

Legend to protein chain colorations for animated signal transduction proteins shown in rotating 3D space filling x-ray crystallographic structures.

PDB Number	Full Names of Protein	URL for structure	Species Represented	Chain data	Chain colours	Reference
1A02	Nfat, Fos and Jun DNA-binding domains bound to DNA	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbl=1A02	<i>Homo sapien</i>	Nfat - fragment DNA binding domain (human) - Chain A; c-Fos - Chain B; c-Jun (C279S mutant) - Chain C; DNA - Chains A, B.	A=red; B=orange; C=yellow; D=DNA backbone=purple and nucleotides=blue. E=DNA backbone=purple and nucleotides=blue.	Chen, L., Glover, J. N., Hogan, P. G., Rao, A., Harrison, S. C.: Structure of the DNA-binding domains from NFAT, Fos and Jun bound specifically to DNA. <i>Nature</i> 392 pp. 42 (1998).
1A0N	Fyn tyrosine kinase SH3 domain complexed with a synthetic peptide P2L corresponding to residues 91-104 of the p85 subunit of phosphatidylinositol 3-kinase	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbl=1A0N&page=0&pid=126561076874485	<i>Homo sapien</i>	PI3K p85 subunit fragment (residues 91-104; PPRPLPVAPGSSLT) (human) - Chain A. Fyn SH3 domain fragment (residues 82 - 148) (human) - Chain B.	A=ice blue; B=pink.	Rossi, C., Waterfield, M. D., Campbell, I. D., Ladbury, J. E.: Structural and thermodynamic characterization of the interaction of the SH3 domain from Fyn with the proline-rich binding site on the p85 subunit of PI3-kinase. <i>Biochemistry</i> 35 pp. 15646 (1996).
1A37	14-3-3 bound to Raf kinase Ser-259 phosphorylation site containing peptide	http://www.rcsb.org/pdb/cgi/explore.cgi?job=summary&pdbl=1A37&page=0&pid=46051076782848	<i>Bos taurus</i>	14-3-3 (bovine) - Chains A, B. Phosphoserine-containing peptide derived from Raf1 (KSQRQRSTpSTPNVHM) - Chains C,D.	A=blue; B=ice blue; C, D=pink.	Liu, D., Bienkowska, J., Petosa, C., Collier, R. J., Fu, H., Liddington, R.: Crystal structure of the zeta isoform of the 14-3-3 protein. <i>Nature</i> 376 pp. 191 (1995).
1A6Q	Protein-serine/threonine phosphatase 2C (PP2C)	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbl=1A6Q&page=0&pid=247511076886214	<i>Homo sapien</i>	Protein-serine phosphatase 2C (human) - Chain A.	A=lime.	Das, A. K., Helps, N. R., Cohen, P. T., Barford, D.: Crystal structure of the protein serine/threonine phosphatase 2C at 2.0 Å resolution. <i>EMBO J</i> 15 pp. 6798 (1996).
1APM	cAMP-dependent protein kinase (PKA) catalytic subunit complexed with inhibitor portion of PKI inhibitor	http://www.rcsb.org/pdb/cgi/explore.cgi?job=summary&pdbl=1APM&page=20&pid=208161076787315	<i>Mus musculus</i>	PKA catalytic subunit (mouse) isoenzyme mutant with Ser 139 replaced by Ala (S139A) - Chain A. 1APM:1 - the peptide inhibitor PKI (5-24; TTYADFIASGRTGRRNAIHD) - Chain B.	A=pink1; B=yellow.	Knighton, D. R., Bell, S. M., Zheng, J. H., Teneyck, L. F., Xuong, N. H., Taylor, S. S., Sowadski, J. M.: 2.0 Ångstrom refined crystal structure of the catalytic subunit of cAMP-dependent protein kinase complexed with a peptide inhibitor and detergent. <i>Acta Crystallogr D Biol Crystallogr</i> 49 pp. 357 (1993).
1AXC	Proliferating cell nuclear antigen (PCNA) binding to p21 WAF CDK inhibitor	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbl=1AXC&page=40&pid=208161076787315	<i>Homo sapien</i>	PCNA (human) - Chains A, C, E. p21/Waf1 fragment: 22 C terminal (residues 139 - 160; GRKRRQTSMTDFYHSKRRLIF) - Chains B, D, F.	A=orange; B=yellow; C=red; D=yellow; E=ochre; F=yellow.	Gulbis, J. M., Kelman, Z., Hurwitz, J., O'Donnell, M., Kuriyan, J.: Structure of the C-terminal region of p21(WAF1/CIP1) complexed with human PCNA. <i>Cell</i> 87 pp. 297 (1996).
1B17	Insulin A and B chains in a complex	http://www.pdb.org/pdb/explore/explore.do?structureid=1B17	<i>Sus scrofa</i>	Insulin A chain (pig) - Chain A. Insulin B chain (pig) - Chain B.	A=yellow; B=purple.	Diao, J.S. Crystallographic titration of cubic insulin crystals: pH affects GluB13 switching and sulfate binding <i>Acta Crystallogr., Sect.D</i> v59 pp.670-76 (2003).
