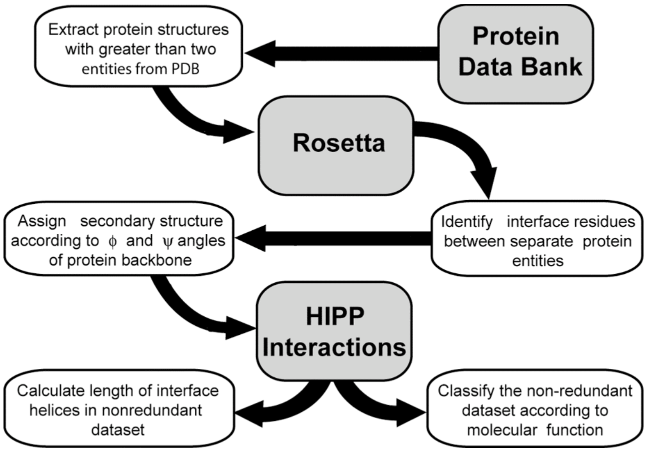
Assessment of helical interfaces in protein-protein interactions

Andrea L. Jochim and Paramjit S. Arora

Department of Chemistry
New York University
New York, NY 10003

Supplementary Information

Methods used to Identify HIPP Interactions



Protein structures were obtained from the Protein Data Bank (http:://www.pdb.org/). In addition to using Rosetta, we created several computer programs to aid in our goal. The key steps to identifying HIPP interactions are listed below.

1) Using the advanced search function on the PDB website, we extract all structures with more than one protein entity.

2) **Perl script to construct individual PDB files for each interacting chain within the parent PDB file**. This script reads a PDB, identifies atoms from different chains that interaction with each other, then creates a new formatted PDB file with those two chains. This process is repeated until all interacting chains have a new PDB file. If the parent PDB file contains more than one structure, only the first structure is considered.

3) **Perl script to identify protein partner chains between separate entities**. This script reads a PDB file, identifies chains that belong to separate entities within the PDB file, and creates a list of the PDB code and partnering chains that are part of the separate entities. This enables us to find those helix interfaces that are between separate protein entities as opposed to helical interfaces between chains in a single protein.

4) **Modifications within Rosetta written in C++ programming language to identify helical interfaces between interacting protein chains**. Rosetta already contains programs that identify interface residues and assigns secondary structure to a protein backbone. Here we link the two routines to find protein chains with interface residues that lie within a helix. We define helical segment as one that contains at least four contiguous residues with ϕ and φ angles that are characteristic of the α-helix ($\phi = -47^\circ \pm 25^\circ$, $\varphi = -57^\circ \pm 25^\circ$). Often, protein-protein interfaces are defined according to geometrically continuous patches of residues on the surface of a protein that exclude solvent by binding to another chain. This definition might include some residues that are not really involved in the interaction or exclude some residues that play a key role in the interaction. Therefore, we use a distance threshold between residues of different chains.

5) The length of each helix involved in HIPP interactions was calculated using a simple C++ program.

6) The PDB structures involved in HIPP interactions were classified according to molecular function. The categories were derived from those listed in the 'Advanced Search' option on the PDB website.

Table S1. Non-redundant Dataset of HIPP interactions

PDB Code	Title	Classification
1A02	STRUCTURE OF THE DNA BINDING DOMAINS OF NFAT, FOS AND JUN BOUND TO DNA	TRANSCRIPTION/DNA
1A2X	COMPLEX OF TROPONIN C WITH A 47 RESIDUE (1-47) FRAGMENT OF TROPONIN I	COMPLEX (SKELETAL MUSCLE/MUSCLE PROTEIN)
1A3R	FAB FRAGMENT (ANTIBODY 8F5) COMPLEXED WITH PEPTIDE FROM HUMAN RHINOVIRUS (SEROTYPE 2) VIRAL CAPSID PROTEIN VP2 (RESIDUES 156-170)	VIRAL PROTEIN/IMMUNE SYSTEM
1A4F	BAR-HEADED GOOSE HEMOGLOBIN (OXY FORM)	OXYGEN TRANSPORT
1A6D	THERMOSOME FROM T. ACIDOPHILUM	CHAPERONIN
1A6T	FAB FRAGMENT OF MAB1-IA MONOCLONAL ANTIBODY TO HUMAN RHINOVIRUS 14 NIM-IA SITE	IMMUNOGLOBULIN
1A81	CRYSTAL STRUCTURE OF THE TANDEM SH2 DOMAIN OF THE SYK KINASE BOUND TO A DUALLY TYROSINE-PHOSPHORYLATED ITAM	COMPLEX (TRANSFERASE/PEPTIDE)
1A93	NMR SOLUTION STRUCTURE OF THE C-MYC-MAX HETERODIMERIC LEUCINE ZIPPER, NMR, MINIMIZED AVERAGE STRUCTURE	LEUCINE ZIPPER
1A9N	CRYSTAL STRUCTURE OF THE SPLICEOSOMAL U2B''-U2A' PROTEIN COMPLEX BOUND TO A FRAGMENT OF U2 SMALL NUCLEAR RNA	RNA BINDING PROTEIN/RNA
1A9X	CARBAMOYL PHOSPHATE SYNTHETASE: CAUGHT IN THE ACT OF GLUTAMINE HYDROLYSIS	AMIDOTRANSFERASE
1ABR	CRYSTAL STRUCTURE OF ABRIN-A	COMPLEX (GLYCOSIDASE/CARBOHYDRATE)
1AD0	AB FRAGMENT OF ENGINEERED HUMAN MONOCLONAL ANTIBODY A5B7	IMMUNOGLOBULIN
1AD9	GG-FAB FRAGMENT OF ENGINEERED HUMAN MONOCLONAL ANTIBODY CTM01	IMMUNOGLOBULIN
1AF0	SERRATIA PROTEASE IN COMPLEX WITH INHIBITOR	COMPLEX (METALLOPROTEASE/INHIBITOR)
1AHG	ASPARTATE AMINOTRANSFERASE HEXAMUTANT	TRANSFERASE (AMINOTRANSFERASE)
1AIP	EF-TU EF-TS COMPLEX FROM THERMUS THERMOPHILUS	COMPLEX OF TWO ELONGATION FACTORS
1ALL	ALLOPHYCOCYANIN	LIGHT-HARVESTING PROTEIN
1AOI	COMPLEX BETWEEN NUCLEOSOME CORE PARTICLE (H3,H4,H2A,H2B) AND 146 BP LONG DNA FRAGMENT	DNA BINDING PROTEIN/DNA
1APY	HUMAN ASPARTYLGLUCOSAMINIDASE	HYDROLASE
1AQW	GLUTATHIONE S-TRANSFERASE IN COMPLEX WITH GLUTATHIONE	TRANSFERASE
1AR1	STRUCTURE AT 2.7 ANGSTROM RESOLUTION OF THE PARACOCCUS DENITRIFICANS TWO-SUBUNIT CYTOCHROME C OXIDASE COMPLEXED	COMPLEX (OXIDOREDUCTASE/ANTIBODY)

	WITH AN ANTIBODY FV FRAGMENT	
1ARO	T7 RNA POLYMERASE COMPLEXED WITH T7 LYSOZYME	COMPLEX (POLYMERASE/HYDROLASE)
1ATI	CRYSTAL STRUCTURE OF GLYCYL-TRNA SYNTHETASE FROM THERMUS THERMOPHILUS	PROTEIN BIOSYNTHESIS
1AVO	PROTEASOME ACTIVATOR REG(ALPHA)	PROTEASOME ACTIVATOR
1AWC	MOUSE GABP ALPHA/BETA DOMAIN BOUND TO DNA	TRANSCRIPTION/DNA
1AXD	STRUCTURE OF GLUTATHIONE S-TRANSFERASE-I BOUND WITH THE LIGAND LACTOYLGLUTATHIONE	COMPLEX (TRANSFERASE/LIGAND)
1AXI	STRUCTURAL PLASTICITY AT THE HGH:HGHBP INTERFACE	COMPLEX (HORMONE/RECEPTOR)
1AY1	ANTI TAQ FAB TP7	IMMUNOGLOBULIN
1AYA	CRYSTAL STRUCTURES OF PEPTIDE COMPLEXES OF THE AMINO-TERMINAL SH2 DOMAIN OF THE SYP TYROSINE PHOSPHATASE	HYDROLASE(SH2 DOMAIN)
1AZS	COMPLEX OF GS-ALPHA WITH THE CATALYTIC DOMAINS OF MAMMALIAN ADENYLYL CYCLASE	COMPLEX (LYASE/HYDROLASE)
1B33	STRUCTURE OF LIGHT HARVESTING COMPLEX OF ALLOPHYCOCYANIN ALPHA AND BETA CHAINS/CORE-LINKER COMPLEX AP*LC7.8	PHOTOSYNTHESIS
1B34	CRYSTAL STRUCTURE OF THE D1D2 SUB-COMPLEX FROM THE HUMAN SNRNP CORE DOMAIN	RNA BINDING PROTEIN
1B35	CRICKET PARALYSIS VIRUS (CRPV)	VIRUS
1B5F	NATIVE CARDOSIN A FROM CYNARA CARDUNCULUS L.	HYDROLASE
1B72	PBX1, HOMEOBOX PROTEIN HOX-B1/DNA TERNARY COMPLEX	PROTEIN/DNA
1B8D	CRYSTAL STRUCTURE OF A PHYCOUROBILIN-CONTAINING PHYCOERYTHRIN	PHOTOSYNTHESIS
1B8H	SLIDING CLAMP, DNA POLYMERASE	TRANSFERASE
1B8I	STRUCTURE OF THE HOMEOTIC UBX/EXD/DNA TERNARY COMPLEX	TRANSCRIPTION/DNA
1BAI	STRUCTURAL BASIS FOR SPECIFICITY OF RETROVIRAL PROTEASES	COMPLEX (PROTEASE/INHIBITOR)
1BB1	CRYSTAL STRUCTURE OF A DESIGNED, THERMOSTABLE HETEROTRIMERIC COILED COIL	DE NOVO PROTEIN DESIGN
1BBJ	CRYSTAL STRUCTURE OF A CHIMERIC FAB' FRAGMENT OF AN ANTIBODY BINDING TUMOUR CELLS	IMMUNOGLOBULIN
1BC5	CHEMOTAXIS RECEPTOR RECOGNITION BY PROTEIN METHYLTRANSFERASE CHER	COMPLEX (METHYLTRANSFERASE/PEPTIDE)
1BFO	CAMPATH-1G IGG2B RAT MONOCLONAL FAB	ANTIBODY

1BH9	HTAFII18/HTAFII28 HETERODIMER CRYSTAL STRUCTURE WITH BOUND PCMBS	TRANSCRIPTION REGULATION COMPLEX
1BLX	P19INK4D/CDK6 COMPLEX	COMPLEX (INHIBITOR PROTEIN/KINASE)
1BOG	ANTI-P24 (HIV-1) FAB FRAGMENT CB41 COMPLEXED WITH AN EPITOPE-HOMOLOGOUS PEPTIDE	COMPLEX (ANTIBODY/PEPTIDE)
1BOM	THREE-DIMENSIONAL STRUCTURE OF BOMBYXIN-II, AN INSULIN-RELATED BRAIN-SECRETORY PEPTIDE OF THE SILKMOTH BOMBYX MORI: COMPARISON WITH INSULIN AND RELAXIN	INSULIN-LIKE BRAIN-SECRETORY PEPTIDE
1BOU	THREE-DIMENSIONAL STRUCTURE OF LIGAB	DIOXYGENASE
1BR1	SMOOTH MUSCLE MYOSIN MOTOR DOMAIN-ESSENTIAL LIGHT CHAIN COMPLEX WITH MGADP.ALF4 BOUND AT THE ACTIVE SITE	MUSCLE PROTEIN
1BRL	THREE-DIMENSIONAL STRUCTURE OF BACTERIAL LUCIFERASE FROM VIBRIO HARVEYI AT 2.4 ANGSTROMS RESOLUTION	LUMINESCENCE
1BS6	PEPTIDE DEFORMYLASE AS NI2+ CONTAINING FORM IN COMPLEX WITH TRIPEPTIDE MET-ALA-SER	HYDROLASE
1BSX	STRUCTURE AND SPECIFICITY OF NUCLEAR RECEPTOR-COACTIVATOR INTERACTIONS	HORMONE/GROWTH FACTOR
1BT6	P11 (S100A10), LIGAND OF ANNEXIN II IN COMPLEX WITH ANNEXIN II N-TERMINUS	COMPLEX (LIGAND/ANNEXIN)
1BUN	STRUCTURE OF BETA2-BUNGAROTOXIN: POTASSIUM CHANNEL BINDING BY KUNITZ MODULES AND TARGETED PHOSPHOLIPASE ACTION	TOXIN
1BVY	COMPLEX OF THE HEME AND FMN-BINDING DOMAINS OF THE CYTOCHROME P450(BM-3)	OXIDOREDUCTASE
1BWV	ACTIVATED RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE (RUBISCO) COMPLEXED WITH THE REACTION INTERMEDIATE ANALOGUE 2-CARBOXYARABINITOL 1,5-BISPHOSPHATE	LYASE
1BXN	THE CRYSTAL STRUCTURE OF RUBISCO FROM ALCALIGENES EUTROPHUS TO 2.7 ANGSTROMS.	LYASE
1C17	A1C12 SUBCOMPLEX OF F1FO ATP SYNTHASE	MEMBRANE PROTEIN
1C1Y	CRYSTAL STRUCTURE OF RAP.GMPPNP IN COMPLEX WITH THE RAS-BINDING-DOMAIN OF C-RAF1 KINASE (RAFRBD).	SIGNALING PROTEIN
1C3A	CRYSTAL STRUCTURE OF FLAVOCETIN-A FROM THE HABU SNAKE VENOM, A NOVEL CYCLIC TETRAMER OF C-TYPE LECTIN-LIKE HETERODIMERS	MEMBRANE PROTEIN
1C4Z	STRUCTURE OF E6AP: INSIGHTS INTO UBIQUITINATION PATHWAY	LIGASE
1C5C	DECARBOXYLASE CATALYTIC ANTIBODY 21D8-HAPTEN COMPLEX	IMMUNE SYSTEM

1C5D	THE CRYSTAL STRUCTURE OF THE FAB FRAGMENT OF A RAT MONOCLONAL ANTIBODY AGAINST THE MAIN IMMUNOGENIC REGION OF THE HUMAN MUSCLE ACETYLCHOLINE RECEPTOR	IMMUNE SYSTEM
1C5F	CRYSTAL STRUCTURE OF THE CYCLOPHILIN-LIKE DOMAIN FROM BRUGIA MALAYI COMPLEXED WITH CYCLOSPORIN A	ISOMERASE/IMMUNE SYSTEM
1C6V	SIV INTEGRASE (CATALYTIC DOMAIN + DNA BIDING DOMAIN COMPRISING RESIDUES 50-293) MUTANT WITH PHE 185 REPLACED BY HIS (F185H)	DNA BINDING PROTEIN
1C9B	CRYSTAL STRUCTURE OF A HUMAN TBP CORE DOMAIN-HUMAN TFIIB CORE DOMAIN COMPLEX BOUND TO AN EXTENDED, MODIFIED ADENOVIRAL MAJOR LATE PROMOTER (ADMLP)	TRANSCRIPTION/DNA
1C9L	PEPTIDE-IN-GROOVE INTERACTIONS LINK TARGET PROTEINS TO THE B-PROPELLER OF CLATHRIN	ENDOCYTOSIS/EXOCYTOSIS
1CBV	AN AUTOANTIBODY TO SINGLE-STRANDED DNA: COMPARISON OF THE THREE-DIMENSIONAL STRUCTURES OF THE UNLIGANDED FAB AND A DEOXYNUCLEOTIDE-FAB COMPLEX	IMMUNE SYSTEM/DNA
1CC1	CRYSTAL STRUCTURE OF A REDUCED, ACTIVE FORM OF THE NI-FE-SE HYDROGENASE FROM DESULFOMICROBIUM BACULATUM	OXIDOREDUCTASE
1CCW	STRUCTURE OF THE COENZYME B12 DEPENDENT ENZYME GLUTAMATE MUTASE FROM CLOSTRIDIUM COCHLEARIUM	ISOMERASE
1CD3	PROCAPSID OF BACTERIOPHAGE PHIX174	VIRUS
1CD9	2:2 COMPLEX OF G-CSF WITH ITS RECEPTOR	CYTOKINE
1CE7	MISTLETOE LECTIN I FROM VISCUM ALBUM	RIBOSOME
1CF7	STRUCTURAL BASIS OF DNA RECOGNITION BY THE HETERODIMERIC CELL CYCLE TRANSCRIPTION FACTOR E2F-DP	TRANSCRIPTION/DNA
1CF8	CONVERGENCE OF CATALYTIC ANTIBODY AND TERPENE CYCLASE MECHANISMS: POLYENE CYCLIZATION DIRECTED BY CARBOCATION-PI INTERACTIONS	CATALYTIC ANTIBODY
1CG5	DEOXY FORM HEMOGLOBIN FROM DASYATIS AKAJEI	OXYGEN TRANSPORT
1CGL	STRUCTURE OF THE CATALYTIC DOMAIN OF FIBROBLAST COLLAGENASE COMPLEXED WITH AN INHIBITOR	METALLOPROTEASE
1CI6	TRANSCRIPTION FACTOR ATF4-C/EBP BETA BZIP HETERODIMER	TRANSCRIPTION
1CLV	ELLOW MEAL WORM ALPHA-AMYLASE IN COMPLEX WITH THE AMARANTH ALPHA-AMYLASE INHIBITOR	HYDROLASE
1CMI	STRUCTURE OF THE HUMAN PIN/LC8 DIMER WITH A BOUND PEPTIDE	OXIDOREDUCTASE/OXIDOREDUCTASE INHIBITOR
1CN3	INTERACTION OF POLYOMAVIRUS INTERNAL PROTEIN VP2 WITH MAJOR CAPSID PROTEIN VP1 AND IMPLICATIONS FOR PARTICIPATION OF	VIRAL PROTEIN

	VP2 IN VIRAL ENTRY	
1CP9	CRYSTAL STRUCTURE OF PENICILLIN G ACYLASE FROM THE BRO1 MUTANT STRAIN OF PROVIDENCIA RETTGERI	HYDROLASE
1CPC	ISOLATION, CRYSTALLIZATION, CRYSTAL STRUCTURE ANALYSIS AND REFINEMENT OF CONSTITUTIVE C-PHYCOCYANIN FROM THE CHROMATICALLY ADAPTING CYANOBACTERIUM FREMYELLA DIPLOSIPHON AT 1.66 ANGSTROMS RESOLUTION	LIGHT HARVESTING PROTEIN
1CQT	CRYSTAL STRUCTURE OF A TERNARY COMPLEX CONTAINING AN OCA-B PEPTIDE, THE OCT-1 POU DOMAIN, AND AN OCTAMER ELEMENT	GENE REGULATION/DNA
1CVU	CRYSTAL STRUCTURE OF ARACHIDONIC ACID BOUND TO THE CYCLOOXYGENASE ACTIVE SITE OF COX-2	OXIDOREDUCTASE
1CZQ	CRYSTAL STRUCTURE OF THE D10-P1/IQN17 COMPLEX: A D-PEPTIDE INHIBITOR OF HIV-1 ENTRY BOUND TO THE GP41 COILED-COIL POCKET.	VIRAL PROTEIN/VIRAL PROTEIN INHIBITOR
1CZY	RYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE TRAF DOMAIN OF HUMAN TRAF2 AND AN LMP1 BINDING PEPTIDE	APOPTOSIS
1D2Z	THREE-DIMENSIONAL STRUCTURE OF A COMPLEX BETWEEN THE DEATH DOMAINS OF PELLE AND TUBE	APOPTOSIS
1D3B	CRYSTAL STRUCTURE OF THE D3B SUBCOMPLEX OF THE HUMAN CORE SNRNP DOMAIN AT 2.0A RESOLUTION	RNA BINDING PROTEIN
1D3U	TATA-BINDING PROTEIN/TRANSCRIPTION FACTOR (II)B/BRE+TATA-BOX COMPLEX FROM PYROCOCCUS WOESEI	GENE REGULATION/DNA
1D4T	CRYSTAL STRUCTURE OF THE XLP PROTEIN SAP IN COMPLEX WITH A SLAM PEPTIDE	SIGNALING PROTEIN
1D6G	MOLECULAR COMPLEX OF CHOLECYSTOKININ-8 AND N-TERMINUS OF THE CHOLECYSTOKININ A RECEPTOR BY NMR SPECTROSCOPY	HORMONE/GROWTH FACTOR
1DEV	CRYSTAL STRUCTURE OF SMAD2 MH2 DOMAIN BOUND TO THE SMAD-BINDING DOMAIN OF SARA	SIGNALING PROTEIN
1DKD	CRYSTAL STRUCTURE OF A GROEL (APICAL DOMAIN) AND A DODECAMERIC PEPTIDE COMPLEX	CHAPERONE
1DKG	CRYSTAL STRUCTURE OF THE NUCLEOTIDE EXCHANGE FACTOR GRPE BOUND TO THE ATPASE DOMAIN OF THE MOLECULAR CHAPERONE DNAK	COMPLEX (HSP24/HSP70)
1DKZ	THE SUBSTRATE BINDING DOMAIN OF DNAK IN COMPLEX WITH A SUBSTRATE PEPTIDE, DETERMINED FROM TYPE 1 NATIVE CRYSTALS	COMPLEX (MOLECULAR CHAPERONE/PEPTIDE)
1DML	CRYSTAL STRUCTURE OF HERPES SIMPLEX UL42 BOUND TO THE C-TERMINUS OF HSV POL	DNA BINDING PROTEIN/TRANSFERASE
1DN0	STRUCTURE OF THE FAB FRAGMENT FROM A HUMAN IGM COLD AGGLUTININ	IMMUNE SYSTEM

1DNU	TRUCTURAL ANALYSES OF HUMAN MYELOPEROXIDASE-THIOCYANATE COMPLEX	OXIDOREDUCTASE
1DOW	CRYSTAL STRUCTURE OF A CHIMERA OF BETA-CATENIN AND ALPHA-CATENIN	CELL ADHESION
1DPJ	THE STRUCTURE OF PROTEINASE A COMPLEXED WITH IA3 PEPTIDE INHIBITOR	HYDROLASE/HYDROLASE INHIBITOR
1DPP	DIPEPTIDE BINDING PROTEIN COMPLEX WITH GLYCYL-L-LEUCINE	COMPLEX (BINDING PROTEIN/PEPTIDE)
1DSZ	STRUCTURE OF THE RXR/RAR DNA-BINDING DOMAIN HETERODIMER IN COMPLEX WITH THE RETINOIC ACID RESPONSE ELEMENT DR1	TRANSCRIPTION/DNA
1DTD	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE LEECH CARBOXYPEPTIDASE INHIBITOR AND THE HUMAN CARBOXYPEPTIDASE A2 (LCI-CPA2)	HYDROLASE/HYDROLASE INHIBITOR
1DY9	INHIBITION OF THE HEPATITIS C VIRUS NS3/4A PROTEASE. THE CRYSTAL STRUCTURES OF TWO PROTEASE-INHIBITOR COMPLEXES (INHIBITOR I)	SERINE PROTEASE
1E3D	[NIFE] HYDROGENASE FROM DESULFOVIBRIO DESULFURICANS ATCC 27774	HYDROGENASE
	RIBONUCLEASE DOMAIN OF COLICIN E3 IN COMPLEX WITH ITS IMMUNITY PROTEIN	RIBONUCLEASE
1E4W	CROSSREACTIVE BINDING OF A CIRCULARIZED PEPTIDE TO AN ANTI-TGFALPHA ANTIBODY FAB-FRAGMENT	COMPLEX (ANTIBODY/ANTIGEN)
	AML1/CBF COMPLEX	TRANSCRIPTION FACTOR
1E6E	DRENODOXIN REDUCTASE/ADRENODOXIN COMPLEX OF MITOCHONDRIAL P450 SYSTEMS	OXIDOREDUCTASE
1E6V	METHYL-COENZYME M REDUCTASE FROM METHANOPYRUS KANDLERI	OXIDOREDUCTASE
1E6Y	METHYL-COENZYME M REDUCTASE FROM METHANOSARCINA BARKERI	OXIDOREDUCTASE
1E8N	PROLYL OLIGOPEPTIDASE FROM PORCINE BRAIN, MUTANT, COMPLEXED WITH PEPTIDE	HYDROLASE
1E8O	CORE OF THE ALU DOMAIN OF THE MAMMALIAN SRP	SIGNALING PROTEIN/RNA
	HSLV-HSLU FROM E.COLI	CHAPERONE
1E9Z	CRYSTAL STRUCTURE OF HELICOBACTER PYLORI UREASE	HYDROLASE
1EAK	CATALYTIC DOMAIN OF PROMMP-2 E404Q MUTANT	HYDROLYSE
1EE4	CRYSTAL STRUCTURE OF YEAST KARYOPHERIN (IMPORTIN) ALPHA IN A COMPLEX WITH A C-MYC NLS PEPTIDE	TRANSPORT PROTEIN

1EEO	CRYSTAL STRUCTURE OF PROTEIN TYROSINE PHOSPHATASE 1B COMPLEXED WITH ACETYL-E-L-E-F-PTYR-M-D-Y-E-NH2	HYDROLASE
1EER	CRYSTAL STRUCTURE OF HUMAN ERYTHROPOIETIN COMPLEXED TO ITS RECEPTOR AT 1.9 ANGSTROMS	COMPLEX (CYTOKINE/RECEPTOR)
1EF1	CRYSTAL STRUCTURE OF THE MOESIN FERM DOMAIN/TAIL DOMAIN COMPLEX	MEMBRANE PROTEIN
1EFP	ELECTRON TRANSFER FLAVOPROTEIN (ETF) FROM PARACOCCUS DENITRIFICANS	ELECTRON TRANSPORT
1EFV	THREE-DIMENSIONAL STRUCTURE OF HUMAN ELECTRON TRANSFER FLAVOPROTEIN TO 2.1 A RESOLUTION	ELECTRON TRANSPORT
1EG4	STRUCTURE OF A DYSTROPHIN WW DOMAIN FRAGMENT IN COMPLEX WITH A BETA-DYSTROGLYCAN PEPTIDE	STRUCTURAL PROTEIN
1EGJ	DOMAIN 4 OF THE BETA COMMON CHAIN IN COMPLEX WITH AN ANTIBODY	IMMUNE SYSTEM
1EGV	CRYSTAL STRUCTURE OF THE DIOL DEHYDRATASE-ADENINYLPENTYLCOBALAMIN COMPLEX FROM KLEBSELLA OXYTOCA UNDER THE ILLUMINATED CONDITION.	LYASE
1EHL	64M-2 ANTIBODY FAB COMPLEXED WITH D(5HT)(6-4)T	IMMUNE SYSTEM
1EIY	HE CRYSTAL STRUCTURE OF PHENYLALANYL-TRNA SYNTHETASE FROM THERMUS THERMOPHILUS COMPLEXED WITH COGNATE TRNAPHE	LIGASE/RNA
1EJ6	REOVIRUS CORE	VIRUS
1EJX	CRYSTAL STRUCTURE OF WILD-TYPE KLEBSIELLA AEROGENES UREASE AT 100K	HYDROLASE
1ELR	CRYSTAL STRUCTURE OF THE TPR2A DOMAIN OF HOP IN COMPLEX WITH THE HSP90 PEPTIDE MEEVD	CHAPERONE
1ELW	CRYSTAL STRUCTURE OF THE TPR1 DOMAIN OF HOP IN COMPLEX WITH A HSC70 PEPTIDE	CHAPERONE
1EM8	CRYSTAL STRUCTURE OF CHI AND PSI SUBUNIT HETERODIMER FROM DNA POL III	GENE REGULATION
1EMU	TRUCTURE OF THE AXIN RGS-HOMOLOGOUS DOMAIN IN COMPLEX WITH A SAMP REPEAT FROM APC	SIGNALING PROTEIN
1EP3	CRYSTAL STRUCTURE OF LACTOCOCCUS LACTIS DIHYDROOROTATE DEHYDROGENASE B. DATA COLLECTED UNDER CRYOGENIC CONDITIONS.	OXIDOREDUCTASE
1EQZ	X-RAY STRUCTURE OF THE NUCLEOSOME CORE PARTICLE AT 2.5 A RESOLUTION	STRUCTURAL PROTEIN/DNA
1ES0	CRYSTAL STRUCTURE OF THE MURINE CLASS II ALLELE I-A(G7) COMPLEXED WITH THE GLUTAMIC ACID DECARBOXYLASE (GAD65)	IMMUNE SYSTEM

	PEPTIDE 207-220	
1EUC	CRYSTAL STRUCTURE OF DEPHOSPHORYLATED PIG HEART, GTP-SPECIFIC SUCCINYL-COA SYNTHETASE	LIGASE
1EUV	X-RAY STRUCTURE OF THE C-TERMINAL ULP1 PROTEASE DOMAIN IN COMPLEX WITH SMT3, THE YEAST ORTHOLOG OF SUMO.	HYDROLASE
1EWP	CRUZAIN BOUND TO MOR-LEU-HPQ	HYDROLASE
1EWY	ANABAENA PCC7119 FERREDOXIN:FERREDOXIN-NADP+-REDUCTASE COMPLEX	OXIDOREDUCTASE
1EXB	STRUCTURE OF THE CYTOPLASMIC BETA SUBUNIT-T1 ASSEMBLY OF VOLTAGE-DEPENDENT K CHANNELS	METAL TRANSPORT
1EYS	RYSTAL STRUCTURE OF PHOTOSYNTHETIC REACTION CENTER FROM A THERMOPHILIC BACTERIUM, THERMOCHROMATIUM TEPIDUM	ELECTRON TRANSPORT
1EYX	CRYSTAL STRUCTURE OF R-PHYCOERYTHRIN AT 2.2 ANGSTROMS	PHOTOSYNTHESIS
1F02	CRYSTAL STRUCTURE OF C-TERMINAL 282-RESIDUE FRAGMENT OF INTIMIN IN COMPLEX WITH TRANSLOCATED INTIMIN RECEPTOR (TIR) INTIMIN-BINDING DOMAIN	CELL ADHESION
1F2R	NMR STRUCTURE OF THE HETERODIMERIC COMPLEX BETWEEN CAD DOMAINS OF CAD AND ICAD	DNA BINDING PROTEIN
1F2T	CRYSTAL STRUCTURE OF ATP-FREE RAD50 ABC-ATPASE	REPLICATION
1F3U	CRYSTAL STRUCTURE OF THE RAP30/74 INTERACTION DOMAINS OF HUMAN TFIIF	TRANSCRIPTION
1F47	THE BACTERIAL CELL-DIVISION PROTEIN ZIPA AND ITS INTERACTION WITH AN FTSZ FRAGMENT REVEALED BY X-RAY CRYSTALLOGRAPHY	CELL CYCLE
1F51	A TRANSIENT INTERACTION BETWEEN TWO PHOSPHORELAY PROTEINS TRAPPED IN A CRYSTAL LATTICE REVEALS THE MECHANISM OF MOLECULAR RECOGNITION AND PHOSPHOTRANSFER IN SINGAL TRANSDUCTION	TRANSFERASE
1F60	CRYSTAL STRUCTURE OF THE YEAST ELONGATION FACTOR COMPLEX EEF1A:EEF1BA	TRANSLATION
1F66	2.6 A CRYSTAL STRUCTURE OF A NUCLEOSOME CORE PARTICLE CONTAINING THE VARIANT HISTONE H2A.Z	STRUCTURAL PROTEIN/DNA
1F6F	CRYSTAL STRUCTURE OF THE TERNARY COMPLEX BETWEEN OVINE PLACENTAL LACTOGEN AND THE EXTRACELLULAR DOMAIN OF THE RAT PROLACTIN RECEPTOR	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR
1F80	HOLO-(ACYL CARRIER PROTEIN) SYNTHASE IN COMPLEX WITH HOLO-(ACYL CARRIER PROTEIN)	TRANSFERASE

1F8V	THE STRUCTURE OF PARIACOTO VIRUS REVEALS A DODECAHEDRAL CAGE OF DUPLEX RNA	VIRUS/RNA
1F93	CRYSTAL STRUCTURE OF A COMPLEX BETWEEN THE DIMERIZATION DOMAIN OF HNF-1 ALPHA AND THE COACTIVATOR DCOH	TRANSCRIPTION
1F99	CRYSTAL STRUCTURE OF R-PHYCOCYANIN FROM POLYSIPHONIA AT 2.4 A RESOLUTION	PHOTOSYNTHESIS
1FCD	HE STRUCTURE OF FLAVOCYTOCHROME C SULFIDE DEHYDROGENASE FROM A PURPLE PHOTOTROPHIC BACTERIUM CHROMATIUM VINOSUM AT 2.5 ANGSTROMS RESOLUTION	ELECTRON TRANSPORT(FLAVOCYTOCHROME)
1FCH	CRYSTAL STRUCTURE OF THE PTS1 COMPLEXED TO THE TPR REGION OF HUMAN PEX5	SIGNALING PROTEIN
1FFT	THE STRUCTURE OF UBIQUINOL OXIDASE FROM ESCHERICHIA COLI	OXIDOREDUCTASE
1FFV	CARBON MONOXIDE DEHYDROGENASE FROM HYDROGENOPHAGA PSEUDOFLAVA	HYDROLASE
1FH0	CRYSTAL STRUCTURE OF HUMAN CATHEPSIN V COMPLEXED WITH AN IRREVERSIBLE VINYL SULFONE INHIBITOR	HYDROLASE
1FHJ	RYSTAL STRUCTURE OF AQUOMET HEMOGLOBIN-I OF THE MANED WOLF (CHRYSOCYON BRACHYURUS) AT 2.0 RESOLUTION.	OXYGEN STORAGE/TRANSPORT
1FIP	THE STRUCTURE OF FIS MUTANT PRO61ALA ILLUSTRATES THAT THE KINK WITHIN THE LONG ALPHA-HELIX IS NOT DUE TO THE PRESENCE OF THE PROLINE RESIDUE	DNA-BINDING PROTEIN
1FIW	THREE-DIMENSIONAL STRUCTURE OF BETA-ACROSIN FROM RAM SPERMATOZOA	HYDROLASE
1FIZ	THREE DIMENSIONAL STRUCTURE OF BETA-ACROSIN FROM BOAR SPERMATOZOA	HYDROLASE
1FJG	TRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT IN COMPLEX WITH THE ANTIBIOTICS STREPTOMYCIN, SPECTINOMYCIN, AND PAROMOMYCIN	RIBOSOME
1FJM	PROTEIN SERINE/THREONINE PHOSPHATASE-1 (ALPHA ISOFORM, TYPE I) COMPLEXED WITH MICROCYSTIN-LR TOXIN	COMPLEX (HYDROLASE/TOXIN)
1FKA	STRUCTURE OF FUNCTIONALLY ACTIVATED SMALL RIBOSOMAL SUBUNIT AT 3.3 A RESOLUTION	RIBOSOME
1FLC	X-RAY STRUCTURE OF THE HAEMAGGLUTININ-ESTERASE-FUSION GLYCOPROTEIN OF INFLUENZA C VIRUS	HYDROLASE
1FLT	VEGF IN COMPLEX WITH DOMAIN 2 OF THE FLT-1 RECEPTOR	COMPLEX (GROWTH FACTOR/TRANSFERASE)
1FM0	MOLYBDOPTERIN SYNTHASE (MOAD/MOAE)	TRANSFERASE
1FN4	CRYSTAL STRUCTURE OF FAB198, AN EFFICIENT PROTECTOR OF	IMMUNE SYSTEM

	ACETYLCHOLINE RECEPTOR AGAINST MYASTHENOGENIC ANTIBODIES	
1FNG	HISTOCOMPATIBILITY ANTIGEN	IMMUNE SYSTEM
1FOS	TWO HUMAN C-FOS:C-JUN:DNA COMPLEXES	TRANSCRIPTION/DNA
1FPR	CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN THE CATALYTIC DOMAIN OF SHP-1 AND AN IN VITRO PEPTIDE SUBSTRATE PY469 DERIVED FROM SHPS-1.	SIGNALING PROTEIN
1FS0	COMPLEX OF GAMMA/EPSILON ATP SYNTHASE FROM E.COLI	HYDROLASE
1FS1	INSIGHTS INTO SCF UBIQUITIN LIGASES FROM THE STRUCTURE OF THE SKP1-SKP2 COMPLEX	LIGASE
1FVU	CRYSTAL STRUCTURE OF BOTROCETIN	TOXIN
1FXW	CRYSTAL STRUCTURE OF THE RECOMBINANT ALPHA1/ALPHA2 CATALYTIC HETERODIMER OF BOVINE BRAIN PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB.	HYDROLASE
1FXY	COAGULATION FACTOR XA-TRYPSIN CHIMERA INHIBITED WITH D-PHE-PRO-ARG-CHLOROMETHYLKETONE	COMPLEX (PROTEASE/INHIBITOR)
1FY4	FUSARIUM OXYSPORUM TRYPSIN AT ATOMIC RESOLUTION	HYDROLASE
1FYH	1:1 COMPLEX BETWEEN AN INTERFERON GAMMA SINGLE-CHAIN VARIANT AND ITS RECEPTOR	IMMUNE SYSTEM
1G1S	P-SELECTIN LECTIN/EGF DOMAINS COMPLEXED WITH PSGL-1 PEPTIDE	IMMUNE SYSTEM, MEMBRANE PROTEIN
1G1X	STRUCTURE OF RIBOSOMAL PROTEINS S15, S6, S18, AND 16S RIBOSOMAL RNA	RIBOSOME
1G2C	HUMAN RESPIRATORY SYNCYTIAL VIRUS FUSION PROTEIN CORE	VIRAL PROTEIN
1G5J	COMPLEX OF BCL-XL WITH PEPTIDE FROM BAD	APOPTOSIS
1G5Q	EPID H67N COMPLEXED WITH SUBSTRATE PEPTIDE DSYTC	OXIDOREDUCTASE
1G6V	COMPLEX OF THE CAMELID HEAVY-CHAIN ANTIBODY FRAGMENT CAB-CA05 WITH BOVINE CARBONIC ANHYDRASE	LYASE/IMMUNE SYSTEM
1G73	CRYSTAL STRUCTURE OF SMAC BOUND TO XIAP-BIR3 DOMAIN	APOPTOSIS/APOPTOSIS INHIBITOR
1G8K	CRYSTAL STRUCTURE ANALYSIS OF ARSENITE OXIDASE FROM ALCALIGENES FAECALIS	OXIDOREDUCTASE
1GAQ	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN FERREDOXIN AND FERREDOXIN-NADP+ REDUCTASE	OXIDOREDUCTASE/ELECTRON TRANSPORT
1GCV	DEOXY FORM HEMOGLOBIN FROM MUSTELUS GRISEUS	OXYGEN STORAGE/TRANSPORT
1GEC	LYCYL ENDOPEPTIDASE-COMPLEX WITH BENZYLOXYCARBONYL-LEUCINE-VALINE-GLYCINE-METHYLENE COVALENTLY BOUND TO CYSTEINE 25	COMPLEX (PROTEINASE/INHIBITOR)

1GGP	CRYSTAL STRUCTURE OF TRICHOSANTHES KIRILOWII LECTIN-1 AND ITS RELATION TO THE TYPE 2 RIBOSOME INACTIVATING PROTEINS	SUGAR BINDING PROTEIN
1GH0	CRYSTAL STRUCTURE OF C-PHYCOCYANIN FROM SPIRULINA PLATENSIS	PHOTOSYNTHESIS
1GHQ	CR2-C3D COMPLEX STRUCTURE	IMMUNE SYSTEM/VIRAL PROTEIN RECEPTOR
1GK8	RUBISCO FROM CHLAMYDOMONAS REINHARDTII	LYASE
1GK9	CRYSTAL STRUCTURES OF PENICILLIN ACYLASE ENZYME-SUBSTRATE COMPLEXES: STRUCTURAL INSIGHTS INTO THE CATALYTIC MECHANISM	ANTIBIOTIC RESISTANCE
1GLC	CATION PROMOTED ASSOCIATION (CPA) OF A REGULATORY AND TARGET PROTEIN IS CONTROLLED BY PHOSPHORYLATION	PHOSPHOTRANSFERASE
1GO3	STRUCTURE OF AN ARCHEAL HOMOLOG OF THE EUKARYOTIC RNA POLYMERASE II RPB4/RPB7 COMPLEX	TRANSFERASE
1GO4	CRYSTAL STRUCTURE OF MAD1-MAD2 REVEALS A CONSERVED MAD2 BINDING MOTIF IN MAD1 AND CDC20.	CELL CYCLE
1GOT	HETEROTRIMERIC COMPLEX OF A GT-ALPHA/GI-ALPHA CHIMERA AND THE GT-BETA-GAMMA SUBUNITS	COMPLEX (GTP-BINDING/TRANSDUCER)
1GPW	STRUCTURAL EVIDENCE FOR AMMONIA TUNNELING ACROSS THE (BETA/ALPHA)8 BARREL OF THE IMIDAZOLE GLYCEROL PHOSPHATE SYNTHASE BIENZYME COMPLEX.	COMPLEX (LYASE/TRANSFERASE)
1GUL	HUMAN GLUTATHIONE TRANSFERASE A4-4 COMPLEX WITH IODOBENZYL GLUTATHIONE	TRANSFERASE
1GVU	ENDOTHIAPEPSIN COMPLEX WITH H189	HYDROLASE
1GXS	CRYSTAL STRUCTURE OF HYDROXYNITRILE LYASE FROM SORGHUM BICOLOR IN COMPLEX WITH INHIBITOR BENZOIC ACID: A NOVEL CYANOGENIC ENZYME	LYASE
1GYB	N77Y POINT MUTANT OF YNTF2 BOUND TO FXFG NUCLEOPORIN REPEAT	NUCLEAR TRANSPORT
1H0H	TUNGSTEN CONTAINING FORMATE DEHYDROGENASE FROM DESULFOVIBRIO GIGAS	DEHYDROGENASE
1H0I	COMPLEX OF A CHITINASE WITH THE NATURAL PRODUCT CYCLOPENTAPEPTIDE ARGIFIN FROM GLIOCLADIU	HYDROLASE
1H2K	FACTOR INHIBITING HIF-1 ALPHA IN COMPLEX WITH HIF-1 ALPHA FRAGMENT PEPTIDE	TRANSCRIPTION ACTIVATOR/INHIBITOR
1H2S	MOLECULAR BASIS OF TRANSMENBRANE SIGNALLING BY SENSORY RHODOPSIN II-TRANSDUCER COMPLEX	MENBRANE PROTEIN COMPLEX
1H3O	CRYSTAL STRUCTURE OF THE HUMAN TAF4-TAF12 (TAFII135-TAFII20) COMPLEX	TRANSCRIPTION/TBP-ASSOCIATED FACTORS

1H4I	ETHYLOBACTERIUM EXTORQUENS METHANOL DEHYDROGENASE	DEHYDROGENASE
1H4L	STRUCTURE AND REGULATION OF THE CDK5-P25(NCK5A) COMPLEX	COMPLEX(CYCLINS/CDK)
1H6W	RYSTAL STRUCTURE OF A HEAT-AND PROTEASE-STABLE FRAGMENT OF THE BACTERIOPHAGE T4 SHORT FIBRE	STRUCTURAL PROTEIN
1H88	CRYSTAL STRUCTURE OF TERNARY PROTEIN-DNA COMPLEX1	TRANSCRIPTION/DNA
1H89	CRYSTAL STRUCTURE OF TERNARY PROTEIN-DNA COMPLEX2	TRANSCRIPTION/DNA
1H8A	CRYSTAL STRUCTURE OF TERNARY PROTEIN-DNA COMPLEX3	TRANSCRIPTION/DNA
1H8T	ECHOVIRUS 11	VIRUS
1H9D	AML1/CBF-BETA/DNA COMPLEX	TRANSCRIPTION/DNA
1HAO	COMPLEX OF HUMAN ALPHA-THROMBIN WITH A 15MER OLIGONUCLEOTIDE GGTTGGTGTGGTTGG (BASED ON NMR MODEL OF DNA	HYDROLASE/HYDROLASE INHIBITOR/DNA
1HBN	METHYL-COENZYME M REDUCTASE	METHANOGENESIS
1HBX	TERNARY COMPLEX OF SAP-1 AND SRF WITH SPECIFIC SRE DNA	GENE REGULATION/DNA
1HCN	TRUCTURE OF HUMAN CHORIONIC GONADOTROPIN AT 2.6 ANGSTROMS RESOLUTION FROM MAD ANALYSIS OF THE SELENOMETHIONYL PROTEIN	HORMONE
1HDM	HISTOCOMPATIBILITY ANTIGEN HLA-DM	IMMUNE SYSTEM
1HDS	ACROMOLECULAR STRUCTURE REFINEMENT BY RESTRAINED LEAST-SQUARES AND INTERACTIVE GRAPHICS AS APPLIED TO SICKLING DEER TYPE III HEMOGLOBIN	OXYGEN TRANSPORT
1HFE	.6 A RESOLUTION STRUCTURE OF THE FE-ONLY HYDROGENASE FROM DESULFOVIBRIO DESULFURICANS	HYDROGENASE
1HIL	STRUCTURAL EVIDENCE FOR INDUCED FIT AS A MECHANISM FOR ANTIGEN-ANTIBODY RECOGNITION	IMMUNOGLOBULIN
1HJB	RYSTAL STRUCTURE OF RUNX-1/AML1/CBFALPHA RUNT DOMAIN AND C/EBPBETA BZIP HOMODIMER BOUND TO A DNA FRAGMENT FROM THE CSF-1R PROMOTER	TRANSCRIPTION/DNA
1HLE	CRYSTAL STRUCTURE OF CLEAVED EQUINE LEUCOCYTE ELASTASE INHIBITOR DETERMINED AT 1.95 ANGSTROMS RESOLUTION	HYDROLASE INHIBITOR(SERINE PROTEINASE)
1HNW	TRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT IN COMPLEX WITH TETRACYCLINE	RIBOSOME
1HNZ	TRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT IN COMPLEX WITH HYGROMYCIN B	RIBOSOME
1HPG	A GLUTAMIC ACID SPECIFIC SERINE PROTEASE UTILIZES A NOVEL HISTIDINE TRIAD IN SUBSTRATE BINDING	HYDROLASE (SERINE PROTEASE)

1HR0	CRYSTAL STRUCTURE OF INITIATION FACTOR IF1 BOUND TO THE 30S RIBOSOMAL SUBUNIT	RIBOSOME
1HR6	YEAST MITOCHONDRIAL PROCESSING PEPTIDASE	HYDROLASE
1HTR	RYSTAL AND MOLECULAR STRUCTURES OF HUMAN PROGASTRICSIN AT 1.62 ANGSTROMS RESOLUTION	ASPARTYL PROTEASE
1HTT	HISTIDYL-TRNA SYNTHETASE	COMPLEX (TRNA SYNTHETASE/HIS-ADENYLATE)
1HUT	THE STRUCTURE OF ALPHA-THROMBIN INHIBITED BY A 15-MER SINGLE-STRANDED DNA APTAMER	HYDROLASE, BLOOD CLOTTING/DNA
1HVU	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 REVERSE TRANSCRIPTASE COMPLEXED WITH A 33-BASE NUCLEOTIDE RNA PSEUDOKNOT	TRANSFERASE/RNA
1HWM	EBULIN,ORTHORHOMBIC CRYSTAL FORM MODEL	HYDROLASE
1HXM	RYSTAL STRUCTURE OF A HUMAN VGAMMA9/VDELTA2 T CELL RECEPTOR	IMMUNE SYSTEM
1HYS	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH A POLYPURINE TRACT RNA:DNA	TRANSFERASE/DNA/RNA
1I1Q	STRUCTURE OF THE COOPERATIVE ALLOSTERIC ANTHRANILATE SYNTHASE FROM SALMONELLA TYPHIMURIUM	LYASE
1I1R	CRYSTAL STRUCTURE OF A CYTOKINE/RECEPTOR COMPLEX	CYTOKINE
1I2M	RAN-RCC1-SO4 COMPLEX	CELL CYCLE
1I6H	RNA POLYMERASE II ELONGATION COMPLEX	TRANSCRIPTION/DNA/RNA
1I73	COMPLEX OF PRO-LEU-L-TRP PHOSPHONATE WITH THE CATALITIC DOMAIN OF MATRIX METALLO PROTEINASE-8 (MET80 FORM)	HYDROLASE
1I7A	EVH1 DOMAIN FROM MURINE HOMER 2B/VESL 2	SIGNALING PROTEIN
1I7S	ANTHRANILATE SYNTHASE FROM SERRATIA MARCESCENS IN COMPLEX WITH ITS END PRODUCT INHIBITOR L-TRYPTOPHAN	LYASE
1I8L	HUMAN B7-1/CTLA-4 CO-STIMULATORY COMPLEX	IMMUNE SYSTEM
1I8M	CRYSTAL STRUCTURE OF A RECOMBINANT ANTI-SINGLE-STRANDED DNA ANTIBODY FRAGMENT COMPLEXED WITH DT5	IMMUNE SYSTEM/DNA
1I94	CRYSTAL STRUCTURES OF THE SMALL RIBOSOMAL SUBUNIT WITH TETRACYCLINE, EDEINE AND IF3	RIBOSOME
1IAK	HISTOCOMPATIBILITY ANTIGEN I-AK	HISTOCOMPATIBILITY ANTIGEN I-AK
1IAR	INTERLEUKIN-4 / RECEPTOR ALPHA CHAIN COMPLEX	CYTOKINE/RECEPTOR
1IAU	HUMAN GRANZYME B IN COMPLEX WITH AC-IEPD-CHO	HYDROLASE
1IBK	TRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT	RIBOSOME

	IN COMPLEX WITH THE ANTIBIOTIC PAROMOMYCIN	
1ID3	CRYSTAL STRUCTURE OF THE YEAST NUCLEOSOME CORE PARTICLE REVEALS FUNDAMENTAL DIFFERENCES IN INTER-NUCLEOSOME INTERACTIONS	STRUCTURAL PROTEIN/DNA
1IHF	INTEGRATION HOST FACTOR/DNA COMPLEX	TRANSCRIPTION/DNA
1IHJ	CRYSTAL STRUCTURE OF THE N-TERMINAL PDZ DOMAIN OF INAD IN COMPLEX WITH A NORPA C-TERMINAL PEPTIDE	SIGNALING PROTEIN
1IJD	CRYSTALLOGRAPHIC STRUCTURE OF THE LH3 COMPLEX FROM RHODOPSEUDOMONAS ACIDOPHILA STRAIN 7050	PHOTOSYNTHESIS
1IK9	CRYSTAL STRUCTURE OF A XRCC4-DNA LIGASE IV COMPLEX	GENE REGULATION/LIGASE
1ILQ	CXCR-1 N-TERMINAL PEPTIDE BOUND TO INTERLEUKIN-8 (MINIMIZED MEAN)	CYTOKINE
1IO4	CRYSTAL STRUCTURE OF RUNX-1/AML1/CBFALPHA RUNT DOMAIN-CBFBETA CORE DOMAIN HETERODIMER AND C/EBPBETA BZIP HOMODIMER BOUND TO A DNA FRAGMENT FROM THE CSF-1R PROMOTER	TRANSCRIPTION/DNA
1IRD	RYSTAL STRUCTURE OF HUMAN CARBONMONOXY-HAEMOGLOBIN AT 1.25 A RESOLUTION	OXYGEN STORAGE/TRANSPORT
1IRS	IRS-1 PTB DOMAIN COMPLEXED WITH A IL-4 RECEPTOR PHOSPHOPEPTIDE, NMR, MINIMIZED AVERAGE STRUCTURE	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)
1IRU	CRYSTAL STRUCTURE OF THE MAMMALIAN 20S PROTEASOME AT 2.75 A RESOLUTION	HYDROLASE
1IS8	CRYSTAL STRUCTURE OF RAT GTPCHI/GFRP STIMULATORY COMPLEX PLUS ZN	HYDROLASE/PROTEIN BINDING
1ISQ	YROCOCCUS FURIOSUS PCNA COMPLEXED WITH RFCL PIP-BOX PEPTIDE	DNA BINDING PROTEIN
1IWP	LYCEROL DEHYDRATASE-CYANOCOBALAMIN COMPLEX OF KLEBSIELLA PNEUMONIAE	LYASE
1IXS	STRUCTURE OF RUVB COMPLEXED WITH RUVA DOMAIN III	HYDROLASE
1IZN	CRYSTAL STRUCTURE OF ACTIN FILAMENT CAPPING PROTEIN CAPZ	PROTEIN BINDING
1J1D	CRYSTAL STRUCTURE OF THE 46KDA DOMAIN OF HUMAN CARDIAC TROPONIN IN THE CA2+ SATURATED FORM	CONTRACTILE PROTEIN
1J2X	RYSTAL STRUCTURE OF RAP74 C-TERMINAL DOMAIN COMPLEXED WITH FCP1 C-TERMINAL PEPTIDE	TRANSCRIPTION
1J34	CRYSTAL STRUCTURE OF MG(II)-AND CA(II)-BOUND GLA DOMAIN OF FACTOR IX COMPLEXED WITH BINDING PROTEIN	PROTEIN BINDING/BLOOD CLOTTING
1J3K	QUADRUPLE MUTANT (N51I+C59R+S108N+I164L) PLASMODIUM FALCIPARUM DIHYDROFOLATE REDUCTASE-THYMIDYLATE SYNTHASE	OXIDOREDUCTASE, TRANSFERASE

	(PFDHFR-TS) COMPLEXED WITH WR99210, NADPH, AND DUMP	
1J4X	HUMAN VH1-RELATED DUAL-SPECIFICITY PHOSPHATASE C124S MUTANT-PEPTIDE COMPLEX	HYDROLASE
1J5O	CRYSTAL STRUCTURE OF MET184ILE MUTANT OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH DOUBLE STRANDED DNA TEMPLATE-PRIMER	TRANSFERASE/IMMUNE SYSTEM/DNA
1J7D	CRYSTAL STRUCTURE OF HMMS2-HUBC13	UNKNOWN FUNCTION
1JAT	MMS2/UBC13 UBIQUITIN CONJUGATING ENZYME COMPLEX	LIGASE
1JB0	CRYSTAL STRUCTURE OF PHOTOSYSTEM I: A PHOTOSYNTHETIC REACTION CENTER AND CORE ANTENNA SYSTEM FROM CYANOBACTERIA	PHOTOSYNTHESIS
1JB7	DNA G-QUARTETS IN A 1.86 A RESOLUTION STRUCTURE OF AN OXYTRICHA NOVA TELOMERIC PROTEIN-DNA COMPLEX	DNA-BINDING PROTEIN/DNA
1JBO	THE 1.45A THREE-DIMENSIONAL STRUCTURE OF C-PHYCOCYANIN FROM THE THERMOPHYLIC CYANOBACTERIUM SYNECHOCOCCUS ELONGATUS	PHOTOSYNTHESIS
1JD5	CRYSTAL STRUCTURE OF DIAP1-BIR2/GRIM	APOPTOSIS
1JDP	CRYSTAL STRUCTURE OF HORMONE/RECEPTOR COMPLEX	SIGNALING PROTEIN
1JEB	HIMERIC HUMAN/MOUSE CARBONMONOXY HEMOGLOBIN (HUMAN ZETA2 / MOUSE BETA2)	OXYGEN STORAGE/TRANSPORT
1JEK	VISNA TM CORE STRUCTURE	VIRAL PROTEIN
1JEQ	CRYSTAL STRUCTURE OF THE KU HETERODIMER	DNA BINDING PROTEIN
1JET	OLIGO-PEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH KAK	COMPLEX (PEPTIDE TRANSPORT/PEPTIDE)
1JEY	CRYSTAL STRUCTURE OF THE KU HETERODIMER BOUND TO DNA	DNA BINDING PROTEIN/DNA
1JFI	CRYSTAL STRUCTURE OF THE NC2-TBP-DNA TERNARY COMPLEX	TRANSCRIPTION/DNA
1JG3	CRYSTAL STRUCTURE OF L-ISOASPARTYL (D-ASPARTYL) O-METHYLTRANSFERASE WITH ADENOSINE & VYP(ISP)HA SUBSTRATE	TRANSFERASE
1JHL	THREE-DIMENSIONAL STRUCTURE OF A HETEROCLITIC ANTIGEN-ANTIBODY CROSS-REACTION COMPLEX	COMPLEX(ANTIBODY-ANTIGEN)
1JJ2	FULLY REFINED CRYSTAL STRUCTURE OF THE HALOARCULA MARISMORTUI LARGE RIBOSOMAL SUBUNIT AT 2.4 ANGSTROM RESOLUTION	RIBOSOME
1JJC	CRYSTAL STRUCTURE AT 2.6A RESOLUTION OF PHENYLALANYL-TRNA SYNTHETASE COMPLEXED WITH PHENYLALANYL-ADENYLATE IN THE PRESENCE OF MANGANESE	LIGASE
1JJO	CRYSTAL STRUCTURE OF MOUSE NEUROSERPIN (CLEAVED FORM)	SIGNALING PROTEIN

1JK0	RIBONUCLEOTIDE REDUCTASE Y2Y4 HETERODIMER	OXIDOREDUCTASE
1JK4	DES 1-6 BOVINE NEUROPHYSIN II COMPLEX WITH VASOPRESSIN	NEUROPEPTIDE
1JK9	HETERODIMER BETWEEN H48F-YSOD1 AND YCCS	OXIDOREDUCTASE
1JLT	VIPOXIN COMPLEX	HYDROLASE
1JMA	CRYSTAL STRUCTURE OF THE HERPES SIMPLEX VIRUS GLYCOPROTEIN D BOUND TO THE CELLULAR RECEPTOR HVEA/HVEM	VIRAL PROTEIN
1JMT	X-RAY STRUCTURE OF A CORE U2AF65/U2AF35 HETERODIMER	RNA BINDING PROTEIN
1JMX	RYSTAL STRUCTURE OF A QUINOHEMOPROTEIN AMINE DEHYDROGENASE FROM PSEUDOMONAS PUTIDA	OXIDOREDUCTASE
1JNH	CRYSTAL STRUCTURE OF FAB-ESTRADIOL COMPLEXES	IMMUNE SYSTEM
1JNR	STRUCTURE OF ADENYLYLSULFATE REDUCTASE FROM THE HYPERTHERMOPHILIC ARCHAEOGLOBUS FULGIDUS AT 1.6 RESOLUTION	OXIDOREDUCTASE
1JRO	CRYSTAL STRUCTURE OF XANTHINE DEHYDROGENASE FROM RHODOBACTER CAPSULATUS	OXIDOREDUCTASE
1JRR	HUMAN PLASMINOGEN ACTIVATOR INHIBITOR-2.[LOOP (66-98) DELETIONMUTANT] COMPLEXED WITH PEPTIDE MIMICKING THE REACTIVE CENTER LOOP	PEPTIDE BINDING PROTEIN
1JSD	CRYSTAL STRUCTURE OF SWINE H9 HAEMAGGLUTININ	VIRAL PROTEIN
1JSM	STRUCTURE OF H5 AVIAN HAEMAGGLUTININ	VIRAL PROTEIN
1JUQ	GGA3 VHS DOMAIN COMPLEXED WITH C-TERMINAL PEPTIDE FROM CATION-DEPENDENT MANNOSE 6-PHOSPHATE RECEPTOR	SIGNALING PROTEIN
1JWI	CRYSTAL STRUCTURE OF BITISCETIN, A VON WILLEBAND FACTOR-DEPENDENT PLATELET AGGREGATION INDUCER.	TOXIN
1JX2	CRYSTAL STRUCTURE OF THE NUCLEOTIDE-FREE DYNAMIN A GTPASE DOMAIN, DETERMINED AS MYOSIN FUSION	HYDROLASE
1JY2	CRYSTAL STRUCTURE OF THE CENTRAL REGION OF BOVINE FIBRINOGEN (E5 FRAGMENT) AT 1.4 ANGSTROMS RESOLUTION	BLOOD CLOTTING
1JYO	STRUCTURE OF THE SALMONELLA VIRULENCE EFFECTOR SPTP IN COMPLEX WITH ITS SECRETION CHAPERONE SICP	CHAPERONE
1JYR	XRAY STRUCTURE OF GRB2 SH2 DOMAIN COMPLEXED WITH A PHOSPHORYLATED PEPTIDE	SIGNALING PROTEIN
1K3A	STRUCTURE OF THE INSULIN-LIKE GROWTH FACTOR 1 RECEPTOR KINASE	TRANSFERASE
1K5N	HLA-B*2709 BOUND TO NONA-PEPTIDE M9	IMMUNE SYSTEM

1K6O	CRYSTAL STRUCTURE OF A TERNARY SAP-1/SRF/C-FOS SRE DNA COMPLEX	TRANSCRIPTION/DNA
1K73	CO-CRYSTAL STRUCTURE OF ANISOMYCIN BOUND TO THE 50S RIBOSOMAL SUBUNIT	RIBOSOME
1K78	PAX5(1-149)+ETS-1(331-440)+DNA	TRANSCRIPTION/DNA
1K8A	CO-CRYSTAL STRUCTURE OF CARBOMYCIN A BOUND TO THE 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1K8I	CRYSTAL STRUCTURE OF MOUSE H2-DM	IMMUNE SYSTEM
1K8K	CRYSTAL STRUCTURE OF ARP2/3 COMPLEX	STRUCTURAL PROTEIN
1K9M	CO-CRYSTAL STRUCTURE OF TYLOSIN BOUND TO THE 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1KA9	IMIDAZOLE GLYCEROL PHOSPHATE SYNTHASE	TRANSFERASE
1KAP	THREE-DIMENSIONAL STRUCTURE OF THE ALKALINE PROTEASE OF PSEUDOMONAS AERUGINOSA: A TWO-DOMAIN PROTEIN WITH A CALCIUM BINDING PARALLEL BETA ROLL MOTIF	ZINC METALLOPROTEASE
1KC8	CO-CRYSTAL STRUCTURE OF BLASTICIDIN S BOUND TO THE 50S RIBOSOMAL SUBUNIT	RIBOSOME
1KCG	NKG2D IN COMPLEX WITH ULBP3	IMMUNE SYSTEM
1KCV	CRYSTAL STRUCTURE OF ANTIBODY PC282	IMMUNE SYSTEM
1KD1	CO-CRYSTAL STRUCTURE OF SPIRAMYCIN BOUND TO THE 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1KD8	X-RAY STRUCTURE OF THE COILED COIL GCN4 ACID BASE HETERODIMER ACID-D12IA16V BASE-D12LA16L	DE NOVO PROTEIN
1KDV	SEUDOMONAS SERINE-CARBOXYL PROTEINASE COMPLEXED WITH THE INHIBITOR AIAF (THIS ENZYME RENAMED "SEDOLISIN" IN 2003)	HYDROLASE
1KDX	KIX DOMAIN OF MOUSE CBP (CREB BINDING PROTEIN) IN COMPLEX WITH PHOSPHORYLATED KINASE INDUCIBLE DOMAIN (PKID) OF RAT CREB (CYCLIC AMP RESPONSE ELEMENT BINDING PROTEIN), NMR 17 STRUCTURES	TRANSCRIPTION REGULATION COMPLEX
1KEG	ANTIBODY 64M-2 FAB COMPLEXED WITH DTT(6-4)TT	IMMUNE SYSTEM/DNA
1KF6	E. COLI QUINOL-FUMARATE REDUCTASE WITH BOUND INHIBITOR HQNO	OXIDOREDUCTASE
1KGC	IMMUNE RECEPTOR	IMMUNE SYSTEM
1KHQ	ORTHORHOMBIC FORM OF PAPAIN/ZLFG-DAM COVALENT COMPLEX	HYDROLASE
1KIG	BOVINE FACTOR XA	COMPLEX (PROTEASE/INHIBITOR)

1KJV	TAP-B-ASSOCIATED RAT MHC CLASS I MOLECULE	IMMUNE SYSTEM
1KMH	CRYSTAL STRUCTURE OF SPINACH CHLOROPLAST F1-ATPASE COMPLEXED WITH TENTOXIN	HYDROLASE
1KN1	CRYSTAL STRUCTURE OF ALLOPHYCOCYANIN	ELECTRON TRANSPORT
1KQF	FORMATE DEHYDROGENASE N FROM E. COLI	OXIDOREDUCTASE
1KQS	THE HALOARCULA MARISMORTUI 50S COMPLEXED WITH A PRETRANSLOCATIONAL INTERMEDIATE IN PROTEIN SYNTHESIS	RIBOSOME
1KSH	COMPLEX OF ARL2 AND PDE DELTA, CRYSTAL FORM 2 (NATIVE)	SIGNALING PROTEIN/HYDROLASE
1KTZ	CRYSTAL STRUCTURE OF THE HUMAN TGF-BETA TYPE II RECEPTOR EXTRACELLULAR DOMAIN IN COMPLEX WITH TGF-BETA3	CYTOKINE/CYTOKINE RECEPTOR
1KU6	FASCICULIN 2-MOUSE ACETYLCHOLINESTERASE COMPLEX	HYDROLASE/TOXIN
1KUG	CRYSTAL STRUCTURE OF A TAIWAN HABU VENOM METALLOPROTEINASE COMPLEXED WITH ITS ENDOGENOUS INHIBITOR PENW	HYDROLASE
1KVE	KILLER TOXIN FROM HALOTOLERANT YEAST	TOXIN
1KX3	X-RAY STRUCTURE OF THE NUCLEOSOME CORE PARTICLE, NCP146, AT 2.0 A RESOLUTION	STRUCTURAL PROTEIN/DNA
1KX5	X-RAY STRUCTURE OF THE NUCLEOSOME CORE PARTICLE, NCP147, AT 1.9 A RESOLUTION	STRUCTURAL PROTEIN/DNA
1KXQ	CAMELID VHH DOMAIN IN COMPLEX WITH PORCINE PANCREATIC ALPHA-AMYLASE	HYDROLASE, IMMUNE SYSTEM
1KYF	AP-2 CLATHRIN ADAPTOR ALPHA-APPENDAGE IN COMPLEX WITH EPS15 DPF PEPTIDE	ENDOCYTOSIS/EXOCYTOSIS
1L2W	CRYSTAL STRUCTURE OF THE YERSINIA VIRULENCE EFFECTOR YOPE CHAPERONE-BINDING DOMAIN IN COMPLEX WITH ITS SECRETION CHAPERONE, SYCE	CHAPERONE
1L4A	X-RAY STRUCTURE OF THE NEURONAL COMPLEXIN/SNARE COMPLEX FROM THE SQUID LOLIGO PEALEI	ENDOCYTOSIS/EXOCYTOSIS
1L4D	RYSTAL STRUCTURE OF MICROPLASMINOGEN-STREPTOKINASE ALPHA DOMAIN COMPLEX	HYDROLASE/HYDROLASE ACTIVATOR
1L6O	XENOPUS DISHEVELLED PDZ DOMAIN	GENE REGULATION
1LB2	STRUCTURE OF THE E. COLI ALPHA C-TERMINAL DOMAIN OF RNA POLYMERASE IN COMPLEX WITH CAP AND DNA	GENE REGULATION/DNA
1LE8	CRYSTAL STRUCTURE OF THE MATA1/MATALPHA2-3A HETERODIMER BOUND TO DNA COMPLEX	TRANSCRIPTION/DNA
1LEN	REFINEMENT OF TWO CRYSTAL FORMS OF LENTIL LECTIN AT 1.8	LECTIN

	ANGSTROMS RESOLUTION	
1LGH	CRYSTAL STRUCTURE OF THE LIGHT-HARVESTING COMPLEX II (B800-850) FROM RHODOSPIRILLUM MOLISCHIANUM	LIGHT HARVESTING COMPLEX
1LIA	CRYSTAL STRUCTURE OF R-PHYCOERYTHRIN FROM POLYSIPHONIA AT 2.8 A RESOLUTION	LIGHT HARVESTING PROTEIN
1LJ2	RECOGNITION OF EIF4G BY ROTAVIRUS NSP3 REVEALS A BASIS FOR MRNA CIRCULARIZATION	VIRAL PROTEIN/ TRANSLATION
1LK3	ENGINEERED HUMAN INTERLEUKIN-10 MONOMER COMPLEXED TO 9D7 FAB FRAGMENT	IMMUNE SYSTEM
1LKK	HUMAN P56-LCK TYROSINE KINASE SH2 DOMAIN IN COMPLEX WITH THE PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU-ILE (PYEEI PEPTIDE)	COMPLEX (TYROSINE KINASE/PEPTIDE)
1LM8	STRUCTURE OF A HIF-1A-PVHL-ELONGINB-ELONGINC COMPLEX	TRANSCRIPTION
1LOE	X-RAY CRYSTAL STRUCTURE DETERMINATION AND REFINEMENT AT 1.9 ANGSTROMS RESOLUTION OF ISOLECTIN I FROM THE SEEDS OF LATHYRUS OCHRUS	LECTIN
1LP1	PROTEIN Z IN COMPLEX WITH AN IN VITRO SELECTED AFFIBODY	IMMUNE SYSTEM
1LPB	THE 2.46 ANGSTROMS RESOLUTION STRUCTURE OF THE PANCREATIC LIPASE COLIPASE COMPLEX INHIBITED BY A C11 ALKYL PHOSPHONATE	HYDROLASE(CARBOXYLIC ESTERASE)
1LQV	CRYSTAL STRUCTURE OF THE ENDOTHELIAL PROTEIN C RECEPTOR WITH PHOSPHOLIPID IN THE GROOVE IN COMPLEX WITH GLA DOMAIN OF PROTEIN C.	BLOOD CLOTTING
1LRW	CRYSTAL STRUCTURE OF METHANOL DEHYDROGENASE FROM P. DENITRIFICANS	OXIDOREDUCTASE
1LSH	LIPID-PROTEIN INTERACTIONS IN LIPOVITELLIN	LIPID BINDING PROTEIN
1LVM	CATALYTICALLY ACTIVE TOBACCO ETCH VIRUS PROTEASE COMPLEXED WITH PRODUCT	VIRAL PROTEIN
1LWU	CRYSTAL STRUCTURE OF FRAGMENT D FROM LAMPREY FIBRINOGEN COMPLEXED WITH THE PEPTIDE GLY-HIS-ARG-PRO-AMIDE	BLOOD CLOTTING
1LYB	CRYSTAL STRUCTURES OF NATIVE AND INHIBITED FORMS OF HUMAN CATHEPSIN D: IMPLICATIONS FOR LYSOSOMAL TARGETING AND DRUG DESIGN	LYSOSOMAL ASPARTIC PROTEASE
1M06	STRUCTURAL STUDIES OF BACTERIOPHAGE ALPHA3 ASSEMBLY, X-RAY CRYSTALLOGRAPHY	VIRUS/DNA
1M18	LIGAND BINDING ALTERS THE STRUCTURE AND DYNAMICS OF NUCLEOSOMAL DNA	STRUCTURAL PROTEIN/DNA

1M19	LIGAND BINDING ALTERS THE STRUCTURE AND DYNAMICS OF NUCLEOSOMAL DNA	STRUCTURAL PROTEIN/DNA
1M1A	LIGAND BINDING ALTERS THE STRUCTURE AND DYNAMICS OF NUCLEOSOMAL DNA	STRUCTURAL PROTEIN/DNA
1M1J	CRYSTAL STRUCTURE OF NATIVE CHICKEN FIBRINOGEN WITH TWO DIFFERENT BOUND LIGANDS	BLOOD CLOTTING
1M1K	CO-CRYSTAL STRUCTURE OF AZITHROMYCIN BOUND TO THE 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1M1N	NITROGENASE MOFE PROTEIN FROM AZOTOBACTER VINELANDII	OXIDOREDUCTASE
1M2T	MISTLETOE LECTIN I FROM VISCUM ALBUM IN COMPLEX WITH ADENINE MONOPHOSPHATE. CRYSTAL STRUCTURE AT 1.9 A RESOLUTION	RIBOSOME INHIBITOR, HYDROLASE
1M45	CRYSTAL STRUCTURE OF MLC1P BOUND TO IQ2 OF MYO2P, A CLASS V MYOSIN	CELL CYCLE PROTEIN
1M4U	CRYSTAL STRUCTURE OF BONE MORPHOGENETIC PROTEIN-7 (BMP-7) IN COMPLEX WITH THE SECRETED ANTAGONIST NOGGIN	HORMONE/GROWTH FACTOR
1M6X	FLPE-HOLLIDAY JUNCTION COMPLEX	LIGASE, LYASE/DNA
1M72	RYSTAL STRUCTURE OF CASPASE-1 FROM SPODOPTERA FRUGIPERDA	HYDROLASE
1M7E	CRYSTAL STRUCTURE OF THE PHOSPHOTYROSINE BINDING DOMAIN(PTB) OF MOUSE DISABLED 2(DAB2):IMPLICATIONS FOR REELING SIGNALING	SIGNALING PROTEIN
1M90	CO-CRYSTAL STRUCTURE OF CCA-PHE-CAPROIC ACID-BIOTIN AND SPARSOMYCIN BOUND TO THE 50S RIBOSOMAL SUBUNIT	RIBOSOME
1MA3	STRUCTURE OF A SIR2 ENZYME BOUND TO AN ACETYLATED P53 PEPTIDE	PROTEIN BINDING, TRANSCRIPTION
1MCI	PRINCIPLES AND PITFALLS IN DESIGNING SITE DIRECTED PEPTIDE LIGANDS	IMMUNOGLOBULIN
1MCP	PHOSPHOCHOLINE BINDING IMMUNOGLOBULIN FAB MC/PC603. AN X-RAY DIFFRACTION STUDY AT 2.7 ANGSTROMS	IMMUNOGLOBULIN
1MCT	THE REFINED 1.6 ANGSTROMS RESOLUTION CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN PORCINE BETA-TRYPSIN AND MCTI-A, A TRYPSIN INHIBITOR OF SQUASH FAMILY	COMPLEX(PROTEINASE/INHIBITOR)
1MDM	INHIBITED FRAGMENT OF ETS-1 AND PAIRED DOMAIN OF PAX5 BOUND TO DNA	TRANSCRIPTION/DNA
1MDY	CRYSTAL STRUCTURE OF MYOD BHLH DOMAIN BOUND TO DNA: PERSPECTIVES ON DNA RECOGNITION AND IMPLICATIONS FOR TRANSCRIPTIONAL ACTIVATION	TRANSCRIPTION/DNA

1MEX	ANTIBODY CATALYSIS OF A BIMOLECULAR CYCLOADDITION REACTION	IMMUNE SYSTEM
1MF4	STRUCTURE-BASED DESIGN OF POTENT AND SELECTIVE INHIBITORS OF PHOSPHOLIPASE A2: CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN PHOSHOLIPASE A2 FROM NAJA NAJA SAGITTIFERA AND A DESIGNED PEPTIDE INHIBITOR AT 1.9 A RESOLUTION	HYDROLASE
1MFG	THE STRUCTURE OF ERBIN PDZ DOMAIN BOUND TO THE CARBOXY-TERMINAL TAIL OF THE ERBB2 RECEPTOR	SIGNALING PROTEIN
1MFQ	CRYSTAL STRUCTURE ANALYSIS OF A TERNARY S-DOMAIN COMPLEX OF HUMAN SIGNAL RECOGNITION PARTICLE	SIGNALING PROTEIN/RNA
1MH2	CRYSTAL STRUCTURE OF A ZINC CONTAINING DIMER OF PHOSPHOLIPASE A2 FROM THE VENOM OF INDIAN COBRA (NAJA NAJA SAGITTIFERA)	HYDROLASE
1MHM	CRYSTAL STRUCTURE OF S-ADENOSYLMETHIONINE DECARBOXYLASE FROM POTATO	LYASE
1MHY	METHANE MONOOXYGENASE HYDROXYLASE	OXIDOREDUCTASE
1MIO	X-RAY CRYSTAL STRUCTURE OF THE NITROGENASE MOLYBDENUM-IRON PROTEIN FROM CLOSTRIDIUM PASTEURIANUM AT 3.0 ANGSTROMS RESOLUTION	MOLYBDENUM-IRON PROTEIN
1MIU	STRUCTURE OF A BRCA2-DSS1 COMPLEX	GENE REGULATION/ANTITUMOR PROTEIN
1MIZ	CRYSTAL STRUCTURE OF AN INTEGRIN BETA3-TALIN CHIMERA	STRUCTURAL PROTEIN
1MJE	STRUCTURE OF A BRCA2-DSS1-SSDNA COMPLEX	GENE REGULATION/ANTITUMOR PROTEIN/DNA
1MJU	1.22 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE FAB FRAGMENT OF ESTEROLYTIC ANTIBODY MS6-12	IMMUNE SYSTEM
1MNM	YEAST MATALPHA2/MCM1/DNA TERNARY TRANSCRIPTION COMPLEX CRYSTAL STRUCTURE	TRANSCRIPTION/DNA
1MOX	RYSTAL STRUCTURE OF HUMAN EPIDERMAL GROWTH FACTOR RECEPTOR (RESIDUES 1-501) IN COMPLEX WITH TGF-ALPHA	TRANSFERASE/GROWTH FACTOR
1MQS	CRYSTAL STRUCTURE OF SLY1P IN COMPLEX WITH AN N-TERMINAL PEPTIDE OF SED5P	ENDOCYTOSIS/EXOCYTOSIS
1MTY	ETHANE MONOOXYGENASE HYDROXYLASE FROM METHYLOCOCCUS CAPSULATUS (BATH)	MONOOXYGENASE
1MVF	MAZE ADDICTION ANTIDOTE	IMMUNE SYSTEM
1MVU	SINGLE CHAIN FV OF C219 HEAVY CHAIN V101L MUTANT IN COMPLEX WITH SYNTHETIC EPITOPE PEPTIDE	IMMUNE SYSTEM
1MZ8	CRYSTAL STRUCTURES OF THE NUCLEASE DOMAIN OF COLE7/IM7 IN COMPLEX WITH A PHOSPHATE ION AND A ZINC ION	TOXIN,HYDROLASE/PROTEIN BINDING

1MZW	CRYSTAL STRUCTURE OF A U4/U6 SNRNP COMPLEX BETWEEN HUMAN SPLICEOSOMAL CYCLOPHILIN H AND A U4/U6-60K PEPTIDE	ISOMERASE
1N0W	CRYSTAL STRUCTURE OF A RAD51-BRCA2 BRC REPEAT COMPLEX	GENE REGULATION/ANTITUMOR PROTEIN
1N1J	CRYSTAL STRUCTURE OF THE NF-YB/NF-YC HISTONE PAIR	DNA BINDING PROTEIN
1N32	TRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT BOUND TO CODON AND NEAR-COGNATE TRANSFER RNA ANTICODON STEM-LOOP MISMATCHED AT THE FIRST CODON POSITION AT THE A SITE WITH PAROMOMYCIN	RIBOSOME
1N5Y	HIV-1 REVERSE TRANSCRIPTASE CROSSLINKED TO POST-TRANSLOCATION AZTMP-TERMINATED DNA (COMPLEX P)	TRANSFERASE/IMMUNE SYSTEM/DNA
1N62	CRYSTAL STRUCTURE OF THE MO,CU-CO DEHYDROGENASE (CODH), N-BUTYLISOCYANIDE-BOUND STATE	OXIDOREDUCTASE
1N6E	TRICORN PROTEASE IN COMPLEX WITH A TRIDECAPEPTIDE CHLOROMETHYL KETONE DERIVATIVE	HYDROLASE
1N6Q	HIV-1 REVERSE TRANSCRIPTASE CROSSLINKED TO PRE-TRANSLOCATION AZTMP-TERMINATED DNA (COMPLEX N)	TRANSFERASE/IMMUNE SYSTEM/DNA
1N7F	CRYSTAL STRUCTURE OF THE SIXTH PDZ DOMAIN OF GRIP1 IN COMPLEX WITH LIPRIN C-TERMINAL PEPTIDE	PROTEIN BINDING
1N7S	HIGH RESOLUTION STRUCTURE OF A TRUNCATED NEURONAL SNARE COMPLEX	TRANSPORT PROTEIN
1N8R	STRUCTURE OF LARGE RIBOSOMAL SUBUNIT IN COMPLEX WITH VIRGINIAMYCIN M	RIBOSOME
1NBW	GLYCEROL DEHYDRATASE REACTIVASE	HYDROLASE
1NCB	CRYSTAL STRUCTURES OF TWO MUTANT NEURAMINIDASE-ANTIBODY COMPLEXES WITH AMINO ACID SUBSTITUTIONS IN THE INTERFACE	HYDROLASE(O-GLYCOSYL)
1NCQ	THE STRUCTURE OF HRV14 WHEN COMPLEXED WITH PLECONARIL, AN ANTIVIRAL COMPOUND	VIRUS
1NCW	CATIONIC CYCLIZATION ANTIBODY 4C6 IN COMPLEX WITH BENZOIC ACID	IMMUNE SYSTEM
1ND2	THE STRUCTURE OF RHINOVIRUS 16	VIRUS
1NEK	COMPLEX II (SUCCINATE DEHYDROGENASE) FROM E. COLI WITH UBIQUINONE BOUND	OXIDOREDUCTASE/ELECTRON TRANSPORT
1NEX	CRYSTAL STRUCTURE OF SCSKP1-SCCDC4-CPD PEPTIDE COMPLEX	LIGASE, CELL CYCLE
1NFD	AN ALPHA-BETA T CELL RECEPTOR (TCR) HETERODIMER IN COMPLEX WITH AN ANTI-TCR FAB FRAGMENT DERIVED FROM A MITOGENIC ANTIBODY	COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN)

1NGM	CRYSTAL STRUCTURE OF A YEAST BRF1-TBP-DNA TERNARY COMPLEX	TRANSCRIPTION/DNA
1NH0	1.03 A STRUCTURE OF HIV-1 PROTEASE: INHIBITOR BINDING INSIDE AND OUTSIDE THE ACTIVE SITE	HYDROLASE/HYDROLASE INHIBITOR
1NH2	CRYSTAL STRUCTURE OF A YEAST TFIIA/TBP/DNA COMPLEX	TRANSCRIPTION/DNA
1NJI	STRUCTURE OF CHLORAMPHENICOL BOUND TO THE 50S RIBOSOMAL SUBUNIT	RIBOSOME
1NJT	COMPLEX STRUCTURE OF HCMV PROTEASE AND A PEPTIDOMIMETIC INHIBITOR	HYDROLASE
1NKP	CRYSTAL STRUCTURE OF MYC-MAX RECOGNIZING DNA	TRANSCRIPTION/DNA
1NKZ	CRYSTAL STRUCTURE OF LH2 B800-850 FROM RPS. ACIDOPHILA AT 2.0 ANGSTROM RESOLUTION	MEMBRANE PROTEIN
1NLN	CRYSTAL STRUCTURE OF HUMAN ADENOVIRUS 2 PROTEINASE WITH ITS 11 AMINO ACID COFACTOR AT 1.6 ANGSTROM RESOLUTION	HYDROLASE
1NLW	CRYSTAL STRUCTURE OF MAD-MAX RECOGNIZING DNA	TRANSCRIPTION/DNA
1NOC	MURINE INDUCIBLE NITRIC OXIDE SYNTHASE OXYGENASE DOMAIN (DELTA 114) COMPLEXED WITH TYPE I E. COLI CHLORAMPHENICOL ACETYL TRANSFERASE AND IMIDAZOLE	COMPLEX (OXIDOREDUCTASE/TRANSFERASE)
1NOP	RYSTAL STRUCTURE OF HUMAN TYROSYL-DNA PHOSPHODIESTERASE (TDP1) IN COMPLEX WITH VANADATE, DNA AND A HUMAN TOPOISOMERASE I-DERIVED PEPTIDE	HYDROLASE/DNA
1-Nov	NODAMURA VIRUS	VIRUS
1NQ7	HARACTERIZATION OF LIGANDS FOR THE ORPHAN NUCLEAR RECEPTOR RORBETA	TRANSCRIPTION
1NRJ	SIGNAL RECOGNITION PARTICLE RECEPTOR BETA-SUBUNIT IN COMPLEX WITH THE SRX DOMAIN FROM THE ALPHA-SUBUNIT	PROTEIN TRANSPORT
1NT2	CRYSTAL STRUCTURE OF FIBRILLARIN/NOP5P COMPLEX	RNA BINDING PROTEIN
1NTV	CRYSTAL STRUCTURE OF THE DISABLED-1 (DAB1) PTB DOMAIN-APOER2 PEPTIDE COMPLEX	SIGNALING PROTEIN
1NVM	RYSTAL STRUCTURE OF A BIFUNCTIONAL ALDOLASE-DEHYDROGENASE : SEQUESTERING A REACTIVE AND VOLATILE INTERMEDIATE	LYASE/OXIDOREDUCTASE
1NVP	HUMAN TFIIA/TBP/DNA COMPLEX	TRANSCRIPTION/DNA
1NX1	CALPAIN DOMAIN VI COMPLEXED WITH CALPASTATIN INHIBITORY DOMAIN C (DIC)	HYDROLASE
1O4X	TERNARY COMPLEX OF THE DNA BINDING DOMAINS OF THE OCT1 AND SOX2 TRANSCRIPTION FACTORS WITH A 19MER OLIGONUCLEOTIDE FROM THE HOXB1 REGULATORY ELEMENT	TRANSCRIPTION/DNA

