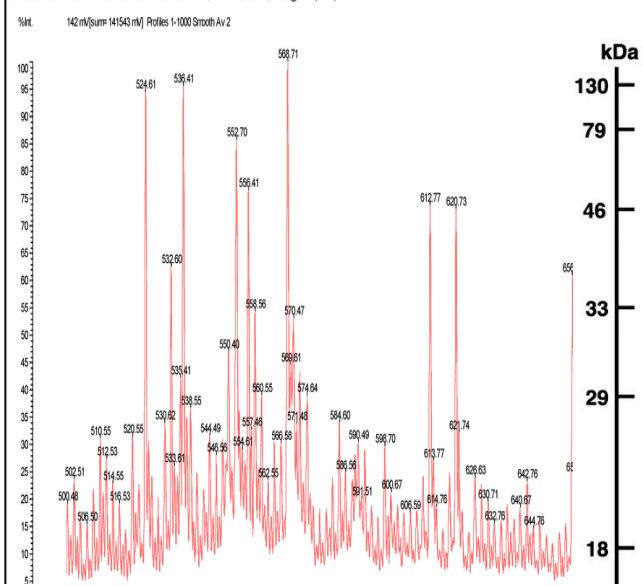
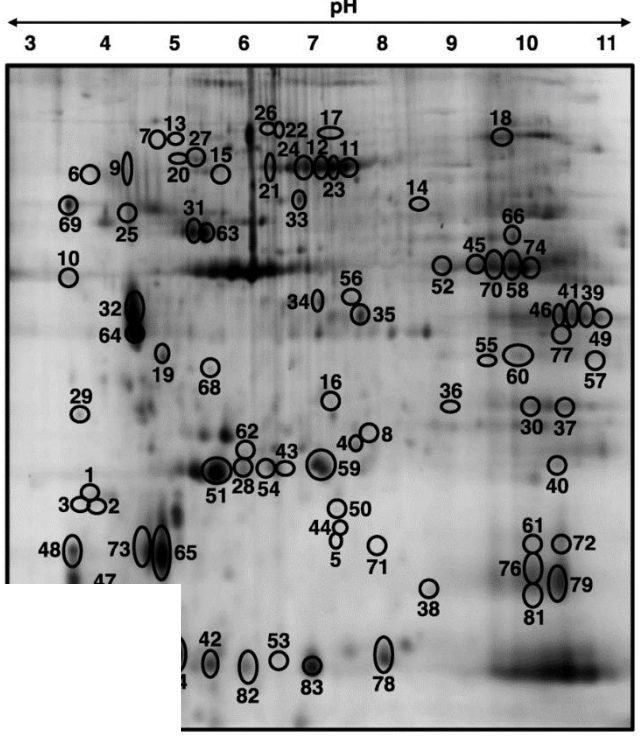
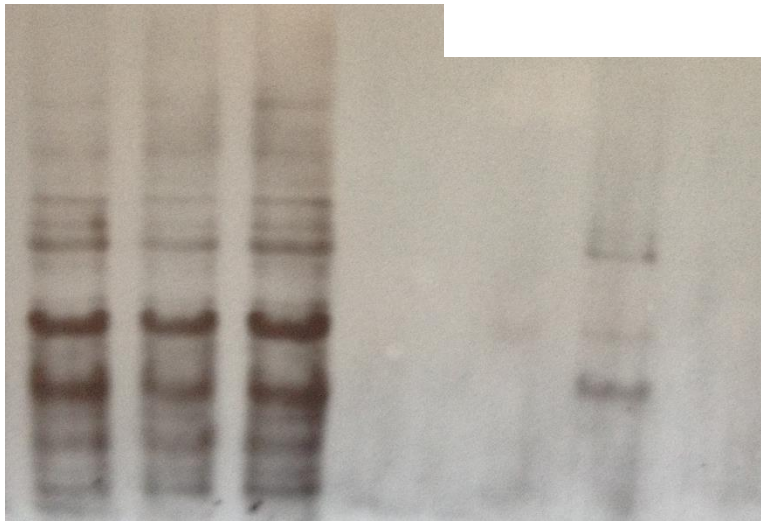
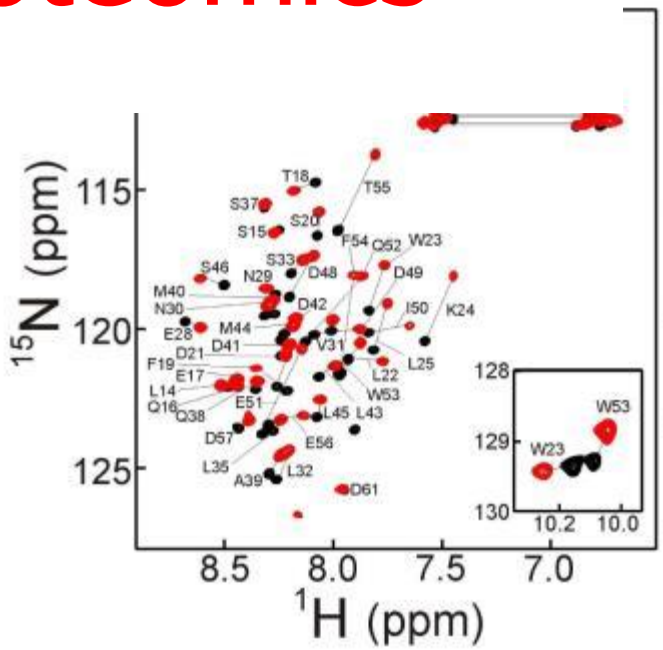


