

Table S1: Hydrogen Bonding Interactions Extracted from the MD Simulations

Molecule Type	Residue i	Residue j	Regions	Occupancy	Comments
P38, peptide, C-tail	R70	D328	$\alpha$ C helix and L16 3/10 helix	95%	MAPK-specific salt bridge interactions
	K66	D328	$\alpha$ C helix and L16 3/10 helix	66%	C-capping interaction of L16 3/10 helix
	F99	K338	$\beta$ 4- $\beta$ 5 and L16 helix	12%	$\beta$ 4- $\beta$ 5 Insert interactions
	K139	P318	$\alpha$ E helix and L16 loop	11%	
	A144	Y323	$\alpha$ E helix and L16 loop	73%	MAPK-specific alanine (see Fig. 2)
	S143	P318	$\alpha$ E helix and L16 loop	9%	
	K76	E344	$\alpha$ C helix and L16 loop	90%	
	R173	Q325	A-loop and L16 loop	19%	
P38, no peptide, C-tail	R70	D328	$\alpha$ C helix and L16 3/10 helix	91%	MAPK-specific salt bridge interactions
	K66	D328	$\alpha$ C helix and L16 3/10 helix	76%	C-capping interaction of L16 3/10 helix
	F99	K338	$\beta$ 4- $\beta$ 5 and L16 helix	12%	$\beta$ 4- $\beta$ 5 Insert interactions

	K139	P318	$\alpha$ E helix and L16 loop	10%	
	A144	Y323	$\alpha$ E helix and L16 loop	6%	MAPK-specific alanine (see Fig. 2)
	S143	P318	$\alpha$ E helix and L16 loop	~0%	
	K76	E344	$\alpha$ C helix and L16 loop	92%	
	R173	Q325	A-loop and L16 loop	~0%	
ERK2, peptide, C-tail	R68	D334	$\alpha$ C helix and L16 3/10 helix	65%	MAPK-specific salt bridge interactions
	M96	K342	$\beta$ 4- $\beta$ 5 and L16 helix	22%	$\beta$ 4- $\beta$ 5 Insert interactions
	I93	K342	$\beta$ 4- $\beta$ 5 and L16 helix	10%	$\beta$ 4- $\beta$ 5 Insert interactions
	K71	E348	$\alpha$ C helix and L16 loop	77%	
	A141	F327	$\alpha$ E helix and L16 loop	85%	MAPK-specific alanine (see Fig. 2)
	S140	A323	$\alpha$ E helix and L16 loop	79%	
	D175	K328	A-loop and L16 loop	40%	
	H178	D335	A-loop and L16 loop	21%	

ERK2, no peptide, C-tail	R68	D330	$\alpha$ C helix and L16 3/10 helix	99%	MAPK-specific salt bridge interactions
	M96	K342	$\beta$ 4- $\beta$ 5 and L16 helix	18%	$\beta$ 4- $\beta$ 5 Insert interactions
	I93	K342	$\beta$ 4- $\beta$ 5 and L16 helix	11%	$\beta$ 4- $\beta$ 5 Insert interactions
	K71	E348	$\alpha$ C helix and L16 loop	67%	
	A141	F327	$\alpha$ E helix and L16 loop	93%	MAPK-specific alanine (see Fig. 2)
	S140	A323	$\alpha$ E helix and L16 loop	7%	
	D175	K328	A-loop and L16 loop	~0%	
	H178	D335	A-loop and L16 loop	~0%	