

Legend to protein chain colorations for animated signal transduction proteins shown in rotating 3D ribbon, stick and ball x-ray crystallographic structures.

PDB Number	Full Names of Protein	URL for structure	Species Represented	Chain data	Chain colours	Reference
1B39	Cyclin-dependent kinase 2 (CDK2) with Thr-160 phosphorylation site - ball model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=1B39	<i>Homo sapien</i>	CDK2 (human) - Chain A.	A=pink; T160 phos. site=blue; ATP=white.	Brown, N.R., Noble, M.E., Lawrie, A.M., Morris, M.C., Tunnah, P., Divita, G., Johnson, L.N., Endicott, J.A. Effects of phosphorylation of threonine 160 on cyclin-dependent kinase 2 structure and activity. <i>J.Biol.Chem.</i> v274 pp.8746-8756 (1999).
1D5R	PTEN phosphoinositide phosphatase - ribbon model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=1D5R	<i>Homo sapien</i>	PTEN catalytic fragment (residues 7-353) Human) - Chain A.	A=yellow	Lee, J.O., Yang, H., Georgescu, M.M., Di Cristofano, A., Maehama, T., Shi, Y., Dixon, J.E., Pandolfi, P., Pavletich, N.P. Crystal structure of the PTEN tumor suppressor: implications for its phosphoinositide phosphatase activity and membrane association. <i>Cell</i> v99 pp.323-334 (1999).
1DM2	CDK2 complexed marine sponge inhibitor hymenialdisine - ball model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=1DM2	<i>Homo sapien</i>	CDK2 (human) - Chain A.	A=pink; inhibitor=white.	Meijer, L., Thunnissen, A.M., White, A.W., Garnier, M., Nikolic, M., Tsai, L.H., Walter, J., Cleverley, K.E., Salinas, P.C., Wu, Y.Z., Biernat, J., Mandelkow, E.M., Kim, S.H., Pettit, G.R. Inhibition of cyclin-dependent kinases, GSK-3beta and CK1 by hymenialdisine, a marine sponge constituent. <i>Chem.Biol.</i> v7 pp.51-63 (2000).
1E0A	Cdc42 complexed with the GTPase binding domain of p21-activated kinase-alpha (PAK α) - stick model	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbId=1E0A	<i>Homo sapien</i>	Cdc42 (G25K) GTP-binding protein, placental isoform fragment (residues 1-184) (human) - Chain A. PAK1 protein-serine/threonine kinase fragment (residues 75-118) (human) - Chain B. 5' guanosyl-imidate triphosphate in complex.	A=dark green; B=light green; GTP=white.	Morreale, A., Venkatesan, M., Mott, H. R., Owen, D., Nieltispach, D., Lowe, P. N., Laue, E. D.: Solution Structure of Cdc42 Bound to the Gtpase Binding Domain of Pak <i>Nat.Struct.Biol.</i> 7 pp. 384 (2000).
1E8Z	Phosphatidylinositol 3-kinase gamma (PI3K γ) p110 catalytic subunit bound with inhibitor staurosporin - ribbon	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=1E8Z	<i>Homo sapien</i>	PI3K p110 catalytic subunit (human) - Chain A. Staurosporin - Inhibitor,	A=pink; Inhibitor=white.	Walker, E.H., Pacold, M.E., Perisic, O., Stephens, L., Hawkins, P.T., Wymann, M.P., Williams, R.L. Structural determinants of phosphoinositide 3-kinase inhibition by wortmannin, LY294002, quercetin, myricetin, and staurosporine. <i>Mol.Cell</i> v6 pp.909-919 (2000).
1EBA	Erythropoietin (Epo) receptor extracellular domain bound to Epo - ball model	http://www.pdb.org/pdb/explore/expl ore.do?structureId=1EBA	<i>Homo sapien</i>	Epo receptor (human) - Chains A, B. Epo (human) - Chains C, D.	A=green; B=purple; C=yellow; D=white.	Livnah, O., Johnson, D.L., Stura, E.A., Farrell, F.X., Barbone, F.P., You, Y., Liu, K.D., Goldsmith, M.A., He, W., Krause, C.D., Pestka, S., Jolliffe, L.K., Wilson, I.A. An antagonist peptide-EPO receptor complex suggests that receptor dimerization is not sufficient for activation. <i>Nat.Struct.Biol.</i> v5 pp.993-1004 (1998).