1O6L	CRYSTAL STRUCTURE OF AN ACTIVATED AKT/PROTEIN KINASE B (PKB-PIF CHIMERA) TERNARY COMPLEX WITH AMP-PNP AND GSK3 PEPTIDE	TRANSFERASE
1O7D	THE STRUCTURE OF THE BOVINE LYSOSOMAL A-MANNOSIDASE SUGGESTS A NOVEL MECHANISM FOR LOW PH ACTIVATION	HYDROLASE
1O7N	NAPHTHALENE 1,2-DIOXYGENASE, TERNARY COMPLEX WITH DIOXYGEN AND INDOLE	OXIDOREDUCTASE
1O9D	STRUCTURAL VIEW OF A FUNGAL TOXIN ACTING ON A 14-3-3 REGULATORY COMPLEX	PROTEIN BINDING
1O9U	GLYCOGEN SYNTHASE KINASE 3 BETA COMPLEXED WITH AXIN PEPTIDE	KINASE
1OAI	COMPLEX BETWEEN TAP UBA DOMAIN AND FXFG NUCLEOPORIN PEPTIDE	NUCLEAR TRANSPORT
1OAO	NIZN[FE4S4] AND NINI[FE4S4] CLUSTERS IN CLOSED AND OPEN ALPHA SUBUNITS OF ACETYL-COA SYNTHASE/CARBON MONOXIDE DEHYDROGENASE	OXIDOREDUCTASE
1OBX	CRYSTAL STRUCTURE OF THE COMPLEX OF PDZ2 OF SYNTENIN WITH AN INTERLEUKIN 5 RECEPTOR ALPHA PEPTIDE.	ADHESION/COMPLEX
1OC0	PLASMINOGEN ACTIVATOR INHIBITOR-1 COMPLEX WITH SOMATOMEDIN B DOMAIN OF VITRONECTIN	SERINE PROTEASE INHIBITOR/COMPLEX
1OEY	HETERODIMER OF P40PHOX AND P67PHOX PB1 DOMAINS FROM HUMAN NADPH OXIDASE	PB1 HETERODIMER/COMPLEX
1OFH	ASYMMETRIC COMPLEX BETWEEN HSLV AND I-DOMAIN DELETED HSLU (H. INFLUENZAE)	HYDROLASE
1OFU	CRYSTAL STRUCTURE OF SULA:FTSZ FROM PSEUDOMONAS AERUGINOSA	BACTERIAL CELL DIVISION INHIBITOR
1OHE	STRUCTURE OF CDC14B PHOSPHATASE WITH A PEPTIDE LIGAND	HYDROLASE
1OHZ	COHESIN-DOCKERIN COMPLEX FROM THE CELLULOSOME OF CLOSTRIDIUM THERMOCELLUM	COHESIN/DOCKERIN COMPLEX
1OJ5	CRYSTAL STRUCTURE OF THE NCO-A1 PAS-B DOMAIN BOUND TO THE STAT6 TRANSACTIVATION DOMAIN LXXLL MOTIF	TRANSCRIPTIONAL COACTIVATOR
1OK7	A CONSERVED PROTEIN BINDING-SITE ON BACTERIAL SLIDING CLAMPS	TRANSFERASE
1OKK	HOMO-HETERODIMERIC COMPLEX OF THE SRP GTPASES	SIGNAL RECOGNITION/COMPLEX
1OO0	CRYSTAL STRUCTURE OF THE DROSOPHILA MAGO NASHI-Y14 COMPLEX	SIGNALING PROTEIN
1OOP	THE CRYSTAL STRUCTURE OF SWINE VESICULAR DISEASE VIRUS	VIRUS
1OP9	COMPLEX OF HUMAN LYSOZYME WITH CAMELID VHH HL6 ANTIBODY FRAGMENT	HYDROLASE
1OQS	CRYSTAL STRUCTURE OF RV4/RV7 COMPLEX	HYDROLASE

1OR7	CRYSTAL STRUCTURE OF ESCHERICHIA COLI SIGMAE WITH THE CYTOPLASMIC DOMAIN OF ITS ANTI-SIGMA RSEA	TRANSCRIPTION
1OSP	CRYSTAL STRUCTURE OF OUTER SURFACE PROTEIN A OF BORRELIA BURGDORFERI COMPLEXED WITH A MURINE MONOCLONAL ANTIBODY FAB	COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN)
1OSV	STRUCTURAL BASIS FOR BILE ACID BINDING AND ACTIVATION OF THE NUCLEAR RECEPTOR FXR	DNA BINDING PROTEIN
1OTC	THE O. NOVA TELOMERE END BINDING PROTEIN COMPLEXED WITH SINGLE STRAND DNA	PROTEIN/DNA
1OTS	STRUCTURE OF THE ESCHERICHIA COLI CLC CHLORIDE CHANNEL AND FAB COMPLEX	MEMBRANE PROTEIN
1OUT	TROUT HEMOGLOBIN I	OXYGEN TRANSPORT
1OUZ	CRYSTAL STRUCTURE OF A MUTANT IHF (BETAE44A) COMPLEXED WITH A VARIANT H' SITE (T44A)	TRANSCRIPTION/DNA
1OW6	PAXILLIN LD4 MOTIF BOUND TO THE FOCAL ADHESION TARGETING (FAT) DOMAIN OF THE FOCAL ADHESION KINASE	TRANSFERASE
1OWF	CRYSTAL STRUCTURE OF A MUTANT IHF (BETAE44A) COMPLEXED WITH THE NATIVE H' SITE	TRANSCRIPTION/DNA
1OWG	CRYSTAL STRUCTURE OF WT IHF COMPLEXED WITH AN ALTERED H' SITE (T44A)	TRANSCRIPTION/DNA
1OXN	STRUCTURE AND FUNCTION ANALYSIS OF PEPTIDE ANTAGONISTS OF MELANOMA INHIBITOR OF APOPTOSIS (ML-IAP)	APOPTOSIS
1OY3	CRYSTAL STRUCTURE OF AN IKBBETA/NF-KB P65 HOMODIMER COMPLEX	DNA BINDING PROTEIN
1OZ7	CRYSTAL STRUCTURE OF ECHICETIN FROM THE VENOM OF INDIAN SAW-SCALED VIPER (ECHIS CARINATUS) AT 2.4 RESOLUTION	TOXIN
1OZB	CRYSTAL STRUCTURE OF SECB COMPLEXED WITH SECA C-TERMINUS	PROTEIN TRANSPORT
1P13	CRYSTAL STRUCTURE OF THE SRC SH2 DOMAIN COMPLEXED WITH PEPTIDE (SDPYANFK)	TRANSFERASE
1P27	CRYSTAL STRUCTURE OF THE HUMAN Y14/MAGOH COMPLEX	RNA BINDING PROTEIN
1P34	CRYSTALLOGRAPHIC STUDIES OF NUCLEOSOME CORE PARTICLES CONTAINING HISTONE 'SIN' MUTANTS	STRUCTURAL PROTEIN/DNA
1P4E	FLPE W330F MUTANT-DNA HOLLIDAY JUNCTION COMPLEX	DNA BINDING PROTEIN/RECOMBINATION/DNA
1P7W	CRYSTAL STRUCTURE OF THE COMPLEX OF PROTEINASE K WITH A DESIGNED HEPTAPEPTIDE INHIBITOR PRO-ALA-PRO-PHE-ALA-SER-ALA AT ATOMIC RESOLUTION	HYDROLASE
1P8J	CRYSTAL STRUCTURE OF THE PROPROTEIN CONVERTASE FURIN	HYDROLASE

1P9U	CORONAVIRUS MAIN PROTEINASE (3CLPRO) STRUCTURE: BASIS FOR DESIGN OF ANTI-SARS DRUGS	HYDROLASE
1PA6	CRYSTAL STRUCTURE OF THE OXYTRICHA NOVA TELOMERE END-BINDING PROTEIN COMPLEXED WITH NONCOGNATE SSDNA GGGGTTTTGAGG	DNA BINDING PROTEIN/DNA
1PBY	STRUCTURE OF THE PHENYLHYDRAZINE ADDUCT OF THE QUINOHEMOPROTEIN AMINE DEHYDROGENASE FROM PARACOCCUS DENITRIFICANS AT 1.7 A RESOLUTION	OXIDOREDUCTASE
1PCA	THREE DIMENSIONAL STRUCTURE OF PORCINE PANCREATIC PROCARBOXYPEPTIDASE A. A COMPARISON OF THE A AND B ZYMOGENS AND THEIR DETERMINANTS FOR INHIBITION AND ACTIVATION	HYDROLASE(C-TERMINAL PEPTIDASE)
1PCX	CRYSTAL STRUCTURE OF THE COPII COAT SUBUNIT, SEC24, COMPLEXED WITH A PEPTIDE FROM THE SNARE PROTEIN BET1	TRANSPORT PROTEIN
1PEG	STRUCTURAL BASIS FOR THE PRODUCT SPECIFICITY OF HISTONE LYSINE METHYLTRANSFERASES	TRANSFERASE
1PFB	STRUCTURAL BASIS FOR SPECIFIC BINDING OF POLYCOMB CHROMODOMAIN TO HISTONE H3 METHYLATED AT K27	PEPTIDE BINDING PROTEIN
1PG5	CRYSTAL STRUCTURE OF THE UNLIGATED (T-STATE) ASPARTATE TRANSCARBAMOYLASE FROM THE EXTREMELY THERMOPHILIC ARCHAEON SULFOLOBUS ACIDOCALDARIUS	TRANSFERASE
1PHN	STRUCTURE OF PHYCOCYANIN FROM CYANIDIUM CALDARIUM AT 1.65A RESOLUTION	ELECTRON TRANSPORT
1PIC	PHOSPHATIDYLINOSITOL 3-KINASE, P85-ALPHA SUBUNIT: C-TERMINAL SH2 DOMAIN COMPLEXED WITH A TYR751 PHOSPHOPEPTIDE FROM THE PDGF RECEPTOR, NMR, MINIMIZED MEAN STRUCTURE	COMPLEX (PHOSPHOTRANSFERASE/RECEPTOR)
1PIN	PIN1 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FROM HOMO SAPIENS	COMPLEX (ISOMERASE/DIPEPTIDE)
1PK1	HETERO SAM DOMAIN STRUCTURE OF PH AND SCM.	TRANSCRIPTION REPRESSION
1PNS	RYSTAL STRUCTURE OF A STREPTOMYCIN DEPENDENT RIBOSOME FROM E. COLI, 30S SUBUNIT OF 70S RIBOSOME. THIS FILE, 1PNS, CONTAINS THE 30S SUBUNIT, TWO TRNAS, AND ONE MRNA MOLECULE. THE 50S RIBOSOMAL SUBUNIT IS IN FILE 1PNU.	RIBOSOME
1PNX	CRYSTAL STRUCTURE OF THE WILD TYPE RIBOSOME FROM E. COLI, 30S SUBUNIT OF 70S RIBOSOME. THIS FILE, 1PNX, CONTAINS ONLY MOLECULES OF THE 30S RIBOSOMAL SUBUNIT. THE 50S SUBUNIT IS IN THE PDB FILE 1PNY.	RIBOSOME
1POI	RYSTAL STRUCTURE OF GLUTACONATE COENZYME A-TRANSFERASE FROM ACIDAMINOCOCCUS FERMENTANS TO 2.55 ANGSTOMS RESOLUTION	TRANSFERASE
1PPL	CRYSTALLOGRAPHIC ANALYSIS OF TRANSITION-STATE MIMICS BOUND	HYDROLASE(ACID PROTEINASE)

	TO PENICILLOPEPSIN: PHOSPHORUS-CONTAINING PEPTIDE ANALOGUES	
1PQ1	CRYSTAL STRUCTURE OF BCL-XL/BIM	APOPTOSIS
1PRT	THE CRYSTAL STRUCTURE OF PERTUSSIS TOXIN	TOXIN
1PSA	STRUCTURE OF A PEPSIN(SLASH)RENIN INHIBITOR COMPLEX REVEALS A NOVEL CRYSTAL PACKING INDUCED BY MINOR CHEMICAL ALTERATIONS IN THE INHIBITOR	HYDROLASE(ACID PROTEINASE)
1PSK	THE CRYSTAL STRUCTURE OF AN FAB FRAGMENT THAT BINDS TO THE MELANOMA-ASSOCIATED GD2 GANGLIOSIDE	IMMUNOGLOBULIN
1PSO	THE CRYSTAL STRUCTURE OF HUMAN PEPSIN AND ITS COMPLEX WITH PEPSTATIN	HYDROLASE (ACID PROTEINASE)
1PUF	RYSTAL STRUCTURE OF HOXA9 AND PBX1 HOMEODOMAINS BOUND TO DNA	TRANSCRIPTION/DNA
1PWW	CRYSTAL STRUCTURE OF ANTHRAX LETHAL FACTOR ACTIVE SITE MUTANT PROTEIN COMPLEXED WITH AN OPTIMISED PEPTIDE SUBSTRATE IN THE PRESENCE OF ZINC.	HYDROLASE
1PXV	THE STAPHOSTATIN-STAPHOPAIN COMPLEX: A FORWARD BINDING INHIBITOR IN COMPLEX WITH ITS TARGET CYSTEINE PROTEASE	HYDROLASE
1PYA	REFINED STRUCTURE OF THE PYRUVOYL-DEPENDENT HISTIDINE DECARBOXYLASE FROM LACTOBACILLUS 30A	CARBOXY-LYASE
1PYO	RYSTAL STRUCTURE OF HUMAN CASPASE-2 IN COMPLEX WITH ACETYL-LEU-ASP-GLU-SER-ASP-CHO	HYDROLASE
1PZL	CRYSTAL STRUCTURE OF HNF4A LBD IN COMPLEX WITH THE LIGAND AND THE COACTIVATOR SRC-1 PEPTIDE	TRANSCRIPTION
1Q1A	STRUCTURE OF THE YEAST HST2 PROTEIN DEACETYLASE IN TERNARY COMPLEX WITH 2'-O-ACETYL ADP RIBOSE AND HISTONE PEPTIDE	GENE REGULATION
1Q1S	OUSE IMPORTIN ALPHA- PHOSPHORYLATED SV40 CN PEPTIDE COMPLEX	PROTEIN TRANSPORT
1Q3L	CHROMODOMAIN OF HP1 COMPLEXED WITH HISTONE H3 TAIL CONTAINING MONOMETHYLLYSINE 9.	STRUCTURAL PROTEIN
1Q3P	RYSTAL STRUCTURE OF THE SHANK PDZ-LIGAND COMPLEX REVEALS A CLASS I PDZ INTERACTION AND A NOVEL PDZ-PDZ DIMERIZATION	PEPTIDE BINDING PROTEIN
1Q40	CRYSTAL STRUCTURE OF THE C. ALBICANS MTR2-MEX67 M DOMAIN COMPLEX	TRANSLATION
1Q5Q	THE RHODOCOCCUS 20S PROTEASOME	HYDROLASE
1Q7L	ZN-BINDING DOMAIN OF THE T347G MUTANT OF HUMAN AMINOACYLASE-I	HYDROLASE
1Q7Y	RYSTAL STRUCTURE OF CCDAP-PUROMYCIN BOUND AT THE PEPTIDYL	RIBOSOME

	TRANSFERASE CENTER OF THE 50S RIBOSOMAL SUBUNIT	
1Q81	CRYSTAL STRUCTURE OF MINIHELIX WITH 3' PUROMYCIN BOUND TO A-SITE OF THE 50S RIBOSOMAL SUBUNIT.	RIBOSOME
1Q82	CRYSTAL STRUCTURE OF CC-PUROMYCIN BOUND TO THE A-SITE OF THE 50S RIBOSOMAL SUBUNIT	RIBOSOME
1Q86	CRYSTAL STRUCTURE OF CCA-PHE-CAP-BIOTIN BOUND SIMULTANEOUSLY AT HALF OCCUPANCY TO BOTH THE A-SITE AND P-SITE OF THE THE 50S RIBOSOMAL SUBUNIT.	RIBOSOME
1Q90	STRUCTURE OF THE CYTOCHROME B6F (PLASTOHYDROQUINONE : PLASTOCYANIN OXIDOREDUCTASE) FROM CHLAMYDOMONAS REINHARDTII	PHOTOSYNTHESIS
1QAV	UNEXPECTED MODES OF PDZ DOMAIN SCAFFOLDING REVEALED BY STRUCTURE OF NNOS-SYNTROPHIN COMPLEX	MEMBRANE PROTEIN/OXIDOREDUCTASE
1QD6	OUTER MEMBRANE PHOSPHOLIPASE A FROM ESCHERICHIA COLI	MEMBRANE PROTEIN
1QDL	THE CRYSTAL STRUCTURE OF ANTHRANILATE SYNTHASE FROM SULFOLOBUS SOLFATARICUS	LYASE
1QGR	STRUCTURE OF IMPORTIN BETA BOUND TO THE IBB DOMAIN OF IMPORTIN ALPHA (II CRYSTAL FORM, GROWN AT LOW PH)	TRANSPORT RECEPTOR
1QH8	NITROGENASE MOFE PROTEIN FROM KLEBSIELLA PNEUMONIAE, AS-CRYSTALLIZED (MIXED OXIDATION) STATE	OXIDOREDUCTASE
1QJJ	STRUCTURE OF ASTACIN WITH A HYDROXAMIC ACID INHIBITOR	HYDROLASE(METALLOPROTEINASE)
1QLS	S100C (S100A11),OR CALGIZZARIN, IN COMPLEX WITH ANNEXIN I N-TERMINUS	COMPLEX (LIGAND/ANNEXIN)
1QNH	LASMODIUM FALCIPARUM CYCLOPHILIN (DOUBLE MUTANT) COMPLEXED WITH CYCLOSPORIN A	COMPLEX (ISOMERASE/IMMUNOSUPPRESSANT)
1QO0	AMIDE RECEPTOR OF THE AMIDASE OPERON OF PSEUDOMONAS AERUGINOSA (AMIC) COMPLEXED WITH THE NEGATIVE REGULATOR AMIR.	BINDING PROTEIN
1QOP	CRYSTAL STRUCTURE OF WILD-TYPE TRYPTOPHAN SYNTHASE COMPLEXED WITH INDOLE PROPANOL PHOSPHATE	LYASE
1QPW	CRYSTAL STRUCTURE DETERMINATION OF PORCINE HEMOGLOBIN AT 1.8A RESOLUTION	OXYGEN TRANSPORT
1QRJ	SOLUTION STRUCTURE OF HTLV-I CAPSID PROTEIN	VIRAL PROTEIN
1QS0	CRYSTAL STRUCTURE OF PSEUDOMONAS PUTIDA 2-OXOISOVALERATE DEHYDROGENASE (BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE, E1B)	OXIDOREDUCTASE
1QS8	CRYSTAL STRUCTURE OF THE P. VIVAX ASPARTIC PROTEINASE PLASMEPSIN COMPLEXED WITH THE INHIBITOR PEPSTATIN A	HYDROLASE

1QSN	RYSTAL STRUCTURE OF TETRAHYMENA GCN5 WITH BOUND COENZYME A AND HISTONE H3 PEPTIDE	TRANSFERASE
1QVF	STRUCTURE OF A DEACYLATED TRNA MINIHELIX BOUND TO THE E SITE OF THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1QVG	STRUCTURE OF CCA OLIGONUCLEOTIDE BOUND TO THE TRNA BINDING SITES OF THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1QYG	NTI-COCAINE ANTIBODY M82G2 COMPLEXED WITH BENZOYLECGONINE	IMMUNE SYSTEM
1QZ0	CRYSTAL STRUCTURE OF THE YERSINIA PESTIS PHOSPHATASE YOPH IN COMPLEX WITH A PHOSPHOTYROSYL MIMETIC-CONTAINING HEXAPEPTIDE	HYDROLASE
1QZ2	CRYSTAL STRUCTURE OF FKBP52 C-TERMINAL DOMAIN COMPLEX WITH THE C-TERMINAL PEPTIDE MEEVD OF HSP90	ISOMERASE/CHAPERONE
1R0A	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE COVALENTLY TETHERED TO DNA TEMPLATE-PRIMER SOLVED TO 2.8 ANGSTROMS	TRANSFERASE/IMMUNE SYSTEM/DNA
1R0N	RYSTAL STRUCTURE OF HETERODIMERIC ECDSYONE RECEPTOR DNA BINDING COMPLEX	TRANSCRIPTION/DNA
1R0O	RYSTAL STRUCTURE OF THE HETERODIMERIC ECDYSONE RECEPTOR DNA-BINDING COMPLEX	TRANSCRIPTION/DNA
1R0R	.1 ANGSTROM RESOLUTION STRUCTURE OF THE COMPLEX BETWEEN THE PROTEIN INHIBITOR, OMTKY3, AND THE SERINE PROTEASE, SUBTILISIN CARLSBERG	HYDROLASE
1R1Q	STRUCTURAL BASIS FOR DIFFERENTIAL RECOGNITION OF TYROSINE PHOSPHORYLATED SITES IN THE LINKER FOR ACTIVATION OF T CELLS (LAT) BY THE ADAPTOR PROTEIN GADS	PEPTIDE BINDING PROTEIN
1R24	FAB FROM MURINE IGG3 KAPPA	IMMUNE SYSTEM
1R2B	CRYSTAL STRUCTURE OF THE BCL6 BTB DOMAIN COMPLEXED WITH A SMRT CO-REPRESSOR PEPTIDE	TRANSCRIPTION
1R4P	SHIGA TOXIN TYPE 2	TOXIN
1R4Q	SHIGA TOXIN	TOXIN
1R6O	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA/ATP-DEPENDENT CLP PROTEASE ADAPTOR PROTEIN CLPS	HYDROLASE
1R8S	ARF1[DELTA1-17]-GDP IN COMPLEX WITH A SEC7 DOMAIN CARRYING THE MUTATION OF THE CATALYTIC GLUTAMATE TO LYSINE	PROTEIN TRANSPORT/EXCHANGE FACTOR
1R9S	RNA POLYMERASE II STRAND SEPARATED ELONGATION COMPLEX, MATCHED NUCLEOTIDE	TRANSCRIPTION/DNA/RNA

1R9T	RNA POLYMERASE II STRAND SEPARATED ELONGATION COMPLEX, MISMATCHED NUCLEOTIDE	TRANSCRIPTION/DNA/RNA
1RB8	THE PHIX174 DNA BINDING PROTEIN J IN TWO DIFFERENT CAPSID ENVIRONMENTS.	VIRUS/DNA
1RBL	STRUCTURE DETERMINATION AND REFINEMENT OF RIBULOSE 1,5 BISPHOSPHATE CARBOXYLASE(SLASH)OXYGENASE FROM SYNECHOCOCCUS PCC6301	LYASE(CARBON-CARBON)
1RDQ	HYDROLYSIS OF ATP IN THE CRYSTAL OF Y204A MUTANT OF CAMP-DEPENDENT PROTEIN KINASE	TRANSFERASE/TRANSFERASE INHIBITOR
1REQ	METHYLMALONYL-COA MUTASE	ISOMERASE
1REW	TRUCTURAL REFINEMENT OF THE COMPLEX OF BONE MORPHOGENETIC PROTEIN 2 AND ITS TYPE IA RECEPTOR	HORMONE/GROWTH FACTOR/SIGNALING PROTEIN
1RFN	HUMAN COAGULATION FACTOR IXA IN COMPLEX WITH P-AMINO BENZAMIDINE	COAGULATION FACTOR
1RH5	THE STRUCTURE OF A PROTEIN CONDUCTING CHANNEL	PROTEIN TRANSPORT
1RIO	STRUCTURE OF BACTERIOPHAGE LAMBDA CI-NTD IN COMPLEX WITH SIGMA-REGION4 OF THERMUS AQUATICUS BOUND TO DNA	TRANSCRIPTION/DNA
1RJL	TRUCTURE OF THE COMPLEX BETWEEN OSPB-CT AND BACTERICIDAL FAB-H6831	IMMUNE SYSTEM
1RLB	RETINOL BINDING PROTEIN COMPLEXED WITH TRANSTHYRETIN	COMPLEX (PROTEIN/PROTEIN)
1RM1	STRUCTURE OF A YEAST TFIIA/TBP/TATA-BOX DNA COMPLEX	TRANSCRIPTION/DNA
1RM6	TRUCTURE OF 4-HYDROXYBENZOYL-COA REDUCTASE FROM THAUERA AROMATICA	OXIDOREDUCTASE
1RP3	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM	TRANSCRIPTION
1RQF	STRUCTURE OF CK2 BETA SUBUNIT CRYSTALLIZED IN THE PRESENCE OF A P21WAF1 PEPTIDE	TRANSFERASE
1RTD	STRUCTURE OF A CATALYTIC COMPLEX OF HIV-1 REVERSE TRANSCRIPTASE: IMPLICATIONS FOR NUCLEOSIDE ANALOG DRUG RESISTANCE	TRANSFERASE/DNA
1RVX	1934 H1 HEMAGGLUTININ IN COMPLEX WITH LSTA	VIRAL PROTEIN
1RXZ	C-TERMINAL REGION OF A. FULGIDUS FEN-1 COMPLEXED WITH A. FULGIDUS PCNA	REPLICATION
1RY1	STRUCTURE OF THE SIGNAL RECOGNITION PARTICLE INTERACTING WITH THE ELONGATION-ARRESTED RIBOSOME	TRANSLATION

1RYP	CRYSTAL STRUCTURE OF THE 20S PROTEASOME FROM YEAST AT 2.4 ANGSTROMS RESOLUTION	MULTICATALYTIC PROTEINASE
1RZO	AGGLUTININ FROM RICINUS COMMUNIS WITH GALACTOAZA	HYDROLASE
1RZX	CRYSTAL STRUCTURE OF A PAR-6 PDZ-PEPTIDE COMPLEX	CELL CYCLE
1S1H	STRUCTURE OF THE RIBOSOMAL 80S-EEF2-SORDARIN COMPLEX FROM YEAST OBTAINED BY DOCKING ATOMIC MODELS FOR RNA AND PROTEIN COMPONENTS INTO A 11.7 A CRYO-EM MAP. THIS FILE, 1S1H, CONTAINS 40S SUBUNIT. THE 60S RIBOSOMAL SUBUNIT IS IN FILE 1S1I.	RIBOSOME
1S32	MOLECULAR RECOGNITION OF THE NUCLEOSOMAL 'SUPERGROOVE'	STRUCTURAL PROTEIN/DNA
1S3S	CRYSTAL STRUCTURE OF AAA ATPASE P97/VCP ND1 IN COMPLEX WITH P47 C	PROTEIN BINDING
1S4V	THE 2.0 A CRYSTAL STRUCTURE OF THE KDEL-TAILED CYSTEINE ENDOPEPTIDASE FUNCTIONING IN PROGRAMMED CELL DEATH OF RICINUS COMMUNIS ENDOSPERM	HYDROLASE
1S5D	CHOLERA HOLOTOXIN WITH AN A-SUBUNIT Y30S MUTATION, CRYSTAL FORM 2	TRANSERASE,TOXIN
1S5L	ARCHITECTURE OF THE PHOTOSYNTHETIC OXYGEN EVOLVING CENTER	PHOTOSYNTHESIS
1S5P	STRUCTURE AND SUBSTRATE BINDING PROPERTIES OF COBB, A SIR2 HOMOLOG PROTEIN DEACETYLASE FROM ESCHERICIA COLI.	HYDROLASE
1S6B	X-RAY CRYSTAL STRUCTURE OF A COMPLEX FORMED BETWEEN TWO HOMOLOGOUS ISOFORMS OF PHOSPHOLIPASE A2 FROM NAJA NAJA SAGITTIFERA: PRINCIPLE OF MOLECULAR ASSOCIATION AND INACTIVATION	HYDROLASE
1S6C	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN KCHIP1 AND KV4.2 N1-30	TRANSPORT PROTEIN
1S70	COMPLEX BETWEEN PROTEIN SER/THR PHOSPHATASE-1 (DELTA) AND THE MYOSIN PHOSPHATASE TARGETING SUBUNIT 1 (MYPT1)	HYDROLASE
1S72	REFINED CRYSTAL STRUCTURE OF THE HALOARCULA MARISMORTUI LARGE RIBOSOMAL SUBUNIT AT 2.4 ANGSTROM RESOLUTION	RIBOSOME
1S9K	CRYSTAL STRUCTURE OF HUMAN NFAT1 AND FOS-JUN ON THE IL-2 ARRE1 SITE	TRANSCRIPTION/DNA
1S9V	CRYSTAL STRUCTURE OF HLA-DQ2 COMPLEXED WITH DEAMIDATED GLIADIN PEPTIDE	IMMUNE SYSTEM
1SA0	TUBULIN-COLCHICINE: STATHMIN-LIKE DOMAIN COMPLEX	CELL CYCLE
1SB2	HIGH RESOLUTION STRUCTURE DETERMINATION OF RHODOCETIN	TOXIN
1SCT	SCAPHARCA TETRAMERIC HEMOGLOBIN, CO-STATE	OXYGEN TRANSPORT

1SDD	CRYSTAL STRUCTURE OF BOVINE FACTOR VAI	BLOOD CLOTTING
1SDX	CRYSTAL STRUCTURE OF THE ZINC SATURATED C-TERMINAL HALF OF BOVINE LACTOFERRIN AT 2.0 A RESOLUTION REVEALS TWO ADDITIONAL ZINC BINDING SITES	TRANSPORT PROTEIN
1SE0	CRYSTAL STRUCTURE OF DIAP1 BIR1 BOUND TO A GRIM PEPTIDE	APOPTOSIS
1SFO	RNA POLYMERASE II STRAND SEPARATED ELONGATION COMPLEX	TRANSCRIPTION/DNA/RNA
1SGF	CRYSTAL STRUCTURE OF 7S NGF: A COMPLEX OF NERVE GROWTH FACTOR WITH FOUR BINDING PROTEINS (SERINE PROTEINASES)	GROWTH FACTOR
1SHC	SHC PTB DOMAIN COMPLEXED WITH A TRKA RECEPTOR PHOSPHOPEPTIDE, NMR, MINIMIZED AVERAGE STRUCTURE	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)
1SHZ	CRYSTAL STRUCTURE OF THE P115RHOGEF RGRGS DOMAIN IN A COMPLEX WITH GALPHA(13):GALPHA(I1) CHIMERA	SIGNALING PROTEIN
1SIO	STRUCTURE OF KUMAMOLISIN-AS COMPLEXED WITH A COVALENTLY-BOUND INHIBITOR, ACIPF	HYDROLASE
1SKR	7 DNA POLYMERASE COMPLEXED TO DNA PRIMER/TEMPLATE AND DDATP	TRANSFERASE/ELECTRON TRANSPORT/DNA
1SKS	BINARY 3' COMPLEX OF T7 DNA POLYMERASE WITH A DNA PRIMER/TEMPLATE CONTAINING A CIS-SYN THYMINE DIMER ON THE TEMPLATE	TRANSFERASE/ELECTRON TRANSPORT/DNA
1SKY	CRYSTAL STRUCTURE OF THE NUCLEOTIDE FREE ALPHA3BETA3 SUB-COMPLEX OF F1-ATPASE FROM THE THERMOPHILIC BACILLUS PS3	ATP SYNTHASE
1SL0	TERNARY 3' COMPLEX OF T7 DNA POLYMERASE WITH A DNA PRIMER/TEMPLATE CONTAINING A DISORDERED CIS-SYN THYMINE DIMER ON THE TEMPLATE AND AN INCOMING NUCLEOTIDE	TRANSFERASE/ELECTRON TRANSPORT/DNA
1SL1	BINARY 5' COMPLEX OF T7 DNA POLYMERASE WITH A DNA PRIMER/TEMPLATE CONTAINING A CIS-SYN THYMINE DIMER ON THE TEMPLATE	TRANSFERASE/ELECTRON TRANSPORT/DNA
1SL2	TERNARY 5' COMPLEX OF T7 DNA POLYMERASE WITH A DNA PRIMER/TEMPLATE CONTAINING A CIS-SYN THYMINE DIMER ON THE TEMPLATE AND AN INCOMING NUCLEOTIDE	TRANSFERASE/ELECTRON TRANSPORT/DNA
1SLU	RAT ANIONIC N143H, E151H TRYPSIN COMPLEXED TO A86H ECOTIN	COMPLEX (SERINE PROTEASE/INHIBITOR)
1SOZ	CRYSTAL STRUCTURE OF DEGS PROTEASE IN COMPLEX WITH AN ACTIVATING PEPTIDE	HYDROLASE
1SR4	CRYSTAL STRUCTURE OF THE HAEMOPHILUS DUCREYI CYTOLETHAL DISTENDING TOXIN	TOXIN
1SUY	NMR STRUCTURE OF THE THKAIA180C-CIIABD COMPLEX (AVERAGE MINIMIZED STRUCTURE)	CIRCADIAN CLOCK PROTEIN

1SV0	CRYSTAL STRUCTURE OF YAN-SAM/MAE-SAM COMPLEX	TRANSCRIPTION
1SVD	THE STRUCTURE OF HALOTHIOBACILLUS NEAPOLITANUS RUBISCO	LYASE
1SY6	RYSTAL STRUCTURE OF CD3GAMMAEPSILON HETERODIMER IN COMPLEX WITH OKT3 FAB FRAGMENT	SIGNALING PROTEIN/ANTIBIOTIC
1SYX	THE CRYSTAL STRUCTURE OF A BINARY U5 SNRNP COMPLEX	TRANSLATION/IMMUNE SYSTEM
1SZA	THE RNA POLYMERASE II CTD IN MRNA PROCESSING: BETA-TURN RECOGNITION AND BETA-SPIRAL MODEL	TRANSCRIPTION
1T03	HIV-1 REVERSE TRANSCRIPTASE CROSSLINKED TO TENOFOVIR TERMINATED TEMPLATE-PRIMER (COMPLEX P)	TRANSFERASE/ANTIBODY/DNA
1T05	HIV-1 REVERSE TRANSCRIPTASE CROSSLINKED TO TEMPLATE-PRIMER WITH TENOFOVIR-DIPHOSPHATE BOUND AS THE INCOMING NUCLEOTIDE SUBSTRATE	TRANSFERASE/DNA
1T0F	CRYSTAL STRUCTURE OF THE TNSA/TNSC(504-555) COMPLEX	DNA BINDING PROTEIN
1T0H	CRYSTAL STRUCTURE OF THE RATTUS NORVEGICUS VOLTAGE GATED CALCIUM CHANNEL BETA SUBUNIT ISOFORM 2A	SIGNALING PROTEIN
1T0K	JOINT X-RAY AND NMR REFINEMENT OF YEAST L30E-MRNA COMPLEX	RIBOSOME
1T0P	STRUCTURAL BASIS OF ICAM RECOGNITION BY INTEGRIN ALPAHLBETA2 REVEALED IN THE COMPLEX STRUCTURE OF BINDING DOMAINS OF ICAM-3 AND ALPHALBETA2 AT 1.65 A	IMMUNE SYSTEM
1T15	CRYSTAL STRUCTURE OF THE BRCA1 BRCT DOMAINS IN COMPLEX WITH THE PHOSPHORYLATED INTERACTING REGION FROM BACH1 HELICASE	ANTITUMOR PROTEIN
1T2K	STRUCTURE OF THE DNA BINDING DOMAINS OF IRF3, ATF-2 AND JUN BOUND TO DNA	TRANSCRIPTION/DNA
1T34	ROTATION MECHANISM FOR TRANSMEMBRANE SIGNALING BY THE ATRIAL NATRIURETIC PEPTIDE RECEPTOR	SIGNALING PROTEIN,MEMBRANE PROTEIN
1T3Q	CRYSTAL STRUCTURE OF QUINOLINE 2-OXIDOREDUCTASE FROM PSEUDOMONAS PUTIDA 86	OXIDOREDUCTASE
1T61	CRYSTAL STRUCTURE OF COLLAGEN IV NC1 DOMAIN FROM PLACENTA BASEMENT MEMBRANE	STRUCTURAL PROTEIN
1T6B	CRYSTAL STRUCTURE OF B. ANTHRACIS PROTECTIVE ANTIGEN COMPLEXED WITH HUMAN ANTHRAX TOXIN RECEPTOR	MEMBRANE PROTEIN/TOXIN
1T6O	NUCLEOCAPSID-BINDING DOMAIN OF THE MEASLES VIRUS P PROTEIN (AMINO ACIDS 457-507) IN COMPLEX WITH AMINO ACIDS 486-505 OF THE MEASLES VIRUS N PROTEIN	VIRAL PROTEIN
1T7P	T7 DNA POLYMERASE COMPLEXED TO DNA PRIMER/TEMPLATE,A NUCLEOSIDE TRIPHOSPHATE, AND ITS PROCESSIVITY FACTOR THIOREDOXIN	TRANSFERASE/DNA

1T7R	RYSTAL STRUCTURE OF THE ANDROGEN RECEPTOR LIGAND BINDING DOMAIN IN COMPLEX WITH A FXXLF MOTIF	HORMONE/GROWTH FACTOR RECEPTOR
1T8E	T7 DNA POLYMERASE TERNARY COMPLEX WITH DCTP AT THE INSERTION SITE.	TRANSFERASE/ELECTRON TRANSPORT/DNA
1TA3	CRYSTAL STRUCTURE OF XYLANASE (GH10) IN COMPLEX WITH INHIBITOR (XIP)	HYDROLASE INHIBITOR/HYDROLASE
1TCE	OLUTION NMR STRUCTURE OF THE SHC SH2 DOMAIN COMPLEXED WITH A TYROSINE-PHOSPHORYLATED PEPTIDE FROM THE T-CELL RECEPTOR, MINIMIZED AVERAGE STRUCTURE	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)
1TDQ	TRUCTURAL BASIS FOR THE INTERACTIONS BETWEEN TENASCINS AND THE C-TYPE LECTIN DOMAINS FROM LECTICANS: EVIDENCE FOR A CROSS-LINKING ROLE FOR TENASCINS	EXTRACELLULAR MATRIX
1TH8	CRYSTAL STRUCTURES OF THE ADP AND ATP BOUND FORMS OF THE BACILLUS ANTI-SIGMA FACTOR SPOIIAB IN COMPLEX WITH THE ANTI-ANTI-SIGMA SPOIIAA: INHIBITORY COMPLEX WITH ADP, CRYSTAL FORM II	TRANSCRIPTION
1TII	ESCHERICHIA COLI HEAT LABILE ENTEROTOXIN TYPE IIB	ENTEROTOXIN
1TK0	7 DNA POLYMERASE TERNARY COMPLEX WITH 8 OXO GUANOSINE AND DDCTP AT THE INSERTION SITE	TRANSFERASE/ELECTRON TRANSPORT/DNA
1TK2	RYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN ALKALINE PROTEINASE SAVINASE AND GRAMICIDIN S AT 1.5A RESOLUTION	HYDROLASE
1TK5	T7 DNA POLYMERASE BINARY COMPLEX WITH 8 OXO GUANOSINE IN THE TEMPLATING STRAND	TRANSFERASE/ELECTRON TRANSPORT/DNA
1TK8	7 DNA POLYMERASE TERNARY COMPLEX WITH 8 OXO GUANOSINE AND DAMP AT THE ELONGATION SITE	TRANSFERASE/ELECTRON TRANSPORT/DNA
1TL9	HIGH RESOLUTION CRYSTAL STRUCTURE OF CALPAIN I PROTEASE CORE IN COMPLEX WITH LEUPEPTIN	HYDROLASE
1TO2	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' WITH CHYMOTRYPSIN INHIBITOR 2 M59K, IN PH 9 CRYOSOAK	HYDROLASE
1TP5	CRYSTAL STRUCTURE OF PDZ3 DOMAIN OF PSD-95 PROTEIN COMPLEXED WITH A PEPTIDE LIGAND KKETWV	PEPTIDE BINDING PROTEIN
1TQE	MECHANISM OF RECRUITMENT OF CLASS II HISTONE DEACETYLASES BY MYOCYTE ENHANCER FACTOR-2	TRANSCRIPTION/PROTEIN BINDING/DNA
1TQY	THE ACTINORHODIN KETOSYNTHASE/CHAIN LENGTH FACTOR	TRANSFERASE
1TTW	CRYSTAL STRUCTURE OF THE YERSINIA PESTIS TYPE III SECRETION CHAPERONE SYCH IN COMPLEX WITH A STABLE FRAGMENT OF YSCM2	CHAPERONE
1TU3	RYSTAL STRUCTURE OF RAB5 COMPLEX WITH RABAPTIN5 C-TERMINAL	PROTEIN TRANSPORT

	DOMAIN	
1TUE	THE X-RAY STRUCTURE OF THE PAPILLOMAVIRUS HELICASE IN COMPLEX WITH ITS MOLECULAR MATCHMAKER E2	REPLICATION
1TWF	RNA POLYMERASE II COMPLEXED WITH UTP AT 2.3 A RESOLUTION	TRANSCRIPTION
1TWQ	CRYSTAL STRUCTURE OF THE C-TERMINAL PGN-BINDING DOMAIN OF HUMAN PGRP-IALPHA IN COMPLEX WITH PGN ANALOG MURAMYL TRIPEPTIDE	IMMUNE SYSTEM, MEMBRANE PROTEIN
1TY4	CRYSTAL STRUCTURE OF A CED-9/EGL-1 COMPLEX	APOPTOSIS
1TYG	STRUCTURE OF THE THIAZOLE SYNTHASE/THIS COMPLEX	BIOSYNTHETIC PROTEIN
1U00	HSCA SUBSTRATE BINDING DOMAIN COMPLEXED WITH THE ISCU RECOGNITION PEPTIDE ELPPVKIHC	CHAPERONE
1U0S	CHEMOTAXIS KINASE CHEA P2 DOMAIN IN COMPLEX WITH RESPONSE REGULATOR CHEY FROM THE THERMOPHILE THERMOTOGA MARITIMA	SIGNALING PROTEIN
1U2G	TRANSHYDROGENASE (DI.ADPR)2(DIII.NADPH)1 ASYMMETRIC COMPLEX	OXIDOREDUCTASE
1U35	CRYSTAL STRUCTURE OF THE NUCLEOSOME CORE PARTICLE CONTAINING THE HISTONE DOMAIN OF MACROH2A	STRUCTURAL PROTEIN/DNA
1U5T	STRUCTURE OF THE ESCRT-II ENDOSOMAL TRAFFICKING COMPLEX	TRANSPORT PROTEIN
1U7B	CRYSTAL STRUCTURE OF HPCNA BOUND TO RESIDUES 331-350 OF THE FLAP ENDONUCLEASE-1 (FEN1)	REPLICATION
1U8T	CRYSTAL STRUCTURE OF CHEY D13K Y106W ALONE AND IN COMPLEX WITH A FLIM PEPTIDE	SIGNALING PROTEIN
1U9L	STRUCTURAL BASIS FOR A NUSA- PROTEIN N INTERACTION	RNA BINDING PROTEIN
1UEA	MMP-3/TIMP-1 COMPLEX	COMPLEX (METALLOPROTEASE/INHIBITOR)
1UEF	CRYSTAL STRUCTURE OF DOK1 PTB DOMAIN COMPLEX	PROTEIN BINDING/TRANSFERASE
1UF2	THE ATOMIC STRUCTURE OF RICE DWARF VIRUS (RDV)	VIRUS
1UGH	CRYSTAL STRUCTURE OF HUMAN URACIL-DNA GLYCOSYLASE IN COMPLEX WITH A PROTEIN INHIBITOR: PROTEIN MIMICRY OF DNA	GLYCOSYLASE
1UGP	CRYSTAL STRUCTURE OF CO-TYPE NITRILE HYDRATASE COMPLEXED WITH N-BUTYRIC ACID	LYASE
1UHE	CRYSTAL STRUCTURE OF ASPARTATE DECARBOXYLASE, ISOASPARGINE COMPLEX	LYASE
1UJK	VHS DOMAIN OF HUMAN GGA1 COMPLEXED WITH C-TERMINAL PHOSPHOPEPTIDE FROM BACE	PROTEIN TRANSPORT/HYDROLASE
1UKH	STRUCTURAL BASIS FOR THE SELECTIVE INHIBITION OF JNK1 BY	TRANSFERASE

	THE SCAFFOLDING PROTEIN JIP1 AND SP600125	
1ULI	IPHENYL DIOXYGENASE (BPHA1A2) DERIVED FROM RHODOCOCCUS SP. STRAIN RHA1	OXIDOREDUCTASE
1UM2	RYSTAL STRUCTURE OF THE VMA1-DERIVED ENDONUCLEASE WITH THE LIGATED EXTEIN SEGMENT	HYDROLASE
1UMD	RANCHED-CHAIN 2-OXO ACID DEHYDROGENASE (E1) FROM THERMUS THERMOPHILUS HB8 WITH 4-METHYL-2-OXOPENTANOATE AS AN INTERMEDIATE	OXIDOREDUCTASE
1UMR	CRYSTAL STRUCTURE OF THE PLATELET ACTIVATOR CONVULXIN, A DISULFIDE LINKED A4B4 CYCLIC TETRAMER FROM THE VENOM OF CROTALUS DURISSUS TERRIFICUS	LECTIN
1UPK	CRYSTAL STRUCTURE OF MO25 IN COMPLEX WITH A C-TERMINAL PEPTIDE OF STRAD	TRANSFERASE
1UPT	STRUCTURE OF A COMPLEX OF THE GOLGIN-245 GRIP DOMAIN WITH ARL1	COMPLEX (GTPASE/GOLGIN)
1USU	THE STRUCTURE OF THE COMPLEX BETWEEN AHA1 AND HSP90	CHAPERONE/COMPLEX
1UVQ	CRYSTAL STRUCTURE OF HLA-DQ0602 IN COMPLEX WITH A HYPOCRETIN PEPTIDE	IMMUNOLOGY
1UW4	THE STRUCTURAL BASIS OF THE INTERACTION BETWEEN NONSENSE MEDIATED DECAY FACTORS UPF2 AND UPF3	RNA-BINDING PROTEIN
1UYW	CRYSTAL STRUCTURE OF THE ANTIFLAVIVIRUS FAB4G2	IMMUNE SYSTEM
1V29	CRYSTAL STRUCTURE OF NITRILE HYDRATASE FROM A THERMOPHILE BACILLUS SMITHII	LYASE
1V4X	RYSTAL STRUCTURE OF BLUEFIN TUNA HEMOGLOBIN DEOXY FORM AT PH5.0	OXYGEN STORAGE/TRANSPORT
1V74	RIBONUCLEASE-INHIBITOR COMPLEX	ANTIBIOTIC/IMMUNE SYSTEM
1V7P	STRUCTURE OF EMS16-ALPHA2-I DOMAIN COMPLEX	TOXIN/CELL ADHESION
1V9T	STRUCTURE OF E. COLI CYCLOPHILIN B K163T MUTANT BOUND TO SUCCINYL-ALA-PRO-ALA-P-NITROANILIDE	ISOMERASE
1VC3	CRYSTAL STRUCTURE OF L-ASPARTATE-ALPHA-DECARBOXYLASE	LYASE
1VF6	2.1 ANGSTROM CRYSTAL STRUCTURE OF THE PALS-1-L27N AND PATJ L27 HETERODIMER COMPLEX	PROTEIN BINDING/PROTEIN TRANSPORT
1VG0	THE CRYSTAL STRUCTURES OF THE REP-1 PROTEIN IN COMPLEX WITH MONOPRENYLATED RAB7 PROTEIN	PROTEIN BINDING/PROTEIN TRANSPORT
1VLF	CRYSTAL STRUCTURE OF PYROGALLOL-PHLOROGLUCINOL TRANSHYDROXYLASE FROM PELOBACTER ACIDIGALLICI COMPLEXED	OXIDOREDUCTASE

	WITH INHIBITOR 1,2,4,5-TETRAHYDROXY-BENZENE	
1VOQ	CRYSTAL STRUCTURE OF FIVE 70S RIBOSOMES FROM ESCHERICHIA COLI IN COMPLEX WITH PROTEIN Y. THIS FILE CONTAINS THE 30S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS FIVE 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
1VQ4	THE STRUCTURE OF THE TRANSITION STATE ANALOGUE "DAA" BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1VQ5	THE STRUCTURE OF THE TRANSITION STATE ANALOGUE "RAA" BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1VQ6	THE STRUCTURE OF C-HPMN AND CCA-PHE-CAP-BIO BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1VQ7	THE STRUCTURE OF THE TRANSITION STATE ANALOGUE "DCA" BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1VQ8	THE STRUCTURE OF CCDA-PHE-CAP-BIO AND THE ANTIBIOTIC SPARSOMYCIN BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1VQP	THE STRUCTURE OF THE TRANSITION STATE ANALOGUE "RAP" BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1VRA	CRYSTAL STRUCTURE OF ARGININE BIOSYNTHESIS BIFUNCTIONAL PROTEIN ARGJ (10175521) FROM BACILLUS HALODURANS AT 2.00 A RESOLUTION	TRANSFERASE
1VS5	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH THE ANTIBIOTIC KASUGAMYIN AT 3.5A RESOLUTION. THIS FILE CONTAINS THE 30S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
1VSA	CRYSTAL STRUCTURE OF A 70S RIBOSOME-TRNA COMPLEX REVEALS FUNCTIONAL INTERACTIONS AND REARRANGEMENTS. THIS FILE, 1VSA, CONTAINS THE 50S RIBOSOME SUBUNIT. 30S RIBOSOME SUBUNIT IS IN THE FILE 2OW8	RIBOSOME
1VSQ	OLUTION NMR STRUCTURE OF THE PRODUCTIVE COMPLEX BETWEEN IIAMANNOSE AND IIBMANNOSE OF THE MANNOSE TRANSPORTER OF THE E. COLI PHOSPHOTRANSFERASE SYSTEM	TRANSFERASE
1VZJ	STRUCTURE OF THE TETRAMERIZATION DOMAIN OF ACETYLCHOLINESTERASE: FOUR-FOLD INTERACTION OF A WWW MOTIF WITH A LEFT-HANDED POLYPROLINE HELIX	HYDROLASE
1W2B	TRIGGER FACTOR RIBOSOME BINDING DOMAIN IN COMPLEX WITH 50S	RIBOSOME
1W2W	CRYSTAL STRUCTURE OF YEAST YPR118W, A METHYLTHIORIBOSE-1-PHOSPHATE ISOMERASE RELATED TO REGULATORY EIF2B SUBUNITS	ISOMERASE
1W7J	CRYSTAL STRUCTURE OF MYOSIN V MOTOR WITH ESSENTIAL LIGHT	MOTOR PROTEIN

	CHAIN + ADP-BEFX- NEAR RIGOR	
1W7V	ZNMG SUBSTITUTED AMINOPEPTIDASE P FROM E. COLI	HYDROLASE
1W85	HE CRYSTAL STRUCTURE OF PYRUVATE DEHYDROGENASE E1 BOUND TO THE PERIPHERAL SUBUNIT BINDING DOMAIN OF E2	OXIDOREDUCTASE
1W8X	STRUCTURAL ANALYSIS OF PRD1	VIRUS
1WA8	SOLUTION STRUCTURE OF THE CFP-10.ESAT-6 COMPLEX. MAJOR VIRULENCE DETERMINANTS OF PATHOGENIC MYCOBACTERIA	TUBERCULOSIS
1WBP	SRPK1 BOUND TO 9MER DOCKING MOTIF PEPTIDE	TRANSFERASE
1WDC	SCALLOP MYOSIN REGULATORY DOMAIN	MUSCLE PROTEIN
1WDD	CRYSTAL STRUCTURE OF ACTIVATED RICE RUBISCO COMPLEXED WITH 2-CARBOXYARABINITOL-1,5-BISPHOSPHATE	LYASE
1WDK	FATTY ACID BETA-OXIDATION MULTIENZYME COMPLEX FROM PSEUDOMONAS FRAGI, FORM I (NATIVE2)	LYASE,OXIDOREDUCTASE/TRANSFERASE
1WDW	STRUCTURAL BASIS OF MUTUAL ACTIVATION OF THE TRYPTOPHAN SYNTHASE A2B2 COMPLEX FROM A HYPERTHERMOPHILE, PYROCOCCUS FURIOSUS	LYASE
1WE3	CRYSTAL STRUCTURE OF THE CHAPERONIN COMPLEX CPN60/CPN10/(ADP)7 FROM THERMUS THERMOPHILUS	CHAPERONE
1WHS	STRUCTURE OF THE COMPLEX OF L-BENZYLSUCCINATE WITH WHEAT SERINE CARBOXYPEPTIDASE II AT 2.0 ANGSTROMS RESOLUTION	SERINE CARBOXYPEPTIDASE
1WKR	CRYSTAL STRUCTURE OF ASPARTIC PROTEINASE FROM IRPEX LACTEUS	HYDROLASE
1WLP	SOLUTION STRUCTURE OF THE P22PHOX-P47PHOX COMPLEX	OXIDOREDUCTASE/SIGNALING PROTEIN
1WLQ	STRUCURE OF GEMININ-CDT1 COMPLEX	CELL CYCLE
1WMH	CRYSTAL STRUCTURE OF A PB1 DOMAIN COMPLEX OF PROTEIN KINASE C IOTA AND PAR6 ALPHA	TRANSFERASE/CELL CYCLE
1WMI	CRYSTAL STRUCTURE OF ARCHAEAL RELE-RELB COMPLEX FROM PYROCOCCUS HORIKOSHII OT3	HYDROLASE/HYDROLASE INHIBITOR
1WMU	CRYSTAL STRUCTURE OF HEMOGLOBIN D FROM THE ALDABRA GIANT TORTOISE, GEOCHELONE GIGANTEA, AT 1.65 A RESOLUTION	OXYGEN STORAGE/TRANSPORT
1WPX	CRYSTAL STRUCTURE OF CARBOXYPEPTIDASE Y INHIBITOR COMPLEXED WITH THE COGNATE PROTEINASE	HYDROLASE
1WQJ	STRUCTURAL BASIS FOR THE REGULATION OF INSULIN-LIKE GROWTH FACTORS (IGFS) BY IGF BINDING PROTEINS (IGFBPS)	PROTEIN BINDING/HORMONE/GROWTH FACTOR
1WQL	UMENE DIOXYGENASE (CUMA1A2) FROM PSEUDOMONAS FLUORESCENS IP01	OXIDOREDUCTASE

1WT9	CRYSTAL STRUCTURE OF AA-X-BP-I, A SNAKE VENOM PROTEIN WITH THE ACTIVITY OF BINDING TO COAGULATION FACTOR X FROM AGKISTRODON ACUTUS	BLOOD CLOTTING
1WTH	CRYSTAL STRUCTURE OF GP5-S351L MUTANT AND GP27 COMPLEX	HYDROLASE/STRUCTURAL PROTEIN
1WUI	ULTRA-HIGH RESOLUTION STRUCTURE OF THE NI-A STATE OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE
1WVE	P-CRESOL METHYLHYDROXYLASE: ALTERATION OF THE STRUCTURE OF THE FLAVOPROTEIN SUBUNIT UPON ITS BINDING TO THE CYTOCHROME SUBUNIT	OXIDOREDUCTASE
1WWW	NGF IN COMPLEX WITH DOMAIN 5 OF THE TRKA RECEPTOR	NERVE GROWTH FACTOR/TRKA COMPLEX
1WXC	CRYSTAL STRUCTURE OF THE COPPER-FREE STREPTOMYCES CASTANEOGLOBISPORUS TYROSINASE COMPLEXED WITH A CADDIE PROTEIN	OXIDOREDUCTASE/METAL TRANSPORT
1WYU	CRYSTAL STRUCTURE OF GLYCINE DECARBOXYLASE (P-PROTEIN) OF THE GLYCINE CLEAVAGE SYSTEM, IN HOLO FORM	OXIDOREDUCTASE
1X11	X11 PTB DOMAIN	COMPLEX (PEPTIDE BINDING MODULE/PEPTIDE)
1X31	CRYSTAL STRUCTURE OF HETEROTETRAMERIC SARCOSINE OXIDASE FROM CORYNEBACTERIUM SP. U-96	OXIDOREDUCTASE
1X75	CCDB:GYRA14 COMPLEX	ISOMERASE/SIGNALING PROTEIN
1X9F	HEMOGLOBIN DODECAMER FROM LUMBRICUS ERYTHROCRUORIN	OXYGEN STORAGE/TRANSPORT
1X9M	T7 DNA POLYMERASE IN COMPLEX WITH AN N-2-ACETYLAMINOFLUORENE-ADDUCTED DNA	TRANSFERASE/ELECTRON TRANSPORT/DNA
1X9S	T7 DNA POLYMERASE IN COMPLEX WITH A PRIMER/TEMPLATE DNA CONTAINING A DISORDERED N-2 AMINOFLUORENE ON THE TEMPLATE, CRYSTALLIZED WITH DIDEOXY-CTP AS THE INCOMING NUCLEOTIDE.	TRANSFERASE/ELECTRON TRANSPORT/DNA
1X9T	THE CRYSTAL STRUCTURE OF HUMAN ADENOVIRUS 2 PENTON BASE IN COMPLEX WITH AN AD2 N-TERMINAL FIBRE PEPTIDE	VIRUS LIKE PARTICLE/PEPTIDE
1XB1	THE STRUCTURE OF THE BIR DOMAIN OF IAP-LIKE PROTEIN 2	APOPTOSIS
1XB2	CRYSTAL STRUCTURE OF BOS TAURUS MITOCHONDRIAL ELONGATION FACTOR TU/TS COMPLEX	TRANSLATION
1XD3	CRYSTAL STRUCTURE OF UCHL3-UBVME COMPLEX	HYDROLASE
1XEW	STRUCTURAL BIOCHEMISTRY OF ATP-DRIVEN DIMERIZATION AND DNA STIMULATED ACTIVATION OF SMC ATPASES.	CELL CYCLE
1XF2	STRUCTURE OF FAB DNA-1 COMPLEXED WITH DT3	IMMUNE SYSTEM/DNA
1XG0	IGH RESOLUTION CRYSTAL STRUCTURE OF PHYCOERYTHRIN 545 FROM	PHOTOSYNTHESIS

	THE MARINE CRYPTOPHYTE RHODOMONAS CS24	
1XG2	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN PECTIN METHYLESTERASE AND ITS INHIBITOR PROTEIN	HYDROLASE/HYDROLASE INHIBITOR
1XIU	CRYSTAL STRUCTURE OF THE AGONIST-BOUND LIGAND-BINDING DOMAIN OF BIOMPHALARIA GLABRATA RXR	TRANSCRIPTION/TRANSFERASE
1XK4	CRYSTAL STRUCTURE OF HUMAN CALPROTECTIN(S100A8/S100A9)	METAL BINDING PROTEIN
1XKP	CRYSTAL STRUCTURE OF THE VIRULENCE FACTOR YOPN IN COMPLEX WITH ITS HETERODIMERIC CHAPERONE SYCN-YSCB	MEMBRANE PROTEIN/CHAPERON
1XME	STRUCTURE OF RECOMBINANT CYTOCHROME BA3 OXIDASE FROM THERMUS THERMOPHILUS	OXIDOREDUCTASE
1XMO	RYSTAL STRUCTURE OF MNM5U34T6A37-TRNALYSUUU COMPLEXED WITH AAG-MRNA IN THE DECODING CENTER	RIBOSOME
1XMQ	CRYSTAL STRUCTURE OF T6A37-ASLLYSUUU AAA-MRNA BOUND TO THE DECODING CENTER	RIBOSOME
1XN2	NEW SUBSTRATE BINDING POCKETS FOR BETA-SECRETASE.	HYDROLASE
1XNQ	STRUCTURE OF AN INOSINE-ADENINE WOBBLE BASE PAIR COMPLEX IN THE CONTEXT OF THE DECODING CENTER	RIBOSOME
1XNR	CRYSTAL STRUCTURE OF AN INOSINE-CYTOSINE WOBBLE BASE PAIR IN THE CONTEXT OF THE DECODING CENTER	RIBOSOME
1XOF	HETEROOLIGOMERIC BETA BETA ALPHA MINIPROTEIN	DE NOVO PROTEIN
1XOU	CRYSTAL STRUCTURE OF THE CESA-ESPA COMPLEX	STRUCTURAL PROTEIN/CHAPERONE
1XQ7	CYCLOPHILIN FROM TRYPANOSOMA CRUZI BOUND TO CYCLOSPORIN A	ISOMERASE
1XR0	STRUCTURAL BASIS OF SNT PTB DOMAIN INTERACTIONS WITH DISTINCT NEUROTROPHIC RECEPTORS	SIGNALING PROTEIN/GROWTH FACTOR RECEPTOR
1XRP	CRYSTAL STRUCTURE OF ACTIVE SITE F1-MUTANT E213Q SOAKED WITH PEPTIDE PRO-LEU-GLY-GLY	HYDROLASE
1XRS	CRYSTAL STRUCTURE OF LYSINE 5,6-AMINOMUTASE IN COMPLEX WITH PLP, COBALAMIN, AND 5'-DEOXYADENOSINE	ISOMERASE
1XS9	A MODEL OF THE TERNARY COMPLEX FORMED BETWEEN MARA, THE ALPHA-CTD OF RNA POLYMERASE AND DNA	TRANSCRIPTION/DNA
1XU2	THE CRYSTAL STRUCTURE OF APRIL BOUND TO BCMA	CYTOKINE, HORMONE/GROWTH FACTOR RECEPTOR
1Y14	CRYSTAL STRUCTURE OF YEAST SUBCOMPLEX OF RPB4 AND RPB7	TRANSFERASE
1Y1W	COMPLETE RNA POLYMERASE II ELONGATION COMPLEX	TRANSFERASE/DNA/RNA
1Y56	CRYSTAL STRUCTURE OF L-PROLINE DEHYDROGENASE FROM	OXIDOREDUCTASE

	P.HORIKOSHII	
1Y5I	THE CRYSTAL STRUCTURE OF THE NARGHI MUTANT NARI-K86A	OXIDOREDUCTASE
1Y75	A NEW FORM OF CATALYTICALLY INACTIVE PHOSPHOLIPASE A2 WITH AN UNUSUAL DISULPHIDE BRIDGE CYS 32- CYS 49 REVEALS RECOGNITION FOR N-ACETYLGLUCOSMINE	HYDROLASE
1Y77	COMPLETE RNA POLYMERASE II ELONGATION COMPLEX WITH SUBSTRATE ANALOGUE GMPCPP	TRANSFERASE/DNA/RNA
1Y7L	O-ACETYLSERINE SULFHYDRYLASE COMPLEX	TRANSFERASE
1Y8Q	SUMO E1 ACTIVATING ENZYME SAE1-SAE2-MG-ATP COMPLEX	LIGASE
1Y96	RYSTAL STRUCTURE OF THE GEMIN6/GEMIN7 HETERODIMER FROM THE HUMAN SMN COMPLEX	RNA BINDING PROTEIN
1YAR	STRUCTURE OF ARCHEABACTERIAL 20S PROTEASOME MUTANT D9S-PA26 COMPLEX	HYDROLASE/HYDROLASE ACTIVATOR
1YC5	SIR2-P53 PEPTIDE-NICOTINAMIDE	HYDROLASE
1YCQ	XENOPUS LAEVIS MDM2 BOUND TO THE TRANSACTIVATION DOMAIN OF HUMAN P53	COMPLEX (ONCOGENE PROTEIN/PEPTIDE)
1YCS	P53-53BP2 COMPLEX	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1YDI	HUMAN VINCULIN HEAD DOMAIN (VH1, 1-258) IN COMPLEX WITH HUMAN ALPHA-ACTININ'S VINCULIN-BINDING SITE (RESIDUES 731-760)	CELL ADHESION, STRUCTURAL PROTEIN
1YEW	CRYSTAL STRUCTURE OF PARTICULATE METHANE MONOOXYGENASE	OXIDOREDUCTASE, MEMBRANE PROTEIN
1YF8	CRYSTAL STRUCTURE OF HIMALAYAN MISTLETOE RIP REVEALS THE PRESENCE OF A NATURAL INHIBITOR AND A NEW FUNCTIONALLY ACTIVE SUGAR-BINDING SITE	HYDROLASE
1YFN	VERSATILE MODES OF PEPTIDE RECOGNITION BY THE AAA+ ADAPTOR PROTEIN SSPB- THE CRYSTAL STRUCTURE OF A SSPB-RSEA COMPLEX	PROTEIN BINDING
1YGU	RYSTAL STRUCTURE OF THE TANDEM PHOSPHATASE DOMAINS OF RPTP CD45 WITH A PTYR PEPTIDE	HYDROLASE
1YHQ	CRYSTAL STRUCTURE OF AZITHROMYCIN BOUND TO THE G2099A MUTANT 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1YHU	CRYSTAL STRUCTURE OF RIFTIA PACHYPTILA C1 HEMOGLOBIN REVEALS NOVEL ASSEMBLY OF 24 SUBUNITS.	OXYGEN STORAGE/TRANSPORT
1YI2	CRYSTAL STRUCTURE OF ERYTHROMYCIN BOUND TO THE G2099A MUTANT 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1YI5	CRYSTAL STRUCTURE OF THE A-COBRATOXIN-ACHBP COMPLEX	TOXIN

1YIJ	CRYSTAL STRUCTURE OF TELITHROMYCIN BOUND TO THE G2099A MUTANT 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1YIT	CRYSTAL STRUCTURE OF VIRGINIAMYCIN M AND S BOUND TO THE 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1YJ5	MOLECULAR ARCHITECTURE OF MAMMALIAN POLYNUCLEOTIDE KINASE, A DNA REPAIR ENZYME	TRANSFERASE
1YJ9	CRYSTAL STRUCTURE OF THE MUTANT 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI CONTAINING A THREE RESIDUE DELETION IN L22	RIBOSOME
1YJN	CRYSTAL STRUCTURE OF CLINDAMYCIN BOUND TO THE G2099A MUTANT 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1YJW	CRYSTAL STRUCTURE OF QUINUPRISTIN BOUND TO THE G2099A MUTANT 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1YK0	STRUCTURE OF NATRIURETIC PEPTIDE RECEPTOR-C COMPLEXED WITH ATRIAL NATRIURETIC PEPTIDE	HORMONE/GROWTH FACTOR RECEPTOR
1YKH	STRUCTURE OF THE MEDIATOR MED7/MED21 (MED7/SRB7) SUBCOMPLEX	GENE REGULATION
1YL3	CRYSTAL STRUCTURE OF 70S RIBOSOME WITH THRS OPERATOR AND TRNAS. LARGE SUBUNIT. THE COORDINATES FOR THE SMALL SUBUNIT ARE IN THE PDB ENTRY 1YL4.	RIBOSOME
1YL4	CRYSTAL STRUCTURE OF 70S RIBOSOME WITH THRS OPERATOR AND TRNAS. 30S SUBUNIT. THE COORDINATES FOR THE 50S SUBUNIT ARE IN THE PDB ENTRY 1YL3	RIBOSOME
1YM0	CRYSTAL STRUCTURE OF EARTHWORM FIBRINOLYTIC ENZYME COMPONENT B: A NOVEL, GLYCOSYLATED TWO-CHAINED TRYPSIN	HYDROLASE
1YMT	MOUSE SF-1 LBD	TRANSCRIPTION
1YNN	TAQ RNA POLYMERASE-RIFAMPICIN COMPLEX	TRANSFERASE
1YQ9	STRUCTURE OF THE UNREADY OXIDIZED FORM OF [NIFE] HYDROGENASE	OXIDOREDUCTASE
1YQW	STRUCTURE OF THE OXIDIZED UNREADY FORM OF NI-FE HYDROGENASE	OXIDOREDUCTASE
1YRN	CRYSTAL STRUCTURE OF THE MATA1/MATALPHA2 HOMEODOMAIN HETERODIMER BOUND TO DNA	DNA BINDING PROTEIN/DNA
1YRO	CRYSTAL STRUCTURE OF BETA14,-GALACTOSYLTRANSFERASE MUTANT ARG228LYS IN COMPLEX WITH ALPHA-LACTALBUMIN IN THE PRESENCE OF UDP-GALACTOSE AND MN	TRANSFERASE ACTIVATOR/TRANSFERASE
1YRQ	STRUCTURE OF THE READY OXIDIZED FORM OF [NIFE]-HYDROGENASE	OXIDOREDUCTASE
1YSH	LOCALIZATION AND DYNAMIC BEHAVIOR OF RIBOSOMAL PROTEIN L30E	STRUCTURAL PROTEIN/RNA
1YTF	YEAST TFIIA/TBP/DNA COMPLEX	TRANSCRIPTION/DNA

1YTV	MALTOSE-BINDING PROTEIN FUSION TO A C-TERMINAL FRAGMENT OF THE V1A VASOPRESSIN RECEPTOR	SUGAR BINDING PROTEIN, HORMONE RECEPTOR
1YUC	HUMAN NUCLEAR RECEPTOR LIVER RECEPTOR HOMOLOGUE-1, LRH-1, BOUND TO PHOSPHOLIPID AND A FRAGMENT OF HUMAN SHP	TRANSCRIPTION REGULATION
1YVL	STRUCTURE OF UNPHOSPHORYLATED STAT1	SIGNALING PROTEIN
1YWT	CRYSTAL STRUCTURE OF THE HUMAN SIGMA ISOFORM OF 14-3-3 IN COMPLEX WITH A MODE-1 PHOSPHOPEPTIDE	SIGNALING PROTEIN/DE NOVO PROTEIN
1YYE	RYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH WAY-202196	TRANSCRIPTION
1YYP	CRYSTAL STRUCTURE OF CYTOMEGALOVIRUS UL44 BOUND TO C-TERMINAL PEPTIDE FROM CMV UL54	REPLICATION/TRANSFERASE
1Z0J	STRUCTURE OF GTP-BOUND RAB22Q64L GTPASE IN COMPLEX WITH THE MINIMAL RAB BINDING DOMAIN OF RABENOSYN-5	PROTEIN TRANSPORT
1Z0K	STRUCTURE OF GTP-BOUND RAB4Q67L GTPASE IN COMPLEX WITH THE CENTRAL RAB BINDING DOMAIN OF RABENOSYN-5	PROTEIN TRANSPORT
1Z3E	CRYSTAL STRUCTURE OF SPX IN COMPLEX WITH THE C-TERMINAL DOMAIN OF THE RNA POLYMERASE ALPHA SUBUNIT	TRANSCRIPTION
1Z56	CO-CRYSTAL STRUCTURE OF LIF1P-LIG4P	LIGASE
1Z5X	HEMIPTERAN ECDYSONE RECEPTOR LIGAND-BINDING DOMAIN COMPLEXED WITH PONASTERONE A	HORMONE/GROWTH FACTOR RECEPTOR
1Z5Y	CRYSTAL STRUCTURE OF THE DISULFIDE-LINKED COMPLEX BETWEEN THE N-TERMINAL DOMAIN OF THE ELECTRON TRANSFER CATALYST DSBD AND THE CYTOCHROME C BIOGENESIS PROTEIN CCMG	OXIDOREDUCTASE/BIOSYNTHETIC PROTEIN
1Z6O	CRYSTAL STRUCTURE OF TRICHOPLUSIA NI SECRETED FERRITIN	METAL BINDING PROTEIN
1Z7M	ATP PHOSPHORIBOSYL TRANSFERASE (HISZG ATP-PRTASE) FROM LACTOCOCCUS LACTIS	TRANSFERASE
1Z7X	X-RAY STRUCTURE OF HUMAN RIBONUCLEASE INHIBITOR COMPLEXED WITH RIBONUCLEASE I	HYDROLASE/HYDROLASE INHIBITOR
1Z9O	1.9 ANGSTROM CRYSTAL STRUCTURE OF THE RAT VAP-A MSP HOMOLOGY DOMAIN IN COMPLEX WITH THE RAT ORP1 FFAT MOTIF	PROTEIN BINDING/LIPID BINDING PROTEIN
1ZAN	CRYSTAL STRUCTURE OF ANTI-NGF AD11 FAB	IMMUNE SYSTEM
1ZAV	RIBOSOMAL PROTEIN L10-L12(NTD) COMPLEX, SPACE GROUP P21	STRUCTURAL PROTEIN
1ZB5	RECOGNITION OF PEPTIDE LIGANDS BY SIGNALLING PROTEIN FROM PORCINE MAMMARY GLAND (SPP-40): CRYSTAL STRUCTURE OF THE COMPLEX OF SPP-40 WITH A PEPTIDE TRP-PRO-TRP AT 2.45A RESOLUTION	SIGNALING PROTEIN

1ZBB	STRUCTURE OF THE 4_601_167 TETRANUCLEOSOME	STRUCTURAL PROTEIN/DNA
1ZBD	STRUCTURAL BASIS OF RAB EFFECTOR SPECIFICITY: CRYSTAL STRUCTURE OF THE SMALL G PROTEIN RAB3A COMPLEXED WITH THE EFFECTOR DOMAIN OF RABPHILIN-3A	G PROTEIN
1ZBX	CRYSTAL STRUCTURE OF A ORC1P-SIR1P COMPLEX	TRANSCRIPTION
1ZDT	THE CRYSTAL STRUCTURE OF HUMAN STEROIDOGENIC FACTOR-1	TRANSCRIPTION
1ZGY	STRUCTURAL AND BIOCHEMICAL BASIS FOR SELECTIVE REPRESSION OF THE ORPHAN NUCLEAR RECEPTOR LRH-1 BY SHP	TRANSCRIPTION
1ZH7	STRUCTURAL AND BIOCHEMICAL BASIS FOR SELECTIVE REPRESSION OF THE ORPHAN NUCLEAR RECEPTOR LRH-1 BY SHP	TRANSCRIPTION
1ZHH	CRYSTAL STRUCTURE OF THE APO FORM OF VIBRIO HARVEYI LUXP COMPLEXED WITH THE PERIPLASMIC DOMAIN OF LUXQ	SIGNALING PROTEIN
1ZLA	X-RAY STRUCTURE OF A KAPOSI'S SARCOMA HERPESVIRUS LANA PEPTIDE BOUND TO THE NUCLEOSOMAL CORE	PROTEIN BINDING/VIRUS/DNA
1ZLH	CRYSTAL STRUCTURE OF THE TICK CARBOXYPEPTIDASE INHIBITOR IN COMPLEX WITH BOVINE CARBOXYPEPTIDASE A	HYDROLASE/HYDROLASE INHIBITOR
1ZO1	IF2, IF1, AND TRNA FITTED TO CRYO-EM DATA OF E. COLI 70S INITIATION COMPLEX	TRANSLATION/RNA
1ZOQ	IRF3-CBP COMPLEX	TRANSCRIPTION/TRANSFERASE
1ZOY	CRYSTAL STRUCTURE OF MITOCHONDRIAL RESPIRATORY COMPLEX II FROM PORCINE HEART AT 2.4 ANGSTROMS	OXIDOREDUCTASE
1ZQ1	TRUCTURE OF GATDE TRNA-DEPENDENT AMIDOTRANSFERASE FROM PYROCOCCUS ABYSSI	LYASE
1ZRT	RHODOBACTER CAPSULATUS CYTOCHROME BC1 COMPLEX WITH STIGMATELLIN BOUND	OXIDOREDUCTASE/METAL TRANSPORT
1ZT2	HETERODIMERIC STRUCTURE OF THE CORE PRIMASE.	REPLICATION, TRANSFERASE
1ZTX	WEST NILE VIRUS ENVELOPE PROTEIN DIII IN COMPLEX WITH NEUTRALIZING E16 ANTIBODY FAB	VIRAL PROTEIN/IMMUNE SYSTEM
1ZUN	CRYSTAL STRUCTURE OF A GTP-REGULATED ATP SULFURYLASE HETERODIMER FROM PSEUDOMONAS SYRINGAE	TRANSFERASE
1ZVV	CRYSTAL STRUCTURE OF A CCPA-CRH-DNA COMPLEX	TRANSCRIPTION/DNA
1ZY1	X-RAY STRUCTURE OF PEPTIDE DEFORMYLASE FROM ARABIDOPSIS THALIANA (ATPDF1A) IN COMPLEX WITH MET-ALA-SER	HYDROLASE
1ZYQ	T7 DNA POLYMERASE IN COMPLEX WITH 8OG AND INCOMING DDATP	TRANSFERASE/ELECTRON TRANSPORT/DNA

2A06	BOVINE CYTOCHROME BC1 COMPLEX WITH STIGMATELLIN BOUND	OXIDOREDUCTASE
2A19	PKR KINASE DOMAIN- EIF2ALPHA- AMP-PNP COMPLEX.	PROTEIN SYNTHESIS/TRANSFERASE
2A1J	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE C-TERMINAL DOMAINS OF HUMAN XPF AND ERCC1	DNA BINDING PROTEIN
2A3I	STRUCTURAL AND BIOCHEMICAL MECHANISMS FOR THE SPECIFICITY OF HORMONE BINDING AND COACTIVATOR ASSEMBLY BY MINERALOCORTICOID RECEPTOR	TRANSFERASE
2A5T	CRYSTAL STRUCTURE OF THE NR1/NR2A LIGAND-BINDING CORES COMPLEX	METAL TRANSPORT,MEMBRANE PROTEIN
2A6H	CRYSTAL STRUCTURE OF THE T. THERMOPHILUS RNA POLYMERASE HOLOENZYME IN COMPLEX WITH ANTIBIOTIC STERPTOLYDIGIN	TRANSFERASE
2A6Q	CRYSTAL STRUCTURE OF YEFM-YOEB COMPLEX	TOXIN INHIBITOR/TOXIN
2A7U	NMR SOLUTION STRUCTURE OF THE E.COLI F-ATPASE DELTA SUBUNIT N-TERMINAL DOMAIN IN COMPLEX WITH ALPHA SUBUNIT N-TERMINAL 22 RESIDUES	HYDROLASE
2A9K	CRYSTAL STRUCTURE OF THE C3BOT-NAD-RALA COMPLEX REVEALS A NOVEL TYPE OF ACTION OF A BACTERIAL EXOENZYME	PROTEIN BINDING/TRANSFERASE
2A9M	STRUCTURAL ANALYSIS OF A TIGHT-BINDING FLUORESCEIN-SCFV; APO FORM	IMMUNE SYSTEM
2AAI	CRYSTALLOGRAPHIC REFINEMENT OF RICIN TO 2.5 ANGSTROMS	GLYCOSIDASE
2AD6	RYSTAL STRUCTURE OF METHANOL DEHYDROGENASE FROM M. W3A1 (FORM C)	OXIDOREDUCTASE
2ADF	CRYSTAL STRUCTURE AND PARATOPE DETERMINATION OF 82D6A3, AN ANTITHROMBOTIC ANTIBODY DIRECTED AGAINST THE VON WILLEBRAND FACTOR A3-DOMAIN	BLOOD CLOTTING/IMMUNE SYSTEM
2AGI	THE LEUPEPTIN-TRYPSIN COVALENT COMPLEX AT 1.14 A RESOLUTION	HYDROLASE
2AGJ	CRYSTAL STRUCTURE OF A GLYCOSYLATED FAB FROM AN IGM CRYOGLOBULIN WITH PROPERTIES OF A NATURAL PROTEOLYTIC ANTIBODY	IMMUNE SYSTEM
2AHM	CRYSTAL STRUCTURE OF SARS-COV SUPER COMPLEX OF NON-STRUCTURAL PROTEINS: THE HEXADECAMER	VIRAL PROTEIN, REPLICATION
2AIG	ADAMALYSIN II WITH PEPTIDOMIMETIC INHIBITOR POL647	COMPLEX (METALLOPROTEASE/INHIBITOR)
2AIJ	FORMYLGLYCINE GENERATING ENZYME C336S MUTANT COVALENTLY BOUND TO SUBSTRATE PEPTIDE CTPSR	HYDROLASE ACTIVATOR,PROTEIN BINDING
2B05	CRYSTAL STRUCTURE OF 14-3-3 GAMMA IN COMPLEX WITH A PHOSPHOSERINE PEPTIDE	CELL CYCLE

2B1N	CRYSTAL STRUCTURE OF A PAPAIN-FOLD PROTEIN WITHOUT THE CATALYTIC CYSTEINE FROM SEEDS OF PACHYRHIZUS EROSUS	SUGAR BINDING PROTEIN
2B1X	CRYSTAL STRUCTURE OF NAPHTHALENE 1,2-DIOXYGENASE FROM RHODOCOCCUS SP.	OXIDOREDUCTASE
2B26	THE CRYSTAL STRUCTURE OF THE PROTEIN COMPLEX OF YEAST HSP40 SIS1 AND HSP70 SSA1	CHAPERONE/PROTEIN TRANSPORT
2B3G	P53N (FRAGMENT 33-60) BOUND TO RPA70N	REPLICATION
2B3T	MOLECULAR BASIS FOR BACTERIAL CLASS 1 RELEASE FACTOR METHYLATION BY PRMC	TRANSLATION
2B42	CRYSTAL STRUCTURE OF THE TRITICUM XYLANSE INHIBITOR-I IN COMPLEX WITH BACILLUS SUBTILIS XYLANASE	HYDROLASE INHIBITOR/HYDROLASE
2B4J	STRUCTURAL BASIS FOR THE RECOGNITION BETWEEN HIV-1 INTEGRASE AND LEDGF/P75	VIRAL PROTEIN, RECOMBINATION
2B59	THE TYPE II COHESIN DOCKERIN COMPLEX	HYDROLASE/STRUCTURAL PROTEIN
2B5I	CYTOKINE RECEPTOR COMPLEX	CYTOKINE/CYTOKINE RECEPTOR
2B5L	CRYSTAL STRUCTURE OF DDB1 IN COMPLEX WITH SIMIAN VIRUS 5 V PROTEIN	PROTEIN BINDING/VIRAL PROTEIN
2B63	COMPLETE RNA POLYMERASE II-RNA INHIBITOR COMPLEX	TRANSFERASE/RNA
2B64	30S RIBOSOMAL SUBUNIT, TRNAS, MRNA AND RELEASE FACTOR RF1 FROM A CRYSTAL STRUCTURE OF THE WHOLE RIBOSOMAL COMPLEX. THIS FILE CONTAINS THE 30S SUBUNIT, TRNAS, MRNA AND RELEASE FACTOR RF1 FROM A CRYSTAL STRUCTURE OF THE WHOLE RIBOSOMAL COMPLEX". THE ENTIRE CRYSTAL STRUCTURE CONTAINS ONE 70S RIBOSOME, TRNAS, MRNA AND RELEASE FACTOR RF1 AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2B66	50S RIBOSOMAL SUBUNIT FROM A CRYSTAL STRUCTURE OF RELEASE FACTOR RF1, TRNAS AND MRNA BOUND TO THE RIBOSOME. THIS FILE CONTAINS THE 50S SUBUNIT FROM A CRYSTAL STRUCTURE OF RELEASE FACTOR RF1, TRNAS AND MRNA BOUND TO THE RIBOSOME AND IS DESCRIBED IN REMARK 400	RIBOSOME
2B6N	THE 1.8 A CRYSTAL STRUCTURE OF A PROTEINASE K LIKE ENZYME FROM A PSYCHROTROPH SERRATIA SPECIES	HYDROLASE
2B7F	CRYSTAL STRUCTURE OF HUMAN T-CELL LEUKEMIA VIRUS PROTEASE, A NOVEL TARGET FOR ANTI-CANCER DESIGN	HYDROLASE
2B7Y	FAVA BEAN LECTIN-GLUCOSE COMPLEX	LECTIN
2B9H	CRYSTAL STRUCTURE OF FUS3 WITH A DOCKING MOTIF FROM STE7	TRANSFERASE
2B9M	30S RIBOSOMAL SUBUNIT, TRNAS, MRNA AND RELEASE FACTOR RF2 FROM A CRYSTAL STRUCTURE OF THE WHOLE RIBOSOMAL COMPLEX.	RIBOSOME

