

Additional file 4. O-linked glycosylation and phosphorylation predicted for Chi2 and Chi3. O-glycosylation at residues that would otherwise be phosphorylated is one illustration of the complex interplay among eukaryotic post-translational modification systems (Caragea C, Sinapov J, Silvescu A, Dobbs D, Honavar V: Glycosylation site prediction using ensembles of Support Vector Machine classifiers. *BMC Bioinformatics*. 2007 Nov 9; 8:438.)

Thresholds of > 0.5 and ≥ 0.4 for potential phosphorylated and O-linked glycosylated sites, respectively.

Sites for which both types of modification were predicted are highlighted in yellow.

Bold letters: modified residue.

position in Chi2	site	score	
		phosphorylation	O-glycosylation
15	VVAMTSSVE	0.67	no
16	VAMTSSVEA	0.54	no
17	AMTSSVEAA	0.60	no
71	VHDGYAAVQ	0.85	no
93	GNNLYGNFG	0.85	no
84	GRGDSWNDQ	1.00	no
109	KARGTKFGL	0.94	no
114	KFGLSIGGW	0.79	no
121	GWTLSDKFS	0.51	no
125	SDKFSSIAS	0.55	no
126	DKFSSIAST	0.83	no
129	SSIASTETG	0.98	no
132	ASTETGRRT	0.94	no
140	TFAKSSVKL	0.73	no
141	FAKSSVKLM	0.85	no
204	LSVASPAGP	0.92	no
236	DLAGSWSK	0.57	no
240	SWSKYTDHQ	0.97	no
248	QANLYEDPN	0.94	no
294	SNGLYSNFT	0.96	no
329	ATEIYDEKL	0.76	no
342	SYDPTSKIF	0.62	no
343	YDPTSKIFT	0.98	no
347	SKIFTSYEG	0.76	no
348	KIFTSYEGP	0.98	no
361	QKLDYIKQY	0.72	no
381	ADAKSGSPR	0.76	no
383	AKSGSPRSL	0.99	no
386	GSPRSLITQ	0.77	no
414	PTSQYANIR	0.91	no
424	GAAVTSAVP	no	0.50
425	AAVTSAVPV	no	0.73
430	AVPVTSSPV	no	0.88
431	VPVTSSPVA	no	0.72
438	VAPVTTVAP	no	0.48
439	APVTTVAPV	0.69	0.75
444	VAPVTSEVP	no	0.69
445	APVTSEVPV	no	0.97
450	EVPVTSSPA	no	0.81

451	VPVTSSPAA	no	0.68
458	AAPVTTVAP	no	0.65
459	APVTTVAPV	0.69	0.81
464	VAPVTSEVP	no	0.85
465	APVTSEVPV	no	0.97
470	EVPVTSSPD	no	0.65
471	VPVTSSPDA	0.99	0.50
472	PVTSSPDAP	0.58	no
478	DAPVTTVAP	no	0.50
479	APVTTVAPV	0.69	0.75
484	VAPVTTVAP	no	0.77
485	APVTSEVPV	no	0.97
490	EVPVTSSPD	no	0.65
491	VPVTSSPDA	0.99	0.50
492	PVTSSPDAP	0.58	no
498	DAPVTTVAP	no	0.56
499	APVTTVAPV	0.69	0.80
504	VAPVTSAVH	no	0.79
505	APVTSAVHV	no	0.83
510	AVHVTCSY	no	0.68
514	TCSSYAPVT	0.66	no
518	YAPVTSSAV	no	0.45
519	APVTSSAVP	no	0.53
525	AVPETTPVE	no	0.67
526	VPETTPVEP	0.99	0.52
536	TTEATPAPT	0.92	0.76
532	VEPVTTEAT	no	0.84
533	EPVTTEATP	no	0.75
540	TPAPTGGPI	no	0.85
550	NPLETLAPT	0.55	0.67
554	TLAPTTTAA	no	0.40
556	APTTTAAAG	no	0.48

position in Chi3	site	score	
		phosphorylation	O-glycosylation
15	VVAMTSSVE	0.67	no
16	VAMTSSVEA	0.54	no
17	AMTSSVEAA	0.60	no
84	EHGDSWNDQ	1.00	no
93	GNSLYGNFG	0.86	no
109	KARGTKFGL	0.94	no
114	KFGLSIGGW	0.79	no
129	SSIASTETG	0.98	no
132	ASTETGRRT	0.94	no
140	TFAKSSVKL	0.73	no
141	FAKSSVKLM	0.85	no
204	LSVASPAGP	0.92	no
236	DLAGSWSK	0.57	no
240	SWSKYTDHQ	0.97	no
248	QANLYEDPN	0.94	no
259	PGAKYSSHN	0.76	no
268	AVQDYIKGG	0.52	no
296	SNGLYSNFT	0.96	no
332	ATEIYDEKL	0.76	no
345	SYDPTSKIF	0.62	no
346	YDPTSKIFT	0.98	no
350	SKIFTSYEG	0.76	no
351	KIFTSYEGP	0.98	no
364	QKLDYIKQY	0.72	no
384	ADAKSGSPR	0.76	no
386	AKSGSPRSL	0.99	no
389	GSPRSLITQ	0.77	no
417	PTSQYANIR	0.91	no
426	AGAVTTVAP	no	0.57
427	GAVTTVAPV	0.78	0.51
432	VAPVTSAAP	no	0.92
433	APVTSAAPV	no	0.80
438	AAPVTSAAP	no	0.93
439	APVTSAAPV	no	0.99
444	AAPVTSSTA	no	0.95
445	APVTSSTAP	no	0.93
446	PVTSSTAPG	no	0.58
447	VTSSSTAPGT	no	0.73
451	TAPGTTPAT	no	0.90
452	APGTTPATP	0.51	0.89
455	TTPATPVTT	0.68	0.88
458	ATPVTTTRAT	0.80	0.97
459	TPVTTTRATP	no	0.85
462	TTRATPAPT	0.97	0.84
466	TPAPTGGPI	no	0.90
471	GGPITNPPV	no	0.52
476	NPPVTSAPT	0.70	0.96
477	PPVTSAPTT	no	0.41
480	TSAPTTTAA	no	0.64
481	SAPTTTAAA	0.52	no
482	APTTTAAAG	no	0.58
508	TLPYSQADC	0.77	no