1BUH	Cyclin-dependent kinase 2 (CDK2) complex with cell cycle-regulatory protein CksHs1	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbl=1BUH&page=100&pid=208161076787315	<i>Homo sapien</i>	CDK2 (human) - Chain A. CksHs1 Human - Chain B.	A=pink; B=ice blue.	Bourne, Y., Watson, M. H., Hickey, M. J., Holmes, W., Rocque, W., Reed, S. I., Tainer, J. A.: Crystal structure and mutational analysis of the human CDK2 kinase complex with cell cycle-regulatory protein CksHs1. <i>Cell</i> 84 pp. 863 (1996).

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1CS4	Adenylate Cyclase C1A and C2A domains complexed with Gs alpha subunit	http://www.pdb.org/pdb/explore/explore.do?structureid=1CS4	<i>Canine familiaris, Rattus norvegicus, Bos taurus</i>	Adenylate cyclase C1A domain (dog) - Chain A. Adenylate cyclase C2A domain (rat) - Chain B. Gs-alpha (cow)- Chain C.	A=yellow; B=tan; C=teal ; ATP=grey.	Tesmer, J.J., Dessauer, C.W., Sunahara, R.K., Murray, L.D., Johnson, R.A., Gilman, A.G., Sprang, S.R. Molecular basis for P-site inhibition of adenylyl cyclase. <i>Biochemistry</i> v39 pp.14464-14471 (2000).
1CVS	Fibroblast growth factor 2 (FGF2) dimer - fibroblast growth factor receptor1 (FGFR1) complex	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbld=1CVS&page=140&pid=208161076787315	<i>Homo sapien</i>	Fibroblast Growth Factor 2; - Chains A, B. Fibroblast Growth Factor Receptor 1 fragment with Ig-like domains 2 and 3 (human) - Chains C, D.	A, B=ice blue; C=pink; D=dark pink.	Plotnikov, A. N., Schlessinger, J., Hubbard, S. R., Mohammadi, M.: Structural Basis of Fgf Receptor Dimerization and Activation <i>Cell</i> (Cambridge,Mass.) 98 pp. 641 (1999).
1CXZ	RhoA complexed with the effector domain of the protein kinase PKN/PRK1	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbld=1CXZ&page=140&pid=208161076787315	<i>Homo sapien</i>	RhoA fragment (residues 1 - 181) (human) - Chain A. PKN fragment (residues 13-98) (human) - Chain B.	A=teal; B=pink	Maesaki, R., Ihara, K., Shimizu, T., Kuroda, S., Kaibuchi, K., Hakoshima, T.: Structural Basis of Rho Effector Recognition Revealed by the Crystal Structure of Human RhoA Complexed with the Effector Domain of Pkn/Prk1 <i>Mol. Cell</i> 4 pp. 793 (1999).
1D0G	Death receptor 5 (DR5) extracellular domain bound to Apo2 ligand/Trail	http://www.pdb.org/pdb/explore/explore.do?structureid=1D0G	<i>Homo sapien</i>	Apo2L/Trail (human) - Chains A, B, C. Death receptor 5 extracellular domain (human) - Chains D, E, F.	A=ice blue; B=purple; C=mauve; D=ochre; E=orange; F=yellow.	Hymowitz, S.G., Christinger, H.W., Fuh, G., Ultsch, M., O'Connell, M., Kelley, R.F., Ashkenazi, A., de Vos, A.M. Triggering cell death: the crystal structure of Apo2L/TRAIL in a complex with death receptor 5. <i>Mol.Cell</i> v4 pp.563-571 , (1999).
1EOA	Cdc42 complexed with the GTPase binding domain of p21-activated kinase (PAK)	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbld=1EOA	<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.	A=teal; B=pink.	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)
1EOO	Fibroblast growth factor 1 (FGF1) dimer - fibroblast growth factor receptor 2 (FGFR2) complex	http://www.rcsb.org/pdb/cgi/explore.cgi?pid=208161076787315&page=180&pdbld=1EOO	<i>Homo sapien</i>	Fibroblast Growth Factor 1 (human) - Chains A, C. Fibroblast Growth Factor Receptor 2 (human) - Chains B, D.	A=ice blue; B=pink; C=ice blue; D=dark pink.	Pellegrini, L., Burke, D. F., Von Delft, F., Mulloy, B., Blu, T. L.: Crystal Structure of Fibroblast Growth Factor Recep Ectodomain Bound to Ligand and Heparin <i>Nature</i> 407 pp. 1029 (2000).
1EBA	Erythropoietin (Epo) receptor extracellular domain bound to Epo	http://www.pdb.org/pdb/explore/explore.do?structureid=1EBA	<i>Homo sapien</i>	Epo receptor (human) - Chains A, B. Epo (human) - Chains C, D.	A=blue; B=ice blue; C=yellow; D=lime.	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).
1EFN	HIV-1 Nef protein in complex with Arg-961 mutant Fyn SH3 Domain	http://www.rcsb.org/pdb/cgi/explore.cgi?pid=251641076811792&page=220&pdbld=1EFN	<i>Homo sapien</i>	Fyn tyrosine kinase fragment of SH3 domain (residues 85-141) (human) - Chains A, C. HIV-1 Nef protein fragment (residues 71-203) - Chains B, D.	A=pink; B=purple.	Lee, C. H., Saksela, K., Mirza, U. A., Chait, B. T., Kuriyan, J.: Crystal structure of the conserved core of HIV-1 Nef complexed with a Src family SH3 domain. <i>Cell</i> 85 pp. 931 (1996).