	THIS FILE CONTAINS THE 30S RIBOSOMAL SUBUNIT, TRNAS, MRNA AND RELEASE FACTOR RF2 FROM A CRYSTAL STRUCTURE OF THE WHOLE RIBOSOMAL COMPLEX". THE ENTIRE CRYSTAL STRUCTURE CONTAINS ONE 70S RIBOSOME, TRNAS, MRNA AND RELEASE FACTOR RF2 AND IS DESCRIBED IN REMARK 400.	
2B9N	50S RIBOSOMAL SUBUNIT FROM A CRYSTAL STRUCTURE OF RELEASE FACTOR RF2, TRNAS AND MRNA BOUND TO THE RIBOSOME. THIS FILE CONTAINS THE 50S SUBUNIT FROM A CRYSTAL STRUCTURE OF RELEASE FACTOR RF1, TRNAS AND MRNA BOUND TO THE RIBOSOME AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2B9O	30S RIBOSOMAL SUBUNIT, TRNAS AND MRNA FROM A CRYSTAL STRUCTURE OF THE WHOLE RIBOSOMAL COMPLEX WITH A STOP CODON IN THE A-SITE. THIS FILE CONTAINS THE 30S SUBUNIT, TRNAS AND MRNA FROM A CRYSTAL STRUCTURE OF THE WHOLE RIBOSOMAL COMPLEX WITH A STOP CODON IN THE A-SITE AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2B9P	50S RIBOSOMAL SUBUNIT FROM A CRYSTAL STRUCTURE OF THE RIBOSOME IN COMPLEX WITH TRNAS AND MRNA WITH A STOP CODON IN THE A-SITE. THIS FILE CONTAINS THE 50S SUBUNIT FROM A CRYSTAL STRUCTURE OF THE RIBOSOME IN COMPLEX WITH TRNAS AND MRNA WITH A STOP CODON IN THE A-SITE AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2B9S	CRYSTAL STRUCTURE OF HETERODIMERIC L. DONOVANI TOPOISOMERASE I-VANADATE-DNA COMPLEX	ISOMERASE/DNA
2BA0	ARCHAEAL EXOSOME CORE	RNA BINDING PROTEIN
2BBA	RYSTAL STRUCTURE AND THERMODYNAMIC CHARACTERIZATION OF THE EPHB4 RECEPTOR IN COMPLEX WITH AN EPHRIN-B2 ANTAGONIST PEPTIDE REVEALS THE DETERMINANTS FOR RECEPTOR SPECIFICITY	SIGNALING PROTEIN
2BBV	THE REFINED THREE-DIMENSIONAL STRUCTURE OF AN INSECT VIRUS AT 2.8 ANGSTROMS RESOLUTION	VIRUS/RNA
2BCG	STRUCTURE OF DOUBLY PRENYLATED YPT1:GDI COMPLEX	PROTEIN TRANSPORT
2BCN	SOLVENT ISOTOPE EFFECTS ON INTERFACIAL PROTEIN ELECTRON TRANSFER BETWEEN CYTOCHROME C AND CYTOCHROME C PEROXIDASE	OXIDOREDUCTASE/ELECTRON TRANSFER
2BE1	STRUCTURE OF THE COMPACT LUMENAL DOMAIN OF YEAST IRE1	TRANSCRIPTION
2BE7	CRYSTAL STRUCTURE OF THE UNLIGANDED (T-STATE) ASPARTATE TRANSCARBAMOYLASE OF THE PSYCHROPHILIC BACTERIUM MORITELLA PROFUNDA	TRANSFERASE
2BEC	CRYSTAL STRUCTURE OF CHP2 IN COMPLEX WITH ITS BINDING REGION IN NHE1 AND INSIGHTS INTO THE MECHANISM OF PH REGULATION	METAL BINDING PROTEIN/TRANSPORT PROTEIN
2BFD	REACTIVITY MODULATION OF HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE BY AN INTERNAL MOLECULAR SWITCH	OXIDOREDUCTASE

2BFU	X-RAY STRUCTURE OF CPMV TOP COMPONENT	VIRUS
2BG9	REFINED STRUCTURE OF THE NICOTINIC ACETYLCHOLINE RECEPTOR AT 4A RESOLUTION.	ION CHANNEL/RECEPTOR
2BGR	CRYSTAL STRUCTURE OF HIV-1 TAT DERIVED NONAPEPTIDES TAT(1-9) BOUND TO THE ACTIVE SITE OF DIPEPTIDYL PEPTIDASE IV (CD26)	HYDROLASE/COMPLEX
2BH1	-RAY STRUCTURE OF THE GENERAL SECRETION PATHWAY COMPLEX OF THE N-TERMINAL DOMAIN OF EPSE AND THE CYTOSOLIC DOMAIN OF EPSL OF VIBRIO CHOLERAE	TRANSPORT PROTEIN
2BKK	RYSTAL STRUCTURE OF AMINOGLYCOSIDE PHOSPHOTRANSFERASE APH (3')-IIIA IN COMPLEX WITH THE INHIBITOR AR_3A	TRANSFERASE/DESIGNED PROTEIN COMPLEX
2BKR	NEDD8 NEDP1 COMPLEX	UBIQUITIN/HYDROLASE COMPLEX
2BKY	CRYSTAL STRUCTURE OF THE ALBA1:ALBA2 HETERODIMER FROM SULFOLOBUS SOLFATARICUS	DNA BINDING PROTEIN
2BL0	PHYSARUM POLYCEPHALUM MYOSIN II REGULATORY DOMAIN	MUSCLE PROTEIN
2BLF	SULFITE DEHYDROGENASE FROM STARKEYA NOVELLA	OXIDOREDUCTASE
2BMO	THE CRYSTAL STRUCTURE OF NITROBENZENE DIOXYGENASE	OXIDOREDUCTASE
2BNU	STRUCTURAL AND KINETIC BASIS FOR HEIGHTENED IMMUNOGENICITY OF T CELL VACCINES	IMMUNE SYSTEM/RECEPTOR
2BO9	HUMAN CARBOXYPEPTIDASE A4 IN COMPLEX WITH HUMAN LATEXIN.	HYDROLASE
2BPT	STRUCTURE OF THE NUP1P:KAP95P COMPLEX	NUCLEAR TRANSPORT
2BQ1	IBONUCLEOTIDE REDUCTASE CLASS 1B HOLOCOMPLEX R1E,R2F FROM SALMONELLA TYPHIMURIUM	OXIDOREDUCTASE
2BR9	14-3-3 PROTEIN EPSILON (HUMAN) COMPLEXED TO PEPTIDE	CELL REGULATOR PROTEIN
2BRR	COMPLEX OF THE NEISSERIAL PORA P1.4 EPITOPE PEPTIDE AND TWO FAB-FRAGMENTS (ANTIBODY MN20B9.34)	ANTIBODY/ANTIGEN COMPLEX
2BS3	GLU C180-> GLN VARIANT QUINOL:FUMARATE REDUCTASE FROM WOLINELLA SUCCINOGENES	OXIDOREDUCTASE
2BSK	CRYSTAL STRUCTURE OF THE TIM9 TIM10 HEXAMERIC COMPLEX	PROTEIN TRANSPORT
2BSQ	FITAB BOUND TO DNA	TRANSCRIPTION REGULATION COMPLEX
2BTO	STRUCTURE OF BTUBA FROM PROSTHECOBACTER DEJONGEII	CYTOSKELETAL PROTEIN
2BTP	14-3-3 PROTEIN THETA (HUMAN) COMPLEXED TO PEPTIDE	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)
2BTV	ATOMIC MODEL FOR BLUETONGUE VIRUS (BTV) CORE	VIRUS

2BUR	CRYSTAL STRUCTURE OF WILD-TYPE PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 IN COMPLEX WITH 4-HYDROXYBENZOATE	OXIDOREDUCTASE
2BV8	THE CRYSTAL STRUCTURE OF PHYCOCYANIN FROM GRACILARIA CHILENSIS.	PHOTOSYNTHESIS
2BWE	THE CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE UBA AND UBL DOMAINS OF DSK2	SIGNALING PROTEIN
2BYK	HISTONE FOLD HETERODIMER OF THE CHROMATIN ACCESSIBILITY COMPLEX	DNA-BINDING PROTEIN
2BYP	CRYSTAL STRUCTURE OF APLYSIA CALIFORNICA ACHBP IN COMPLEX WITH ALPHA-CONOTOXIN IMI	RECEPTOR COMPLEX
2BZ6	ORALLY AVAILABLE FACTOR7A INHIBITOR	HYDROLASE
2C1D	CRYSTAL STRUCTURE OF SOXXA FROM P. PANTOTROPHUS	OXIDOREDUCTASE
2C23	14-3-3 PROTEIN BETA (HUMAN) IN COMPLEX WITH EXOENZYME S PEPTIDE	SIGNALING PROTEIN/COMPLEX
2C2L	CRYSTAL STRUCTURE OF THE CHIP U-BOX E3 UBIQUITIN LIGASE	HEAT-SHOCK PROTEIN COMPLEX
2C35	SUBUNITS RPB4 AND RPB7 OF HUMAN RNA POLYMERASE II	POLYMERASE
2C3I	CRYSTAL STRUCTURE OF HUMAN PIM1 IN COMPLEX WITH IMIDAZOPYRIDAZIN I	COMPLEX TRANSFERASE/PEPTIDE
2C5K	N-TERMINAL DOMAIN OF TLG1 COMPLEXED WITH N-TERMINUS OF VPS51	PROTEIN TRANSPORT/COMPLEX
2C5W	PENICILLIN-BINDING PROTEIN 1A (PBP-1A) ACYL-ENZYME COMPLEX (CEFOTAXIME) FROM STREPTOCOCCUS PNEUMONIAE	PEPTIDOGLYCAN SYNTHESIS
2C63	14-3-3 PROTEIN ETA (HUMAN) COMPLEXED TO PEPTIDE	SIGNALING PROTEIN/PEPTIDE COMPLEX
2C7J	PHYCOERYTHROCYANIN FROM MASTIGOCLADUS LAMINOSUS, 295 K, 3.0 A	ELECTRON TRANSPORT
2CCH	THE CRYSTAL STRUCTURE OF CDK2 CYCLIN A IN COMPLEX WITH A SUBSTRATE PEPTIDE DERIVED FROM CDC MODIFIED WITH A GAMMA-LINKED ATP ANALOGUE	COMPLEX(TRANSFERASE/CELL DIVISION)
2CDF	STRUCTURE AND BINDING KINETICS OF THREE DIFFERENT HUMAN CD1D-ALPHA-GALACTOSYLCERAMIDE-SPECIFIC T CELL RECEPTORS (TCR 5E)	CELL RECEPTOR
2CE8	AN EH1 PEPTIDE BOUND TO THE GROUCHO-TLE WD40 DOMAIN.	TRANSCRIPTION REGULATION
2CG5	STRUCTURE OF AMINOADIPATE-SEMIALDEHYDE DEHYDROGENASE-PHOSPHOPANTETHEINYL TRANSFERASE IN COMPLEX WITH CYTOSOLIC ACYL CARRIER PROTEIN AND COENZYME A	TRANSFERASE/HYDROLASE (COMPLEX)

2CH4	COMPLEX BETWEEN BACTERIAL CHEMOTAXIS HISTIDINE KINASE CHEA DOMAINS P4 AND P5 AND RECEPTOR-ADAPTOR PROTEIN CHEW	TRANSFERASE/CHEMOTAXIS
2CHO	BACTEROIDES THETAIOTAOMICRON HEXOSAMINIDASE WITH O-GLCNACASE ACTIVITY	HYDROLASE
2CI9	CK1 SH2-DOMAIN IN COMPLEX WITH A DODECAPHOSPHOPEPTIDE FROM EPEC PROTEIN TIR	SH2-DOMAIN/COMPLEX
2CJS	STRUCTURAL BASIS FOR A MUNC13-1 HOMODIMER- MUNC13-1- RIM HETERODIMER SWITCH: C2-DOMAINS AS VERSATILE PROTEIN-PROTEIN INTERACTION MODULES	EXOCYTOSIS
2CKF	CRYSTAL STRUCTURE OF THE TERMINAL COMPONENT OF THE PAH-HYDROXYLATING DIOXYGENASE FROM SPHINGOMONAS SP CHY-1	OXIDOREDUCTASE
2CKL	RING1B-BMI1 E3 CATALYTIC DOMAIN STRUCTURE	TRANSCRIPTION REGULATION COMPLEX
2CLY	SUBCOMPLEX OF THE STATOR OF BOVINE MITOCHONDRIAL ATP SYNTHASE	HYDROLASE
2CNM	RIMI - RIBOSOMAL S18 N-ALPHA-PROTEIN ACETYLTRANSFERASE IN COMPLEX WITH A BISUBSTRATE INHIBITOR (CTERM-ARG-ARG-PHE-TYR-ARG-ALA-N-ALPHA-ACETYL-S-COA).	TRANSFERASE
2CV5	CRYSTAL STRUCTURE OF HUMAN NUCLEOSOME CORE PARTICLE	STRUCTURAL PROTEIN/DNA
2CVY	STRUCTURES OF YEAST RIBONUCLEOTIDE REDUCTASE I	OXIDOREDUCTASE
2CWG	CRYSTALLOGRAPHIC REFINEMENT AND STRUCTURE ANALYSIS OF THE COMPLEX OF WHEAT GERM AGGLUTININ WITH A BIVALENT SIALOGLYCOPEPTIDE FROM GLYCOPHORIN A	LECTIN(AGGLUTININ)
2CZV	CRYSTAL STRUCTURE OF ARCHEAL RNASE P PROTEIN PH1481P IN COMPLEX WITH PH1877P	HYDROLASE
2D0O	TRCUTURE OF DIOL DEHYDRATASE-REACTIVATING FACTOR COMPLEXED WITH ADP AND MG2+	CHAPERONE
2D0V	CRYSTAL STRUCTURE OF METHANOL DEHYDROGENASE FROM HYPHOMICROBIUM DENITRIFICANS	OXIDOREDUCTASE
2D1P	RYSTAL STRUCTURE OF HETEROHEXAMERIC TUSBCD PROTEINS, WHICH ARE CRUCIAL FOR THE TRNA MODIFICATION	TRANSLATION
2D3O	STRUCTURE OF RIBOSOME BINDING DOMAIN OF THE TRIGGER FACTOR ON THE 50S RIBOSOMAL SUBUNIT FROM D. RADIODURANS	RIBOSOME
2D5R	CRYSTAL STRUCTURE OF A TOB-HCAF1 COMPLEX	TRANSCRIPTION
2D5W	THE CRYSTAL STRUCTURE OF OLIGOPEPTIDE BINDING PROTEIN FROM THERMUS THERMOPHILUS HB8 COMPLEXED WITH PENTAPEPTIDE	PEPTIDE BINDING PROTEIN
2D5X	CRYSTAL STRUCTURE OF CARBONMONOXY HORSE HEMOGLOBIN COMPLEXED WITH L35	OXYGEN STORAGE/TRANSPORT

2D6F	RYSTAL STRUCTURE OF GLU-TRNA(GLN) AMIDOTRANSFERASE IN THE COMPLEX WITH TRNA(GLN)	LIGASE/RNA
2D74	CRYSTAL STRUCTURE OF TRANSLATION INITIATION FACTOR AIF2BETAGAMMA HETERODIMER	TRANSLATION
2D7C	CRYSTAL STRUCTURE OF HUMAN RAB11 IN COMPLEX WITH FIP3 RAB-BINDING DOMAIN	PROTEIN TRANSPORT
2D7D	STRUCTURAL INSIGHTS INTO THE CRYPTIC DNA DEPENDENT ATP-ASE ACTIVITY OF UVRB	HYDROLASE/DNA
2DE6	HE REDUCED COMPLEX BETWEEN OXYGENASE AND FERREDOXIN IN CARBAZOLE 1,9A-DIOXYGENASE	OXIDOREDUCTASE
2DEW	CRYSTAL STRUCTURE OF HUMAN PEPTIDYLARGININE DEIMINASE 4 IN COMPLEX WITH HISTONE H3 N-TERMINAL TAIL INCLUDING ARG8	HYDROLASE
2DFK	CRYSTAL STRUCTURE OF THE CDC42-COLLYBISTIN II COMPLEX	CELL CYCLE
2DJF	CRYSTAL STRUCTURE OF HUMAN DIPEPTIDYL PEPTIDASE I (CATHEPSIN C) IN COMPLEX WITH THE INHIBITOR GLY-PHE-CHN2	HYDROLASE
2DOH	THE X-RAY CRYSTALLOGRAPHIC STRUCTURE OF THE ANGIOGENESIS INHIBITOR, ANGIOSTATIN, BOUND A TO A PEPTIDE FROM THE GROUP A STREPTOCOCCAL SURFACE PROTEIN PAM	HYDROLASE
2DPP	CRYSTAL STRUCTURE OF THERMOSTABLE BACILLUS SP. RAPC8 NITRILE HYDRATASE	LYASE
2DS2	CRYSTAL STRUCTURE OF MABINLIN II	PLANT PROTEIN
2DS8	STRUCTURE OF THE ZBD-XB COMPLEX	METAL BINDING PROTEIN, PROTEIN BINDING
2DVQ	RYSTAL STRUCTURE ANALYSIS OF THE N-TERMINAL BROMODOMAIN OF HUMAN BRD2 COMPLEXED WITH ACETYLATED HISTONE H4 PEPTIDE	TRANSCRIPTION
2DVW	STRUCTURE OF THE ONCOPROTEIN GANKYRIN IN COMPLEX WITH S6 ATPASE OF THE 26S PROTEASOME	CELL CYCLE/PROTEIN-BINDING
2DXC	RECOMBINANT THIOCYANATE HYDROLASE, FULLY-MATURED FORM	HYDROLASE
2DYO	THE CRYSTAL STRUCTURE OF SACCHAROMYCES CEREVISIAE ATG5-ATG16(1-57) COMPLEX	PROTEIN TURNOVER/PROTEIN TURNOVER
2DYR	BOVINE HEART CYTOCHROME C OXIDASE AT THE FULLY OXIDIZED STATE	OXIDOREDUCTASE
2DZN	CRYSTAL STRUCTURE ANALYSIS OF YEAST NAS6P COMPLEXED WITH THE PROTEASOME SUBUNIT, RPT3	PROTEIN BINDING
2E1M	RYSTAL STRUCTURE OF L-GLUTAMATE OXIDASE FROM STREPTOMYCES SP. X-119-6	OXIDOREDUCTASE

2E2D	FLEXIBILITY AND VARIABILITY OF TIMP BINDING: X-RAY STRUCTURE OF THE COMPLEX BETWEEN COLLAGENASE-3/MMP-13 AND TIMP-2	HYDROLASE/HYDROLASE INHIBITOR
2E2H	RNA POLYMERASE II ELONGATION COMPLEX AT 5 MM MG2+ WITH GTP	TRANSCRIPTION/DNA/RNA
2E2I	RNA POLYMERASE II ELONGATION COMPLEX IN 5 MM MG+2 WITH 2'-DGTP	TRANSCRIPTION/DNA/RNA
2E2J	RNA POLYMERASE II ELONGATION COMPLEX IN 5 MM MG+2 WITH GMPCPP	TRANSCRIPTION/DNA/RNA
2E3K	:RYSTAL STRUCTURE OF THE HUMAN BRD2 SECOND BROMODOMAIN IN COMPLEXED WITH THE ACETYLATED HISTONE H4 PEPTIDE	TRANSCRIPTION
2E3X	RYSTAL STRUCTURE OF RUSSELL'S VIPER VENOM METALLOPROTEINASE	HYDROLASE, BLOOD CLOTTING, TOXIN
2E5L	A SNAPSHOT OF THE 30S RIBOSOMAL SUBUNIT CAPTURING MRNA VIA THE SHINE- DALGARNO INTERACTION	RIBOSOME
2E7 4	CRYSTAL STRUCTURE OF THE CYTOCHROME B6F COMPLEX FROM M.LAMINOSUS	PHOTOSYNTHESIS
2E9W	CRYSTAL STRUCTURE OF THE EXTRACELLULAR DOMAIN OF KIT IN COMPLEX WITH STEM CELL FACTOR (SCF)	TRANSFERASE/HORMONE
2E9X	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX	REPLICATION
2EAX	CRYSTAL STRUCTURE OF HUMAN PGRP-IBETAC IN COMPLEX WITH GLYCOSAMYL MURAMYL PENTAPEPTIDE	SUGAR BINDING PROTEIN
2EFH	ARA7-GDP/ATVPS9A(D185N)	TRANSPORT PROTEIN
2EHB	THE STRUCTURE OF THE C-TERMINAL DOMAIN OF THE PROTEIN KINASE ATSOS2 BOUND TO THE CALCIUM SENSOR ATSOS3	SIGNALLING PROTEIN/TRANSFERASE
2EJF	CRYSTAL STRUCTURE OF THE BIOTIN PROTEIN LIGASE (MUTATIONS R48A AND K111A) AND BIOTIN CARBOXYL CARRIER PROTEIN COMPLEX FROM PYROCOCCUS HORIKOSHII OT3	LIGASE
2EQ7	RYSTAL STRUCTURE OF LIPOAMIDE DEHYDROGENASE FROM THERMUS THERMOPHILUS HB8 WITH PSBDO	OXIDOREDUCTASE
2F2A	STRUCTURE OF TRNA-DEPENDENT AMIDOTRANSFERASE GATCAB COMPLEXED WITH GLN	LIGASE
2F2L	CRYSTAL STRUCTURE OF TRACHEAL CYTOTOXIN (TCT) BOUND TO THE ECTODOMAIN COMPLEX OF PEPTIDOGLYCAN RECOGNITION PROTEINS LCA (PGRP-LCA) AND LCX (PGRP-LCX)	MEMBRANE PROTEIN, IMMUNE SYSTEM, TOXIN
2F31	CRYSTAL STRUCTURE OF THE AUTOINHIBITORY SWITCH IN FORMIN MDIA1; THE DID/DAD COMPLEX	STRUCTURAL PROTEIN
2F4M	THE MOUSE PNGASE-HR23 COMPLEX REVEALS A COMPLETE REMODULATION OF THE PROTEIN-PROTEIN INTERFACE COMPARED TO	HYDROLASE

	ITS YEAST ORTHOLOGS	
2F4V	30S RIBOSOME + DESIGNER ANTIBIOTIC	RIBOSOME
2F5Z	RYSTAL STRUCTURE OF HUMAN DIHYDROLIPOAMIDE DEHYDROGENASE (E3) COMPLEXED TO THE E3-BINDING DOMAIN OF HUMAN E3-BINDING PROTEIN	OXIDOREDUCTASE/PROTEIN BINDING
2F69	TERNARY COMPLEX OF SET7/9 BOUND TO ADOHCY AND A TAF10 PEPTIDE	TRANSFERASE
2F6A	COLLAGEN ADHESIN AND COLLAGEN COMPLEX STRUCTURE	CELL ADHESION/STRUCTURAL PROTEIN
2F6M	STRUCTURE OF A VPS23-C:VPS28-N SUBCOMPLEX	TRANSPORT PROTEIN
2F8E	FOOT AND MOUTH DISEASE VIRUS RNA-DEPENDENT RNA POLYMERASE IN COMPLEX WITH URIDYLYLATED VPG PROTEIN	TRANSFERASE
2F8N	9 ANGSTROM X-RAY STRUCTURE OF HYBRID MACROH2A NUCLEOSOMES	STRUCTURAL PROTEIN/DNA
2F8X	CRYSTAL STRUCTURE OF ACTIVATED NOTCH, CSL AND MAML ON HES-1 PROMOTER DNA SEQUENCE	TRANSCRIPTION/DNA
2F9D	2.5 ANGSTROM RESOLUTION STRUCTURE OF THE SPLICEOSOMAL PROTEIN P14 BOUND TO REGION OF SF3B155	RNA BINDING PROTEIN
2F9I	RYSTAL STRUCTURE OF THE CARBOXYLTRANSFERASE SUBUNIT OF ACC FROM STAPHYLOCOCCUS AUREUS	TRANSFERASE
2F9N	CRYSTAL STRUCTURE OF THE RECOMBINANT HUMAN ALPHA I TRYPTASE MUTANT K192Q/D216G IN COMPLEX WITH LEUPEPTIN	HYDROLASE
2F9Y	HE CRYSTAL STRUCTURE OF THE CARBOXYLTRANSFERASE SUBUNIT OF ACC FROM ESCHERICHIA COLI	LIGASE
2F9Z	COMPLEX BETWEEN THE CHEMOTAXIS DEAMIDASE CHED AND THE CHEMOTAXIS PHOSPHATASE CHEC FROM THERMOTOGA MARITIMA	SIGNALING PROTEIN
2FCW	STRUCTURE OF A COMPLEX BETWEEN THE PAIR OF THE LDL RECEPTOR LIGAND-BINDING MODULES 3-4 AND THE RECEPTOR ASSOCIATED PROTEIN (RAP).	LIPID TRANSPORT/ENDOCYTOSIS/CHAPERONE
2FDB	CRYSTAL STRUCTURE OF FIBROBLAST GROWTH FACTOR (FGF)8B IN COMPLEX WITH FGF RECEPTOR (FGFR) 2C	HORMONE/GROWTH FACTOR/TRANSFERASE
2FEP	STRUCTURE OF TRUNCATED CCPA IN COMPLEX WITH P-SER-HPR AND SULFATE IONS	TRANSCRIPTION
2FEW	COMPLEX OF ENZYME IIAMTL AND PHOSPHORYLATED ENZYME IIBMTL FROM ESCHERICHIA COLI NMR, RESTRAINED REGULARIZED MEAN STRUCTURE	TRANSFERASE
2FF4	MYCOBACTERIUM TUBERCULOSIS EMBR IN COMPLEX WITH LOW AFFINITY PHOSPHOPEPTIDE	TRANSCRIPTION

2FFF	OPEN FORM OF A CLASS A TRANSPEPTIDASE DOMAIN	MEMBRANE PROTEIN, TRANSFERASE
2FFK	OLUTION STRUCTURE OF THE COMPLEX BETWEEN POXVIRUS-ENCODED CC CHEMOKINE INHIBITOR VCCI AND HUMAN MIP-1BETA, MINIMIZED AVERAGE STRUCTURE	VIRUS/VIRAL PROTEIN/CYTOKINE
2FFU	CRYSTAL STRUCTURE OF HUMAN PPGALNACT-2 COMPLEXED WITH UDP AND EA2	TRANSFERASE
2FGE	CRYSTAL STRUCTURE OF PRESEQUENCE PROTEASE PREP FROM ARABIDOPSIS THALIANA	HYDROLASE, PLANT PROTEIN
2FH5	THE STRUCTURE OF THE MAMMALIAN SRP RECEPTOR	TRANSPORT PROTEIN
2FHE	FASCIOLA HEPATICA GLUTATHIONE S-TRANSFERASE ISOFORM 1 IN COMPLEX WITH GLUTATHIONE	TRANSFERASE
2FHH	RYSTAL STRUCTURE OF MYCOBACTERIUM TUBERCULOSIS PROTEASOME IN COMPLEX WITH A PEPTIDYL BORONATE INHIBITOR MLN-273	HYDROLASE
2FHZ	MOLECULAR BASIS OF INHIBITION OF THE RIBONUCLEASE ACTIVITY IN COLICIN E5 BY ITS COGNATE IMMUNITY PROTEIN	IMMUNE SYSTEM, HYDROLASE
2FIB	RECOMBINANT HUMAN GAMMA-FIBRINOGEN CARBOXYL TERMINAL FRAGMENT (RESIDUES 143-411) COMPLEXED TO THE PEPTIDE GLY-PRO-ARG-PRO AT PH 6.0	COMPLEX (BLOOD COAGULATION/PEPTIDE)
2FJ7	CRYSTAL STRUCTURE OF NUCLEOSOME CORE PARTICLE CONTAINING A POLY (DA.DT) SEQUENCE ELEMENT	STRUCTURAL PROTEIN/DNA
2FL5	COFACTOR-CONTAINING ANTIBODIES: CRYSTAL STRUCTURE OF THE ORIGINAL YELLOW ANTIBODY	IMMUNE SYSTEM
2FM8	CRYSTAL STRUCTURE OF THE SALMONELLA SECRETION CHAPERONE INVB IN COMPLEX WITH SIPA	CHAPERONE/CELL INVASION
2FMM	CRYSTAL STRUCTURE OF EMSY-HP1 COMPLEX	TRANSCRIPTION
2FO1	CRYSTAL STRUCTURE OF THE CSL-NOTCH-MASTERMIND TERNARY COMPLEX BOUND TO DNA	GENE REGULATION/SIGNALLING PROTEIN/DNA
2FO5	CRYSTAL STRUCTURE OF RECOMBINANT BARLEY CYSTEINE ENDOPROTEASE B ISOFORM 2 (EP-B2) IN COMPLEX WITH LEUPEPTIN	HYDROLASE
2FOM	DENGUE VIRUS NS2B/NS3 PROTEASE	VIRAL PROTEIN/PROTEASE
2FP7	WEST NILE VIRUS NS2B/NS3PROTEASE IN COMPLEX WITH BZ-NLE-LYS-ARG-ARG-H	VIRAL PROTEIN/PROTEASE
2FR4	STRUCTURE OF FAB DNA-1 COMPLEXED WITH A STEM-LOOP DNA LIGAND	IMMUNE SYSTEM/DNA
2FSE	CRYSTALLOGRAPHIC STRUCTURE OF A RHEUMATOID ARTHRITIS MHC SUSCEPTIBILITY ALLELE, HLA-DR1 (DRB1*0101), COMPLEXED WITH THE IMMUNODOMINANT DETERMINANT OF HUMAN TYPE II COLLAGEN	IMMUNE SYSTEM, STRUCTURAL PROTEIN

2FTS	RYSTAL STRUCTURE OF THE GLYCINE RECEPTOR-GEPHYRIN COMPLEX	STRUCTURAL PROTEIN
2FTX	CRYSTAL STRUCTURE OF THE YEAST KINETOCHORE SPC24/SPC25 GLOBULAR DOMAIN	STRUCTURAL PROTEIN, PROTEIN BINDING
2FU5	STRUCTURE OF RAB8 IN COMPLEX WITH MSS4	SIGNALING PROTEIN
2FUG	CRYSTAL STRUCTURE OF THE HYDROPHILIC DOMAIN OF RESPIRATORY COMPLEX I FROM THERMUS THERMOPHILUS	OXIDOREDUCTASE
2FYM	CRYSTAL STRUCTURE OF E. COLI ENOLASE COMPLEXED WITH THE MINIMAL BINDING SEGMENT OF RNASE E.	LYASE
2FYZ	STRUCTURAL OF MUMPS VIRUS FUSION PROTEIN CORE	PROTEIN BINDING
2FZC	THE STRUCTURE OF WILD-TYPE E. COLI ASPARTATE TRANSCARBAMOYLASE IN COMPLEX WITH NOVEL T STATE INHIBITORS AT 2.10 RESOLUTION	TRANSFERASE
2G1T	A SRC-LIKE INACTIVE CONFORMATION IN THE ABL TYROSINE KINASE DOMAIN	TRANSFERASE
2G2L	CRYSTAL STRUCTURE OF THE SECOND PDZ DOMAIN OF SAP97 IN COMPLEX WITH A GLUR-A C-TERMINAL PEPTIDE	MEMBRANE PROTEIN
2G2R	GREEN-FLUORESCENT ANTIBODY 11G10 IN COMPLEX WITH ITS HAPTEN (NITRO-STILBENE DERIVATIVE)	IMMUNE SYSTEM
2G2U	CRYSTAL STRUCTURE OF THE SHV-1 BETA-LACTAMASE/BETA-LACTAMASE INHIBITOR PROTEIN (BLIP) COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
2G30	BETA APPENDAGE OF AP2 COMPLEXED WITH ARH PEPTIDE	ENDOCYTOSIS/EXOCYTOSIS
2G38	A PE/PPE PROTEIN COMPLEX FROM MYCOBACTERIUM TUBERCULOSIS	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
2G3V	CRYSTAL STRUCTURE OF CAGS (HP0534, CAG13) FROM HELICOBACTER PYLORI	UNKNOWN FUNCTION
2G58	CRYSTAL STRUCTURE OF A COMPLEX OF PHOSPHOLIPASE A2 WITH A DESIGNED PEPTIDE INHIBITOR DEHYDRO-ILE-ALA-ARG-SER AT 0.98 A RESOLUTION	HYDROLASE
2G5L	STREPTAVIDIN IN COMPLEX WITH NANOTAG	PEPTIDE BINDING PROTEIN
2G77	CRYSTAL STRUCTURE OF GYP1 TBC DOMAIN IN COMPLEX WITH RAB33 GTPASE BOUND TO GDP AND ALF3	HYDROLASE ACTIVATOR/PROTEIN TRANSPORT
2GA9	CRYSTAL STRUCTURE OF THE HETERODIMERIC VACCINIA VIRUS POLYADENYLATE POLYMERASE WITH BOUND ATP-GAMMA-S	TRANSFERASE
2GAG	HETEROTETERAMERIC SARCOSINE: STRUCTURE OF A DIFLAVIN METALOENZYME AT 1.85 A RESOLUTION	OXIDOREDUCTASE
2GBW	CRYSTAL STRUCTURE OF BIPHENYL 2,3-DIOXYGENASE FROM SPHINGOMONAS YANOIKUYAE B1	OXIDOREDUCTASE

2GC7	SUBSTRATE REDUCED, COPPER FREE COMPLEX OF METHYLAMINE DEHYDROGENASE, AMICYANIN AND CYTOCHROME C551I FROM PARACOCCUS DENITRIFICANS.	OXIDOREDUCTASE, ELECTRON TRANSPORT
2GEZ	CRYSTAL STRUCTURE OF POTASSIUM-INDEPENDENT PLANT ASPARAGINASE	HYDROLASE
2GFB	CRYSTAL STRUCTURE OF A CATALYTIC FAB HAVING ESTERASE-LIKE ACTIVITY	IMMUNOGLOBULIN
2GH0	GROWTH FACTOR/RECEPTOR COMPLEX	HORMONE/GROWTH FACTOR
2GHT	CTD-SPECIFIC PHOSPHATASE SCP1 IN COMPLEX WITH PEPTIDE FROM C-TERMINAL DOMAIN OF RNA POLYMERASE II	HYDROLASE
2GIA	CRYSTAL STRUCTURES OF TRYPANOSOMA BRUCIEI MRP1/MRP2	TRANSLATION
2GJE	STRUCTURE OF A GUIDERNA-BINDING PROTEIN COMPLEX BOUND TO A GRNA	TRANSLATION/RNA
2GJX	RYSTALLOGRAPHIC STRUCTURE OF HUMAN BETA-HEXOSAMINIDASE A	HYDROLASE
2GKW	KEY CONTACTS PROMOTE RECONGNITO OF BAFF-R BY TRAF3	APOPTOSIS
2GO5	STRUCTURE OF SIGNAL RECOGNITION PARTICLE RECEPTOR (SR) IN COMPLEX WITH SIGNAL RECOGNITION PARTICLE (SRP) AND RIBOSOME NASCENT CHAIN COMPLEX	TRANSLATION/RNA
2GPH	DOCKING MOTIF INTERACTIONS IN THE MAP KINASE ERK2	TRANSFERASE
2GPO	ESTROGEN RELATED RECEPTOR-GAMMA LIGAND BINDING DOMAIN COMPLEXED WITH A SYNTHETIC PEPTIDE FROM RIP140	TRANSCRIPTION
2GRL	CRYSTAL STRUCTURE OF DCT/ICF10 COMPLEX	TRANSCRIPTION
2GS6	CRYSTAL STRUCTURE OF THE ACTIVE EGFR KINASE DOMAIN IN COMPLEX WITH AN ATP ANALOG-PEPTIDE CONJUGATE	TRANSFERASE
2GSK	STRUCTURE OF THE BTUB:TONB COMPLEX	SIGNALING PROTEIN/MEMBRANE PROTEIN
2GSM	CATALYTIC CORE (SUBUNITS I AND II) OF CYTOCHROME C OXIDASE FROM RHODOBACTER SPHAEROIDES	OXIDOREDUCTASE
2GSR	STRUCTURE OF PORCINE CLASS PI GLUTATHIONE S-TRANSFERASE	COMPLEX (TRANSFERASE/INHIBITOR)
2GUZ	STRUCTURE OF THE TIM14-TIM16 COMPLEX OF THE MITOCHONDRIAL PROTEIN IMPORT MOTOR	CHAPERONE, PROTEIN TRANSPORT
2GV2	MDM2 IN COMPLEX WITH AN 8-MER P53 PEPTIDE ANALOGUE	LIGASE
2GV5	CRYSTAL STRUCTURE OF SFI1P/CDC31P COMPLEX	CELL CYCLE
2GWF	STRUCTURE OF A USP8-NRDP1 COMPLEX	HYDROLASE/LIGASE

2GY7	ANGIOPOIETIN-2/TIE2 COMPLEX CRYSTAL STRUCTURE	SIGNALING PROTEIN
2GY9	STRUCTURE OF THE 30S SUBUNIT OF A PRE-TRANSLOCATIONAL E. COLI RIBOSOME OBTAINED BY FITTING ATOMIC MODELS FOR RNA AND PROTEIN COMPONENTS INTO CRYO-EM MAP EMD-1056	RIBOSOME
2GYA	STRUCTURE OF THE 50S SUBUNIT OF A PRE-TRANSLOCATIONAL E. COLI RIBOSOME OBTAINED BY FITTING ATOMIC MODELS FOR RNA AND PROTEIN COMPONENTS INTO CRYO-EM MAP EMD-1056	RIBOSOME
2GYB	STRUCTURE OF THE 30S SUBUNIT OF A SECM-STALLED E. COLI RIBOSOME COMPLEX OBTAINED BY FITTING ATOMIC MODELS FOR RNA AND PROTEIN COMPONENTS INTO CRYO-EM MAP EMD-1143	RIBOSOME
2GYC	STRUCTURE OF THE 50S SUBUNIT OF A SECM-STALLED E. COLI RIBOSOME COMPLEX OBTAINED BY FITTING ATOMIC MODELS FOR RNA AND PROTEIN COMPONENTS INTO CRYO-EM MAP EMD-1143	RIBOSOME
2H1C	CRYSTAL STRUCTURE OF FITACB FROM NEISSERIA GONORRHOEAE	GENE REGULATION
2H1O	STRUCTURE OF FITAB BOUND TO IR36 DNA FRAGMENT	GENE REGULATION/DNA COMPLEX
2H3N	CRYSTAL STRUCTURE OF A SURROGATE LIGHT CHAIN (LAMBDA5 AND VPREB) HOMODIMER	IMMUNE SYSTEM
2H4C	STRUCTURE OF DABOIATOXIN (HETERODIMERIC PLA2 VENOM)	HYDROLASE
2H6F	ROTEIN FARNESYLTRANSFERASE COMPLEXED WITH A FARNESYLATED DDPTASACVLS PEPTIDE PRODUCT AT 1.5A RESOLUTION	TRANSFERASE
2H88	AVIAN MITOCHONDRIAL RESPIRATORY COMPLEX II AT 1.8 ANGSTROM RESOLUTION	OXIDOREDUCTASE
2H9A	CORRINOID IRON-SULFUR PROTEIN	OXIDOREDUCTASE
2HAL	AN EPISULFIDE CATION (THIIRANIUM RING) TRAPPED IN THE ACTIVE SITE OF HAV 3C PROTEINASE INACTIVATED BY PEPTIDE-BASED KETONE INHIBITORS	HYDROLASE
2HAN	STRUCTURAL BASIS OF HETERODIMERIC ECDYSTEROID RECEPTOR INTERACTION WITH NATURAL RESPONSE ELEMENT HSP27 GENE PROMOTER	TRANSCRIPTION/DNA
2HC4	CRYSTAL STRUCTURE OF THE LBD OF VDR OF DANIO RERIO IN COMPLEX WITH CALCITRIOL	GENE REGULATION
2HDI	CRYSTAL STRUCTURE OF THE COLICIN I RECEPTOR CIR FROM E.COLI IN COMPLEX WITH RECEPTOR BINDING DOMAIN OF COLICIN IA.	PROTEIN TRANSPORT,ANTIMICROBIAL PROTEIN
2HDX	CRYSTAL STRUCTURE OF THE SRC HOMOLOGY-2 DOMAIN OF SH2-B IN COMPLEX WITH JAK2 PTYR813 PHOSPHOPEPTIDE	SIGNALING PROTEIN
2HGI	RYSTAL STRUCTURE OF THE 70S THERMUS THERMOPHILUS RIBOSOME SHOWING HOW THE 16S 3'-END MIMICKS MRNA E AND P CODONS. THIS ENTRY 2HGI CONTAINS 30S RIBOSOMAL SUBUNIT. THE 50S	RIBOSOME

	RIBOSOMAL SUBUNIT CAN BE FOUND IN PDB ENTRY 2HGJ.	
2HGR	70S T.TH. RIBOSOME FUNCTIONAL COMPLEX WITH MRNA AND E- AND P-SITE TRNAS AT 4.5A. THIS ENTRY 2HGR CONTAINS 30S RIBOSOMAL SUBUNIT. THE 50S RIBOSOMAL SUBUNIT CAN BE FOUND IN PDB ENTRY 2HGU.	RIBOSOME
2HGU	70S T.TH. RIBOSOME FUNCTIONAL COMPLEX WITH MRNA AND E- AND P-SITE TRNAS AT 4.5A. THIS ENTRY 2HGU CONTAINS 50S RIBOSOMAL SUBUNIT. THE 30S RIBOSOMAL SUBUNIT CAN BE FOUND IN PDB ENTRY 2HGR.	RIBOSOME
2HHH	RYSTAL STRUCTURE OF KASUGAMYCIN BOUND TO THE 30S RIBOSOMAL SUBUNIT	RIBOSOME
2HKQ	CRYSTAL STRUCTURE OF THE C-TERMINAL DOMAIN OF HUMAN EB1 IN COMPLEX WITH THE CAP-GLY DOMAIN OF HUMAN DYNACTIN-1 (P150-GLUED)	STRUCTURAL PROTEIN
2HLB	A STRUCTURAL BASIS FOR NUCLEOTIDE EXCHANGE ON G-ALPHA-I SUBUNITS AND RECEPTOR COUPLING SPECIFICITY	SIGNALING PROTEIN
2HLD	CRYSTAL STRUCTURE OF YEAST MITOCHONDRIAL F1-ATPASE	HYDROLASE
2HMH	CRYSTAL STRUCTURE OF SOCS3 IN COMPLEX WITH GP130(PTYR757) PHOSPHOPEPTIDE.	CYTOKINE REGULATOR
2HMI	HIV-1 REVERSE TRANSCRIPTASE/FRAGMENT OF FAB 28/DNA COMPLEX	IMMUNE SYSTEM/DNA
2HPE	COMPARISON OF THE STRUCTURES OF HIV-2 PROTEASE COMPLEXES IN THREE CRYSTAL SPACE GROUPS WITH AN HIV-1 PROTEASE COMPLEX STRUCTURE	HYDROLASE(ACID PROTEASE)
2HPL	CRYSTAL STRUCTURE OF THE MOUSE P97/PNGASE COMPLEX	HYDROLASE
2HQS	CRYSTAL STRUCTURE OF TOLB/PAL COMPLEX	TRANSPORT PROTEIN/LIPOPROTEIN
2HRK	TRUCTURAL BASIS OF YEAST AMINOACYL-TRNA SYNTHETASE COMPLEX FORMATION REVEALED BY CRYSTAL STRUCTURES OF TWO BINARY SUB-COMPLEXES	LIGASE/RNA BINDING PROTEIN
2HT0	IHF BOUND TO DOUBLY NICKED DNA	TRANSCRIPTION/DNA
2HT9	THE STRUCTURE OF DIMERIC HUMAN GLUTAREDOXIN 2	OXIDOREDUCTASE
2HTM	RYSTAL STRUCTURE OF TTHA0676 FROM THERMUS THERMOPHILUS HB8	BIOSYNTHETIC PROTEIN
2HU2	CTBP/BARS IN TERNARY COMPLEX WITH NAD(H) AND RRTGAPPAL PEPTIDE	OXIDOREDUCTASE
2HUE	STRUCTURE OF THE H3-H4 CHAPERONE ASF1 BOUND TO HISTONES H3 AND H4	DNA BINDING PROTEIN
2HVY	CRYSTAL STRUCTURE OF AN H/ACA BOX RNP FROM PYROCOCCUS FURIOSUS	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA

2HY5	CRYSTAL STRUCTURE OF DSREFH	TRANSFERASE
2HYI	TRUCTURE OF THE HUMAN EXON JUNCTION COMPLEX WITH A TRAPPED DEAD-BOX HELICASE BOUND TO RNA	HYDROLASE/RNA BINDING PROTEIN/RNA
2HZM	STRUCTURE OF THE MEDIATOR HEAD SUBCOMPLEX MED18/20	TRANSCRIPTION
2I04	X-RAY CRYSTAL STRUCTURE OF MAGI-1 PDZ1 BOUND TO THE C-TERMINAL PEPTIDE OF HPV18 E6	PEPTIDE BINDING PROTEIN
2I0I	X-RAY CRYSTAL STRUCTURE OF SAP97 PDZ3 BOUND TO THE C-TERMINAL PEPTIDE OF HPV18 E6	PEPTIDE BINDING PROTEIN
2I0Q	CRYSTAL STRUCTURE OF A TELOMERE SINGLE-STRAND DNA-PROTEIN COMPLEX FROM O. NOVA WITH FULL-LENGTH ALPHA AND BETA TELOMERE PROTEINS	STRUCTURAL PROTEIN/DNA
2I2P	CRYSTAL STRUCTURE OF RIBOSOME WITH MESSENGER RNA AND THE ANTICODON STEM-LOOP OF P-SITE TRNA. THIS FILE CONTAINS THE 30S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2I2T	CRYSTAL STRUCTURE OF RIBOSOME WITH MESSENGER RNA AND THE ANTICODON STEM-LOOP OF P-SITE TRNA. THIS FILE CONTAINS THE 50S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2I2U	CRYSTAL STRUCTURE OF RIBOSOME WITH MESSENGER RNA AND THE ANTICODON STEM-LOOP OF P-SITE TRNA. THIS FILE CONTAINS THE 30S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2I2V	CRYSTAL STRUCTURE OF RIBOSOME WITH MESSENGER RNA AND THE ANTICODON STEM-LOOP OF P-SITE TRNA. THIS FILE CONTAINS THE 50S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2I2X	RYSTAL STRUCTURE OF METHANOL:COBALAMIN METHYLTRANSFERASE COMPLEX MTABC FROM METHANOSARCINA BARKERI	TRANSFERASE
2I3H	STRUCTURE OF AN ML-IAP/XIAP CHIMERA BOUND TO A 4-MER PEPTIDE (AVPW)	INHIBITOR/APOPTOSIS
2I3S	BUB3 COMPLEX WITH BUB1 GLEBS MOTIF	CELL CYCLE
2I5N	1.96 A X-RAY STRUCTURE OF PHOTOSYNTHETIC REACTION CENTER FROM RHODOPSEUDOMONAS VIRIDIS:CRYSTALS GROWN BY MICROFLUIDIC TECHNIQUE	PHOTOSYNTHESIS
2I6O	RYSTAL STRUCTURE OF THE COMPLEX OF THE ARCHAEAL SULFOLOBUS	HYDROLASE

	PTP-FOLD PHOSPHATASE WITH PHOSPHOPEPTIDES N-G-(P)Y-K-N	
2IAL	STRUCTURAL BASIS FOR RECOGNITION OF MUTANT SELF BY A TUMOR-SPECIFIC, MHC CLASS II-RESTRICTED TCR	IMMUNE SYSTEM
2IBG	CRYSTAL STRUCTURE OF HEDGEHOG BOUND TO THE FNIII DOMAINS OF IHOG	PROTEIN BINDING
2ID4	THE 1.9 A STRUCTURE OF KEX2 IN COMPLEX WITH AN AC-R-E-R-K-CHLOROMETHYL KETONE INHIBITOR.	HYDROLASE
2IDO	STRUCTURE OF THE E. COLI POL III EPSILON-HOT PROOFREADING COMPLEX	TRANSFERASE
2IJ0	STRUCTURAL BASIS OF T CELL SPECIFICITY AND ACTIVATION BY THE BACTERIAL SUPERANTIGEN TOXIC SHOCK SYNDROME TOXIN-1	PROTEIN BINDING
2INC	NATIVE TOLUENE/O-XYLENE MONOOXYGENASE HYDROXYLASE X-RAY CRYSTAL STRUCTURE	OXIDOREDUCTASE
2INP	STRUCTURE OF THE PHENOL HYDROXYLASE-REGULATORY PROTEIN COMPLEX	OXIDOREDUCTASE
2IOU	MAJOR TROPISM DETERMINANT P1 (MTD-P1) VARIANT COMPLEXED WITH BORDETELLA BROCHISEPTICA VIRULENCE FACTOR PERTACTIN EXTRACELLULAR DOMAIN (PRN-E).	VIRAL PROTEIN/MEMBRANE PROTEIN
2IQ6	CRYSTAL STRUCTURE OF THE AMINOPEPTIDASE FROM VIBRIO PROTEOLYTICUS IN COMPLEXATION WITH LEUCYL-LEUCYL-LEUCINE.	HYDROLASE
2ISQ	CRYSTAL STRUCTURE OF O-ACETYLSERINE SULFHYDRYLASE FROM ARABIDOPSIS THALIANA IN COMPLEX WITH C-TERMINAL PEPTIDE FROM ARABIDOPSIS SERINE ACETYLTRANSFERASE	TRANSFERASE
2ISS	TRUCTURE OF THE PLP SYNTHASE HOLOENZYME FROM THERMOTOGA MARITIMA	LYASE, TRANSFERASE
2IUH	CRYSTAL STRUCTURE OF THE PI3-KINASE P85 N-TERMINAL SH2 DOMAIN IN COMPLEX WITH C-KIT PHOSPHOTYROSYL PEPTIDE	TRANSFERASE
2IVF	THYLBENZENE DEHYDROGENASE FROM AROMATOLEUM AROMATICUM	OXIDOREDUCTASE
2IW5	STRUCTURAL BASIS FOR COREST-DEPENDENT DEMETHYLATION OF NUCLEOSOMES BY THE HUMAN LSD1 HISTONE DEMETHYLASE	OXIDOREDUCTASE/REPRESSOR COMPLEX
2IWB	MECR1 UNBOUND EXTRACELLULAR ANTIBIOTIC-SENSOR DOMAIN.	ANTIBIOTIC RESISTANCE
2IX2	CRYSTAL STRUCTURE OF THE HETEROTRIMERIC PCNA FROM SULFOLOBUS SOLFATARICUS	REPLICATION
2IXP	CRYSTAL STRUCTURE OF THE PP2A PHOSPHATASE ACTIVATOR YPA1 PTPA1 IN COMPLEX WITH MODEL SUBSTRATE	ISOMERASE
2IYB	STRUCTURE OF COMPLEX BETWEEN THE 3RD LIM DOMAIN OF TES AND THE EVH1 DOMAIN OF MENA	METAL-BINDING

2IZ2	CRYSTAL STRUCTURE OF THE LIGAND BINDING DOMAIN OF FUSHI TARAZU FACTOR 1 FROM DROSOPHILA MELANOGASTER	DNA BINDING PROTEIN
2IZX	MOLECULAR BASIS OF AKAP SPECIFICITY FOR PKA REGULATORY SUBUNITS	KINASE
2J00	STRUCTURE OF THE THERMUS THERMOPHILUS 70S RIBOSOME COMPLEXED WITH MRNA, TRNA AND PAROMOMYCIN (PART 1 OF 4). THIS FILE CONTAINS THE 30S SUBUNIT, MRNA, A-, P- AND E-SITE TRNAS AND PAROMOMYCIN FOR MOLECULE I.	RIBOSOME
2J0Q	THE CRYSTAL STRUCTURE OF THE EXON JUNCTION COMPLEX AT 3.2 A RESOLUTION	HYDROLASE/RNA
2J1K	CAV-2 FIBRE HEAD IN COMPLEX WITH CAR D1	VIRUS/RECEPTOR COMPLEX
2J28	MODEL OF E. COLI SRP BOUND TO 70S RNCS	PROTEIN/RNA COMPLEX
2J2Z	X-RAY STRUCTURE OF THE CHAPERONE PAPD IN COMPLEX WITH THE PILUS TERMINATOR SUBUNIT PAPH AT 2.3 ANGSTROM RESOLUTION	CHAPERONE/SURFACE ACTIVE PROTEIN
2J37	MODEL OF MAMMALIAN SRP BOUND TO 80S RNCS	RIBOSOME
2J3W	THE CRYSTAL STRUCTURE OF THE BET3-TRS31-SEDLIN COMPLEX.	VESICLE TRANSPORT
2J4U	E.COLI OMPC- CAMEL LACTOFERRIN COMPLEX	MEMBRANE PROTEIN/HYDROLASE COMPLEX
2J7A	RYSTAL STRUCTURE OF CYTOCHROME C NITRITE REDUCTASE NRFHA COMPLEX FROM DESULFOVIBRIO VULGARIS	OXIDOREDUCTASE
2J7Y	TRUCTURE OF 17-EPIESTRIOL-BOUND ESTROGEN RECEPTOR BETA LBD IN COMPLEX WITH LXXLL MOTIF FROM NCOA5	TRANSCRIPTION
2J8C	X-RAY HIGH RESOLUTION STRUCTURE OF THE PHOTOSYNTHETIC REACTION CENTER FROM RB. SPHAEROIDES AT PH 8 IN THE NEUTRAL STATE	ELECTRON TRANSPORT
2J8S	RUG EXPORT PATHWAY OF MULTIDRUG EXPORTER ACRB REVEALED BY DARPIN INHIBITORS	MEMBRANE PROTEIN/COMPLEX
2J9A	BLLAP IN COMPLEX WITH MICROGININ FR1	HYDROLASE
2J9U	2 ANGSTROM X-RAY STRUCTURE OF THE YEAST ESCRT-I VPS28 C-TERMINUS IN COMPLEX WITH THE NZF-N DOMAIN FROM ESCRT-II	PROTEIN TRANSPORT
2JA5	PD LESION CONTAINING RNA POLYMERASE II ELONGATION COMPLEX A	TRANSFERASE
2JA6	PD LESION CONTAINING RNA POLYMERASE II ELONGATION COMPLEX B	TRANSFERASE
2JA7	PD LESION CONTAINING RNA POLYMERASE II ELONGATION COMPLEX C	TRANSFERASE
2JA8	PD LESION CONTAINING RNA POLYMERASE II ELONGATION COMPLEX D	TRANSFERASE
2JAM	RYSTAL STRUCTURE OF HUMAN CALMODULIN-DEPENDENT PROTEIN	TRANSFERASE

	KINASE I G	
2JBY	A VIRAL PROTEIN UNEXPECTEDLY MIMICS THE STRUCTURE AND FUNCTION OF PRO-SURVIVAL BCL-2	APOPTOSIS
2JD5	SKY1P BOUND TO NPL3P-DERIVED SUBSTRATE PEPTIDE	TRANSFERASE
2JDI	GROUND STATE STRUCTURE OF F1-ATPASE FROM BOVINE HEART MITOCHONDRIA (BOVINE F1-ATPASE CRYSTALLISED IN THE ABSENCE OF AZIDE)	HYDROLASE
2JDL	STRUCTURE OF C-TERMINAL REGION OF ACIDIC P2 RIBOSOMAL PROTEIN COMPLEXED WITH TRICHOSANTHIN	HYDROLASE
2JDQ	C-TERMINAL DOMAIN OF INFLUENZA A VIRUS POLYMERASE PB2 SUBUNIT IN COMPLEX WITH HUMAN IMPORTIN ALPHA5	PROTEIN TRANSPORT
2JE6	STRUCTURE OF A 9-SUBUNIT ARCHAEAL EXOSOME	HYDROLASE
2JEA	STRUCTURE OF A 9-SUBUNIT ARCHAEAL EXOSOME BOUND TO RNA	HYDROLASE
2JES	PORTAL PROTEIN FROM BACTERIOPHAGE SPP1	VIRAL PROTEIN
2JET	CRYSTAL STRUCTURE OF A TRYPSIN-LIKE MUTANT (S189D, A226G) CHYMOTRYPSIN.	HYDROLASE
2JGB	TRUCTURE OF HUMAN EIF4E HOMOLOGOUS PROTEIN 4EHP WITH M7GTP	TRANSLATION
2JKG	PLASMODIUM FALCIPARUM PROFILIN	PROTEIN-BINDING
2JKI	COMPLEX OF HSP90 N-TERMINAL AND SGT1 CS DOMAIN	CHAPERONE
2JKR	AP2 CLATHRIN ADAPTOR CORE WITH DILEUCINE PEPTIDE RM(PHOSPHOS)QIKRLLSE	ENDOCYTOSIS
2JL5	INSIGHTS INTO TRANSLATIONAL TERMINATION FROM THE STRUCTURE OF RF2 BOUND TO THE RIBOSOME (PART 1 OF 4). THIS FILE CONTAINS THE 30S SUBUNIT.	RIBOSOME
2JOD	PAC1-RSHORT N-TERMINAL EC DOMAIN PACAP(6-38) COMPLEX	SIGNALING PROTEIN
2JZN	OLUTION NMR STRUCTURE OF THE PRODUCTIVE COMPLEX BETWEEN IIAMANNOSE AND IIBMANNOSE OF THE MANNOSE TRANSPORTER OF THE E. COLI PHOSPHOTRANSFERASE SYSTEM	TRANSFERASE
2KIN	KINESIN (MONOMERIC) FROM RATTUS NORVEGICUS	MOTOR PROTEIN
2NL9	CRYSTAL STRUCTURE OF THE MCL-1:BIM BH3 COMPLEX	APOPTOSIS
2NM1	STRUCTURE OF BONT/B IN COMPLEX WITH ITS PROTEIN RECEPTOR	TOXIN,HYDROLASE
2NMV	DAMAGE DETECTION BY THE UVRABC PATHWAY: CRYSTAL STRUCTURE OF UVRB BOUND TO FLUORESCEIN-ADDUCTED DNA	HYDROLASE/DNA
2NN6	TRUCTURE OF THE HUMAN RNA EXOSOME COMPOSED OF RRP41, RRP45,	HYDROLASE/TRANSFERASE

	RRP46, RRP43, MTR3, RRP42, CSL4, RRP4, AND RRP40	
2NNA	STRUCTURE OF THE MHC CLASS II MOLECULE HLA-DQ8 BOUND WITH A DEAMIDATED GLUTEN PEPTIDE	IMMUNE SYSTEM
2NNU	CRYSTAL STRUCTURE OF THE PAPILLOMAVIRUS DNA TETHERING COMPLEX E2:BRD4	TRANSCRIPTION
2NNW	ALTERNATIVE CONFORMATIONS OF NOP56/58-FIBRILLARIN COMPLEX AND IMPLICATION FOR INDUCED-FIT ASSENLY OF BOX C/D RNPS	TRANSFERASE
2NPI	CLP1-ATP-PCF11 COMPLEX	TRANSCRIPTION
2NPM	CRYSTAL STRUCTURE OF CRYPTOSPORIDIUM PARVUM 14-3-3 PROTEIN IN COMPLEX WITH PEPTIDE	PROTEIN BINDING
2NPS	CRYSTAL STRUCTURE OF THE EARLY ENDOSOMAL SNARE COMPLEX	TRANSPORT PROTEIN
2NPT	RYSTAL STRUCTURE OF THE COMPLEX OF HUMAN MITOGEN ACTIVATED PROTEIN KINASE KINASE 5 PHOX DOMAIN (MAP2K5-PHOX) WITH HUMAN MITOGEN ACTIVATED PROTEIN KINASE KINASE KINASE 2 PHOX DOMAIN (MAP3K2-PHOX)	TRANSFERASE
2NQA	CATALYTIC DOMAIN OF HUMAN CALPAIN 8	HYDROLASE/HYDROLASE INHIBITOR
2NQB	DROSOPHILA NUCLEOSOME STRUCTURE	STRUCTURAL PROTEIN/DNA
2NQD	CRYSTAL STRUCTURE OF CYSTEINE PROTEASE INHIBITOR, CHAGASIN, IN COMPLEX WITH HUMAN CATHEPSIN L	HYDROLASE INHIBITOR/HYDROLASE
2NS1	CRYSTAL STRUCTURE OF THE E. COLI AMMONIA CHANNEL AMTB COMPLEXED WITH THE SIGNAL TRANSDUCTION PROTEIN GLNK	TRANSPORT PROTEIN/SIGNALING PROTEIN
2NS8	HOW AN IN VITRO SELECTED PEPTIDE MIMICS THE ANTIBIOTIC TETRACYCLINE TO INDUCE TET REPRESSOR	TRANSCRIPTION
2NTS	CRYSTAL STRUCTURE OF SEK-HVB5.1	TOXIN/IMMUNE SYSTEM
2NTY	ROP4-GDP-PRONE8	SIGNALING PROTEIN
2NU8	C123AT MUTANT OF E. COLI SUCCINYL-COA SYNTHETASE	LIGASE
2NUD	THE STRUCTURE OF THE TYPE III EFFECTOR AVRB COMPLEXED WITH A HIGH-AFFINITY RIN4 PEPTIDE	TOXIN/PROTEIN BINDING
2NUT	CRYSTAL STRUCTURE OF THE HUMAN SEC23A/24A HETERODIMER, COMPLEXED WITH THE SNARE PROTEIN SEC22B	PROTEIN TRANSPORT
2NV2	STRUCTURE OF THE PLP SYNTHASE COMPLEX PDX1/2 (YAAD/E) FROM BACILLUS SUBTILIS	LYASE/TRANSFERASE
2NVQ	RNA POLYMERASE II ELONGATION COMPLEX IN 150 MM MG+2 WITH 2'DUTP	TRANSCRIPTION/DNA/RNA
2NVT	RNA POLYMERASE II ELONGATION COMPLEX IN 150 MM MG+2 WITH	TRANSCRIPTION/DNA/RNA

	GMPCPP	
2NVX	RNA POLYMERASE II ELONGATION COMPLEX IN 5 MM MG+2 WITH 2'-DUTP	TRANSCRIPTION/DNA/RNA
2NVZ	RNA POLYMERASE II ELONGATION COMPLEX WITH UTP, UPDATED 11/2006	TRANSCRIPTION/DNA/RNA
2NW2	CRYSTAL STRUCTURE OF ELS4 TCR AT 1.4A	IMMUNE SYSTEM
2NXX	CRYSTAL STRUCTURE OF THE LIGAND-BINDING DOMAINS OF THE T.CASTANEUM (COLEOPTERA) HETERODIMER ECRUSP BOUND TO PONASTERONE A	HORMONE/GROWTH FACTOR
2NZD	NUCLEOSOME CORE PARTICLE CONTAINING 145 BP OF DNA	STRUCTURAL PROTEIN/DNA
2NZU	STRUCTURAL MECHANISM FOR THE FINE-TUNING OF CCPA FUNCTION BY THE SMALL MOLECULE EFFECTORS G6P AND FBP	TRANSCRIPTION
2O01	THE STRUCTURE OF A PLANT PHOTOSYSTEM I SUPERCOMPLEX AT 3.4 ANGSTROM RESOLUTION	PHOTOSYNTHESIS
2O02	HOSPHORYLATION INDEPENDENT INTERACTIONS BETWEEN 14-3-3 AND EXOENZYME S: FROM STRUCTURE TO PATHOGENESIS	PROTEIN BINDING/TOXIN
2O1R	TRUCTURAL GENOMICS, THE CRYSTAL STRUCTURE OF A CONSERVED PUTATIVE PROTEIN FROM HAEMOPHILUS INFLUENZAE RD KW20	MEMBRANE PROTEIN
2O26	STRUCTURE OF A CLASS III RTK SIGNALING ASSEMBLY	CYTOKINE/SIGNALING PROTEIN
2O3B	CRYSTAL STRUCTURE COMPLEX OF NUCLEASE A (NUCA) WITH INTRA-CELLULAR INHIBITOR NUIA	HYDROLASE/HYDROLASE INHIBITOR
2O5G	ALMODULIN-SMOOTH MUSCLE LIGHT CHAIN KINASE PEPTIDE COMPLEX	METAL BINDING PROTEIN
2O8B	HUMAN MUTSALPHA (MSH2/MSH6) BOUND TO ADP AND A G T MISPAIR	DNA BINDING PROTEIN/DNA
2O8C	HUMAN MUTSALPHA (MSH2/MSH6) BOUND TO ADP AND AN O6-METHYL-GUANINE T MISPAIR	DNA BINDING PROTEIN/DNA
2O8D	HUMAN MUTSALPHA (MSH2/MSH6) BOUND TO ADP AND A G DU MISPAIR	DNA BINDING PROTEIN/DNA
2O8E	HUMAN MUTSALPHA (MSH2/MSH6) BOUND TO A G T MISPAIR, WITH ADP BOUND TO MSH2 ONLY	DNA BINDING PROTEIN/DNA
2O8F	HUMAN MUTSALPHA (MSH2/MSH6) BOUND TO DNA WITH A SINGLE BASE T INSERT	DNA BINDING PROTEIN/DNA
2O8M	CRYSTAL STRUCTURE OF THE S139A MUTANT OF HEPATITIS C VIRUS NS3/4A PROTEASE	VIRAL PROTEIN
2O97	CRYSTAL STRUCTURE OF E. COLI HU HETERODIMER	DNA BINDING PROTEIN
2OBH	CENTRIN-XPC PEPTIDE	CELL CYCLE

2OD8	STRUCTURE OF A PEPTIDE DERIVED FROM CDC9 BOUND TO PCNA	PROTEIN BINDING
2ODE	CRYSTAL STRUCTURE OF THE HETERODIMERIC COMPLEX OF HUMAN RGS8 AND ACTIVATED GI ALPHA 3	SIGNALING PROTEIN
2ODG	COMPLEX OF BARRIER-TO-AUTOINTEGRATION FACTOR AND LEM-DOMAIN OF EMERIN	MEMBRANE PROTEIN, PROTEIN BINDING
2OF5	OLIGOMERIC DEATH DOMAIN COMPLEX	APOPTOSIS
2OGX	THE CRYSTAL STRUCTURE OF THE MOLYBDENUM STORAGE PROTEIN FROM AZOTOBACTER VINELANDII LOADED WITH POLYOXOTUNGSTATES (WSTO)	METAL BINDING PROTEIN
2OIZ	CRYSTAL STRUCTURE OF THE TRYPTAMINE-DERIVED (INDOL-3-ACETAMIDE)-TTQ ADDUCT OF AROMATIC AMINE DEHYDROGENASE	OXIDOREDUCTASE
2OK0	FAB ED10-DNA COMPLEX	IMMUNE SYSTEM/DNA
2OKR	CRYSTAL STRUCTURE OF THE P38A-MAPKAP KINASE 2 HETERODIMER	TRANSFERASE
2OM7	STRUCTURAL BASIS FOR INTERACTION OF THE RIBOSOME WITH THE SWITCH REGIONS OF GTP-BOUND ELONGATION FACTORS	RIBOSOME
2ONK	ABC TRANSPORTER MODBC IN COMPLEX WITH ITS BINDING PROTEIN MODA	MEMBRANE PROTEIN
2OQ1	TANDEM SH2 DOMAINS OF ZAP-70 WITH 19-MER ZETA1 PEPTIDE	TRANSFERASE
2OT0	FRUCTOSE-1,6-BISPHOSPHATE ALDOLASE FROM RABBIT MUSCLE IN COMPLEX WITH A C-TERMINAL PEPTIDE OF WISKOTT-ALDRICH SYNDROME PROTEIN	LYASE
2OT3	CRYSTAL STRUCTURE OF RABEX-5 VPS9 DOMAIN IN COMPLEX WITH NUCLEOTIDE FREE RAB21	PROTEIN TRANSPORT
2OTJ	3-DEOXYTEDANOLIDE BOUND TO THE LARGE SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
2OTL	GIRODAZOLE BOUND TO THE LARGE SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
2OVH	PROGESTERONE RECEPTOR WITH BOUND ASOPRISNIL AND A PEPTIDE FROM THE CO-REPRESSOR SMRT	TRANSCRIPTION
2OVK	CRYSTAL STRUCTURE OF RIGOR-LIKE SQUID MYOSIN S1	CONTRACTILE PROTEIN
2OVR	STRUCTURE OF THE SKP1-FBW7-CYCLINEDEGN COMPLEX	TRANSCRIPTION/CELL CYCLE
2OX0	CRYSTAL STRUCTURE OF JMJD2A COMPLEXED WITH HISTONE H3 PEPTIDE DIMETHYLATED AT LYS9	OXIDOREDUCTASE
2OXG	THE SOXYZ COMPLEX OF PARACOCCUS PANTOTROPHUS	TRANSPORT PROTEIN
2OXQ	STRUCTURE OF THE UBCH5 :CHIP U-BOX COMPLEX	LIGASE

2OXW	HUMAN MMP-12 COMPLEXED WITH THE PEPTIDE IAG	HYDROLASE
2OZ1	THE SOXAX COMPLEX OF RHODOVULUM SULFIDOPHILUM	ELECTRON TRANSPORT
2OZB	STRUCTURE OF A HUMAN PRP31-15.5K-U4 SNRNA COMPLEX	RNA BINDING PROTEIN/RNA
2OZN	THE COHESIN-DOCKERIN COMPLEX OF NAGJ AND NAGH FROM CLOSTRIDIUM PERFRINGENS	TOXIN
2P0R	STRUCTURE OF HUMAN CALPAIN 9 IN COMPLEX WITH LEUPEPTIN	HYDROLASE
2P0W	HUMAN HISTONE ACETYLTRANSFERASE 1 (HAT1)	TRANSFERASE
2P1L	STRUCTURE OF THE BCL-XL:BECLIN 1 COMPLEX	APOPTOSIS
2P1M	TIR1-ASK1 COMPLEX STRUCTURE	SIGNALING PROTEIN
2P1T	CRYSTAL STRUCTURE OF THE LIGAND BINDING DOMAIN OF THE RETINOID X RECEPTOR ALPHA IN COMPLEX WITH 3-(2'-METHOXY)-TETRAHYDRONAPHTYL CINNAMIC ACID AND A FRAGMENT OF THE COACTIVATOR TIF-2	HORMONE RECEPTOR
2P3U	CRYSTAL STRUCTURE OF HUMAN FACTOR XA COMPLEXED WITH 3-CHLORO-N-(4-CHLORO-2-{[(5-CHLOROPYRIDIN-2-YL) AMINO]CARBONYL}-6-METHOXYPHENYL)-4-[(1-METHYL-1H-IMIDAZOL-2-YL)METHYL]THIOPHENE-2-CARBOXAMIDE {PFIZER 320663}	BLOOD CLOTTING
2P49	COMPLEX OF A CAMELID SINGLE-DOMAIN VHH ANTIBODY FRAGMENT WITH RNASE A AT 1.4A RESOLUTION: NATIVE MONO_1 CRYSTAL FORM	HYDROLASE/IMMUNE SYSTEM
2P54	A CRYSTAL STRUCTURE OF PPAR ALPHA BOUND WITH SRC1 PEPTIDE AND GW735	TRANSCRIPTION
2P58	STRUCTURE OF THE YERSINIA PESTIS TYPE III SECRETION SYSTEM NEEDLE PROTEIN YSCF IN COMPLEX WITH ITS CHAPERONES YSCE/YSCG	TRANSPORT PROTEIN/CHAPERONE
2P5T	MOLECULAR AND STRUCTURAL CHARACTERIZATION OF THE PEZAT CHROMOSOMAL TOXIN-ANTITOXIN SYSTEM OF THE HUMAN PATHOGEN STREPTOCOCCUS PNEUMONIAE	TRANSCRIPTION REGULATOR
2P7V	CRYSTAL STRUCTURE OF THE ESCHERICHIA COLI REGULATOR OF SIGMA 70, RSD, IN COMPLEX WITH SIGMA 70 DOMAIN 4	TRANSCRIPTION
2PA8	X-RAY CRYSTAL STRUCTURE OF THE D/L SUBCOMPLEX OF THE SULFOLOBUS SOLFATARICUS RNA POLYMERASE	TRANSFERASE
2PBI	THE MULTIFUNCTIONAL NATURE OF GBETA5/RGS9 REVEALED FROM ITS CRYSTAL STRUCTURE	SIGNALING PROTEIN
2PBK	CRYSTAL STRUCTURE OF KSHV PROTEASE IN COMPLEX WITH HEXAPEPTIDE PHOSPHONATE INHIBITOR	VIRAL PROTEIN
2PC4	CRYSTAL STRUCTURE OF FRUCTOSE-BISPHOSPHATE ALDOLASE FROM	LYASE

	PLASMODIUM FALCIPARUM IN COMPLEX WITH TRAP-TAIL DETERMINED AT 2.4 ANGSTROM RESOLUTION	
2PEH	CRYSTAL STRUCTURE OF THE UHM DOMAIN OF HUMAN SPF45 IN COMPLEX WITH SF3B155-ULM5	PROTEIN BINDING
2PEM	CRYSTAL STRUCTURE OF RBCX IN COMPLEX WITH SUBSTRATE	CHAPERONE
2PHK	THE CRYSTAL STRUCTURE OF A PHOSPHORYLASE KINASE PEPTIDE SUBSTRATE COMPLEX: KINASE SUBSTRATE RECOGNITION	COMPLEX (TRANSFERASE/PEPTIDE)
2PI2	FULL-LENGTH REPLICATION PROTEIN A SUBUNITS RPA14 AND RPA32	REPLICATION, DNA BINDING PROTEIN
2PJR	HELICASE PRODUCT COMPLEX	HYDROLASE/DNA
2PJW	THE VPS27/HSE1 COMPLEX IS A GAT DOMAIN-BASED SCAFFOLD FOR UBIQUITIN-DEPENDENT SORTING	ENDOCYTOSIS/EXOCYTOSIS
2PJX	CRYSTAL STRUCTURE OF THE MUNC18C/SYNTAXIN4 N-PEPTIDE COMPLEX	ENDOCYTOSIS/EXOCYTOSIS
2PK9	STRUCTURE OF THE PHO85-PHO80 CDK-CYCLIN COMPLEX OF THE PHOSPHATE-RESPONSIVE SIGNAL TRANSDUCTION PATHWAY	SIGNALING PROTEIN,TRANSFERASE/CELL CYCLE
2PKA	REFINED 2 ANGSTROMS X-RAY CRYSTAL STRUCTURE OF PORCINE PANCREATIC KALLIKREIN A, A SPECIFIC TRYPSIN-LIKE SERINE PROTEINASE. CRYSTALLIZATION, STRUCTURE DETERMINATION, CRYSTALLOGRAPHIC REFINEMENT, STRUCTURE AND ITS COMPARISON WITH BOVINE TRYPSIN	SERINE PROTEINASE
2PKQ	CRYSTAL STRUCTURE OF THE PHOTOSYNTHETIC A2B2-GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE, COMPLEXED WITH NADP	OXIDOREDUCTASE
2PLD	NUCLEAR MAGNETIC RESONANCE STRUCTURE OF AN SH2 DOMAIN OF PHOSPHOLIPASE C-GAMMA1 COMPLEXED WITH A HIGH AFFINITY BINDING PEPTIDE	PHOSPHORIC DIESTER HYDROLASE
2PM7	CRYSTAL STRUCTURE OF YEAST SEC13/31 EDGE ELEMENT OF THE COPII VESICULAR COAT, SELENOMETHIONINE VERSION	PROTEIN TRANSPORT
2PMS	CRYSTAL STRUCTURE OF THE COMPLEX OF HUMAN LACTOFERRIN N-LOBE AND LACTOFERRIN-BINDING DOMAIN OF PNEUMOCOCCAL SURFACE PROTEIN A	METAL TRANSPORT, HYDROLASE
2PNZ	CRYSTAL STRUCTURE OF THE P. ABYSSI EXOSOME RNASE PH RING COMPLEXED WITH UDP AND GMP	HYDROLASE/HYDROLASE
2PO1	CRYSTAL STRUCTURE OF THE P. ABYSSI EXOSOME RNASE PH RING COMPLEXED WITH A SINGLE STRANDED 10-MER POLY(A) RNA	HYDROLASE/HYDROLASE/RNA
2POP	THE CRYSTAL STRUCTURE OF TAB1 AND BIR1 COMPLEX	SIGNALING PROTEIN/APOPTOSIS
2POY	CRYPTOSPORIDIUM PARVUM CYCLOPHILIN TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE CGD2_4120 IN COMPLEX WITH CYCLOSPORIN A	ISOMERASE
2PPB	CRYSTAL STRUCTURE OF THE T. THERMOPHILUS RNAP POLYMERASE	TRANSFERASE/DNA/RNA

	ELONGATION COMPLEX WITH THE NTP SUBSTRATE ANALOG AND ANTIBIOTIC STREPTOLYDIGIN	
2PQR	CRYSTAL STRUCTURE OF YEAST FIS1 COMPLEXED WITH A FRAGMENT OF YEAST CAF4	APOPTOSIS
2PSM	CRYSTAL STRUCTURE OF INTERLEUKIN 15 IN COMPLEX WITH INTERLEUKIN 15 RECEPTOR ALPHA	CYTOKINE
2PT7	CRYSTAL STRUCTURE OF CAG VIRB11 (HP0525) AND AN INHIBITORY PROTEIN (HP1451)	HYDROLASE/PROTEIN BINDING
2PU9	RYSTAL SRTUCTURE OF THE BINARY COMPLEX BETWEEN FERREDOXIN: THIOREDOXIN REDUCTASE AND THIOREDOXIN F	ELECTRON TRANSPORT
2PUX	CRYSTAL STRUCTURE OF MURINE THROMBIN IN COMPLEX WITH THE EXTRACELLULAR FRAGMENT OF MURINE PAR3	HYDROLASE
2PUY	CRYSTAL STRUCTURE OF THE BHC80 PHD FINGER	TRANSCRIPTION
2PV2	CRYSTALLOGRAPHIC STRUCTURE OF SURA FIRST PEPTIDYL-PROLYL ISOMERASE DOMAIN COMPLEXED WITH PEPTIDE NFTLKFWDIFRK	ISOMERASE
2PVF	RYSTAL STRUCTURE OF TYROSINE PHOSPHORYLATED ACTIVATED FGF RECEPTOR 2 (FGFR2) KINASE DOMAIN IN COMPLEX WITH ATP ANALOG AND SUBSTRATE PEPTIDE	TRANSFERASE
2PYO	DROSOPHILA NUCLEOSOME CORE	STRUCTURAL PROTEIN/DNA
2Q0N	STRUCTURE OF HUMAN P21 ACTIVATING KINASE 4 (PAK4) IN COMPLEX WITH A CONSENSUS PEPTIDE	TRANSFERASE
2Q0O	CRYSTAL STRUCTURE OF AN ANTI-ACTIVATION COMPLEX IN BACTERIAL QUORUM SENSING	TRANSCRIPTION
2Q1Z	CRYSTAL STRUCTURE OF RHODOBACTER SPHAEROIDES SIGE IN COMPLEX WITH THE ANTI-SIGMA CHRR	TRANSCRIPTION
2Q26	FHV VIRUS LIKE PARTICLE	VIRUS/RNA
2Q2E	RYSTAL STRUCTURE OF THE TOPOISOMERASE VI HOLOENZYME FROM METHANOSARCINA MAZEI	ISOMERASE
2Q3C	2.1 A RESOLUTION CRYSTAL STRUCTURE OF O-ACETYLSERINE SULFHYDRYLASE (OASS) HOLOENZYME FROM MYCOBACTERIUM TUBERCULOSIS IN COMPLEX WITH THE INHIBITORY PEPTIDE DFSI	TRANSFERASE
2Q3N	AGGLUTININ FROM ABRUS PRECATORIUS (APA-I)	PLANT PROTEIN
2Q3Y	ANCESTRAL CORTICIOD RECEPTOR IN COMPLEX WITH DOC	TRANSCRIPTION
2Q3Z	RANSGLUTAMINASE 2 UNDERGOES LARGE CONFORMATIONAL CHANGE UPON ACTIVATION	TRANSFERASE
2Q5W	HE X-RAY CRYSTAL STRUCTURE OF MOLYBDOPTERIN SYNTHASE FROM	TRANSFERASE