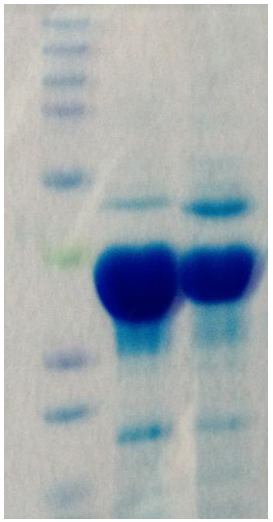

kDa
130
79
46
33
29
18


pH
3
4
5
6
7
8
9
10
11

Proteomics

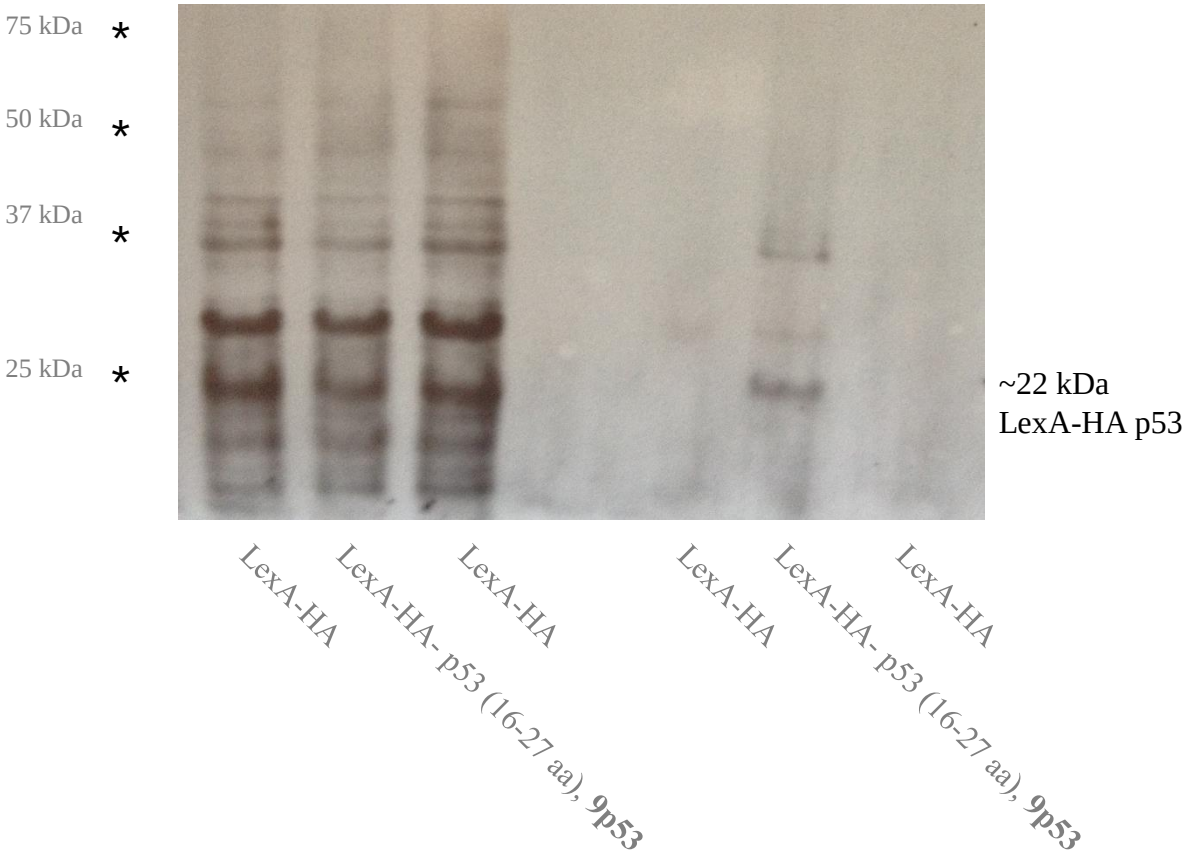



15N (ppm)
115
120
125
1H (ppm)
8.5
8.0
7.5
7.0
128
129
130
10.2