1ES7	Bone morphogenetic protein (BMP) receptor Ia extracellular domain bound to BMP-2	http://www.pdb.org/pdb/explore/explore.do?structureid=1ES7	<i>Homo sapien</i>	BMP-2 (human) - Chains A, C. BMP-2 receptor Ia extracellular domain (human) - Chains B, D.	A=lime; B=ochre; C=green; D=ochre.	Kirsch, T., Sebald, W., Dreyer, M.K. Crystal structure of the BMP-2-BRIA ectodomain complex. <i>Nat.Struct.Biol.</i> v7 pp.492-496 (2000).

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1F1J	Caspase-7 in complex with Acetyl-Asp-Glu-Val-Asp-Cho	http://www.pdb.org/pdb/explore/explre.do?structureid=1F1J	<i>Homo sapien</i>	p20 cleaved caspase 7 - Chain A. p10 cleaved caspase 7 (human) - Chain B. Ace-Asp-Glu-Val-Asp-Cho - Chains C,D.	A=ice blue; B=orange; C, D=yellow.	Wei, Y., Fox, T., Chambers, S.P., Sintchak, J., Coll, J.T., Golec, J.M., Swenson, L., Wilson, K.P., Charifson, P.S. The structures of caspases-1, -3, -7 and -8 reveal the basis for substrate and inhibitor selectivity. <i>Chem.Biol.</i> v7 pp.423-432 (2000).
1FAP	FKBP12-rapamycin complex interacting with PI3K-related kinase FRAP fragment	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbld=1FAP&page=240&pid=7391076804597	<i>Homo sapien</i>	FK506-binding protein (human)- Chain A. FRAP (human) - Chain B.	A=ice-blue; B=pink.	Choi, J., Chen, J., Schreiber, S. L., Clardy, J.: Structure of the FKBP12-rapamycin complex interacting with the binding domain of human FRAP. <i>Science</i> 273 pp. 239 (1996).
1FPR	SHP-1 tyrosine phosphatase catalytic domain and an in vitro peptide substrate Py469 derived from SHPS-1	http://www.rcsb.org/pdb/cgi/explore.cgi?job=summary&pdbld=1FPR&page=	<i>Homo sapien</i>	Protein-tyrosine phosphatase 1C catalytic domain fragment (human) - Chain A. Peptide PY469 -Chain B.	A=lime; B=red.	Yang, J., Cheng, Z., Niu, Z., Zhao, Z. J., Zhou, G. W.: Structural Basis for Substrate Specificity of Protein Tyrosine Phosphatase Shp-1 <i>J.Biol.Chem.</i> 275 pp. 4066 (2000).
1FQ1	Cyclin-dependent kinase 2 (CDK2) complexed with KAP	http://www.pdb.org/pdb/explore/explre.do?structureid=1FQ1	<i>Homo sapien</i>	KAP CDK phosphatase (human) - Chain A. Cyclin-dependent kinase 2 (human) - Chain B.	A= lime B=pink.	Song, H., Hanlon, N., Brown, N.R., Noble, M.E., Johnson, L.N., Barford, D. Phosphoprotein-protein interactions revealed by the crystal structure of kinase-associated phosphatase in complex with phosphoCDK2. <i>Mol.Cell</i> v7 pp.615-626 (2001).
1G1F	Protein tyrosine phosphatase 1B (PTP1B) complexed with a tri-phosphorylated peptide (Rdi(Ptr)Etd(Ptr)(Ptr)Rk) from the insulin receptor kinase	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbld=1G1F&page=280&pid=7391076804597	<i>Homo sapien</i>	Protein Tyrosine Phosphatase 1B catalytic domain fragment (human) - Chain A. Tri-phosphorylated peptide from the insulin receptor tyrosine kinase (RDIpYETDpYpYRK)- Chain B.	A=lime; B=pink.	Salmeen, A., Andersen, J. N., Myers, M. P., Tonks, N. K., Barford, D.: Molecular Basis for Dephosphorylation of the Activation Segment of the Insulin Receptor by Protein Tyrosine Phosphatase 1B <i>Mol. Cell</i> 6 pp. 1401 (2000).
1G3N	p18(Ink4C)-cyclin-dependent kinase 6 - cyclin K ternary complex	http://www.rcsb.org/pdb/cgi/explore.cgi?pid=7391076804597&page=300&pdbld=1G3N	<i>Homo sapien</i>	CDK6 (human) - Chains A, E. CDK6 inhibitor p18 Ink4C (human) - Chains B, F. Cyclin K (human) - Chains C, G.	A= pink; B= yellow; C=blue; E, F, G=black.	Jeffrey, P. D., Tong, L., Pavletich, N. P.: Structural Basis of Inhibition of Cdk-Cyclin Complexes by Ink4 Inhibitors <i>Genes Dev.</i> 24 pp. 3115 (2000).