	STAPHYLOCOCCUS AUREUS	
2Q5Y	CRYSTAL STRUCTURE OF THE C-TERMINAL DOMAIN OF HNUP98	PROTEIN TRANSPORT
2Q86	STRUCTURE OF THE MOUSE INVARIANT NKT CELL RECEPTOR VALPHA14	IMMUNE SYSTEM
2Q8B	STRUCTURE OF THE MALARIA ANTIGEN AMA1 IN COMPLEX WITH A GROWTH-INHIBITORY ANTIBODY	IMMUNE SYSTEM
2QA4	A MORE COMPLETE STRUCTURE OF THE THE L7/L12 STALK OF THE HALOARCULA MARISMORTUI 50S LARGE RIBOSOMAL SUBUNIT	RIBOSOME
2QAC	THE CLOSED MTIP-MYOSINA-TAIL COMPLEX FROM THE MALARIA PARASITE INVASION MACHINERY	MEMBRANE PROTEIN
2QAG	CRYSTAL STRUCTURE OF HUMAN SEPTIN TRIMER 2/6/7	CELL CYCLE, STRUCTURAL PROTEIN
2QAL	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH NEOMYCIN. THIS FILE CONTAINS THE 30S SUBUNIT OF THE FIRST 70S RIBOSOME, WITH NEOMYCIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2QAS	RYSTAL STRUCTURE OF CAULOBACTER CRESCENTUS SSPB ORTHOLOG	HYDROLASE ACTIVATOR
2QBW	THE CRYSTAL STRUCTURE OF PDZ-FIBRONECTIN FUSION PROTEIN	UNKNOWN FUNCTION
2QBY	CRYSTAL STRUCTURE OF A HETERODIMER OF CDC6/ORC1 INITIATORS BOUND TO ORIGIN DNA (FROM S. SOLFATARICUS)	REPLICATION/DNA
2QDY	CRYSTAL STRUCTURE OF FE-TYPE NHASE FROM RHODOCOCCUS ERYTHROPOLIS AJ270	LYASE
2QE7	CRYSTAL STRUCTURE OF THE F1-ATPASE FROM THE THERMOALKALIPHILIC BACTERIUM BACILLUS SP. TA2.A1	HYDROLASE
2QEJ	CRYSTAL STRUCTURE OF A STAPHYLOCOCCUS AUREUS PROTEIN (SSL7) IN COMPLEX WITH FC OF HUMAN IGA1	IMMUNE SYSTEM
2QEX	NEGAMYCIN BINDS TO THE WALL OF THE NASCENT CHAIN EXIT TUNNEL OF THE 50S RIBOSOMAL SUBUNIT	RIBOSOME
2QFA	CRYSTAL STRUCTURE OF A SURVIVIN-BOREALIN-INCENP CORE COMPLEX	CELL CYCLE/CELL CYCLE/CELL CYCLE
2QFC	CRYSTAL STRUCTURE OF BACILLUS THURINGIENSIS PLCR COMPLEXED WITH PAPR	TRANSCRIPTION REGULATION
2QHR	CRYSTAL STRUCTURE OF THE 13F6-1-2 FAB FRAGMENT BOUND TO ITS EBOLA VIRUS GLYCOPROTEIN PEPTIDE EPITOPE.	IMMUNE SYSTEM/VIRAL PROTEIN
2QI9	ABC-TRANSPORTER BTUCD IN COMPLEX WITH ITS PERIPLASMIC BINDING PROTEIN BTUF	MEMBRANE PROTEIN
2QIY	YEAST DEUBIQUITINASE UBP3 AND BRE5 COFACTOR COMPLEX	SIGNALING PROTEIN/HYDROLASE

2QJY	RYSTAL STRUCTURE OF RHODOBACTER SPHAEROIDES DOUBLE MUTANT WITH STIGMATELLIN AND UQ2	OXIDOREDUCTASE
2QK7	COVALENT S-F HETERODIMER OF STAPHYLOCOCCAL GAMMA-HEMOLYSIN	TOXIN
2QKH	CRYSTAL STRUCTURE OF THE EXTRACELLULAR DOMAIN OF HUMAN GIP RECEPTOR IN COMPLEX WITH THE HORMONE GIP	SIGNALING PROTEIN/HORMONE
2QKL	THE CRYSTAL STRUCTURE OF FISSION YEAST MRNA DECAPPING ENZYME DCP1-DCP2 COMPLEX	HYDROLASE
2QKW	STRUCTURAL BASIS FOR ACTIVATION OF PLANT IMMUNITY BY BACTERIAL EFFECTOR PROTEIN AVRPTO	TRANSFERASE
2QL2	CRYSTAL STRUCTURE OF THE BASIC-HELIX-LOOP-HELIX DOMAINS OF THE HETERODIMER E47/NEUROD1 BOUND TO DNA	TRANSCRIPTION/DNA
2QLL	HUMAN LIVER GLYCOGEN PHOSPHORYLASE- GL COMPLEX	TRANSFERASE
2QLV	CRYSTAL STRUCTURE OF THE HETEROTRIMER CORE OF THE S. CEREVISIAE AMPK HOMOLOG SNF1	TRANSFERASE/PROTEIN BINDING
2QM6	CRYSTAL STRUCTURE OF HELICOBACTER PYLORI GAMMA-GLUTAMYLTRANSPEPTIDASE IN COMPLEX WITH GLUTAMATE	TRANSFERASE
2QME	CRYSTAL STRUCTURE OF HUMAN RAC3 IN COMPLEX WITH CRIB DOMAIN OF HUMAN P21-ACTIVATED KINASE 1 (PAK1)	SIGNALING PROTEIN/TRANSFERASE
2QN6	STRUCTURE OF AN ARCHAEAL HETEROTRIMERIC INITIATION FACTOR 2 REVEALS A NUCLEOTIDE STATE BETWEEN THE GTP AND THE GDP STATES	TRANSLATION
2QOG	CROTOXIN B, THE BASIC PLA2 FROM CROTALUS DURISSUS TERRIFICUS.	HYDROLASE
2QOS	CRYSTAL STRUCTURE OF COMPLEMENT PROTEIN C8 IN COMPLEX WITH A PEPTIDE CONTAINING THE C8 BINDING SITE ON C8	IMMUNE SYSTEM
2QOU	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH SPECTINOMYCIN. THIS FILE CONTAINS THE 30S SUBUNIT OF THE FIRST 70S RIBOSOME, WITH SPECTINOMYCIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES.	RIBOSOME
2QRD	CRYSTAL STRUCTURE OF THE ADENYLATE SENSOR FROM AMP-ACTIVATED PROTEIN KINASE IN COMPLEX WITH ADP AND ATP	TRANSFERASE
2QRV	STRUCTURE OF DNMT3A-DNMT3L C-TERMINAL DOMAIN COMPLEX	TRANSFERASE/TRANSFERASE REGULATOR
2QSC	CRYSTAL STRUCTURE ANALYSIS OF ANTI-HIV-1 V3-FAB F425-B4E8 IN COMPLEX WITH A V3-PEPTIDE	IMMUNE SYSTEM
2QSF	CRYSTAL STRUCTURE OF THE RAD4-RAD23 COMPLEX	DNA BINDING PROTEIN
2QSG	CRYSTAL STRUCTURE OF RAD4-RAD23 BOUND TO A UV-DAMAGED DNA	DNA BINDING PROTEIN/DNA

2QSH	CRYSTAL STRUCTURE OF RAD4-RAD23 BOUND TO A MISMATCH DNA	DNA BINDING PROTEIN/DNA
2QSS	BOVINE HEMOGLOBIN AT PH 6.3	OXYGEN BINDING
2QT5	CRYSTAL STRUCTURE OF GRIP1 PDZ12 IN COMPLEX WITH THE FRAS1 PEPTIDE	PEPTIDE BINDING PROTEIN
2QTV	TRUCTURE OF SEC23-SAR1 COMPLEXED WITH THE ACTIVE FRAGMENT OF SEC31	PROTEIN TRANSPORT
2QU0	RYSTAL STRUCTURE DETERMINATION OF SHEEP METHEMOGLOBIN AT 2.7 ANGSTROM RESOLUTION	OXYGEN STORAGE, OXYGEN TRANSPORT
2QWO	RYSTAL STRUCTURE OF DISULFIDE-BOND-CROSSLINKED COMPLEX OF BOVINE HSC70 (1-394AA)R171C AND BOVINE AUXILIN (810-910AA) D876C IN THE ADP*PI FORM #1	CHAPERONE
2QXV	STRUCTURAL BASIS OF EZH2 RECOGNITION BY EED	GENE REGULATION
2R17	UNCTIONAL ARCHITECTURE OF THE RETROMER CARGO-RECOGNITION COMPLEX	PROTEIN TRANSPORT
2R25	COMPLEX OF YPD1 AND SLN1-R1 WITH BOUND MG2+ AND BEF3-	SIGNALING PROTEIN/TRANSFERASE
2R40	CRYSTAL STRUCTURE OF 20E BOUND ECR/USP	GENE REGULATION
2R5Y	TRUCTURE OF SCR/EXD COMPLEX BOUND TO A CONSENSUS HOX-EXD SITE	TRANSCRIPTION/DNA
2R5Z	STRUCTURE OF SCR/EXD COMPLEX BOUND TO A DNA SEQUENCE DERIVED FROM THE FKH GENE	TRANSCRIPTION/DNA
2R6A	CRYSTAL FORM BH1	REPLICATION
2R7G	STRUCTURE OF THE RETINOBLASTOMA PROTEIN POCKET DOMAIN IN COMPLEX WITH ADENOVIRUS E1A CR1 DOMAIN	TRANSCRIPTION REPRESSOR, CELL CYCLE
2R7Z	CISPLATIN LESION CONTAINING RNA POLYMERASE II ELONGATION COMPLEX	TRANSCRIPTION, TRANSFERASE/DNA/RNA
2R80	PIGEON HEMOGLOBIN (OXY FORM)	OXYGEN BINDING
2R8S	HIGH RESOLUTION STRUCTURE OF A SPECIFIC SYNTHETIC FAB BOUND TO P4-P6 RNA RIBOZYME DOMAIN	IMMUNE SYSTEM/RNA
2R92	ELONGATION COMPLEX OF RNA POLYMERASE II WITH ARTIFICIAL RDRP SCAFFOLD	TRANSFERASE/RNA
2R93	ELONGATION COMPLEX OF RNA POLYMERASE II WITH A HEPATITIS DELTA VIRUS-DERIVED RNA STEM LOOP	TRANSFERASE/RNA
2R9B	STRUCTURAL ANALYSIS OF PLASMEPSIN 2 FROM PLASMODIUM FALCIPARUM COMPLEXED WITH A PEPTIDE-BASED INHIBITOR	HYDROLASE

2R9P	HUMAN MESOTRYPSIN COMPLEXED WITH BOVINE PANCREATIC TRYPSIN INHIBITOR(BPTI)	HYDROLASE/HYDROLASE INHIBITOR
2R9Q	CRYSTAL STRUCTURE OF 2'-DEOXYCYTIDINE 5'-TRIPHOSPHATE DEAMINASE FROM AGROBACTERIUM TUMEFACIENS	HYDROLASE
2RAO	X RAY CRYSTAL STRUCTURE OF RABBIT HEMOGLOBIN (OXY FORM) AT 2.0 ANGSTROM RESOLUTION	OXYGEN BINDING
2RD5	STRUCTURAL BASIS FOR THE REGULATION OF N-ACETYLGLUTAMATE KINASE BY PII IN ARABIDOPSIS THALIANA	PROTEIN BINDING
2REM	CRYSTAL STRUCTURE OF OXIDOREDUCTASE DSBA FROM XYLELLA FASTIDIOSA	OXIDOREDUCTASE
2RET	THE CRYSTAL STRUCTURE OF A BINARY COMPLEX OF TWO PSEUDOPILINS: EPSI AND EPSJ FROM THE TYPE 2 SECRETION SYSTEM OF VIBRIO VULNIFICUS	PROTEIN TRANSPORT
2REX	CRYSTAL STRUCTURE OF THE EFFECTOR DOMAIN OF PLXNB1 BOUND WITH RND1 GTPASE	SIGNALING PROTEIN/LIPOPROTEIN
2RF4	CRYSTAL STRUCTURE OF THE RNA POLYMERASE I SUBCOMPLEX A14/43	TRANSFERASE
2RFI	CRYSTAL STRUCTURE OF CATALYTIC DOMAIN OF HUMAN EUCHROMATIC HISTONE METHYLTRANSFERASE 1 IN COMPLEX WITH SAH AND DIMETHYLATED H3K9 PEPTIDE	TRANSFERASE
2RFK	SUBSTRATE RNA POSITIONING IN THE ARCHAEAL H/ACA RIBONUCLEOPROTEIN COMPLEX	ISOMERASE/RNA
2RFT	CRYSTAL STRUCTURE OF INFLUENZA B VIRUS HEMAGGLUTININ IN COMPLEX WITH LSTA RECEPTOR ANALOG	VIRAL PROTEIN
2RHK	CRYSTAL STRUCTURE OF INFLUENZA A NS1A PROTEIN IN COMPLEX WITH F2F3 FRAGMENT OF HUMAN CELLULAR FACTOR CPSF30	VIRAL PROTEIN/NUCLEAR PROTEIN
2RHS	PHERS FROM STAPHYLOCOCCUS HAEMOLYTICUS- RATIONAL PROTEIN ENGINEERING AND INHIBITOR STUDIES	LIGASE
2RI7	CRYSTAL STRUCTURE OF PHD FINGER-LINKER-BROMODOMAIN Y17E MUTANT FROM HUMAN BPTF IN THE H3(1-9)K4ME2 BOUND STATE	TRANSCRIPTION/NUCLEAR PROTEIN
2RII	CRYSTAL STRUCTURE OF HUMAN PEROXIREDOXIN I IN COMPLEX WITH SULFIREDOXIN	OXIDOREDUCTASE COMPLEX
2RJE	CRYSTAL STRUCTURE OF L3MBTL1 IN COMPLEX WITH H4K20ME2 (RESIDUES 17-25), ORTHORHOMBIC FORM II	TRANSCRIPTION
2RMC	CRYSTAL STRUCTURE OF MURINE CYCLOPHILIN C COMPLEXED WITH IMMUNOSUPPRESSIVE DRUG CYCLOSPORIN A	COMPLEX (ISOMERASE/IMMUNOSUPPRESSANT)
2STA	ANIONIC SALMON TRYPSIN IN COMPLEX WITH SQUASH SEED INHIBITOR (CUCURBITA MAXIMA TRYPSIN INHIBITOR I)	HYDROLASE/HYDROLASE INHIBITOR

2UU9	TRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT COMPLEXED WITH A VALINE-ASL WITH CMO5U IN POSITION 34 BOUND TO AN MRNA WITH A GUG-CODON IN THE A-SITE AND PAROMOMYCIN.	RIBOSOME
2UWJ	STRUCTURE OF THE HETEROTRIMERIC COMPLEX WHICH REGULATES TYPE III SECRETION NEEDLE FORMATION	CHAPERONE
2UXB	CRYSTAL STRUCTURE OF AN EXTENDED TRNA ANTICODON STEM LOOP IN COMPLEX WITH ITS COGNATE MRNA GGGU IN THE CONTEXT OF THE THERMUS THERMOPHILUS 30S SUBUNIT.	RIBOSOME
2UYZ	NON-COVALENT COMPLEX BETWEEN UBC9 AND SUMO1	LIGASE
2UZX	STRUCTURE OF THE HUMAN RECEPTOR TYROSINE KINASE MET IN COMPLEX WITH THE LISTERIA MONOCYTOGENES INVASION PROTEIN INLB: CRYSTAL FORM I	SIGNALING PROTEIN/RECEPTOR COMPLEX
2V17	STRUCTURE OF THE COMPLEX OF ANTIBODY MN423 WITH A FRAGMENT OF TAU PROTEIN	IMMUNE SYSTEM
2V1C	CRYSTAL STRUCTURE AND MUTATIONAL STUDY OF RECOR PROVIDE INSIGHT INTO ITS ROLE IN DNA REPAIR	RECOMBINATION
2V1T	CRYSTAL STRUCTURE OF RAT TOM20-ALDH PRESEQUENCE COMPLEX	OXIDOREDUCTASE
2V36	CRYSTAL STRUCTURE OF GAMMA-GLUTAMYL TRANSFERASE FROM BACILLUS SUBTILIS	TRANSFERASE
2V3B	CRYSTAL STRUCTURE OF THE ELECTRON TRANSFER COMPLEX RUBREDOXIN - RUBREDOXIN REDUCTASE FROM PSEUDOMONAS AERUGINOSA.	OXIDOREDUCTASE
2V3S	STRUCTURAL INSIGHTS INTO THE RECOGNITION OF SUBSTRATES AND ACTIVATORS BY THE OSR1 KINASE	TRANSFERASE
2V46	STRUCTURE OF THE RIBOSOME RECYCLING FACTOR BOUND TO THE THERMUS THERMOPHILUS 70S RIBOSOME WITH MRNA, ASL-PHE AND TRNA-FMET (PART 1 OF 4). THIS FILE CONTAINS THE 30S SUBUNIT, MRNA, P-SITE ASL, E-SITE TRNA AND RRF FOR MOLECULE 1.	RIBOSOME
2V4J	THE CRYSTAL STRUCTURE OF DESULFOVIBRIO VULGARIS DISSIMILATORY SULFITE REDUCTASE BOUND TO DSRC PROVIDES NOVEL INSIGHTS INTO THE MECHANISM OF SULFATE RESPIRATION	OXIDOREDUCTASE
2V52	STRUCTURE OF MAL-RPEL2 COMPLEXED TO G-ACTIN	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN
2V53	CRYSTAL STRUCTURE OF A SPARC-COLLAGEN COMPLEX	CELL ADHESION
2V55	MECHANISM OF MULTI-SITE PHOSPHORYLATION FROM A ROCK-I:RHOE COMPLEX STRUCTURE	TRANSFERASE
2V5E	THE STRUCTURE OF THE GDNF\:CORECEPTOR COMPLEX\: INSIGHTS INTO RET SIGNALLING AND HEPARIN BINDING.	RECEPTOR/GLYCOPROTEIN COMPLEX

2V5H	CONTROLLING THE STORAGE OF NITROGEN AS ARGININE: THE COMPLEX OF PII AND ACETYLGLUTAMATE KINASE FROM SYNECHOCOCCUS ELONGATUS PCC 7942	TRANSCRIPTION
2V5P	COMPLEX STRUCTURE OF HUMAN IGF2R DOMAINS 11-13 BOUND TO IGF-II	RECEPTOR/GLYCOPROTEIN COMPLEX
2V5Q	CRYSTAL STRUCTURE OF WILD-TYPE PLK-1 KINASE DOMAIN IN COMPLEX WITH A SELECTIVE DARPIN	TRANSFERASE COMPLEX
2V5W	CRYSTAL STRUCTURE OF HDAC8-SUBSTRATE COMPLEX	HYDROLASE
2V6X	STRACTURAL INSIGHT INTO THE INTERACTION BETWEEN ESCRT-III AND VPS4	PROTEIN TRANSPORT
2V89	CRYSTAL STRUCTURE OF RAG2-PHD FINGER IN COMPLEX WITH H3K4ME3 PEPTIDE AT 1.1A RESOLUTION	PROTEIN BINDING
2V8C	MOUSE PROFILIN IIA IN COMPLEX WITH THE PROLINE-RICH DOMAIN OF VASP	PROTEIN-BINDING
2V8Q	RYSTAL STRUCTURE OF THE REGULATORY FRAGMENT OF MAMMALIAN AMPK IN COMPLEXES WITH AMP	TRANSFERASE
2V8S	VTI1B HABC DOMAIN - EPSINR ENTH DOMAIN COMPLEX	PROTEIN TRANSPORT
2V8Y	RYSTALLOGRAPHIC AND MASS SPECTROMETRIC CHARACTERISATION OF EIF4E WITH N7-CAP DERIVATIVES	TRANSLATION
2VBC	RYSTAL STRUCTURE OF THE NS3 PROTEASE-HELICASE FROM DENGUE VIRUS	HYDROLASE
2VBJ	OLECULAR BASIS OF HUMAN XPC GENE RECOGNITION AND CLEAVAGE BY ENGINEERED HOMING ENDONUCLEASE HETERODIMERS	HYDROLASE
2VDB	TRUCTURE OF HUMAN SERUM ALBUMIN WITH S-NAPROXEN AND THE GA MODULE	PROTEIN BINDING
2VDC	THE 9.5 A RESOLUTION STRUCTURE OF GLUTAMATE SYNTHASE FROM CRYO-ELECTRON MICROSCOPY AND ITS OLIGOMERIZATION BEHAVIOR IN SOLUTION: FUNCTIONAL IMPLICATIONS.	OXIDOREDUCTASE
2VDR	INTEGRIN ALPHAIIBBETA3 HEADPIECE BOUND TO A CHIMERIC FIBRINOGEN GAMMA CHAIN PEPTIDE, LGGAKQRGDV	CELL ADHESION/IMMUNE SYSTEM COMPLEX
2VDU	STRUCTURE OF TRM8-TRM82, THE YEAST TRNA M7G METHYLATION COMPLEX	TRANSFERASE
2VDW	UANOSINE N7 METHYL-TRANSFERASE SUB-COMPLEX (D1-D12) OF THE VACCINIA VIRUS MRNA CAPPING ENZYME	TRANSFERASE
2VE7	CRYSTAL STRUCTURE OF A BONSAI VERSION OF THE HUMAN NDC80 COMPLEX	CELL CYCLE

2VGO	CRYSTAL STRUCTURE OF AURORA B KINASE IN COMPLEX WITH REVERSINE INHIBITOR	TRANSFERASE
2VHM	STRUCTURE OF PDF BINDING HELIX IN COMPLEX WITH THE RIBOSOME (PART 1 OF 4)	RIBOSOME
2VIF	CRYSTAL STRUCTURE OF SOCS6 SH2 DOMAIN IN COMPLEX WITH A C-KIT PHOSPHOPEPTIDE	SIGNALING PROTEIN
2VJE	RYSTAL STRUCTURE OF THE MDM2-MDMX RING DOMAIN HETERODIMER	LIGASE
2VJH	HE STRUCTURE OF PHYCOERYTHRIN FROM GLOEOBACTER VIOLACEUS	PHOTOSYNTHESIS
2VJT	IE STRUCTURE OF ALLOPHYCOCYANIN FROM GLOEOBACTER VIOLACEUS	PHOTOSYNTHESIS
2VLQ	F86A MUTANT OF E9 DNASE DOMAIN IN COMPLEX WITH IM9	PROTEIN-BINDING
2VML	HE MONOCLINIC STRUCTURE OF PHYCOCYANIN FROM GLOEOBACTER VIOLACEUS	PHOTOSYNTHESIS
2VN6	THE CLOSTRIDIUM CELLULOLYTICUM DOCKERIN DISPLAYS A DUAL BINDING MODE FOR ITS COHESIN PARTNER	CELL ADHESION
2VOF	STRUCTURE OF MOUSE A1 BOUND TO THE PUMA BH3-DOMAIN	APOPTOSIS
2VPB	DECODING OF METHYLATED HISTONE H3 TAIL BY THE PYGO-BCL9 WNT SIGNALING COMPLEX	GENE REGULATION
2VQE	MODIFIED URIDINES WITH C5-METHYLENE SUBSTITUENTS AT THE FIRST POSITION OF THE TRNA ANTICODON STABILIZE U-G WOBBLE PAIRING DURING DECODING	RIBOSOME
2VSK	IENDRA VIRUS ATTACHMENT GLYCOPROTEIN IN COMPLEX WITH HUMAN CELL SURFACE RECEPTOR EPHRINB2	HYDROLASE
2VSO	CRYSTAL STRUCTURE OF A TRANSLATION INITIATION COMPLEX	HYDROLASE/TRANSLATION
2VT1	CRYSTAL STRUCTURE OF THE CYTOPLASMIC DOMAIN OF SPA40, THE SPECIFICITY SWITCH FOR THE SHIGELLA FLEXNERI TYPE III SECRETION SYSTEM	MEMBRANE PROTEIN
2VUM	ALPHA-AMANITIN INHIBITED COMPLETE RNA POLYMERASE II ELONGATION COMPLEX	TRANSFERASE
2VUT	CRYSTAL STRUCTURE OF NAD-BOUND NMRA-AREA ZINC FINGER COMPLEX	TRANSCRIPTION
2VXC	STRUCTURE OF THE CRB2-BRCT2 DOMAIN COMPLEX WITH PHOSPHOPEPTIDE.	CELL CYCLE
2VYN	TRUCTURE OF E.COLI GAPDH RAT SPERM GAPDH HETEROTETRAMER	OXIDOREDUCTASE
2VZG	CRYSTAL STRUCTURE OF THE C-TERMINAL CALPONIN HOMOLOGY DOMAIN OF ALPHA-PARVIN IN COMPLEX WITH PAXILLIN LD2 MOTIF	CELL ADHESION

2YU9	RNA POLYMERASE II ELONGATION COMPLEX IN 150 MM MG+2 WITH UTP	TRANSCRIPTION/DNA/RNA
2YVJ	RYSTAL STRUCTURE OF THE FERREDOXIN-FERREDOXIN REDUCTASE (BPHA3-BPHA4)COMPLEX	OXIDOREDUCTASE/ELECTRON TRANSPORT
2Z23	CRYSTAL STRUCTURE OF Y.PESTIS OLIGO PEPTIDE BINDING PROTEIN OPPA WITH TRI-LYSINE LIGAND	PEPTIDE BINDING PROTEIN
2Z2Q	CRYSTAL STRUCTURE OF FLOCK HOUSE VIRUS	VIRUS/RNA
2Z3C	A MECHANISTIC VIEW OF ENZYME INHIBITION AND PEPTIDE HYDROLYSIS IN THE ACTIVE SITE OF THE SARS-COV 3C-LIKE PEPTIDASE	HYDROLASE
2Z3F	RYSTAL STRUCTURE OF SPCIA1/ASF1 COMPLEXED WITH CAC2 PEPTIDE	CHAPERONE
2Z3N	COMPLEX STRUCTURE OF LF-TRANSFERASE AND PEPTIDE B	TRANSFERASE
2Z3Q	CRYSTAL STRUCTURE OF THE IL-15/IL-15RA COMPLEX	CYTOKINE/CYTOKINE RECEPTOR
2Z4K	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH PAROMOMYCIN AND RIBOSOME RECYCLING FACTOR (RRF). THIS FILE CONTAINS THE 30S SUBUNIT OF THE FIRST 70S RIBOSOME, WITH PAROMOMYCIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2Z5I	CRYSTAL STRUCTURE OF THE HEAD-TO-TAIL JUNCTION OF TROPOMYOSIN	CONTRACTILE PROTEIN
2Z5K	COMPLEX OF TRANSPORTIN 1 WITH TAP NLS	TRANSPORT PROTEIN/RNA BINDING PROTEIN
2Z65	CRYSTAL STRUCTURE OF THE HUMAN TLR4 TV3 HYBRID-MD-2-ERITORAN COMPLEX	IMMUNE SYSTEM
2Z6W	CRYSTAL STRUCTURE OF HUMAN CYCLOPHILIN D IN COMPLEX WITH CYCLOSPORIN A	ISOMERASE
2Z7X	CRYSTAL STRUCTURE OF THE TLR1-TLR2 HETERODIMER INDUCED BY BINDING OF A TRI-ACYLATED LIPOPEPTIDE	IMMUNE SYSTEM
2Z9I	RYSTAL STRUCTURE OF RV0983 FROM MYCOBACTERIUM TUBERCULOSIS-PROTEOLYTICALLY ACTIVE FORM	HYDROLASE
2ZA4	CRYSTAL STRUCTURAL ANALYSIS OF BARNASE-BARSTAR COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
2ZAE	CRYSTAL STRUCTURE OF PROTEIN PH1601P IN COMPLEX WITH PROTEIN PH1771P OF ARCHAEAL RIBONUCLEASE P FROM PYROCOCCUS HORIKOSHII OT3	HYDROLASE
2ZBK	CRYSTAL STRUCTURE OF AN INTACT TYPE II DNA TOPOISOMERASE: INSIGHTS INTO DNA TRANSFER MECHANISMS	ISOMERASE
2ZD7	HE STRUCTURE OF VPS75 (VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN 75)	PROTEIN TRANSPORT

2ZDI	CRYSTAL STRUCTURE OF PREFOLDIN FROM PYROCOCCUS HORIKOSHII OT3	CHAPERONE
2ZET	CRYSTAL STRUCTURE OF THE SMALL GTPASE RAB27B COMPLEXED WITH THE SLP HOMOLOGY DOMAIN OF SLAC2-A/MELANOPHILIN	SIGNALING PROTEIN
2ZFB	CRYSTAL STRUCTURE OF PARROT HEMOGLOBIN (PSITTACULA KRAMERI) AT PH 7.5	METAL BINDING PROTEIN
2ZFD	THE CRYSTAL STRUCTURE OF PLANT SPECIFIC CALCIUM BINDING PROTEIN ATCBL2 IN COMPLEX WITH THE REGULATORY DOMAIN OF ATCIPK14	SIGNALING PROTEIN/TRANSFERASE
2ZFO	STRUCTURE OF THE PARTIALLY UNLIGANDED MET STATE OF 400 KDA HEMOGLOBIN: INSIGHTS INTO LIGAND-INDUCED STRUCTURAL CHANGES OF GIANT HEMOGLOBINS	OXYGEN BINDING, TRANSPORT PROTEIN
2ZIV	CRYSTAL STRUCTURE OF THE MUS81-EME1 COMPLEX	HYDROLASE
2ZJD	CRYSTAL STRUCTURE OF LC3-P62 COMPLEX	APOPTOSIS INHIBITOR/APOPTOSIS
2ZJP	THIOPEPTIDE ANTIBIOTIC NOSIHEPTIDE BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF DEINOCOCCUS RADIODURANS	RIBOSOME
2ZJQ	INTERACTION OF L7 WITH L11 INDUCED BY MICROCCOCIN BINDING TO THE DEINOCOCCUS RADIODURANS 50S SUBUNIT	RIBOSOME
2ZJR	REFINED NATIVE STRUCTURE OF THE LARGE RIBOSOMAL SUBUNIT (50S) FROM DEINOCOCCUS RADIODURANS	RIBOSOME
2ZL4	CRYSTAL STRUCTURE OF H.PYLORI CLPP S99A IN COMPLEX WITH THE PEPTIDE AAAA	HYDROLASE
2ZMI	CRYSTAL STRUCTURE OF RAT VITAMIN D RECEPTOR BOUND TO ADAMANTYL VITAMIN D ANALOGS: STRUCTURAL BASIS FOR VITAMIN D RECEPTOR ANTAGONISM AND/OR PARTIAL AGONISM	TRANSCRIPTION
2ZNE	CRYSTAL STRUCTURE OF ZN2+-BOUND FORM OF DES3-23ALG-2 COMPLEXED WITH ALIX ABS PEPTIDE	APOPTOSIS
2ZNL	CRYSTAL STRUCTURE OF PA-PB1 COMPLEX FORM INFLUENZA VIRUS RNA POLYMERASE	TRANSCRIPTION
2ZPY	RYSTAL STRUCTURE OF THE MOUSE RADXIN FERM DOMAIN COMPLEXED WITH THE MOUSE CD44 CYTOPLASMIC PEPTIDE	CELL ADHESION
2ZS6	HA3 SUBCOMPONENT OF BOTULINUM TYPE C PROGENITOR TOXIN	TOXIN
2ZSI	STRUCTURAL BASIS OF GIBBERELLIN(GA4)-INDUCED DELLA RECOGNITION BY THE GIBBERELLIN RECEPTOR	HORMONE RECEPTOR
3B3Q	CRYSTAL STRUCTURE OF A SYNAPTIC ADHESION COMPLEX	CELL ADHESION
3B5N	STRUCTURE OF THE YEAST PLASMA MEMBRANE SNARE COMPLEX	MEMBRANE PROTEIN

3B6F	NUCLEOSOME CORE PARTICLE TREATED WITH CISPLATIN	STRUCTURAL PROTEIN/DNA
3B6G	NUCLEOSOME CORE PARTICLE TREATED WITH OXALIPLATIN	STRUCTURAL PROTEIN/DNA
3B7S	[E296Q]LTA4H IN COMPLEX WITH RSR SUBSTRATE	HYDROLASE
3B82	STRUCTURE OF THE EEF2-EXOA(E546H)-NAD+ COMPLEX	BIOSYNTHETIC PROTEIN/TRANSFERASE
3B8E	CRYSTAL STRUCTURE OF THE SODIUM-POTASSIUM PUMP	HYDROLASE/TRANSPORT PROTEIN
3B95	EUHMT1 (GLP) ANKYRIN REPEAT DOMAIN (STRUCTURE 2)	TRANSFERASE/STRUCTUAL PROTEIN
3BBN	HOMOLOGY MODEL FOR THE SPINACH CHLOROPLAST 30S SUBUNIT FITTED TO 9.4A CRYO-EM MAP OF THE 70S CHLORORIBOSOME.	RIBOSOME
3BBO	HOMOLOGY MODEL FOR THE SPINACH CHLOROPLAST 50S SUBUNIT FITTED TO 9.4A CRYO-EM MAP OF THE 70S CHLORORIBOSOME	RIBOSOME
3BBP	RAB6-GTP:GCC185 RAB BINDING DOMAIN COMPLEX	PROTEIN TRANSPORT/SPLICING
3BC1	CRYSTAL STRUCTURE OF THE COMPLEX RAB27A-SLP2A	SIGNALING PROTEIN/TRANSPORT PROTEIN
3BCQ	RYSTAL STRUCTURE OF OXY-HEMOGLOBIN FROM BRYCON CEPHALUS	TRANSPORT PROTEIN/OXYGEN BINDING
3BDW	HUMAN CD94/NKG2A	IMMUNE SYSTEM RECEPTOR
3BEJ	STRUCTURE OF HUMAN FXR IN COMPLEX WITH MFA-1 AND CO-ACTIVATOR PEPTIDE	TRANSCRIPTION REGULATOR
3BEV	11MER STRUCTURE OF AN MHC CLASS I MOLECULE FROM B21 CHICKENS ILLUSTRATE PROMISCUOUS PEPTIDE BINDING	IMMUNE SYSTEM
3BG1	ARCHITECTURE OF A COAT FOR THE NUCLEAR PORE MEMBRANE	PROTEIN TRANSPORT, HYDROLASE
3BH7	CRYSTAL STRUCTURE OF THE RP2-ARL3 COMPLEX BOUND TO GDP-ALF4	SIGNALING PROTEIN
3BIN	STRUCTURE OF THE DAL-1 AND TSLC1 (372-383) COMPLEX	CELL ADHESION
3BJ1	MET-PERCH HEMOGLOBIN AT PH 5.7	OXYGEN BINDING
3BL2	CRYSTAL STRUCTURE OF M11, THE BCL-2 HOMOLOG OF MURINE GAMMA-HERPESVIRUS 68, COMPLEXED WITH MOUSE BECLIN1 (RESIDUES 106-124)	VIRAL PROTEIN/APOPTOSIS
3BLH	CRYSTAL STRUCTURE OF HUMAN CDK9/CYCLINT1	TRANSCRIPTION
3BLX	YEAST ISOCITRATE DEHYDROGENASE (APO FORM)	OXIDOREDUCTASE
3BO0	RIBOSOME-SECY COMPLEX	RIBOSOME
3BOM	CRYSTAL STRUCTURE OF TROUT HEMOGLOBIN AT 1.35 ANGSTROM RESOLUTION	OXYGEN STORAGE/TRANSPORT
3BOO	STRUCTURE OF THE C. BOTULINUM NEUROTOXIN SEROTYPE A WITH AN	TOXIN/TOXIN INHIBITOR

	INHIBITORY PEPTIDE BOUND	
3BP8	CRYSTAL STRUCTURE OF MLC/EIIB COMPLEX	TRANSCRIPTION
3BPQ	CRYSTAL STRUCTURE OF RELB-RELE ANTITOXIN-TOXIN COMPLEX FROM METHANOCOCCUS JANNASCHII	TOXIN
3BQO	CRYSTAL STRUCTURE OF TRF1 TRFH DOMAIN AND TIN2 PEPTIDE COMPLEX	DNA BINDING PROTEIN
3BRV	NEMO/IKKB ASSOCIATION DOMAIN STRUCTURE	TRANSFERASE/TRANSCRIPTION
3BS4	CRYSTAL STRUCTURE OF UNCHARACTERIZED PROTEIN PH0321 FROM PYROCOCCUS HORIKOSHII IN COMPLEX WITH AN UNKNOWN PEPTIDE	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
3BS5	CRYSTAL STRUCTURE OF HCNK2-SAM/DHYP-SAM COMPLEX	SIGNALING PROTEIN/MEMBRANE PROTEIN
3BTP	CRYSTAL STRUCTURE OF AGROBACTERIUM TUMEFACIENS VIRE2 IN COMPLEX WITH ITS CHAPERONE VIRE1: A NOVEL FOLD AND IMPLICATIONS FOR DNA BINDING	DNA BINDING PROTEIN, CHAPERONE
3BTS	CRYSTAL STRUCTURE OF A TERNARY COMPLEX OF THE TRANSCRIPTIONAL REPRESSOR GAL80P (GAL80S0 [G301R]) AND THE ACIDIC ACTIVATION DOMAIN OF GAL4P (AA 854-874) FROM SACCHAROMYCES CEREVISIAE WITH NAD	TRANSCRIPTION
3BU3	CRYSTAL STRUCTURE OF THE INSULIN RECEPTOR KINASE IN COMPLEX WITH IRS2 KRLB PEPTIDE	TRANSFERASE
3BU8	CRYSTAL STRUCTURE OF TRF2 TRFH DOMAIN AND TIN2 PEPTIDE COMPLEX	DNA BINDING PROTEIN
3BUX	CRYSTAL STRUCTURE OF C-CBL-TKB DOMAIN COMPLEXED WITH ITS BINDING MOTIF IN C-MET	LIGASE/SIGNALING PROTEIN
3BWU	CRYSTAL STRUCTURE OF THE TERNARY COMPLEX OF FIMD (N-TERMINAL DOMAIN, FIMDN) WITH FIMC AND THE N-TERMINALLY TRUNCATED PILUS SUBUNIT FIMF (FIMFT)	CHAPERONE, STRUCTURAL, MEMBRANE PROTEIN
3BX4	CRYSTAL STRUCTURE OF THE SNAKE VENOM TOXIN AGGRETIN	TOXIN
3BZI	MOLECULAR AND STRUCTURAL BASIS OF POLO-LIKE KINASE 1 SUBSTRATE RECOGNITION: IMPLICATIONS IN CENTROSOMAL LOCALIZATION	TRANSFERASE
3C01	CRYSTAL STRUCTURAL OF NATIVE SPAS C-TERMINAL DOMAIN	MEMBRANE PROTEIN, PROTEIN TRANSPORT
3C0T	STRUCTURE OF THE SCHIZOSACCHAROMYCES POMBE MEDIATOR SUBCOMPLEX MED8C/18	TRANSCRIPTION
3C1B	THE EFFECT OF H3 K79 DIMETHYLATION AND H4 K20 TRIMETHYLATION ON NUCLEOSOME AND CHROMATIN STRUCTURE	STRUCTURAL PROTEIN/DNA
3C2G	CRYSTAL COMPLEX OF SYS-1/POP-1 AT 2.5A RESOLUTION	CELL ADHESION/TRANSCRIPTION

3C3R	ALIX BRO1 CHMP4C COMPLEX	TRANSPORT PROTEIN
3C5I	CRYSTAL STRUCTURE OF PLASMODIUM KNOWLESI CHOLINE KINASE, PKH_134520	TRANSFERASE
3C5J	CRYSTAL STRUCTURE OF HLA DR52C	MEMBRANE PROTEIN
3C5T	RYSTAL STRUCTURE OF THE LIGAND-BOUND GLUCAGON-LIKE PEPTIDE-1 RECEPTOR EXTRACELLULAR DOMAIN	SIGNALING PROTEIN/SIGNALING PROTEIN
3C5W	OMPLEX BETWEEN PP2A-SPECIFIC METHYLESTERASE PME-1 AND PP2A CORE ENZYME	HYDROLASE
3C5X	CRYSTAL STRUCTURE OF THE PRECURSOR MEMBRANE PROTEIN-ENVELOPE PROTEIN HETERODIMER FROM THE DENGUE 2 VIRUS AT LOW PH	VIRAL PROTEIN
3C66	YEAST POLY(A) POLYMERASE IN COMPLEX WITH FIP1 RESIDUES 80-105	TRANSFERASE
3C7B	STRUCTURE OF THE DISSIMILATORY SULFITE REDUCTASE FROM ARCHAEOGLOBUS FULGIDUS	OXIDOREDUCTASE
3C7K	OLECULAR ARCHITECTURE OF GALPHAO AND THE STRUCTURAL BASIS FOR RGS16-MEDIATED DEACTIVATION	SIGNALING PROTEIN
3C94	EXOI/SSB-CT COMPLEX	HYDROLASE
3C9A	IGH RESOLUTION CRYSTAL STRUCTURE OF ARGOS BOUND TO THE EGF DOMAIN OF SPITZ	HORMONE/SIGNALING PROTEIN
3C9Q	CRYSTAL STRUCTURE OF THE UNCHARACTERIZED HUMAN PROTEIN C8ORF32 WITH BOUND PEPTIDE	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
3CB8	4FE-4S-PYRUVATE FORMATE-LYASE ACTIVATING ENZYME IN COMPLEX WITH ADOMET AND A PEPTIDE SUBSTRATE	OXIDOREDUCTASE
3CBL	RYSTAL STRUCTURE OF HUMAN FELINE SARCOMA VIRAL ONCOGENE HOMOLOGUE (V-FES) IN COMPLEX WITH STAUROSPORINE AND A CONSENSUS PEPTIDE	TRANSFERASE
3CC2	HE REFINED CRYSTAL STRUCTURE OF THE HALOARCULA MARISMORTUI LARGE RIBOSOMAL SUBUNIT AT 2.4 ANGSTROM RESOLUTION WITH RRNA SEQUENCE FOR THE 23S RRNA AND GENOME-DERIVED SEQUENCES FOR R-PROTEINS	RIBOSOME
3CC4	CO-CRYSTAL STRUCTURE OF ANISOMYCIN BOUND TO THE 50S RIBOSOMAL SUBUNIT	RIBOSOME
3CC7	STRUCTURE OF ANISOMYCIN RESISTANT 50S RIBOSOMAL SUBUNIT: 23S RRNA MUTATION C2487U	RIBOSOME
3CD6	CO-CYSTAL OF LARGE RIBOSOMAL SUBUNIT MUTANT G2616A WITH CC-PUROMYCIN	RIBOSOME

3CDK	CRYSTAL STRUCTURE OF THE CO-EXPRESSED SUCCINYL-COA TRANSFERASE A AND B COMPLEX FROM BACILLUS SUBTILIS	TRANSFERASE
3CDW	CRYSTAL STRUCTURE OF COXSACKIEVIRUS B3 RNA-DEPENDENT RNA POLYMERASE (3DPOL) IN COMPLEX WITH PROTEIN PRIMER VPG AND A PYROPHOSPHATE	TRANSFERASE/VIRAL PROTEIN
3CF4	STRUCTURE OF THE CODH COMPONENT OF THE M. BARKERI ACDS COMPLEX	OXIDOREDUCTASE
3CF5	THIOPEPTIDE ANTIBIOTIC THIOSTREPTON BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF DEINOCOCCUS RADIODURANS	RIBOSOME
3CFB	HIGH-RESOLUTION STRUCTURE OF BLUE FLUORESCENT ANTIBODY EP2-19G2 IN COMPLEX WITH STILBENE HAPTEN AT 100K	IMMUNE SYSTEM
3CFS	STRUCTURAL BASIS OF THE INTERACTION OF RBAP46/RBAP48 WITH HISTONE H4	HISTONE/CHAPERONE
3CHX	CRYSTAL STRUCTURE OF METHYLOSINUS TRICHOSPORIUM OB3B PARTICULATE METHANE MONOOXYGENASE (PMMO)	MEMBRANE PROTEIN
3CI0	THE CRYSTAL STRUCTURE OF THE GSPK-GSPI-GSPJ COMPLEX FROM ENTEROTOXIGENIC ESCHERICHIA COLI TYPE 2 SECRETION SYSTEM	PROTEIN TRANSPORT
3CIP	COMPLEX OF DICTYOSTELIUM DISCOIDEUM ACTIN WITH GELSOLIN	STRUCTURAL PROTEIN
3CJH	TIM8-TIM13 COMPLEX	PROTEIN TRANSPORT
3CJI	STRUCTURE OF SENECA VALLEY VIRUS-001	VIRUS
3CJS	MINIMAL RECOGNITION COMPLEX BETWEEN PRMA AND RIBOSOMAL PROTEIN L11	TRANSFERASE/RIBOSOMAL PROTEIN
3CK4	A HETEROSPECIFIC LEUCINE ZIPPER TETRAMER	PROTEIN BINDING
3CL3	CRYSTAL STRUCTURE OF A VFLIP-IKKGAMMA COMPLEX: INSIGHTS INTO VIRAL ACTIVATION OF THE IKK SIGNALOSOME	VIRAL PROTEIN/SIGNALING PROTEIN
3CLF	HIV NEUTRALIZING MONOCLONAL ANTIBODY YZ23	IMMUNE SYSTEM
3CLS	CRYSTAL STRUCTURE OF THE R236C MUTANT OF ETF FROM METHYLOPHILUS METHYLOTROPHUS	ELECTRON TRANSPORT
3CMA	THE STRUCTURE OF CCA AND CCA-PHE-CAP-BIO BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
3CME	THE STRUCTURE OF CA AND CCA-PHE-CAP-BIO BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
3CMO	HIV NEUTRALIZING MONOCLONAL ANTIBODY YZ18	IMMUNE SYSTEM
3CPT	MP1-P14 SCAFFOLDING COMPLEX	PROTEIN BINDING
3CQC	NUCLEOPORIN NUP107/NUP133 INTERACTION COMPLEX	PROTEIN TRANSPORT

3CQW	CRYSTAL STRUCTURE OF AKT-1 COMPLEXED WITH SUBSTRATE PEPTIDE AND INHIBITOR	TRANSFERASE
3CR3	STRUCTURE OF A TRANSIENT COMPLEX BETWEEN DHA-KINASE SUBUNITS DHAM AND DHAL FROM LACTOCOCCUS LACTIS	TRANSFERASE
3CRK	CRYSTAL STRUCTURE OF THE PDHK2-L2 COMPLEX.	TRANSFERASE
3CRP	A HETEROSPECIFIC LEUCINE ZIPPER TETRAMER	PROTEIN BINDING
3CUQ	INTEGRATED STRUCTURAL AND FUNCTIONAL MODEL OF THE HUMAN ESCRT-II COMPLEX	PROTEIN TRANSPORT
3CV0	STRUCTURE OF PEROXISOMAL TARGETING SIGNAL 1 (PTS1) BINDING DOMAIN OF TRYPANOSOMA BRUCEI PEROXIN 5 (TBPEX5)COMPLEXED TO T. BRUCEI PHOSPHOGLUCOISOMERASE (PGI) PTS1 PEPTIDE	TRANSPORT PROTEIN
3CWW	CRYSTAL STRUCTURE OF IDE-BRADYKININ COMPLEX	HYDROLASE
3CX8	CRYSTAL STRUCTURE OF PDZRHOGEF RGRGS DOMAIN IN A COMPLEX WITH GALPHA-13 BOUND TO GTP-GAMMA-S	SIGNALING PROTEIN
3CXB	CRYSTAL STRUCTURE OF SIFA AND SKIP	SIGNALING PROTEIN
3CYY	THE CRYSTAL STRUCTURE OF ZO-1 PDZ2 IN COMPLEX WITH THE CX43 PEPTIDE	PEPTIDE BINDING PROTEIN
3CZU	CRYSTAL STRUCTURE OF THE HUMAN EPHRIN A2- EPHRIN A1 COMPLEX	TRANSFERASE/SIGNALING PROTEIN
3D1K	R/T INTERMEDIATE QUATERNARY STRUCTURE OF AN ANTARCTIC FISH HEMOGLOBIN IN AN ALPHA(CO)-BETA(PENTACOORDINATE) STATE	OXYGEN BINDING
3D1M	CRYSTAL STRUCTURE OF SONIC HEDGEHOG BOUND TO THE THIRD FNIII DOMAIN OF CDO	SIGNALING PROTEIN / CELL ADHESION
3D24	CRYSTAL STRUCTURE OF LIGAND-BINDING DOMAIN OF ESTROGEN-RELATED RECEPTOR ALPHA (ERRALPHA) IN COMPLEX WITH THE PEROXISOME PROLIFERATORS-ACTIVATED RECEPTOR COACTIVATOR-1ALPHA BOX3 PEPTIDE (PGC-1ALPHA)	TRANSCRIPTION
3D2F	CRYSTAL STRUCTURE OF A COMPLEX OF SSE1P AND HSP70	CHAPERONE
3D31	MODBC FROM METHANOSARCINA ACETIVORANS	TRANSPORT PROTEIN
3D32	COMPLEX OF GABA(A) RECEPTOR-ASSOCIATED PROTEIN (GABARAP) WITH A SYNTHETIC PEPTIDE	TRANSPORT PROTEIN
3D3T	CRYSTAL STRUCTURE OF HIV-1 CRF01_AE IN COMPLEX WITH THE SUBSTRATE P1-P6	HYDROLASE
3D3X	CRYSTAL STRUCTURE OF BOTULINUM NEUROTOXIN SEROTYPE E CATALYTIC DOMAIN IN COMPLEX WITH SNAP-25 SUBSTRATE PEPTIDE	HYDROLASE
3D48	CRYSTAL STRUCTURE OF A PROLACTIN RECEPTOR ANTAGONIST BOUND	HORMONE/HORMONE RECEPTOR

	TO THE EXTRACELLULAR DOMAIN OF THE PROLACTIN RECEPTOR	
3D54	STUCTURE OF PURLQS FROM THERMOTOGA MARITIMA	LIGASE
3D5A	STRUCTURAL BASIS FOR TRANSLATION TERMINATION ON THE 70S RIBOSOME. THIS FILE CONTAINS THE 30S SUBUNIT, RELEASE FACTOR 1 (RF1), TWO TRNA, AND MRNA MOLECULES OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AS DESCRIBED IN REMARK 400.	RIBOSOME
3D5O	STRUCTURAL RECOGNITION AND FUNCTIONAL ACTIVATION OF FCRR BY INNATE PENTRAXINS	IMMUNE SYSTEM
3D8A	CO-CRYSTAL STRUCTURE OF TRAM-TRAD COMPLEX.	DNA BINDING PROTEIN
3D9A	HIGH RESOLUTION CRYSTAL STRUCTURE STRUCTURE OF HYHEL10 FAB COMPLEXED TO HEN EGG LYSOZYME	HYDROLASE/IMMUNE SYSTEM
3D9N	SNAPSHOTS OF THE RNA PROCESSING FACTOR SCAF8 BOUND TO DIFFERENT PHOSPHORYLATED FORMS OF THE CARBOXY-TERMINAL DOMAIN OF RNA-POLYMERASE II	TRANSCRIPTION
3D9T	CIAP1-BIR3 IN COMPLEX WITH N-TERMINAL PEPTIDE FROM CASPASE-9 (ATPFQE)	APOPTOSIS
3DAC	STRUCTURE OF THE HUMAN MDMX PROTEIN BOUND TO THE P53 TUMOR SUPPRESSOR TRANSACTIVATION DOMAIN	CELL CYCLE
3DBJ	ALLOPHYCOCYANIN FROM THERMOSYNECHOCOCCUS VULCANUS	PHOTOSYNTHESIS
3DBO	CRYSTAL STRUCTURE OF A MEMBER OF THE VAPBC FAMILY OF TOXIN-ANTITOXIN SYSTEMS, VAPBC-5, FROM MYCOBACTERIUM TUBERCULOSIS	TOXIN/ANTITOXIN
3DD2	RYSTAL STRUCTURE OF AN RNA APTAMER BOUND TO HUMAN THROMBIN	HYDROLASE/RNA
3DD7	STRUCTURE OF DOCH66Y IN COMPLEX WITH THE C-TERMINAL DOMAIN OF PHD	RIBOSOME INHIBITOR
3DDC	CRYSTAL STRUCTURE OF NORE1A IN COMPLEX WITH RAS	HYDROLASE/APOPTOSIS
3DEG	COMPLEX OF ELONGATING ESCHERICHIA COLI 70S RIBOSOME AND EF4(LEPA)-GMPPNP	RIBOSOME
3DEP	STRUCTURAL BASIS FOR SPECIFIC SUBSTRATE RECOGNITION BY THE CHLOROPLAST SIGNAL RECOGNITION PARTICLE PROTEIN CPSRP43	PROTEIN TRANSPORT, MEMBRANE PROTEIN
3DGP	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN TFB5 AND THE C-TERMINAL DOMAIN OF TFB2	TRANSCRIPTION
3DHW	CRYSTAL STRUCTURE OF METHIONINE IMPORTER METNI	MEMBRANE PROTEIN/HYDROLASE
3DIN	CRYSTAL STRUCTURE OF THE PROTEIN-TRANSLOCATION COMPLEX FORMED BY THE SECY CHANNEL AND THE SECA ATPASE	MEMBRANE PROTEIN, PROTEIN TRANSPORT
3DIW	C-TERMINAL BETA-CATENIN BOUND TIP-1 STRUCTURE	SIGNALING PROTEIN/CELL ADHESION

3DKT	CRYSTAL STRUCTURE OF THERMOTOGA MARITIMA ENCAPSULIN	STRUCTURAL PROTEIN/VIRUS LIKE PARTICLE
3DL8	STRUCTURE OF THE COMPLEX OF AQUIFEX AEOLICUS SECYEG AND BASCILLUS SUBTILIS SECA	PROTEIN TRANSPORT
3DLL	THE OXAZOLIDINONE ANTIBIOTICS PERTURB THE RIBOSOMAL PEPTIDYL-TRANSFERASE CENTER AND EFFECT TRNA POSITIONING	RIBOSOME
3DLQ	CRYSTAL STRUCTURE OF THE IL-22/IL-22R1 COMPLEX	CYTOKINE/CYTOKINE RECEPTOR
3DM1	YSTAL STRUCTURE OF THE COMPLEX OF HUMAN CHROMOBOX HOMOLOG 3 (CBX3) WITH PEPTIDE	TRANSCRIPTION
3DNJ	HE STRUCTURE OF THE CAULOBACTER CRESCENTUS CLPS PROTEASE ADAPTOR PROTEIN IN COMPLEX WITH A N-END RULE PEPTIDE	PEPTIDE BINDING PROTEIN
3DPL	STRUCTURAL INSIGHTS INTO NEDD8 ACTIVATION OF CULLIN-RING LIGASES: CONFORMATIONAL CONTROL OF CONJUGATION.	LIGASE
3DQB	CRYSTAL STRUCTURE OF THE ACTIVE G-PROTEIN-COUPLED RECEPTOR OPSIN IN COMPLEX WITH A C-TERMINAL PEPTIDE DERIVED FROM THE GALPHA SUBUNIT OF TRANSDUCIN	SIGNALING PROTEIN
3DRA	CANDIDA ALBICANS PROTEIN GERANYLGERANYLTRANSFERASE-I COMPLEXED WITH GGPP	TRANSFERASE
3DS4	HIV-1 CAPSID C-TERMINAL DOMAIN MUTANT (L211S) IN COMPLEX WITH AN INHIBITOR OF PARTICLE ASSEMBLY (CAI)	VIRAL PROTEIN
3DSF	CRYSTAL STRUCTURE OF ANTI-OSTEOPONTIN ANTIBODY 23C3 IN COMPLEX WITH W43A MUTATED EPITOPE PEPTIDE	IMMUNE SYSTEM
3DSS	CRYSTAL STRUCTURE OF RABGGTASE(DELTA LRR; DELTA IG)	TRANSFERASE
3DWG	CRYSTAL STRUCTURE OF A SULFUR CARRIER PROTEIN COMPLEX FOUND IN THE CYSTEINE BIOSYNTHETIC PATHWAY OF MYCOBACTERIUM TUBERCULOSIS	TRANSFERASE
3DWL	CRYSTAL STRUCTURE OF FISSION YEAST ARP2/3 COMPLEX LACKING THE ARP2 SUBUNIT	STRUCTURAL PROTEIN
3DXE	CRYSTAL STRUCTURE OF THE INTRACELLULAR DOMAIN OF HUMAN APP (T668A MUTANT) IN COMPLEX WITH FE65-PTB2	PROTEIN BINDING
3DXR	CRYSTAL STRUCTURE OF THE YEAST INTER-MEMBRANE SPACE CHAPERONE ASSEMBLY TIM9.10	PROTEIN TRANSPORT
3DZU	INTACT PPAR GAMMA - RXR ALPHA NUCLEAR RECEPTOR COMPLEX ON DNA BOUND WITH BVT.13, 9-CIS RETINOIC ACID AND NCOA2 PEPTIDE	TRANSCRIPTION/DNA
3DZY	INTACT PPAR GAMMA - RXR ALPHA NUCLEAR RECEPTOR COMPLEX ON DNA BOUND WITH ROSIGLITAZONE, 9-CIS RETINOIC ACID AND NCOA2 PEPTIDE	TRANSCRIPTION/DNA

3EO0	INTACT PPAR GAMMA - RXR ALPHA NUCLEAR RECEPTOR COMPLEX ON DNA BOUND WITH GW9662, 9-CIS RETINOIC ACID AND NCOA2 PEPTIDE	TRANSCRIPTION/DNA
3E0J	X-RAY STRUCTURE OF THE COMPLEX OF REGULATORY SUBUNITS OF HUMAN DNA POLYMERASE DELTA	TRANSFERASE
3E1K	CRYSTAL STRUCTURE OF KLUYVEROMYCES LACTIS GAL80P IN COMPLEX WITH THE ACIDIC ACTIVATION DOMAIN OF GAL4P	TRANSCRIPTION
3E1R	MIDBODY TARGETING OF THE ESCRT MACHINERY BY A NON-CANONICAL COILED-COIL IN CEP55	CELL CYCLE/TRANSPORT PROTEIN
3E5A	CRYSTAL STRUCTURE OF AURORA A IN COMPLEX WITH VX-680 AND TPX2	TRANSFERASE
3E7C	GLUCOCORTICOID RECEPTOR LBD BOUND TO GSK866	TRANSCRIPTION
3E9 5	CRYSTAL STRUCTURE OF THE PLASMODIUM FALCIPARUM UBIQUITIN CONJUGATING ENZYME COMPLEX, PFUBC13-PFUEV1A	LIGASE
3E9J	STRUCTURE OF THE CHARGE-TRANSFER INTERMEDIATE OF THE TRANSMEMBRANE REDOX CATALYST DSBB	OXIDOREDUCTASE
3EAB	CRYSTAL STRUCTURE OF SPASTIN MIT IN COMPLEX WITH ESCRT III	CELL CYCLE
3ECH	THE MARR-FAMILY REPRESSOR MEXR IN COMPLEX WITH ITS ANTIREPRESSOR ARMR	TRANSCRIPTION, TRANSCRIPTION REGULATION
3EJ9	STRUCTURAL AND MECHANISTIC ANALYSIS OF TRANS-3-CHLOROACRYLIC ACID DEHALOGENASE ACTIVITY	HYDROLASE
3EJB	CRYSTAL STRUCTURE OF P450BIOI IN COMPLEX WITH TETRADECANOIC ACID LIGATED ACYL CARRIER PROTEIN	OXIDOREDUCTASE/LIPID TRANSPORT
3EJJ	STRUCTURE OF M-CSF BOUND TO THE FIRST THREE DOMAINS OF FMS	CYTOKINE/SIGNALING PROTEIN
3ENH	CRYSTAL STRUCTURE OF CGI121/BUD32/KAE1 COMPLEX	HYDROLASE/UNKNOWN FUNCTION
3ENO	CRYSTAL STRUCTURE OF PYROCOCCUS FURIOSUS PCC1 IN COMPLEX WITH THERMOPLASMA ACIDOPHILUM KAE1	HYDROLASE/UNKNOWN FUNCTION
3EO0	STRUCTURE OF THE TRANSFORMING GROWTH FACTOR-BETA NEUTRALIZING ANTIBODY GC-1008	IMMUNE SYSTEM
3EOY	STRUCTURE OF REOVIRUS SIGMA1 IN COMPLEX WITH ITS RECEPTOR JUNCTIONAL ADHESION MOLECULE-A	VIRAL PROTEIN/CELL ADHESION
3ERY	DIFFERENT THERMODYNAMIC BINDING MECHANISMS AND PEPTIDE FINE SPECIFICITIES ASSOCIATED WITH A PANEL OF STRUCTURALLY SIMILAR HIGH-AFFINITY T CELL RECEPTORS	IMMUNE SYSTEM
3EWE	CRYSTAL STRUCTURE OF THE NUP85/SEH1 COMPLEX	PROTEIN TRANSPORT,STRUCTURAL PROTEIN

3EX7	THE CRYSTAL STRUCTURE OF EJC IN ITS TRANSITION STATE	HYDROLASE/RNA BINDING PROTEIN/RNA
3EXE	CRYSTAL STRUCTURE OF THE PYRUVATE DEHYDROGENASE (E1P) COMPONENT OF HUMAN PYRUVATE DEHYDROGENASE COMPLEX	OXIDOREDUCTASE
3EZQ	CRYSTAL STRUCTURE OF THE FAS/FADD DEATH DOMAIN COMPLEX	APOPTOSIS
3F1E	CRYSTAL STRUCTURE OF A TRANSLATION TERMINATION COMPLEX FORMED WITH RELEASE FACTOR RF2. THIS FILE CONTAINS THE 30S SUBUNIT, RF2, TWO TRNA, AND MRNA MOLECULES OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AS DESCRIBED IN REMARK 400.	RIBOSOME
3F2K	TRUCTURE OF THE TRANSPOSASE DOMAIN OF HUMAN HISTONE-LYSINE N-METHYLTRANSFERASE SETMAR	TRANSFERASE
3F2O	CRYSTAL STRUCTURE OF HUMAN SPLA/RYANODINE RECEPTOR DOMAIN AND SOCS BOX CONTAINING 1 (SPSB1) IN COMPLEX WITH A 20-RESIDUE VASA PEPTIDE	APOPTOSIS/HYDROLASE
3F6Q	CRYSTAL STRUCTURE OF INTEGRIN-LINKED KINASE ANKYRIN REPEAT DOMAIN IN COMPLEX WITH PINCH1 LIM1 DOMAIN	SIGNALING PROTEIN/SIGNALING PROTEIN
3F6U	CRYSTAL STRUCTURE OF HUMAN ACTIVATED PROTEIN C (APC) COMPLEXED WITH PPACK	HYDROLASE
3F75	ACTIVATED TOXOPLASMA GONDII CATHEPSIN L (TGCPL) IN COMPLEX WITH ITS PROPEPTIDE	HYDROLASE
3F9X	STRUCTURAL INSIGHTS INTO LYSINE MULTIPLE METHYLATION BY SET DOMAIN METHYLTRANSFERASES, SET8-Y334F / H4-LYS20ME2 / ADOHCY	TRANSFERASE
3FAP	ATOMIC STRUCTURES OF THE RAPAMYCIN ANALOGS IN COMPLEX WITH BOTH HUMAN FKBP12 AND FRB DOMAIN OF FRAP	CELL CYCLE
3FBI	STRUCTURE OF THE MEDIATOR SUBMODULE MED7N/31	TRANSCRIPTION
3FDO	STRUCTURE OF HUMAN MDMX IN COMPLEX WITH HIGH AFFINITY PEPTIDE	CELL CYCLE
3FIV	CRYSTAL STRUCTURE OF FELINE IMMUNODEFICIENCY VIRUS PROTEASE COMPLEXED WITH A SUBSTRATE	COMPLEX (ACID PROTEINASE/SUBSTRATE)
3GTU	LIGAND-FREE HETERODIMERIC HUMAN GLUTATHIONE S-TRANSFERASE M2-3 (EC 2.5.1.18), MONOCLINIC CRYSTAL FORM	TRANSFERASE
3PCC	TRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 4-HYDROXYBENZOATE	DIOXYGENASE
3PRO	ALPHA-LYTIC PROTEASE COMPLEXED WITH C-TERMINAL TRUNCATED PRO REGION	PRO REGION
3RUB	CRYSTAL STRUCTURE OF THE UNACTIVATED FORM OF RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE(SLASH)OXYGENASE FROM TOBACCO	LYASE(CARBON-CARBON)

	REFINED AT 2.0-ANGSTROMS RESOLUTION	
3YGS	APAF-1 CARD IN COMPLEX WITH PRODOMAIN OF PROCASPASE-9	APOPTOSIS
43C9	CRYSTALLOGRAPHIC STRUCTURE OF THE ESTEROLYTIC AND AMIDOLYTIC 43C9 ANTIBODY	IMMUNOGLOBULIN
4SGA	STRUCTURES OF PRODUCT AND INHIBITOR COMPLEXES OF STREPTOMYCES GRISEUS PROTEASE A AT 1.8 ANGSTROMS RESOLUTION. A MODEL FOR SERINE PROTEASE CATALYSIS	HYDROLASE (SERINE PROTEINASE)
4UBP	STRUCTURE OF BACILLUS PASTEURII UREASE INHIBITED WITH ACETOHYDROXAMIC ACID AT 1.55 A RESOLUTION	HYDROLASE
5AP R	STRUCTURES OF COMPLEXES OF RHIZOPUSPEPSIN WITH PEPSTATIN AND OTHER STATINE-CONTAINING INHIBITORS	HYDROLASE (ACID PROTEINASE)
6RLX	X-RAY STRUCTURE OF HUMAN RELAXIN AT 1.5 ANGSTROMS. COMPARISON TO INSULIN AND IMPLICATIONS FOR RECEPTOR BINDING DETERMINANTS	HORMONE(MUSCLE RELAXANT)
8PCH	CRYSTAL STRUCTURE OF PORCINE CATHEPSIN H DETERMINED AT 2.1 ANGSTROM RESOLUTION: LOCATION OF THE MINI-CHAIN C-TERMINAL CARBOXYL GROUP DEFINES CATHEPSIN H AMINOPEPTIDASE FUNCTION	HYDROLASE
8RUC	ACTIVATED SPINACH RUBISCO COMPLEXED WITH 2-CARBOXYARABINITOL BISPHOSPHATE	LYASE (CARBON-CARBON)
8TLN	TRUCTURAL COMPARISON SUGGESTS THAT THERMOLYSIN AND RELATED NEUTRAL PROTEASES UNDERGO HINGE-BENDING MOTION DURING CATALYSIS	HYDROLASE(METALLOPROTEINASE)

Table S2. Full dataset of HIPP interactions

PDB Code	Title	Classification
10GS	HUMAN GLUTATHIONE S-TRANSFERASE P1-1, COMPLEX WITH TER117	COMPLEX (TRANSFERASE/INHIBITOR)
1A00	HEMOGLOBIN (VAL BETA1 MET, TRP BETA37 TYR) MUTANT	OXYGEN TRANSPORT
1A01	HEMOGLOBIN (VAL BETA1 MET, TRP BETA37 ALA) MUTANT	OXYGEN TRANSPORT
1A02	STRUCTURE OF THE DNA BINDING DOMAINS OF NFAT, FOS AND JUN BOUND TO DNA	TRANSCRIPTION/DNA
1A07	C-SRC (SH2 DOMAIN) COMPLEXED WITH ACE-MALONYL TYR-GLU-(N,N-DIPENTYL AMINE)	COMPLEX (TRANSFERASE/PEPTIDE)
1A08	C-SRC (SH2 DOMAIN) COMPLEXED WITH ACE-DIFLUORO PHOSPHOTYR-GLU-(N,N-DIPENTYL AMINE)	COMPLEX (TRANSFERASE/PEPTIDE)
1A09	C-SRC (SH2 DOMAIN) COMPLEXED WITH ACE-FORMYL PHOSPHOTYR-GLU-(N,N-DIPENTYL AMINE)	COMPLEX (TRANSFERASE/PEPTIDE)
1A1A	C-SRC (SH2 DOMAIN WITH C188A MUTATION) COMPLEXED WITH ACE-FORMYL PHOSPHOTYR-GLU-(N,N-DIPENTYL AMINE)	COMPLEX (TRANSFERASE/PEPTIDE)
1A1B	C-SRC (SH2 DOMAIN) COMPLEXED WITH ACE-PHOSPHOTYR-GLU-(N,N-DIPENTYL AMINE)	COMPLEX (TRANSFERASE/PEPTIDE)
1A1C	C-SRC (SH2 DOMAIN) COMPLEXED WITH ACE-PHOSPHOTYR-GLU-(N-ME(-(CH2)3-CYCLOPENTYL))	COMPLEX (TRANSFERASE/PEPTIDE)
1A1E	C-SRC (SH2 DOMAIN) COMPLEXED WITH ACE-PHOSPHOTYR-GLU-(3-BUTYLPIPERIDINE)	COMPLEX (TRANSFERASE/PEPTIDE)
1A1M	MHC CLASS I MOLECULE B*5301 COMPLEXED WITH PEPTIDE TPYDINQML FROM GAG PROTEIN OF HIV2	COMPLEX (ANTIGEN/PEPTIDE)
1A1N	MHC CLASS I MOLECULE B*3501 COMPLEXED WITH PEPTIDE VPLRPMTY FROM THE NEF PROTEIN (75-82) OF HIV1	COMPLEX (ANTIGEN/PEPTIDE)
1A1O	MHC CLASS I MOLECULE B*5301 COMPLEXED WITH PEPTIDE LS6 (KPIVQYDNF) FROM THE MALARIA PARASITE P. FALCIPARUM	COMPLEX (ANTIGEN/PEPTIDE)
1A1R	HCV NS3 PROTEASE DOMAIN:NS4A PEPTIDE COMPLEX	VIRAL PROTEIN
1A22	HUMAN GROWTH HORMONE BOUND TO SINGLE RECEPTOR	COMPLEX (HORMONE/RECEPTOR)
1A2C	STRUCTURE OF THROMBIN INHIBITED BY AERUGINOSIN298-A FROM A BLUE-GREEN ALGA	COMPLEX (SERINE PROTEASE/INHIBITOR)
1A2K	GDPRAN-NTF2 COMPLEX	COMPLEX (TRANSPORT/NUCLEAR PROTEIN)
1A2X	COMPLEX OF TROPONIN C WITH A 47 RESIDUE (1-47) FRAGMENT OF TROPONIN I	COMPLEX (SKELETAL MUSCLE/MUSCLE PROTEIN)
1A2Y	HEN EGG WHITE LYSOZYME, D18A MUTANT, IN COMPLEX WITH MOUSE MONOCLONAL ANTIBODY D1.3	COMPLEX (IMMUNOGLOBULIN/HYDROLASE)

1A30	HIV-1 PROTEASE COMPLEXED WITH A TRIPEPTIDE INHIBITOR	COMPLEX (ASPARTIC PROTEASE/INHIBITOR)
1A37	14-3-3 PROTEIN ZETA BOUND TO PS-RAF259 PEPTIDE	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)
1A38	14-3-3 PROTEIN ZETA BOUND TO R18 PEPTIDE	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)
1A3B	COMPLEX OF HUMAN ALPHA-THROMBIN WITH THE BIFUNCTIONAL BORONATE INHIBITOR BOROLOG1	COMPLEX (SERINE PROTEASE/INHIBITOR)
1A3E	COMPLEX OF HUMAN ALPHA-THROMBIN WITH THE BIFUNCTIONAL BORONATE INHIBITOR BOROLOG2	COMPLEX (SERINE PROTEASE/INHIBITOR)
1A3L	CATALYSIS OF A DISFAVORED REACTION: AN ANTIBODY EXO DIELS-ALDERASE-TSA-INHIBITOR COMPLEX AT 1.95 A RESOLUTION	IMMUNOGLOBULIN
1A3N	DEOXY HUMAN HEMOGLOBIN	OXYGEN TRANSPORT
1A3O	ARTIFICIAL MUTANT (ALPHA Y42H) OF DEOXY HEMOGLOBIN	OXYGEN TRANSPORT
1A3R	FAB FRAGMENT (ANTIBODY 8F5) COMPLEXED WITH PEPTIDE FROM HUMAN RHINOVIRUS (SEROTYPE 2) VIRAL CAPSID PROTEIN VP2 (RESIDUES 156-170)	VIRAL PROTEIN/IMMUNE SYSTEM
1A46	THROMBIN COMPLEXED WITH HIRUGEN AND A BETA-STRAND MIMETIC INHIBITOR	COMPLEX (SERINE PROTEASE/INHIBITOR)
1A4F	BAR-HEADED GOOSE HEMOGLOBIN (OXY FORM)	OXYGEN TRANSPORT
1A4J	DIELS ALDER CATALYTIC ANTIBODY GERMLINE PRECURSOR	IMMUNOGLOBULIN
1A4K	DIELS ALDER CATALYTIC ANTIBODY WITH TRANSITION STATE ANALOGUE	IMMUNOGLOBULIN
1A4W	CRYSTAL STRUCTURES OF THROMBIN WITH THIAZOLE-CONTAINING INHIBITORS: PROBES OF THE S1' BINDING SITE	COMPLEX (SERINE PROTEASE/INHIBITORS)
1A4Y	RIBONUCLEASE INHIBITOR-ANGIOGENIN COMPLEX	COMPLEX (INHIBITOR/NUCLEASE)
1A5A	CRYO-CRYSTALLOGRAPHY OF A TRUE SUBSTRATE, INDOLE-3-GLYCEROL PHOSPHATE, BOUND TO A MUTANT (ALPHAD60N) TRYPTOPHAN SYNTHASE ALPHA2BETA2 COMPLEX REVEALS THE CORRECT ORIENTATION OF ACTIVE SITE ALPHA GLU 49	LYASE
1A5B	CRYO-CRYSTALLOGRAPHY OF A TRUE SUBSTRATE, INDOLE-3-GLYCEROL PHOSPHATE, BOUND TO A MUTANT (ALPHA D60N) TRYPTOPHAN SYNTHASE ALPHA2BETA2 COMPLEX REVEALS THE CORRECT ORIENTATION OF ACTIVE SITE ALPHA GLU 49	LYASE
1A5F	FAB FRAGMENT OF A MONOCLONAL ANTI-E-SELECTIN ANTIBODY	IMMUNOGLOBULIN
1A5G	HUMAN THROMBIN COMPLEXED WITH NOVEL SYNTHETIC PEPTIDE MIMETIC INHIBITOR AND HIRUGEN	COMPLEX (SERINE PROTEASE/INHIBITOR)
1A5K	K217E VARIANT OF KLEBSIELLA AEROGENES UREASE	HYDROLASE

1A5L	K217C VARIANT OF KLEBSIELLA AEROGENES UREASE	HYDROLASE
1A5M	K217A VARIANT OF KLEBSIELLA AEROGENES UREASE	HYDROLASE
1A5N	K217A VARIANT OF KLEBSIELLA AEROGENES UREASE, CHEMICALLY RESCUED BY FORMATE AND NICKEL	HYDROLASE
1A5O	K217C VARIANT OF KLEBSIELLA AEROGENES UREASE, CHEMICALLY RESCUED BY FORMATE AND NICKEL	HYDROLASE
1A5S	CRYSTAL STRUCTURE OF WILD-TYPE TRYPTOPHAN SYNTHASE COMPLEXED WITH 5-FLUOROINDOLE PROPANOL PHOSPHATE AND L-SER BOUND AS AMINO ACRYLATE TO THE BETA SITE	COMPLEX (LYASE/INHIBITOR)
1A61	THROMBIN COMPLEXED WITH A BETA-MIMETIC THIAZOLE-CONTAINING INHIBITOR	COMPLEX (SERINE PROTEASE/INHIBITOR)
1A6A	THE STRUCTURE OF AN INTERMEDIATE IN CLASS II MHC MATURATION: CLIP BOUND TO HLA-DR3	COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN)
1A6D	THERMOSOME FROM T. ACIDOPHILUM	CHAPERONIN
1A6E	THERMOSOME-MG-ADP-ALF3 COMPLEX	CHAPERONIN
1A6T	FAB FRAGMENT OF MAB1-IA MONOCLONAL ANTIBODY TO HUMAN RHINOVIRUS 14 NIM-IA SITE	IMMUNOGLOBULIN
1A6Z	HFE (HUMAN) HEMOCHROMATOSIS PROTEIN	MHC CLASS I COMPLEX
1A81	CRYSTAL STRUCTURE OF THE TANDEM SH2 DOMAIN OF THE SYK KINASE BOUND TO A DUALLY TYROSINE-PHOSPHORYLATED ITAM	COMPLEX (TRANSFERASE/PEPTIDE)
1A8G	HIV-1 PROTEASE IN COMPLEX WITH SDZ283-910	COMPLEX (ACID PROTEINASE/INHIBITOR)
1A8K	CRYSTALLOGRAPHIC ANALYSIS OF HUMAN IMMUNODEFICIENCY VIRUS 1 PROTEASE WITH AN ANALOG OF THE CONSERVED CA-P2 SUBSTRATE: INTERACTIONS WITH FREQUENTLY OCCURRING GLUTAMIC ACID RESIDUE AT P2' POSITION OF SUBSTRATES	COMPLEX (ASPARTYL PROTEASE/PEPTIDE)
1A93	NMR SOLUTION STRUCTURE OF THE C-MYC-MAX HETERODIMERIC LEUCINE ZIPPER, NMR, MINIMIZED AVERAGE STRUCTURE	LEUCINE ZIPPER
1A94	STRUCTURAL BASIS FOR SPECIFICITY OF RETROVIRAL PROTEASES	COMPLEX (ASPARTYL PROTEASE/PEPTIDE)
1A9B	DECAMER-LIKE CONFORMATION OF A NANO-PEPTIDE BOUND TO HLA-B3501 DUE TO NONSTANDARD POSITIONING OF THE C-TERMINUS	COMPLEX (MHC CLASS I/PEPTIDE)
1A9E	DECAMER-LIKE CONFORMATION OF A NANO-PEPTIDE BOUND TO HLA-B3501 DUE TO NONSTANDARD POSITIONING OF THE C-TERMINUS	COMPLEX (MHC CLASS I/PEPTIDE)
1A9N	CRYSTAL STRUCTURE OF THE SPLICEOSOMAL U2B''-U2A' PROTEIN COMPLEX BOUND TO A FRAGMENT OF U2 SMALL NUCLEAR RNA	RNA BINDING PROTEIN/RNA
1A9X	CARBAMOYL PHOSPHATE SYNTHETASE: CAUGHT IN THE ACT OF	AMIDOTRANSFERASE

	GLUTAMINE HYDROLYSIS	
1AA1	ACTIVATED SPINACH RUBISCO IN COMPLEX WITH THE PRODUCT 3-PHOSPHOGLYCERATE	OXIDOREDUCTASE
1AB9	CRYSTAL STRUCTURE OF BOVINE GAMMA-CHYMOTRYPSIN	COMPLEX (SERINE PROTEASE/PEPTIDE)
1ABI	STRUCTURE OF THE HIRULOG 3-THROMBIN COMPLEX AND NATURE OF THE S' SUBSITES OF SUBSTRATES AND INHIBITORS	HYDROLASE(SERINE PROTEINASE)
1ABJ	STRUCTURE OF THE HIRULOG 3-THROMBIN COMPLEX AND NATURE OF THE S' SUBSITES OF SUBSTRATES AND INHIBITORS	HYDROLASE(SERINE PROTEINASE)
1ABR	CRYSTAL STRUCTURE OF ABRIN-A	COMPLEX (GLYCOSIDASE/CARBOHYDRATE)
1ABW	DEOXY RHB1.1 (RECOMBINANT HEMOGLOBIN)	COMPLEX (OXYGEN TRANSPORT/PEPTIDE)
1ABY	CYANOMET RHB1.1 (RECOMBINANT HEMOGLOBIN)	OXYGEN TRANSPORT
1ACB	CRYSTAL AND MOLECULAR STRUCTURE OF THE BOVINE ALPHA-CHYMOTRYPSIN-EGLIN C COMPLEX AT 2.0 ANGSTROMS RESOLUTION	HYDROLASE(SERINE PROTEASE)
1ACM	ARGININE 54 IN THE ACTIVE SITE OF ESCHERICHIA COLI ASPARTATE TRANSCARBAMOYLASE IS CRITICAL FOR CATALYSIS: A SITE-SPECIFIC MUTAGENESIS, NMR AND X-RAY CRYSTALLOGRAPHY STUDY	TRANSFERASE (CARBAMOYL-P,ASPARTATE)
1ACY	CRYSTAL STRUCTURE OF THE PRINCIPAL NEUTRALIZING SITE OF HIV-1	COMPLEX(ANTIBODY/HIV-1 FRAGMENT)
1AD0	AB FRAGMENT OF ENGINEERED HUMAN MONOCLONAL ANTIBODY A5B7	IMMUNOGLOBULIN
1AD8	COMPLEX OF THROMBIN WITH AND INHIBITOR CONTAINING A NOVEL P1 MOIETY	COMPLEX (SERINE PROTEASE/INHIBITOR)
1AD9	GG-FAB FRAGMENT OF ENGINEERED HUMAN MONOCLONAL ANTIBODY CTM01	IMMUNOGLOBULIN
1ADQ	CRYSTAL STRUCTURE OF A HUMAN IGM RHEUMATOID FACTOR FAB IN COMPLEX WITH ITS AUTOANTIGEN IGG FC	COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN)
1AE6	IGG-FAB FRAGMENT OF MOUSE MONOCLONAL ANTIBODY CTM01	IMMUNOGLOBULIN
1AF0	SERRATIA PROTEASE IN COMPLEX WITH INHIBITOR	COMPLEX (METALLOPROTEASE/INHIBITOR)
1AFQ	RYSTAL STRUCTURE OF BOVINE GAMMA-CHYMOTRYPSIN COMPLEXED WITH A SYNTHETIC INHIBITOR	COMPLEX (SERINE PROTEASE/INHIBITOR)
1AFV	HIV-1 CAPSID PROTEIN (P24) COMPLEX WITH FAB25.3	VIRAL PROTEIN/IMMUNE SYSTEM
1AGB	ANTAGONIST HIV-1 GAG PEPTIDES INDUCE STRUCTURAL CHANGES IN HLA B8-HIV-1 GAG PEPTIDE (GGRKKYKL-3R MUTATION)	HISTOCOMPATIBILITY COMPLEX
1AGC	ANTAGONIST HIV-1 GAG PEPTIDES INDUCE STRUCTURAL CHANGES IN HLA B8-HIV-1 GAG PEPTIDE (GGKKKYQL-7Q MUTATION)	HISTOCOMPATIBILITY COMPLEX

1AGD	ANTAGONIST HIV-1 GAG PEPTIDES INDUCE STRUCTURAL CHANGES IN HLA B8-HIV-1 GAG PEPTIDE (GGKKKYKL-INDEX PEPTIDE)	HISTOCOMPATIBILITY COMPLEX
1AGF	ANTAGONIST HIV-1 GAG PEPTIDES INDUCE STRUCTURAL CHANGES IN HLA B8-HIV-1 GAG PEPTIDE (GGKKRYKL-5R MUTATION)	HISTOCOMPATIBILITY COMPLEX
1AGR	COMPLEX OF ALF4-ACTIVATED GI-ALPHA-1 WITH RGS4	COMPLEX (SIGNAL TRANSDUCTION/REGULATOR)
1AHG	ASPARTATE AMINOTRANSFERASE HEXAMUTANT	TRANSFERASE (AMINOTRANSFERASE)
1AHJ	NITRILE HYDRATASE	LYASE
1AHW	A COMPLEX OF EXTRACELLULAR DOMAIN OF TISSUE FACTOR WITH AN INHIBITORY FAB (5G9)	COMPLEX (IMMUNOGLOBULIN/TISSUE FACTOR)
1AI1	HIV-1 V3 LOOP MIMIC	COMPLEX (ANTIBODY/PEPTIDE)
1AI4	PENICILLIN ACYLASE COMPLEXED WITH 3,4-DIHYDROXYPHENYLACETIC ACID	ANTIBIOTIC RESISTANCE
1AI5	PENICILLIN ACYLASE COMPLEXED WITH M-NITROPHENYLACETIC ACID	ANTIBIOTIC RESISTANCE
1AI6	PENICILLIN ACYLASE WITH P-HYDROXYPHENYLACETIC ACID	ANTIBIOTIC RESISTANCE
1AI7	PENICILLIN ACYLASE COMPLEXED WITH PHENOL	ANTIBIOTIC RESISTANCE
1AI8	HUMAN ALPHA-THROMBIN TERNARY COMPLEX WITH THE EXOSITE INHIBITOR HIRUGEN AND ACTIVE SITE INHIBITOR PHCH2OCO-D-DPA-PRO-BOROMPG	COMPLEX (BLOOD COAGULATION/INHIBITOR)
1AIF	ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A) FAB FROM MOUSE	IMMUNOGLOBULIN
1AIG	OTOSYNTHETIC REACTION CENTER FROM RHODOBACTER SPHAEROIDES IN THE D+QB-CHARGE SEPARATED STATE	PHOTOSYNTHETIC REACTION CENTER
1AIJ	OTOSYNTHETIC REACTION CENTER FROM RHODOBACTER SPHAEROIDES IN THE CHARGE-NEUTRAL DQAQB STATE	PHOTOSYNTHETIC REACTION CENTER
1AIK	HIV GP41 CORE STRUCTURE	VIRAL PROTEIN
1AIP	EF-TU EF-TS COMPLEX FROM THERMUS THERMOPHILUS	COMPLEX OF TWO ELONGATION FACTORS
1AIX	HUMAN ALPHA-THROMBIN TERNARY COMPLEX WITH EXOSITE INHIBITOR HIRUGEN AND ACTIVE SITE INHIBITOR PHCH2OCO-D-DPA-PRO-BOROVAL	COMPLEX (BLOOD COAGULATION/INHIBITOR)
1AJ9	R-STATE HUMAN CARBONMONOXYHEMOGLOBIN ALPHA-A53S	OXYGEN TRANSPORT
1AJP	PENICILLIN ACYLASE COMPLEXED WITH 2,5-DIHYDROXYPHENYLACETIC ACID	ANTIBIOTIC RESISTANCE
1AJQ	PENICILLIN ACYLASE COMPLEXED WITH THIOPHENEACETIC ACID	ANTIBIOTIC RESISTANCE
1AJS	REFINEMENT AND COMPARISON OF THE CRYSTAL STRUCTURES OF PIG	AMINOTRANSFERASE