10.0
W53
W23



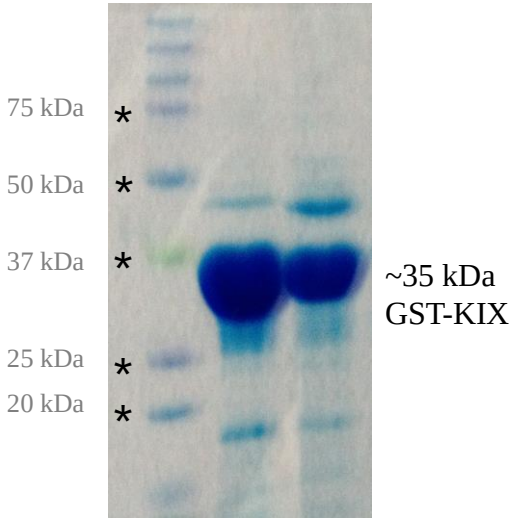
Western blotting with anti-HA antibody

Input of LexA-HA proteins Pull-down with GST-KIX

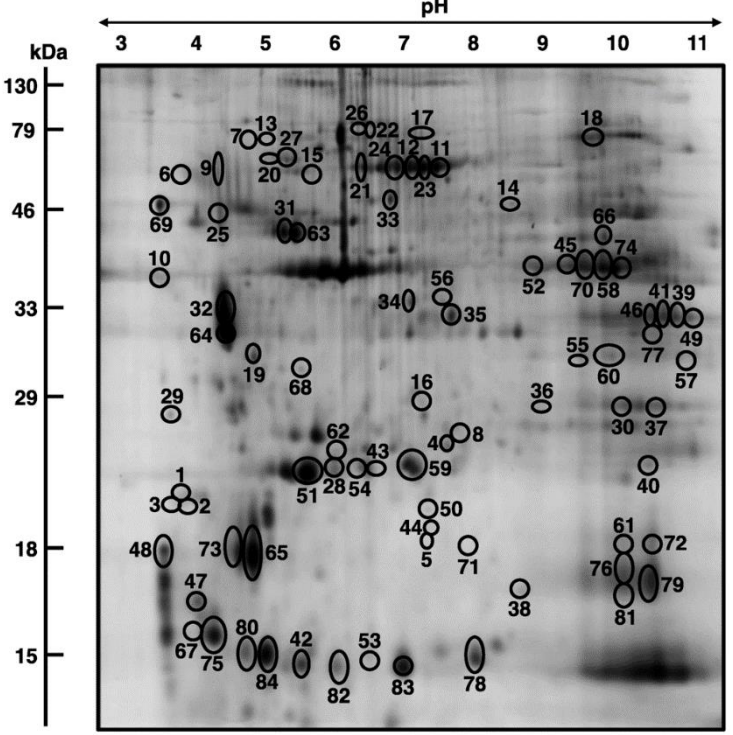