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1F3M	p21-activated kinase-alpha (PAKa) autoregulatory domain complexed with its catalytic domain - ball and ribbon model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=1F3M	<i>Homo sapien</i>	PAKalpha autoregulatory domain (residues 70-149) (human) - Chaiins A, B. PAKalpha catalytic domain fragment (residues 249-545) (human) - Chaiins C, D.	A=yellow; B=pink; C=purple; D=green.	Lei, M., Lu, W., Meng, W., Parrini, M.C., Eck, M.J., Mayer, B.J., Harrison, S.C. Structure of PAK1 in an autoinhibited conformation reveals a multistage activation switch. <i>Cell</i> v102 pp.387-397 (2000).
1FAO	Pleckstrin homology domain from dual adaptor of phosphotyrosine and 3-phosphoinositides (DAPP1/PHISH) complexed with inositol 1,3,4,5-tetraphosphate - ball model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=1FAO	<i>Homo sapien</i>	Pleckstrin homology domain from DAPP1/PHISH (human) - Chain A. Inositol 1,3,4,5-tetraphosphate (IP4).	A=purple; IP4=white.	Ferguson, K.M., Kavran, J.M., Sankaran, V.G., Fournier, E., Isakoff, S.J., Skolnik, E.Y., Lemmon, M.A. Structural basis for discrimination of 3-phosphoinositides by pleckstrin homology domains. <i>Mol.Cell</i> v6 pp.373-384 (2000).
1FMK	Src protein-tyrosine kinase with SH2, SH3, catalytic domain and C-terminus - wire model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=1FMK	<i>Homo sapien</i>	Src fragment (residues 86-836) (human) containing: catalytic domain - Region A (conserved kinase residues are shown in purple); SH2 domain - Region B; and SH3 domain -Region C.	A=blue; B=red; C=green,	Xu, W., Harrison, S.C., Eck, M.J. Three-dimensional structure of the tyrosine kinase c-Src. <i>Nature</i> v385 pp.595-602 (1997).
1FMK	Src protein-tyrosine kinase - ribbon model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=1FMK	<i>Homo sapien</i>	Src fragment (residues 86-836) (human) - Chain A.	A=pink.	Xu, W., Harrison, S.C., Eck, M.J. Three-dimensional structure of the tyrosine kinase c-Src. <i>Nature</i> v385 pp.595-602 (1997).
1FYN	Fyn protein-tyrosine kinase SH3 domain with proline-containing polypeptide from 3BP-2 - ball model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=1FYN	<i>Homo sapien</i>	Fyn protein-tyrosine kinase SH3 domain (human) - Chain A. Proline-containing peptide (PPAYPPPPVP) from 3BP-2 (human) - Chain B.	A=purple; B=yellow.	Musacchio, A., Saraste, M., Wilmanns, M. High-resolution crystal structures of tyrosine kinase SH3 domains complexed with proline-rich peptides. <i>Nat.Struct.Biol.</i> v1 pp.546-551 (1994).
1GRI	Growth factor bound protein 2 (Grb2) - ribbon model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=1GRI	<i>Homo sapien</i>	Grb2 (human) - non-SH2 - Region A. SH2 domains - Regions B, C.	A=purple; B,C=green.	Maignan, S., Guilloteau, J.P., Fromage, N., Arnoux, B., Becquart, J., Ducruix, A. Crystal structure of the mammalian Grb2 adaptor. <i>Science</i> v268 pp.291-293 (1995).
1IAN	p38 MAPK alpha- ball model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=1IAN	<i>Homo sapien</i>	p38 (human) - Chain A. 4-[5-(3-iodo-phenyl)-2-(4-methanesulfinyl-phenyl)-1H-imidazol-4-yl]-pyridine - Inhibitor.	A=pink; Inhibitor=yellow.	Tong, L., Pav, S., White, D.M., Rogers, S., Crane, K.M., Cywin, C.L., Brown, M.L., Pargellis, C.A. A highly specific inhibitor of human p38 MAP kinase binds in the ATP pocket. <i>Nat.Struct.Biol.</i> v4 pp.311-316 (1997).