	CYTOSOLIC ASPARTATE AMINOTRANSFERASE AND ITS COMPLEX WITH 2-METHYLASPARTATE	
1AK4	HUMAN CYCLOPHILIN A BOUND TO THE AMINO-TERMINAL DOMAIN OF HIV-1 CAPSID	VIRAL PROTEIN/ISOMERASE
1AKJ	COMPLEX OF THE HUMAN MHC CLASS I GLYCOPROTEIN HLA-A2 AND THE T CELL CORECEPTOR CD8	COMPLEX (MHC I/PEPTIDE/CD8)
1AKS	CRYSTAL STRUCTURE OF THE FIRST ACTIVE AUTOLYSATE FORM OF THE PORCINE ALPHA TRYPSIN	SERINE PROTEASE
1AL0	PROCAPSID OF BACTERIOPHAGE PHIX174	VIRUS
1ALL	ALLOPHYCOCYANIN	LIGHT-HARVESTING PROTEIN
1AM4	COMPLEX BETWEEN CDC42HS.GMPPNP AND P50 RHOGAP (H. SAPIENS)	COMPLEX (GTPASE-ACTIVATING/GTP-BINDING)
1AO7	COMPLEX BETWEEN HUMAN T-CELL RECEPTOR, VIRAL PEPTIDE (TAX), AND HLA-A 0201	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1AOI	COMPLEX BETWEEN NUCLEOSOME CORE PARTICLE (H3,H4,H2A,H2B) AND 146 BP LONG DNA FRAGMENT	DNA BINDING PROTEIN/DNA
1AOK	VIPOXIN COMPLEX	HYDROLASE
1AON	CRYSTAL STRUCTURE OF THE ASYMMETRIC CHAPERONIN COMPLEX GROEL/GROES/(ADP)7	COMPLEX (GROEL/GROES)
1AOT	NMR STRUCTURE OF THE FYN SH2 DOMAIN COMPLEXED WITH A PHOSPHOTYROSYL PEPTIDE, MINIMIZED AVERAGE STRUCTURE	COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN)
1AP2	SINGLE CHAIN FV OF C219	IMMUNOGLOBULIN
1APH	CONFORMATIONAL CHANGES IN CUBIC INSULIN CRYSTALS IN THE PH RANGE 7-11	HORMONE
1APM	2.0 ANGSTROM REFINED CRYSTAL STRUCTURE OF THE CATALYTIC SUBUNIT OF CAMP-DEPENDENT PROTEIN KINASE COMPLEXED WITH A PEPTIDE INHIBITOR AND DETERGENT	TRANSFERASE(PHOSPHOTRANSFERASE)
1APV	CRYSTALLOGRAPHIC ANALYSIS OF TRANSITION STATE MIMICS BOUND TO PENICILLOPEPSIN: DIFLUOROSTATINE-AND DIFLUOROSTATONE-CONTAINING PEPTIDES	HYDROLASE(ACID PROTEINASE)
1APY	HUMAN ASPARTYLGLUCOSAMINIDASE	HYDROLASE
1APZ	JMAN ASPARTYLGLUCOSAMINIDASE COMPLEX WITH REACTION PRODUCT	COMPLEX (HYDROLASE/PEPTIDE)
1AQD	HLA-DR1 (DRA, DRB1 0101) HUMAN CLASS II HISTOCOMPATIBILITY PROTEIN (EXTRACELLULAR DOMAIN) COMPLEXED WITH ENDOGENOUS PEPTIDE	COMPLEX (MHC PROTEIN/ANTIGEN)
1AQK	THREE-DIMENSIONAL STRUCTURE OF A HUMAN FAB WITH HIGH AFFINITY FOR TETANUS TOXOID	IMMUNOGLOBULIN

1AQV	GLUTATHIONE S-TRANSFERASE IN COMPLEX WITH P-BROMOBENZYLGLUTATHIONE	COMPLEX (TRANSFERASE/PEPTIDE)
1AQW	GLUTATHIONE S-TRANSFERASE IN COMPLEX WITH GLUTATHIONE	TRANSFERASE
1AQX	GLUTATHIONE S-TRANSFERASE IN COMPLEX WITH MEISENHEIMER COMPLEX	TRANSFERASE
1AR1	STRUCTURE AT 2.7 ANGSTROM RESOLUTION OF THE PARACOCCUS DENITRIFICANS TWO-SUBUNIT CYTOCHROME C OXIDASE COMPLEXED WITH AN ANTIBODY FV FRAGMENT	COMPLEX (OXIDOREDUCTASE/ANTIBODY)
1ARO	T7 RNA POLYMERASE COMPLEXED WITH T7 LYSOZYME	COMPLEX (POLYMERASE/HYDROLASE)
1AS4	CLEAVED ANTICHYMOTRYPSIN A349R	SERPIN
1AT1	CRYSTAL STRUCTURES OF PHOSPHONOACETAMIDE LIGATED T AND PHOSPHONOACETAMIDE AND MALONATE LIGATED R STATES OF ASPARTATE CARBAMOYLTRANSFERASE AT 2.8-ANGSTROMS RESOLUTION AND NEUTRAL P*H	TRANSFERASE (CARBAMOYL-P,ASPARTATE)
1ATI	CRYSTAL STRUCTURE OF GLYCYL-TRNA SYNTHETASE FROM THERMUS THERMOPHILUS	PROTEIN BIOSYNTHESIS
1AUI	HUMAN CALCINEURIN HETERODIMER	HYDROLASE
1AUS	ACTIVATED UNLIGANDED SPINACH RUBISCO	LYASE (CARBON-CARBON)
1AVA	AMY2/BASI PROTEIN-PROTEIN COMPLEX FROM BARLEY SEED	HYDROLASE INHIBITION
1AVF	ACTIVATION INTERMEDIATE 2 OF HUMAN GASTRICSIN FROM HUMAN STOMACH	ASPARTYL PROTEASE
1AVO	PROTEASOME ACTIVATOR REG(ALPHA)	PROTEASOME ACTIVATOR
1AVP	STRUCTURE OF HUMAN ADENOVIRUS 2 PROTEINASE WITH ITS 11 AMINO ACID COFACTOR	HYDROLASE
1AVZ	V-1 NEF PROTEIN IN COMPLEX WITH WILD TYPE FYN SH3 DOMAIN	COMPLEX (MYRISTYLATION/TRANSFERASE)
1AW8	PYRUVOYL DEPENDENT ASPARTATE DECARBOXYLASE	DECARBOXYLASE
1AWC	MOUSE GABP ALPHA/BETA DOMAIN BOUND TO DNA	TRANSCRIPTION/DNA
1AWF	NOVEL COVALENT THROMBIN INHIBITOR FROM PLANT EXTRACT	COMPLEX (PROTEASE/INHIBITOR)
1AWH	NOVEL COVALENT THROMBIN INHIBITOR FROM PLANT EXTRACT	COMPLEX (PROTEASE/INHIBITOR)
1AWI	HUMAN PLATELET PROFILIN COMPLEXED WITH THE L-PRO10 PEPTIDE	COMPLEX (ACTIN-BINDING PROTEIN/PEPTIDE)
1AXC	HUMAN PCNA	COMPLEX (DNA-BINDING PROTEIN/DNA)
1AXD	STRUCTURE OF GLUTATHIONE S-TRANSFERASE-I BOUND WITH THE LIGAND LACTOYLGLUTATHIONE	COMPLEX (TRANSFERASE/LIGAND)

1AXI	STRUCTURAL PLASTICITY AT THE HGH:HGHBP INTERFACE	COMPLEX (HORMONE/RECEPTOR)
1AY1	ANTI TAQ FAB TP7	IMMUNOGLOBULIN
1AY6	THROMBIN INHIBITOR FROM THEONALLA, CYCLOTHEANAMIDE-BASED MACROCYCLIC TRIPEPTIDE MOTIF	COMPLEX (SERINE PROTEASE/INHIBITOR)
1AY7	RIBONUCLEASE SA COMPLEX WITH BARSTAR	COMPLEX (ENZYME/INHIBITOR)
1AYA	CRYSTAL STRUCTURES OF PEPTIDE COMPLEXES OF THE AMINO-TERMINAL SH2 DOMAIN OF THE SYP TYROSINE PHOSPHATASE	HYDROLASE(SH2 DOMAIN)
1AYB	CRYSTAL STRUCTURES OF PEPTIDE COMPLEXES OF THE AMINO-TERMINAL SH2 DOMAIN OF THE SYP TYROSINE PHOSPHATASE	HYDROLASE(SH2 DOMAIN)
1AYY	GLYCOSYLASPARAGINASE	HYDROLASE
1AZS	COMPLEX OF GS-ALPHA WITH THE CATALYTIC DOMAINS OF MAMMALIAN ADENYLYL CYCLASE	COMPLEX (LYASE/HYDROLASE)
1AZZ	FIDDLER CRAB COLLAGENASE COMPLEXED TO ECOTIN	COMPLEX (SERINE PROTEASE/INHIBITOR)
1B05	STRUCTURE OF OLIGO-PEPTIDE BINDING PROTEIN COMPLEXED WITH LYS-CYS-LYS	PEPTIDE BINDING PROTEIN
1B0G	CLASS I HISTOCOMPATIBILITY ANTIGEN (HLA-A2.1)/BETA 2-MICROGLOBULIN/PEPTIDE P1049 COMPLEX	HISTOCOMPATIBILITY ANTIGEN
1B0H	OLIGO-PEPTIDE BINDING PROTEIN COMPLEXED WITH LYSYL-NAPTHYLALANYL-LYSINE	PEPTIDE BINDING PROTEIN
1B0R	CRYSTAL STRUCTURE OF HLA-A*0201 COMPLEXED WITH A PEPTIDE WITH THE CARBOXYL-TERMINAL GROUP SUBSTITUTED BY A METHYL GROUP	SIGNALING PROTEIN
1B17	PH AFFECTS GLU B13 SWITCHING AND SULFATE BINDING IN CUBIC INSULIN CRYSTALS (PH 5.00 COORDINATES)	HORMONE/GROWTH FACTOR
1B18	PH AFFECTS GLU B13 SWITCHING AND SULFATE BINDING IN CUBIC INSULIN CRYSTALS (PH 5.53 COORDINATES)	HORMONE/GROWTH FACTOR
1B19	PH AFFECTS GLU B13 SWITCHING AND SULFATE BINDING IN CUBIC INSULIN CRYSTALS (PH 5.80 COORDINATES)	HORMONE/GROWTH FACTOR
1B1H	OLIGO-PEPTIDE BINDING PROTEIN/TRIPEPTIDE (LYS HPE LYS) COMPLEX	SIGNALING PROTEIN
1B27	STRUCTURAL RESPONSE TO MUTATION AT A PROTEIN-PROTEIN INTERFACE	HYDROLASE/HYDROLASE INHIBITOR
1B2A	PH AFFECTS GLU B13 SWITCHING AND SULFATE BINDING IN CUBIC INSULIN CRYSTALS (PH 6.00 COORDINATES)	HORMONE/GROWTH FACTOR
1B2B	PH AFFECTS GLU B13 SWITCHING AND SULFATE BINDING IN CUBIC	HORMONE/GROWTH FACTOR

	INSULIN CRYSTALS (PH 6.16 COORDINATES)	
1B2C	PH AFFECTS GLU B13 SWITCHING AND SULFATE BINDING IN CUBIC INSULIN CRYSTALS (PH 6.26 COORDINATES)	HORMONE/GROWTH FACTOR
1B2G	PH AFFECTS GLU B13 SWITCHING AND SULFATE BINDING IN CUBIC INSULIN CRYSTALS (PH 9.00 COORDINATES)	HORMONE/GROWTH FACTOR
1B2H	OLIGO-PEPTIDE BINDING PROTEIN COMPLEXED WITH LYSYL-ORNITHYL-LYSINE	PEPTIDE BINDING PROTEIN
1B2U	STRUCTURAL RESPONSE TO MUTATION AT A PROTEIN-PROTEIN INTERFACE	HYDROLASE/HYDROLASE INHIBITOR
1B2W	COMPARISON OF THE THREE-DIMENSIONAL STRUCTURES OF A HUMANIZED AND A CHIMERIC FAB OF AN ANTI-GAMMA-INTERFERON ANTIBODY	IMMUNE SYSTEM
1B32	OLIGO-PEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH KMK	PEPTIDE BINDING PROTEIN
1B33	STRUCTURE OF LIGHT HARVESTING COMPLEX OF ALLOPHYCOCYANIN ALPHA AND BETA CHAINS/CORE-LINKER COMPLEX AP*LC7.8	PHOTOSYNTHESIS
1B34	CRYSTAL STRUCTURE OF THE D1D2 SUB-COMPLEX FROM THE HUMAN SNRNP CORE DOMAIN	RNA BINDING PROTEIN
1B35	CRICKET PARALYSIS VIRUS (CRPV)	VIRUS
1B3F	OLIGO-PEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH KHK	PEPTIDE BINDING PROTEIN
1B3G	OLIGO-PEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH KIK	PEPTIDE BINDING PROTEIN
1B3H	OLIGO-PEPTIDE BINDING PROTEIN COMPLEXED WITH LYSYL-CYCLOHEXYLALANYL-LYSINE	PEPTIDE BINDING PROTEIN
1B3L	OLIGO-PEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH KGK	PEPTIDE BINDING PROTEIN
1B3S	STRUCTURAL RESPONSE TO MUTATION AT A PROTEIN-PROTEIN INTERFACE	HYDROLASE/HYDROLASE INHIBITOR
1B41	HUMAN ACETYLCHOLINESTERASE COMPLEXED WITH FASCICULIN-II, GLYCOSYLATED PROTEIN	HYDROLASE/TOXIN
1B46	OLIGO-PEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH KPK	PEPTIDE BINDING PROTEIN
1B4H	OLIGO-PEPTIDE BINDING PROTEIN COMPLEXED WITH LYSYL-DIAMINOBUTYRIC ACID-LYSINE	PEPTIDE BINDING PROTEIN
1B4J	COMPARISON OF THE THREE-DIMENSIONAL STRUCTURES OF A HUMANIZED AND A CHIMERIC FAB OF AN ANTI-GAMMA-INTERFERON ANTIBODY	ANTIBODY ENGINEERING
1B4U	PROTOCATECHUATE 4,5-DIOXYGENASE (LIGAB) IN COMPLEX WITH PROTOCATECHUATE (PCA)	DIOXYGENASE

1B4Z	OLIGO-PEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH KDK	PEPTIDE BINDING PROTEIN
1B51	OLIGO-PEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH KSK	PEPTIDE BINDING PROTEIN
1B52	OLIGO-PEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH KTK	PEPTIDE BINDING PROTEIN
1B5F	NATIVE CARDOSIN A FROM CYNARA CARDUNCULUS L.	HYDROLASE
1B5G	HUMAN THROMBIN COMPLEXED WITH NOVEL SYNTHETIC PEPTIDE MIMETIC INHIBITOR AND HIRUGEN	COMPLEX (SERINE PROTEASE/INHIBITOR)
1B5H	OLIGO-PEPTIDE BINDING PROTEIN COMPLEXED WITH LYSYL-DIAMINOPROPANOIC ACID-LYSINE	PEPTIDE BINDING PROTEIN
1B5I	OLIGO-PEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH KNK	PEPTIDE BINDING PROTEIN
1B5J	OLIGO-PEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH KQK	PEPTIDE BINDING PROTEIN
1B6C	CRYSTAL STRUCTURE OF THE CYTOPLASMIC DOMAIN OF THE TYPE I TGF-BETA RECEPTOR IN COMPLEX WITH FKBP12	COMPLEX (ISOMERASE/PROTEIN KINASE)
1B6H	OLIGO-PEPTIDE BINDING PROTEIN COMPLEXED WITH LYSYL-NORVALYL-LYSINE	PEPTIDE BINDING PROTEIN
1B70	PHENYLALANYL TRNA SYNTHETASE COMPLEXED WITH PHENYLALANINE	LIGASE
1B72	PBX1, HOMEOBOX PROTEIN HOX-B1/DNA TERNARY COMPLEX	PROTEIN/DNA
1B7H	OLIGO-PEPTIDE BINDING PROTEIN COMPLEXED WITH LYSYL-NORLEUCYL-LYSINE	PEPTIDE BINDING PROTEIN
1B7T	MYOSIN DIGESTED BY PAPAIN	MYOSIN
1B7X	STRUCTURE OF HUMAN ALPHA-THROMBIN Y225I MUTANT BOUND TO D-PHE-PRO-ARG-CHLOROMETHYLKETONE	HYDROLASE/HYDROLASE INHIBITOR
1B7Y	HENYLALANYL TRNA SYNTHETASE COMPLEXED WITH PHENYLALANINYL-ADENYLATE	LIGASE
1B86	HUMAN DEOXYHAEMOGLOBIN-2,3-DIPHOSPHOGLYCERATE COMPLEX	HAEMOGLOBIN
1B8D	CRYSTAL STRUCTURE OF A PHYCOUROBILIN-CONTAINING PHYCOERYTHRIN	PHOTOSYNTHESIS
1B8H	SLIDING CLAMP, DNA POLYMERASE	TRANSFERASE
1B8I	STRUCTURE OF THE HOMEOTIC UBX/EXD/DNA TERNARY COMPLEX	TRANSCRIPTION/DNA
1B9E	HUMAN INSULIN MUTANT SERB9GLU	HORMONE/GROWTH FACTOR
1B9X	STRUCTURAL ANALYSIS OF PHOSDUCIN AND ITS PHOSPHORYLATION-REGULATED INTERACTION WITH TRANSDUCIN	SIGNALING PROTEIN
1B9Y	STRUCTURAL ANALYSIS OF PHOSDUCIN AND ITS PHOSPHORYLATION-REGULATED INTERACTION WITH TRANSDUCIN BETA-GAMMA	SIGNALING PROTEIN

1BA8	THROMBIN INHIBITOR WITH A RIGID TRIPEPTIDYL ALDEHYDES	COMPLEX (SERINE PROTEASE/INHIBITOR)
1BAB	HEMOGLOBIN THIONVILLE: AN ALPHA-CHAIN VARIANT WITH A SUBSTITUTION OF A GLUTAMATE FOR VALINE AT NA-1 AND HAVING AN ACETYLATED METHIONINE NH2 TERMINUS	OXYGEN TRANSPORT
1BAF	2.9 ANGSTROMS RESOLUTION STRUCTURE OF AN ANTI-DINITROPHENYL-SPIN-LABEL MONOCLONAL ANTIBODY FAB FRAGMENT WITH BOUND HAPTEN	IMMUNOGLOBULIN
1BAI	STRUCTURAL BASIS FOR SPECIFICITY OF RETROVIRAL PROTEASES	COMPLEX (PROTEASE/INHIBITOR)
1BB0	THROMBIN INHIBITORS WITH RIGID TRIPEPTIDYL ALDEHYDES	COMPLEX (SERINE PROTEASE/INHIBITOR)
1BB1	CRYSTAL STRUCTURE OF A DESIGNED, THERMOSTABLE HETEROTRIMERIC COILED COIL	DE NOVO PROTEIN DESIGN
1BBB	A THIRD QUATERNARY STRUCTURE OF HUMAN HEMOGLOBIN A AT 1.7-ANGSTROMS RESOLUTION	OXYGEN TRANSPORT
1BBD	THREE DIMENSIONAL STRUCTURE OF THE FAB FRAGMENT OF A NEUTRALIZING ANTIBODY TO HUMAN RHINOVIRUS SEROTYPE 2	IMMUNOGLOBULIN
1BBJ	CRYSTAL STRUCTURE OF A CHIMERIC FAB' FRAGMENT OF AN ANTIBODY BINDING TUMOUR CELLS	IMMUNOGLOBULIN
1BBR	THE STRUCTURE OF RESIDUES 7-16 OF THE A ALPHA CHAIN OF HUMAN FIBRINOGEN BOUND TO BOVINE THROMBIN AT 2.3 ANGSTROMS RESOLUTION	SERINE PROTEASE
1BC5	CHEMOTAXIS RECEPTOR RECOGNITION BY PROTEIN METHYLTRANSFERASE CHER	COMPLEX (METHYLTRANSFERASE/PEPTIDE)
1BCC	CYTOCHROME BC1 COMPLEX FROM CHICKEN	OXIDOREDUCTASE
1BCP	BINARY COMPLEX OF PERTUSSIS TOXIN AND ATP	TOXIN
1BCS	COMPLEX OF THE WHEAT SERINE CARBOXYPEPTIDASE, CPDW-II, WITH THE MICROBIAL PEPTIDE ALDEHYDE INHIBITOR, CHYMOSTATIN, AND ARGININE AT 100 DEGREES KELVIN	COMPLEX (SERINE PROTEASE/INHIBITOR)
1BCU	ALPHA-THROMBIN COMPLEXED WITH HIRUGEN AND PROFLAVIN	COMPLEX (SERINE PROTEASE INHIBITOR)
1BD2	COMPLEX BETWEEN HUMAN T-CELL RECEPTOR B7, VIRAL PEPTIDE (TAX) AND MHC CLASS I MOLECULE HLA-A 0201	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1BDJ	COMPLEX STRUCTURE OF HPT DOMAIN AND CHEY	COMPLEX (CHEMOTAXIS/TRANSFERASE)
1BE3	CYTOCHROME BC1 COMPLEX FROM BOVINE	ELECTRON TRANSPORT
1BE9	THE THIRD PDZ DOMAIN FROM THE SYNAPTIC PROTEIN PSD-95 IN COMPLEX WITH A C-TERMINAL PEPTIDE DERIVED FROM CRIPT.	PEPTIDE RECOGNITION
1BEN	INSULIN COMPLEXED WITH 4-HYDROXYBENZAMIDE	HORMONE

1BEU	TRP SYNTHASE (D60N-IPP-SER) WITH K+	CARBON-OXYGEN LYASE
1BFO	CAMPATH-1G IGG2B RAT MONOCLONAL FAB	ANTIBODY
1BGS	RECOGNITION BETWEEN A BACTERIAL RIBONUCLEASE, BARNASE, AND ITS NATURAL INHIBITOR, BARSTAR	ENDONUCLEASE
1BGX	TAQ POLYMERASE IN COMPLEX WITH TP7, AN INHIBITORY FAB	COMPLEX (POLYMERASE/INHIBITOR)
1BGY	CYTOCHROME BC1 COMPLEX FROM BOVINE	ELECTRON TRANSPORT
1BH8	HTAFII18/HTAFII28 HETERODIMER CRYSTAL STRUCTURE	TRANSCRIPTION REGULATION COMPLEX
1BH9	HTAFII18/HTAFII28 HETERODIMER CRYSTAL STRUCTURE WITH BOUND PCMBS	TRANSCRIPTION REGULATION COMPLEX
1BHF	P56LCK SH2 DOMAIN INHIBITOR COMPLEX	COMPLEX (SH2 DOMAIN/INHIBITOR)
1BHH	FREE P56LCK SH2 DOMAIN	SH2 DOMAIN
1BHX	X-RAY STRUCTURE OF THE COMPLEX OF HUMAN ALPHA THROMBIN WITH THE INHIBITOR SDZ 229-357	SERINE PROTEASE
1BI4	CATALYTIC DOMAIN OF HIV-1 INTEGRASE	DNA INTEGRATION
1BI7	MECHANISM OF G1 CYCLIN DEPENDENT KINASE INHIBITION FROM THE STRUCTURE OF THE CDK6-P16INK4A TUMOR SUPPRESSOR COMPLEX	COMPLEX (KINASE/ANTI-ONCOGENE)
1BI8	MECHANISM OF G1 CYCLIN DEPENDENT KINASE INHIBITION FROM THE STRUCTURES CDK6-P19INK4D INHIBITOR COMPLEX	COMPLEX (KINASE/INHIBITOR)
1BII	THE CRYSTAL STRUCTURE OF H-2DD MHC CLASS I IN COMPLEX WITH THE HIV-1 DERIVED PEPTIDE P18-110	COMPLEX (MHC I/PEPTIDE)
1BIQ	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 1 BETA CHAIN MUTANT E238A	OXIDOREDUCTASE
1BJ1	VASCULAR ENDOTHELIAL GROWTH FACTOR IN COMPLEX WITH A NEUTRALIZING ANTIBODY	COMPLEX (ANTIBODY/ANTIGEN)
1BJ3	CRYSTAL STRUCTURE OF COAGULATION FACTOR IX-BINDING PROTEIN (IX-BP) FROM VENOM OF HABU SNAKE WITH A HETERODIMER OF C-TYPE LECTIN DOMAINS	COLLAGEN BINDING PROTEIN
1BJO	THE STRUCTURE OF PHOSPHOSERINE AMINOTRANSFERASE FROM E. COLI IN COMPLEX WITH ALPHA-METHYL-L-GLUTAMATE	AMINOTRANSFERASE
1BJR	COMPLEX FORMED BETWEEN PROTEOLYTICALLY GENERATED LACTOFERRIN FRAGMENT AND PROTEINASE K	COMPLEX (HYDROLASE/IRON TRANSPORT)
1BK6	KARYOPHERIN ALPHA (YEAST) + SV40 T ANTIGEN NLS	COMPLEX (PROTEIN TRANSPORT/PEPTIDE)
1BKC	CATALYTIC DOMAIN OF TNF-ALPHA CONVERTING ENZYME (TACE)	ZN-ENDOPEPTIDASE

1BKD	COMPLEX OF HUMAN H-RAS WITH HUMAN SOS-1	COMPLEX(ONCOGENE PROTEIN/EXCHANGE FACTR)
1BKS	TRYPTOPHAN SYNTHASE (E.C.4.2.1.20) FROM SALMONELLA TYPHIMURIUM	LYASE
1BLL	X-RAY CRYSTALLOGRAPHIC DETERMINATION OF THE STRUCTURE OF BOVINE LENS LEUCINE AMINOPEPTIDASE COMPLEXED WITH AMASTATIN: FORMULATION OF A CATALYTIC MECHANISM FEATURING A GEM-DIOLATE TRANSITION STATE	HYDROLASE(ALPHA-AMINOACYLPEPTIDE)
1BLX	P19INK4D/CDK6 COMPLEX	COMPLEX (INHIBITOR PROTEIN/KINASE)
1BM3	IMMUNOGLOBULIN OPG2 FAB-PEPTIDE COMPLEX	IMMUNE SYSTEM
1BMB	GRB2-SH2 DOMAIN IN COMPLEX WITH KPFY*VNVEF (PKF270-974)	HORMONE/GROWTH FACTOR
1BMF	BOVINE MITOCHONDRIAL F1-ATPASE	ATP PHOSPHORYLASE
1BML	COMPLEX OF THE CATALYTIC DOMAIN OF HUMAN PLASMIN AND STREPTOKINASE	BLOOD CLOTTING
1BMM	HUMAN ALPHA-THROMBIN COMPLEXED WITH [S-(R*,R*)]-4-[(AMINOIMINOMETHYL)AMINO]-N-[[1-[3-HYDROXY-2-[(2-NAPHTHALENYLSULFONYL)AMINO]-1-OXOPROPYL]-2-PYRROLIDINYL] METHYL]BUTANAMIDE (BMS-186282)	COMPLEX (SERINE PROTEASE/INHIBITOR)
1BMN	HUMAN ALPHA-THROMBIN COMPLEXED WITH [S-(R*,R*)]-1-(AMINOIMINOMETHYL)-N-[[1-[N-[(2-NAPHTHALENYLSULFONYL)-L-SERYL]-PYRROLIDINYL]METHYL]-3-PIPERIDENECARBOXAMIDE (BMS-189090)	COMPLEX (SERINE PROTEASE/INHIBITOR)
1BMQ	CRYSTAL STRUCTURE OF THE COMPLEX OF INTERLEUKIN-1BETA CONVERTING ENZYME (ICE) WITH A PEPTIDE BASED INHIBITOR, (3S)-N-METHANESULFONYL-3-({1-[N-(2-NAPHTOYL)-L-VALYL]-L-PROLYL }AMINO)-4-OXOBUTANAMIDE	HYDROLASE
1BOG	ANTI-P24 (HIV-1) FAB FRAGMENT CB41 COMPLEXED WITH AN EPITOPE-HOMOLOGOUS PEPTIDE	COMPLEX (ANTIBODY/PEPTIDE)
1BOM	THREE-DIMENSIONAL STRUCTURE OF BOMBYXIN-II, AN INSULIN-RELATED BRAIN-SECRETORY PEPTIDE OF THE SILKMOTH BOMBYX MORI: COMPARISON WITH INSULIN AND RELAXIN	INSULIN-LIKE BRAIN-SECRETORY PEPTIDE
1BOU	THREE-DIMENSIONAL STRUCTURE OF LIGAB	DIOXYGENASE
1BP3	HE XRAY STRUCTURE OF A GROWTH HORMONE-PROLACTIN RECEPTOR COMPLEX	HORMONE/GROWTH FACTOR
1BPH	CONFORMATIONAL CHANGES IN CUBIC INSULIN CRYSTALS IN THE PH RANGE 7-11	HORMONE
1BPL	GLYCOSYLTRANSFERASE	GLYCOSYLTRANSFERASE
1BQH	MURINE CD8AA ECTODOMAIN FRAGMENT IN COMPLEX WITH H-2KB/VSV8	IMMUNE SYSTEM

1BQL	STRUCTURE OF AN ANTI-HEL FAB FRAGMENT COMPLEXED WITH BOBWHITE QUAIL LYSOZYME	COMPLEX (ANTIBODY/ANTIGEN)
1BQM	HIV-1 RT/HBY 097	NUCLEOTIDYLTRANSFERASE
1BQN	TYR 188 LEU HIV-1 RT/HBY 097	NUCLEOTIDYLTRANSFERASE
1BQP	THE STRUCTURE OF THE PEA LECTIN-D-MANNOPYRANOSE COMPLEX	PLANT PROTEIN
1BQQ	CRYSTAL STRUCTURE OF THE MT1-MMP--TIMP-2 COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
1BR1	SMOOTH MUSCLE MYOSIN MOTOR DOMAIN-ESSENTIAL LIGHT CHAIN COMPLEX WITH MGADP.ALF4 BOUND AT THE ACTIVE SITE	MUSCLE PROTEIN
1BR4	SMOOTH MUSCLE MYOSIN MOTOR DOMAIN-ESSENTIAL LIGHT CHAIN COMPLEX WITH MGADP.BEF3 BOUND AT THE ACTIVE SITE	MUSCLE PROTEIN
1BR8	IMPLICATIONS FOR FUNCTION AND THERAPY OF A 2.9A STRUCTURE OF BINARY-COMPLEXED ANTITHROMBIN	BLOOD CLOTTING
1BRC	RELOCATING A NEGATIVE CHARGE IN THE BINDING POCKET OF TRYPSIN	COMPLEX(PROTEINASE/INHIBITOR)
1BRL	THREE-DIMENSIONAL STRUCTURE OF BACTERIAL LUCIFERASE FROM VIBRIO HARVEYI AT 2.4 ANGSTROMS RESOLUTION	LUMINESCENCE
1BRS	PROTEIN-PROTEIN RECOGNITION: CRYSTAL STRUCTURAL ANALYSIS OF A BARNASE-BARSTAR COMPLEX AT 2.0-A RESOLUTION	ENDONUCLEASE
1BS6	PEPTIDE DEFORMYLASE AS NI2+ CONTAINING FORM IN COMPLEX WITH TRIPEPTIDE MET-ALA-SER	HYDROLASE
1BS8	PEPTIDE DEFORMYLASE AS ZN2+ CONTAINING FORM IN COMPLEX WITH TRIPEPTIDE MET-ALA-SER	HYDROLASE
1BSX	STRUCTURE AND SPECIFICITY OF NUCLEAR RECEPTOR-COACTIVATOR INTERACTIONS	HORMONE/GROWTH FACTOR
1BT6	P11 (S100A10), LIGAND OF ANNEXIN II IN COMPLEX WITH ANNEXIN II N-TERMINUS	COMPLEX (LIGAND/ANNEXIN)
1BTH	STRUCTURE OF THROMBIN COMPLEXED WITH BOVINE PANCREATIC TRYPSIN INHIBITOR	COMPLEX (SERINE PROTEASE/INHIBITOR)
1BUH	CRYSTAL STRUCTURE OF THE HUMAN CDK2 KINASE COMPLEX WITH CELL CYCLE-REGULATORY PROTEIN CKSHS1	TRANSFERASE
1BUI	STRUCTURE OF THE TERNARY MICROPLASMIN-STAPHYLOKINASE-MICROPLASMIN COMPLEX: A PROTEINASE-COFACTOR-SUBSTRATE COMPLEX IN ACTION.	HYDROLASE
1BUN	STRUCTURE OF BETA2-BUNGAROTOXIN: POTASSIUM CHANNEL BINDING BY KUNITZ MODULES AND TARGETED PHOSPHOLIPASE ACTION	TOXIN
1BUV	CRYSTAL STRUCTURE OF THE MT1-MMP-TIMP-2 COMPLEX	HYDROLASE/HYDROLASE INHIBITOR

1BUW	RYSTAL STRUCTURE OF S-NITROSO-NITROSYL HUMAN HEMOGLOBIN A	OXYGEN STORAGE/TRANSPORT
1BVK	HUMANIZED ANTI-LYSOZYME FV COMPLEXED WITH LYSOZYME	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE)
1BVN	PIG PANCREATIC ALPHA-AMYLASE IN COMPLEX WITH THE PROTEINACEOUS INHIBITOR TENDAMISTAT	HYDROLASE/HYDROLASE INHIBITOR
1BVY	COMPLEX OF THE HEME AND FMN-BINDING DOMAINS OF THE CYTOCHROME P450(BM-3)	OXIDOREDUCTASE
1BWV	ACTIVATED RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE (RUBISCO) COMPLEXED WITH THE REACTION INTERMEDIATE ANALOGUE 2-CARBOXYARABINITOL 1,5-BISPHOSPHATE	LYASE
1BX2	CRYSTAL STRUCTURE OF HLA-DR2 (DRA*0101,DRB1*1501) COMPLEXED WITH A PEPTIDE FROM HUMAN MYELIN BASIC PROTEIN	IMMUNE SYSTEM
1BXG	HENYLALANINE DEHYDROGENASE STRUCTURE IN TERNARY COMPLEX WITH NAD+ AND BETA-PHENYLPROPIONATE	AMINO ACID DEHYDROGENASE
1BXI	CRYSTAL STRUCTURE OF THE ESCHERICHIA COLI COLICIN E9 DNASE DOMAIN WITH ITS COGNATE IMMUNITY PROTEIN IM9	IMMUNE SYSTEM
1BXL	STRUCTURE OF BCL-XL/BAK PEPTIDE COMPLEX, NMR, MINIMIZED AVERAGE STRUCTURE	COMPLEX (APOPTOSIS/PEPTIDE)
1BXN	HE CRYSTAL STRUCTURE OF RUBISCO FROM ALCALIGENES EUTROPHUS TO 2.7 ANGSTROMS.	LYASE
1BXR	TRUCTURE OF CARBAMOYL PHOSPHATE SYNTHETASE COMPLEXED WITH THE ATP ANALOG AMPPNP	AMIDOTRANSFERASE
1BZ0	HEMOGLOBIN A (HUMAN, DEOXY, HIGH SALT)	OXYGEN STORAGE/TRANSPORT
1BZ1	HEMOGLOBIN (ALPHA + MET) VARIANT	OXYGEN STORAGE/TRANSPORT
1BZ7	FAB FRAGMENT FROM MURINE ASCITES	IMMUNE SYSTEM
1BZ9	CRYSTAL STRUCTURE OF MURINE CLASS I MHC H2-DB COMPLEXED WITH A SYNTHETIC PEPTIDE P1027	MURINE CLASS I MHC/PEPTIDE COMPLEX
1BZH	CYCLIC PEPTIDE INHIBITOR OF HUMAN PTP1B	HYDROLASE
1BZQ	OMPLEX OF A DROMEDARY SINGLE-DOMAIN VHH ANTIBODY FRAGMENT WITH RNASE A	HYDROLASE/IMMUNE SYSTEM
1BZZ	HEMOGLOBIN (ALPHA V1M) MUTANT	OXYGEN STORAGE/TRANSPORT
1C08	CRYSTAL STRUCTURE OF HYHEL-10 FV-HEN LYSOZYME COMPLEX	IMMUNE SYSTEM/HYDROLASE
1C0F	CRYSTAL STRUCTURE OF DICTYOSTELIUM CAATP-ACTIN IN COMPLEX WITH GELSOLIN SEGMENT 1	CONTRACTILE PROTEIN
1C0G	RYSTAL STRUCTURE OF 1:1 COMPLEX BETWEEN GELSOLIN SEGMENT 1	CONTRACTILE PROTEIN

	AND A DICTYOSTELIUM/TETRAHYMENA CHIMERA ACTIN (MUTANT 228: Q228K/T229A/A230Y/E360H)	
1C0T	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH BM+21.1326	TRANSFERASE
1C0U	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH BM+50.0934	TRANSFERASE
1C12	INSIGHT IN ODORANT PERCEPTION: THE CRYSTAL STRUCTURE AND BINDING CHARACTERISTICS OF ANTIBODY FRAGMENTS DIRECTED AGAINST THE MUSK ODORANT TRASEOLIDE	IMMUNE SYSTEM
1C17	A1C12 SUBCOMPLEX OF F1FO ATP SYNTHASE	MEMBRANE PROTEIN
1C1B	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH GCA-186	TRANSFERASE
1C1C	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH TNK-6123	TRANSFERASE
1C1E	CRYSTAL STRUCTURE OF A DIELS-ALDERASE CATALYTIC ANTIBODY 1E9 IN COMPLEX WITH ITS HAPTEN	IMMUNE SYSTEM
1C1U	RECRUITING ZINC TO MEDIATE POTENT, SPECIFIC INHIBITION OF SERINE PROTEASES	BLOOD CLOTTING
1C1V	RECRUITING ZINC TO MEDIATE POTENT, SPECIFIC INHIBITION OF SERINE PROTEASES	BLOOD CLOTTING
1C1W	RECRUITING ZINC TO MEDIATE POTENT, SPECIFIC INHIBITION OF SERINE PROTEASES	BLOOD CLOTTING
1C1Y	CRYSTAL STRUCTURE OF RAP.GMPPNP IN COMPLEX WITH THE RAS-BINDING-DOMAIN OF C-RAF1 KINASE (RAFRBD).	SIGNALING PROTEIN
1C29	CRYSTAL STRUCTURE OF THE COMPLEX OF BACTERIAL TRYPTOPHAN SYNTHASE WITH THE TRANSITION STATE ANALOGUE INHIBITOR 4-(2-HYDROXYPHENYLTHIO)-1-BUTENYLPHOSPHONIC ACID	LYASE/LYASE INHIBITOR
1C30	CRYSTAL STRUCTURE OF CARBAMOYL PHOSPHATE SYNTHETASE: SMALL SUBUNIT MUTATION C269S	LIGASE
1C3A	CRYSTAL STRUCTURE OF FLAVOCETIN-A FROM THE HABU SNAKE VENOM, A NOVEL CYCLIC TETRAMER OF C-TYPE LECTIN-LIKE HETERODIMERS	MEMBRANE PROTEIN
1C3O	CRYSTAL STRUCTURE OF THE CARBAMOYL PHOSPHATE SYNTHETASE: SMALL SUBUNIT MUTANT C269S WITH BOUND GLUTAMINE	LIGASE
1C40	BAR-HEADED GOOSE HEMOGLOBIN (AQUOMET FORM)	OXYGEN STORAGE/TRANSPORT
1C4Z	STRUCTURE OF E6AP: INSIGHTS INTO UBIQUITINATION PATHWAY	LIGASE
1C5B	DECARBOXYLASE CATALYTIC ANTIBODY 21D8 UNLIGANDED FORM	IMMUNE SYSTEM

1C5C	DECARBOXYLASE CATALYTIC ANTIBODY 21D8-HAPTEN COMPLEX	IMMUNE SYSTEM
1C5D	THE CRYSTAL STRUCTURE OF THE FAB FRAGMENT OF A RAT MONOCLONAL ANTIBODY AGAINST THE MAIN IMMUNOGENIC REGION OF THE HUMAN MUSCLE ACETYLCHOLINE RECEPTOR	IMMUNE SYSTEM
1C5F	CRYSTAL STRUCTURE OF THE CYCLOPHILIN-LIKE DOMAIN FROM BRUGIA MALAYI COMPLEXED WITH CYCLOSPORIN A	ISOMERASE/IMMUNE SYSTEM
1C5L	STRUCTURAL BASIS FOR SELECTIVITY OF A SMALL MOLECULE, S1-BINDING, SUB-MICROMOLAR INHIBITOR OF UROKINASE TYPE PLASMINOGEN ACTIVATOR	BLOOD CLOTTING
1C5M	STRUCTURAL BASIS FOR SELECTIVITY OF A SMALL MOLECULE, S1-BINDING, SUB-MICROMOLAR INHIBITOR OF UROKINASE TYPE PLASMINOGEN ACTIVATOR	BLOOD CLOTTING
1C5N	STRUCTURAL BASIS FOR SELECTIVITY OF A SMALL MOLECULE, S1-BINDING, SUB-MICROMOLAR INHIBITOR OF UROKINASE TYPE PLASMINOGEN ACTIVATOR	BLOOD CLOTTING
1C5O	STRUCTURAL BASIS FOR SELECTIVITY OF A SMALL MOLECULE, S1-BINDING, SUB-MICROMOLAR INHIBITOR OF UROKINASE TYPE PLASMINOGEN ACTIVATOR	BLOOD CLOTTING
1C6V	SIV INTEGRASE (CATALYTIC DOMAIN + DNA BIDING DOMAIN COMPRISING RESIDUES 50-293) MUTANT WITH PHE 185 REPLACED BY HIS (F185H)	DNA BINDING PROTEIN
1C7B	DEOXY RHB1.0 (RECOMBINANT HEMOGLOBIN)	OXYGEN STORAGE/TRANSPORT
1C7C	DEOXY RHB1.1 (RECOMBINANT HEMOGLOBIN)	OXYGEN STORAGE/TRANSPORT
1C7D	DEOXY RHB1.2 (RECOMBINANT HEMOGLOBIN)	OXYGEN STORAGE/TRANSPORT
1C8O	2.9 A STRUCTURE OF CLEAVED VIRAL SERPIN CRMA	VIRAL PROTEIN
1C8V	CRYSTAL STRUCTURE OF THE COMPLEX OF BACTERIAL TRYPTOPHAN SYNTHASE WITH THE TRANSITION STATE ANALOGUE INHIBITOR 4-(2-HYDROXYPHENYLTHIO)-BUTYLPHOSPHONIC ACID	LYASE
1C9B	CRYSTAL STRUCTURE OF A HUMAN TBP CORE DOMAIN-HUMAN TFIIB CORE DOMAIN COMPLEX BOUND TO AN EXTENDED, MODIFIED ADENOVIRAL MAJOR LATE PROMOTER (ADMLP)	TRANSCRIPTION/DNA
1C9D	CRYSTAL STRUCTURE OF THE COMPLEX OF BACTERIAL TRYPTOPHAN SYNTHASE WITH THE TRANSITION STATE ANALOGUE INHIBITOR 4-(2-HYDROXY-4-FLUOROPHENYLTHIO)-BUTYLPHOSPHONIC ACID	LYASE
1C9I	PEPTIDE-IN-GROOVE INTERACTIONS LINK TARGET PROTEINS TO THE B-PROPELLER OF CLATHRIN	ENDOCYTOSIS/EXOCYTOSIS
1C9L	PEPTIDE-IN-GROOVE INTERACTIONS LINK TARGET PROTEINS TO THE B-PROPELLER OF CLATHRIN	ENDOCYTOSIS/EXOCYTOSIS

1C9T	COMPLEX OF BDELLASTASIN WITH BOVINE TRYPSIN	HYDROLASE/HYDROLASE INHIBITOR
1CA0	BOVINE CHYMOTRYPSIN COMPLEXED TO APPI	COMPLEX (SERINE PROTEASE/INHIBITOR)
1CA8	THROMBIN INHIBITORS WITH RIGID TRIPEPTIDYL ALDEHYDES	COMPLEX (SERINE PROTEASE/INHIBITOR)
1CA9	STRUCTURE OF TNF RECEPTOR ASSOCIATED FACTOR 2 IN COMPLEX WITH A PEPTIDE FROM TNF-R2	TNF SIGNALING
1CAU	DETERMINATION OF THREE CRYSTAL STRUCTURES OF CANAVALIN BY MOLECULAR REPLACEMENT	SEED STORAGE PROTEIN
1CAW	DETERMINATION OF THREE CRYSTAL STRUCTURES OF CANAVALIN BY MOLECULAR REPLACEMENT	SEED STORAGE PROTEIN
1CAX	DETERMINATION OF THREE CRYSTAL STRUCTURES OF CANAVALIN BY MOLECULAR REPLACEMENT	SEED STORAGE PROTEIN
1CB7	LUTAMATE MUTASE FROM CLOSTRIDIUM COCHLEARIUM RECONSTITUTED WITH METHYL-COBALAMIN	ISOMERASE
1CBV	AN AUTOANTIBODY TO SINGLE-STRANDED DNA: COMPARISON OF THE THREE-DIMENSIONAL STRUCTURES OF THE UNLIGANDED FAB AND A DEOXYNUCLEOTIDE-FAB COMPLEX	IMMUNE SYSTEM/DNA
1CBW	BOVINE CHYMOTRYPSIN COMPLEXED TO BPTI	COMPLEX (SERINE PROTEASE/INHIBITOR)
1CC0	CRYSTAL STRUCTURE OF THE RHOA.GDP-RHOGDI COMPLEX	SIGNALING PROTEIN
1CC1	CRYSTAL STRUCTURE OF A REDUCED, ACTIVE FORM OF THE NI-FE-SE HYDROGENASE FROM DESULFOMICROBIUM BACULATUM	OXIDOREDUCTASE
1CCW	STRUCTURE OF THE COENZYME B12 DEPENDENT ENZYME GLUTAMATE MUTASE FROM CLOSTRIDIUM COCHLEARIUM	ISOMERASE
1CD1	CD1(MOUSE) ANTIGEN PRESENTING MOLECULE	CD1
1CD3	PROCAPSID OF BACTERIOPHAGE PHIX174	VIRUS
1CD9	2:2 COMPLEX OF G-CSF WITH ITS RECEPTOR	CYTOKINE
1CDK	CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT (E.C.2.7.1.37) (PROTEIN KINASE A) COMPLEXED WITH PROTEIN KINASE INHIBITOR PEPTIDE FRAGMENT 5-24 (PKI(5-24) ISOELECTRIC VARIANT CA) AND MN2+ ADENYLYL IMIDODIPHOSPHATE (MNAMP-PNP) AT PH 5.6 AND 7C AND 4C	COMPLEX (TRANSFERASE/INHIBITOR)
1CDL	TARGET ENZYME RECOGNITION BY CALMODULIN: 2.4 ANGSTROMS STRUCTURE OF A CALMODULIN-PEPTIDE COMPLEX	CALCIUM-BINDING PROTEIN
1CDM	MODULATION OF CALMODULIN PLASTICITY IN MOLECULAR RECOGNITION ON THE BASIS OF X-RAY STRUCTURES	CALCIUM-BINDING PROTEIN
1CE1	1.9A STRUCTURE OF THE THERAPEUTIC ANTIBODY CAMPATH-1H FAB IN COMPLEX WITH A SYNTHETIC PEPTIDE ANTIGEN	ANTIBODY

1CE6	MHC CLASS I H-2DB COMPLEXED WITH A SENDAI VIRUS NUCLEOPROTEIN PEPTIDE	MHC CLASS I
1CE7	MISTLETOE LECTIN I FROM VISCUM ALBUM	RIBOSOME
1CE8	CARBAMOYL PHOSPHATE SYNTHETASE FROM ESCHERICHIS COLI WITH COMPLEXED WITH THE ALLOSTERIC LIGAND IMP	LIGASE IMP
1CF0	HUMAN PLATELET PROFILIN COMPLEXED WITH AN L-PRO10-IODOTYROSINE PEPTIDE	COMPLEX (ACTIN-BINDING PROTEIN/PEPTIDE)
1CF7	STRUCTURAL BASIS OF DNA RECOGNITION BY THE HETERODIMERIC CELL CYCLE TRANSCRIPTION FACTOR E2F-DP	TRANSCRIPTION/DNA
1CF8	CONVERGENCE OF CATALYTIC ANTIBODY AND TERPENE CYCLASE MECHANISMS: POLYENE CYCLIZATION DIRECTED BY CARBOCATION-PI INTERACTIONS	CATALYTIC ANTIBODY
1CFN	ANTI-P24 (HIV-1) FAB FRAGMENT CB41 COMPLEXED WITH AN EPITOPE-RELATED PEPTIDE	POLYSPECIFICITY
1CFQ	ANTI-P24 (HIV-1) FAB FRAGMENT CB41	POLYSPECIFICITY
1CFS	ANTI-P24 (HIV-1) FAB FRAGMENT CB41 COMPLEXED WITH AN EPITOPE-UNRELATED PEPTIDE	POLYSPECIFICITY
1CFT	ANTI-P24 (HIV-1) FAB FRAGMENT CB41 COMPLEXED WITH AN EPITOPE-UNRELATED D-PEPTIDE	POLYSPECIFICITY
1CG5	DEOXY FORM HEMOGLOBIN FROM DASYATIS AKAJEI	OXYGEN TRANSPORT
1CG8	CO FORM HEMOGLOBIN FROM DASYATIS AKAJEI	OXYGEN TRANSPORT
1CG9	COMPLEX RECOGNITION OF THE SUPERTYPIC BW6-DETERMINANT ON HLA-B AND-C MOLECULES BY THE MONOCLONAL ANTIBODY SFR8-B6	MHC CLASS I
1CGI	HREE-DIMENSIONAL STRUCTURE OF THE COMPLEXES BETWEEN BOVINE CHYMOTRYPSINOGEN*A AND TWO RECOMBINANT VARIANTS OF HUMAN PANCREATIC SECRETORY TRYPSIN INHIBITOR (KAZAL-TYPE)	SERINE PROTEASE/INHIBITOR COMPLEX
1CGJ	HREE-DIMENSIONAL STRUCTURE OF THE COMPLEXES BETWEEN BOVINE CHYMOTRYPSINOGEN*A AND TWO RECOMBINANT VARIANTS OF HUMAN PANCREATIC SECRETORY TRYPSIN INHIBITOR (KAZAL-TYPE)	SERINE PROTEASE/INHIBITOR COMPLEX
1CGL	STRUCTURE OF THE CATALYTIC DOMAIN OF FIBROBLAST COLLAGENASE COMPLEXED WITH AN INHIBITOR	METALLOPROTEASE
1CGS	LOCAL AND TRANSMITTED CONFORMATIONAL CHANGES ON COMPLEXATION OF AN ANTI-SWEETENER FAB	IMMUNOGLOBULIN
1CHO	CRYSTAL AND MOLECULAR STRUCTURES OF THE COMPLEX OF ALPHA-*CHYMOTRYPSIN WITH ITS INHIBITOR TURKEY OVOMUCOID THIRD DOMAIN AT 1.8 ANGSTROMS RESOLUTION	COMPLEX(SERINE PROTEINASE-INHIBITOR)

1CI6	TRANSCRIPTION FACTOR ATF4-C/EBP BETA BZIP HETERODIMER	TRANSCRIPTION
1CIC	IDIOTOPE-ANTI-IDIOTOPE FAB-FAB COMPLEX; D1.3-E225	IMMUNOGLOBULIN
1CIQ	COMPLEX OF TWO FRAGMENTS OF CI2, RESIDUES 1-40 AND 41-64	SERINE PROTEASE INHIBITOR
1CJF	PROFILIN BINDS PROLINE-RICH LIGANDS IN TWO DISTINCT AMIDE BACKBONE ORIENTATIONS	STRUCTURAL REGULATION PROTEIN
1CJK	COMPLEX OF GS-ALPHA WITH THE CATALYTIC DOMAINS OF MAMMALIAN ADENYLYL CYCLASE: COMPLEX WITH ADENOSINE 5'-(ALPHA THIO)-TRIPHOSPHATE (RP), MG, AND MN	LYASE/LYASE/SIGNALING PROTEIN
1CJR	X-RAY CRYSTALLOGRAPHIC STUDIES OF DENATURATION IN RIBONUCLEASE S	HYDROLASE
1CJT	COMPLEX OF GS-ALPHA WITH THE CATALYTIC DOMAINS OF MAMMALIAN ADENYLYL CYCLASE: COMPLEX WITH BETA-L-2',3'-DIDEOXYATP, MN, AND MG	LYASE/LYASE/SIGNALING PROTEIN
1CJU	COMPLEX OF GS-ALPHA WITH THE CATALYTIC DOMAINS OF MAMMALIAN ADENYLYL CYCLASE: COMPLEX WITH BETA-L-2',3'-DIDEOXYATP AND MG	LYASE/LYASE/SIGNALING PROTEIN
1CJV	COMPLEX OF GS-ALPHA WITH THE CATALYTIC DOMAINS OF MAMMALIAN ADENYLYL CYCLASE: COMPLEX WITH BETA-L-2',3'-DIDEOXYATP, MG, AND ZN	LYASE/LYASE/SIGNALING PROTEIN
1CK0	ANTI-ANTI-IDIOTYPIC ANTIBODY AGAINST HUMAN ANGIOTENSIN II, UNLIGANDED FORM	IMMUNOGLOBULIN
1CKN	STRUCTURE OF GUANYLYLATED MRNA CAPPING ENZYME COMPLEXED WITH GTP	CAPPING ENZYME
1CL7	ANTI HIV1 PROTEASE FAB	IMMUNE SYSTEM
1CLO	ANTI-CARCINOEMBRYONIC ANTIGEN MONOCLONAL ANTIBODY A5B7	IMMUNOGLOBULIN
1CLS	CROSS-LINKED HUMAN HEMOGLOBIN DEOXY	OXYGEN TRANSPORT
1CLV	ELLOW MEAL WORM ALPHA-AMYLASE IN COMPLEX WITH THE AMARANTH ALPHA-AMYLASE INHIBITOR	HYDROLASE
1CLY	IGG FAB (HUMAN IGG1, KAPPA) CHIMERIC FRAGMENT (CBR96) COMPLEXED WITH LEWIS Y NONOATE METHYL ESTER	IMMUNOGLOBULIN
1CLZ	IGG FAB (IGG3, KAPPA) FRAGMENT (MBR96) COMPLEXED WITH LEWIS Y NONOATE METHYL ESTER	IMMUNOGLOBULIN
1CM1	MOTIONS OF CALMODULIN-SINGLE-CONFORMER REFINEMENT	COMPLEX (CALCIUM-BINDING/TRANSFERASE)
1CMI	STRUCTURE OF THE HUMAN PIN/LC8 DIMER WITH A BOUND PEPTIDE	OXIDOREDUCTASE/OXIDOREDUCTASE INHIBITOR
1CMK	CRYSTAL STRUCTURES OF THE MYRISTYLATED CATALYTIC SUBUNIT OF CAMP-DEPENDENT PROTEIN KINASE REVEAL OPEN AND CLOSED	PHOSPHOTRANSFERASE

	CONFORMATIONS	
1CMX	STRUCTURAL BASIS FOR THE SPECIFICITY OF UBIQUITIN C-TERMINAL HYDROLASES	HYDROLASE
1CMY	THE MUTATION BETA99 ASP-TYR STABILIZES Y-A NEW, COMPOSITE QUATERNARY STATE OF HUMAN HEMOGLOBIN	OXYGEN TRANSPORT
1CN3	INTERACTION OF POLYOMAVIRUS INTERNAL PROTEIN VP2 WITH MAJOR CAPSID PROTEIN VP1 AND IMPLICATIONS FOR PARTICIPATION OF VP2 IN VIRAL ENTRY	VIRAL PROTEIN
1CN4	ERYTHROPOIETIN COMPLEXED WITH EXTRACELLULAR DOMAINS OF ERYTHROPOIETIN RECEPTOR	HAEMATOPOIETIC CYTOKINE
1COH	STRUCTURE OF HAEMOGLOBIN IN THE DEOXY QUATERNARY STATE WITH LIGAND BOUND AT THE ALPHA HAEMS	OXYGEN TRANSPORT
1COW	BOVINE MITOCHONDRIAL F1-ATPASE COMPLEXED WITH AUROVERTIN B	HYDROGEN ION TRANSPORT
1CP3	CRYSTAL STRUCTURE OF THE COMPLEX OF APOPAIN WITH THE TETRAPEPTIDE INHIBITOR ACE-DVAD-FMC	COMPLEX (PROTEASE/INHIBITOR)
1CP9	CRYSTAL STRUCTURE OF PENICILLIN G ACYLASE FROM THE BRO1 MUTANT STRAIN OF PROVIDENCIA RETTGERI	HYDROLASE
1CPC	ISOLATION, CRYSTALLIZATION, CRYSTAL STRUCTURE ANALYSIS AND REFINEMENT OF CONSTITUTIVE C-PHYCOCYANIN FROM THE CHROMATICALLY ADAPTING CYANOBACTERIUM FREMYELLA DIPLOSIPHON AT 1.66 ANGSTROMS RESOLUTION	LIGHT HARVESTING PROTEIN
1CPH	CONFORMATIONAL CHANGES IN CUBIC INSULIN CRYSTALS IN THE PH RANGE 7-11	HORMONE
1CPI	REGIOSELECTIVE STRUCTURAL AND FUNCTIONAL MIMICRY OF PEPTIDES. DESIGN OF HYDROLYTICALLY STABLE CYCLIC PEPTIDOMIMETIC INHIBITORS OF HIV-1 PROTEASE	COMPLEX (ACID PROTEINASE/PEPTIDE)
1CQ4	CI2 MUTANT WITH TETRAGLUTAMINE (MGQQQQGM) REPLACING MET59	HYDROLASE INHIBITOR
1CQH	HIGH RESOLUTION SOLUTION NMR STRUCTURE OF MIXED DISULFIDE INTERMEDIATE BETWEEN HUMAN THIOREDOXIN (C35A, C62A, C69A, C73A) MUTANT AND A 13 RESIDUE PEPTIDE COMPRISING ITS TARGET SITE IN HUMAN REF-1 (RESIDUES 59-71 OF THE P50 SUBUNIT OF NFKB), NMR, MINIMIZED AVERAGE STRUCTURE	COMPLEX (ELECTRON TRANSPORT/PEPTIDE)
1CQI	CRYSTAL STRUCTURE OF THE COMPLEX OF ADP AND MG2+ WITH DEPHOSPHORYLATED E. COLI SUCCINYL-COA SYNTHETASE	LIGASE
1CQJ	CRYSTAL STRUCTURE OF DEPHOSPHORYLATED E. COLI SUCCINYL-COA SYNTHETASE	LIGASE
1CQT	CRYSTAL STRUCTURE OF A TERNARY COMPLEX CONTAINING AN OCA-B PEPTIDE, THE OCT-1 POU DOMAIN, AND AN OCTAMER ELEMENT	GENE REGULATION/DNA

1CR9	CRYSTAL STRUCTURE OF THE ANTI-PRION FAB 3F4	IMMUNE SYSTEM
1CS0	CRYSTAL STRUCTURE OF CARBAMOYL PHOSPHATE SYNTHETASE COMPLEXED AT CYS269 IN THE SMALL SUBUNIT WITH THE TETRAHEDRAL MIMIC L-GLUTAMATE GAMMA-SEMIALDEHYDE	LIGASE
1CS4	COMPLEX OF GS-ALPHA WITH THE CATALYTIC DOMAINS OF MAMMALIAN ADENYLYL CYCLASE: COMPLEX WITH 2'-DEOXY-ADENOSINE 3'-MONOPHOSPHATE, PYROPHOSPHATE AND MG	LYASE/LYASE/SIGNALING PROTEIN
1CSE	THE HIGH-RESOLUTION X-RAY CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN SUBTILISIN CARLSBERG AND EGLIN C, AN ELASTASE INHIBITOR FROM THE LEECH HIRUDO MEDICINALIS. STRUCTURAL ANALYSIS, SUBTILISIN STRUCTURE AND INTERFACE GEOMETRY	COMPLEX(SERINE PROTEINASE-INHIBITOR)
1CSO	CRYSTAL STRUCTURE OF THE OMTKY3 P1 VARIANT OMTKY3-ILE18I IN COMPLEX WITH SGPB	HYDROLASE/HYDROLASE INHIBITOR
1CSZ	SYK TYROSINE KINASE C-TERMINAL SH2 DOMAIN COMPLEXED WITH A PHOSPHOPEPTIDEFROM THE GAMMA CHAIN OF THE HIGH AFFINITY IMMUNOGLOBIN G RECEPTOR, NMR	COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
1CT0	CRYSTAL STRUCTURE OF THE OMTKY3 P1 VARIANT OMTKY3-SER18I IN COMPLEX WITH SGPB	HYDROLASE/HYDROLASE INHIBITOR
1CT2	CRYSTAL STRUCTURE OF THE OMTKY3 P1 VARIANT OMTKY3-THR18I IN COMPLEX WITH SGPB	HYDROLASE/HYDROLASE INHIBITOR
1CT4	CRYSTAL STRUCTURE OF THE OMTKY3 P1 VARIANT OMTKY3-VAL18I IN COMPLEX WITH SGPB	HYDROLASE/HYDROLASE INHIBITOR
1CT8	CATALYTIC ANTIBODY 7C8 COMPLEX	IMMUNE SYSTEM
1CTP	STRUCTURE OF THE MAMMALIAN CATALYTIC SUBUNIT OF CAMP-DEPENDENT PROTEIN KINASE AND AN INHIBITOR PEPTIDE DISPLAYS AN OPEN CONFORMATION	TRANSFERASE(PHOSPHOTRANSFERASE)
1CU4	CRYSTAL STRUCTURE OF THE ANTI-PRION FAB 3F4 IN COMPLEX WITH ITS PEPTIDE EPITOPE	IMMUNE SYSTEM
1CVU	CRYSTAL STRUCTURE OF ARACHIDONIC ACID BOUND TO THE CYCLOOXYGENASE ACTIVE SITE OF COX-2	OXIDOREDUCTASE
1CVW	CRYSTAL STRUCTURE OF ACTIVE SITE-INHIBITED HUMAN COAGULATION FACTOR VIIA (DES-GLA)	HYDROLASE
1CW2	CRYSTAL STRUCTURE OF THE COMPLEX OF BACTERIAL TRYPTOPHAN SYNTHASE WITH THE TRANSITION STATE ANALOGUE INHIBITOR 4-(2-HYDROXYPHENYLSULFINYL)-BUTYLPHOSPHONIC ACID	LYASE
1CWD	JMAN P56LCK TYROSINE KINASE COMPLEXED WITH PHOSPHONOPEPTIDE	COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
1CWE	JMAN P56LCK TYROSINE KINASE COMPLEXED WITH PHOSPHONOPEPTIDE	COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)

1CX9	CRYSTAL STRUCTURE OF THE COMPLEX OF BACTERIAL TRYPTOPHAN SYNTHASE WITH THE TRANSITION STATE ANALOGUE INHIBITOR 4-(2-AMINOPHENYLTHIO)-BUTYLPHOSPHONIC ACID	LYASE
1CXP	CRYOGENIC CRYSTAL STRUCTURE OF HUMAN MYELOPEROXIDASE ISOFORM C	OXIDOREDUCTASE
1CXZ	RYSTAL STRUCTURE OF HUMAN RHOA COMPLEXED WITH THE EFFECTOR DOMAIN OF THE PROTEIN KINASE PKN/PRK1	SIGNALING PROTEIN
1CZ8	VASCULAR ENDOTHELIAL GROWTH FACTOR IN COMPLEX WITH AN AFFINITY MATURED ANTIBODY	IMMUNE SYSTEM
1CZQ	CRYSTAL STRUCTURE OF THE D10-P1/IQN17 COMPLEX: A D-PEPTIDE INHIBITOR OF HIV-1 ENTRY BOUND TO THE GP41 COILED-COIL POCKET.	VIRAL PROTEIN/VIRAL PROTEIN INHIBITOR
1CZY	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE TRAF DOMAIN OF HUMAN TRAF2 AND AN LMP1 BINDING PEPTIDE	APOPTOSIS
1CZZ	STRUCTURE OF TNF RECEPTOR ASSOCIATED FACTOR 2 IN COMPLEX WITH A 17-RESIDUE CD40 PEPTIDE	APOPTOSIS
1D00	STRUCTURE OF TNF RECEPTOR ASSOCIATED FACTOR 2 IN COMPLEX WITH A 5-RESIDUE CD40 PEPTIDE	APOPTOSIS
1D01	STRUCTURE OF TNF RECEPTOR ASSOCIATED FACTOR 2 IN COMPLEX WITH A HUMAN CD30 PEPTIDE	APOPTOSIS
1D09	PARTATE TRANSCARBAMOYLASE COMPLEXED WITH N-PHOSPHONACETYL-L-ASPARTATE (PALA)	TRANSFERASE
1D0A	STRUCTURE OF TNF RECEPTOR ASSOCIATED FACTOR 2 (TRAF2) IN COMPLEX WITH A HUMAN OX40 PEPTIDE	APOPTOSIS
1D0J	STRUCTURE OF TNF RECEPTOR ASSOCIATED FACTOR 2 IN COMPLEX WITH A M4-1BB PEPTIDE	APOPTOSIS
1D2V	RYSTAL STRUCTURE OF BROMIDE-BOUND HUMAN MYELOPEROXIDASE ISOFORM C AT PH 5.5	OXIDOREDUCTASE
1D2Z	THREE-DIMENSIONAL STRUCTURE OF A COMPLEX BETWEEN THE DEATH DOMAINS OF PELLE AND TUBE	APOPTOSIS
1D3B	CRYSTAL STRUCTURE OF THE D3B SUBCOMPLEX OF THE HUMAN CORE SNRNP DOMAIN AT 2.0A RESOLUTION	RNA BINDING PROTEIN
1D3D	CRYSTAL STRUCTURE OF HUMAN ALPHA THROMBIN IN COMPLEX WITH BENZOTHIOPHENE INHIBITOR 4	BLOOD CLOTTING
1D3P	CRYSTAL STRUCTURE OF HUMAN APLHA-THROMBIN IN COMPLEX WITH BENZO[B]THIOPHENE INHIBITOR 3	BLOOD CLOTTING
1D3Q	CRYSTAL STRUCTURE OF HUMAN ALPHA THROMBIN IN COMPLEX WITH BENZO[B]THIOPHENE INHIBITOR 2	BLOOD CLOTTING

1D3T	CRYSTAL STRUCTURE OF HUMAN ALPHA THROMBIN IN COMPLEX WITH BENZO[B]THIOPHENE INHIBITOR 1	BLOOD CLOTTING
1D3U	TATA-BINDING PROTEIN/TRANSCRIPTION FACTOR (II)B/BRE+TATA-BOX COMPLEX FROM PYROCOCCUS WOESEI	GENE REGULATION/DNA
1D4P	CRYSTAL STRUCTURE OF HUMAN ALPHA THROMBIN IN COMPLEX WITH 5-AMIDINOINDOLE-4-BENZYLPIPERIDINE INHIBITOR	BLOOD CLOTTING
1D4T	CRYSTAL STRUCTURE OF THE XLP PROTEIN SAP IN COMPLEX WITH A SLAM PEPTIDE	SIGNALING PROTEIN
1D4W	CRYSTAL STRUCTURE OF THE XLP PROTEIN SAP IN COMPLEX WITH SLAM PHOSPHOPEPTIDE	SIGNALING PROTEIN
1D4X	CRYSTAL STRUCTURE OF CAENORHABDITIS ELEGANS MG-ATP ACTIN COMPLEXED WITH HUMAN GELSOLIN SEGMENT 1 AT 1.75 A RESOLUTION.	CONTRACTILE PROTEIN
1D5B	UNLIGANDED MATURE OXY-COPE CATALYTIC ANTIBODY	IMMUNE SYSTEM
1D5D	THE ROLE OF PHENYLALANINE 8 IN THE STABILIZATION OF THE S PROTEIN-S PEPTIDE INTERACTION: PACKING AND CAVITIES	HYDROLASE
1D5E	THE ROLE OF PHENYLALANINE 8 IN THE STABILIZATION OF THE S PROTEIN-S PEPTIDE INTERACTION: PACKING AND CAVITIES	HYDROLASE
1D5H	RNASE S(F8A). MUTANT RIBONUCLEASE S.	HYDROLASE
1D5I	UNLIGANDED GERMLINE PRECURSOR OF AN OXY-COPE CATALYTIC ANTIBODY	IMMUNE SYSTEM
1D5L	CRYSTAL STRUCTURE OF CYANIDE-BOUND HUMAN MYELOPEROXIDASE ISOFORM C AT PH 5.5	OXIDOREDUCTASE
1D5M	X-RAY CRYSTAL STRUCTURE OF HLA-DR4 COMPLEXED WITH PEPTIDE AND SEB	IMMUNE SYSTEM
1D5S	CRYSTAL STRUCTURE OF CLEAVED ANTITRYPSIN POLYMER	HYDROLASE INHIBITOR
1D5Z	X-RAY CRYSTAL STRUCTURE OF HLA-DR4 COMPLEXED WITH PEPTIDOMIMETIC AND SEB	IMMUNE SYSTEM
1D6E	CRYSTAL STRUCTURE OF HLA-DR4 COMPLEX WITH PEPTIDOMIMETIC AND SEB	IMMUNE SYSTEM
1D6G	MOLECULAR COMPLEX OF CHOLECYSTOKININ-8 AND N-TERMINUS OF THE CHOLECYSTOKININ A RECEPTOR BY NMR SPECTROSCOPY	HORMONE/GROWTH FACTOR
1D6R	CRYSTAL STRUCTURE OF CANCER CHEMOPREVENTIVE BOWMAN-BIRK INHIBITOR IN TERNARY COMPLEX WITH BOVINE TRYPSIN AT 2.3 A RESOLUTION. STRUCTURAL BASIS OF JANUS-FACED SERINE PROTEASE INHIBITOR SPECIFICITY	HYDROLASE

1D6V	CONFORMATION EFFECTS IN BIOLOGICAL CATALYSIS INTRODUCED BY OXY-COPE ANTIBODY MATURATION	IMMUNE SYSTEM
1D7W	CRYSTAL STRUCTURE OF HUMAN MYELOPEROXIDASE ISOFORM C COMPLEXED WITH CYANIDE AND BROMIDE AT PH 4.0	OXIDOREDUCTASE
1D8D	CO-CRYSTAL STRUCTURE OF RAT PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH A K-RAS4B PEPTIDE SUBSTRATE AND FPP ANALOG AT 2.0A RESOLUTION	TRANSFERASE
1D8E	ZINC-DEPLETED FTASE COMPLEXED WITH K-RAS4B PEPTIDE SUBSTRATE AND FPP ANALOG.	TRANSFERASE
1D9K	CRYSTAL STRUCTURE OF COMPLEX BETWEEN D10 TCR AND PMHC I-AK/CA	IMMUNE SYSTEM
1DAN	COMPLEX OF ACTIVE SITE INHIBITED HUMAN BLOOD COAGULATION FACTOR VIIA WITH HUMAN RECOMBINANT SOLUBLE TISSUE FACTOR	COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND)
1DAZ	STRUCTURAL AND KINETIC ANALYSIS OF DRUG RESISTANT MUTANTS OF HIV-1 PROTEASE	HYDROLASE
1DBA	THREE-DIMENSIONAL STRUCTURE OF AN ANTI-STEROID FAB' AND PROGESTERONE-FAB' COMPLEX	IMMUNOGLOBULIN
1DBB	THREE-DIMENSIONAL STRUCTURE OF AN ANTI-STEROID FAB' AND PROGESTERONE-FAB' COMPLEX	IMMUNOGLOBULIN
1DBJ	MOLECULAR BASIS OF CROSS-REACTIVITY AND THE LIMITS OF ANTIBODY-ANTIGEN COMPLEMENTARITY	IMMUNOGLOBULIN
1DBK	MOLECULAR BASIS OF CROSS-REACTIVITY AND THE LIMITS OF ANTIBODY-ANTIGEN COMPLEMENTARITY	IMMUNOGLOBULIN
1DBM	MOLECULAR BASIS OF CROSS-REACTIVITY AND THE LIMITS OF ANTIBODY-ANTIGEN COMPLEMENTARITY	IMMUNOGLOBULIN
1DCE	RYSTAL STRUCTURE OF RAB GERANYLGERANYLTRANSFERASE FROM RAT BRAIN	TRANSFERASE
1DD3	RYSTAL STRUCTURE OF RIBOSOMAL PROTEIN L12 FROM THERMOTOGA MARITIMA	RIBOSOME
1DD4	RYSTAL STRUCTURE OF RIBOSOMAL PROTEIN L12 FROM THERMOTOGA MARITIM	RIBOSOME
1DDH	MHC CLASS I H-2DD HEAVY CHAIN COMPLEXED WITH BETA-2 MICROGLOBULIN AND AN IMMUNODOMINANT PEPTIDE P18-I10 FROM THE HUMAN IMMUNODEFICIENCY VIRUS ENVELOPE GLYCOPROTEIN 120	COMPLEX (HISTOCOMPATIBILITY/ANTIGEN)
1DE4	HEMOCHROMATOSIS PROTEIN HFE COMPLEXED WITH TRANSFERRIN RECEPTOR	METAL TRANSPORT INHIBITOR/RECEPTOR
1DE7	INTERACTION OF FACTOR XIII ACTIVATION PEPTIDE WITH ALPHA-THROMBIN: CRYSTAL STRUCTURE OF THE ENZYME-SUBSTRATE COMPLEX	HYDROLASE/BLOOD CLOTTING

1DEE	CRYSTAL STRUCTURE AT 2.7A RESOLUTION OF A COMPLEX BETWEEN A STAPHYLOCOCCUS AUREUS DOMAIN AND A FAB FRAGMENT OF A HUMAN IGM ANTIBODY	IMMUNE SYSTEM
1DEI	DESHEPTAPEPTIDE (B24-B30) INSULIN	HORMONE
1DEJ	CRYSTAL STRUCTURE OF A DICTYOSTELIUM/TETRAHYMENA CHIMERA ACTIN (MUTANT 646: Q228K/T229A/A230Y/A231K/S232E/E360H) IN COMPLEX WITH HUMAN GELSOLIN SEGMENT 1	CONTRACTILE PROTEIN
1DEV	CRYSTAL STRUCTURE OF SMAD2 MH2 DOMAIN BOUND TO THE SMAD-BINDING DOMAIN OF SARA	SIGNALING PROTEIN
1DF0	CRYSTAL STRUCTURE OF M-CALPAIN	HYDROLASE
1DFB	STRUCTURE OF A HUMAN MONOCLONAL ANTIBODY FAB FRAGMENT AGAINST GP41 OF HUMAN IMMUNODEFICIENCY VIRUS TYPE I	IMMUNOGLOBULIN
1DFJ	RIBONUCLEASE INHIBITOR COMPLEXED WITH RIBONUCLEASE A	COMPLEX (ENDONUCLEASE/INHIBITOR)
1DFK	NUCLEOTIDE-FREE SCALLOP MYOSIN S1-NEAR RIGOR STATE	CONTRACTILE PROTEIN
1DFL	SCALLOP MYOSIN S1 COMPLEXED WITH MGADP:VANADATE-TRANSITION STATE	CONTRACTILE PROTEIN
1DGH	HUMAN ERYTHROCYTE CATALASE 3-AMINO-1,2,4-TRIAZOLE COMPLEX	OXIDOREDUCTASE
1DGR	REFINED CRYSTAL STRUCTURE OF CANAVALIN FROM JACK BEAN	PLANT PROTEIN
1DGW	STRUCTURE OF THE RHOMBOHEDRAL CRYSTAL OF CANAVALIN FROM JACK BEAN	PLANT PROTEIN
1DHK	STRUCTURE OF PORCINE PANCREATIC ALPHA-AMYLASE	COMPLEX (HYDROLASE/INHIBITOR)
1DII	CRYSTAL STRUCTURE OF P-CRESOL METHYLHYDROXYLASE AT 2.5 A RESOLUTION	OXIDOREDUCTASE
1DIO	DIOL DEHYDRATASE-CYANOCOBALAMIN COMPLEX FROM KLEBSIELLA OXYTOCA	LYASE
1DIQ	CRYSTAL STRUCTURE OF P-CRESOL METHYLHYDROXYLASE WITH SUBSTRATE BOUND	OXIDOREDUCTASE
1DIT	COMPLEX OF A DIVALENT INHIBITOR WITH THROMBIN	COMPLEX (HYDROLASE/INHIBITOR)
1DJ7	CRYSTAL STRUCTURE OF FERREDOXIN THIOREDOXIN REDUCTASE	ELECTRON TRANSPORT
1DJS	IGAND-BINDING PORTION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2 IN COMPLEX WITH FGF1	HORMONE/GROWTH FACTOR/RECEPTOR
1DKD	CRYSTAL STRUCTURE OF A GROEL (APICAL DOMAIN) AND A DODECAMERIC PEPTIDE COMPLEX	CHAPERONE
1DKE	NI BETA HEME HUMAN HEMOGLOBIN	OXYGEN STORAGE/TRANSPORT

1DKF	CRYSTAL STRUCTURE OF A HETERODIMERIC COMPLEX OF RAR AND RXR LIGAND-BINDING DOMAINS	HORMONE/GROWTH FACTOR RECEPTOR
1DKG	CRYSTAL STRUCTURE OF THE NUCLEOTIDE EXCHANGE FACTOR GRPE BOUND TO THE ATPASE DOMAIN OF THE MOLECULAR CHAPERONE DNAK	COMPLEX (HSP24/HSP70)
1DKX	THE SUBSTRATE BINDING DOMAIN OF DNAK IN COMPLEX WITH A SUBSTRATE PEPTIDE, DETERMINED FROM TYPE 1 SELENOMETHIONYL CRYSTALS	COMPLEX (MOLECULAR CHAPERONE/PEPTIDE)
1DKY	THE SUBSTRATE BINDING DOMAIN OF DNAK IN COMPLEX WITH A SUBSTRATE PEPTIDE, DETERMINED FROM TYPE 2 NATIVE CRYSTALS	COMPLEX (MOLECULAR CHAPERONE/PEPTIDE)
1DKZ	THE SUBSTRATE BINDING DOMAIN OF DNAK IN COMPLEX WITH A SUBSTRATE PEPTIDE, DETERMINED FROM TYPE 1 NATIVE CRYSTALS	COMPLEX (MOLECULAR CHAPERONE/PEPTIDE)
1DLH	CRYSTAL STRUCTURE OF THE HUMAN CLASS II MHC PROTEIN HLA-DR1 COMPLEXED WITH AN INFLUENZA VIRUS PEPTIDE	HISTOCOMPATIBILITY ANTIGEN
1DLO	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1	NUCLEOTIDYLTRANSFERASE
1DM0	SHIGA TOXIN	TOXIN
1DM4	SER195ALA MUTANT OF HUMAN THROMBIN COMPLEXED WITH FIBRINOPEPTIDE A (7-16)	HYDROLASE
1DML	CRYSTAL STRUCTURE OF HERPES SIMPLEX UL42 BOUND TO THE C-TERMINUS OF HSV POL	DNA BINDING PROTEIN/TRANSFERASE
1DN0	STRUCTURE OF THE FAB FRAGMENT FROM A HUMAN IGM COLD AGGLUTININ	IMMUNE SYSTEM
1DN2	FC FRAGMENT OF HUMAN IGG1 IN COMPLEX WITH AN ENGINEERED 13 RESIDUE PEPTIDE DCAWHLGELVWCT-NH2	IMMUNE SYSTEM
1DNU	STRUCTURAL ANALYSES OF HUMAN MYELOPEROXIDASE-THIOCYANATE COMPLEX	OXIDOREDUCTASE
1DNW	HUMAN MYELOPEROXIDASE-CYANIDE-THIOCYANATE COMPLEX	OXIDOREDUCTASE
1DOA	STRUCTURE OF THE RHO FAMILY GTP-BINDING PROTEIN CDC42 IN COMPLEX WITH THE MULTIFUNCTIONAL REGULATOR RHOGDI	CELL CYCLE
1DOJ	RYSTAL STRUCTURE OF HUMAN ALPHA-THROMBIN*RWJ-51438 COMPLEX AT 1.7 A	HYDROLASE/HYDROLASE INHIBITOR
1DOW	CRYSTAL STRUCTURE OF A CHIMERA OF BETA-CATENIN AND ALPHA-CATENIN	CELL ADHESION
1DP5	THE STRUCTURE OF PROTEINASE A COMPLEXED WITH A IA3 MUTANT INHIBITOR	HYDROLASE/HYDROLASE INHIBITOR
1DPH	CONFORMATIONAL CHANGES IN CUBIC INSULIN CRYSTALS IN THE PH RANGE 7-11	HORMONE