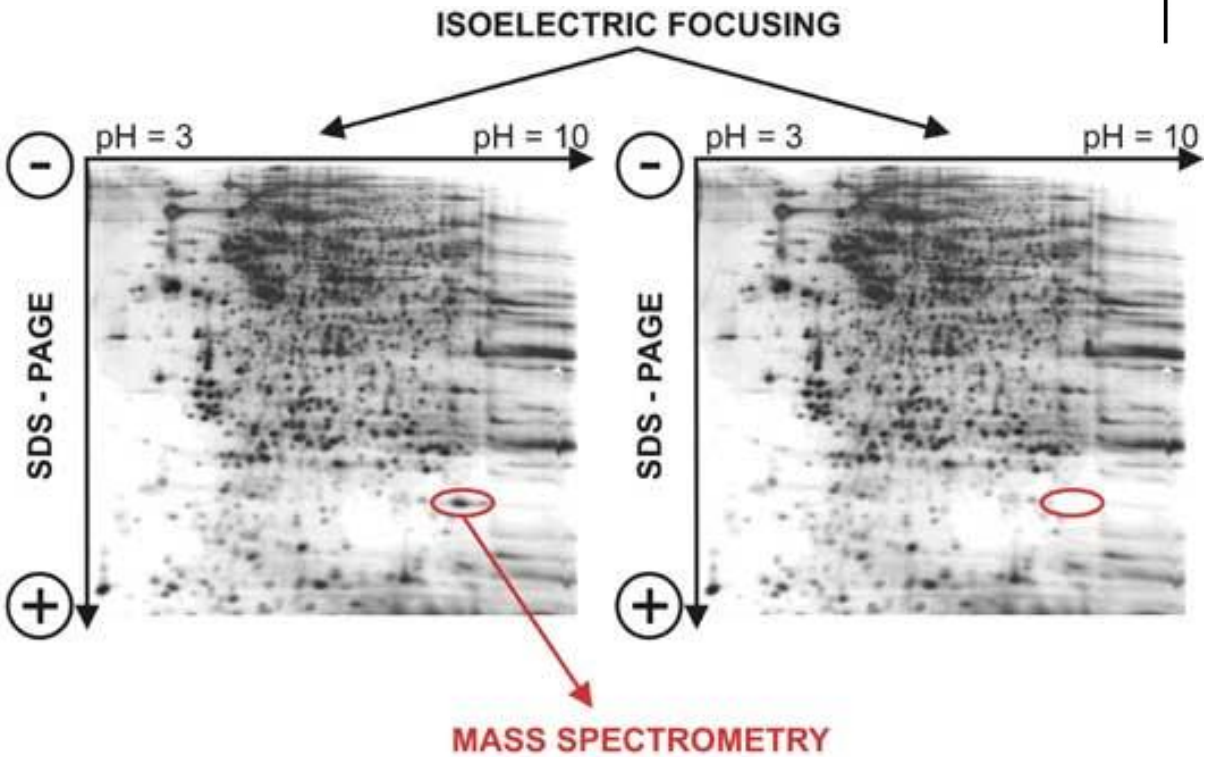
SDS-PAGE

Purified GST-KIX protein



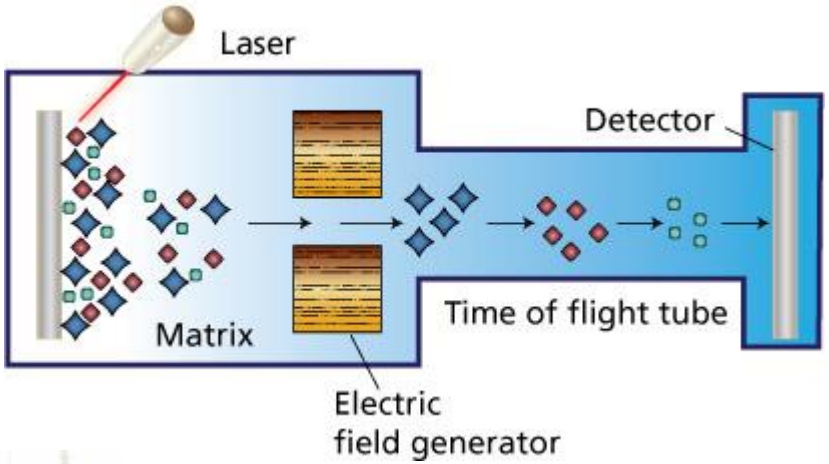
Two-dimensional gel electrophoresis

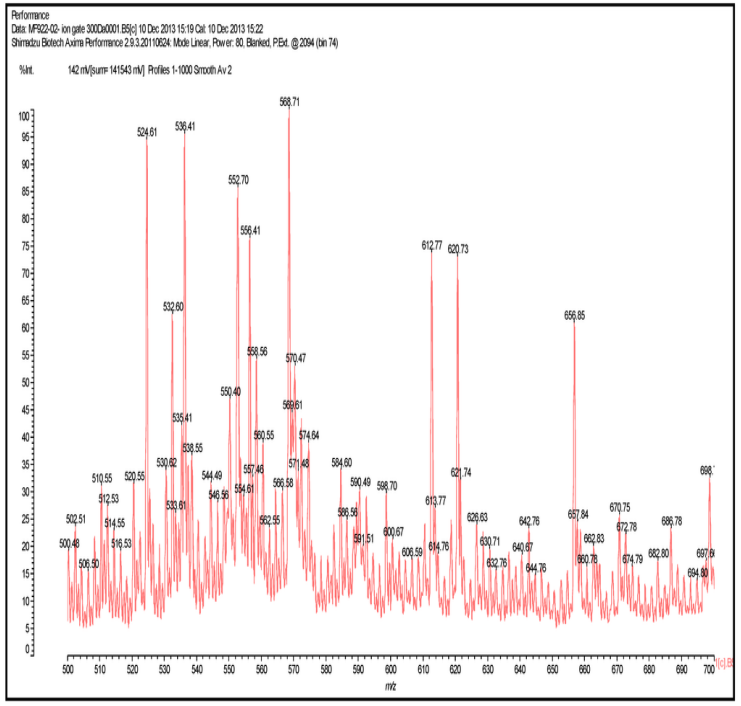




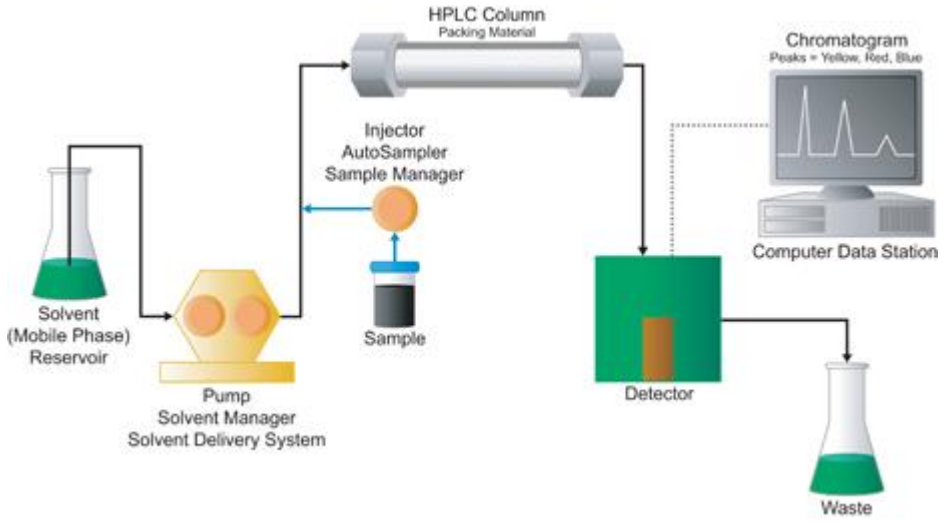