1IR3	Insulin receptor-tyrosine kinase catalytic domain with peptide substrate - stick model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=1IR3	<i>Homo sapien</i>	Insulin receptor kinase catalytic domain - (human) Chain A. Peptide substrate - Chain B.	A=pink; B=yellow; ATP analog=white.	Hubbard, S.R. Crystal structure of the activated insulin receptor tyrosine kinase in complex with peptide substrate and ATP analog. <i>EMBO J.</i> v16 pp.5572-5581 (1997).
1MCO	Immunoglobulin - ball model	http://www.rcsb.org/pdb/explore.do?s tructureId=1MCO	<i>Homo sapien</i>	IgG - Chains A,B,C,D.	A,B,C,D=blue.	Guddat, L.W., Herron, J.N., Edmundson, A.B. Three-Dimensional Structure of a Human Immunoglobulin with a Hinge Deletion. <i>Proteins.Struct.,Funct., Genet.</i> v16 pp.246 (1993).

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1NTS	DNA double helix - stick model	http://www.rcsb.org/pdb/static.do?p=explorer/viewers/jmol.jsp?structureId=1NTS	Synthetic construct	DNA - Chains A,B.	Multi-coloured.	Znosko, B.M., Barnes III, T.W., Krugh, T.R., Turner, D.H. NMR Studies of DNA Single Strands and DNA:RNA Hybrids With and Without 1-Propynylation at C5 of Oligopyrimidines J.Am.Chem.Soc. v125 pp.6090-6097 (2003).
1PTU	Protein-tyrosine phosphatase 1B complexed with a phosphotyrosine-containing hexapeptide - stick model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=1PTU	<i>Homo sapien</i>	Protein-tyrosine phosphatase 1B (human) - Chain A. Phosphorylated hexapeptide substrate - Chain B (phosphorylated tyrosine is light blue).	A=purple; B=yellow.	Jia, Z., Barford, D., Flint, A.J., Tonks, N.K. Structural basis for phosphotyrosine peptide recognition by protein tyrosine phosphatase 1B. Science v268 pp.1754-1758 (1995).
1QB0	Cdc25B dual specificity phosphatase - ribbon model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=1QB0	<i>Homo sapien</i>	Cdc25B (human) - Chain A.	A=yellow.	Reynolds, R.A., Yem, A.W., Wolfe, C.L., Deibel Jr., M.R., Chidester, C.G., Watenpugh, K.D. Crystal structure of the catalytic subunit of Cdc25B required for G2/M phase transition of the cell cycle. J.Mol.Biol. v293 pp.559-568 (1999).
1QB3	Cyclin-dependent kinase regulatory subunit (Cks1) - ball model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=1QB3	<i>Saccharomyc es cerevisiae</i>	Cks1 (budding yeast) - Chains A, B, C.	A=pink; B=purple; C=green.	Bourne, Y., Watson, M.H., Arvai, A.S., Bernstein, S.L., Reed, S.I., Tainer, J.A. Crystal structure and mutational analysis of the <i>Saccharomyces cerevisiae</i> cell cycle regulatory protein Cks1: implications for domain swapping, anion binding and protein interactions. Structure Fold.Des. v8 pp.841-850, (2000).
1QJA	14-3-3 zeta dimer complexed with Raf1 phosphorylated serine-containing peptide - stick and ball model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=1QJA	<i>Homo sapien</i>	14-3-3 zeta (human) - Chains A,B. Phosphorylated serine -containing peptide - Chains C,D (phosphorylated serine is light blue).	A=purple; B=green; C,D=yellow.	Rittinger, K., Budman, J., Xu, J., Volinia, S., Cantley, L.C., Smerdon, S.J., Gambin, S.J., Yaffe, M.B. Structural analysis of 14-3-3 phosphopeptide complexes identifies a dual role for the nuclear export signal of 14-3-3 in ligand binding. Mol.Cell v4 pp.153-166 (1999).