1DPJ	THE STRUCTURE OF PROTEINASE A COMPLEXED WITH IA3 PEPTIDE INHIBITOR	HYDROLASE/HYDROLASE INHIBITOR
1DPP	DIPEPTIDE BINDING PROTEIN COMPLEX WITH GLYCYL-L-LEUCINE	COMPLEX (BINDING PROTEIN/PEPTIDE)
1DQJ	CRYSTAL STRUCTURE OF THE ANTI-LYSOZYME ANTIBODY HYHEL-63 COMPLEXED WITH HEN EGG WHITE LYSOZYME	IMMUNE SYSTEM/HYDROLASE
1DQM	CRYSTAL STRUCTURE OF ANTI-LYSOZYME ANTIBODY	IMMUNE SYSTEM
1DQQ	CRYSTAL STRUCTURE OF ANTI-LYSOZYME ANTIBODY HYHEL-63	IMMUNE SYSTEM
1DS2	CRYSTAL STRUCTURE OF SGPB:OMTKY3-COO-LEU18I	HYDROLASE/HYDROLASE INHIBITOR
1DS5	DIMERIC CRYSTAL STRUCTURE OF THE ALPHA SUBUNIT IN COMPLEX WITH TWO BETA PEPTIDES MIMICKING THE ARCHITECTURE OF THE TETRAMERIC PROTEIN KINASE CK2 HOLOENZYME.	TRANSFERASE
1DS6	CRYSTAL STRUCTURE OF A RAC-RHOGDI COMPLEX	SIGNALING PROTEIN
1DS8	OTOSYNTHETIC REACTION CENTER FROM RHODOBACTER SPHAEROIDES IN THE CHARGE-NEUTRAL DQAQB STATE WITH THE PROTON TRANSFER INHIBITOR CD2+	PHOTOSYNTHESIS
1DSZ	STRUCTURE OF THE RXR/RAR DNA-BINDING DOMAIN HETERODIMER IN COMPLEX WITH THE RETINOIC ACID RESPONSE ELEMENT DR1	TRANSCRIPTION/DNA
1DTD	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE LEECH CARBOXYPEPTIDASE INHIBITOR AND THE HUMAN CARBOXYPEPTIDASE A2 (LCI-CPA2)	HYDROLASE/HYDROLASE INHIBITOR
1DTQ	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH PETT-1 (PETT131A94)	HYDROLASE/TRANSFERASE
1DTT	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH PETT-2 (PETT130A94)	HYDROLASE/TRANSFERASE
1DTW	HUMAN BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE	OXIDOREDUCTASE
1DUY	CRYSTAL STRUCTURE OF HLA-A*0201/OCTAMERIC TAX PEPTIDE COMPLEX	IMMUNE SYSTEM
1DUZ	HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN (HLA-A 0201) IN COMPLEX WITH A NONAMERIC PEPTIDE FROM HTLV-1 TAX PROTEIN	IMMUNE SYSTEM
1DV3	OTOSYNTHETIC REACTION CENTER FROM RHODOBACTER SPHAEROIDES IN THE CHARGE-SEPARATED D+QAQB-STATE WITH THE PROTON TRANSFER INHIBITOR CD2+	PHOTOSYNTHESIS
1DV6	OTOSYNTHETIC REACTION CENTER FROM RHODOBACTER SPHAEROIDES IN THE CHARGE-NEUTRAL DQAQB STATE WITH THE PROTON TRANSFER INHIBITOR ZN2+	PHOTOSYNTHESIS
1DVA	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE PEPTIDE	HYDROLASE/HYDROLASE INHIBITOR

	EXOSITE INHIBITOR E-76 AND COAGULATION FACTOR VIIA	
1DVF	IDIOTOPIC ANTIBODY D1.3 FV FRAGMENT-ANTIIDIOTOPIC ANTIBODY E5.2 FV FRAGMENT COMPLEX	COMPLEX (IDIOTOPE-ANTIIDIOTOPE)
1DW6	STRUCTURAL AND KINETIC ANALYSIS OF DRUG RESISTANT MUTANTS OF HIV-1 PROTEASE	HYDROLASE/HYDROLASE INHIBITOR
1DX5	RYSTAL STRUCTURE OF THE THROMBIN-THROMBOMODULIN COMPLEX	SERINE PROTEINASE
1DXP	INHIBITION OF THE HEPATITIS C VIRUS NS3/4A PROTEASE. THE CRYSTAL STRUCTURES OF TWO PROTEASE-INHIBITOR COMPLEXES (APO STRUCTURE)	SERINE PROTEASE
1DXR	HOTOSYNTHETIC REACTION CENTER FROM RHODOPSEUDOMONAS VIRIDIS-HIS L168 PHE MUTANT (TERBUTRYN COMPLEX)	PHOTOSYNTHETIC REACTION CENTER
1DXT	HIGH-RESOLUTION X-RAY STUDY OF DEOXY RECOMBINANT HUMAN HEMOGLOBINS SYNTHESIZED FROM BETA-GLOBINS HAVING MUTATED AMINO TERMINI	OXYGEN TRANSPORT
1DXU	HIGH-RESOLUTION X-RAY STUDY OF DEOXY RECOMBINANT HUMAN HEMOGLOBINS SYNTHESIZED FROM BETA-GLOBINS HAVING MUTATED AMINO TERMINI	OXYGEN TRANSPORT
1DXV	HIGH-RESOLUTION X-RAY STUDY OF DEOXY RECOMBINANT HUMAN HEMOGLOBINS SYNTHESIZED FROM BETA-GLOBINS HAVING MUTATED AMINO TERMINI	OXYGEN TRANSPORT
1DY8	INHIBITION OF THE HEPATITIS C VIRUS NS3/4A PROTEASE. THE CRYSTAL STRUCTURES OF TWO PROTEASE-INHIBITOR COMPLEXES (INHIBITOR II)	SERINE PROTEASE
1DY9	INHIBITION OF THE HEPATITIS C VIRUS NS3/4A PROTEASE. THE CRYSTAL STRUCTURES OF TWO PROTEASE-INHIBITOR COMPLEXES (INHIBITOR I)	SERINE PROTEASE
1DZB	CRYSTAL STRUCTURE OF PHAGE LIBRARY-DERIVED SINGLE-CHAIN FV FRAGMENT 1F9 IN COMPLEX WITH TURKEY EGG-WHITE LYSOZYME	COMPLEX (ANTIBODY ANTIGEN)
1.00E+08	STRUCTURAL MODEL OF THE [FE]-HYDROGENASE/CYTOCHROME C553 COMPLEX COMBINING NMR AND SOFT-DOCKING	HYDROGENASE
1E0F	CRYSTAL STRUCTURE OF THE HUMAN ALPHA-THROMBIN-HAEMADIN COMPLEX: AN EXOSITE II-BINDING INHIBITOR	COAGULATION/CRYSTAL STRUCTURE/HEPARIN-B
1.00E+14	PHOTOSYNTHETIC REACTION CENTER MUTANT WITH PHE M197 REPLACED WITH ARG (CHAIN M, FM197R) AND GLY M203 REPLACED WITH ASP (CHAIN M, GM203D)	PHOTOSYNTHETIC REACTION CENTER
1E1C	METHYLMALONYL-COA MUTASE H244A MUTANT	ISOMERASE
1E1H	RYSTAL STRUCTURE OF RECOMBINANT BOTULINUM NEUROTOXIN TYPE A LIGHT CHAIN, SELF-INHIBITING ZN ENDOPEPTIDASE.	NEUROTOXIN

1E1Q	BOVINE MITOCHONDRIAL F1-ATPASE AT 100K	ATP PHOSPHORYLASE
1E1R	BOVINE MITOCHONDRIAL F1-ATPASE INHIBITED BY MG2+ADP AND ALUMINIUM FLUORIDE	ATP PHOSPHORYLASE
1.00E+27	NONSTANDARD PEPTIDE BINDING OF HLA-B*5101 COMPLEXED WITH HIV IMMUNODOMINANT EPITOPE KM1(LPPVVAKEI)	HLA B51
1.00E+28	NONSTANDARD PEPTIDE BINDING OF HLA-B*5101 COMPLEXED WITH HIV IMMUNODOMINANT EPITOPE KM2(TAFTIPSI)	HLA B51
1E3A	A SLOW PROCESSING PRECURSOR PENICILLIN ACYLASE FROM ESCHERICHIA COLI	ANTIBIOTIC RESISTANCE
1E3D	[NIFE] HYDROGENASE FROM DESULFOVIBRIO DESULFURICANS ATCC 27774	HYDROGENASE
1E3U	MAD STRUCTURE OF OXA10 CLASS D BETA-LACTAMASE	BETA-LACTAMASE
1E3W	RAT BRAIN 3-HYDROXYACYL-COA DEHYDROGENASE BINARY COMPLEX WITH NADH AND 3-KETO BUTYRATE	DEHYDROGENASE
1.00E+44	RIBONUCLEASE DOMAIN OF COLICIN E3 IN COMPLEX WITH ITS IMMUNITY PROTEIN	RIBONUCLEASE
1E4E	D-ALANYL-D-LACATE LIGASE	LIGASE
1E4K	CRYSTAL STRUCTURE OF SOLUBLE HUMAN IGG1 FC FRAGMENT-FC-GAMMA RECEPTOR III COMPLEX	COMPLEX
1E4W	CROSSREACTIVE BINDING OF A CIRCULARIZED PEPTIDE TO AN ANTI-TGFALPHA ANTIBODY FAB-FRAGMENT	COMPLEX (ANTIBODY/ANTIGEN)
1E4X	CROSSREACTIVE BINDING OF A CIRCULARIZED PEPTIDE TO AN ANTI-TGFALPHA ANTIBODY FAB-FRAGMENT	COMPLEX (ANTIBODY/ANTIGEN)
1.00E+50	AML1/CBF COMPLEX	TRANSCRIPTION FACTOR
1E6D	PHOTOSYNTHETIC REACTION CENTER MUTANT WITH TRP M115 REPLACED WITH PHE (CHAIN M, WM115F) PHE M197 REPLACED WITH ARG (CHAIN M, FM197R)	PHOTOSYNTHETIC REACTION CENTER
1E6E	DRENODOXIN REDUCTASE/ADRENODOXIN COMPLEX OF MITOCHONDRIAL P450 SYSTEMS	OXIDOREDUCTASE
1E6O	CRYSTAL STRUCTURE OF FAB13B5 AGAINST HIV-1 CAPSID PROTEIN P24	IMMUNOGLOBULIN
1E6V	METHYL-COENZYME M REDUCTASE FROM METHANOPYRUS KANDLERI	OXIDOREDUCTASE
1E6Y	METHYL-COENZYME M REDUCTASE FROM METHANOSARCINA BARKERI	OXIDOREDUCTASE
1E7P	QUINOL:FUMARATE REDUCTASE FROM WOLINELLA SUCCINOGENES	OXIDOREDUCTASE
1.00E+80	ENDOTHIAPEPSIN COMPLEX WITH RENIN INHIBITOR MERCK-KGAA-	HYDROLASE (ACID PROTEINASE)

	EMD56133	
1E8N	PROLYL OLIGOPEPTIDASE FROM PORCINE BRAIN, MUTANT, COMPLEXED WITH PEPTIDE	HYDROLASE
1E8O	CORE OF THE ALU DOMAIN OF THE MAMMALIAN SRP	SIGNALING PROTEIN/RNA
1.00E+91	STRUCTURE OF THE COMPLEX OF THE MAD1-SIN3B INTERACTION DOMAINS	EUKARYOTIC TRANSCRIPTIONAL REGULATION
1.00E+94	HSLV-HSLU FROM E.COLI	CHAPERONE
1E9H	THR 160 PHOSPHORYLATED CDK2-HUMAN CYCLIN A3 COMPLEX WITH THE INHIBITOR INDIRUBIN-5-SULPHONATE BOUND	COMPLEX (PROTEIN KINASE/CYCLIN)
1E9Y	CRYSTAL STRUCTURE OF HELICOBACTER PYLORI UREASE IN COMPLEX WITH ACETOHYDROXAMIC ACID	HYDROLASE
1E9Z	CRYSTAL STRUCTURE OF HELICOBACTER PYLORI UREASE	HYDROLASE
1EAK	CATALYTIC DOMAIN OF PROMMP-2 E404Q MUTANT	HYDROLYSE
1EAP	CRYSTAL STRUCTURE OF A CATALYTIC ANTIBODY WITH A SERINE PROTEASE ACTIVE SITE	CATALYTIC ANTIBODY
1EAY	CHEY-BINDING (P2) DOMAIN OF CHEA IN COMPLEX WITH CHEY FROM ESCHERICHIA COLI	SIGNAL TRANSDUCTION COMPLEX
1EB1	COMPLEX STRUCTURE OF HUMAN THROMBIN WITH N-METHYL-ARGININE INHIBITOR	SERINE PROTEINASE
1EBD	DIHYDROLIPOAMIDE DEHYDROGENASE COMPLEXED WITH THE BINDING DOMAIN OF THE DIHYDROLIPOAMIDE ACETYLASE	COMPLEX (OXIDOREDUCTASE/TRANSFERASE)
1EBK	STRUCTURAL AND KINETIC ANALYSIS OF DRUG RESISTANT MUTANTS OF HIV-1 PROTEASE	HYDROLASE/HYDROLASE INHIBITOR
1ED3	CRYSTAL STRUCTURE OF RAT MINOR HISTOCOMPATIBILITY ANTIGEN COMPLEX RT1-AA/MTF-E.	IMMUNE SYSTEM
1EE4	CRYSTAL STRUCTURE OF YEAST KARYOPHERIN (IMPORTIN) ALPHA IN A COMPLEX WITH A C-MYC NLS PEPTIDE	TRANSPORT PROTEIN
1EE5	YEAST KARYOPHERIN (IMPORTIN) ALPHA IN A COMPLEX WITH A NUCLEOPLASMIN NLS PEPTIDE	TRANSPORT PROTEIN
1EEO	CRYSTAL STRUCTURE OF PROTEIN TYROSINE PHOSPHATASE 1B COMPLEXED WITH ACETYL-E-L-E-F-PTYR-M-D-Y-E-NH2	HYDROLASE
1EER	CRYSTAL STRUCTURE OF HUMAN ERYTHROPOIETIN COMPLEXED TO ITS RECEPTOR AT 1.9 ANGSTROMS	COMPLEX (CYTOKINE/RECEPTOR)
1EET	HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH THE INHIBITOR MSC204	VIRAL PROTEIN, TRANSFERASE

1EEY	CRYSTAL STRUCTURE DETERMINATION OF HLA A2 COMPLEXED TO PEPTIDE GP2 WITH THE SUBSTITUTION (I2L/V5L/L9V)	IMMUNE SYSTEM
1EEZ	CRYSTAL STRUCTURE DETERMINATION OF HLA-A2.1 COMPLEXED TO GP2 PEPTIDE VARIANT(I2L/V5L)	IMMUNE SYSTEM
1EF1	CRYSTAL STRUCTURE OF THE MOESIN FERM DOMAIN/TAIL DOMAIN COMPLEX	MEMBRANE PROTEIN
1EF2	CRYSTAL STRUCTURE OF MANGANESE-SUBSTITUTED KLEBSIELLA AEROGENES UREASE	HYDROLASE
1EFN	HIV-1 NEF PROTEIN IN COMPLEX WITH R96I MUTANT FYN SH3 DOMAIN	COMPLEX (SH3 DOMAIN/VIRAL ENHANCER)
1EFP	ELECTRON TRANSFER FLAVOPROTEIN (ETF) FROM PARACOCCUS DENITRIFICANS	ELECTRON TRANSPORT
1EFR	BOVINE MITOCHONDRIAL F1-ATPASE COMPLEXED WITH THE PEPTIDE ANTIBIOTIC EFRAPEPTIN	COMPLEX (ION TRANSPORT/INHIBITOR)
1EFU	ELONGATION FACTOR COMPLEX EF-TU/EF-TS FROM ESCHERICHIA COLI	COMPLEX (TWO ELONGATION FACTORS)
1EFV	THREE-DIMENSIONAL STRUCTURE OF HUMAN ELECTRON TRANSFER FLAVOPROTEIN TO 2.1 A RESOLUTION	ELECTRON TRANSPORT
1EFX	STRUCTURE OF A COMPLEX BETWEEN THE HUMAN NATURAL KILLER CELL RECEPTOR KIR2DL2 AND A CLASS I MHC LIGAND HLA-CW3	IMMUNE SYSTEM
1EG4	STRUCTURE OF A DYSTROPHIN WW DOMAIN FRAGMENT IN COMPLEX WITH A BETA-DYSTROGLYCAN PEPTIDE	STRUCTURAL PROTEIN
1EG9	NAPHTHALENE 1,2-DIOXYGENASE WITH INDOLE BOUND IN THE ACTIVE SITE.	OXIDOREDUCTASE
1EGJ	DOMAIN 4 OF THE BETA COMMON CHAIN IN COMPLEX WITH AN ANTIBODY	IMMUNE SYSTEM
1EGM	CRYSTAL STRUCTURE OF DIOL DEHYDRATASE-CYANOCOBALAMIN COMPLEX AT 100K.	LYASE
1EGP	PROTEINASE INHIBITOR EGLIN C WITH HYDROLYSED REACTIVE CENTER	PROTEINASE INHIBITOR
1EGV	CRYSTAL STRUCTURE OF THE DIOL DEHYDRATASE-ADENINYLPENTYLCOBALAMIN COMPLEX FROM KLEBSELLA OXYTOCA UNDER THE ILLUMINATED CONDITION.	LYASE
1EHK	CRYSTAL STRUCTURE OF THE ABERRANT BA3-CYTOCHROME-C OXIDASE FROM THERMUS THERMOPHILUS	OXIDOREDUCTASE
1EHL	64M-2 ANTIBODY FAB COMPLEXED WITH D(5HT)(6-4)T	IMMUNE SYSTEM
1EIY	HE CRYSTAL STRUCTURE OF PHENYLALANYL-TRNA SYNTHETASE FROM THERMUS THERMOPHILUS COMPLEXED WITH COGNATE TRNAPHE	LIGASE/RNA
1EJ4	COCRYSTAL STRUCTURE OF EIF4E/4E-BP1 PEPTIDE	TRANSLATION

1EJ6	REOVIRUS CORE	VIRUS
1EJ7	RYSTAL STRUCTURE OF UNACTIVATED TOBACCO RUBISCO WITH BOUND PHOSPHATE IONS	LYASE
1EJH	EIF4E/EIF4G PEPTIDE/7-METHYL-GDP	TRANSLATION
1EJL	MOUSE IMPORTIN ALPHA-SV40 LARGE T ANTIGEN NLS PEPTIDE COMPLEX	PROTEIN BINDING
1EJM	CRYSTAL STRUCTURE OF THE BPTI ALA16LEU MUTANT IN COMPLEX WITH BOVINE TRYPSIN	HYDROLASE/INHIBITOR
1EJO	FAB FRAGMENT OF NEUTRALISING MONOCLONAL ANTIBODY 4C4 COMPLEXED WITH G-H LOOP FROM FMDV.	IMMUNE SYSTEM
1EJR	CRYSTAL STRUCTURE OF THE D221A VARIANT OF KLEBSIELLA AEROGENES UREASE	HYDROLASE
1EJS	CRYSTAL STRUCTURE OF THE H219N VARIANT OF KLEBSIELLA AEROGENES UREASE	HYDROLASE
1EJT	CRYSTAL STRUCTURE OF THE H219Q VARIANT OF KLEBSIELLA AEROGENES UREASE	HYDROLASE
1EJU	CRYSTAL STRUCTURE OF THE H320N VARIANT OF KLEBSIELLA AEROGENES UREASE	HYDROLASE
1EJV	CRYSTAL STRUCTURE OF THE H320Q VARIANT OF KLEBSIELLA AEROGENES UREASE	HYDROLASE
1EJW	RYSTAL STRUCTURE OF WILD-TYPE KLEBSIELLA AEROGENES UREASE AT 298K	HYDROLASE
1EJX	RYSTAL STRUCTURE OF WILD-TYPE KLEBSIELLA AEROGENES UREASE AT 100K	HYDROLASE
1EJY	MOUSE IMPORTIN ALPHA-NUCLEOPLASMIN NLS PEPTIDE COMPLEX	PROTEIN BINDING
1ELR	CRYSTAL STRUCTURE OF THE TPR2A DOMAIN OF HOP IN COMPLEX WITH THE HSP90 PEPTIDE MEEVD	CHAPERONE
1ELW	CRYSTAL STRUCTURE OF THE TPR1 DOMAIN OF HOP IN COMPLEX WITH A HSC70 PEPTIDE	CHAPERONE
1EM8	CRYSTAL STRUCTURE OF CHI AND PSI SUBUNIT HETERODIMER FROM DNA POL III	GENE REGULATION
1EMT	FAB ANTIBODY FRAGMENT OF AN C60 ANTIFULLERENE ANTIBODY	IMMUNE SYSTEM
1EMU	TRUCTURE OF THE AXIN RGS-HOMOLOGOUS DOMAIN IN COMPLEX WITH A SAMP REPEAT FROM APC	SIGNALING PROTEIN
1EMV	CRYSTAL STRUCTURE OF COLICIN E9 DNASE DOMAIN WITH ITS	IMMUNE SYSTEM

	COGNATE IMMUNITY PROTEIN IM9 (1.7 ANGSTROMS)	
1ENT	X-RAY ANALYSES OF ASPARTIC PROTEINASES. THE THREE-DIMENSIONAL STRUCTURE AT 2.1 ANGSTROMS RESOLUTION OF ENDOTHIAPEPSIN	HYDROLASE(ACID PROTEINASE)
1EO2	CRYSTAL STRUCTURE OF ACINETOBACTER SP. ADP1 PROTOCATECHUATE 3,4-DIOXYGENASE	OXIDOREDUCTASE
1EO8	INFLUENZA VIRUS HEMAGGLUTININ COMPLEXED WITH A NEUTRALIZING ANTIBODY	VIRAL PROTEIN/IMMUNE SYSTEM
1EO9	CRYSTAL STRUCTURE OF ACINETOBACTER SP. ADP1 PROTOCATECHUATE 3,4-DIOXYGENASE AT PH < 7.0	OXIDOREDUCTASE
1EOA	CRYSTAL STRUCTURE OF ACINETOBACTER SP. ADP1 PROTOCATECHUATE 3,4-DIOXYGENASE IN COMPLEX WITH CYANIDE	OXIDOREDUCTASE
1EOB	CRYSTAL STRUCTURE OF ACINETOBACTER SP. ADP1 PROTOCATECHUATE 3,4-DIOXYGENASE IN COMPLEX WITH 3,4-DIHYDROXYBENZOATE	OXIDOREDUCTASE
1EOC	CRYSTAL STRUCTURE OF ACINETOBACTER SP. ADP1 PROTOCATECHUATE 3,4-DIOXYGENASE IN COMPLEX WITH 4-NITROCATECHOL	OXIDOREDUCTASE
1EP1	CRYSTAL STRUCTURE OF LACTOCOCCUS LACTIS DIHYDROOROTATE DEHYDROGENASE B	OXIDOREDUCTASE
1EP2	CRYSTAL STRUCTURE OF LACTOCOCCUS LACTIS DIHYDROOROTATE DEHYDROGENASE B COMPLEXED WITH OROTATE	OXIDOREDUCTASE
1EP3	CRYSTAL STRUCTURE OF LACTOCOCCUS LACTIS DIHYDROOROTATE DEHYDROGENASE B. DATA COLLECTED UNDER CRYOGENIC CONDITIONS.	OXIDOREDUCTASE
1EPL	A STRUCTURAL COMPARISON OF 21 INHIBITOR COMPLEXES OF THE ASPARTIC PROTEINASE FROM ENDOTHIA PARASITICA	HYDROLASE(ACID PROTEINASE)
1EPM	A STRUCTURAL COMPARISON OF 21 INHIBITOR COMPLEXES OF THE ASPARTIC PROTEINASE FROM ENDOTHIA PARASITICA	HYDROLASE(ACID PROTEINASE)
1EPN	A STRUCTURAL COMPARISON OF 21 INHIBITOR COMPLEXES OF THE ASPARTIC PROTEINASE FROM ENDOTHIA PARASITICA	HYDROLASE(ACID PROTEINASE)
1EPO	DIRECT OBSERVATION BY X-RAY ANALYSIS OF THE TETRAHEDRAL "INTERMEDIATE" OF ASPARTIC PROTEINASES	HYDROLASE(ACID PROTEINASE)
1EPQ	ANALYSES OF LIGAND BINDING IN FIVE ENDOTHIAPEPSIN CRYSTAL COMPLEXES AND THEIR USE IN THE DESIGN AND EVALUATION OF NOVEL RENIN INHIBITORS	HYDROLASE(ACID PROTEINASE)
1EPT	REFINED 1.8 ANGSTROMS RESOLUTION CRYSTAL STRUCTURE OF PORCINE EPSILON-TRYPSIN	HYDROLASE (SERINE PROTEASE)
1EQY	COMPLEX BETWEEN RABBIT MUSCLE ALPHA-ACTIN: HUMAN GELSOLIN DOMAIN 1	CONTRACTILE PROTEIN

1EQZ	X-RAY STRUCTURE OF THE NUCLEOSOME CORE PARTICLE AT 2.5 A RESOLUTION	STRUCTURAL PROTEIN/DNA
1ER8	THE ACTIVE SITE OF ASPARTIC PROTEINASES	HYDROLASE (ACID PROTEINASE)
1ES0	CRYSTAL STRUCTURE OF THE MURINE CLASS II ALLELE I-A(G7) COMPLEXED WITH THE GLUTAMIC ACID DECARBOXYLASE (GAD65) PEPTIDE 207-220	IMMUNE SYSTEM
1ES7	COMPLEX BETWEEN BMP-2 AND TWO BMP RECEPTOR IA ECTODOMAINS	CYTOKINE
1ESV	COMPLEX BETWEEN LATRUNCULIN A:RABBIT MUSCLE ALPHA ACTIN:HUMAN GELSOLIN DOMAIN 1	CONTRACTILE PROTEIN
1ETZ	THE THREE-DIMENSIONAL STRUCTURE OF AN ANTI-SWEETENER FAB, NC10.14, SHOWS THE EXTENT OF STRUCTURAL DIVERSITY IN ANTIGEN RECOGNITION BY IMMUNOGLOBULINS	IMMUNE SYSTEM
1EUC	CRYSTAL STRUCTURE OF DEPHOSPHORYLATED PIG HEART, GTP-SPECIFIC SUCCINYL-COA SYNTHETASE	LIGASE
1EUI	ESCHERICHIA COLI URACIL-DNA GLYCOSYLASE COMPLEX WITH URACIL-DNA GLYCOSYLASE INHIBITOR PROTEIN	COMPLEX (HYDROLASE/INHIBITOR)
1EUV	X-RAY STRUCTURE OF THE C-TERMINAL ULP1 PROTEASE DOMAIN IN COMPLEX WITH SMT3, THE YEAST ORTHOLOG OF SUMO.	HYDROLASE
1EV3	STRUCTURE OF THE RHOMBOHEDRAL FORM OF THE M-CRESOL/INSULIN R6 HEXAMER	HORMONE/GROWTH FACTOR
1EV6	STRUCTURE OF THE MONOCLINIC FORM OF THE M-CRESOL/INSULIN R6 HEXAMER	HORMONE/GROWTH FACTOR
1EVR	THE STRUCTURE OF THE RESORCINOL/INSULIN R6 HEXAMER	HORMONE/GROWTH FACTOR
1EVT	CRYSTAL STRUCTURE OF FGF1 IN COMPLEX WITH THE EXTRACELLULAR LIGAND BINDING DOMAIN OF FGF RECEPTOR 1 (FGFR1)	GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1EWP	CRUZAIN BOUND TO MOR-LEU-HPQ	HYDROLASE
1EWY	ANABAENA PCC7119 FERREDOXIN:FERREDOXIN-NADP+-REDUCTASE COMPLEX	OXIDOREDUCTASE
1EXB	STRUCTURE OF THE CYTOPLASMIC BETA SUBUNIT-T1 ASSEMBLY OF VOLTAGE-DEPENDENT K CHANNELS	METAL TRANSPORT
1EYS	CRYSTAL STRUCTURE OF PHOTOSYNTHETIC REACTION CENTER FROM A THERMOPHILIC BACTERIUM, THERMOCHROMATIUM TEPIDUM	ELECTRON TRANSPORT
1EYX	CRYSTAL STRUCTURE OF R-PHYCOERYTHRIN AT 2.2 ANGSTROMS	PHOTOSYNTHESIS
1EZQ	RYSTAL STRUCTURE OF HUMAN COAGULATION FACTOR XA COMPLEXED WITH RPR128515	HYDROLASE
1EZS	CRYSTAL STRUCTURE OF ECOTIN MUTANT M84R, W67A, G68A, Y69A,	HYDROLASE/INHIBITOR

	D70A BOUND TO RAT ANIONIC TRYPSIN II	
1EZU	ECOTIN Y69F, D70P BOUND TO D102N TRYPSIN	HYDROLASE/INHIBITOR
1EZV	STRUCTURE OF THE YEAST CYTOCHROME BC1 COMPLEX CO-CRYSTALLIZED WITH AN ANTIBODY FV-FRAGMENT	OXIDOREDUCTASE/ELECTRON TRANSPORT
1EZX	CRYSTAL STRUCTURE OF A SERPIN:PROTEASE COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
1EZZ	CRYSTAL STRUCTURE OF E. COLI ASPARTATE TRANSCARBAMOYLASE P268A MUTANT IN THE T-STATE	TRANSFERASE
1F02	CRYSTAL STRUCTURE OF C-TERMINAL 282-RESIDUE FRAGMENT OF INTIMIN IN COMPLEX WITH TRANSLOCATED INTIMIN RECEPTOR (TIR) INTIMIN-BINDING DOMAIN	CELL ADHESION
1F0R	RYSTAL STRUCTURE OF HUMAN COAGULATION FACTOR XA COMPLEXED WITH RPR208815	HYDROLASE
1F0S	RYSTAL STRUCTURE OF HUMAN COAGULATION FACTOR XA COMPLEXED WITH RPR208707	HYDROLASE
1F11	F124 FAB FRAGMENT FROM A MONOCLONAL ANTI-PRES2 ANTIBODY	IMMUNE SYSTEM
1F1B	CRYSTAL STRUCTURE OF E. COLI ASPARTATE TRANSCARBAMOYLASE P268A MUTANT IN THE R-STATE IN THE PRESENCE OF N-PHOSPHONACETYL-L-ASPARTATE	TRANSFERASE
1F1J	CRYSTAL STRUCTURE OF CASPASE-7 IN COMPLEX WITH ACETYL-ASP-GLU-VAL-ASP-CHO	HYDROLASE, APOPTOSIS
1F1W	RC SH2 THREF1TRP MUTANT COMPLEXED WITH THE PHOSPHOPEPTIDE S(PTR)VNVQN	TRANSFERASE
1F2R	NMR STRUCTURE OF THE HETERODIMERIC COMPLEX BETWEEN CAD DOMAINS OF CAD AND ICAD	DNA BINDING PROTEIN
1F2S	RYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN BOVINE BETA-TRYPSIN AND MCTI-A, A TRYPSIN INHIBITOR OF SQUASH FAMILY AT 1.8 A RESOLUTION	HYDROLASE/HYDROLASE INHIBITOR
1F2T	CRYSTAL STRUCTURE OF ATP-FREE RAD50 ABC-ATPASE	REPLICATION
1F2U	CRYSTAL STRUCTURE OF RAD50 ABC-ATPASE	REPLICATION
1F34	CRYSTAL STRUCTURE OF ASCARIS PEPSIN INHIBITOR-3 BOUND TO PORCINE PEPSIN	HYDROLASE/HYDROLASE INHIBITOR
1F3D	CATALYTIC ANTIBODY 4B2 IN COMPLEX WITH ITS AMIDINIUM HAPTEN.	IMMUNE SYSTEM
1F3J	HISTOCOMPATIBILITY ANTIGEN I-AG7	IMMUNE SYSTEM
1F3M	CRYSTAL STRUCTURE OF HUMAN SERINE/THREONINE KINASE PAK1	TRANSFERASE
1F3U	CRYSTAL STRUCTURE OF THE RAP30/74 INTERACTION DOMAINS OF	TRANSCRIPTION

	HUMAN TFIIF	
1F3V	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE N-TERMINAL DOMAIN OF TRADD AND THE TRAF DOMAIN OF TRAF2	APOPTOSIS
1F45	HUMAN INTERLEUKIN-12	CYTOKINE/CYTPKINE
1F47	THE BACTERIAL CELL-DIVISION PROTEIN ZIPA AND ITS INTERACTION WITH AN FTSZ FRAGMENT REVEALED BY X-RAY CRYSTALLOGRAPHY	CELL CYCLE
1F4X	CRYSTAL STRUCTURE OF AN ANTI-CARBOHYDRATE ANTIBODY DIRECTED AGAINST VIBRIO CHOLERAE O1 IN COMPLEX WITH ANTIGEN	IMMUNE SYSTEM
1F4Y	CRYSTAL STRUCTURE OF AN ANTI-CARBOHYDRATE ANTIBODY DIRECTED AGAINST VIBRIO CHOLERAE O1 IN COMPLEX WITH ANTIGEN	IMMUNE SYSTEM
1F51	A TRANSIENT INTERACTION BETWEEN TWO PHOSPHORELAY PROTEINS TRAPPED IN A CRYSTAL LATTICE REVEALS THE MECHANISM OF MOLECULAR RECOGNITION AND PHOSPHOTRANSFER IN SINGAL TRANSDUCTION	TRANSFERASE
1F58	IGG1 FAB FRAGMENT (58.2) COMPLEX WITH 24-RESIDUE PEPTIDE (RESIDUES 308-333 OF HIV-1 GP120 (MN ISOLATE) WITH ALA TO AIB SUBSTITUTION AT POSITION 323	VIRAL PROTEIN/IMMUNE SYSTEM
1F59	IMPORTIN-BETA-FXFG NUCLEOPORIN COMPLEX	TRANSPORT PROTEIN RECEPTOR
1F5Q	CRYSTAL STRUCTURE OF MURINE GAMMA HERPESVIRUS CYCLIN COMPLEXED TO HUMAN CYCLIN DEPENDENT KINASE 2	TRANSFERASE
1F60	CRYSTAL STRUCTURE OF THE YEAST ELONGATION FACTOR COMPLEX EEF1A:EEF1BA	TRANSLATION
1F66	2.6 A CRYSTAL STRUCTURE OF A NUCLEOSOME CORE PARTICLE CONTAINING THE VARIANT HISTONE H2A.Z	STRUCTURAL PROTEIN/DNA
1F6F	CRYSTAL STRUCTURE OF THE TERNARY COMPLEX BETWEEN OVINE PLACENTAL LACTOGEN AND THE EXTRACELLULAR DOMAIN OF THE RAT PROLACTIN RECEPTOR	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR
1F6M	CRYSTAL STRUCTURE OF A COMPLEX BETWEEN THIOREDOXIN REDUCTASE, THIOREDOXIN, AND THE NADP+ ANALOG, AADP+	OXIDOREDUCTASE
1F6N	CRYSTAL STRUCTURE ANALYSIS OF THE MUTANT REACTION CENTER PRO L209-> TYR FROM THE PHOTOSYNTHETIC PURPLE BACTERIUM RHODOBACTER SPHAEROIDES	PHOTOSYNTHESIS
1F7A	HOW DOES A SYMMETRIC DIMER RECOGNIZE AN ASYMMETRIC SUBSTRATE? A SUBSTRATE COMPLEX OF HIV-1 PROTEASE.	HYDROLASE
1F80	HOLO-(ACYL CARRIER PROTEIN) SYNTHASE IN COMPLEX WITH HOLO-(ACYL CARRIER PROTEIN)	TRANSFERASE
1F8A	STRUCTURAL BASIS FOR THE PHOSPHOSERINE-PROLINE RECOGNITION	ISOMERASE

	BY GROUP IV WW DOMAINS	
1F8T	FAB (LNKB-2) OF MONOCLONAL ANTIBODY, CRYSTAL STRUCTURE	IMMUNE SYSTEM
1F8U	CRYSTAL STRUCTURE OF MUTANT E202Q OF HUMAN ACETYLCHOLINESTERASE COMPLEXED WITH GREEN MAMBA VENOM PEPTIDE FASCICULIN-II	HYDROLASE/TOXIN
1F8V	THE STRUCTURE OF PARIACOTO VIRUS REVEALS A DODECAHEDRAL CAGE OF DUPLEX RNA	VIRUS/RNA
1F90	FAB FRAGMENT OF MONOCLONAL ANTIBODY (LNKB-2) AGAINST HUMAN INTERLEUKIN-2 IN COMPLEX WITH ANTIGENIC PEPTIDE	IMMUNE SYSTEM
1F93	CRYSTAL STRUCTURE OF A COMPLEX BETWEEN THE DIMERIZATION DOMAIN OF HNF-1 ALPHA AND THE COACTIVATOR DCOH	TRANSCRIPTION
1F95	SOLUTION STRUCTURE OF DYNEIN LIGHT CHAIN 8 (DLC8) AND BIM PEPTIDE COMPLEX	CONTRACTILE PROTEIN/APOPTOSIS
1F99	CRYSTAL STRUCTURE OF R-PHYCOCYANIN FROM POLYSIPHONIA AT 2.4 A RESOLUTION	PHOTOSYNTHESIS
1F9E	CASPASE-8 SPECIFICITY PROBED AT SUBSITE S4: CRYSTAL STRUCTURE OF THE CASPASE-8-Z-DEVD-CHO	APOPTOSIS
1FAI	THREE-DIMENSIONAL STRUCTURE OF TWO CRYSTAL FORMS OF FAB R19.9, FROM A MONOCLONAL ANTI-ARSONATE ANTIBODY	IMMUNOGLOBULIN
1FAK	HUMAN TISSUE FACTOR COMPLEXED WITH COAGULATION FACTOR VIIA INHIBITED WITH A BPTI-MUTANT	BLOOD CLOTTING
1FAP	HE STRUCTURE OF THE IMMUNOPHILIN-IMMUNOSUPPRESSANT FKBP12-RAPAMYCIN COMPLEX INTERACTING WITH HUMAN FRAP	COMPLEX (ISOMERASE/KINASE)
1FAV	THE STRUCTURE OF AN HIV-1 SPECIFIC CELL ENTRY INHIBITOR IN COMPLEX WITH THE HIV-1 GP41 TRIMERIC CORE	VIRAL PROTEIN
1FAW	GRAYLAG GOOSE HEMOGLOBIN (OXY FORM)	OXYGEN STORAGE/TRANSPORT
1FBI	RYSTAL STRUCTURE OF A CROSS-REACTION COMPLEX BETWEEN FAB F9.13.7 AND GUINEA-FOWL LYSOZYME	COMPLEX (ANTIBODY/ANTIGEN)
1FBV	STRUCTURE OF A CBL-UBCH7 COMPLEX: RING DOMAIN FUNCTION IN UBIQUITIN-PROTEIN LIGASES	LIGASE
1FCC	CRYSTAL STRUCTURE OF THE C2 FRAGMENT OF STREPTOCOCCAL PROTEIN G IN COMPLEX WITH THE FC DOMAIN OF HUMAN IGG	COMPLEX (ANTIBODY/ANTIGEN)
1FCD	HE STRUCTURE OF FLAVOCYTOCHROME C SULFIDE DEHYDROGENASE FROM A PURPLE PHOTOTROPHIC BACTERIUM CHROMATIUM VINOSUM AT 2.5 ANGSTROMS RESOLUTION	ELECTRON TRANSPORT(FLAVOCYTOCHROME)
1FCH	CRYSTAL STRUCTURE OF THE PTS1 COMPLEXED TO THE TPR REGION OF HUMAN PEX5	SIGNALING PROTEIN

1FDH	STRUCTURE OF HUMAN FOETAL DEOXYHAEMOGLOBIN	OXYGEN TRANSPORT
1FDL	CRYSTALLOGRAPHIC REFINEMENT OF THE THREE-DIMENSIONAL STRUCTURE OF THE FAB D1.3-LYSOZYME COMPLEX AT 2.5-ANGSTROMS RESOLUTION	COMPLEX (ANTIBODY-ANTIGEN)
1FE8	CRYSTAL STRUCTURE OF THE VON WILLEBRAND FACTOR A3 DOMAIN IN COMPLEX WITH A FAB FRAGMENT OF IGG RU5 THAT INHIBITS COLLAGEN BINDING	IMMUNE SYSTEM
1FEJ	STRUCTURAL IMPLICATIONS OF DRUG RESISTANT MUTANTS OF HIV-1 PROTEASE: HIGH RESOLUTION CRYSTAL STRUCTURES OF THE MUTANT PROTEASE/SUBSTRATE ANALOG COMPLEXES	HYDROLASE/HYDROLASE INHIBITOR
1FEV	CRYSTAL STRUCTURE OF THE ALA4AIB MUTATION IN RNASE S	HYDROLASE
1FF0	STRUCTURAL IMPLICATIONS OF DRUG RESISTANT MUTANTS OF HIV-1 PROTEASE: HIGH RESOLUTION CRYSTAL STRUCTURES OF THE MUTANT PROTEASE/SUBSTRATE ANALOG COMPLEXES.	HYDROLASE/HYDROLASE INHIBITOR
1FFF	STRUCTURAL IMPLICATIONS OF DRUG RESISTANT MUTANTS OF HIV-1 PROTEASE : HIGH RESOLUTION CRYSTAL STRUCTURES OF THE MUTANT PROTEASE/SUBSTRATE ANALOG COMPLEXES.	HYDROLASE/HYDROLASE INHIBITOR
1FFG	CHEY-BINDING DOMAIN OF CHEA IN COMPLEX WITH CHEY AT 2.1 A RESOLUTION	TRANSFERASE/SIGNALING PROTEIN
1FFI	STRUCTURAL IMPLICATIONS OF DRUG RESISTANT MUTANTS OF HIV-1 PROTEASE: HIGH RESOLUTION CRYSTAL STRUCTURES OF THE MUTANT PROTEASE/SUBSTRATE ANALOG COMPLEXES	HYDROLASE/HYDROLASE INHIBITOR
1FFK	CRYSTAL STRUCTURE OF THE LARGE RIBOSOMAL SUBUNIT FROM HALOARCULA MARISMORTUI AT 2.4 ANGSTROM RESOLUTION	RIBOSOME
1FFN	CRYSTAL STRUCTURE OF MURINE CLASS I H-2DB COMPLEXED WITH PEPTIDE GP33(C9M)	IMMUNE SYSTEM/SIGNALING PROTEIN
1FFO	CRYSTAL STRUCTURE OF MURINE CLASS I H-2DB COMPLEXED WITH SYNTHETIC PEPTIDE GP33 (C9M/K1A)	IMMUNE SYSTEM/SIGNALING PROTEIN
1FFP	CRYSTAL STRUCTURE OF MURINE CLASS I H-2DB COMPLEXED WITH PEPTIDE GP33 (C9M/K1S)	IMMUNE SYSTEM/SIGNALING PROTEIN
1FFS	CHEY-BINDING DOMAIN OF CHEA IN COMPLEX WITH CHEY FROM CRYSTALS SOAKED IN ACETYL PHOSPHATE	TRANSFERASE/SIGNALING PROTEIN
1FFT	THE STRUCTURE OF UBIQUINOL OXIDASE FROM ESCHERICHIA COLI	OXIDOREDUCTASE
1FFU	CARBON MONOXIDE DEHYDROGENASE FROM HYDROGENOPHAGA PSEUDOFLAVA WHICH LACKS THE MO-PYRANOPTERIN MOIETY OF THE MOLYBDENUM COFACTOR	HYDROLASE
1FFV	CARBON MONOXIDE DEHYDROGENASE FROM HYDROGENOPHAGA PSEUDOFLAVA	HYDROLASE

1FFW	CHEY-BINDING DOMAIN OF CHEA IN COMPLEX WITH CHEY WITH A BOUND IMIDO DIPHOSPHATE	TRANSFERASE/SIGNALING PROTEIN
1FFX	TUBULIN:STATHMIN-LIKE DOMAIN COMPLEX	STRUCTURAL PROTEIN
1FFZ	LARGE RIBOSOMAL SUBUNIT COMPLEXED WITH R(CC)-DA-PUROMYCIN	RIBOSOME
1FG2	CRYSTAL STRUCTURE OF THE LCMV PEPTIDIC EPITOPE GP33 IN COMPLEX WITH THE MURINE CLASS I MHC MOLECULE H-2DB	IMMUNE SYSTEM
1FG6	STRUCTURAL IMPLICATIONS OF DRUG RESISTANT MUTANTS OF HIV-1 PROTEASE: HIGH RESOLUTION CRYSTAL STRUCTURES OF THE MUTANT PROTEASE/SUBSTRATE ANALOG COMPLEXES	HYDROLASE/HYDROLASE INHIBITOR
1FG9	3:1 COMPLEX OF INTERFERON-GAMMA RECEPTOR WITH INTERFERON-GAMMA DIMER	IMMUNE SYSTEM
1FGC	STRUCTURAL IMPLICATIONS OF DRUG RESISTANT MUTANTS OF HIV-1 PROTEASE: HIGH RESOLUTION CRYSTAL STRUCTURES OF THE MUTANT PROTEASE/SUBSTRATE ANALOG COMPLEXES	HYDROLASE/HYDROLASE INHIBITOR
1FGN	MONOCLONAL MURINE ANTIBODY 5G9-ANTI-HUMAN TISSUE FACTOR	IMMUNOGLOBULIN
1FGO	LIPOXYGENASE-1 (SOYBEAN) AT 100K, Q495A MUTANT	OXIDOREDUCTASE
1FH0	CRYSTAL STRUCTURE OF HUMAN CATHEPSIN V COMPLEXED WITH AN IRREVERSIBLE VINYL SULFONE INHIBITOR	HYDROLASE
1FH5	CRYSTAL STRUCTURE OF THE FAB FRAGMENT OF THE MONOCLONAL ANTIBODY MAK33	IMMUNE SYSTEM
1FHJ	RYSTAL STRUCTURE OF AQUOMET HEMOGLOBIN-I OF THE MANED WOLF (CHRYSOCYON BRACHYURUS) AT 2.0 RESOLUTION.	OXYGEN STORAGE/TRANSPORT
1FI8	RAT GRANZYME B [N66Q] COMPLEXED TO ECOTIN [81-84 IEPD]	HYDROLASE/HYDROLASE INHIBITOR
1FIG	ROUTES TO CATALYSIS: STRUCTURE OF A CATALYTIC ANTIBODY AND COMPARISON WITH ITS NATURAL COUNTERPART	IMMUNOGLOBULIN
1FIN	CYCLIN A-CYCLIN-DEPENDENT KINASE 2 COMPLEX	COMPLEX (TRANSFERASE/CYCLIN)
1FIP	THE STRUCTURE OF FIS MUTANT PRO61ALA ILLUSTRATES THAT THE KINK WITHIN THE LONG ALPHA-HELIX IS NOT DUE TO THE PRESENCE OF THE PROLINE RESIDUE	DNA-BINDING PROTEIN
1FIQ	CRYSTAL STRUCTURE OF XANTHINE OXIDASE FROM BOVINE MILK	OXIDOREDUCTASE
1FIW	THREE-DIMENSIONAL STRUCTURE OF BETA-ACROSIN FROM RAM SPERMATOZOA	HYDROLASE
1FIZ	THREE DIMENSIONAL STRUCTURE OF BETA-ACROSIN FROM BOAR SPERMATOZOA	HYDROLASE
1FJ1	LYME DISEASE ANTIGEN OSPA IN COMPLEX WITH NEUTRALIZING	IMMUNE SYSTEM

	ANTIBODY FAB LA-2	
1FJG	TRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT IN COMPLEX WITH THE ANTIBIOTICS STREPTOMYCIN, SPECTINOMYCIN, AND PAROMOMYCIN	RIBOSOME
1FJM	PROTEIN SERINE/THREONINE PHOSPHATASE-1 (ALPHA ISOFORM, TYPE I) COMPLEXED WITH MICROCYSTIN-LR TOXIN	COMPLEX (HYDROLASE/TOXIN)
1FJS	CRYSTAL STRUCTURE OF THE INHIBITOR ZK-807834 (CI-1031) COMPLEXED WITH FACTOR XA	BLOOD CLOTTING
1FK9	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH DMP-266(EFAVIRENZ)	TRANSFERASE
1FKA	STRUCTURE OF FUNCTIONALLY ACTIVATED SMALL RIBOSOMAL SUBUNIT AT 3.3 A RESOLUTION	RIBOSOME
1FKO	CRYSTAL STRUCTURE OF NNRTI RESISTANT K103N MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH DMP-266(EFAVIRENZ)	TRANSFERASE
1FKP	CRYSTAL STRUCTURE OF NNRTI RESISTANT K103N MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH NEVIRAPINE	TRANSFERASE
1FL3	CRYSTAL STRUCTURE OF THE BLUE FLUORESCENT ANTIBODY (19G2) IN COMPLEX WITH STILBENE HAPTEN AT 277K	IMMUNE SYSTEM
1FL5	THE UNLIGANDED GERMLINE PRECURSOR TO THE SULFIDE OXIDASE CATALYTIC ANTIBODY 28B4.	IMMUNE SYSTEM
1FL6	HE HAPTEN COMPLEXED GERMLINE PRECURSOR TO SULFIDE OXIDASE CATALYTIC ANTIBODY 28B4	IMMUNE SYSTEM
1FL7	HUMAN FOLLICLE STIMULATING HORMONE	HORMONE/GROWTH FACTOR
1FLC	X-RAY STRUCTURE OF THE HAEMAGGLUTININ-ESTERASE-FUSION GLYCOPROTEIN OF INFLUENZA C VIRUS	HYDROLASE
1FLR	4-4-20 FAB FRAGMENT	IMMUNOGLOBULIN
1FLT	VEGF IN COMPLEX WITH DOMAIN 2 OF THE FLT-1 RECEPTOR	COMPLEX (GROWTH FACTOR/TRANSFERASE)
1FM0	MOLYBDOPTERIN SYNTHASE (MOAD/MOAE)	TRANSFERASE
1FM2	HE 2 ANGSTROM CRYSTAL STRUCTURE OF CEPHALOSPORIN ACYLASE	HYDROLASE
1FM6	THE 2.1 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HETERODIMER OF THE HUMAN RXRALPHA AND PPARGAMMA LIGAND BINDING DOMAINS RESPECTIVELY BOUND WITH 9-CIS RETINOIC ACID AND ROSIGLITAZONE AND CO-ACTIVATOR PEPTIDES.	TRANSCRIPTION
1FM9	THE 2.1 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HETERODIMER OF THE HUMAN RXRALPHA AND PPARGAMMA LIGAND BINDING DOMAINS RESPECTIVELY BOUND WITH 9-CIS RETINOIC ACID AND GI262570 AND CO-ACTIVATOR PEPTIDES.	TRANSCRIPTION

1FMA	MOLYBDOPTERIN SYNTHASE (MOAD/MOAE)	TRANSFERASE
1FMO	CRYSTAL STRUCTURE OF A POLYHISTIDINE-TAGGED RECOMBINANT CATALYTIC SUBUNIT OF CAMP-DEPENDENT PROTEIN KINASE COMPLEXED WITH THE PEPTIDE INHIBITOR PKI(5-24) AND ADENOSINE	COMPLEX (PHOSPHOTRANSFERASE/INHIBITOR)
1FN3	CRYSTAL STRUCTURE OF NICKEL RECONSTITUTED HEMOGLOBIN-A CASE FOR PERMANENT, T-STATE HEMOGLOBIN	OXYGEN STORAGE/TRANSPORT
1FN4	CRYSTAL STRUCTURE OF FAB198, AN EFFICIENT PROTECTOR OF ACETYLCHOLINE RECEPTOR AGAINST MYASTHENOGENIC ANTIBODIES	IMMUNE SYSTEM
1FN8	FUSARIUM OXYSPORUM TRYPSIN AT ATOMIC RESOLUTION	HYDROLASE
1FNE	HISTOCOMPATIBILITY ANTIGEN	IMMUNE SYSTEM
1FNG	HISTOCOMPATIBILITY ANTIGEN	IMMUNE SYSTEM
1FNP	CRYSTAL STRUCTURE ANALYSIS OF THE MUTANT REACTION CENTER PRO L209-> PHE FROM THE PHOTOSYNTHETIC PURPLE BACTERIUM RHODOBACTER SPHAEROIDES	PHOTOSYNTHESIS
1FNQ	CRYSTAL STRUCTURE ANALYSIS OF THE MUTANT REACTION CENTER PRO L209-> GLU FROM THE PHOTOSYNTHETIC PURPLE BACTERIUM RHODOBACTER SPHAEROIDES	PHOTOSYNTHESIS
1FNS	CRYSTAL STRUCTURE OF THE VON WILLEBRAND FACTOR (VWF) A1 DOMAIN I546V MUTANT IN COMPLEX WITH THE FUNCTION BLOCKING FAB NMC4	IMMUNE SYSTEM
1FNT	CRYSTAL STRUCTURE OF THE 20S PROTEASOME FROM YEAST IN COMPLEX WITH THE PROTEASOME ACTIVATOR PA26 FROM TRYPANOSOME BRUCEI AT 3.2 ANGSTROMS RESOLUTION	HYDROLASE/HYDROLASE ACTIVATOR
1FO0	MURINE ALLOREACTIVE SCFV TCR-PEPTIDE-MHC CLASS I MOLECULE COMPLEX	IMMUNE SYSTEM
1FOE	CRYSTAL STRUCTURE OF RAC1 IN COMPLEX WITH THE GUANINE NUCLEOTIDE EXCHANGE REGION OF TIAM1	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALI
1FOR	STRUCTURE DETERMINATION OF AN FAB FRAGMENT THAT NEUTRALIZES HUMAN RHINOVIRUS AND ANALYSIS OF THE FAB-VIRUS COMPLEX	IMMUNOGLOBULIN
1FOS	TWO HUMAN C-FOS:C-JUN:DNA COMPLEXES	TRANSCRIPTION/DNA
1FP4	CRYSTAL STRUCTURE OF THE ALPHA-H195Q MUTANT OF NITROGENASE	OXIDOREDUCTASE
1FPC	ACTIVE SITE MIMETIC INHIBITION OF THROMBIN	COMPLEX (SERINE PROTEASE/INHIBITOR)
1FPH	THE INTERACTION OF THROMBIN WITH FIBRINOGEN: A STRUCTURAL BASIS FOR ITS SPECIFICITY	HYDROLASE(SERINE PROTEINASE)
1FPP	PROTEIN FARNESYLTRANSFERASE COMPLEX WITH FARNESYL	PRENYLTRANSFERASE

	DIPHOSPHATE	
1FPR	CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN THE CATALYTIC DOMAIN OF SHP-1 AND AN IN VITRO PEPTIDE SUBSTRATE PY469 DERIVED FROM SHPS-1.	SIGNALING PROTEIN
1FPT	THREE-DIMENSIONAL STRUCTURE OF THE COMPLEX BETWEEN THE FAB FRAGMENT OF AN NEUTRALIZING ANTIBODY FOR TYPE 1 POLIOVIRUS AND ITS VIRAL EPITOPE	COMPLEX (ANTIBODY/PV-1 FRAGMENT)
1FQ1	CRYSTAL STRUCTURE OF KINASE ASSOCIATED PHOSPHATASE (KAP) IN COMPLEX WITH PHOSPHO-CDK2	HYDROLASE/TRANSFERASE
1FQJ	CRYSTAL STRUCTURE OF THE HETEROTRIMERIC COMPLEX OF THE RGS DOMAIN OF RGS9, THE GAMMA SUBUNIT OF PHOSPHODIESTERASE AND THE GT/I1 CHIMERA ALPHA SUBUNIT [(RGS9)-(PDEGAMMA)-(GT/I1ALPHA)-(GDP)-(ALF4-)-(MG2+)]	SIGNALING PROTEIN
1FQK	CRYSTAL STRUCTURE OF THE HETERODIMERIC COMPLEX OF THE RGS DOMAIN OF RGS9, AND THE GT/I1 CHIMERA ALPHA SUBUNIT [(RGS9)-(GT/I1ALPHA)-(GDP)-(ALF4-)-(MG2+)]	SIGNALING PROTEIN
1FQV	INSIGHTS INTO SCF UBIQUITIN LIGASES FROM THE STRUCTURE OF THE SKP1-SKP2 COMPLEX	LIGASE
1FQX	CRYSTAL STRUCTURE OF THE COMPLEX OF HIV-1 PROTEASE WITH A PEPTIDOMIMETIC INHIBITOR	HYDROLASE
1FR2	CRYSTAL STRUCTURE OF THE E9 DNASE DOMAIN WITH A MUTANT IMMUNITY PROTEIN IM9(E41A)	IMMUNE SYSTEM
1FRF	CRYSTAL STRUCTURE OF THE NI-FE HYDROGENASE FROM DESULFOVIBRIO FRUCTOSOVORANS	OXIDOREDUCTASE
1FRG	CRYSTAL STRUCTURE, SEQUENCE, AND EPITOPE MAPPING OF A PEPTIDE COMPLEX OF AN ANTI-INFLUENZA HA PEPTIDE ANTIBODY FAB 26(SLASH)9: FINE-TUNING ANTIBODY SPECIFICITY	VIRAL PROTEIN/IMMUNE SYSTEM
1FRT	CRYSTAL STRUCTURE OF THE COMPLEX OF RAT NEONATAL FC RECEPTOR WITH FC	COMPLEX (RECEPTOR/IMMUNOGLOBULIN)
1FRV	CRYSTAL STRUCTURE OF THE OXIDIZED FORM OF NI-FE HYDROGENASE	OXIDOREDUCTASE
1FS0	COMPLEX OF GAMMA/EPSILON ATP SYNTHASE FROM E.COLI	HYDROLASE
1FS1	INSIGHTS INTO SCF UBIQUITIN LIGASES FROM THE STRUCTURE OF THE SKP1-SKP2 COMPLEX	LIGASE
1FS2	INSIGHTS INTO SCF UBIQUITIN LIGASES FROM THE STRUCTURE OF THE SKP1-SKP2 COMPLEX	LIGASE
1FSK	COMPLEX FORMATION BETWEEN A FAB FRAGMENT OF A MONOCLONAL IGG ANTIBODY AND THE MAJOR ALLERGEN FROM BIRCH POLLEN BET V 1	IMMUNE SYSTEM

1FSS	ACETYLCHOLINESTERASE (E.C. 3.1.1.7) COMPLEXED WITH FASCICULIN-II	COMPLEX (SERINE ESTERASE/TOXIN)
1FSX	HE X-RAY STRUCTURE DETERMINATION OF BOVINE CARBONMONOXY HB AT 2.1 A RESOLUTION AND ITS RELATIONSHIP TO THE QUATERNARY STRUCTURE OF OTHER HB CRYSTAL FORMS	OXYGEN STORAGE/TRANSPORT
1FT1	CRYSTAL STRUCTURE OF PROTEIN FARNESYLTRANSFERASE AT 2.25 ANGSTROMS RESOLUTION	TRANSFERASE
1FT2	CO-CRYSTAL STRUCTURE OF PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH A FARNESYL DIPHOSPHATE SUBSTRATE	TRANSFERASE
1FU2	FIRST PROTEIN STRUCTURE DETERMINED FROM X-RAY POWDER DIFFRACTION DATA	HORMONE/GROWTH FACTOR
1FU5	NMR STRUCTURE OF THE N-SH2 DOMAIN OF THE P85 SUBUNIT OF PI3-KINASE COMPLEXED TO A DOUBLY PHOSPHORYLATED PEPTIDE DERIVED FROM POLYOMAVIRUS MIDDLE T ANTIGEN	PEPTIDE BINDING PROTEIN
1FUB	FIRST PROTEIN STRUCTURE DETERMINED FROM X-RAY POWDER DIFFRACTION DATA	HORMONE/GROWTH FACTOR
1FUY	CRYSTAL STRUCTURE OF BETAA169L/BETAC170W DOUBLE MUTANT OF TRYPTOPHAN SYNTHASE COMPLEXED WITH 5-FLUORO-INDOLE-PROPANOL PHOSPHATE	LYASE
1FV1	STRUCTURAL BASIS FOR THE BINDING OF AN IMMUNODOMINANT PEPTIDE FROM MYELIN BASIC PROTEIN IN DIFFERENT REGISTERS BY TWO HLA-DR2 ALLELES	IMMUNE SYSTEM
1FVD	X-RAY STRUCTURES OF THE ANTIGEN-BINDING DOMAINS FROM THREE VARIANTS OF HUMANIZED ANTI-P185-HER2 ANTIBODY 4D5 AND COMPARISON WITH MOLECULAR MODELING	IMMUNOGLOBULIN
1FVE	X-RAY STRUCTURES OF THE ANTIGEN-BINDING DOMAINS FROM THREE VARIANTS OF HUMANIZED ANTI-P185-HER2 ANTIBODY 4D5 AND COMPARISON WITH MOLECULAR MODELING	IMMUNOGLOBULIN
1FVU	CRYSTAL STRUCTURE OF BOTROCETIN	TOXIN
1FVV	THE STRUCTURE OF CDK2/CYCLIN A IN COMPLEX WITH AN OXINDOLE INHIBITOR	TRANSFERASE, CELL CYCLE
1FWA	KLEBSIELLA AEROGENES UREASE, C319A VARIANT AT PH 7.5	HYDROLASE
1FWB	KLEBSIELLA AEROGENES UREASE, C319A VARIANT AT PH 6.5	HYDROLASE
1FWC	KLEBSIELLA AEROGENES UREASE, C319A VARIANT AT PH 8.5	HYDROLASE
1FWD	KLEBSIELLA AEROGENES UREASE, C319A VARIANT AT PH 9.4	HYDROLASE
1FWE	KLEBSIELLA AEROGENES UREASE, C319A VARIANT WITH ACETOHYDROXAMIC ACID (AHA) BOUND	HYDROLASE

1FWF	KLEBSIELLA AEROGENES UREASE, C319D VARIANT	HYDROLASE
1FWG	KLEBSIELLA AEROGENES UREASE, C319S VARIANT	HYDROLASE
1FWH	KLEBSIELLA AEROGENES UREASE, C319Y VARIANT	HYDROLASE
1FWI	KLEBSIELLA AEROGENES UREASE, H134A VARIANT	HYDROLASE
1FWJ	KLEBSIELLA AEROGENES UREASE, NATIVE	HYDROLASE
1FX0	CRYSTAL STRUCTURE OF THE CHLOROPLAST F1-ATPASE FROM SPINACH	HYDROLASE
1FXH	MUTANT OF PENICILLIN ACYLASE IMPAIRED IN CATALYSIS WITH PHENYLACETIC ACID IN THE ACTIVE SITE	HYDROLASE
1FXK	CRYSTAL STRUCTURE OF ARCHAEAL PREFOLDIN (GIMC).	CHAPERONE
1FXT	STRUCTURE OF A CONJUGATING ENZYME-UBIQUITIN THIOLESTER COMPLEX	LIGASE
1FXV	PENICILLIN ACYLASE MUTANT IMPAIRED IN CATALYSIS WITH PENICILLIN G IN THE ACTIVE SITE	HYDROLASE
1FXW	CRYSTAL STRUCTURE OF THE RECOMBINANT ALPHA1/ALPHA2 CATALYTIC HETERODIMER OF BOVINE BRAIN PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB.	HYDROLASE
1FXY	COAGULATION FACTOR XA-TRYPSIN CHIMERA INHIBITED WITH D-PHE-PRO-ARG-CHLOROMETHYLKETONE	COMPLEX (PROTEASE/INHIBITOR)
1FY4	FUSARIUM OXYSPORUM TRYPSIN AT ATOMIC RESOLUTION	HYDROLASE
1FY5	FUSARIUM OXYSPORUM TRYPSIN AT ATOMIC RESOLUTION	HYDROLASE
1FYH	1:1 COMPLEX BETWEEN AN INTERFERON GAMMA SINGLE-CHAIN VARIANT AND ITS RECEPTOR	IMMUNE SYSTEM
1FYR	DIMER FORMATION THROUGH DOMAIN SWAPPING IN THE CRYSTAL STRUCTURE OF THE GRB2-SH2 AC-PYVNV COMPLEX	HORMONE/GROWTH FACTOR
1FYT	CRYSTAL STRUCTURE OF A COMPLEX OF A HUMAN ALPHA/BETA-T CELL RECEPTOR, INFLUENZA HA ANTIGEN PEPTIDE, AND MHC CLASS II MOLECULE, HLA-DR1	IMMUNE SYSTEM
1FYZ	METHANE MONOOXYGENASE HYDROXYLASE, FORM II REDUCED BY SOAKING	OXIDOREDUCTASE
1FZ0	METHANE MONOOXYGENASE HYDROXYLASE, FORM II MIXED-VALENT GROWN ANAEROBICALLY	OXIDOREDUCTASE
1FZ1	METHANE MONOOXYGENASE HYDROXYLASE, FORM III OXIDIZED	OXIDOREDUCTASE
1FZ2	METHANE MONOOXYGENASE HYDROXYLASE, FORM II MIXED-VALENT GENERATED BY CRYSTAL SOAKING	OXIDOREDUCTASE

1FZ3	METHANE MONOOXYGENASE HYDROXYLASE, FORM III SOAK AT PH 6.2 (0.1 M PIPES)	OXIDOREDUCTASE
1FZ4	METHANE MONOOXYGENASE HYDROXYLASE, FORM III SOAKED AT PH 8.5 (0.1 M TRIS)	OXIDOREDUCTASE
1FZ5	METHANE MONOOXYGENASE HYDROXYLASE, FORM II CRYSTALLIZED ANAEROBICALLY FROM REDUCED ENZYME	OXIDOREDUCTASE
1FZ6	METHANE MONOOXYGENASE HYDROXYLASE, FORM II SOAKED IN 1 M METHANOL	OXIDOREDUCTASE
1FZ7	METHANE MONOOXYGENASE HYDROXYLASE, FORM III SOAKED IN 0.9 M ETHANOL	OXIDOREDUCTASE
1FZ8	ETHANE MONOOXYGENASE HYDROXYLASE, FORM II COCRYSTALLIZED WITH DIBROMOMETHANE	OXIDOREDUCTASE
1FZ9	ETHANE MONOOXYGENASE HYDROXYLASE, FORM II COCRYSTALLIZED WITH IODOETHANE	OXIDOREDUCTASE
1FZA	CRYSTAL STRUCTURE OF FIBRINOGEN FRAGMENT D	BLOOD COAGULATION
1FZB	CRYSTAL STRUCTURE OF CROSSLINKED FRAGMENT D	BLOOD COAGULATION
1FZC	CRYSTAL STRUCTURE OF FRAGMENT DOUBLE-D FROM HUMAN FIBRIN WITH TWO DIFFERENT BOUND LIGANDS	BLOOD COAGULATION
1FZE	CRYSTAL STRUCTURE OF FRAGMENT DOUBLE-D FROM HUMAN FIBRIN	BLOOD COAGULATION
1FZF	CRYSTAL STRUCTURE OF FRAGMENT DOUBLE-D FROM HUMAN FIBRIN WITH THE PEPTIDE LIGAND GLY-HIS-ARG-PRO-AMIDE	BLOOD COAGULATION
1FZG	RYSTAL STRUCTURE OF FRAGMENT D FROM HUMAN FIBRINOGEN WITH THE PEPTIDE LIGAND GLY-HIS-ARG-PRO-AMIDE	BLOOD COAGULATION
1FZH	ETHANE MONOOXYGENASE HYDROXYLASE, FORM II PRESSURIZED WITH XENON GAS	OXIDOREDUCTASE
1FZI	ETHANE MONOOXYGENASE HYDROXYLASE, FORM I PRESSURIZED WITH XENON GAS	OXIDOREDUCTASE
1FZJ	MHC CLASS I NATURAL MUTANT H-2KBM1 HEAVY CHAIN COMPLEXED WITH BETA-2 MICROGLOBULIN AND VESICULAR STOMATITIS VIRUS NUCLEOPROTEIN	IMMUNE SYSTEM
1FZK	MHC CLASS I NATURAL MUTANT H-2KBM1 HEAVY CHAIN COMPLEXED WITH BETA-2 MICROGLOBULIN AND SENDAI VIRUS NUCLEOPROTEIN	IMMUNE SYSTEM
1FZM	MHC CLASS I NATURAL MUTANT H-2KBM8 HEAVY CHAIN COMPLEXED WITH BETA-2 MICROGLOBULIN AND VESICULAR STOMATITIS VIRUS NUCLEOPROTEIN	IMMUNE SYSTEM
1FZO	MHC CLASS I NATURAL MUTANT H-2KBM8 HEAVY CHAIN COMPLEXED WITH BETA-2 MICROGLOBULIN AND SENDAI VIRUS NUCLEOPROTEIN	IMMUNE SYSTEM

1G08	CARBONMONOXY LIGANDED BOVINE HEMOGLOBIN PH 5.0	OXYGEN STORAGE/TRANSPORT
1G09	CARBONMONOXY LIGANDED BOVINE HEMOGLOBIN PH 7.2	OXYGEN STORAGE/TRANSPORT
1G0A	CARBONMONOXY LIGANDED BOVINE HEMOGLOBIN PH 8.5	OXYGEN STORAGE/TRANSPORT
1G0B	CARBONMONOXY LIGANDED EQUINE HEMOGLOBIN PH 8.5	OXYGEN STORAGE/TRANSPORT
1G0U	A GATED CHANNEL INTO THE PROTEASOME CORE PARTICLE	HYDROLASE
1G0V	THE STRUCTURE OF PROTEINASE A COMPLEXED WITH A IA3 MUTANT, MVV	HYDROLASE/HYDROLASE INHIBITOR
1G1F	CRYSTAL STRUCTURE OF PROTEIN TYROSINE PHOSPHATASE 1B COMPLEXED WITH A TRI-PHOSPHORYLATED PEPTIDE (RDI(PTR) ETD(PTR)(PTR)RK) FROM THE INSULIN RECEPTOR KINASE	HYDROLASE, SIGNALING PROTEIN
1G1G	CRYSTAL STRUCTURE OF PROTEIN TYROSINE PHOSPHATASE 1B COMPLEXED WITH A MONO-PHOSPHORYLATED PEPTIDE (ETDY(PTR) RKGGKGLL) FROM THE INSULIN RECEPTOR KINASE	HYDROLASE, SIGNALING PROTEIN
1G1H	CRYSTAL STRUCTURE OF PROTEIN TYROSINE PHOSPHATASE 1B COMPLEXED WITH A BIS-PHOSPHORYLATED PEPTIDE (ETD(PTR)(PTR) RKGGKGLL) FROM THE INSULIN RECEPTOR KINASE	HYDROLASE, SIGNALING PROTEIN
1G1S	P-SELECTIN LECTIN/EGF DOMAINS COMPLEXED WITH PSGL-1 PEPTIDE	IMMUNE SYSTEM, MEMBRANE PROTEIN
1G1X	STRUCTURE OF RIBOSOMAL PROTEINS S15, S6, S18, AND 16S RIBOSOMAL RNA	RIBOSOME
1G20	IGATP-BOUND AND NUCLEOTIDE-FREE STRUCTURES OF A NITROGENASE PROTEIN COMPLEX BETWEEN LEU127DEL-FE PROTEIN AND THE MOFE PROTEIN	OXIDOREDUCTASE
1G21	IGATP-BOUND AND NUCLEOTIDE-FREE STRUCTURES OF A NITROGENASE PROTEIN COMPLEX BETWEEN LEU127DEL-FE PROTEIN AND THE MOFE PROTEIN	OXIDOREDUCTASE
1G2C	HUMAN RESPIRATORY SYNCYTIAL VIRUS FUSION PROTEIN CORE	VIRAL PROTEIN
1G30	THROMBIN INHIBITOR COMPLEX	HYDROLASE
1G32	THROMBIN INHIBITOR COMPLEX	HYDROLASE
1G3F	NMR STRUCTURE OF A 9 RESIDUE PEPTIDE FROM SMAC/DIABLO COMPLEXED TO THE BIR3 DOMAIN OF XIAP	APOPTOSIS
1G3I	RYSTAL STRUCTURE OF THE HSLUV PROTEASE-CHAPERONE COMPLEX	CHAPERONE/HYDROLASE
1G3J	CRYSTAL STRUCTURE OF THE XTCF3-CBD/BETA-CATENIN ARMADILLO REPEAT COMPLEX	TRANSCRIPTION
1G3N	STRUCTURE OF A P18(INK4C)-CDK6-K-CYCLIN TERNARY COMPLEX	CELL CYCLE, SIGNALING PROTEIN

1G4A	CRYSTAL STRUCTURES OF THE HSLVU PEPTIDASE-ATPASE COMPLEX REVEAL AN ATP-DEPENDENT PROTEOLYSIS MECHANISM	CHAPERONE/HYDROLASE
1G4B	CRYSTAL STRUCTURES OF THE HSLVU PEPTIDASE-ATPASE COMPLEX REVEAL AN ATP-DEPENDENT PROTEOLYSIS MECHANISM	CHAPERONE/HYDROLASE
1G4U	CRYSTAL STRUCTURE OF THE SALMONELLA TYROSINE PHOSPHATASE AND GTPASE ACTIVATING PROTEIN SPTP BOUND TO RAC1	SIGNALING PROTEIN
1G4Y	1.60 A CRYSTAL STRUCTURE OF THE GATING DOMAIN FROM SMALL CONDUCTANCE POTASSIUM CHANNEL COMPLEXED WITH CALCIUM-CALMODULIN	SIGNALING PROTEIN
1G5J	COMPLEX OF BCL-XL WITH PEPTIDE FROM BAD	APOPTOSIS
1G5Q	EPID H67N COMPLEXED WITH SUBSTRATE PEPTIDE DSYTC	OXIDOREDUCTASE
1G65	CRYSTAL STRUCTURE OF EPOXOMICIN:20S PROTEASOME REVEALS A MOLECULAR BASIS FOR SELECTIVITY OF ALPHA,BETA-EPOXYKETONE PROTEASOME INHIBITORS	HYDROLASE
1G6R	A FUNCTIONAL HOT SPOT FOR ANTIGEN RECOGNITION IN A SUPERAGONIST TCR/MHC COMPLEX	IMMUNE SYSTEM
1G6V	COMPLEX OF THE CAMELID HEAVY-CHAIN ANTIBODY FRAGMENT CAB-CA05 WITH BOVINE CARBONIC ANHYDRASE	LYASE/IMMUNE SYSTEM
1G72	ATALYTIC MECHANISM OF QUINOPROTEIN METHANOL DEHYDROGENASE: A THEORETICAL AND X-RAY CRYSTALLOGRAPHIC INVESTIGATION	OXIDOREDUCTASE
1G73	CRYSTAL STRUCTURE OF SMAC BOUND TO XIAP-BIR3 DOMAIN	APOPTOSIS/APOPTOSIS INHIBITOR
1G7A	1.2 A STRUCTURE OF T3R3 HUMAN INSULIN AT 100 K	HORMONE/GROWTH FACTOR
1G7B	1.3 A STRUCTURE OF T3R3 HUMAN INSULIN AT 100 K	HORMONE/GROWTH FACTOR
1G7C	YEAST EEF1A:EEF1BA IN COMPLEX WITH GDPNP	TRANSLATION
1G7H	CRYSTAL STRUCTURE OF HEN EGG WHITE LYSOZYME (HEL) COMPLEXED WITH THE MUTANT ANTI-HEL MONOCLONAL ANTIBODY D1.3(VLW92A)	HYDROLASE INHIBITOR/HYDROLASE
1G7I	CRYSTAL STRUCTURE OF HEN EGG WHITE LYSOZYME (HEL) COMPLEXED WITH THE MUTANT ANTI-HEL MONOCLONAL ANTIBODY D1.3 (VLW92F)	HYDROLASE INHIBITOR/HYDROLASE
1G7J	CRYSTAL STRUCTURE OF HEN EGG WHITE LYSOZYME (HEL) COMPLEXED WITH THE MUTANT ANTI-HEL MONOCLONAL ANTIBODY D1.3 (VLW92H)	HYDROLASE INHIBITOR/HYDROLASE
1G7L	CRYSTAL STRUCTURE OF HEN EGG WHITE LYSOZYME (HEL) COMPLEXED WITH THE MUTANT ANTI-HEL MONOCLONAL ANTIBODY D1.3 (VLW92S)	HYDROLASE INHIBITOR/HYDROLASE
1G7M	CRYSTAL STRUCTURE OF HEN EGG WHITE LYSOZYME (HEL) COMPLEXED WITH THE MUTANT ANTI-HEL MONOCLONAL ANTIBODY D1.3 (VLW92V)	HYDROLASE INHIBITOR/HYDROLASE
1G7P	CRYSTAL STRUCTURE OF MHC CLASS I H-2KB HEAVY CHAIN COMPLEXED WITH BETA-2 MICROGLOBULIN AND YEAST ALPHA-	IMMUNE SYSTEM

	GLUCOSIDASE	
1G7Q	CRYSTAL STRUCTURE OF MHC CLASS I H-2KB HEAVY CHAIN COMPLEXED WITH BETA-2 MICROGLOBULIN AND MUC1 VNTR PEPTIDE SAPDTRPA	IMMUNE SYSTEM
1G8K	CRYSTAL STRUCTURE ANALYSIS OF ARSENITE OXIDASE FROM ALCALIGENES FAECALIS	OXIDOREDUCTASE
1G9M	HIV-1 HXBC2 GP120 ENVELOPE GLYCOPROTEIN COMPLEXED WITH CD4 AND INDUCED NEUTRALIZING ANTIBODY 17B	VIRAL PROTEIN/IMMUNE SYSTEM
1G9N	HIV-1 YU2 GP120 ENVELOPE GLYCOPROTEIN COMPLEXED WITH CD4 AND INDUCED NEUTRALIZING ANTIBODY 17B	VIRAL PROTEIN/IMMUNE SYSTEM
1G9V	HIGH RESOLUTION CRYSTAL STRUCTURE OF DEOXY HEMOGLOBIN COMPLEXED WITH A POTENT ALLOSTERIC EFFECTOR	OXYGEN STORAGE/TRANSPORT
1GAF	48G7 HYBRIDOMA LINE FAB COMPLEXED WITH HAPTEN 5-(PARA-NITROPHENYL PHOSPHONATE)-PENTANOIC ACID	CATALYTIC ANTIBODY
1GAG	CRYSTAL STRUCTURE OF THE INSULIN RECEPTOR KINASE IN COMPLEX WITH A BISUBSTRATE INHIBITOR	TRANSFERASE, SIGNALING PROTEIN
1GAQ	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN FERREDOXIN AND FERREDOXIN-NADP+ REDUCTASE	OXIDOREDUCTASE/ELECTRON TRANSPORT
1GBU	DEOXY (BETA-(C93A,C112G)) HUMAN HEMOGLOBIN	OXYGEN TRANSPORT
1GBV	(ALPHA-OXY, BETA-(C112G)DEOXY) T-STATE HUMAN HEMOGLOBIN	OXYGEN TRANSPORT
1GC1	HIV-1 GP120 CORE COMPLEXED WITH CD4 AND A NEUTRALIZING HUMAN ANTIBODY	VIRAL PROTEIN/RECEPTOR/IMMUNE SYSTEM
1GCV	DEOXY FORM HEMOGLOBIN FROM MUSTELUS GRISEUS	OXYGEN STORAGE/TRANSPORT
1GCW	CO FORM HEMOGLOBIN FROM MUSTELUS GRISEUS	OXYGEN STORAGE/TRANSPORT
1GDN	FUSARIUM OXYSPORUM TRYPSIN AT ATOMIC RESOLUTION	HYDROLASE
1GDQ	FUSARIUM OXYSPORUM TRYPSIN AT ATOMIC RESOLUTION	HYDROLASE
1GDU	FUSARIUM OXYSPORUM TRYPSIN AT ATOMIC RESOLUTION	HYDROLASE
1GEC	LYCYL ENDOPEPTIDASE-COMPLEX WITH BENZYLOXYCARBONYL-LEUCINE-VALINE-GLYCINE-METHYLENE COVALENTLY BOUND TO CYSTEINE 25	COMPLEX (PROTEINASE/INHIBITOR)
1GFW	THE 2.8 ANGSTROM CRYSTAL STRUCTURE OF CASPASE-3 (APOPAIN OR CPP32)IN COMPLEX WITH AN ISATIN SULFONAMIDE INHIBITOR.	HYDROLASE
1GG2	G PROTEIN HETEROTRIMER MUTANT GI_ALPHA_1(G203A) BETA_1 GAMMA_2 WITH GDP BOUND	COMPLEX (GTP-BINDING/TRANSDUCER)
1GG6	CRYSTAL STUCTURE OF GAMMA CHYMOTRYPSIN WITH N-ACETYL-PHENYLALANINE TRIFLUOROMETHYL KETONE BOUND AT THE ACTIVE	HYDROLASE/HYDROLASE INHIBITOR

	SITE	
1GGB	MAJOR ANTIGEN-INDUCED DOMAIN REARRANGEMENTS IN AN ANTIBODY	IMMUNOGLOBULIN
1GGC	MAJOR ANTIGEN-INDUCED DOMAIN REARRANGEMENTS IN AN ANTIBODY	IMMUNOGLOBULIN
1GGD	CRYSTAL STUCTURE OF GAMMA CHYMOTRYPSIN WITH N-ACETYL-LEUCIL-PHENYLALANINE ALDEHYDE BOUND AT THE ACTIVE SITE	HYDROLASE/HYDROLASE INHIBITOR
1GGI	CRYSTAL STRUCTURE OF AN HIV-1 NEUTRALIZING ANTIBODY 50.1 IN COMPLEX WITH ITS V3 LOOP PEPTIDE ANTIGEN	IMMUNOGLOBULIN
1GGP	CRYSTAL STRUCTURE OF TRICHOSANTHES KIRILOWII LECTIN-1 AND ITS RELATION TO THE TYPE 2 RIBOSOME INACTIVATING PROTEINS	SUGAR BINDING PROTEIN
1GH0	CRYSTAL STRUCTURE OF C-PHYCOCYANIN FROM SPIRULINA PLATENSIS	PHOTOSYNTHESIS
1GH6	RETINOBLASTOMA POCKET COMPLEXED WITH SV40 LARGE T ANTIGEN	ANTITUMOR PROTEIN
1GHA	A SECOND ACTIVE SITE IN CHYMOTRYPSIN? THE X-RAY CRYSTAL STRUCTURE OF N-ACETYL-D-TRYPTOPHAN BOUND TO GAMMA-CHYMOTRYPSIN	HYDROLASE(SERINE PROTEINASE)
1GHD	CRYSTAL STRUCTURE OF THE GLUTARYL-7-AMINOCEPHALOSPORANIC ACID ACYLASE BY MAD PHASING	HYDROLASE
1GHF	ANTI-ANTI-IDIOTYPE GH1002 FAB FRAGMENT	ANTIBODY FAB FRAGMENT
1GHQ	CR2-C3D COMPLEX STRUCTURE	IMMUNE SYSTEM/VIRAL PROTEIN RECEPTOR
1GHV	A NOVEL SERINE PROTEASE INHIBITION MOTIF INVOLVING A MULTI-CENTERED SHORT HYDROGEN BONDING NETWORK AT THE ACTIVE SITE	BLOOD CLOTTING
1GHW	A NOVEL SERINE PROTEASE INHIBITION MOTIF INVOLVING A MULTI-CENTERED SHORT HYDROGEN BONDING NETWORK AT THE ACTIVE SITE	BLOOD CLOTTING
1GHX	A NOVEL SERINE PROTEASE INHIBITION MOTIF INVOLVING A MULTI-CENTERED SHORT HYDROGEN BONDING NETWORK AT THE ACTIVE SITE	BLOOD CLOTTING
1GHY	A NOVEL SERINE PROTEASE INHIBITION MOTIF INVOLVING A MULTI-CENTERED SHORT HYDROGEN BONDING NETWORK AT THE ACTIVE SITE	BLOOD CLOTTING
1GIG	REFINED THREE-DIMENSIONAL STRUCTURE OF THE FAB FRAGMENT OF A MURINE IGG1, LAMBDA ANTIBODY	IMMUNOGLOBULIN
1GJ4	SELECTIVITY AT S1, H2O DISPLACEMENT, UPA, TPA, SER190/ALA190 PROTEASE, STRUCTURE-BASED DRUG DESIGN	BLOOD CLOTTING, HYDROLASE
1GJ5	SELECTIVITY AT S1, H2O DISPLACEMENT, UPA, TPA, SER190/ALA190 PROTEASE, STRUCTURE-BASED DRUG DESIGN	BLOOD CLOTTING, HYDROLASE
1GJA	ENGINEERING INHIBITORS HIGHLY SELECTIVE FOR THE S1 SITES OF SER190 TRYPSIN-LIKE SERINE PROTEASE DRUG TARGETS	BLOOD CLOTTING, HYDROLASE
1GK0	STRUCTURE-BASED PREDICTION OF MODIFICATIONS IN	HYDROLASE