Matrix-assisted laser desorption/ionization (MALDI)

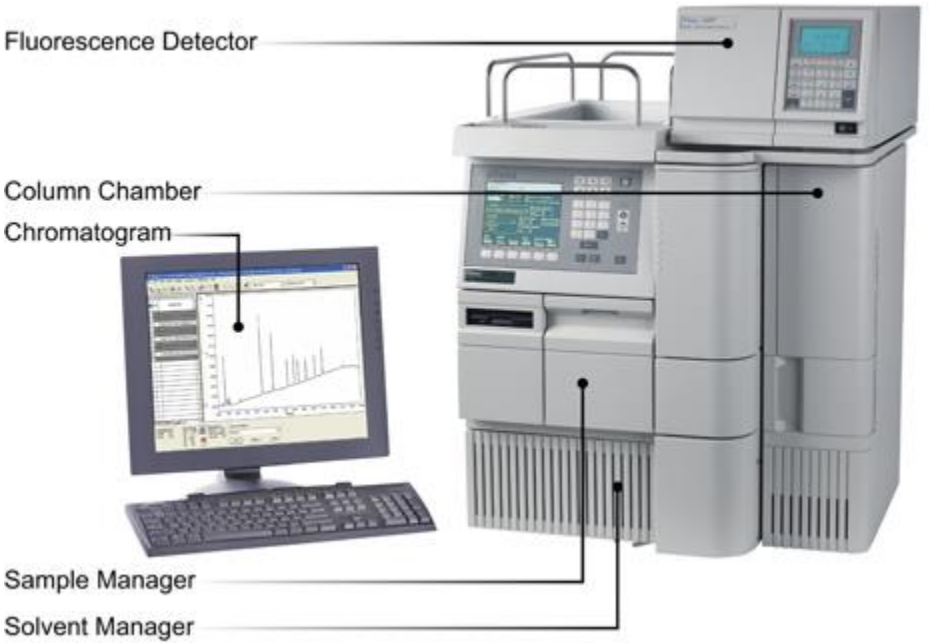
TOF (time-of-flight mass spectrometer)
ionization process, UV lasers (337 nm)
peptides, Trypsin (K/R)



