

9H2 Antibody Responses to EGFR Array of Overlapping phosphotyrosine Peptides Sorted by Sequence

Array Well Position #	EGFR phosphotyrosine Peptide*	9H2 Antibody ELISA	Relation to Deduced Epitope
1	empty (control)	0.068	
2	IATGMV GALLLLLVVALGIGL	0.078	
3	GALLLLLVVALGIGLFMRRRH	0.068	
4	LVVALGIGLFMRRRHIVRKRT	0.067	
5	IGLFMRRRHIVRKRTLRLQL	0.065	
6	RRHIVRKRTLRLQLQERELVE	0.068	
7	KRTLRLQLQERELVEPLTPSG	0.064	
8	LLQERELVEPLTPSGEAPNQA	0.064	
9	LVEPLTPSGEAPNQALLRILK	0.068	
10	PSGEAPNQALLRILKETEFKK	0.068	
11	NQALLRILKETEFKKIKVLGS	0.068	
12	ILKETEFKKIKVLGSGAFGTV	0.074	
13	FKKIKVLGSGAFGTVYKGLWI	0.078	
14	LGSGAFGTVYKGLWIPEGEKV	0.278	
15	GTVYKGLWIPEGEKVKIPVAI	0.169	
16	LWIPEGEKVKIPVAIKELREA	0.071	
17	EKVKIPVAIKELREATSPKAN	0.079	
18	VAIKELREATSPKANKEILDE	0.075	
19	REATSPKANKEILDEAYVMAS	0.094	
20	KANKEILDEAYVMASVDNPHV	0.099	
21	LDEAYVMASVDNPHVCRLGI	0.148	
22	MASVDNPHVCRLGICLTSTV	0.07	
23	PHVCRLGICLTSTVQLITQL	0.071	
24	LGICLTSTVQLITQLMPFGCL	0.07	
25	STVQLITQLMPFGCLLDYVRE	0.194	homologous
26	TQLMPFGCLLDYVREHKDNIG	0.627	homologous
27	GCLLDYVREHKDNIGSQYLLN	2.357	overlap
28	VREHKDNIGSQYLLNWCVQIA	2.653	partial
29	NIGSQYLLNWCVQIAKGMNYL	3.295	overlap
30	LLNWCVQIAKGMNYLEDRLV	1.639	partial
31	QIAKGMNYLEDRLVHRDLAA	1.831	partial
32	NYLEDRLVHRDLAARNVLVK	0.331	partial
33	RLVHRDLAARNVLVKTPQHVK	0.077	

34	LAARNVLVKTQPQHVKITDFGL	0.083	
35	LVKTPQHVKITDFGLAKLLGA	0.091	
36	HVKITDFGLAKLLGAEKEYH	0.121	
37	FGLAKLLGAEKEYHAEGGKV	0.139	
38	LGAEKEYHAEGGKVPIKWMA	0.089	
39	EYHAEGGKVPIKWMALESILH	0.11	
40	GKVPIKWMALESILHRIYTHQ	0.105	
41	WMALESILHRIYTHQSDVWSY	0.113	
42	ILHRIYTHQSDVWSYGVTVWE	0.133	
43	THQSDVWSYGVTVWELMTFGS	0.109	
44	WSYGVTVWELMTFGSKPYDGI	0.174	
45	VWELMTFGSKPYDGIPASEIS	0.123	
46	FGSKPYDGIPASEISSILEKG	0.088	
47	DGIPASEISSILEKGERLPQP	0.069	
48	EISSILEKGERLPQPPICTID	0.073	
49	EKGERLPQPPICTIDVYMIMV	0.112	
50	PQPPICTIDVYMIMVKCWMID	0.105	
51	TIDVYMIMVKCWMIDADSRPK	0.126	
52	IMVKCWMIDADSRPKFRELII	0.074	
53	MIDADSRPKFRELIIIEFSKMA	0.073	
54	RPKFRELIIIEFSKMARDPQRY	0.133	
55	LIIIEFSKMARDPQRYLVIQGD	2.552	partial
56	KMARDPQRYLVIQGDERMHLPL	2.974	partial
57	QRYLVIQGDERMHLPSPTDSN	3.145	partial
58	QGDERMHLPSPTDSNFYRALM	0.395	
59	HLPSPDSNFYRALMDEEDMD	0.257	
60	DSNFYRALMDEEDMDDVVDAD	0.263	
61	ALMDEEDMDDVVDADAYLIPQ	0.426	Identical
62	DMDDVVDADAYLIPQQGFSS	1.791	Identical
63	DADEYLIPQQGFSSPSTSRT	3.147	Identical
64	IPQQGFSSPSTSRTPLLSSL	0.138	
65	FSSPSTSRTPLLSSLSATSNN	0.094	
66	SRTPLLSSLSATSNNSTVACI	0.075	
67	SSLSATSNNSTVACIDRNLQ	0.07	
68	SNNSTVACIDRNLQSCPIKE	0.074	
69	ACIDRNLQSCPIKEDSFLQR	0.079	
70	GLQSCPIKEDSFLQRYSSDPT	0.133	
71	IKEDSFLQRYSSDPTGALTED	0.161	
72	LQRYSSDPTGALTEDSIDDTF	0.092	

73	DPTGALTEDSIDDTFLPVPEY	0.084	
74	TEDSIDDTFLPVPEYINQSVP	0.833	homologous
75	DTFLPVPEYINQSVPKRPAGS	2.481	homologous
76	PEYINQSVPKRPAGSVQNPVY	2.653	homologous
77	SVPKRPAGSVQNPVYHNQPLN	0.106	
78	AGSVQNPVYHNQPLNPAPSRD	0.161	
79	PVYHNQPLNPAPSRDPHYQDP	0.175	
80	PLNPAPSRDPHYQDPHSTAVG	0.096	
81	SRDPHYQDPHSTAVGNPEYLN	3.236	overlap
82	QDPHSTAVGNPEYLNTVQPTC	3.609	Identical
83	AVGNPEYLNTVQPTCVNSTFD	3.585	Identical
84	YLNTVQPTCVNSTFDSPAHPWA	3.475	Identical
85	PTCVNSTFDSPAHPWAQKGS HQ	0.077	
86	TFDSPAHPWAQKGS HQISLDNP	0.072	
87	HWAQKGS HQISLDNPDYQQDF	0.08	
88	SHQISLDNPDYQQDFFPKEAK	0.102	
89	DNPDYQQDFFPKEAKPNGIFK	0.184	
90	QDFFPKEAKPNGIFKGS TAEN	0.12	
91	EAKPNGIFKGS TAENAEYLRV	3.599	Identical
92	IFKGS TAENAEYLRVAPQSSE	4	Identical
93	AENAEYLRVAPQSSEFIGA	3.35	Identical
94	empty (control)	0.075	
95	empty (control)	0.073	
96	empty (control)	0.072	

*EGFR residues 646-1210, Length=21, Offset=6.