	GLUTARYLAMIDASE TO ALLOW SINGLE-STEP ENZYMATIC PRODUCTION OF 7-AMINOCEPHALOSPORANIC ACID FROM CEPHALOSPORIN C	
1GK1	STRUCTURE-BASED PREDICTION OF MODIFICATIONS IN GLUTARYLAMIDASE TO ALLOW SINGLE-STEP ENZYMATIC PRODUCTION OF 7-AMINOCEPHALOSPORANIC ACID FROM CEPHALOSPORIN C	HYDROLASE
1GK8	RUBISCO FROM CHLAMYDOMONAS REINHARDTII	LYASE
1GK9	CRYSTAL STRUCTURES OF PENICILLIN ACYLASE ENZYME-SUBSTRATE COMPLEXES: STRUCTURAL INSIGHTS INTO THE CATALYTIC MECHANISM	ANTIBIOTIC RESISTANCE
1GKF	CRYSTAL STRUCTURES OF PENICILLIN ACYLASE ENZYME-SUBSTRATE COMPLEXES: STRUCTURAL INSIGHTS INTO THE CATALYTIC MECHANISM	ANTIBIOTIC RESISTANCE
1GKT	NEUTRON LAUE DIFFRACTION STRUCTURE OF ENDOTHIAPEPSIN COMPLEXED WITH TRANSITION STATE ANALOGUE INHIBITOR H261	COMPLEX (PROTEASE/INHIBITOR)
1GL0	TRUCTURE OF THE COMPLEX BETWEEN BOVINE ALPHA-CHYMOTRYPSIN AND PMP-D2V, AN INHIBITOR FROM THE INSECT LOCUSTA MIGRATORIA	COMPLEX (PROTEASE/INHIBITOR)
1GL1	TRUCTURE OF THE COMPLEX BETWEEN BOVINE ALPHA-CHYMOTRYPSIN AND PMP-C, AN INHIBITOR FROM THE INSECT LOCUSTA MIGRATORIA	COMPLEX (PROTEASE/INHIBITOR)
1GLA	STRUCTURE OF THE REGULATORY COMPLEX OF ESCHERICHIA COLI IIIGLC WITH GLYCEROL KINASE	PHOSPHOTRANSFERASE
1GLB	STRUCTURE OF THE REGULATORY COMPLEX OF ESCHERICHIA COLI IIIGLC WITH GLYCEROL KINASE	PHOSPHOTRANSFERASE
1GLC	CATION PROMOTED ASSOCIATION (CPA) OF A REGULATORY AND TARGET PROTEIN IS CONTROLLED BY PHOSPHORYLATION	PHOSPHOTRANSFERASE
1GLD	CATION PROMOTED ASSOCIATION (CPA) OF A REGULATORY AND TARGET PROTEIN IS CONTROLLED BY PHOSPHORYLATION	PHOSPHOTRANSFERASE
1GLE	CATION PROMOTED ASSOCIATION (CPA) OF A REGULATORY AND TARGET PROTEIN IS CONTROLLED BY PHOSPHORYLATION	PHOSPHOTRANSFERASE
1GLI	DEOXYHEMOGLOBIN T38W (ALPHA CHAINS), V1G (ALPHA AND BETA CHAINS)	OXYGEN TRANSPORT
1GM7	CRYSTAL STRUCTURES OF PENICILLIN ACYLASE ENZYME-SUBSTRATE COMPLEXES: STRUCTURAL INSIGHTS INTO THE CATALYTIC MECHANISM	HYDROLASE
1GM8	CRYSTAL STRUCTURES OF PENICILLIN ACYLASE ENZYME-SUBSTRATE COMPLEXES: STRUCTURAL INSIGHTS INTO THE CATALYTIC MECHANISM	HYDROLASE
1GM9	CRYSTAL STRUCTURES OF PENICILLIN ACYLASE ENZYME-SUBSTRATE COMPLEXES: STRUCTURAL INSIGHTS INTO THE CATALYTIC MECHANISM	HYDROLASE
1GMC	THE X-RAY CRYSTAL STRUCTURE OF THE TETRAHEDRAL INTERMEDIATE OF GAMMA-CHYMOTRYPSIN IN HEXANE	HYDROLASE(SERINE PROTEASE)

1GMD	X-RAY CRYSTAL STRUCTURE OF GAMMA-CHYMOTRYPSIN IN HEXANE	HYDROLASE(SERINE PROTEASE)
1GMH	REFINED CRYSTAL STRUCTURE OF "AGED" AND "NON-AGED" ORGANOPHOSPHORYL CONJUGATES OF GAMMA-CHYMOTRYPSIN	HYDROLASE(SERINE PROTEINASE)
1GO3	STRUCTURE OF AN ARCHEAL HOMOLOG OF THE EUKARYOTIC RNA POLYMERASE II RPB4/RPB7 COMPLEX	TRANSFERASE
1GO4	CRYSTAL STRUCTURE OF MAD1-MAD2 REVEALS A CONSERVED MAD2 BINDING MOTIF IN MAD1 AND CDC20.	CELL CYCLE
1GOT	HETEROTRIMERIC COMPLEX OF A GT-ALPHA/GI-ALPHA CHIMERA AND THE GT-BETA-GAMMA SUBUNITS	COMPLEX (GTP-BINDING/TRANSDUCER)
1GP2	G PROTEIN HETEROTRIMER GI_ALPHA_1 BETA_1 GAMMA_2 WITH GDP BOUND	COMPLEX (GTP-BINDING/TRANSDUCER)
1GPQ	STRUCTURE OF IVY COMPLEXED WITH ITS TARGET, HEWL	LYSOZYME/INHIBITOR COMPLEX
1GPW	STRUCTURAL EVIDENCE FOR AMMONIA TUNNELING ACROSS THE (BETA/ALPHA)8 BARREL OF THE IMIDAZOLE GLYCEROL PHOSPHATE SYNTHASE BIENZYME COMPLEX.	COMPLEX (LYASE/TRANSFERASE)
1GRN	CRYSTAL STRUCTURE OF THE CDC42/CDC42GAP/ALF3 COMPLEX.	GENE REGULATION
1GRU	OLUTION STRUCTURE OF GROES-ADP7-GROEL-ATP7 COMPLEX BY CRYO-EM	CHAPERONIN
1GSS	THREE-DIMENSIONAL STRUCTURE OF CLASS PI GLUTATHIONE S-TRANSFERASE FROM HUMAN PLACENTA IN COMPLEX WITH S-HEXYLGLUTATHIONE AT 2.8 ANGSTROMS RESOLUTION	TRANSFERASE(GLUTATHIONE)
1GUA	HUMAN RAP1A, RESIDUES 1-167, DOUBLE MUTANT (E30D,K31E) COMPLEXED WITH GPPNHP AND THE RAS-BINDING-DOMAIN OF HUMAN C-RAF1, RESIDUES 51-131	COMPLEX (GTP-BINDING/ATP-BINDING)
1GUJ	INSULIN AT PH 2: STRUCTURAL ANALYSIS OF THE CONDITIONS PROMOTING INSULIN FIBRE FORMATION.	HORMONE
1GUL	HUMAN GLUTATHIONE TRANSFERASE A4-4 COMPLEX WITH IODOBENZYL GLUTATHIONE	TRANSFERASE
1GUX	RB POCKET BOUND TO E7 LXCXE MOTIF	COMPLEX (TRANSCRIPTION REG/PEPTIDE)
1GVE	AFLATOXIN ALDEHYDE REDUCTASE (AKR7A1) FROM RAT LIVER	OXIDOREDUCTASE
1GVT	ENDOTHIAPEPSIN COMPLEX WITH CP-80,794	HYDROLASE
1GVU	ENDOTHIAPEPSIN COMPLEX WITH H189	HYDROLASE
1GVW	ENDOTHIAPEPSIN COMPLEX WITH PD-130,328	HYDROLASE
1GWQ	HUMAN OESTROGEN RECEPTOR ALPHA LIGAND-BINDING DOMAIN IN COMPLEX WITH RALOXIFENE CORE AND TIF2 NRBOX2 PEPTIDE	NUCLEAR RECEPTOR

1GWR	HUMAN OESTROGEN RECEPTOR ALPHA LIGAND-BINDING DOMAIN IN COMPLEX WITH 17BETA-OESTRADIOL AND TIF2 NRBOX3 PEPTIDE	NUCLEAR RECEPTOR
1GX7	BEST MODEL OF THE ELECTRON TRANSFER COMPLEX BETWEEN CYTOCHROME C3 AND [FE]-HYDROGENASE	OXIDOREDUCTASE
1GXD	PROMMP-2/TIMP-2 COMPLEX	HYDROLASE
1GXS	CRYSTAL STRUCTURE OF HYDROXYNITRILE LYASE FROM SORGHUM BICOLOR IN COMPLEX WITH INHIBITOR BENZOIC ACID: A NOVEL CYANOGENIC ENZYME	LYASE
1GY3	PCDK2/CYCLIN A IN COMPLEX WITH MGADP, NITRATE AND PEPTIDE SUBSTRATE	CELL CYCLE REGULATORY PROTEIN KINASE
1GYB	N77Y POINT MUTANT OF YNTF2 BOUND TO FXFG NUCLEOPORIN REPEAT	NUCLEAR TRANSPORT
1GZL	CRYSTAL STRUCTURE OF C14LINKMID/IQN17: A CROSS-LINKED INHIBITOR OF HIV-1 ENTRY BOUND TO THE GP41 HYDROPHOBIC POCKET	GLYCOPROTEIN
1GZS	RYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE GEF DOMAIN OF THE SALMONELLA TYPHIMURIUM SOPE TOXIN AND HUMAN CDC42	COMPLEX (TOXIN/CELL CYCLE PROTEIN)
1GZX	OXY T STATE HAEMOGLOBIN: OXYGEN BOUND AT ALL FOUR HAEMS	OXYGEN TRANSPORT
1H0D	CRYSTAL STRUCTURE OF HUMAN ANGIOGENIN IN COMPLEX WITH FAB FRAGMENT OF ITS MONOCLONAL ANTIBODY MAB 26-2F	COMPLEX (ANTIBODY/HYDROLASE)
1H0G	COMPLEX OF A CHITINASE WITH THE NATURAL PRODUCT CYCLOPENTAPEPTIDE ARGADIN FROM CLONOSTACHYS	HYDROLASE
1H0H	TUNGSTEN CONTAINING FORMATE DEHYDROGENASE FROM DESULFOVIBRIO GIGAS	DEHYDROGENASE
1H0I	COMPLEX OF A CHITINASE WITH THE NATURAL PRODUCT CYCLOPENTAPEPTIDE ARGIFIN FROM GLIOCLADIU	HYDROLASE
1H15	X-RAY CRYSTAL STRUCTURE OF HLA-DRA1*0101/DRB5*0101 COMPLEXED WITH A PEPTIDE FROM EPSTEIN BARR VIRUS DNA POLYMERASE	COMPLEX (MHC/ANTIGEN)
1H1L	NITROGENASE MO-FE PROTEIN FROM KLEBSIELLA PNEUMONIAE, NIFV MUTANT	OXIDOREDUCTASE
1H1P	TRUCTURE OF HUMAN THR160-PHOSPHO CDK2/CYCLIN A COMPLEXED WITH THE INHIBITOR NU2058	TRANSFERASE
1H1Q	TRUCTURE OF HUMAN THR160-PHOSPHO CDK2/CYCLIN A COMPLEXED WITH THE INHIBITOR NU6094	TRANSFERASE
1H1R	TRUCTURE OF HUMAN THR160-PHOSPHO CDK2/CYCLIN A COMPLEXED WITH THE INHIBITOR NU6086	TRANSFERASE
1H1S	TRUCTURE OF HUMAN THR160-PHOSPHO CDK2/CYCLIN A COMPLEXED	TRANSFERASE

	WITH THE INHIBITOR NU6102	
1H1V	GELSOLIN G4-G6/ACTIN COMPLEX	ACTIN-BINDING
1H24	CDK2/CYCLIN A IN COMPLEX WITH A 9 RESIDUE RECRUITMENT PEPTIDE FROM E2F	TRANSFERASE
1H25	CDK2/CYCLIN A IN COMPLEX WITH AN 11-RESIDUE RECRUITMENT PEPTIDE FROM RETINOBLASTOMA-ASSOCIATED PROTEIN	TRANSFERASE
1H26	CDK2/CYCLIN A IN COMPLEX WITH AN 11-RESIDUE RECRUITMENT PEPTIDE FROM P53	CELL CYCLE
1H27	CDK2/CYCLIN A IN COMPLEX WITH AN 11-RESIDUE RECRUITMENT PEPTIDE FROM P27	CELL CYCLE
1H28	CDK2/CYCLIN A IN COMPLEX WITH AN 11-RESIDUE RECRUITMENT PEPTIDE FROM P107	CELL CYCLE
1H2A	SINGLE CRYSTALS OF HYDROGENASE FROM DESULFOVIBRIO VULGARIS	OXIDOREDUCTASE
1H2G	ALTERED SUBSTRATE SPECIFICITY MUTANT OF PENICILLIN ACYLASE	AMIDOHYDROLASE
1H2K	FACTOR INHIBITING HIF-1 ALPHA IN COMPLEX WITH HIF-1 ALPHA FRAGMENT PEPTIDE	TRANSCRIPTION ACTIVATOR/INHIBITOR
1H2L	FACTOR INHIBITING HIF-1 ALPHA IN COMPLEX WITH HIF-1 ALPHA FRAGMENT PEPTIDE	TRANSCRIPTION ACTIVATOR/INHIBITOR
1H2M	FACTOR INHIBITING HIF-1 ALPHA IN COMPLEX WITH HIF-1 ALPHA FRAGMENT PEPTIDE	TRANSCRIPTION ACTIVATOR/INHIBITOR
1H2R	THREE-DIMENSIONAL STRUCTURE OF NI-FE HYDROGENASE FROM DESULFIVIBRIO VULGARIS MIYAZAKI F IN THE REDUCED FORM AT 1.4 A RESOLUTION	OXIDOREDUCTASE
1H2S	MOLECULAR BASIS OF TRANSMENBRANE SIGNALLING BY SENSORY RHODOPSIN II-TRANSDUCER COMPLEX	MENBRANE PROTEIN COMPLEX
1H2U	STRUCTURE OF THE HUMAN NUCLEAR CAP-BINDING-COMPLEX (CBC) IN COMPLEX WITH A CAP ANALOGUE M7GPPPG	NUCLEAR PROTEIN
1H31	OXIDISED SOXAX COMPLEX FROM RHODOVULUM SULFIDOPHILUM	ELECTRON TRANSFER
1H3O	CRYSTAL STRUCTURE OF THE HUMAN TAF4-TAF12 (TAFII135-TAFII20) COMPLEX	TRANSCRIPTION/TBP-ASSOCIATED FACTORS
1H4I	METHYLOBACTERIUM EXTORQUENS METHANOL DEHYDROGENASE	DEHYDROGENASE
1H4J	ETHYLOBACTERIUM EXTORQUENS METHANOL DEHYDROGENASE D303E MUTANT	DEHYDROGENASE
1H4L	STRUCTURE AND REGULATION OF THE CDK5-P25(NCK5A) COMPLEX	COMPLEX(CYCLINS/CDK)
1H59	COMPLEX OF IGFBP-5 WITH IGF-I	INSULIN

1H5R	HYMIDYLYLTRANSFERASE COMPLEXED WITH THIMIDINE AND GLUCOSE-1-PHOSPATE	TRANSFERASE
1H5T	HYMIDYLYLTRANSFERASE COMPLEXED WITH THYMIDYLYLDIPHOSPHATE-GLUCOSE	TRANSFERASE
1H6K	NUCLEAR CAP BINDING COMPLEX	NUCLEAR PROTEIN
1H6W	RYSTAL STRUCTURE OF A HEAT-AND PROTEASE-STABLE FRAGMENT OF THE BACTERIOPHAGE T4 SHORT FIBRE	STRUCTURAL PROTEIN
1H88	CRYSTAL STRUCTURE OF TERNARY PROTEIN-DNA COMPLEX1	TRANSCRIPTION/DNA
1H89	CRYSTAL STRUCTURE OF TERNARY PROTEIN-DNA COMPLEX2	TRANSCRIPTION/DNA
1H8A	CRYSTAL STRUCTURE OF TERNARY PROTEIN-DNA COMPLEX3	TRANSCRIPTION/DNA
1H8E	(ADP.ALF4)2(ADP.SO4) BOVINE F1-ATPASE (ALL THREE CATALYTIC SITES OCCUPIED)	ATP PHOSPHORYLASE
1H8H	BOVINE MITOCHONDRIAL F1-ATPASE CRYSTALLISED IN THE PRESENCE OF 5MM AMPPNP	ATP PHOSPHORYLASE
1H8I	X-RAY CRYSTAL STRUCTURE OF HUMAN ALPHA-THROMBIN WITH A TRIPEPTIDE PHOSPHONATE INHIBITOR.	SERINE PROTEASE
1H8T	ECHOVIRUS 11	VIRUS
1H9D	AML1/CBF-BETA/DNA COMPLEX	TRANSCRIPTION/DNA
1H9H	COMPLEX OF EETI-II WITH PORCINE TRYPSIN	HYDROLASE INHIBITOR
1H9I	COMPLEX OF EETI-II MUTANT WITH PORCINE TRYPSIN	COMPLEX (SERINE PROTEASE/INHIBITOR)
1H9S	OLYBDATE BOUND COMPLEX OF DIMOP DOMAIN OF MODE FROM E.COLI	TRANSCRIPTION REGULATOR
1HA7	STRUCTURE OF A LIGHT-HARVESTING PHYCOBILIPROTEIN, C-PHYCOCYANIN FROM SPIRULINA PLATENSIS AT 2.2A RESOLUTION	PHOTOSYNTHESIS
1HAB	CROSSLINKED HAEMOGLOBIN	OXYGEN TRANSPORT
1HAC	CROSSLINKED HAEMOGLOBIN	OXYGEN TRANSPORT
1HAH	THE ISOMORPHOUS STRUCTURES OF PRETHROMBIN2, HIRUGEN-AND PPACK-THROMBIN: CHANGES ACCOMPANYING ACTIVATION AND EXOSITE BINDING TO THROMBIN	COMPLEX(SERINE PROTEINASE/INHIBITOR)
1HAI	THE ISOMORPHOUS STRUCTURES OF PRETHROMBIN2, HIRUGEN-AND PPACK-THROMBIN: CHANGES ACCOMPANYING ACTIVATION AND EXOSITE BINDING TO THROMBIN	HYDROLASE(SERINE PROTEINASE)
1HAO	COMPLEX OF HUMAN ALPHA-THROMBIN WITH A 15MER OLIGONUCLEOTIDE GGTTGGTGTGGTTGG (BASED ON NMR MODEL OF DNA	HYDROLASE/HYDROLASE INHIBITOR/DNA

1HAP	COMPLEX OF HUMAN ALPHA-THROMBIN WITH A 15MER OLIGONUCLEOTIDE GGTTGGTGTGGTTGG (BASED ON X-RAY MODEL OF DNA)	HYDROLASE/HYDROLASE INHIBITOR/DNA
1HBA	HIGH-RESOLUTION X-RAY STUDY OF DEOXYHEMOGLOBIN ROTHSCHILD 37BETA TRP-> ARG: A MUTATION THAT CREATES AN INTERSUBUNIT CHLORIDE-BINDING SITE	OXYGEN TRANSPORT
1HBB	HIGH-RESOLUTION X-RAY STUDY OF DEOXYHEMOGLOBIN ROTHSCHILD 37BETA TRP-> ARG: A MUTATION THAT CREATES AN INTERSUBUNIT CHLORIDE-BINDING SITE	OXYGEN TRANSPORT
1HBH	STRUCTURE OF DEOXYHAEMOGLOBIN OF THE ANTARCTIC FISH PAGOTHENIA BERNACCHII AND STRUCTURAL BASIS OF THE ROOT EFFECT	OXYGEN CARRIER
1HBM	METHYL-COENZYME M REDUCTASE ENZYME PRODUCT COMPLEX	METHANOGENESIS
1HBN	METHYL-COENZYME M REDUCTASE	METHANOGENESIS
1HBO	METHYL-COENZYME M REDUCTASE MCR-RED1-SILENT	METHANOGENESIS
1HBR	R-STATE FORM OF CHICKEN HEMOGLOBIN D	OXYGEN STORAGE/TRANSPORT
1HBS	REFINED CRYSTAL STRUCTURE OF DEOXYHEMOGLOBIN S. I. RESTRAINED LEAST-SQUARES REFINEMENT AT 3.0-ANGSTROMS RESOLUTION	OXYGEN TRANSPORT
1HBT	HUMAN ALPHA-THROMBIN COMPLEXED WITH A PEPTIDYL PYRIDINIUM METHYL KETONE CONTAINING BIVALENT INHIBITOR	HYDROLASE
1HBU	METHYL-COENZYME M REDUCTASE IN THE MCR-RED1-SILENT STATE IN COMPLEX WITH COENZYME M	METHANOGENESIS
1HBX	TERNARY COMPLEX OF SAP-1 AND SRF WITH SPECIFIC SRE DNA	GENE REGULATION/DNA
1HC9	A-BUNGAROTOXIN COMPLEXED WITH HIGH AFFINITY PEPTIDE	COMPLEX (TOXIN/PEPTIDE)
1HCG	STRUCTURE OF HUMAN DES(1-45) FACTOR XA AT 2.2 ANGSTROMS RESOLUTION	COAGULATION FACTOR
1HCN	STRUCTURE OF HUMAN CHORIONIC GONADOTROPIN AT 2.6 ANGSTROMS RESOLUTION FROM MAD ANALYSIS OF THE SELENOMETHIONYL PROTEIN	HORMONE
1HCO	THE STRUCTURE OF HUMAN CARBONMONOXY HAEMOGLOBIN AT 2.7 ANGSTROMS RESOLUTION	OXYGEN TRANSPORT
1HCS	NMR STRUCTURE OF THE HUMAN SRC SH2 DOMAIN COMPLEX	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)
1HDA	A NOVEL ALLOSTERIC MECHANISM IN HAEMOGLOBIN. STRUCTURE OF BOVINE DEOXYHAEMOGLOBIN, ABSENCE OF SPECIFIC CHLORIDE-BINDING SITES AND ORIGIN OF THE CHLORIDE-LINKED BOHR EFFECT IN BOVINE AND HUMAN HAEMOGLOBIN	OXYGEN TRANSPORT
1HDB	ANALYSIS OF THE CRYSTAL STRUCTURE, MOLECULAR MODELING AND	OXYGEN TRANSPORT

	INFRARED SPECTROSCOPY OF THE DISTAL BETA-HEME POCKET VALINE67(E11)-THREONINE MUTATION OF HEMOGLOBIN	
1HDM	HISTOCOMPATIBILITY ANTIGEN HLA-DM	IMMUNE SYSTEM
1HDS	ACROMOLECULAR STRUCTURE REFINEMENT BY RESTRAINED LEAST-SQUARES AND INTERACTIVE GRAPHICS AS APPLIED TO SICKLING DEER TYPE III HEMOGLOBIN	OXYGEN TRANSPORT
1HDT	STRUCTURE OF A RETRO-BINDING PEPTIDE INHIBITOR COMPLEXED WITH HUMAN ALPHA-THROMBIN	COMPLEX (SERINE PROTEINASE/INHIBITOR)
1HE1	RYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE GAP DOMAIN OF THE PSEUDOMONAS AERUGINOSA EXOS TOXIN AND HUMAN RAC	SIGNALLING COMPLEX
1HE8	RAS G12V-PI 3-KINASE GAMMA COMPLEX	COMPLEX (PHOSPHOINOSITIDE KINASE/RAS)
1HEZ	ANTIBODY-ANTIGEN COMPLEX	ANTIBODY
1HFE	1.6 A RESOLUTION STRUCTURE OF THE FE-ONLY HYDROGENASE FROM DESULFOVIBRIO DESULFURICANS	HYDROGENASE
1HGA	HIGH RESOLUTION CRYSTAL STRUCTURES AND COMPARISONS OF T STATE DEOXYHAEMOGLOBIN AND TWO LIGANDED T-STATE AEMOGLOBINS: T(ALPHA-OXY)HAEMOGLOBIN AND T(MET)HAEMOGLOBIN	OXYGEN TRANSPORT
1HGB	HIGH RESOLUTION CRYSTAL STRUCTURES AND COMPARISONS OF T STATE DEOXYHAEMOGLOBIN AND TWO LIGANDED T-STATE AEMOGLOBINS: T(ALPHA-OXY)HAEMOGLOBIN AND T(MET)HAEMOGLOBIN	OXYGEN TRANSPORT
1HGC	HIGH RESOLUTION CRYSTAL STRUCTURES AND COMPARISONS OF T STATE DEOXYHAEMOGLOBIN AND TWO LIGANDED T-STATE AEMOGLOBINS: T(ALPHA-OXY)HAEMOGLOBIN AND T(MET)HAEMOGLOBIN	OXYGEN TRANSPORT
1HGD	BINDING OF INFLUENZA VIRUS HEMAGGLUTININ TO ANALOGS OF ITS CELL-SURFACE RECEPTOR, SIALIC ACID: ANALYSIS BY PROTON NUCLEAR MAGNETIC RESONANCE SPECTROSCOPY AND X-RAY CRYSTALLOGRAPHY	VIRAL PROTEIN
1HGE	BINDING OF INFLUENZA VIRUS HEMAGGLUTININ TO ANALOGS OF ITS CELL-SURFACE RECEPTOR, SIALIC ACID: ANALYSIS BY PROTON NUCLEAR MAGNETIC RESONANCE SPECTROSCOPY AND X-RAY CRYSTALLOGRAPHY	VIRAL PROTEIN
1HGF	BINDING OF INFLUENZA VIRUS HEMAGGLUTININ TO ANALOGS OF ITS CELL-SURFACE RECEPTOR, SIALIC ACID: ANALYSIS BY PROTON NUCLEAR MAGNETIC RESONANCE SPECTROSCOPY AND X-RAY CRYSTALLOGRAPHY	VIRAL PROTEIN
1HGG	BINDING OF INFLUENZA VIRUS HEMAGGLUTININ TO ANALOGS OF ITS CELL-SURFACE RECEPTOR, SIALIC ACID: ANALYSIS BY PROTON NUCLEAR MAGNETIC RESONANCE SPECTROSCOPY AND X-RAY CRYSTALLOGRAPHY	VIRAL PROTEIN
1HGH	BINDING OF INFLUENZA VIRUS HEMAGGLUTININ TO ANALOGS OF ITS	VIRAL PROTEIN

	CELL-SURFACE RECEPTOR, SIALIC ACID: ANALYSIS BY PROTON NUCLEAR MAGNETIC RESONANCE SPECTROSCOPY AND X-RAY CRYSTALLOGRAPHY	
1HGI	BINDING OF INFLUENZA VIRUS HEMAGGLUTININ TO ANALOGS OF ITS CELL-SURFACE RECEPTOR, SIALIC ACID: ANALYSIS BY PROTON NUCLEAR MAGNETIC RESONANCE SPECTROSCOPY AND X-RAY CRYSTALLOGRAPHY	VIRAL PROTEIN
1HGJ	BINDING OF INFLUENZA VIRUS HEMAGGLUTININ TO ANALOGS OF ITS CELL-SURFACE RECEPTOR, SIALIC ACID: ANALYSIS BY PROTON NUCLEAR MAGNETIC RESONANCE SPECTROSCOPY AND X-RAY CRYSTALLOGRAPHY	VIRAL PROTEIN
1HGT	STRUCTURE OF THE HIRUGEN AND HIRULOG 1 COMPLEXES OF ALPHA-THROMBIN	HYDROLASE(SERINE PROTEASE)
1HH4	RAC1-RHOGDI COMPLEX INVOLVED IN NADPH OXIDASE ACTIVATION	SINGAL PROTEIN INHIBITOR COMPLEX
1HH6	ANTI-P24 (HIV-1) FAB FRAGMENT CB41 COMPLEXED WITH A PEPTIDE	COMPLEX (ANTIBODY/PEPTIDE)
1HH9	ANTI-P24 (HIV-1) FAB FRAGMENT CB41 COMPLEXED WITH A PEPTIDE	COMPLEX (ANTIBODY/PEPTIDE)
1HHG	THE ANTIGENIC IDENTITY OF PEPTIDE(SLASH)MHC COMPLEXES: A COMPARISON OF THE CONFORMATION OF FIVE PEPTIDES PRESENTED BY HLA-A2	HISTOCOMPATIBILITY ANTIGEN
1HHH	THE ANTIGENIC IDENTITY OF PEPTIDE(SLASH)MHC COMPLEXES: A COMPARISON OF THE CONFORMATION OF FIVE PEPTIDES PRESENTED BY HLA-A2	HISTOCOMPATIBILITY ANTIGEN
1HHI	THE ANTIGENIC IDENTITY OF PEPTIDE(SLASH)MHC COMPLEXES: A COMPARISON OF THE CONFORMATION OF FIVE PEPTIDES PRESENTED BY HLA-A2	HISTOCOMPATIBILITY ANTIGEN
1HHJ	THE ANTIGENIC IDENTITY OF PEPTIDE(SLASH)MHC COMPLEXES: A COMPARISON OF THE CONFORMATION OF FIVE PEPTIDES PRESENTED BY HLA-A2	HISTOCOMPATIBILITY ANTIGEN
1HHK	THE ANTIGENIC IDENTITY OF PEPTIDE(SLASH)MHC COMPLEXES: A COMPARISON OF THE CONFORMATION OF FIVE PEPTIDES PRESENTED BY HLA-A2	HISTOCOMPATIBILITY ANTIGEN
1HHO	STRUCTURE OF HUMAN OXYHAEMOGLOBIN AT 2.1 ANGSTROMS RESOLUTION	OXYGEN TRANSPORT
1HI6	ANTI-P24 (HIV-1) FAB FRAGMENT CB41 COMPLEXED WITH A PEPTIDE	COMPLEX (ANTIBODY/PEPTIDE)
1HIA	KALLIKREIN COMPLEXED WITH HIRUSTASIN	COMPLEX (PROTEASE/INHIBITOR)
1HIL	STRUCTURAL EVIDENCE FOR INDUCED FIT AS A MECHANISM FOR ANTIGEN-ANTIBODY RECOGNITION	IMMUNOGLOBULIN
1HIN	STRUCTURAL EVIDENCE FOR INDUCED FIT AS A MECHANISM FOR ANTIBODY-ANTIGEN RECOGNITION	IMMUNOGLOBULIN

1HIV	CRYSTAL STRUCTURE OF A COMPLEX OF HIV-1 PROTEASE WITH A DIHYDROETHYLENE-CONTAINING INHIBITOR: COMPARISONS WITH MOLECULAR MODELING	HYDROLASE(ACID PROTEINASE)
1HJA	LYS 18 VARIANT OF TURKEY OVOMUCOID INHIBITOR THIRD DOMAIN COMPLEXED WITH ALPHA-CHYMOTRYPSIN	COMPLEX (HYDROLASE/INHIBITOR)
1HJB	CRYSTAL STRUCTURE OF RUNX-1/AML1/CBFALPHA RUNT DOMAIN AND C/EBPBETA BZIP HOMODIMER BOUND TO A DNA FRAGMENT FROM THE CSF-1R PROMOTER	TRANSCRIPTION/DNA
1HKL	FREE AND LIGANDED FORM OF AN ESTEROLYTIC CATALYTIC ANTIBODY	CATALYTIC ANTIBODY
1HL3	CTBP/BARS IN TERNARY COMPLEX WITH NAD(H) AND PIDLSKK PEPTIDE	TRANCRIPTION CO-REPRESSOR
1HL6	A NOVEL MODE OF RBD-PROTEIN RECOGNITION IN THE Y14-MAGO COMPLEX	SIGNAL PROTEIN
1HLE	CRYSTAL STRUCTURE OF CLEAVED EQUINE LEUCOCYTE ELASTASE INHIBITOR DETERMINED AT 1.95 ANGSTROMS RESOLUTION	HYDROLASE INHIBITOR(SERINE PROTEINASE)
1HLT	THE STRUCTURE OF A NONADECAPEPTIDE OF THE FIFTH EGF DOMAIN OF THROMBOMODULIN COMPLEXED WITH THROMBIN	COMPLEX(SERINE PROTEINASE/INHIBITOR)
1HLU	STRUCTURE OF BOVINE BETA-ACTIN-PROFILIN COMPLEX WITH ACTIN BOUND ATP PHOSPHATES SOLVENT ACCESSIBLE	COMPLEX (ACETYLATION/ACTIN-BINDING)
1HMV	HE STRUCTURE OF UNLIGANDED REVERSE TRANSCRIPTASE FROM THE HUMAN IMMUNODEFICIENCY VIRUS TYPE 1	NUCLEOTIDYLTRANSFERASE
1HNI	STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN A COMPLEX WITH THE NONNUCLEOSIDE INHIBITOR ALPHA-APA R 95845 AT 2.8 ANGSTROMS RESOLUTION	NUCLEOTIDYLTRANSFERASE
1HNV	STRUCTURE OF HIV-1 RT(SLASH)TIBO R 86183 COMPLEX REVEALS SIMILARITY IN THE BINDING OF DIVERSE NONNUCLEOSIDE INHIBITORS	NUCLEOTIDYLTRANSFERASE
1HNW	TRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT IN COMPLEX WITH TETRACYCLINE	RIBOSOME
1HNX	TRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT IN COMPLEX WITH PACTAMYCIN	RIBOSOME
1HNZ	TRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT IN COMPLEX WITH HYGROMYCIN B	RIBOSOME
1HOC	THE THREE-DIMENSIONAL STRUCTURE OF H-2DB AT 2.4 ANGSTROMS RESOLUTION: IMPLICATIONS FOR ANTIGEN-DETERMINANT SELECTION	HISTOCOMPATIBILITY ANTIGEN
1HPG	A GLUTAMIC ACID SPECIFIC SERINE PROTEASE UTILIZES A NOVEL HISTIDINE TRIAD IN SUBSTRATE BINDING	HYDROLASE (SERINE PROTEASE)
1HPZ	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1	TRANSFERASE

1HQ3	CRYSTAL STRUCTURE OF THE HISTONE-CORE-OCTAMER IN KCL/PHOSPHATE	DNA BINDING PROTEIN
1HQ4	STRUCTURE OF NATIVE CATALYTIC ANTIBODY HA5-19A4	IMMUNE SYSTEM
1HQ6	TRUCTURE OF PYRUVOYL-DEPENDENT HISTIDINE DECARBOXYLASE AT PH 8	LYASE
1HQE	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1	TRANSFERASE
1HQM	RYSTAL STRUCTURE OF THERMUS AQUATICUS CORE RNA POLYMERASE-INCLUDES COMPLETE STRUCTURE WITH SIDE-CHAINS (EXCEPT FOR DISORDERED REGIONS)-FURTHER REFINED FROM ORIGINAL DEPOSITION-CONTAINS ADDITIONAL SEQUENCE INFORMATION	TRANSCRIPTION
1HQR	CRYSTAL STRUCTURE OF A SUPERANTIGEN BOUND TO THE HIGH-AFFINITY, ZINC-DEPENDENT SITE ON MHC CLASS II	IMMUNE SYSTEM
1HQU	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1	TRANSFERASE
1HQY	UCLEOTIDE-DEPENDENT CONFORMATIONAL CHANGES IN A PROTEASE-ASSOCIATED ATPASE HSLU	CHAPERONE
1HR0	CRYSTAL STRUCTURE OF INITIATION FACTOR IF1 BOUND TO THE 30S RIBOSOMAL SUBUNIT	RIBOSOME
1HR6	YEAST MITOCHONDRIAL PROCESSING PEPTIDASE	HYDROLASE
1HR7	YEAST MITOCHONDRIAL PROCESSING PEPTIDASE BETA-E73Q MUTANT	HYDROLASE
1HR8	YEAST MITOCHONDRIAL PROCESSING PEPTIDASE BETA-E73Q MUTANT COMPLEXED WITH CYTOCHROME C OXIDASE IV SIGNAL PEPTIDE	HYDROLASE
1HR9	YEAST MITOCHONDRIAL PROCESSING PEPTIDASE BETA-E73Q MUTANT COMPLEXED WITH MALATE DEHYDROGENASE SIGNAL PEPTIDE	HYDROLASE
1HRP	CRYSTAL STRUCTURE OF HUMAN CHORIONIC GONADOTROPIN	HORMONE
1HRT	THE STRUCTURE OF A COMPLEX OF BOVINE ALPHA-THROMBIN AND RECOMBINANT HIRUDIN AT 2.8 ANGSTROMS RESOLUTION	HYDROLASE(SERINE PROTEINASE)
1HSA	THE THREE-DIMENSIONAL STRUCTURE OF HLA-B27 AT 2.1 ANGSTROMS RESOLUTION SUGGESTS A GENERAL MECHANISM FOR TIGHT PEPTIDE BINDING TO MHC	HISTOCOMPATIBILITY ANTIGEN
1HSB	DIFFERENT LENGTH PEPTIDES BIND TO HLA-AW68 SIMILARLY AT THEIR ENDS BUT BULGE OUT IN THE MIDDLE	HISTOCOMPATIBILITY ANTIGEN
1HT1	UCLEOTIDE-DEPENDENT CONFORMATIONAL CHANGES IN A PROTEASE-ASSOCIATED ATPASE HSLU	CHAPERONE
1HT2	UCLEOTIDE-DEPENDENT CONFORMATIONAL CHANGES IN A PROTEASE-ASSOCIATED ATPASE HSLU	CHAPERONE

1HTE	X-RAY CRYSTALLOGRAPHIC STUDIES OF A SERIES OF PENICILLIN-DERIVED ASYMMETRIC INHIBITORS OF HIV-1 PROTEASE	HYDROLASE(ACID PROTEINASE)
1HTL	MUTATION OF A BURIED RESIDUE CAUSES LACK OF ACTIVITY BUT NO CONFORMATIONAL CHANGE: CRYSTAL STRUCTURE OF E. COLI HEAT-LABILE ENTEROTOXIN MUTANT VAL 97--> LYS	ENTEROTOXIN
1HTM	STRUCTURE OF INFLUENZA HAEMAGGLUTININ AT THE PH OF MEMBRANE FUSION	VIRAL PROTEIN
1HTR	CRYSTAL AND MOLECULAR STRUCTURES OF HUMAN PROGASTRICSIN AT 1.62 ANGSTROMS RESOLUTION	ASPARTYL PROTEASE
1HTT	HISTIDYL-TRNA SYNTHETASE	COMPLEX (TRNA SYNTHETASE/HIS-ADENYLATE)
1HTV	CRYSTAL STRUCTURE OF DESTRIPEPTIDE (B28-B30) INSULIN	HORMONE/GROWTH FACTOR
1HUT	THE STRUCTURE OF ALPHA-THROMBIN INHIBITED BY A 15-MER SINGLE-STRANDED DNA APTAMER	HYDROLASE, BLOOD CLOTTING/DNA
1HV4	CRYSTAL STRUCTURE ANALYSIS OF BAR-HEAD GOOSE HEMOGLOBIN (DEOXY FORM)	OXYGEN STORAGE/TRANSPORT
1HVU	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 REVERSE TRANSCRIPTASE COMPLEXED WITH A 33-BASE NUCLEOTIDE RNA PSEUDOKNOT	TRANSFERASE/RNA
1HWG	1:2 COMPLEX OF HUMAN GROWTH HORMONE WITH ITS SOLUBLE BINDING PROTEIN	COMPLEX (HORMONE/RECEPTOR)
1HWH	1:1 COMPLEX OF HUMAN GROWTH HORMONE MUTANT G120R WITH ITS SOLUBLE BINDING PROTEIN	COMPLEX (HORMONE/RECEPTOR)
1HWM	EBULIN,ORTHORHOMBIC CRYSTAL FORM MODEL	HYDROLASE
1HWN	EBULIN COMPLEXED WITH GALACTOSE, TRIGONAL CRYSTAL FORM	HYDROLASE
1HWO	EBULIN COMPLEXED WITH LACTOSE, TRIGONAL CRYSTAL FORM	HYDROLASE
1HWP	EBULIN COMPLEXED WITH PTEROIC ACID, TRIGONAL CRYSTAL FORM	HYDROLASE
1HX1	CRYSTAL STRUCTURE OF A BAG DOMAIN IN COMPLEX WITH THE HSC70 ATPASE DOMAIN	CHAPERONE/CHAPERONE INHIBITOR
1HXE	SERINE PROTEASE	COMPLEX (SERINE PROTEASE/INHIBITOR)
1HXF	HUMAN THROMBIN COMPLEX WITH HIRUDIN VARIANT	COMPLEX (SERINE PROTEASE/INHIBITOR)
1HXM	CRYSTAL STRUCTURE OF A HUMAN VGAMMA9/VDELTA2 T CELL RECEPTOR	IMMUNE SYSTEM
1HXY	CRYSTAL STRUCTURE OF STAPHYLOCOCCAL ENTEROTOXIN H IN COMPLEX WITH HUMAN MHC CLASS II	IMMUNE SYSTEM/TOXIN
1HYM	HYDROLYZED TRYPSIN INHIBITOR (CMTI-V, MINIMIZED AVERAGE NMR STRUCTURE)	HYDROLASE (SERINE PROTEINASE)

1HYR	CRYSTAL STRUCTURE OF HUMAN MICA IN COMPLEX WITH NATURAL KILLER CELL RECEPTOR NKG2D	IMMUNE SYSTEM
1HYS	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH A POLYPURINE TRACT RNA:DNA	TRANSFERASE/DNA/RNA
1HZH	CRYSTAL STRUCTURE OF THE INTACT HUMAN IGG B12 WITH BROAD AND POTENT ACTIVITY AGAINST PRIMARY HIV-1 ISOLATES: A TEMPLATE FOR HIV VACCINE DESIGN	IMMUNE SYSTEM
1HZZ	THE ASYMMETRIC COMPLEX OF THE TWO NUCLEOTIDE-BINDING COMPONENTS (DI, DIII) OF PROTON-TRANSLOCATING TRANSHYDROGENASE	OXIDOREDUCTASE
1I1A	CRYSTAL STRUCTURE OF THE NEONATAL FC RECEPTOR COMPLEXED WITH A HETERODIMERIC FC	IMMUNE SYSTEM
1I1F	CRYSTAL STRUCTURE OF HUMAN CLASS I MHC (HLA-A2.1) COMPLEXED WITH BETA 2-MICROGLOBULIN AND HIV-RT VARIANT PEPTIDE I1Y	IMMUNE SYSTEM
1I1Q	STRUCTURE OF THE COOPERATIVE ALLOSTERIC ANTHRANILATE SYNTHASE FROM SALMONELLA TYPHIMURIUM	LYASE
1I1R	CRYSTAL STRUCTURE OF A CYTOKINE/RECEPTOR COMPLEX	CYTOKINE
1I1Y	CRYSTAL STRUCTURE OF HUMAN CLASS I MHC (HLA-A2.1) COMPLEXED WITH BETA 2-MICROGLOBULIN AND HIV-RT VARIANT PEPTIDE I1Y	IMMUNE SYSTEM
1I2M	RAN-RCC1-SO4 COMPLEX	CELL CYCLE
1I3O	CRYSTAL STRUCTURE OF THE COMPLEX OF XIAP-BIR2 AND CASPASE 3	APOPTOSIS
1I3Q	RNA POLYMERASE II CRYSTAL FORM I AT 3.1 A RESOLUTION	TRANSCRIPTION
1I4D	CRYSTAL STRUCTURE ANALYSIS OF RAC1-GDP COMPLEXED WITH ARFAPTIN (P21)	SIGNALING PROTEIN
1I4E	CRYSTAL STRUCTURE OF THE CASPASE-8/P35 COMPLEX	APOPTOSIS/HYDROLASE
1I4F	CRYSTAL STRUCTURE OF HLA-A*0201/MAGE-A4-PEPTIDE COMPLEX	IMMUNE SYSTEM
1I4L	CRYSTAL STRUCTURE ANALYSIS OF RAC1-GDP IN COMPLEX WITH ARFAPTIN (P41)	SIGNALING PROTEIN
1I4O	CRYSTAL STRUCTURE OF THE XIAP/CASPASE-7 COMPLEX	APOPTOSIS/HYDROLASE
1I4T	CRYSTAL STRUCTURE ANALYSIS OF RAC1-GMPPNP IN COMPLEX WITH ARFAPTIN	SIGNALING PROTEIN
1I50	RNA POLYMERASE II CRYSTAL FORM II AT 2.8 A RESOLUTION	TRANSCRIPTION
1I51	CRYSTAL STRUCTURE OF CASPASE-7 COMPLEXED WITH XIAP	HYDROLASE/HYDROLASE INHIBITOR
1I5K	STRUCTURE AND BINDING DETERMINANTS OF THE RECOMBINANT KRINGLE-2 DOMAIN OF HUMAN PLASMINOGEN TO AN INTERNAL	BLOOD CLOTTING

	PEPTIDE FROM A GROUP A STREPTOCOCCAL SURFACE PROTEIN	
1I5O	CRYSTAL STRUCTURE OF MUTANT R105A OF E. COLI ASPARTATE TRANSCARBAMOYLASE	TRANSFERASE
1I6H	RNA POLYMERASE II ELONGATION COMPLEX	TRANSCRIPTION/DNA/RNA
1I6V	THERMUS AQUATICUS CORE RNA POLYMERASE-RIFAMPICIN COMPLEX	TRANSCRIPTION
1I72	HUMAN S-ADENOSYLMETHIONINE DECARBOXYLASE WITH COVALENTLY BOUND PYRUVOYL GROUP AND COVALENTLY BOUND 5'-DEOXY-5'-[N-METHYL-N-(2-AMINOOXYETHYL) AMINO]ADENOSINE	LYASE
1I73	COMPLEX OF PRO-LEU-L-TRP PHOSPHONATE WITH THE CATALITIC DOMAIN OF MATRIX METALLO PROTEINASE-8 (MET80 FORM)	HYDROLASE
1I79	HUMAN S-ADENOSYLMETHIONINE DECARBOXYLASE WITH COVALENTLY BOUND PYRUVOYL GROUP AND COVALENTLY BOUND 5'-DEOXY-5'-[(3-HYDRAZINOPROPYL)METHYLAMINO]ADENOSINE	LYASE
1I7A	EVH1 DOMAIN FROM MURINE HOMER 2B/VESL 2	SIGNALING PROTEIN
1I7B	HUMAN S-ADENOSYLMETHIONINE DECARBOXYLASE WITH COVALENTLY BOUND PYRUVOYL GROUP AND COVALENTLY BOUND S-ADENOSYLMETHIONINE METHYL ESTER	LYASE
1I7C	HUMAN S-ADENOSYLMETHIONINE DECARBOXYLASE WITH COVALENTLY BOUND PYRUVOYL GROUP AND COMPLEXED WITH METHYLGLYOXAL BIS-(GUANYLHYDRAZONE)	LYASE
1I7M	HUMAN S-ADENOSYLMETHIONINE DECARBOXYLASE WITH COVALENTLY BOUND PYRUVOYL GROUP AND COMPLEXED WITH 4-AMIDINOINDAN-1-ONE-2'-AMIDINOHYDRAZONE	LYASE
1I7R	CRYSTAL STRUCTURE OF CLASS I MHC A2 IN COMPLEX WITH PEPTIDE P1058	IMMUNE SYSTEM
1I7S	ANTHRANILATE SYNTHASE FROM SERRATIA MARCESCENS IN COMPLEX WITH ITS END PRODUCT INHIBITOR L-TRYPTOPHAN	LYASE
1I7T	CRYSTAL STRUCTURE OF CLASS I MHC A2 IN COMPLEX WITH PEPTIDE P1049-5V	IMMUNE SYSTEM
1I7U	CRYSTAL STRUCTURE OF CLASS I MHC A2 IN COMPLEX WITH PEPTIDE P1049-6V	IMMUNE SYSTEM
1I7W	BETA-CATENIN/PHOSPHORYLATED E-CADHERIN COMPLEX	CELL ADHESION
1I7X	BETA-CATENIN/E-CADHERIN COMPLEX	CELL ADHESION
1I7Y	CRYSTAL STRUCTURE OF C-PHYCOCYANIN OF SYNECHOCOCCUS VULCANUS AT 2.5 ANGSTROMS.	PHOTOSYNTHESIS
1I7Z	ANTIBODY GNC92H2 BOUND TO LIGAND	IMMUNE SYSTEM

1I84	RYO-EM STRUCTURE OF THE HEAVY MEROMYOSIN SUBFRAGMENT OF CHICKEN GIZZARD SMOOTH MUSCLE MYOSIN WITH REGULATORY LIGHT CHAIN IN THE DEPHOSPHORYLATED STATE. ONLY C ALPHAS PROVIDED FOR REGULATORY LIGHT CHAIN. ONLY BACKBONE ATOMS PROVIDED FOR S2 FRAGMENT.	CONTRACTILE PROTEIN
1I8L	HUMAN B7-1/CTLA-4 CO-STIMULATORY COMPLEX	IMMUNE SYSTEM
1I8M	RYSTAL STRUCTURE OF A RECOMBINANT ANTI-SINGLE-STRANDED DNA ANTIBODY FRAGMENT COMPLEXED WITH DT5	IMMUNE SYSTEM/DNA
1I94	CRYSTAL STRUCTURES OF THE SMALL RIBOSOMAL SUBUNIT WITH TETRACYCLINE, EDEINE AND IF3	RIBOSOME
1I9C	LUTAMATE MUTASE FROM CLOSTRIDIUM COCHLEARIUM: COMPLEX WITH ADENOSYLCOBALAMIN AND SUBSTRATE	ISOMERASE
1I9I	ATIVE CRYSTAL STRUCTURE OF THE RECOMBINANT MONOCLONAL WILD TYPE ANTI-TESTOSTERONE FAB FRAGMENT	IMMUNE SYSTEM
1I9J	TESTOSTERONE COMPLEX STRUCTURE OF THE RECOMBINANT MONOCLONAL WILD TYPE ANTI-TESTOSTERONE FAB FRAGMENT	IMMUNE SYSTEM
1I9R	STRUCTURE OF CD40L IN COMPLEX WITH THE FAB FRAGMENT OF HUMANIZED 5C8 ANTIBODY	CYTOKINE/IMMUNE SYSTEM
1IA0	KIF1A HEAD-MICROTUBULE COMPLEX STRUCTURE IN ATP-FORM	TRANSPORT PROTEIN
1IAI	IDIOTYPE-ANTI-IDIOTYPE FAB COMPLEX	COMPLEX (IMMUNOGLOBULIN IGG1/IGG2A)
1IAK	HISTOCOMPATIBILITY ANTIGEN I-AK	HISTOCOMPATIBILITY ANTIGEN I-AK
1IAO	CLASS II MHC I-AD IN COMPLEX WITH OVALBUMIN PEPTIDE 323-339	MHC II
1IAR	INTERLEUKIN-4 / RECEPTOR ALPHA CHAIN COMPLEX	CYTOKINE/RECEPTOR
1IAU	HUMAN GRANZYME B IN COMPLEX WITH AC-IEPD-CHO	HYDROLASE
1IB1	CRYSTAL STRUCTURE OF THE 14-3-3 ZETA:SEROTONIN N-ACETYLTRANSFERASE COMPLEX	SIGNALING PROTEIN/TRANSFERASE
1IBC	CRYSTAL STRUCTURE OF INHIBITED INTERLEUKIN-1BETA CONVERTING ENZYME	COMPLEX (HYDROLASE/PEPTIDE)
1IBE	DEOXY-HAEMOGLOBIN TRAPPED IN THE HIGH-AFFINITY (R) STATE	OXYGEN TRANSPORT
1IBG	STRUCTURE AND SPECIFICITY OF THE ANTI-DIGOXIN ANTIBODY 40-50	IMMUNOGLOBULIN
1IBK	TRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT IN COMPLEX WITH THE ANTIBIOTIC PAROMOMYCIN	RIBOSOME
1IBL	TRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT IN COMPLEX WITH A MESSENGER RNA FRAGMENT AND COGNATE TRANSFER RNA ANTICODON STEM-LOOP BOUND AT THE A SITE AND WITH THE ANTIBIOTIC PAROMOMYCIN	RIBOSOME

1IBM	STRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT IN COMPLEX WITH A MESSENGER RNA FRAGMENT AND COGNATE TRANSFER RNA ANTICODON STEM-LOOP BOUND AT THE A SITE	RIBOSOME
1IBR	COMPLEX OF RAN WITH IMPORTIN BETA	CELL CYCLE,TRANSLATION
1IBT	STRUCTURE OF THE D53,54N MUTANT OF HISTIDINE DECARBOXYLASE AT-170 C	LYASE
1IBU	STRUCTURE OF THE D53,54N MUTANT OF HISTIDINE DECARBOXYLASE AT 25 C	LYASE
1IBV	STRUCTURE OF THE D53,54N MUTANT OF HISTIDINE DECARBOXYLASE BOUND WITH HISTIDINE METHYL ESTER AT-170 C	LYASE
1IBW	STRUCTURE OF THE D53,54N MUTANT OF HISTIDINE DECARBOXYLASE BOUND WITH HISTIDINE METHYL ESTER AT 25 C	LYASE
1IC4	CRYSTAL STRUCTURE OF HYHEL-10 FV MUTANT(HD32A)-HEN LYSOZYME COMPLEX	PROTEIN BINDING/HYDROLASE
1IC5	CRYSTAL STRUCTURE OF HYHEL-10 FV MUTANT(HD99A)-HEN LYSOZYME COMPLEX	PROTEIN BINDING/HYDROLASE
1IC7	CRYSTAL STRUCTURE OF HYHEL-10 FV MUTANT(HD32A99A)-HEN LYSOZYME COMPLEX	PROTEIN BINDING/HYDROLASE
1ICE	STRUCTURE AND MECHANISM OF INTERLEUKIN-1BETA CONVERTING ENZYME	CYTOKINE
1ICF	CRYSTAL STRUCTURE OF MHC CLASS II ASSOCIATED P41 II FRAGMENT IN COMPLEX WITH CATHEPSIN L	HYDROLASE
1ID3	CRYSTAL STRUCTURE OF THE YEAST NUCLEOSOME CORE PARTICLE REVEALS FUNDAMENTAL DIFFERENCES IN INTER-NUCLEOSOME INTERACTIONS	STRUCTURAL PROTEIN/DNA
1ID5	CRYSTAL STRUCTURE OF BOVINE THROMBIN COMPLEX WITH PROTEASE INHIBITOR ECOTIN	HYDROLASE
1IE7	PHOSPHATE INHIBITED BACILLUS PASTEURII UREASE CRYSTAL STRUCTURE	HYDROLASE
1IEA	HISTOCOMPATIBILITY ANTIGEN	HISTOCOMPATIBILITY ANTIGEN
1IEB	HISTOCOMPATIBILITY ANTIGEN	HISTOCOMPATIBILITY ANTIGEN
1IGC	IGG1 FAB FRAGMENT (MOPC21) COMPLEX WITH DOMAIN III OF PROTEIN G FROM STREPTOCOCCUS	COMPLEX (ANTIBODY/BINDING PROTEIN)
1IGF	CRYSTAL STRUCTURES OF AN ANTIBODY TO A PEPTIDE AND ITS COMPLEX WITH PEPTIDE ANTIGEN AT 2.8 ANGSTROMS	IMMUNOGLOBULIN
1IGI	26-10 FAB:DIGOXIN COMPLEX-AFFINITY AND SPECIFICITY DUE TO	IMMUNOGLOBULIN

	SURFACE COMPLEMENTARITY	
1IGJ	26-10 FAB:DIGOXIN COMPLEX-AFFINITY AND SPECIFICITY DUE TO SURFACE COMPLEMENTARITY	IMMUNOGLOBULIN
1IGT	STRUCTURE OF IMMUNOGLOBULIN	IMMUNOGLOBULIN
1IGY	STRUCTURE OF IMMUNOGLOBULIN	IMMUNOGLOBULIN
1IHF	INTEGRATION HOST FACTOR/DNA COMPLEX	TRANSCRIPTION/DNA
1IHJ	CRYSTAL STRUCTURE OF THE N-TERMINAL PDZ DOMAIN OF INAD IN COMPLEX WITH A NORPA C-TERMINAL PEPTIDE	SIGNALING PROTEIN
1IHS	CRYSTAL STRUCTURE OF THE COMPLEX OF HUMAN ALPHA-THROMBIN AND NON-HYDROLYZABLE BIFUNCTIONAL INHIBITORS, HIRUTONIN-2 AND HIRUTONIN-6	HYDROLASE(SERINE PROTEINASE)
1IHT	CRYSTAL STRUCTURE OF THE COMPLEX OF HUMAN ALPHA-THROMBIN AND NON-HYDROLYZABLE BIFUNCTIONAL INHIBITORS, HIRUTONIN-2 AND HIRUTONIN-6	HYDROLASE(SERINE PROTEINASE)
1II8	CRYSTAL STRUCTURE OF THE P. FURIOSUS RAD50 ATPASE DOMAIN	REPLICATION
1IIQ	CRYSTAL STRUCTURE OF HIV-1 PROTEASE COMPLEXED WITH A HYDROXYETHYLAMINE PEPTIDOMIMETIC INHIBITOR	HYDROLASE, HYDROLASE INHIBITOR
1IJD	CRYSTALLOGRAPHIC STRUCTURE OF THE LH3 COMPLEX FROM RHODOPSEUDOMONAS ACIDOPHILA STRAIN 7050	PHOTOSYNTHESIS
1IJE	NUCLEOTIDE EXCHANGE INTERMEDIATES IN THE EEF1A-EEF1BA COMPLEX	TRANSLATION
1IJF	NUCLEOTIDE EXCHANGE MECHANISMS IN THE EEF1A-EEF1BA COMPLEX	TRANSLATION
1IJK	THE VON WILLEBRAND FACTOR MUTANT (I546V) A1 DOMAIN-BOTROCETIN COMPLEX	BLOOD CLOTTING/TOXIN
1IK9	CRYSTAL STRUCTURE OF A XRCC4-DNA LIGASE IV COMPLEX	GENE REGULATION/LIGASE
1IKV	K103N MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH EFIVARENZ	TRANSFERASE
1IKW	WILD TYPE HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH EFAVIRENZ	TRANSFERASE
1IKX	K103N MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH THE INHIBITOR PNU142721	TRANSFERASE
1IKY	HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH THE INHIBITOR MSC194	TRANSFERASE
1IL1	CRYSTAL STRUCTURE OF G3-519, AN ANTI-HIV MONOCLONAL ANTIBODY	IMMUNE SYSTEM
1ILQ	CXCR-1 N-TERMINAL PEPTIDE BOUND TO INTERLEUKIN-8 (MINIMIZED	CYTOKINE

	MEAN)	
1IM3	RYSTAL STRUCTURE OF THE HUMAN CYTOMEGALOVIRUS PROTEIN US2 BOUND TO THE MHC CLASS I MOLECULE HLA-A2/TAX	VIRAL PROTEIN/IMMUNE SYSTEM
1IM9	CRYSTAL STRUCTURE OF THE HUMAN NATURAL KILLER CELL INHIBITORY RECEPTOR KIR2DL1 BOUND TO ITS MHC LIGAND HLA-CW4	IMMUNE SYSTEM
1IND	HOW THE ANTI-(METAL CHELATE) ANTIBODY CHA255 IS SPECIFIC FOR THE METAL ION OF ITS ANTIGEN: X-RAY STRUCTURES FOR TWO FAB'(SLASH)HAPTEN COMPLEXES WITH DIFFERENT METALS IN THE CHELATE	IMMUNOGLOBULIN
1INE	HOW THE ANTI-(METAL CHELATE) ANTIBODY CHA255 IS SPECIFIC FOR THE METAL ION OF ITS ANTIGEN: X-RAY STRUCTURES FOR TWO FAB'(SLASH)HAPTEN COMPLEXES WITH DIFFERENT METALS IN THE CHELATE	IMMUNOGLOBULIN
1INQ	STRUCTURE OF MINOR HISTOCOMPATIBILITY ANTIGEN PEPTIDE, H13A, COMPLEXED TO H2-DB	IMMUNE SYSTEM
1IO4	CRYSTAL STRUCTURE OF RUNX-1/AML1/CBFALPHA RUNT DOMAIN-CBFBETA CORE DOMAIN HETERODIMER AND C/EBPBETA BZIP HOMODIMER BOUND TO A DNA FRAGMENT FROM THE CSF-1R PROMOTER	TRANSCRIPTION/DNA
1IOD	RYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE COAGULATION FACTOR X BINDING PROTEIN FROM SNAKE VENOM AND THE GLA DOMAIN OF FACTOR X	HYDROLASE/HYDROLASE INHIBITOR
1IOE	HUMAN COAGULATION FACTOR XA IN COMPLEX WITH M55532	HYDROLASE
1IQ1	CRYSTAL STRUCTURE OF THE IMPORTIN-ALPHA(44-54)-IMPORTIN-ALPHA(70-529) COMPLEX	PROTEIN TRANSPORT
1IQ5	ALMODULIN/NEMATODE CA2+/CALMODULIN DEPENDENT KINASE KINASE FRAGMENT	METAL BINDING PROTEIN/PROTEIN BINDING
1IQD	HUMAN FACTOR VIII C2 DOMAIN COMPLEXED TO HUMAN MONOCLONAL BO2C11 FAB.	IMMUNE SYSTEM/BLOOD CLOTTING
1IQE	HUMAN COAGULATION FACTOR XA IN COMPLEX WITH M55590	HYDROLASE
1IQF	HUMAN COAGULATION FACTOR XA IN COMPLEX WITH M55165	HYDROLASE
1IQG	HUMAN COAGULATION FACTOR XA IN COMPLEX WITH M55159	HYDROLASE
1IQH	HUMAN COAGULATION FACTOR XA IN COMPLEX WITH M55143	HYDROLASE
1IQI	HUMAN COAGULATION FACTOR XA IN COMPLEX WITH M55125	HYDROLASE
1IQJ	HUMAN COAGULATION FACTOR XA IN COMPLEX WITH M55124	HYDROLASE
1IQK	HUMAN COAGULATION FACTOR XA IN COMPLEX WITH M55113	HYDROLASE
1IQL	HUMAN COAGULATION FACTOR XA IN COMPLEX WITH M54476	HYDROLASE

1IQM	HUMAN COAGULATION FACTOR XA IN COMPLEX WITH M54471	HYDROLASE
1IQN	HUMAN COAGULATION FACTOR XA IN COMPLEX WITH M55192	HYDROLASE
1IQW	CRYSTAL STRUCTURE OF THE FAB FRAGMENT OF THE MOUSE ANTI-HUMAN FAS ANTIBODY HFE7A	IMMUNE SYSTEM
1IR1	CRYSTAL STRUCTURE OF SPINACH RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE (RUBISCO) COMPLEXED WITH CO2, MG2+ AND 2-CARBOXYARABINITOL-1,5-BISPHOSPHATE	LYASE
1IR2	CRYSTAL STRUCTURE OF ACTIVATED RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE (RUBISCO) FROM GREEN ALGA, CHLAMYDOMONAS REINHARDTII COMPLEXED WITH 2-CARBOXYARABINITOL-1,5-BISPHOSPHATE (2-CABP)	LYASE
1IR3	PHOSPHORYLATED INSULIN RECEPTOR TYROSINE KINASE IN COMPLEX WITH PEPTIDE SUBSTRATE AND ATP ANALOG	COMPLEX (TRANSFERASE/SUBSTRATE)
1IRD	RYSTAL STRUCTURE OF HUMAN CARBONMONOXY-HAEMOGLOBIN AT 1.25 A RESOLUTION	OXYGEN STORAGE/TRANSPORT
1IRE	CRYSTAL STRUCTURE OF CO-TYPE NITRILE HYDRATASE FROM PSEUDONOCARDIA THERMOPHILA	LYASE
1IRS	IRS-1 PTB DOMAIN COMPLEXED WITH A IL-4 RECEPTOR PHOSPHOPEPTIDE, NMR, MINIMIZED AVERAGE STRUCTURE	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)
1IRU	CRYSTAL STRUCTURE OF THE MAMMALIAN 20S PROTEASOME AT 2.75 A RESOLUTION	HYDROLASE
1IS0	CRYSTAL STRUCTURE OF A COMPLEX OF THE SRC SH2 DOMAIN WITH CONFORMATIONALLY CONSTRAINED PEPTIDE INHIBITOR	TRANSFERASE
1IS7	CRYSTAL STRUCTURE OF RAT GTPCHI/GFRP STIMULATORY COMPLEX	HYDROLASE/PROTEIN BINDING
1IS8	CRYSTAL STRUCTURE OF RAT GTPCHI/GFRP STIMULATORY COMPLEX PLUS ZN	HYDROLASE/PROTEIN BINDING
1ISQ	YROCOCCUS FURIOSUS PCNA COMPLEXED WITH RFCL PIP-BOX PEPTIDE	DNA BINDING PROTEIN
1IVO	RYSTAL STRUCTURE OF THE COMPLEX OF HUMAN EPIDERMAL GROWTH FACTOR AND RECEPTOR EXTRACELLULAR DOMAINS.	TRANSFERASE/SIGNALING PROTEIN
1IVP	HE CRYSTALLOGRAPHIC STRUCTURE OF THE PROTEASE FROM HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 WITH TWO SYNTHETIC PEPTIDIC TRANSITION STATE ANALOG INHIBITORS	HYDROLASE(ACID PROTEINASE)
1IVQ	HE CRYSTALLOGRAPHIC STRUCTURE OF THE PROTEASE FROM HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 WITH TWO SYNTHETIC PEPTIDIC TRANSITION STATE ANALOG INHIBITORS	HYDROLASE(ACID PROTEINASE)
1IW7	CRYSTAL STRUCTURE OF THE RNA POLYMERASE HOLOENZYME FROM THERMUS THERMOPHILUS AT 2.6A RESOLUTION	TRANSFERASE

1IWA	RUBISCO FROM GALDIERIA PARTITA	LYASE
1IWB	CRYSTAL STRUCTURE OF DIOL DEHYDRATASE	LYASE
1IWH	CRYSTAL STRUCTURE OF HORSE CARBONMONOXYHEMOGLOBIN-BEZAFIBRATE COMPLEX AT 1.55A RESOLUTION: A NOVEL ALLOSTERIC BINDING SITE IN R-STATE HEMOGLOBIN	OXYGEN STORAGE/TRANSPORT
1IWP	GLYCEROL DEHYDRATASE-CYANOCOBALAMIN COMPLEX OF KLEBSIELLA PNEUMONIAE	LYASE
1IWQ	CRYSTAL STRUCTURE OF MARCKS CALMODULIN BINDING DOMAIN PEPTIDE COMPLEXED WITH CA2+/CALMODULIN	METAL BINDING PROTEIN/PROTEIN BINDING
1IXR	RUVA-RUVB COMPLEX	HYDROLASE
1IXS	STRUCTURE OF RUVB COMPLEXED WITH RUVA DOMAIN III	HYDROLASE
1IXX	CRYSTAL STRUCTURE OF COAGULATION FACTORS IX/X-BINDING PROTEIN (IX/X-BP) FROM VENOM OF HABU SNAKE WITH A HETERODIMER OF C-TYPE LECTIN DOMAINS	COAGULATION FACTOR BINDING
1IYJ	STRUCTURE OF A BRCA2-DSS1 COMPLEX	GENE REGULATION/ANTITUMOR PROTEIN
1IZA	ROLE OF B13 GLU IN INSULIN ASSEMBLY: THE HEXAMER STRUCTURE OF RECOMBINANT MUTANT (B13 GLU-> GLN) INSULIN	HORMONE
1IZB	ROLE OF B13 GLU IN INSULIN ASSEMBLY: THE HEXAMER STRUCTURE OF RECOMBINANT MUTANT (B13 GLU-> GLN) INSULIN	HORMONE
1IZL	CRYSTAL STRUCTURE OF PHOTOSYSTEM II	PHOTOSYNTHESIS
1IZN	CRYSTAL STRUCTURE OF ACTIN FILAMENT CAPPING PROTEIN CAPZ	PROTEIN BINDING
1J19	CRYSTAL STRUCTURE OF THE RADXIN FERM DOMAIN COMPLEXED WITH THE ICAM-2 CYTOPLASMIC PEPTIDE	CELL ADHESION
1J1D	CRYSTAL STRUCTURE OF THE 46KDA DOMAIN OF HUMAN CARDIAC TROPONIN IN THE CA2+ SATURATED FORM	CONTRACTILE PROTEIN
1J1E	CRYSTAL STRUCTURE OF THE 52KDA DOMAIN OF HUMAN CARDIAC TROPONIN IN THE CA2+ SATURATED FORM	CONTRACTILE PROTEIN
1J1O	CRYSTAL STRUCTURE OF HYHEL-10 FV MUTANT LY50F COMPLEXED WITH HEN EGG WHITE LYSOZYME	IMMUNE SYSTEM/HYDROLASE
1J1P	CRYSTAL STRUCTURE OF HYHEL-10 FV MUTANT LS91A COMPLEXED WITH HEN EGG WHITE LYSOZYME	IMMUNE SYSTEM/HYDROLASE
1J1X	CRYSTAL STRUCTURE OF HYHEL-10 FV MUTANT LS93A COMPLEXED WITH HEN EGG WHITE LYSOZYME	IMMUNE SYSTEM/HYDROLASE
1J2J	CRYSTAL STRUCTURE OF GGA1 GAT N-TERMINAL REGION IN COMPLEX WITH ARF1 GTP FORM	PROTEIN TRANSPORT

1J2X	CRYSTAL STRUCTURE OF RAP74 C-TERMINAL DOMAIN COMPLEXED WITH FCP1 C-TERMINAL PEPTIDE	TRANSCRIPTION
1J34	CRYSTAL STRUCTURE OF MG(II)-AND CA(II)-BOUND GLA DOMAIN OF FACTOR IX COMPLEXED WITH BINDING PROTEIN	PROTEIN BINDING/BLOOD CLOTTING
1J35	CRYSTAL STRUCTURE OF CA(II)-BOUND GLA DOMAIN OF FACTOR IX COMPLEXED WITH BINDING PROTEIN	PROTEIN BINDING/BLOOD CLOTTING
1J3I	WILD-TYPE PLASMODIUM FALCIPARUM DIHYDROFOLATE REDUCTASE-THYMIDYLATE SYNTHASE (PFDHFR-TS) COMPLEXED WITH WR99210, NADPH, AND DUMP	OXIDOREDUCTASE, TRANSFERASE
1J3J	DOUBLE MUTANT (C59R+S108N) PLASMODIUM FALCIPARUM DIHYDROFOLATE REDUCTASE-THYMIDYLATE SYNTHASE (PFDHFR-TS) COMPLEXED WITH PYRIMETHAMINE, NADPH, AND DUMP	OXIDOREDUCTASE, TRANSFERASE
1J3K	QUADRUPLE MUTANT (N51I+C59R+S108N+I164L) PLASMODIUM FALCIPARUM DIHYDROFOLATE REDUCTASE-THYMIDYLATE SYNTHASE (PFDHFR-TS) COMPLEXED WITH WR99210, NADPH, AND DUMP	OXIDOREDUCTASE, TRANSFERASE
1J3Y	DIRECT OBSERVATION OF PHOTOLYSIS-INDUCED TERTIARY STRUCTURAL CHANGES IN HUMAN HEMOGLOBIN; CRYSTAL STRUCTURE OF ALPHA(FE)-BETA(NI) HEMOGLOBIN (LASER PHOTOLYSED)	OXYGEN STORAGE/TRANSPORT
1J3Z	DIRECT OBSERVATION OF PHOTOLYSIS-INDUCED TERTIARY STRUCTURAL CHANGES IN HUMAN HAEMOGLOBIN; CRYSTAL STRUCTURE OF ALPHA(FE-CO)-BETA(NI) HEMOGLOBIN (LASER UNPHOTOLYSED)	OXYGEN STORAGE/TRANSPORT
1J40	DIRECT OBSERVATION OF PHOTOLYSIS-INDUCED TERTIARY STRUCTURAL CHANGES IN HUMAN HAEMOGLOBIN; CRYSTAL STRUCTURE OF ALPHA(NI)-BETA(FE-CO) HEMOGLOBIN (LASER UNPHOTOLYSED)	OXYGEN STORAGE/TRANSPORT
1J41	DIRECT OBSERVATION OF PHOTOLYSIS-INDUCED TERTIARY STRUCTURAL CHANGES IN HUMAN HAEMOGLOBIN; CRYSTAL STRUCTURE OF ALPHA(NI)-BETA(FE) HEMOGLOBIN (LASER PHOTOLYSED)	OXYGEN STORAGE/TRANSPORT
1J4X	HUMAN VH1-RELATED DUAL-SPECIFICITY PHOSPHATASE C124S MUTANT-PEPTIDE COMPLEX	HYDROLASE
1J5E	STRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT	RIBOSOME
1J5O	CRYSTAL STRUCTURE OF MET184ILE MUTANT OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH DOUBLE STRANDED DNA TEMPLATE-PRIMER	TRANSFERASE/IMMUNE SYSTEM/DNA
1J73	CRYSTAL STRUCTURE OF AN UNSTABLE INSULIN ANALOG WITH NATIVE ACTIVITY.	HORMONE/GROWTH FACTOR
1J7D	CRYSTAL STRUCTURE OF HMMS2-HUBC13	UNKNOWN FUNCTION
1J7S	CRYSTAL STRUCTURE OF DEOXY HBALPHAYQ, A MUTANT OF HBA	OXYGEN STORAGE/TRANSPORT
1J7V	HUMAN IL-10 / IL-10R1 COMPLEX	CYTOKINE/RECEPTOR

1J7W	CRYSTAL STRUCTURE OF DEOXY HBBETAYQ, A SITE DIRECTED MUTANT OF HBA	OXYGEN STORAGE/TRANSPORT
1J7Y	CRYSTAL STRUCTURE OF PARTIALLY LIGATED MUTANT OF HBA	OXYGEN STORAGE/TRANSPORT
1J7Z	OSMOLYTE STABILIZATION OF RIBONUCLEASE	HYDROLASE
1J80	OSMOLYTE STABILIZATION OF RNASE	HYDROLASE
1J81	OSMOLYTE STABILIZATION OF RNASE	HYDROLASE
1J82	OSMOLYTE STABILIZATION OF RNASE	HYDROLASE
1J8H	CRYSTAL STRUCTURE OF A COMPLEX OF A HUMAN ALPHA/BETA-T CELL RECEPTOR, INFLUENZA HA ANTIGEN PEPTIDE, AND MHC CLASS II MOLECULE, HLA-DR4	IMMUNE SYSTEM
1J9C	CRYSTAL STRUCTURE OF TISSUE FACTOR-FACTOR VIIA COMPLEX	BLOOD CLOTTING
1-Jan	COMPLEX OF PRO-LEU-GLY-HYDROXYLAMINE WITH THE CATALYTIC DOMAIN OF MATRIX METALLO PROTEINASE-8 (PHE79 FORM)	COMPLEX (METALLOPROTEASE/INHIBITOR)
1JAP	COMPLEX OF PRO-LEU-GLY-HYDROXYLAMINE WITH THE CATALYTIC DOMAIN OF MATRIX METALLO PROTEINASE-8 (MET80 FORM)	COMPLEX (METALLOPROTEASE/INHIBITOR)
1JAT	MMS2/UBC13 UBIQUITIN CONJUGATING ENZYME COMPLEX	LIGASE
1JB0	CRYSTAL STRUCTURE OF PHOTOSYSTEM I: A PHOTOSYNTHETIC REACTION CENTER AND CORE ANTENNA SYSTEM FROM CYANOBACTERIA	PHOTOSYNTHESIS
1JB7	DNA G-QUARTETS IN A 1.86 A RESOLUTION STRUCTURE OF AN OXYTRICHA NOVA TELOMERIC PROTEIN-DNA COMPLEX	DNA-BINDING PROTEIN/DNA
1JBO	THE 1.45A THREE-DIMENSIONAL STRUCTURE OF C-PHYCOCYANIN FROM THE THERMOPHYLIC CYANOBACTERIUM SYNECHOCOCCUS ELONGATUS	PHOTOSYNTHESIS
1JBP	CRYSTAL STRUCTURE OF THE CATALYTIC SUBUNIT OF CAMP-DEPENDENT PROTEIN KINASE COMPLEXED WITH A SUBSTRATE PEPTIDE, ADP AND DETERGENT	TRANSFERASE
1JBU	COAGULATION FACTOR VII ZYMOGEN (EGF2/PROTEASE) IN COMPLEX WITH INHIBITORY EXOSITE PEPTIDE A-183	HYDROLASE
1JCA	NON-STANDARD DESIGN OF UNSTABLE INSULIN ANALOGUES WITH ENHANCED ACTIVITY	HORMONE/GROWTH FACTOR
1JCH	CRYSTAL STRUCTURE OF COLICIN E3 IN COMPLEX WITH ITS IMMUNITY PROTEIN	RIBOSOME INHIBITOR, HYDROLASE
1JCQ	CRYSTAL STRUCTURE OF HUMAN PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH FARNESYL DIPHOSPHATE AND THE PEPTIDOMIMETIC INHIBITOR L-739,750	TRANSFERASE
1JCR	CRYSTAL STRUCTURE OF RAT PROTEIN FARNESYLTRANSFERASE	TRANSFERASE

	COMPLEXED WITH THE NON-SUBSTRATE TETRAPEPTIDE INHIBITOR CVFM AND FARNESYL DIPHOSPHATE SUBSTRATE	
1JCS	CRYSTAL STRUCTURE OF RAT PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH THE PEPTIDE SUBSTRATE TKCVFM AND AN ANALOG OF FARNESYL DIPHOSPHATE	TRANSFERASE
1JD2	CRYSTAL STRUCTURE OF THE YEAST 20S PROTEASOME:TMC-95A COMPLEX: A NON-COVALENT PROTEASOME INHIBITOR	HYDROLASE
1JD5	CRYSTAL STRUCTURE OF DIAP1-BIR2/GRIM	APOPTOSIS
1JD6	CRYSTAL STRUCTURE OF DIAP1-BIR2/HID COMPLEX	APOPTOSIS
1JDB	CARBAMOYL PHOSPHATE SYNTHETASE FROM ESCHERICHIA COLI	LIGASE
1JDH	CRYSTAL STRUCTURE OF BETA-CATENIN AND HTCF-4	TRANSCRIPTION
1JDP	CRYSTAL STRUCTURE OF HORMONE/RECEPTOR COMPLEX	SIGNALING PROTEIN
1JEB	HIMERIC HUMAN/MOUSE CARBONMONOXY HEMOGLOBIN (HUMAN ZETA2 / MOUSE BETA2)	OXYGEN STORAGE/TRANSPORT
1JEK	VISNA TM CORE STRUCTURE	VIRAL PROTEIN
1JEN	HUMAN S-ADENOSYLMETHIONINE DECARBOXYLASE	S-ADENOSYLMETHIONINE DECARBOXYLASE
1JEQ	CRYSTAL STRUCTURE OF THE KU HETERODIMER	DNA BINDING PROTEIN
1JET	OLIGO-PEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH KAK	COMPLEX (PEPTIDE TRANSPORT/PEPTIDE)
1JEU	OLIGO-PEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH KEK	COMPLEX (PEPTIDE TRANSPORT/PEPTIDE)
1JEV	OLIGO-PEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH KWK	COMPLEX (PEPTIDE TRANSPORT/PEPTIDE)
1JEY	CRYSTAL STRUCTURE OF THE KU HETERODIMER BOUND TO DNA	DNA BINDING PROTEIN/DNA
1JF1	CRYSTAL STRUCTURE OF HLA-A2*0201 IN COMPLEX WITH A DECAMERIC ALTERED PEPTIDE LIGAND FROM THE MART-1/MELAN-A	IMMUNE SYSTEM
1JFF	REFINED STRUCTURE OF ALPHA-BETA TUBULIN FROM ZINC-INDUCED SHEETS STABILIZED WITH TAXOL	STRUCTURAL PROTEIN
1JFI	CRYSTAL STRUCTURE OF THE NC2-TBP-DNA TERNARY COMPLEX	TRANSCRIPTION/DNA
1JFQ	ANTIGEN-BINDING FRAGMENT OF THE MURINE ANTI-PHENYLARSONATE ANTIBODY 36-71, "FAB 36-71"	IMMUNE SYSTEM
1JG3	CRYSTAL STRUCTURE OF L-ISOASPARTYL (D-ASPARTYL) O-METHYLTRANSFERASE WITH ADENOSINE & VYP(ISP)HA SUBSTRATE	TRANSFERASE
1JGD	HLA-B*2709 BOUND TO DECA-PEPTIDE S10R	IMMUNE SYSTEM
1JGE	HLA-B*2705 BOUND TO NONA-PEPTIDE M9	IMMUNE SYSTEM

1JGL	RYSTAL STRUCTURE OF IMMUNOGLOBULIN FAB FRAGMENT COMPLEXED WITH 17-BETA-ESTRADIOL	IMMUNE SYSTEM
1JGU	STRUCTURAL BASIS FOR DISFAVORED ELIMINATION REACTION IN CATALYTIC ANTIBODY 1D4	IMMUNE SYSTEM
1JGV	STRUCTURAL BASIS FOR DISFAVORED ELIMINATION REACTION IN CATALYTIC ANTIBODY 1D4	IMMUNE SYSTEM
1JGW	PHOTOSYNTHETIC REACTION CENTER MUTANT WITH THR M 21 REPLACED WITH LEU	PHOTOSYNTHESIS
1JGX	PHOTOSYNTHETIC REACTION CENTER MUTANT WITH THR M 21 REPLACED WITH ASP	PHOTOSYNTHESIS
1JGY	PHOTOSYNTHETIC REACTION CENTER MUTANT WITH TYR M 76 REPLACED WITH PHE	PHOTOSYNTHESIS
1JGZ	PHOTOSYNTHETIC REACTION CENTER MUTANT WITH TYR M 76 REPLACED WITH LYS	PHOTOSYNTHESIS
1JH0	PHOTOSYNTHETIC REACTION CENTER MUTANT WITH GLU L 205 REPLACED TO LEU	PHOTOSYNTHESIS
1JHK	CRYSTAL STRUCTURE OF THE ANTI-ESTRADIOL ANTIBODY 57-2	IMMUNE SYSTEM
1JHL	THREE-DIMENSIONAL STRUCTURE OF A HETEROCLITIC ANTIGEN-ANTIBODY CROSS-REACTION COMPLEX	COMPLEX(ANTIBODY-ANTIGEN)
1JHT	CRYSTAL STRUCTURE OF HLA-A2*0201 IN COMPLEX WITH A NONAMERIC ALTERED PEPTIDE LIGAND (ALGIGILTV) FROM THE MART-1/MELAN-A.	IMMUNE SYSTEM
1JIW	CRYSTAL STRUCTURE OF THE APR-APRIN COMPLEX	HYDROLASE/HYROLASE INHIBITOR
1JJ2	FULLY REFINED CRYSTAL STRUCTURE OF THE HALOARCULA MARISMORTUI LARGE RIBOSOMAL SUBUNIT AT 2.4 ANGSTROM RESOLUTION	RIBOSOME
1JJC	CRYSTAL STRUCTURE AT 2.6A RESOLUTION OF PHENYLALANYL-TRNA SYNTHETASE COMPLEXED WITH PHENYLALANYL-ADENYLATE IN THE PRESENCE OF MANGANESE	LIGASE
1JJO	CRYSTAL STRUCTURE OF MOUSE NEUROSERPIN (CLEAVED FORM)	SIGNALING PROTEIN
1JJU	TRUCTURE OF A QUINOHEMOPROTEIN AMINE DEHYDROGENASE WITH A UNIQUE REDOX COFACTOR AND HIGHLY UNUSUAL CROSSLINKING	ELECTRON TRANSPORT PROTEIN
1JK0	RIBONUCLEOTIDE REDUCTASE Y2Y4 HETERODIMER	OXIDOREDUCTASE
1JK4	DES 1-6 BOVINE NEUROPHYSIN II COMPLEX WITH VASOPRESSIN	NEUROPEPTIDE
1JK8	CRYSTAL STRUCTURE OF A HUMAN INSULIN PEPTIDE-HLA-DQ8 COMPLEX	IMMUNE SYSTEM
1JK9	HETERODIMER BETWEEN H48F-YSOD1 AND YCCS	OXIDOREDUCTASE