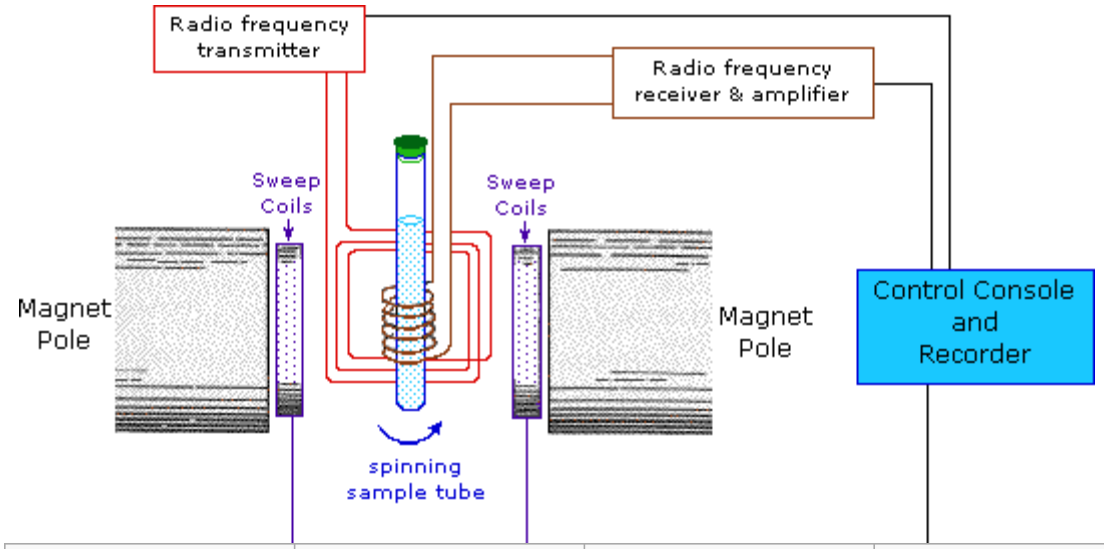


HPLC High Performance Liquid Chromatography





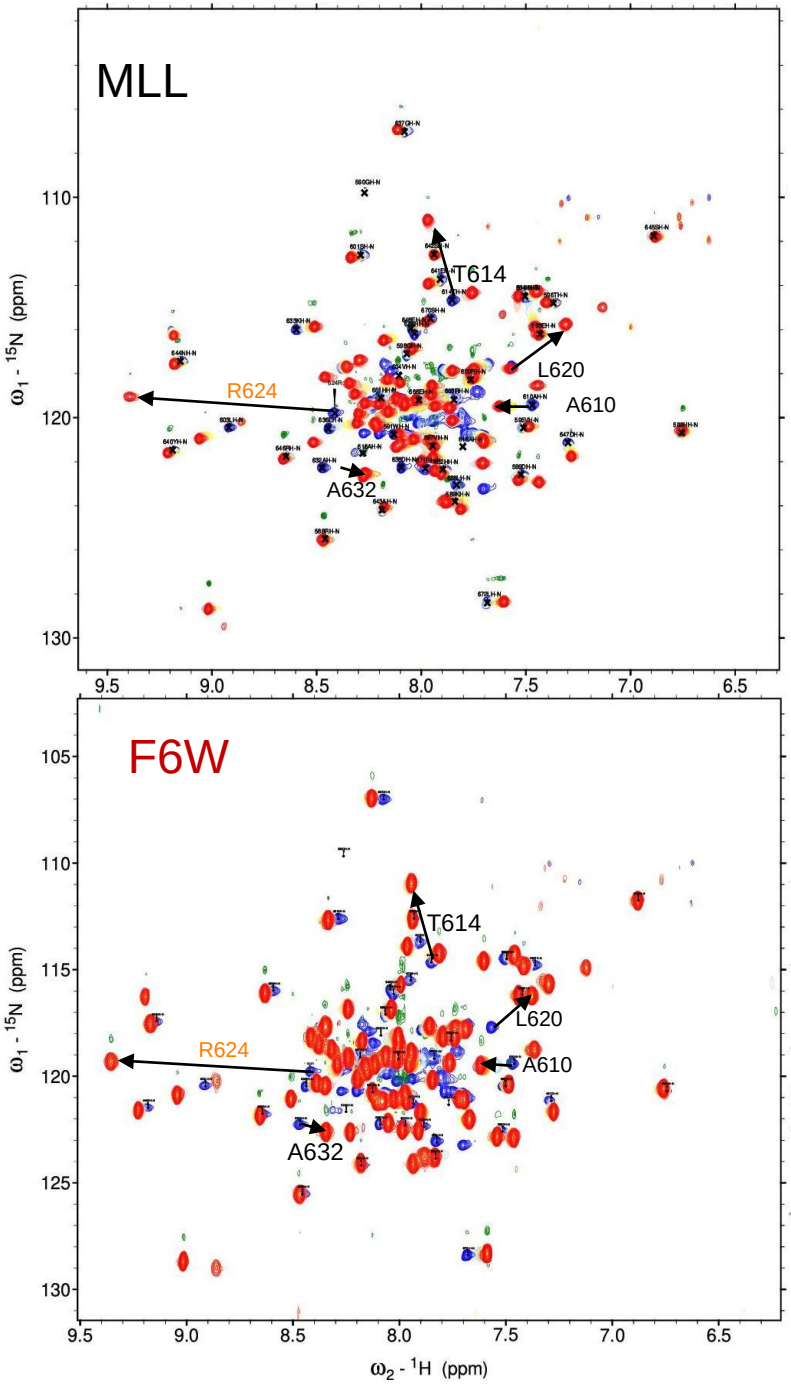
NMR Nuclear magnetic resonance

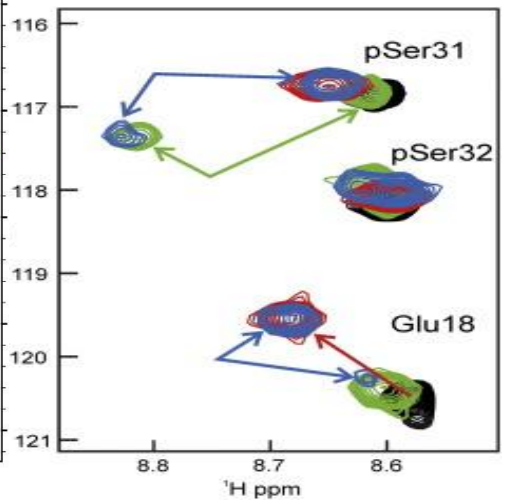


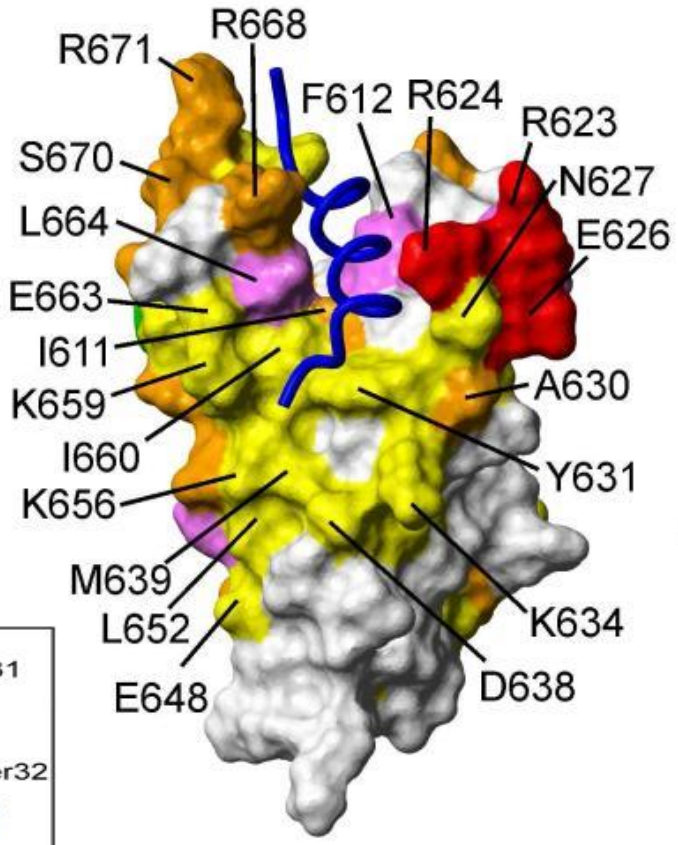
Isotope	Mag Moment (μ, nm)	Nuclear Spin	Natural Abundance (%)	Gyromagnetic Ratio	NMR Frequency at 500 MHz
^{1}H	2.79284734(3)	1/2	**~100**	267.522	-500
^{2}H	0.857438228(9)	1	0.015	41.066	-76.753
^{3}H	2.97896244(4)	1/2	0	285.349	-533.32
^{10}B	1.80064478(6)	3	19.9	28.747	-53.718
^{11}B	2.6886489	3/2	80.1	85.847	-160.42
^{13}C	0.7024118(14)	1/2	1.1	67.238	-125.725
^{14}N	0.40376100(6)	1	**99.6**	19.338	-36.132
^{15}N	-0.28318884(5)	1/2	0.37	-27.126	50.782
^{17}O	-1.89379(9)	5/2	0.04	-36.281	67.782
^{19}F	2.628868(8)	1/2	~100	251.815	-470.47
^{31}P	1.13160(3)	1/2	~100	108.394	-202.606