1G6R	Superagonist T cell antigen receptor (TCR)/major histochemistry complex (MHC)	http://www.pdb.org/pdb/explore/explre.do?structureid=1G6R	<i>Mus musculus</i>	T cell receptor-alpha (mouse)- Chain A. T cell receptor-beta (mouse) - Chain B. MHC class I (mouse)- Chain C. Beta-2 microglobulin (mouse) - Chain D; Siyr peptide - Chain E.	A=orange; B=yellow; C=green; D=red; E=blue.	Degano, M., Garcia, K.C., Apostolopoulos, V., Rudolph, M.G., Teyton, L., Wilson, I.A. A functional hot spot for antigen recognition in a superagonist TCR/MHC complex. <i>Immunity</i> v12 pp.251-261 (2000).
1GNG	Glycogen synthase kinase-3 (GSK3) complex with Frattide peptide	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbld=1GNG&page=320&pid=7391076804597	<i>Homo sapien</i>	Glycogen Synthase Kinase-3 beta fragment (residues 27-393) (human) - Chains A, B. Frattide fragment (residues 188-226; SQPETRTRGDGDDPHRLQLVLSGNLIK EAVRRLHSRRLQ) - Chains X, Y.	A=pink; B=black; X=yellow; Y=black.	Bax, B., Carter, P. S., Lewis, C., Guy, A. R., Bridges, A., Pettman, R. Tanner G., Mannix, C., Culbert, A. A., Brown, M. J. B., Smith, D. G., Reith, A. D.: The Structure of Phosphorylated Gsk-3Beta Complexed with a Peptide, Frattide, that Inhibits Beta-Cateni Phosphorylation <i>Structure (London)</i> 9 pp. 1143 (2001).
1GOT	Trimeric G protein complex of alpha, beta and gamma subunits	http://www.pdb.org/pdb/explore/explre.do?structureid=1GOT	<i>Bos taurus</i>	G-alpha (Gt-alpha bovine residues 216-294 replaced with Gi alpha rat residues 220-298) - Chain A. G -beta (cow) - Chain B. G-gamma (cow) - Chain C.	A=teal B=green C=ice blue.	Lambright, D.G., Sondek, J., Bohm, A., Skiba, N.P., Hamm, H.E., Sigler, P.B. The 2.0 A crystal structure of a heterotrimeric G protein. <i>Nature</i> v379 pp.311-319 (1996).

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1H10	Pleckstrin homology domain of Protein Kinase B/Akt bound to Ins(1,3,4,5)-tetrakisphosphate	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbld=1H10&page=360&pid=7391076804597	<i>Homo sapien</i>	Protein Kinase B-alpha (Akt1) Pleckstrin homology domain fragment (residues 1-123) (human) - Chain A. Inositol (1,3,4,5)-tetrakisphosphate - Other.	A=pink; other=white.	Thomas, C. C., Deak, M., Alessi, D. R., Van Aalten, D. M. F.: High Resolution Structure of the Pleckstrin Homology Domain of Protein Kinase B/Akt Bound to Phosphatidylinositol (3,4,5)-Trisphosphate <i>Curr.Biol.</i> 12 pp. 1256 (2002)
1H90	Phosphatidylinositol 3-kinase (PI3K), p85 subunit: C-terminal SH2 domain complexed with a Tyr-751 phosphorylation site containing peptide from the platelet-derived growth factor receptor	http://www.rcsb.org/pdb/cgi/explore.cgi?pid=7391076804597&page=380&pdbld=1H90	<i>Homo sapien</i>	Phosphatidylinositol 3-kinase C-terminal SH2 domain fragment (residues 617-724) (human) - Chain A. Platelet-derived growth factor receptor fragment tyrosine phosphorylated pentapeptide (residues 751-755) - Chain B.	A=red; B=yellow.	Paupit, R. A., Dennis, C. A., Derbyshire, D. J., Breeze, A. L., Weston, S. A., Rowsell, S., Murshudov, G. N.: NMR Trial Models: Experiences with the Colicin Immunity Protein Im7 and the P85Alpha C-Terminal Sh2-Peptide Complex <i>Acta Crystalloar.,Sect.D.</i>
1HE8	Ras G12V - Phosphatidylinositol 3-kinase (PI3K) complex	http://www.rcsb.org/pdb/cgi/explore.cgi?pid=7391076804597&page=380&pdbld=1HE8	<i>Homo sapien</i>	Phosphatidylinositol 3-kinase p110 catalytic subunit (human). -Chain A. p21/H-Ras-1 (human) - Chain B.	A=red; B=teal.	Pacold, M. E., Suire, S., Perisic, O., Lara-Gonzalez, S., Davis, C. T., Walker, E. H., Hawkins, P. T., Stephens, L., Eccleston, J. F., Williams, R. L.: Crystal Structure and Functional Analysis of Ras Binding to its Effector Phosphoinositide 3-Kinase Gamma Cell(Cambridge,Mass.) 103 pp. 931 (2000).