1QMZ	Cyclin-dependent kinase 2 (CDK2) complexed with cyclin A - ribbon and ball model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=1QMZ	<i>Homo sapien</i>	CDK2 - (human) Chains A,B. Cyclin A fragment (residues 174-432) (human). Chains C, D. Substrate heptapeptide - Chains E, F.	A, B=pink; C, D=purple; E, F=yellow; ATP=white.	Brown, N.R., Noble, M.E., Endicott, J.A., Johnson, L.N. The Structural Basis for Specificity of Substrate and Recruitment Peptides for Cyclin-Dependent Kinases Nat. Cell Biol. v1 pp.438 (1999).
1RVD	H-Ras small G protein G12V constitutively active mutant - ribbon model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=1RVD	<i>Homo sapien</i>	H-Ras (residues 1-166) (human) - Chain A.	A=green; GTP=white	Ahmadian, M.R., Zor, T., Vogt, D., Kabsch, W., Selinger, Z., Wittinghofer, A., Scheffzek, K. Guanosine triphosphatase stimulation of oncogenic Ras mutants. Proc.Natl.Acad.Sci.USA v96 pp.7065-7070 (1999).
1WQ1	Ras complexed with Ras-GTPase activating protein (GAP) - ribbon model	http://www.rcsb.org/pdb/cgi/explore.c gi?job=graphics&pdbId=1WQ1	<i>Homo sapien</i>	H-Ras catalytic domain fragment (residues 1-166) (human) - Chain A. p120 GAP catalytic domain fragment (residues 714-1047) (human) - Chain B.	A=green; B=purple; GTP=white.	Scheffzek, K., Ahmadian, M. R., Kabsch, W., Wiesmuller, L., Lautwein, A., Schmitz, F., Wittinghofer, A.: The Ras-RasGAP complex: structural basis for GTPase activation and its loss in oncogenic Ras mutants. Science 277 pp. 333 (1997).

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1ZEH	Insulin - ball model	http://www.rcsb.org/pdb/explore.do?structureId=1ZEH	<i>Homo sapien</i>	Insulin (human) - Chains A,B.	A,B=green.	Whittingham, J.L., Edwards, D.J., Antson, A.A., Clarkson, J.M., Dodson, G.G. Interactions of phenol and m-cresol in the insulin hexamer, and their effect on the association properties of B28 pro --> Asp insulin analogues. <i>Biochemistry</i> v37 pp.11516-11523 (1998).
2CSN	Casein kinase 1 (CK1) catalytic subunit - ribbon model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=2CSN	<i>Schizosaccha romyces pombe</i>	CK1 catalytic subunit fragment (residues 2-298) (fission yeast) - Chain A.	A=pink; ATP=white.	Xu, R.M., Carmel, G., Kuret, J., Cheng, X. Structural basis for selectivity of the isoquinoline sulfonamide family of protein kinase inhibitors. <i>Proc.Natl.Acad.Sci.USA</i> v93 pp.6308-6313 (1996).
2HNP	Protein-tyrosine phosphatase 1B ribbon model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=2HNP	<i>Homo sapien</i>	Protein-tyrosine phosphatase 1B (human) - Chain A	A=yellow.	Barford, D., Flint, A.J., Tonks, N.K. Crystal structure of human protein tyrosine phosphatase 1B. <i>Science</i> v263 pp.1397-1404 (1994).
4ERK	Extracellular-regulated kinase 2 (ERK2) complexed with drug-ribbon model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=4ERK	<i>Rattus norvegicus</i>	ERK2 (rat) -Chain A. Olomoucine - Inhibitor.	A=pink; Inhibitor=white.	Wang, Z., Canagarajah, B.J., Boehm, J.C., Kassisa, S., Cobb, M.H., Young, P.R., Abdel-Meguid, S., Adams, J.L., Goldsmith, E.J. Structural basis of inhibitor selectivity in MAP kinases. <i>Structure</i> v6 pp.1117-1128 (1998).
4Q21	H-Ras small G protein - inactive form bound to GDP - ribbon model	http://www.rcsb.org/pdb/explore/expl ore.do?structureId=4Q21	<i>Homo sapien</i>	H-Ras (human) - Chain A.	A=green; GDP=white.	Milburn, M.V., Tong, L., deVos, A.M., Brunger, A., Yamaizumi, Z., Nishimura, S., Kim, S.H. Molecular switch for signal transduction: structural differences between active and inactive forms of protooncogenic ras proteins. <i>Science</i> v247 pp.939-945 (1990).