Chemical shift conditioned by binding

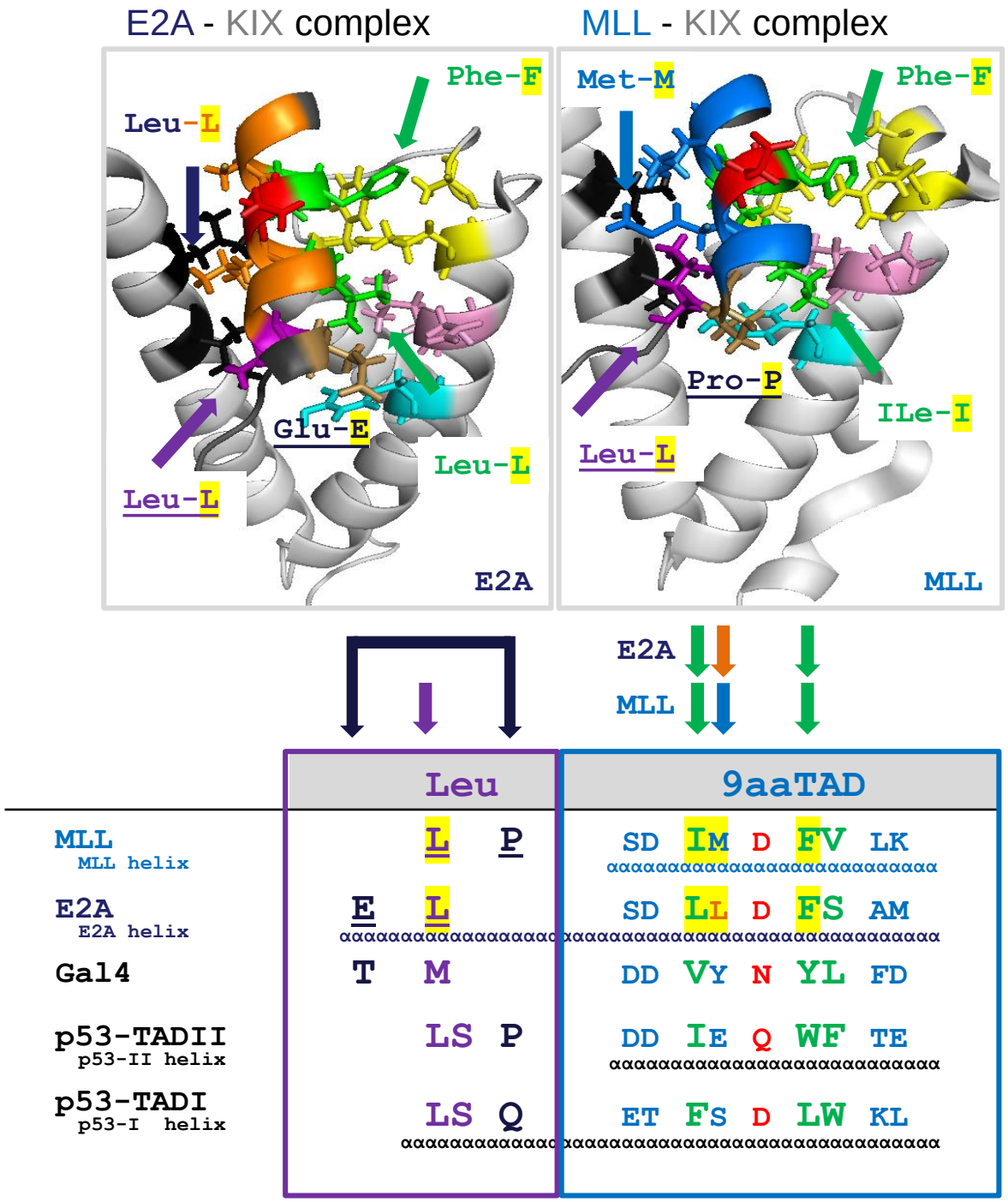
nuclear magnetic resonance MMR
spectra are recorded in solution
1H-15N HSQC spectra







Mapping the interactions of the p53 transactivation domain with the KIX domain of CBP.
Lee CW1, Arai M, Martinez-Yamout MA, Dyson HJ, Wright PE.


E2A - KIX complex
MLL - KIX complex
Phe-F
Leu-L
Glu-E
Leu-L
Leu-L
E2A
Met-M
Phe-F
Pro-P
ILe-I
Leu-L
MLL
E2A
MLL
Leu
9aaTAD
MLL
MLL helix
L P
SD IM D FV LK
E2A
E2A helix
E L
SD LL D FS AM
Gal4
T M
DD VY N YL FD
p53-TADII
p53-II helix
LS P
DD IE Q WF TE
p53-TADI
p53-I helix
LS Q
ET FS D LW KL