1I51	Caspase-7 in complex with Xenopus inhibitor of apoptosis (XIAP)	http://www.pdb.org/pdb/explore/explore.do?structureid=1I51	<i>Homo sapien</i>	p20 cleaved caspase 7 (human) - Chains A,C. p10 cleaved caspase 7 (human) - Chains B,D. Xiap-Bir2 (human) - Chains E,F.	A=ice blue; B=orange; C=ice blue; D=orange; E=lime.	Chai, J., Shiozaki, E., Srinivasula, S.M., Wu, Q., Datta, P., Ainemri, E.S., Shi, Y., Dataa, P. Structural basis of caspase-7 inhibition by XIAP. <i>Cell</i> v104 pp.769-780 (2001).
1IRU	Mammalian 20S proteasome complex	http://www.rcsb.org/pdb/cgi/explore.cgi?pid=42221076905197&page=20&pdbld=1IRU	<i>Bos taurus</i>	The following 20S proteasome proteins are from cow. 20S proteasome protein 1 - Chain A, O. 20S proteasome protein 2 - Chain B, P. 20S proteasome protein 3 - Chain C, Q. 20S proteasome protein 4 - Chain D, R. 20S proteasome protein 5 - Chain E, S. 20S proteasome protein 6 - Chain F, T. 20S proteasome protein 7 - Chain G, U. 20S proteasome protein 8 - Chain H, V. 20S proteasome protein 9 - Chain I, W. 20S proteasome protein 10 - Chain J, X. 20S proteasome protein 12 - Chain K, Y. 20S proteasome protein 13 - Chain L, Z. 20S proteasome protein 14 - Chain M, 1. 20S proteasome protein 15 - Chain N, 2.	All of the non-identical chains are coloured separately.	Unno, M., Mizushima, T., Morimoto, Y., Tomisugi, Y., Tanaka, K., Yasuoka, N., Tsukihara, T.: The Structure of the Mammalian 20S Proteasome at 2.75 A Resolution Structure 10 pp. 609 (2002).
1ITB	Interleukin-1 (IL1) type-1 receptor complexed with interleukin-1 beta	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbld=1ITB	<i>Homo sapien</i>	Interleukin-1 (human) - Chain A. Interleukin-1 receptor type 1 extracellular domain (human) - Chain B.	A=lime; B=ice blue.	Vigers, G. P., Anderson, L. J., Caffes, P., Brandhuber, B. J.: Crystal structure of the type-I interleukin-1 receptor complexed with interleukin-1beta. <i>Nature</i> 386 pp. 190 (1997).
1JSU	Cyclin-dependent kinase 2 (CDK2)/cyclin A complexed with p27 KIP1	http://www.pdb.org/pdb/explore/explore.do?structureid=1JSU	<i>Homo sapien</i>	Cyclin-dependent kinase 2 (human) - Chain A. Cyclin A fragment (residues 173-432) (human) - Chain B. p27 KIP1 CDK Inhibitor fragment (residues 22-106) (human) - Chain C.	A=pink B=blue C=tan.	Russo, A.A., Jeffrey, P.D., Patten, A.K., Massague, J., Pavletich, N.P. Crystal structure of the p27Kip1 cyclin-dependent-kinase inhibitor bound to the cyclin A-Cdk2 complex. <i>Nature</i> v382 pp.325-331 (1996).

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1JWH	Casein kinase 2 (CK2) holoenzyme alpha and beta subunit quaternary complex	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbld=1JWH&page=480&pid=251641076811792	<i>Homo sapien</i>	Casein kinase 2 catalytic subunit (human) - Chains A, B. Casein kinase 2 regulatory subunit (human) - Chains C, D.	A=pink; B=dark pink; C=iceblue; D=blue	Niefind, K., Guerra, B., Ermakowa, I., Issinger, O. G.: Crystal Structure of Human Protein Kinase Ck2: Insights Into Basic Properties of the Ck2 Holoenzyme Embo J. 20 pp. 5320 (2001).
1KX3	Histones H2A, H2B, H3 and H4 with DNA in nucleosomes core complexes	http://www.pdb.org/pdb/explore/explore.do?structureld=1KX3	<i>Xenopus laevis</i>	Histone H3 (frog) - Chains A,E. Histone H4 (frog)- Chains B,F. Histone H2A.1 (frog) - Chains C,G. Histone H2B.1(frog) - Chains D,H. DNA backbone + DNA nucleotides (human) - Chain I.	A=red; B=orange; C=green; D=yellow; E=pink; F=ochre; G=lime; H=tan; I=DNA backbone= purple and nucleotides=blue.	Davey, C.A., Sargent, D.F., Luger, K., Maeder, A.W., Richmond, T.J. Solvent Mediated Interactions in the Structure of the Nucleosome Core Particle at 1.9 Å Resolution J.Mol.Biol. v319 pp.1097-1113 (2002).
1KZO	Protein farnesyltransferase complexed with farnesylated K- Ras4B peptide product and farnesyl diphosphate substrate bound simultaneously	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbld=1KZO	<i>Rattus norvegicus</i>	Protein farnesyltransferase (Ftase) subunit (rat) - Chain A. Protein farnesyltransferase subunit (rat) - Chain B. Farnesylated K-Ras4B peptide (transforming protein P21B) - Chain C.	A=ice blue; B=orange; C=lime.	Long, S. B., Casey, P. J., Beese, L. S.: The Reaction Path of Protein Farnesyltransferase at Atomic Resolution Nature 419 pp. 645 (2002).
1LAR	LAR receptor tyrosine phosphatase tandem phosphatase domains	http://www.rcsb.org/pdb/cgi/explore.cgi?job=summary&pdbld=1LAR&page=	<i>Homo sapien</i>	Protein-tyrosine phosphatase LAR (human) - Chains A, B.	A=lime; B=dark green.	Nam, H.-J., Poy, F., Krueger, N., Saito, H., Frederick, C. A.: Crystal Structure of the Tandem Phosphatase Domains of Rptp Lar Cell (Cambridge,Mass.) 97 pp. 449 (1999).
1MF8	Calcineurin (PP2B)-calmodulin - cyclophilin-cyclosporin complex	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbld=1MF8&page=180&pid=272281076886928	<i>Homo sapien</i>	Calmodulin-dependent Calcineurin A catalytic subunit fragment (residues 20-392) (human) - Chain A. Calcineurin B regulatory subunit isoform 1(human) - Chain B. Cyclophilin A (Peptidyl-Prolyl Cis-Trans Isomerase A) -Chain C. Cyclosporin A - Chain D.	A=lime; B=blue; C=yellow; D=white.	Jin, L., Harrison, S. C.: Crystal Structure of Human Calcineurin Complexed with Cyclosporin a and Human Cyclophilin Proc.Natl.Acad.Sci.USA 99 pp. 13522 (2002).
1N8Z	ErbB2 (HER2) receptor tyrosine kinase extracelleular domain complexed with herceptin monoclonal antibody Fab fragment	http://www.rcsb.org/pdb/cgi/explore.cgi?pid=251641076811792&page=660&pdbld=1N8Z	<i>Homo sapien</i>	Herceptin Fab (antibody fragment) - Light chain - Chain A. Herceptin Fab (antibody fragment) - Heavy chain - Chain B. Receptor protein-tyrosine kinase ErbB2 extracellular domain fragment (human) - Chain C.	A=orange; B=yellow; C=pink.	Cho, H.-S., Mason, K., Ramyar, K. X., Stanley, A. M., Gabelli, S. B., Denney Jr., D. W., Leahy, D. J.: Structure of the Extracellular Region of Her2 Alone and in Complex with the Herceptin Fab Nature 421 pp. 756 (2003).
1NT9	RNA polymerase 2 complex	http://www.pdb.org/pdb/explore/explore.do?structureld=1NT9	<i>Saccharomyces cerevisiae</i>	Rpb1, B220 - Chain A. Rpb2, B150 - Chain B. Rpb3, B44.5 - Chain C. Rpb4, B32 - Chain D. Rpb5, Abc27 - Chain E. Rpb6, Abc23 - Chain F. Rpb7, B16 - Chain G. Rpb8, Abc14.4 - Chain H. Rpb9, B12.6 - Chain I. Rpb10, Abc10b - Chain J. Rpb11, B13.6 - Chain K. Rpb12, Abc10a - Chain L.. All of these correspond to budding yeast proteins.	A=blue; B=ochre; C=lime D=purple; E=teal; F=tan; G=pink; H=yellow; I=green; J=orange; K=red; L=white.	Armache, K.-J., Kettenberger, H., Cramer, P. Architecture of initiation-competent 12-subunit RNA polymerase II Proc.Natl.Acad.Sci.USA v100 pp.6964-6968 (2003).

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1NVV	Ras-GTP of the Ras-specific nucleotide exchange factor Sos	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbld=1NVV&page=40&pid=5031076904128	<i>Homo sapien</i>	Transforming Protein p21/H-Ras fragment (residues 1-166) (human) - Chain A. Transforming Protein p21/H-Ras fragment (residues 1-166) (human) - Chain B. Son of Sevenless protein homolog 1guanine nucleotide exchnage factor fragment (residues 566-1046) (human) - Chain C.	A=teal; B=green; C=yellow.	Margarit, S. M., Sondermann, H., Hall, B. E., Nagar, B., Hoelz, A., Pirruccello, M., Bar-Sagi, D., Kuriyan, J.: Structural Evidence for Feedback Activation by Rasgtp of the Ras-Specific Nucleotide Exchange Factor SOS Cell (Cambridge,Mass.) 112 pp. 685 (2003).
1O6K	Protein kinase B/Akt kinase domain S474D complexed with glycogen synthase kinase 3 peptide and AMP-PnP	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbld=1O6K&page=720&pid=126561076874485	<i>Homo sapien</i>	Protein Kinase B-beta (Akt2) catalytic domain fragment (residues 146-481) (human) - Chain A. Glycogen synthase kinase-3 fragment (residues 3-12) - Chain C.	A=pink; B=lime; C=white.	Yang, J., Cron, P., Good, V. M., Thompson, V., Hemmings, B. A., Barford, D.: Crystal Structure of an Activated Akt/Protein Kinase B Ternary Complex with Gsk-3 Peptide and AMP-Pnp Nat.Struct.Biol. 9 pp. 940 (2002).
1OMW	G protein coupled receptor kinase 2 (GRK2/BARK) complexed with G-beta/gamma subunits	http://www.pdb.org/pdb/explore/explore.do?structureld=1OMW	<i>Bos taurus</i>	GRK2 (cow) -Chain A. G-beta (cow) - Chain B. G-gamma (cow) - Chain C.	A=pink B=green C=ice blue.	Lodowski, D.T., Pitcher, J.A., Capel, W.D., Lefkowitz, R.J., Tesmer, J.J.G. Keeping G proteins at Bay: A Complex Between G Protein-Coupled Receptor Kinase 2 and G-Beta-Gamma Science v300 pp.1256-1262 (2003).
1P9M	Interleukin-6 (IL6) alpha/interleukin-6 beta receptorand interleukin-6	http://www.rcsb.org/pdb/cgi/explore.cgi?pid=240311076894386&page=20&pdbld=1P9M	<i>Homo sapien</i>	Interleukin-6 receptor (GP130) extracellular domains D1-D3 fragment (human) - Chain A. Interleukin-6 (human) - Chain B. Interleukin-6 receptor extracellular domains D2-D3 fragment (human) - Chain C.	A=ice blue; B=orange; C=blue.	Boulanger, M. J., Chow, D. C., Brevnova, E. E., Garcia, K. C.: Hexameric Structure and Assembly of the Interleukin-6/II-6 Alpha-Receptor/Gp130 Complex Science 300 pp. 2101 (2003).
1PNX	30S Ribosome RNA and protein complex	http://www.pdb.org/pdb/explore/explore.do?structureld=1PNX	<i>Escherichia coli</i>	rRNA backbone + rRNA nucleotides - Chains A,B. Nineteen 30S ribosomal proteins are shown. All proteins and rRNA are from <i>E. coli</i> .	A=rRNA backbone= purple and nucleotides=blue; B=rRNA backbone=purple and nucleotides=blue; Each protein chain is differentially coloured.	Vila-Sanjurjo, A., Ridgeway, W.K., Seymaner, V., Zhang, W., Santoso, S., Yu, K., Cate, J.H.D. X-ray crystal structures of the WT and a hyper-accurate ribosome from Escherichia coli Proc.Natl.Acad.Sci.USA v100 pp.8682-8687 (2003).
1PNY	50S Ribosome RNA and protein complex	http://www.pdb.org/pdb/explore/explore.do?structureld=1PNY	<i>Escherichia coli</i>	rRNA backbone + rRNA nucleotides - Chains A,B. Thirty one 50S ribosomal proteins are shown. All proteins and rRNA are from <i>E. coli</i> .	A=rRNA backbone= purple and nucleotides=blue; B=rRNA backbone=purple and nucleotides=blue; Each protein chain is differentially coloured.	Vila-Sanjurjo, A., Ridgeway, W.K., Seymaner, V., Zhang, W., Santoso, S., Yu, K., Cate, J.H.D. X-ray crystal structures of the WT and a hyper-accurate ribosome from Escherichia coli Proc.Natl.Acad.Sci.USA v100 pp.8682-8687 (2003).

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1Q4K	Polo-like kinase 1 (PLK1) polo-box domain in a complex with a phosphopeptide	http://www.rcsb.org/pdb/cgi/explore.cgi?pid=126561076874485&page=820&pdbld=1Q4K	<i>Homo sapien</i>	Protein kinase Plk1 Polo box domain (human) - Chains B, A, C. Phospho-Peptide (MQSpTPL) - Chains D, E, F.	A=pink; B=black; C=black; D=yellow; E, F=black	Cheng, K., Lowe, E. D., Sinclair, J., Nigg, E. A., Johnson, L. N.: The Crystal Structure of the Polo Box Domain of Human Polo-Loke Kinase-1 (Plk1) <i>Embo J.</i> 22 pp. 5757 (2003).
1RQQ	Insulin receptor tyrosine kinase in a complex with the SH2 domain of adapter APS anda substrate inhibitor	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbld=1RQQ&page=880&pid=126561076874485	<i>Homo sapien</i>	Insulin receptor kinase domain fragment (human) - Chains A, B. Adaptor protein Aps SH2 domain fragment - Chains C, D - Bisubstrate Inhibitor - Chains E, F.	A=pink; B=dark pink; C=ice blue; D=blue; E=yellow; F=dark yellow.	Hu, J., Liu, J., Ghirlando, R., Saltiel, A. R., Hubbard, S. R.: Structural Basis for Recruitment of the Adapter Protein Aps to the Activated Insulin Receptor <i>Mol.Cell</i> 12 pp. 1379 (2003).
1SHC	Shc PTB domain complexed with a phosphopeptide from the TrkA receptor-tyrosine kinase	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbld=1SHC&page=900&pid=126561076874485	<i>Homo sapien</i>	Shc PTB domain fragment (human) -Chain A. TrkA receptor phosphopeptide - Chain B.	A=ice blue; B=yellow.	Zhou, M. M., Ravichandran, K. S., Olejniczak, E. F., Petros, A. M., Meadows, R. P., Sattler, M., Harlan, J. E., Wade, W. S., Burakoff, S. J., Fesik, S. W.: Structure and ligand recognition of the phosphotyrosine binding domain of Shc. <i>Nature</i> 378 pp. 584 (1995).
1TUP	Tumor suppressor p53 complexed with DNA	http://www.pdb.org/pdb/explore/explre.do?structureld=1TUP	<i>Homo sapien</i>	p53 (human) - Chains A, B, C. DNA - Chains D, E.	A=lime; B=yellow; C=teal; D=DNA backbone= purple and nucleotides=blue. E=DNA backbone=purple and nucleotides=blue.	Cho, Y., Gorina, S., Jeffrey, P.D., Pavletich, N.P. Crystal structure of a p53 tumor suppressor-DNA complex: understanding tumorigenic mutations. <i>Science</i> v265 pp.346-355 (1994).
1WQ1	Ras complexed with Ras-GTPase activating protein (GAP)	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbld=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=teal; B=red.	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. <i>Science</i> 277 pp. 333 (1997).
1WWW	Nerve growth factor in complex with domain 5 of the TrkA receptor-tyrosine kinase	http://www.rcsb.org/pdb/cgi/explore.cgi?job=summary&pdbld=1WWW&page=	<i>Homo sapien</i>	Nerve growth factor (human) -Chains A, B. TrkA receptor extracellular domain 5 fragment (human) - Chains C,D.	A=ice blue; B=blue; C=pink; D=dark pink.	Wiesmann, C., Ultsch, M. H., Bass, S. H., De Vos, A. M.: Crystal Structure of Nerve Growth Factor in Complex with the Ligand-Binding Domain of the Trka Receptor Receptor <i>Nature</i> 401 pp. 184 (1999)
2NGR	Cdc42 bound to the active and catalytically compromised forms of the Cdc42-GTPase activating protein (GAP)	http://www.rcsb.org/pdb/cgi/explore.cgi?job=graphics&pdbld=2NGR	<i>Homo sapien</i>	Cdc42 (G25K) GTP-binding protein, placental isoform (human) - Chain A. Cdc42 GAP C-terminal active domain R305A mutant) (human) - Chain B.	A=teal; B=yellow.	Nassar, N., Hoffman, G. R., Manor, D., Clardy, J. C., Cerione, R. A.: Structures of Cdc42 bound to the active and catalytically compromised forms of Cdc42GAP. <i>Nat Struct Biol</i> 5 pp. 1047 (1998).

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CaMK2	Calmodulin-dependent kinase 2 oligomer complexed with calmodulin (artistic composite - (CaMK2 catalytic domain represented with phosphorylase kinase catalytic domain)	http://www.pdb.org/pdb/explore/explore.do?structureId=1HKX http://www.pdb.org/pdb/explore/explore.do?structureId=1CDM http://www.pdb.org/pdb/explore/explore.do?structureId=1PHK	<i>Mus musculus</i> , <i>Bos taurus</i> , <i>Oryctolagus cuniculus</i>	Calmodulin-dependent kinase 2alpha fragment association domain (residues 336-478) (mouse)(1HKX) - Chain A. Calmodulin (1CDM) (cow)- Chain B. Phosphorylase kinase gamma catalytic subunit fragment (residues 1-298) (rabbit) (1PHK) - Chain C.	A=light and dark pink; B=blue; C=light and dark pink.	Hoelz, A., Nairn, A.C., Kuriyan, J. Crystal Structure of a Tetradecameric Assembly of the Association Domain of Ca ²⁺ /Calmodulin-Dependent Kinase II Molecular Cell v11 pp.1241 (2003); Meador, W.E., Means, A.R., Quioco, F.A. Modulation of calmodulin plasticity in molecular recognition on the basis of x-ray structures. Science v262 pp.1718-1721 (1993); Owen, D.J., Noble, M.E., Garman, E.F., Papageorgiou, A.C., Johnson, L.N. Two structures of the catalytic domain of phosphorylase kinase: an active protein kinase complexed with substrate analogue and product. Structure v3 pp.467-482 (1995).
EGFR+PM	Epidermal growth factor (EGF) receptor-tyrosine kinase domain dimer shown with plasma membrane and extracellular EGF domain (artistic composite)	http://www.pdb.org/pdb/explore/explore.do?structureId=1M14 http://www.pdb.org/pdb/explore/explore.do?structureId=1IVO	<i>Homo sapien</i>	EGF receptor tyrosine kinase fragment domain (residues 671-998) (human) (1M14) - Chains A, B. EGF receptor extracellular domains I, II, III and IV (human) (1IVO) - Chain C, D. EGF (residues 1-53) (human) (1IVO) - Chains E, F. Plasma membrane - P.M..	A,B,C,D=dark pink; E,F=orange; P.M.=grey.	Stamos, J., Sliwkowski, M.X., Eigenbrot, C. Structure of the epidermal growth factor receptor kinase domain alone and in complex with a 4-anilinoquinazoline inhibitor. J.Biol.Chem. v277 pp.46265-46272 (2002); Ogiso, H., Ishitani, R., Nureki, O., Fukai, S., Yamanaka, M., Kim, J.H., Saito, K., Inoue, M., Shirouzu, M., Yokoyama, S. Crystal Structure of the Complex of Human Epidermal Growth Factor and Receptor Extracellular Domains. Cell (Cambridge,Mass.) v110 pp.775-787 (2002).