1JKG	STRUCTURAL BASIS FOR THE RECOGNITION OF A NUCLEOPORIN FG-REPEAT BY THE NTF2-LIKE DOMAIN OF TAP-P15 MRNA NUCLEAR EXPORT FACTOR	TRANSPORT PROTEIN
1JKH	CRYSTAL STRUCTURE OF Y181C MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH DMP-266(EFAVIRENZ)	TRANSFERASE
1JKJ	E. COLI SCS	LIGASE
1JKY	CRYSTAL STRUCTURE OF THE ANTHRAX LETHAL FACTOR (LF): WILD-TYPE LF COMPLEXED WITH THE N-TERMINAL SEQUENCE OF MAPKK2	TOXIN
1JL4	CRYSTAL STRUCTURE OF THE HUMAN CD4 N-TERMINAL TWO DOMAIN FRAGMENT COMPLEXED TO A CLASS II MHC MOLECULE	IMMUNE SYSTEM
1JLA	CRYSTAL STRUCTURE OF Y181C MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH TNK-651	TRANSFERASE
1JLB	CRYSTAL STRUCTURE OF Y181C MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH NEVIRAPINE	TRANSFERASE
1JLC	CRYSTAL STRUCTURE OF Y181C MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH PETT-2	TRANSFERASE
1JLE	CRYSTAL STRUCTURE OF Y188C MUTANT HIV-1 REVERSE TRANSCRIPTASE	TRANSFERASE
1JLF	CRYSTAL STRUCTURE OF Y188C MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH NEVIRAPINE	TRANSFERASE
1JLG	CRYSTAL STRUCTURE OF Y188C MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH UC-781	TRANSFERASE
1JLL	CRYSTAL STRUCTURE ANALYSIS OF THE E197BETAA MUTANT OF E. COLI SCS	LIGASE
1JLQ	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH 739W94	TRANSFERASE
1JLT	VIPOXIN COMPLEX	HYDROLASE
1JLU	CRYSTAL STRUCTURE OF THE CATALYTIC SUBUNIT OF CAMP-DEPENDENT PROTEIN KINASE COMPLEXED WITH A PHOSPHORYLATED SUBSTRATE PEPTIDE AND DETERGENT	TRANSFERASE
1JMA	CRYSTAL STRUCTURE OF THE HERPES SIMPLEX VIRUS GLYCOPROTEIN D BOUND TO THE CELLULAR RECEPTOR HVEA/HVEM	VIRAL PROTEIN
1JMO	CRYSTAL STRUCTURE OF THE HEPARIN COFACTOR II-S195A THROMBIN COMPLEX	BLOOD CLOTTING
1JMT	X-RAY STRUCTURE OF A CORE U2AF65/U2AF35 HETERODIMER	RNA BINDING PROTEIN
1JMU	CRYSTAL STRUCTURE OF THE REOVIRUS MU1/SIGMA3 COMPLEX	VIRAL PROTEIN

1JMX	RYSTAL STRUCTURE OF A QUINOHEMOPROTEIN AMINE DEHYDROGENASE FROM PSEUDOMONAS PUTIDA	OXIDOREDUCTASE
1JMZ	RYSTAL STRUCTURE OF A QUINOHEMOPROTEIN AMINE DEHYDROGENASE FROM PSEUDOMONAS PUTIDA WITH INHIBITOR	OXIDOREDUCTASE
1JN5	STRUCTURAL BASIS FOR THE RECOGNITION OF A NUCLEOPORIN FG-REPEAT BY THE NTF2-LIKE DOMAIN OF TAP-P15 MRNA EXPORT FACTOR	TRANSPORT PROTEIN
1JN6	CRYSTAL STRUCTURE OF FAB-ESTRADIOL COMPLEXES	IMMUNE SYSTEM
1JN9	STRUCTURE OF PUTATIVE ASPARAGINASE ENCODED BY ESCHERICHIA COLI YBIK GENE	HYDROLASE
1JNH	CRYSTAL STRUCTURE OF FAB-ESTRADIOL COMPLEXES	IMMUNE SYSTEM
1JNL	CRYSTAL STRUCTURE OF FAB-ESTRADIOL COMPLEXES	IMMUNE SYSTEM
1JNN	CRYSTAL STRUCTURE OF FAB-ESTRADIOL COMPLEXES	IMMUNE SYSTEM
1JNR	STRUCTURE OF ADENYLYLSULFATE REDUCTASE FROM THE HYPERTHERMOPHILIC ARCHAEOGLOBUS FULGIDUS AT 1.6 RESOLUTION	OXIDOREDUCTASE
1JNZ	STRUCTURE OF ADENYLYLSULFATE REDUCTASE FROM THE HYPERTHERMOPHILIC ARCHAEOGLOBUS FULGIDUS AT 1.6 RESOLUTION	OXIDOREDUCTASE
1JOU	CRYSTAL STRUCTURE OF NATIVE S195A THROMBIN WITH AN UNOCCUPIED ACTIVE SITE	BLOOD CLOTTING
1JOW	CRYSTAL STRUCTURE OF A COMPLEX OF HUMAN CDK6 AND A VIRAL CYCLIN	CELL CYCLE/TRANSFERASE
1JPF	CRYSTAL STRUCTURE OF THE LCMV PEPTIDIC EPITOPE GP276 IN COMPLEX WITH THE MURINE CLASS I MHC MOLECULE H-2DB	IMMUNE SYSTEM
1JPG	CRYSTAL STRUCTURE OF THE LCMV PEPTIDIC EPITOPE NP396 IN COMPLEX WITH THE MURINE CLASS I MHC MOLECULE H-2DB	IMMUNE SYSTEM
1JPL	GGA3 VHS DOMAIN COMPLEXED WITH C-TERMINAL PEPTIDE FROM CATION-INDEPENDENT MANNOSE 6-PHOSPHATE RECEPTOR	SIGNALING PROTEIN
1JPP	THE STRUCTURE OF A BETA-CATENIN BINDING REPEAT FROM ADENOMATOUS POLYPOSIS COLI (APC) IN COMPLEX WITH BETA-CATENIN	CELL ADHESION
1JPS	CRYSTAL STRUCTURE OF TISSUE FACTOR IN COMPLEX WITH HUMANIZED FAB D3H44	IMMUNE SYSTEM
1JPW	CRYSTAL STRUCTURE OF A HUMAN TCF-4 / BETA-CATENIN COMPLEX	CELL ADHESION
1JQ7	HCMV PROTEASE DIMER-INTERFACE MUTANT, S225Y COMPLEXED TO INHIBITOR BILC 408	HYDROLASE

1JQ8	DESIGN OF SPECIFIC INHIBITORS OF PHOSPHOLIPASE A2: CRYSTAL STRUCTURE OF A COMPLEX FORMED BETWEEN PHOSPHOLIPASE A2 FROM DABOIA RUSSELLI PULCHELLA AND A DESIGNED PENTAPEPTIDE LEU-ALA-ILE-TYR-SER AT 2.0 RESOLUTION	HYDROLASE
1JQ9	RYSTAL STRUCTURE OF A COMPLEX FORMED BETWEEN PHOSPHOLIPASE A2 FROM DABOIA RUSSELLI PULCHELLA AND A DESIGNED PENTAPEPTIDE PHE-LEU-SER-TYR-LYS AT 1.8 RESOLUTION	HYDROLASE
1JQJ	MECHANISM OF PROCESSIVITY CLAMP OPENING BY THE DELTA SUBUNIT WRENCH OF THE CLAMP LOADER COMPLEX OF E. COLI DNA POLYMERASE III: STRUCTURE OF THE BETA-DELTA COMPLEX	TRANSFERASE
1JQL	MECHANISM OF PROCESSIVITY CLAMP OPENING BY THE DELTA SUBUNIT WRENCH OF THE CLAMP LOADER COMPLEX OF E. COLI DNA POLYMERASE III: STRUCTURE OF BETA-DELTA (1-140)	TRANSFERASE
1JR3	CRYSTAL STRUCTURE OF THE PROCESSIVITY CLAMP LOADER GAMMA COMPLEX OF E. COLI DNA POLYMERASE III	TRANSFERASE
1JRO	CRYSTAL STRUCTURE OF XANTHINE DEHYDROGENASE FROM RHODOBACTER CAPSULATUS	OXIDOREDUCTASE
1JRP	CRYSTAL STRUCTURE OF XANTHINE DEHYDROGENASE INHIBITED BY ALLOXANTHINE FROM RHODOBACTER CAPSULATUS	OXIDOREDUCTASE
1JRR	HUMAN PLASMINOGEN ACTIVATOR INHIBITOR-2.[LOOP (66-98) DELETIONMUTANT] COMPLEXED WITH PEPTIDE MIMICKING THE REACTIVE CENTER LOOP	PEPTIDE BINDING PROTEIN
1JRS	HEMIACETAL COMPLEX BETWEEN LEUPEPTIN AND TRYPSIN	HYDROLASE (SERINE PROTEASE)
1JRT	HEMIACETAL COMPLEX BETWEEN LEUPEPTIN AND TRYPSIN	HYDROLASE (SERINE PROTEASE)
1JSD	CRYSTAL STRUCTURE OF SWINE H9 HAEMAGGLUTININ	VIRAL PROTEIN
1JSH	CRYSTAL STRUCTURE OF H9 HAEMAGGLUTININ COMPLEXED WITH LSTA RECEPTOR ANALOG	VIRAL PROTEIN
1JSI	CRYSTAL STRUCTURE OF H9 HAEMAGGLUTININ BOUND TO LSTC RECEPTOR ANALOG	VIRAL PROTEIN
1JSM	STRUCTURE OF H5 AVIAN HAEMAGGLUTININ	VIRAL PROTEIN
1JSN	STRUCTURE OF AVIAN H5 HAEMAGGLUTININ COMPLEXED WITH LSTA RECEPTRO ANALOG	VIRAL PROTEIN
1JSO	STRUCTURE OF AVIAN H5 HAEMAGGLUTININ BOUND TO LSTC RECEPTOR ANALOG	VIRAL PROTEIN
1JST	PHOSPHORYLATED CYCLIN-DEPENDENT KINASE-2 BOUND TO CYCLIN A	COMPLEX (PROTEIN KINASE/CYCLIN)
1JSU	P27(KIP1)/CYCLIN A/CDK2 COMPLEX	COMPLEX (TRANSFERASE/CYCLIN/INHIBITOR)
1JTD	CRYSTAL STRUCTURE OF BETA-LACTAMASE INHIBITOR PROTEIN-II IN	HYDROLASE/INHIBITOR

	COMPLEX WITH TEM-1 BETA-LACTAMASE	
1JTG	CRYSTAL STRUCTURE OF TEM-1 BETA-LACTAMASE / BETA-LACTAMASE INHIBITOR PROTEIN COMPLEX	HYDROLASE
1JTH	CRYSTAL STRUCTURE AND BIOPHYSICAL PROPERTIES OF A COMPLEX BETWEEN THE N-TERMINAL REGION OF SNAP25 AND THE SNARE REGION OF SYNTAXIN 1A	ENDOCYTOSIS/EXOCYTOSIS
1JTO	DEGENERATE INTERFACES IN ANTIGEN-ANTIBODY COMPLEXES	ANTIBODY,HYDROLASE
1JTP	DEGENERATE INTERFACES IN ANTIGEN-ANTIBODY COMPLEXES	ANTIBODY, HYDROLASE
1JTT	DEGENERATE INTERFACES IN ANTIGEN-ANTIBODY COMPLEXES	IMMUNE SYSTEM, LYSOZYME
1JU5	TERNARY COMPLEX OF AN CRK SH2 DOMAIN, CRK-DERIVED PHOPHOPEPTIDE, AND ABL SH3 DOMAIN BY NMR SPECTROSCOPY	PROTEIN BINDING/TRANSFERASE
1JUF	STRUCTURE OF MINOR HISTOCOMPATIBILITY ANTIGEN PEPTIDE, H13B, COMPLEXED TO H2-DB	IMMUNE SYSTEM
1JUQ	GGA3 VHS DOMAIN COMPLEXED WITH C-TERMINAL PEPTIDE FROM CATION-DEPENDENT MANNOSE 6-PHOSPHATE RECEPTOR	SIGNALING PROTEIN
1JV2	CRYSTAL STRUCTURE OF THE EXTRACELLULAR SEGMENT OF INTEGRIN ALPHAVBETA3	CELL ADHESION
1JVQ	CRYSTAL STRUCTURE AT 2.6A OF THE TERNARY COMPLEX BETWEEN ANTITHROMBIN, A P14-P8 REACTIVE LOOP PEPTIDE, AND AN EXOGENOUS TETRAPEPTIDE	BLOOD CLOTTING, HYDROLASE INHIBITOR
1JVZ	STRUCTURE OF CEPHALOSPORIN ACYLASE IN COMPLEX WITH GLUTARYL-7-AMINOCEPHALOSPORANIC ACID	HYDROLASE
1JW0	TRUCTURE OF CEPHALOSPORIN ACYLASE IN COMPLEX WITH GLUTARATE	HYDROLASE
1JW9	STRUCTURE OF THE NATIVE MOEB-MOAD PROTEIN COMPLEX	LIGASE
1JWA	STRUCTURE OF THE ATP-BOUND MOEB-MOAD PROTEIN COMPLEX	LIGASE
1JWB	STRUCTURE OF THE COVALENT ACYL-ADENYLATE FORM OF THE MOEB-MOAD PROTEIN COMPLEX	LIGASE
1JWG	VHS DOMAIN OF HUMAN GGA1 COMPLEXED WITH CATION-INDEPENDENT M6PR C-TERMINAL PEPTIDE	PROTEIN TRANSPORT/PROTEIN BINDING
1JWH	CRYSTAL STRUCTURE OF HUMAN PROTEIN KINASE CK2 HOLOENZYME	TRANSFERASE
1JWI	CRYSTAL STRUCTURE OF BITISCETIN, A VON WILLEBAND FACTOR-DEPENDENT PLATELET AGGREGATION INDUCER.	TOXIN
1JWM	CRYSTAL STRUCTURE OF THE COMPLEX OF THE MHC CLASS II MOLECULE HLA-DR1(HA PEPTIDE 306-318) WITH THE SUPERANTIGEN SEC3	IMMUNE SYSTEM

1JWS	CRYSTAL STRUCTURE OF THE COMPLEX OF THE MHC CLASS II MOLECULE HLA-DR1 (HA PEPTIDE 306-318) WITH THE SUPERANTIGEN SEC3 VARIANT 3B1	IMMUNE SYSTEM
1JWU	CRYSTAL STRUCTURE OF THE COMPLEX OF THE MHC CLASS II MOLECULE HLA-DR1 (HA PEPTIDE 306-318) WITH THE SUPERANTIGEN SEC3 VARIANT 3B2	IMMUNE SYSTEM
1JWY	CRYSTAL STRUCTURE OF THE DYNAMIN A GTPASE DOMAIN COMPLEXED WITH GDP, DETERMINED AS MYOSIN FUSION	HYDROLASE
1JX2	CRYSTAL STRUCTURE OF THE NUCLEOTIDE-FREE DYNAMIN A GTPASE DOMAIN, DETERMINED AS MYOSIN FUSION	HYDROLASE
1JX9	PENICILLIN ACYLASE, MUTANT	HYDROLASE
1JXP	BK STRAIN HEPATITIS C VIRUS (HCV) NS3-NS4A	VIRAL PROTEIN COMPLEX
1JXQ	STRUCTURE OF CLEAVED, CARD DOMAIN DELETED CASPASE-9	HYDROLASE
1JY2	CRYSTAL STRUCTURE OF THE CENTRAL REGION OF BOVINE FIBRINOGEN (E5 FRAGMENT) AT 1.4 ANGSTROMS RESOLUTION	BLOOD CLOTTING
1JY3	CRYSTAL STRUCTURE OF THE CENTRAL REGION OF BOVINE FIBRINOGEN (E5 FRAGMENT) AT 1.4 ANGSTROMS RESOLUTION	BLOOD CLOTTING
1JY7	THE STRUCTURE OF HUMAN METHEMOGLOBIN. THE VARIATION OF A THEME	OXYGEN STORAGE/TRANSPORT
1JYO	STRUCTURE OF THE SALMONELLA VIRULENCE EFFECTOR SPTP IN COMPLEX WITH ITS SECRETION CHAPERONE SICP	CHAPERONE
1JYQ	XRAY STRUCTURE OF GRB2 SH2 DOMAIN COMPLEXED WITH A HIGHLY AFFINE PHOSPHO PEPTIDE	SIGNALING PROTEIN
1JYR	XRAY STRUCTURE OF GRB2 SH2 DOMAIN COMPLEXED WITH A PHOSPHORYLATED PEPTIDE	SIGNALING PROTEIN
1JZD	DSBC-DSBDALPHA COMPLEX	OXIDOREDUCTASE
1K0Y	X-RAY CRYSTALLOGRAPHIC ANALYSES OF SYMMETRICAL ALLOSTERIC EFFECTORS OF HEMOGLOBIN. COMPOUNDS DESIGNED TO LINK PRIMARY AND SECONDARY BINDING SITES	OXYGEN STORAGE/TRANSPORT
1K1K	TRUCTURE OF MUTANT HUMAN CARBONMONOXYHEMOGLOBIN C (BETA E6K) AT 2.0 ANGSTROM RESOLUTION IN PHOSPHATE BUFFER.	OXYGEN STORAGE/TRANSPORT
1K1T	COMBINING MUTATIONS IN HIV-1 PROTEASE TO UNDERSTAND MECHANISMS OF RESISTANCE	HYDROLASE/HYDROLASE INHIBITOR
1K1U	COMBINING MUTATIONS IN HIV-1 PROTEASE TO UNDERSTAND MECHANISMS OF RESISTANCE	HYDROLASE/HYDROLASE INHIBITOR
1K21	HUMAN THROMBIN-INHIBITOR COMPLEX	HYDROLASE

1K22	HUMAN THROMBIN-INHIBITOR COMPLEX	HYDROLASE
1K2C	COMBINING MUTATIONS IN HIV-1 PROTEASE TO UNDERSTAND MECHANISMS OF RESISTANCE	HYDROLASE/HYDROLASE INHIBITOR
1K2D	CRYSTAL STRUCTURE OF THE AUTOIMMUNE MHC CLASS II I-AU COMPLEXED WITH MYELIN BASIC PROTEIN 1-11 AT 2.2A	IMMUNE SYSTEM
1K2X	CRYSTAL STRUCTURE OF PUTATIVE ASPARAGINASE ENCODED BY ESCHERICHIA COLI YBIK GENE	HYDROLASE
1K3A	STRUCTURE OF THE INSULIN-LIKE GROWTH FACTOR 1 RECEPTOR KINASE	TRANSFERASE
1K3B	CRYSTAL STRUCTURE OF HUMAN DIPEPTIDYL PEPTIDASE I (CATHEPSIN C): EXCLUSION DOMAIN ADDED TO AN ENDOPEPTIDASE FRAMEWORK CREATES THE MACHINE FOR ACTIVATION OF GRANULAR SERINE PROTEASES	HYDROLASE
1K3U	CRYSTAL STRUCTURE OF WILD-TYPE TRYPTOPHAN SYNTHASE COMPLEXED WITH N-[1H-INDOL-3-YL-ACETYL]ASPARTIC ACID	LYASE
1K3Z	X-RAY CRYSTAL STRUCTURE OF THE IKBB/NF-KB P65 HOMODIMER COMPLEX	TRANSCRIPTION
1K4C	POTASSIUM CHANNEL KCSA-FAB COMPLEX IN HIGH CONCENTRATION OF K+	MEMBRANE PROTEIN
1K4D	POTASSIUM CHANNEL KCSA-FAB COMPLEX IN LOW CONCENTRATION OF K+	MEMBRANE PROTEIN
1K4W	X-RAY STRUCTURE OF THE ORPHAN NUCLEAR RECEPTOR ROR BETA LIGAND-BINDING DOMAIN IN THE ACTIVE CONFORMATION	HORMONE/GROWTH FACTOR
1K56	OXA 10 CLASS D BETA-LACTAMASE AT PH 6.5	HYDROLASE
1K57	OXA 10 CLASS D BETA-LACTAMASE AT PH 6.0	HYDROLASE
1K5D	CRYSTAL STRUCTURE OF RAN-GPPNHP-RANBP1-RANGAP COMPLEX	SIGNALING PROTEIN/SIGNALING ACTIVATOR
1K5G	CRYSTAL STRUCTURE OF RAN-GDP-ALFX-RANBP1-RANGAP COMPLEX	SIGNALING PROTEIN/SIGNALING ACTIVATOR
1K5M	CRYSTAL STRUCTURE OF A HUMAN RHINOVIRUS TYPE 14:HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 V3 LOOP CHIMERIC VIRUS MN-III-2	VIRUS
1K5N	HLA-B*2709 BOUND TO NONA-PEPTIDE M9	IMMUNE SYSTEM
1K5Q	PENICILLIN ACYLASE, MUTANT COMPLEXED WITH PAA	HYDROLASE
1K5S	PENICILLIN ACYLASE, MUTANT COMPLEXED WITH PPA	HYDROLASE
1K6L	OTOSYNETHETIC REACTION CENTER FROM RHODOBACTER SPHAEROIDES	PHOTOSYNTHESIS
1K6N	E(L212)A,D(L213)A DOUBLE MUTANT STRUCTURE OF PHOTOSYNTHETIC	PHOTOSYNTHESIS

	REACTION CENTER FROM RHODOBACTER SPHAEROIDES	
1K6O	CRYSTAL STRUCTURE OF A TERNARY SAP-1/SRF/C-FOS SRE DNA COMPLEX	TRANSCRIPTION/DNA
1K6Q	CRYSTAL STRUCTURE OF ANTIBODY FAB FRAGMENT D3	IMMUNE SYSTEM
1K73	CO-CRYSTAL STRUCTURE OF ANISOMYCIN BOUND TO THE 50S RIBOSOMAL SUBUNIT	RIBOSOME
1K74	THE 2.3 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HETERODIMER OF THE HUMAN PPARGAMMA AND RXRALPHA LIGAND BINDING DOMAINS RESPECTIVELY BOUND WITH GW409544 AND 9-CIS RETINOIC ACID AND CO-ACTIVATOR PEPTIDES.	TRANSCRIPTION
1K78	PAX5(1-149)+ETS-1(331-440)+DNA	TRANSCRIPTION/DNA
1K7D	PENICILLIN ACYLASE MUTANT WITH PHENYL PROPRIONIC ACID	HYDROLASE
1K7E	CRYSTAL STRUCTURE OF WILD-TYPE TRYPTOPHAN SYNTHASE COMPLEXED WITH N-[1H-INDOL-3-YL-ACETYL]GLYCINE ACID	LYASE
1K7F	CRYSTAL STRUCTURE OF WILD-TYPE TRYPTOPHAN SYNTHASE COMPLEXED WITH N-[1H-INDOL-3-YL-ACETYL]VALINE ACID	LYASE
1K7L	THE 2.5 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HUMAN PPARALPHA LIGAND BINDING DOMAIN BOUND WITH GW409544 AND A CO-ACTIVATOR PEPTIDE.	TRANSCRIPTION
1K7X	CRYSTAL STRUCTURE OF THE BETA-SER178PRO MUTANT OF TRYPTOPHAN SYNTHASE	LYASE
1K83	CRYSTAL STRUCTURE OF YEAST RNA POLYMERASE II COMPLEXED WITH THE INHIBITOR ALPHA AMANITIN	TRANSCRIPTION
1K8A	CO-CRYSTAL STRUCTURE OF CARBOMYCIN A BOUND TO THE 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1K8D	CRYSTAL STRUCTURE OF THE NON-CLASSICAL MHC CLASS IB QA-2 COMPLEXED WITH A SELF PEPTIDE	IMMUNE SYSTEM
1K8I	CRYSTAL STRUCTURE OF MOUSE H2-DM	IMMUNE SYSTEM
1K8K	CRYSTAL STRUCTURE OF ARP2/3 COMPLEX	STRUCTURAL PROTEIN
1K8R	CRYSTAL STRUCTURE OF RAS-BRY2RBD COMPLEX	SIGNALING PROTEIN
1K8X	CRYSTAL STRUCTURE OF ALPHAT183V MUTANT OF TRYPTOPHAN SYNTHASE FROM SALMONELLA TYPHIMURIUM	LYASE
1K8Y	RYSTAL STRUCTURE OF THE TRYPTOPHAN SYNTHASE BETA-SER178PRO MUTANT COMPLEXED WITH D,L-ALPHA-GLYCEROL-3-PHOSPHATE	LYASE
1K8Z	RYSTAL STRUCTURE OF THE TRYPTOPHAN SYNTHASE BETA-SER178PRO MUTANT COMPLEXED WITH N-[1H-INDOL-3-YL-ACETYL]GLYCINE ACID	LYASE

1K90	CRYSTAL STRUCTURE OF THE ADENYLYL CYCLASE DOMAIN OF ANTHRAX EDEMA FACTOR (EF) IN COMPLEX WITH CALMODULIN AND 3' DEOXY-ATP	TOXIN,LYASE/METAL BINDING PROTEIN
1K93	CRYSTAL STRUCTURE OF THE ADENYLYL CYCLASE DOMAIN OF ANTHRAX EDEMA FACTOR (EF) IN COMPLEX WITH CALMODULIN	TOXIN,LYASE/METAL BINDING PROTEIN
1K9M	CO-CRYSTAL STRUCTURE OF TYLOSIN BOUND TO THE 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1KA9	IMIDAZOLE GLYCEROL PHOSPHATE SYNTHASE	TRANSFERASE
1KAP	THREE-DIMENSIONAL STRUCTURE OF THE ALKALINE PROTEASE OF PSEUDOMONAS AERUGINOSA: A TWO-DOMAIN PROTEIN WITH A CALCIUM BINDING PARALLEL BETA ROLL MOTIF	ZINC METALLOPROTEASE
1KB5	MURINE T-CELL RECEPTOR VARIABLE DOMAIN/FAB COMPLEX	COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1KB9	YEAST CYTOCHROME BC1 COMPLEX	OXIDOREDUCTASE/ELECTRON TRANSPORT
1KBG	MHC CLASS I H-2KB PRESENTED GLYCOPEPTIDE RGY8-6H-GAL2	IMMUNE SYSTEM
1KBY	STRUCTURE OF PHOTOSYNTHETIC REACTION CENTER WITH BACTERIOCHLOROPHYLL-BACTERIOPHEOPHYTIN HETERODIMER	PHOTOSYNTHESIS
1KC2	STRUCTURE OF THE TRIPLE (LYS(BETA)D3ALA, ASP(BETA)C8ALA, ASPCD2ALA) MUTANT OF THE SRC SH2 DOMAIN BOUND TO THE PQPYEEIPI PEPTIDE	TRANSFERASE
1KC5	CRYSTAL STRUCTURE OF ANTIBODY PC287 IN COMPLEX WITH PS1 PEPTIDE	IMMUNE SYSTEM
1KC8	CO-CRYSTAL STRUCTURE OF BLASTICIDIN S BOUND TO THE 50S RIBOSOMAL SUBUNIT	RIBOSOME
1KCG	NKG2D IN COMPLEX WITH ULBP3	IMMUNE SYSTEM
1KCR	CRYSTAL STRUCTURE OF ANTIBODY PC283 IN COMPLEX WITH PS1 PEPTIDE	IMMUNE SYSTEM
1KCS	CRYSTAL STRUCTURE OF ANTIBODY PC282 IN COMPLEX WITH PS1 PEPTIDE	IMMUNE SYSTEM
1KCU	CRYSTAL STRUCTURE OF ANTIBODY PC287	IMMUNE SYSTEM
1KCV	CRYSTAL STRUCTURE OF ANTIBODY PC282	IMMUNE SYSTEM
1KD1	CO-CRYSTAL STRUCTURE OF SPIRAMYCIN BOUND TO THE 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1KD2	CRYSTAL STRUCTURE OF HUMAN DEOXYHEMOGLOBIN IN ABSENCE OF ANY ANIONS	OXYGEN STORAGE/TRANSPORT
1KD8	X-RAY STRUCTURE OF THE COILED COIL GCN4 ACID BASE	DE NOVO PROTEIN

	HETERODIMER ACID-D12IA16V BASE-D12LA16L	
1KD9	X-RAY STRUCTURE OF THE COILED COIL GCN4 ACID BASE HETERODIMER ACID-D12LA16L BASE-D12LA16L	DE NOVO PROTEIN
1KDD	X-RAY STRUCTURE OF THE COILED COIL GCN4 ACID BASE HETERODIMER ACID-D12LA16I BASE-D12LA16L	DE NOVO PROTEIN
1KDQ	CRYSTAL STRUCTURE ANALYSIS OF THE MUTANT S189D RAT CHYMOTRYPSIN	HYDROLASE
1KDV	SEUDOMONAS SERINE-CARBOXYL PROTEINASE COMPLEXED WITH THE INHIBITOR AIAF (THIS ENZYME RENAMED "SEDOLISIN" IN 2003)	HYDROLASE
1KDX	KIX DOMAIN OF MOUSE CBP (CREB BINDING PROTEIN) IN COMPLEX WITH PHOSPHORYLATED KINASE INDUCIBLE DOMAIN (PKID) OF RAT CREB (CYCLIC AMP RESPONSE ELEMENT BINDING PROTEIN), NMR 17 STRUCTURES	TRANSCRIPTION REGULATION COMPLEX
1KDY	SEUDOMONAS SERINE-CARBOXYL PROTEINASE COMPLEXED WITH THE INHIBITOR AIPF (THIS ENZYME RENAMED "SEDOLISIN" IN 2003)	HYDROLASE
1KDZ	SEUDOMONAS SERINE-CARBOXYL PROTEINASE COMPLEXED WITH THE INHIBITOR TYROSTATIN (THIS ENZYME RENAMED "SEDOLISIN" IN 2003)	HYDROLASE
1KE1	SEUDOMONAS SERINE-CARBOXYL PROTEINASE COMPLEXED WITH THE INHIBITOR PSEUDOTYROSTATIN (THIS ENZYME RENAMED "SEDOLISIN" IN 2003)	HYDROLASE
1KE2	SEUDOMONAS SERINE-CARBOXYL PROTEINASE COMPLEXED WITH THE INHIBITOR CHYMOSTATIN (THIS ENZYME RENAMED "SEDOLISIN" IN 2003)	HYDROLASE
1KEC	PENICILLIN ACYLASE MUTANT WITH PHENYL PROPRIONIC ACID	HYDROLASE
1KEE	INACTIVATION OF THE AMIDOTRANSFERASE ACTIVITY OF CARBAMOYL PHOSPHATE SYNTHETASE BY THE ANTIBIOTIC ACIVICIN	LIGASE
1KEG	ANTIBODY 64M-2 FAB COMPLEXED WITH DTT(6-4)TT	IMMUNE SYSTEM/DNA
1KEL	CATALYTIC ANTIBODY 28B4 FAB FRAGMENT COMPLEXED WITH HAPTEN (1-[N-4'-NITROBENZYL-N-4'-CARBOXYBUTYLAMINO] METHYLPHOSPHONIC ACID)	CATALYTIC ANTIBODY
1KEM	CATALYTIC ANTIBODY 28B4 FAB FRAGMENT	CATALYTIC ANTIBODY
1KEN	INFLUENZA VIRUS HEMAGGLUTININ COMPLEXED WITH AN ANTIBODY THAT PREVENTS THE HEMAGGLUTININ LOW PH FUSOGENIC TRANSITION	VIRAL PROTEIN/IMMUNE SYSTEM
1KF6	E. COLI QUINOL-FUMARATE REDUCTASE WITH BOUND INHIBITOR HQNO	OXIDOREDUCTASE
1KF9	PHAGE DISPLAY DERIVED VARIANT OF HUMAN GROWTH HORMONE COMPLEXED WITH TWO COPIES OF THE EXTRACELLULAR DOMAIN OF ITS RECEPTOR	HORMONE/GROWTH FACTOR

1KFA	CRYSTAL STRUCTURE OF FAB FRAGMENT COMPLEXED WITH GIBBERELLIN A4	IMMUNE SYSTEM
1KFB	CRYSTAL STRUCTURE OF ALPHAT183V MUTANT OF TRYPTOPHAN SYNTHASE FROM SALMONELLA TYPHIMURIUM WITH INDOLE GLYCEROL PHOSPHATE	LYASE
1KFC	CRYSTAL STRUCTURE OF ALPHAT183V MUTANT OF TRYPTOPHAN SYNTHASE FROM SALMONELLA TYPHIMURIUM WITH INDOLE PROPANOL PHOSPHATE	LYASE
1KFE	CRYSTAL STRUCTURE OF ALPHAT183V MUTANT OF TRYPTOPHAN SYNTHASE FROM SALMONELLA TYPHIMURIUM WITH L-SER BOUND TO THE BETA SITE	LYASE
1KFJ	CRYSTAL STRUCTURE OF WILD-TYPE TRYPTOPHAN SYNTHASE COMPLEXED WITH L-SERINE	LYASE
1KFK	CRYSTAL STRUCTURE OF TRYPTOPHAN SYNTHASE FROM SALMONELLA TYPHIMURIUM	LYASE
1KFU	CRYSTAL STRUCTURE OF HUMAN M-CALPAIN FORM II	HYDROLASE
1KFX	CRYSTAL STRUCTURE OF HUMAN M-CALPAIN FORM I	HYDROLASE
1KFY	QUINOL-FUMARATE REDUCTASE WITH QUINOL INHIBITOR 2-[1-(4-CHLORO-PHENYL)-ETHYL]-4,6-DINITRO-PHENOL	OXIDOREDUCTASE
1KG0	STRUCTURE OF THE EPSTEIN-BARR VIRUS GP42 PROTEIN BOUND TO THE MHC CLASS II RECEPTOR HLA-DR1	VIRAL PROTEIN/IMMUNE SYSTEM
1KGC	IMMUNE RECEPTOR	IMMUNE SYSTEM
1KHP	MONOCLINIC FORM OF PAPAIN/ZLFG-DAM COVALENT COMPLEX	HYDROLASE
1KHQ	ORTHORHOMBIC FORM OF PAPAIN/ZLFG-DAM COVALENT COMPLEX	HYDROLASE
1KI1	GUANINE NUCLEOTIDE EXCHANGE REGION OF INTERSECTIN IN COMPLEX WITH CDC42	SIGNALING PROTEIN
1KI6	CRYSTAL STRUCTURE OF THYMIDINE KINASE FROM HERPES SIMPLEX VIRUS TYPE I COMPLEXED WITH A 5-IODOURACIL ANHYDROHEXITOL NUCLEOSIDE	PHOSPHOTRANSFERASE
1KIG	BOVINE FACTOR XA	COMPLEX (PROTEASE/INHIBITOR)
1KIL	THREE-DIMENSIONAL STRUCTURE OF THE COMPLEXIN/SNARE COMPLEX	MEMBRANE PROTEIN
1KIP	FV MUTANT Y(B 32)A (VH DOMAIN) OF MOUSE MONOCLONAL ANTIBODY D1.3 COMPLEXED WITH HEN EGG WHITE LYSOZYME	COMPLEX (IMMUNOGLOBULIN/HYDROLASE)
1KIQ	FV MUTANT Y(B 101)F (VH DOMAIN) OF MOUSE MONOCLONAL ANTIBODY D1.3 COMPLEXED WITH HEN EGG WHITE LYSOZYME	COMPLEX (IMMUNOGLOBULIN/HYDROLASE)

1KIR	FV MUTANT Y(A 50)S (VL DOMAIN) OF MOUSE MONOCLONAL ANTIBODY D1.3 COMPLEXED WITH HEN EGG WHITE LYSOZYME	COMPLEX (IMMUNOGLOBULIN/HYDROLASE)
1KIU	FIMH ADHESIN Q133N MUTANT-FIMC CHAPERONE COMPLEX WITH METHYL-ALPHA-D-MANNOSE	CHAPERONE/CELL ADHESION
1KJ2	MURINE ALLOREACTIVE SCFV TCR-PEPTIDE-MHC CLASS I MOLECULE COMPLEX	IMMUNE SYSTEM
1KJ3	MHC CLASS I H-2KB MOLECULE COMPLEXED WITH PKB1 PEPTIDE	IMMUNE SYSTEM
1KJ4	SUBSTRATE SHAPE DETERMINES SPECIFICITY OF RECOGNITION RECOGNITION FOR HIV-1 PROTEASE: ANALYSIS OF CRYSTAL STRUCTURES OF SIX SUBSTRATE COMPLEXES	HYDROLASE
1KJ7	SUBSTRATE SHAPE DETERMINES SPECIFICITY OF RECOGNITION RECOGNITION FOR HIV-1 PROTEASE: ANALYSIS OF CRYSTAL STRUCTURES OF SIX SUBSTRATE COMPLEXES	HYDROLASE
1KJF	SUBSTRATE SHAPE DETERMINES SPECIFICITY OF RECOGNITION RECOGNITION FOR HIV-1 PROTEASE: ANALYSIS OF CRYSTAL STRUCTURES OF SIX SUBSTRATE COMPLEXES	HYDROLASE
1KJG	SUBSTRATE SHAPE DETERMINES SPECIFICITY OF RECOGNITION RECOGNITION FOR HIV-1 PROTEASE: ANALYSIS OF CRYSTAL STRUCTURES OF SIX SUBSTRATE COMPLEXES	HYDROLASE
1KJH	SUBSTRATE SHAPE DETERMINES SPECIFICITY OF RECOGNITION RECOGNITION FOR HIV-1 PROTEASE: ANALYSIS OF CRYSTAL STRUCTURES OF SIX SUBSTRATE COMPLEXES	HYDROLASE
1KJM	TAP-A-ASSOCIATED RAT MHC CLASS I MOLECULE	IMMUNE SYSTEM
1KJV	TAP-B-ASSOCIATED RAT MHC CLASS I MOLECULE	IMMUNE SYSTEM
1KJY	CRYSTAL STRUCTURE OF HUMAN G[ALPHA]I1 BOUND TO THE GOLOCO MOTIF OF RGS14	SIGNALING PROTEIN
1KK7	SCALLOP MYOSIN IN THE NEAR RIGOR CONFORMATION	CONTRACTILE PROTEIN
1KK8	SCALLOP MYOSIN (S1-ADP-BEFX) IN THE ACTIN-DETACHED CONFORMATION	CONTRACTILE PROTEIN
1KKL	L.CASEI HPRK/P IN COMPLEX WITH B.SUBTILIS HPR	TRANSFERASE,HYDROLASE/TRANSPORT PROTEIN
1KKM	L.CASEI HPRK/P IN COMPLEX WITH B.SUBTILIS P-SER-HPR	TRANSFERASE,HYDROLASE/TRANSPORT PROTEIN
1KLF	FIMH ADHESIN-FIMC CHAPERONE COMPLEX WITH D-MANNOSE	CHAPERONE/ADHESIN COMPLEX
1KLG	CRYSTAL STRUCTURE OF HLA-DR1/TPI(23-37, THR28-->ILE MUTANT) COMPLEXED WITH STAPHYLOCOCCAL ENTEROTOXIN C3 VARIANT 3B2 (SEC3-3B2)	IMMUNE SYSTEM/TOXIN
1KLI	COFACTOR-AND SUBSTRATE-ASSISTED ACTIVATION OF FACTOR VIIA	HYDROLASE

1KLJ	CRYSTAL STRUCTURE OF UNINHIBITED FACTOR VIIA	HYDROLASE
1KLM	HIV-1 REVERSE TRANSCRIPTASE COMPLEXED WITH BHAP U-90152	NUCLEOTIDYLTRANSFERASE
1KLQ	THE MAD2 SPINDLE CHECKPOINT PROTEIN UNDERGOES SIMILAR MAJOR CONFORMATIONAL CHANGES UPON BINDING TO EITHER MAD1 OR CDC20	CELL CYCLE
1KLU	CRYSTAL STRUCTURE OF HLA-DR1/TPI(23-37) COMPLEXED WITH STAPHYLOCOCCAL ENTEROTOXIN C3 VARIANT 3B2 (SEC3-3B2)	IMMUNE SYSTEM/TOXIN
1KMC	CRYSTAL STRUCTURE OF THE CASPASE-7 / XIAP-BIR2 COMPLEX	APOPTOSIS/HYDROLASE
1KMH	CRYSTAL STRUCTURE OF SPINACH CHLOROPLAST F1-ATPASE COMPLEXED WITH TENTOXIN	HYDROLASE
1KMI	CRYSTAL STRUCTURE OF AN E.COLI CHEMOTAXIS PROTEIN, CHEZ	SIGNALING PROTEIN
1KN1	CRYSTAL STRUCTURE OF ALLOPHYCOCYANIN	ELECTRON TRANSPORT
1KN2	CATALYTIC ANTIBODY D2.3 COMPLEX	IMMUNE SYSTEM
1KN4	CATALYTIC ANTIBODY D2.3 COMPLEX	IMMUNE SYSTEM
1KNO	CRYSTAL STRUCTURE OF THE COMPLEX OF A CATALYTIC ANTIBODY FAB WITH A TRANSITION STATE ANALOG: STRUCTURAL SIMILARITIES IN ESTERASE-LIKE ABZYMES	CATALYTIC ANTIBODY
1KO6	CRYSTAL STRUCTURE OF C-TERMINAL AUTOPROTEOLYTIC DOMAIN OF NUCLEOPORIN NUP98	TRANSFERASE
1KPR	THE HUMAN NON-CLASSICAL MAJOR HISTOCOMPATIBILITY COMPLEX MOLECULE HLA-E	IMMUNE SYSTEM
1KPS	STRUCTURAL BASIS FOR E2-MEDIATED SUMO CONJUGATION REVEALED BY A COMPLEX BETWEEN UBIQUITIN CONJUGATING ENZYME UBC9 AND RANGAP1	LIGASE/PROTEIN TRANSPORT
1KPU	HIGH RESOLUTION CRYSTAL STRUCTURE OF THE MHC CLASS I COMPLEX H-2KB/VSV8	IMMUNE SYSTEM
1KPV	HIGH RESOLUTION CRYSTAL STRUCTURE OF THE MHC CLASS I COMPLEX H-2KB/SEV9	IMMUNE SYSTEM
1KQF	FORMATE DEHYDROGENASE N FROM E. COLI	OXIDOREDUCTASE
1KQG	FORMATE DEHYDROGENASE N FROM E. COLI	OXIDOREDUCTASE
1KQM	SCALLOP MYOSIN S1-AMPPNP IN THE ACTIN-DETACHED CONFORMATION	CONTRACTILE PROTEIN
1KQS	THE HALOARCULA MARISMORTUI 50S COMPLEXED WITH A PRETRANSLOCATIONAL INTERMEDIATE IN PROTEIN SYNTHESIS	RIBOSOME
1KRA	CRYSTAL STRUCTURE OF KLEBSIELLA AEROGENES UREASE, ITS APOENZYME AND TWO ACTIVE SITE MUTANTS	HYDROLASE (UREA AMIDO)

1KRB	CRYSTAL STRUCTURE OF KLEBSIELLA AEROGENES UREASE, ITS APOENZYME AND TWO ACTIVE SITE MUTANTS	HYDROLASE (UREA AMIDO)
1KRC	CRYSTAL STRUCTURE OF KLEBSIELLA AEROGENES UREASE, ITS APOENZYME AND TWO ACTIVE SITE MUTANTS	HYDROLASE (UREA AMIDO)
1KRL	CRYSTAL STRUCTURE OF RACEMIC DL-MONELLIN IN P-1	PLANT PROTEIN
1KSG	COMPLEX OF ARL2 AND PDE DELTA, CRYSTAL FORM 1	SIGNALING PROTEIN/HYDROLASE
1KSH	COMPLEX OF ARL2 AND PDE DELTA, CRYSTAL FORM 2 (NATIVE)	SIGNALING PROTEIN/HYDROLASE
1KSJ	COMPLEX OF ARL2 AND PDE DELTA, CRYSTAL FORM 2 (SEMET)	SIGNALING PROTEIN/HYDROLASE
1KSN	RYSTAL STRUCTURE OF HUMAN COAGULATION FACTOR XA COMPLEXED WITH FXV673	HYDROLASE
1KT2	CRYSTAL STRUCTURE OF CLASS II MHC MOLECULE IEK BOUND TO MOTH CYTOCHROME C PEPTIDE	IMMUNE SYSTEM
1KTD	CRYSTAL STRUCTURE OF CLASS II MHC MOLECULE IEK BOUND TO PIGEON CYTOCHROME C PEPTIDE	IMMUNE SYSTEM
1KTK	COMPLEX OF STREPTOCOCCAL PYROGENIC ENTEROTOXIN C (SPEC) WITH A HUMAN T CELL RECEPTOR BETA CHAIN (VBETA2.1)	IMMUNE SYSTEM
1KTL	THE HUMAN NON-CLASSICAL MAJOR HISTOCOMPATIBILITY COMPLEX MOLECULE HLA-E	IMMUNE SYSTEM
1KTP	CRYSTAL STRUCTURE OF C-PHYCOCYANIN OF SYNECHOCOCCUS VULCANUS AT 1.6 ANGSTROMS	PHOTOSYNTHESIS
1KTS	THROMBIN INHIBITOR COMPLEX	HYDROLASE/BLOOD CLOTTING
1KTT	THROMBIN INHIBITOR COMPLEX	HYDROLASE/BLOOD CLOTTING
1KTZ	CRYSTAL STRUCTURE OF THE HUMAN TGF-BETA TYPE II RECEPTOR EXTRACELLULAR DOMAIN IN COMPLEX WITH TGF-BETA3	CYTOKINE/CYTOKINE RECEPTOR
1KU6	FASCICULIN 2-MOUSE ACETYLCHOLINESTERASE COMPLEX	HYDROLASE/TOXIN
1KUG	CRYSTAL STRUCTURE OF A TAIWAN HABU VENOM METALLOPROTEINASE COMPLEXED WITH ITS ENDOGENOUS INHIBITOR PENW	HYDROLASE
1KUK	CRYSTAL STRUCTURE OF A TAIWAN HABU VENOM METALLOPROTEINASE COMPLEXED WITH PEKW.	HYDROLASE
1KV6	X-RAY STRUCTURE OF THE ORPHAN NUCLEAR RECEPTOR ERR3 LIGAND-BINDING DOMAIN IN THE CONSTITUTIVELY ACTIVE CONFORMATION	GENE REGULATION
1KVD	KILLER TOXIN FROM HALOTOLERANT YEAST	TOXIN
1KVE	KILLER TOXIN FROM HALOTOLERANT YEAST	TOXIN
1KWO	SCALLOP MYOSIN S1-ATPGAMMAS-P-PDM IN THE ACTIN-DETACHED	CONTRACTILE PROTEIN

	CONFORMATION	
1KX3	X-RAY STRUCTURE OF THE NUCLEOSOME CORE PARTICLE, NCP146, AT 2.0 A RESOLUTION	STRUCTURAL PROTEIN/DNA
1KX4	X-RAY STRUCTURE OF THE NUCLEOSOME CORE PARTICLE, NCP146B, AT 2.6 A RESOLUTION	STRUCTURAL PROTEIN/DNA
1KX5	X-RAY STRUCTURE OF THE NUCLEOSOME CORE PARTICLE, NCP147, AT 1.9 A RESOLUTION	STRUCTURAL PROTEIN/DNA
1KXP	CRYSTAL STRUCTURE OF HUMAN VITAMIN D-BINDING PROTEIN IN COMPLEX WITH SKELETAL ACTIN	CONTRACTILE PROTEIN/PROTEIN BINDING
1KXQ	CAMELID VHH DOMAIN IN COMPLEX WITH PORCINE PANCREATIC ALPHA-AMYLASE	HYDROLASE, IMMUNE SYSTEM
1KXT	CAMELID VHH DOMAINS IN COMPLEX WITH PORCINE PANCREATIC ALPHA-AMYLASE	HYDROLASE, IMMUNE SYSTEM
1KXV	CAMELID VHH DOMAINS IN COMPLEX WITH PORCINE PANCREATIC ALPHA-AMYLASE	HYDROLASE, IMMUNE SYSTEM
1KY7	THE AP-2 CLATHRIN ADAPTOR ALPHA-APPENDAGE IN COMPLEX WITH AMPHIPHYSIN FXDXF	ENDOCYTOSIS/EXOCYTOSIS
1KYD	AP-2 CLATHRIN ADAPTOR ALPHA-APPENDAGE IN COMPLEX WITH EPSIN DPW PEPTIDE	ENDOCYTOSIS/EXOCYTOSIS
1KYE	FACTOR XA IN COMPLEX WITH (R)-2-(3-ADAMANTAN-1-YL-UREIDO)-3-(3-CARBAMIMIDOYL-PHENYL)-N-PHENETHYL-PROPIONAMIDE	HYDROLASE
1KYF	AP-2 CLATHRIN ADAPTOR ALPHA-APPENDAGE IN COMPLEX WITH EPS15 DPF PEPTIDE	ENDOCYTOSIS/EXOCYTOSIS
1KYI	HSLUV (H. INFLUENZAE)-NLVS VINYL SULFONE INHIBITOR COMPLEX	CHAPERONE/HYDROLASE
1KYO	YEAST CYTOCHROME BC1 COMPLEX WITH BOUND SUBSTRATE CYTOCHROME C	OXIDOREDUCTASE/ELECTRON TRANSPORT
1KYU	AP-2 CLATHRIN ADAPTOR ALPHA-APPENDAGE IN COMPLEX WITH EPS15 DPF PEPTIDE	ENDOCYTOSIS/EXOCYTOSIS
1KZ7	CRYSTAL STRUCTURE OF THE DH/PH FRAGMENT OF MURINE DBS IN COMPLEX WITH THE PLACENTAL ISOFORM OF HUMAN CDC42	SIGNALING PROTEIN
1KZG	DBSCDC42(Y889F)	SIGNALING PROTEIN
1KZO	ROTEIN FARNESYLTRANSFERASE COMPLEXED WITH FARNESYLATED K-RAS4B PEPTIDE PRODUCT AND FARNESYL DIPHOSPHATE SUBSTRATE BOUND SIMULTANEOUSLY	TRANSFERASE
1KZP	ROTEIN FARNESYLTRANSFERASE COMPLEXED WITH A FARNESYLATED K-RAS4B PEPTIDE PRODUCT	TRANSFERASE

1KZU	NTEGRAL MEMBRANE PERIPHERAL LIGHT HARVESTING COMPLEX FROM RHODOPSEUDOMONAS ACIDOPHILA STRAIN 10050	LIGHT-HARVESTING PROTEIN
1KZY	CRYSTAL STRUCTURE OF THE 53BP1 BRCT REGION COMPLEXED TO TUMOR SUPPRESSOR P53	DNA BINDING PROTEIN, PROTEIN BINDING
1L0A	DOWNSTREAM REGULATOR TANK BINDS TO THE CD40 RECOGNITION SITE ON TRAF3	SIGNALING PROTEIN
1L0N	NATIVE STRUCTURE OF BOVINE MITOCHONDRIAL CYTOCHROME BC1 COMPLEX	OXIDOREDUCTASE
1L0O	CRYSTAL STRUCTURE OF THE BACILLUS STEAROTHERMOPHILUS ANTI-SIGMA FACTOR SPOIIAB WITH THE SPORULATION SIGMA FACTOR SIGMAF	PROTEIN BINDING
1L0V	QUINOL-FUMARATE REDUCTASE WITH MENAQUINOL MOLECULES	OXIDOREDUCTASE
1L0X	TCR BETA CHAIN COMPLEXED WITH STREPTOCOCCAL SUPERANTIGEN SPEA	IMMUNE SYSTEM
1L0Y	T CELL RECEPTOR BETA CHAIN COMPLEXED WITH SUPERANTIGEN SPEA SOAKED WITH ZINC	IMMUNE SYSTEM
1L1O	STRUCTURE OF THE HUMAN REPLICATION PROTEIN A (RPA) TRIMERIZATION CORE	DNA BINDING PROTEIN
1L2I	HUMAN ESTROGEN RECEPTOR ALPHA LIGAND-BINDING DOMAIN IN COMPLEX WITH (R,R)-5,11-CIS-DIETHYL-5,6,11,12-TETRAHYDROCHRYSENE-2,8-DIOL AND A GLUCOCORTICOID RECEPTOR INTERACTING PROTEIN 1 NR BOX II PEPTIDE	TRANSCRIPTION RECEPTOR/COACTIVATOR
1L2O	SCALLOP MYOSIN S1-ADP-P-PDM IN THE ACTIN-DETACHED CONFORMATION	CONTRACTILE PROTEIN
1L2W	CRYSTAL STRUCTURE OF THE YERSINIA VIRULENCE EFFECTOR YOPE CHAPERONE-BINDING DOMAIN IN COMPLEX WITH ITS SECRETION CHAPERONE, SYCE	CHAPERONE
1L3R	CRYSTAL STRUCTURE OF A TRANSITION STATE MIMIC OF THE CATALYTIC SUBUNIT OF CAMP-DEPENDENT PROTEIN KINASE	TRANSFERASE
1L4A	X-RAY STRUCTURE OF THE NEURONAL COMPLEXIN/SNARE COMPLEX FROM THE SQUID LOLIGO PEALEI	ENDOCYTOSIS/EXOCYTOSIS
1L4D	CRYSTAL STRUCTURE OF MICROPLASMINOGEN-STREPTOKINASE ALPHA DOMAIN COMPLEX	HYDROLASE/HYDROLASE ACTIVATOR
1L4Z	X-RAY CRYSTAL STRUCTURE OF THE COMPLEX OF MICROPLASMINOGEN WITH ALPHA DOMAIN OF STREPTOKINASE IN THE PRESENCE CADMIUM IONS	HYDROLASE/BLOOD CLOTTING
1L5G	CRYSTAL STRUCTURE OF THE EXTRACELLULAR SEGMENT OF INTEGRIN AVB3 IN COMPLEX WITH AN ARG-GLY-ASP LIGAND	CELL ADHESION

1L5H	FEMO-COFACTOR DEFICIENT NITROGENASE MOFE PROTEIN	OXIDOREDUCTASE
1L6O	XENOPUS DISHEVELLED PDZ DOMAIN	GENE REGULATION
1L6X	FC FRAGMENT OF RITUXIMAB BOUND TO A MINIMIZED VERSION OF THE B-DOMAIN FROM PROTEIN A CALLED Z34C	IMMUNE SYSTEM
1L7I	CRYSTAL STRUCTURE OF THE ANTI-ERBB2 FAB2C4	IMMUNE SYSTEM
1L7T	CRYSTAL STRUCTURE ANALYSIS OF THE ANTI-TESTOSTERONE FAB FRAGMENT	IMMUNE SYSTEM
1L7V	BACTERIAL ABC TRANSPORTER INVOLVED IN B12 UPTAKE	TRANSPORT PROTEIN/HYDROLASE
1L7Z	CRYSTAL STRUCTURE OF CA2+/CALMODULIN COMPLEXED WITH MYRISTOYLATED CAP-23/NAP-22 PEPTIDE	METAL BINDING PROTEIN/PROTEIN BINDING
1L9B	X-RAY STRUCTURE OF THE CYTOCHROME-C(2)-PHOTOSYNTHETIC REACTION CENTER ELECTRON TRANSFER COMPLEX FROM RHODOBACTER SPHAEROIDES IN TYPE II CO-CRYSTALS	PHOTOSYNTHESIS
1L9J	X-RAY STRUCTURE OF THE CYTOCHROME-C(2)-PHOTOSYNTHETIC REACTION CENTER ELECTRON TRANSFER COMPLEX FROM RHODOBACTER SPHAEROIDES IN TYPE I CO-CRYSTALS	PHOTOSYNTHESIS
1LA6	HE CRYSTAL STRUCTURE OF TREMATOMUS NEWNESI HEMOGLOBIN IN A PARTIAL HEMICHROME STATE	OXYGEN STORAGE/TRANSPORT
1LB1	CRYSTAL STRUCTURE OF THE DBL AND PLECKSTRIN HOMOLOGY DOMAINS OF DBS IN COMPLEX WITH RHOA	SIGNALING PROTEIN
1LB2	STRUCTURE OF THE E. COLI ALPHA C-TERMINAL DOMAIN OF RNA POLYMERASE IN COMPLEX WITH CAP AND DNA	GENE REGULATION/DNA
1LCJ	SH2 (SRC HOMOLOGY-2) DOMAIN OF HUMAN P56-LCK TYROSINE KINASE COMPLEXED WITH THE 11 RESIDUE PHOSPHOTYROSYL PEPTIDE EPQPYEEIPIYL	COMPLEX (KINASE/PEPTIDE)
1LCK	SH3-SH2 DOMAIN FRAGMENT OF HUMAN P56-LCK TYROSINE KINASE COMPLEXED WITH THE 10 RESIDUE SYNTHETIC PHOSPHOTYROSYL PEPTIDE TEGQPYQPQPA	COMPLEX (KINASE/PEPTIDE)
1LD7	CO-CRYSTAL STRUCTURE OF HUMAN FARNESYLTRANSFERASE WITH FARNESYLDIPHOSPHATE AND INHIBITOR COMPOUND 66	TRANSFERASE
1LD8	CO-CRYSTAL STRUCTURE OF HUMAN FARNESYLTRANSFERASE WITH FARNESYLDIPHOSPHATE AND INHIBITOR COMPOUND 49	TRANSFERASE
1LD9	THE THREE-DIMENSIONAL STRUCTURE OF AN H-2LD PEPTIDE COMPLEX EXPLAINS THE UNIQUE INTERACTION OF LD WITH BETA2M AND PEPTIDE	MAJOR HISTOCOMPATIBILITY COMPLEX
1LDJ	STRUCTURE OF THE CUL1-RBX1-SKP1-F BOXSKP2 SCF UBIQUITIN LIGASE COMPLEX	LIGASE

1LDK	STRUCTURE OF THE CUL1-RBX1-SKP1-F BOXSKP2 SCF UBIQUITIN LIGASE COMPLEX	LIGASE
1LDP	CRYSTAL STRUCTURE OF MURINE MHC CLASS I H-2LD WITH A MIXTURE OF BOUND PEPTIDES	COMPLEX (MHC I/PEPTIDE)
1LE8	CRYSTAL STRUCTURE OF THE MATA1/MATALPHA2-3A HETERODIMER BOUND TO DNA COMPLEX	TRANSCRIPTION/DNA
1LEG	CRYSTAL STRUCTURE OF H-2KB BOUND TO THE DEV8 PEPTIDE	IMMUNE SYSTEM
1LEK	CRYSTAL STRUCTURE OF H-2KBM3 BOUND TO DEV8	IMMUNE SYSTEM
1LEM	THE MONOSACCHARIDE BINDING SITE OF LENTIL LECTIN: AN X-RAY AND MOLECULAR MODELLING STUDY	LECTIN
1LEN	REFINEMENT OF TWO CRYSTAL FORMS OF LENTIL LECTIN AT 1.8 ANGSTROMS RESOLUTION	LECTIN
1LEW	CRYSTAL STRUCTURE OF MAP KINASE P38 COMPLEXED TO THE DOCKING SITE ON ITS NUCLEAR SUBSTRATE MEF2A	TRANSFERASE
1LEZ	CRYSTAL STRUCTURE OF MAP KINASE P38 COMPLEXED TO THE DOCKING SITE ON ITS ACTIVATOR MKK3B	TRANSFERASE
1LF8	COMPLEX OF GGA3-VHS DOMAIN AND CI-MPR C-TERMINAL PHOSPHOPEPTIDE	SIGNALING PROTEIN
1LFD	CRYSTAL STRUCTURE OF THE ACTIVE RAS PROTEIN COMPLEXED WITH THE RAS-INTERACTING DOMAIN OF RALGDS	COMPLEX (RALGDS/RAS)
1LFL	DEOXY HEMOGLOBIN (90% RELATIVE HUMIDITY)	OXYGEN STORAGE/TRANSPORT
1LFQ	OXY HEMOGLOBIN (93% RELATIVE HUMIDITY)	OXYGEN STORAGE/TRANSPORT
1LFT	OXY HEMOGLOBIN (90% RELATIVE HUMIDITY)	OXYGEN STORAGE/TRANSPORT
1LFV	OXY HEMOGLOBIN (88% RELATIVE HUMIDITY)	OXYGEN STORAGE/TRANSPORT
1LFY	OXY HEMOGLOBIN (84% RELATIVE HUMIDITY)	OXYGEN STORAGE/TRANSPORT
1LFZ	OXY HEMOGLOBIN (25% METHANOL)	OXYGEN STORAGE/TRANSPORT
1LGH	CRYSTAL STRUCTURE OF THE LIGHT-HARVESTING COMPLEX II (B800-850) FROM RHODOSPIRILLUM MOLISCHIANUM	LIGHT HARVESTING COMPLEX
1LHC	JMAN ALPHA-THROMBIN COMPLEXED WITH AC-(D)PHE-PRO-BOROARG-OH	COMPLEX (SERINE PROTEASE/INHIBITOR)
1LHD	UMAN ALPHA-THROMBIN COMPLEXED WITH AC-(D)PHE-PRO-BOROLYS-OH	COMPLEX (SERINE PROTEASE/INHIBITOR)
1LHE	HUMAN ALPHA-THROMBIN COMPLEXED WITH AC-(D)PHE-PRO-BORO-N-BUTYL-AMIDINO-GLYCINE-OH	COMPLEX (SERINE PROTEASE/INHIBITOR)
1LHF	HUMAN ALPHA-THROMBIN COMPLEXED WITH AC-(D)PHE-PRO-BORO-HOMOLYS-OH	COMPLEX (SERINE PROTEASE/INHIBITOR)

1LHG	HUMAN ALPHA-THROMBIN COMPLEXED WITH AC-(D)PHE-PRO-BOROORNITHINE-OH	COMPLEX (SERINE PROTEASE/INHIBITOR)
1LI1	THE 1.9-A CRYSTAL STRUCTURE OF THE NONCOLLAGENOUS (NC1) DOMAIN OF HUMAN PLACENTA COLLAGEN IV SHOWS STABILIZATION VIA A NOVEL TYPE OF COVALENT MET-LYS CROSS-LINK	STRUCTURAL PROTEIN
1LIA	CRYSTAL STRUCTURE OF R-PHYCOERYTHRIN FROM POLYSIPHONIA AT 2.8 A RESOLUTION	LIGHT HARVESTING PROTEIN
1LJ2	RECOGNITION OF EIF4G BY ROTAVIRUS NSP3 REVEALS A BASIS FOR MRNA CIRCULARIZATION	VIRAL PROTEIN/ TRANSLATION
1LJW	CRYSTAL STRUCTURE OF HUMAN CARBONMONOXY HEMOGLOBIN AT 2.16 A: A SNAPSHOT OF THE ALLOSTERIC TRANSITION	OXYGEN STORAGE/TRANSPORT
1LK2	1.35A CRYSTAL STRUCTURE OF H-2KB COMPLEXED WITH THE GNYSFYAL PEPTIDE	IMMUNE SYSTEM
1LK3	ENGINEERED HUMAN INTERLEUKIN-10 MONOMER COMPLEXED TO 9D7 FAB FRAGMENT	IMMUNE SYSTEM
1LK6	STRUCTURE OF DIMERIC ANTITHROMBIN COMPLEXED WITH A P14-P9 REACTIVE LOOP PEPTIDE AND AN EXOGENOUS TRIPEPTIDE	BLOOD CLOTTING
1LKK	HUMAN P56-LCK TYROSINE KINASE SH2 DOMAIN IN COMPLEX WITH THE PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU-ILE (PYEEI PEPTIDE)	COMPLEX (TYROSINE KINASE/PEPTIDE)
1LKL	HUMAN P56-LCK TYROSINE KINASE SH2 DOMAIN IN COMPLEX WITH THE PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU-GLY (PYEEG PEPTIDE)	COMPLEX (TYROSINE KINASE/PEPTIDE)
1LKY	STRUCTURE OF THE WILD-TYPE TEL-SAM POLYMER	TRANSCRIPTION
1LM8	STRUCTURE OF A HIF-1A-PVHL-ELONGINB-ELONGINC COMPLEX	TRANSCRIPTION
1LNA	A STRUCTURAL ANALYSIS OF METAL SUBSTITUTIONS IN THERMOLYSIN	METALLOPROTEASE
1LNB	A STRUCTURAL ANALYSIS OF METAL SUBSTITUTIONS IN THERMOLYSIN	HYDROLASE (METALLOPROTEASE)
1LNC	A STRUCTURAL ANALYSIS OF METAL SUBSTITUTIONS IN THERMOLYSIN	HYDROLASE (METALLOPROTEASE)
1LND	A STRUCTURAL ANALYSIS OF METAL SUBSTITUTIONS IN THERMOLYSIN	HYDROLASE (METALLOPROTEASE)
1LNE	A STRUCTURAL ANALYSIS OF METAL SUBSTITUTIONS IN THERMOLYSIN	HYDROLASE (METALLOPROTEASE)
1LNF	A STRUCTURAL ANALYSIS OF METAL SUBSTITUTIONS IN THERMOLYSIN	HYDROLASE (METALLOPROTEASE)
1LNU	CRYSTAL STRUCTURE OF CLASS II MHC MOLECULE IAB BOUND TO EALPHA3K PEPTIDE	SUGAR BINDING PROTEIN
1LO0	CATALYTIC RETRO-DIELS-ALDERASE TRANSITION STATE ANALOGUE COMPLEX	IMMUNE SYSTEM

1LO2	RETRO-DIELS-ALDERASE CATALYTIC ANTIBODY	IMMUNE SYSTEM
1LO3	RETRO-DIELS-ALDERASE CATALYTIC ANTIBODY: PRODUCT ANALOGUE	IMMUNE SYSTEM
1LO4	RETRO-DIELS-ALDERASE CATALYTIC ANTIBODY 9D9	IMMUNE SYSTEM
1LO5	CRYSTAL STRUCTURE OF THE D227A VARIANT OF STAPHYLOCOCCAL ENTEROTOXIN A IN COMPLEX WITH HUMAN MHC CLASS II	IMMUNE SYSTEM/TOXIN
1LOA	THREE-DIMENSIONAL STRUCTURES OF COMPLEXES OF LATHYRUS OCHRUS ISOLECTIN I WITH GLUCOSE AND MANNOSE: FINE SPECIFICITY OF THE MONOSACCHARIDE-BINDING SITE	LECTIN
1LOB	THREE-DIMENSIONAL STRUCTURES OF COMPLEXES OF LATHYRUS OCHRUS ISOLECTIN I WITH GLUCOSE AND MANNOSE: FINE SPECIFICITY OF THE MONOSACCHARIDE-BINDING SITE	LECTIN
1LOC	INTERACTION OF A LEGUME LECTIN WITH TWO COMPONENTS OF THE BACTERIAL CELL WALL	LECTIN
1LOD	INTERACTION OF A LEGUME LECTIN WITH TWO COMPONENTS OF THE BACTERIAL CELL WALL	LECTIN
1LOE	X-RAY CRYSTAL STRUCTURE DETERMINATION AND REFINEMENT AT 1.9 ANGSTROMS RESOLUTION OF ISOLECTIN I FROM THE SEEDS OF LATHYRUS OCHRUS	LECTIN
1LOF	X-RAY STRUCTURE OF A BIANTENNARY OCTASACCHARIDE-LECTIN COMPLEX AT 2.3 ANGSTROMS RESOLUTION	LECTIN
1LOG	X-RAY STRUCTURE OF A (ALPHA-MAN(1-3)BETA-MAN(1-4)GLCNAC)-LECTIN COMPLEX AT 2.1 ANGSTROMS RESOLUTION	LECTIN
1LOT	CRYSTAL STRUCTURE OF THE COMPLEX OF ACTIN WITH VITAMIN D-BINDING PROTEIN	TRANSPORT PROTEIN, STRUCTURAL PROTEIN
1LP1	PROTEIN Z IN COMPLEX WITH AN IN VITRO SELECTED AFFIBODY	IMMUNE SYSTEM
1LP9	XENOREACTIVE COMPLEX AHIII 12.2 TCR BOUND TO P1049/HLA-A2.1	IMMUNE SYSTEM
1LPB	THE 2.46 ANGSTROMS RESOLUTION STRUCTURE OF THE PANCREATIC LIPASE COLIPASE COMPLEX INHIBITED BY A C11 ALKYL PHOSPHONATE	HYDROLASE(CARBOXYLIC ESTERASE)
1LPG	CRYSTAL STRUCTURE OF FXA IN COMPLEX WITH 79.	HYDROLASE
1LPH	LYS(B28)PRO(B29)-HUMAN INSULIN	HORMONE
1LPK	CRYSTAL STRUCTURE OF FXA IN COMPLEX WITH 125.	HYDROLASE
1LPZ	CRYSTAL STRUCTURE OF FXA IN COMPLEX WITH 41.	HYDROLASE
1LQ8	CRYSTAL STRUCTURE OF CLEAVED PROTEIN C INHIBITOR	BLOOD CLOTTING

1LQB	CRYSTAL STRUCTURE OF A HYDROXYLATED HIF-1 ALPHA PEPTIDE BOUND TO THE PVHL/ELONGIN-C/ELONGIN-B COMPLEX	GENE REGULATION
1LQD	CRYSTAL STRUCTURE OF FXA IN COMPLEX WITH 45.	HYDROLASE
1LQG	ESCHERICHIA COLI URACIL-DNA GLYCOSYLASE COMPLEX WITH URACIL-DNA GLYCOSYLASE INHIBITOR PROTEIN	HYDROLASE/HYDROLASE INHIBITOR
1LQM	ESCHERICHIA COLI URACIL-DNA GLYCOSYLASE COMPLEX WITH URACIL-DNA GLYCOSYLASE INHIBITOR PROTEIN	HYDROLASE/HYDROLASE INHIBITOR
1LQS	CRYSTAL STRUCTURE OF HUMAN CYTOMEGALOVIRUS IL-10 BOUND TO SOLUBLE HUMAN IL-10R1	IMMUNE SYSTEM
1LQV	CRYSTAL STRUCTURE OF THE ENDOTHELIAL PROTEIN C RECEPTOR WITH PHOSPHOLIPID IN THE GROOVE IN COMPLEX WITH GLA DOMAIN OF PROTEIN C.	BLOOD CLOTTING
1LRW	CRYSTAL STRUCTURE OF METHANOL DEHYDROGENASE FROM P. DENITRIFICANS	OXIDOREDUCTASE
1LSH	LIPID-PROTEIN INTERACTIONS IN LIPOVITELLIN	LIPID BINDING PROTEIN
1LT3	HEAT-LABILE ENTEROTOXIN DOUBLE MUTANT N40C/G166C	ENTEROTOXIN
1LT4	HEAT-LABILE ENTEROTOXIN MUTANT S63K	ENTEROTOXIN
1LT9	RYSTAL STRUCTURE OF RECOMBINANT HUMAN FIBRINOGEN FRAGMENT D	BLOOD CLOTTING
1LTA	2.2 ANGSTROMS CRYSTAL STRUCTURE OF E. COLI HEAT-LABILE ENTEROTOXIN (LT) WITH BOUND GALACTOSE	ENTEROTOXIN
1LTB	2.6 ANGSTROMS CRYSTAL STRUCTURE OF PARTIALLY-ACTIVATED E. COLI HEAT-LABILE ENTEROTOXIN (LT)	ENTEROTOXIN
1LTG	THE ARG7LYS MUTANT OF HEAT-LABILE ENTEROTOXIN EXHIBITS GREAT FLEXIBILITY OF ACTIVE SITE LOOP 47-56 OF THE A SUBUNIT	ENTEROTOXIN
1LTI	HEAT-LABILE ENTEROTOXIN (LT-I) COMPLEX WITH T-ANTIGEN	ENTEROTOXIN
1LTJ	RYSTAL STRUCTURE OF RECOMBINANT HUMAN FIBRINOGEN FRAGMENT D WITH THE PEPTIDE LIGANDS GLY-PRO-ARG-PRO-AMIDE AND GLY-HIS-ARG-PRO-AMIDE	BLOOD CLOTTING
1LTS	REFINED STRUCTURE OF E. COLI HEAT LABILE ENTEROTOXIN, A CLOSE RELATIVE OF CHOLERA TOXIN	TOXIN
1LTT	LACTOSE BINDING TO HEAT-LABILE ENTEROTOXIN REVEALED BY X-RAY CRYSTALLOGRAPHY	TOXIN
1LTX	STRUCTURE OF RAB ESCORT PROTEIN-1 IN COMPLEX WITH RAB GERANYLGERANYL TRANSFERASE AND ISOPRENOID	TRANSFERASE/PROTEIN BINDING
1LUC	BACTERIAL LUCIFERASE	FLAVOPROTEIN

1LUJ	CRYSTAL STRUCTURE OF THE BETA-CATENIN/ICAT COMPLEX	STRUCTURAL PROTEIN
1LVB	CATALYTICALLY INACTIVE TOBACCO ETCH VIRUS PROTEASE COMPLEXED WITH SUBSTRATE	VIRAL PROTEIN
1LVC	CRYSTAL STRUCTURE OF THE ADENYLYL CYCLASE DOMAIN OF ANTHRAX EDEMA FACTOR (EF) IN COMPLEX WITH CALMODULIN AND 2' DEOXY, 3' ANTHRANILOYL ATP	LYASE
1LVM	CATALYTICALLY ACTIVE TOBACCO ETCH VIRUS PROTEASE COMPLEXED WITH PRODUCT	VIRAL PROTEIN
1LW0	CRYSTAL STRUCTURE OF T215Y MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH NEVIRAPINE	TRANSFERASE
1LW2	CRYSTAL STRUCTURE OF T215Y MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH 1051U91	TRANSFERASE
1LW6	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' WITH CHYMOTRYPSIN INHIBITOR 2 AT 1.5 ANGSTROM RESOLUTION	HYDROLASE
1LWC	CRYSTAL STRUCTURE OF M184V MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH NEVIRAPINE	TRANSFERASE
1LWE	CRYSTAL STRUCTURE OF M41L/T215Y MUTANT HIV-1 REVERSE TRANSCRIPTASE (RTMN) IN COMPLEX WITH NEVIRAPINE	TRANSFERASE
1LWF	CRYSTAL STRUCTURE OF A MUTANT HIV-1 REVERSE TRANSCRIPTASE (RTMQ+M184V: M41L/D67N/K70R/M184V/T215Y) IN COMPLEX WITH NEVIRAPINE	TRANSFERASE
1LWU	CRYSTAL STRUCTURE OF FRAGMENT D FROM LAMPREY FIBRINOGEN COMPLEXED WITH THE PEPTIDE GLY-HIS-ARG-PRO-AMIDE	BLOOD CLOTTING
1LX5	CRYSTAL STRUCTURE OF THE BMP7/ACTRII EXTRACELLULAR DOMAIN COMPLEX	GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1LYA	CRYSTAL STRUCTURES OF NATIVE AND INHIBITED FORMS OF HUMAN CATHEPSIN D: IMPLICATIONS FOR LYSOSOMAL TARGETING AND DRUG DESIGN	LYSOSOMAL ASPARTIC PROTEASE
1LYB	CRYSTAL STRUCTURES OF NATIVE AND INHIBITED FORMS OF HUMAN CATHEPSIN D: IMPLICATIONS FOR LYSOSOMAL TARGETING AND DRUG DESIGN	LYSOSOMAL ASPARTIC PROTEASE
1LYW	CATHEPSIN D AT PH 7.5	ASPARTIC PROTEASE
1LZQ	CRYSTAL STRUCTURE OF THE COMPLEX OF MUTANT HIV-1 PROTEASE (A71V, V82T, I84V) WITH AN ETHYLENAMINE PEPTIDOMIMETIC INHIBITOR BOC-PHE-PSI[CH2CH2NH]-PHE-GLU-PHE-NH2	HYDROLASE/HYDROLASE INHIBITOR
1LZW	STRUCTURAL BASIS OF CLPS-MEDIATED SWITCH IN CLPA SUBSTRATE RECOGNITION	CHAPERONE

1M05	HLA B8 IN COMPLEX WITH AN EPSTEIN BARR VIRUS DETERMINANT	IMMUNE SYSTEM
1M06	STRUCTURAL STUDIES OF BACTERIOPHAGE ALPHA3 ASSEMBLY, X-RAY CRYSTALLOGRAPHY	VIRUS/DNA
1M0B	HIV-1 PROTEASE IN COMPLEX WITH AN ETHYLENEAMINE INHIBITOR	HYDROLASE
1M10	CRYSTAL STRUCTURE OF THE COMPLEX OF GLYCOPROTEIN IB ALPHA AND THE VON WILLEBRAND FACTOR A1 DOMAIN	BLOOD CLOTTING
1M18	LIGAND BINDING ALTERS THE STRUCTURE AND DYNAMICS OF NUCLEOSOMAL DNA	STRUCTURAL PROTEIN/DNA
1M19	LIGAND BINDING ALTERS THE STRUCTURE AND DYNAMICS OF NUCLEOSOMAL DNA	STRUCTURAL PROTEIN/DNA
1M1A	LIGAND BINDING ALTERS THE STRUCTURE AND DYNAMICS OF NUCLEOSOMAL DNA	STRUCTURAL PROTEIN/DNA
1M1D	TETRAHYMENA GCN5 WITH BOUND BISUBSTRATE ANALOG INHIBITOR	TRANSFERASE
1M1E	BETA-CATENIN ARMADILLO REPEAT DOMAIN BOUND TO ICAT	STRUCTURAL PROTEIN
1M1J	CRYSTAL STRUCTURE OF NATIVE CHICKEN FIBRINOGEN WITH TWO DIFFERENT BOUND LIGANDS	BLOOD CLOTTING
1M1K	CO-CRYSTAL STRUCTURE OF AZITHROMYCIN BOUND TO THE 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1M1N	NITROGENASE MOFE PROTEIN FROM AZOTOBACTER VINELANDII	OXIDOREDUCTASE
1M1X	CRYSTAL STRUCTURE OF THE EXTRACELLULAR SEGMENT OF INTEGRIN ALPHA VBETA3 BOUND TO MN2+	CELL ADHESION
1M1Y	CHEMICAL CROSSLINK OF NITROGENASE MOFE PROTEIN AND FE PROTEIN	OXIDOREDUCTASE
1M27	CRYSTAL STRUCTURE OF SAP/FYNSH3/SLAM TERNARY COMPLEX	SIGNALING PROTEIN, TRANSFERASE
1M2O	CRYSTAL STRUCTURE OF THE SEC23-SAR1 COMPLEX	PROTEIN TRANSPORT/SIGNALING PROTEIN
1M2T	MISTLETOE LECTIN I FROM VISCUM ALBUM IN COMPLEX WITH ADENINE MONOPHOSPHATE. CRYSTAL STRUCTURE AT 1.9 A RESOLUTION	RIBOSOME INHIBITOR, HYDROLASE
1M2V	CRYSTAL STRUCTURE OF THE YEAST SEC23/24 HETERODIMER	PROTEIN TRANSPORT
1M2Z	CRYSTAL STRUCTURE OF A DIMER COMPLEX OF THE HUMAN GLUCOCORTICOID RECEPTOR LIGAND-BINDING DOMAIN BOUND TO DEXAMETHASONE AND A TIF2 COACTIVATOR MOTIF	HORMONE/HORMONE ACTIVATOR
1M34	NITROGENASE COMPLEX FROM AZOTOBACTER VINELANDII STABILIZED BY ADP-TETRAFLUOROALUMINATE	OXIDOREDUCTASE
1M3X	OTOSYNTHETIC REACTION CENTER FROM RHODOBACTER SPHAEROIDES	PHOTOSYNTHESIS

1M45	CRYSTAL STRUCTURE OF MLC1P BOUND TO IQ2 OF MYO2P, A CLASS V MYOSIN	CELL CYCLE PROTEIN
1M46	CRYSTAL STRUCTURE OF MLC1P BOUND TO IQ4 OF MYO2P, A CLASS V MYOSIN	CELL CYCLE PROTEIN
1M4H	CRYSTAL STRUCTURE OF BETA-SECRETASE COMPLEXED WITH INHIBITOR OM00-3	HYDROLASE
1M4U	CRYSTAL STRUCTURE OF BONE MORPHOGENETIC PROTEIN-7 (BMP-7) IN COMPLEX WITH THE SECRETED ANTAGONIST NOGGIN	HORMONE/GROWTH FACTOR
1M56	STRUCTURE OF CYTOCHROME C OXIDASE FROM RHODOBACTOR SPHAEROIDES (WILD TYPE)	OXIDOREDUCTASE
1M5A	CRYSTAL STRUCTURE OF 2-CO(2+)-INSULIN AT 1.2A RESOLUTION	HORMONE/GROWTH FACTOR
1M5N	CRYSTAL STRUCTURE OF HEAT REPEATS (1-11) OF IMPORTIN B BOUND TO THE NON-CLASSICAL NLS(67-94) OF PTHRP	PROTEIN TRANSPORT
1M63	CRYSTAL STRUCTURE OF CALCINEURIN-CYCLOPHILIN-CYCLOSPORIN SHOWS COMMON BUT DISTINCT RECOGNITION OF IMMUNOPHILIN-DRUG COMPLEXES	HYDROLASE/ISOMERASE
1M6O	CRYSTAL STRUCTURE OF HLA B*4402 IN COMPLEX WITH HLA DPA*0201 PEPTIDE	IMMUNE SYSTEM
1M6V	CRYSTAL STRUCTURE OF THE G359F (SMALL SUBUNIT) POINT MUTANT OF CARBAMOYL PHOSPHATE SYNTHETASE	LIGASE
1M6X	FLPE-HOLLIDAY JUNCTION COMPLEX	LIGASE, LYASE/DNA
1M72	:RYSTAL STRUCTURE OF CASPASE-1 FROM SPODOPTERA FRUGIPERDA	HYDROLASE
1M7D	CRYSTAL STRUCTURE OF A MONOCLONAL FAB SPECIFIC FOR SHIGELLA FLEXNERI Y LIPOPOLYSACCHARIDE COMPLEXED WITH A TRISACCHARIDE	IMMUNE SYSTEM
1M7E	CRYSTAL STRUCTURE OF THE PHOSPHOTYROSINE BINDING DOMAIN(PTB) OF MOUSE DISABLED 2(DAB2):IMPLICATIONS FOR REELING SIGNALING	SIGNALING PROTEIN
1M7I	CRYSTAL STRUCTURE OF A MONOCLONAL FAB SPECIFIC FOR SHIGELLA FLEXNERI Y LIPOPOLYSACCHARIDE COMPLEXED WITH A PENTASACCHARIDE	IMMUNE SYSTEM
1M8Q	MOLECULAR MODELS OF AVERAGED RIGOR CROSSBRIDGES FROM TOMOGRAMS OF INSECT FLIGHT MUSCLE	CONTRACTILE PROTEIN
1M90	CO-CRYSTAL STRUCTURE OF CCA-PHE-CAPROIC ACID-BIOTIN AND SPARSOMYCIN BOUND TO THE 50S RIBOSOMAL SUBUNIT	RIBOSOME
1M93	1.65 A STRUCTURE OF CLEAVED VIRAL SERPIN CRMA	VIRAL PROTEIN

1M9C	X-RAY CRYSTAL STRUCTURE OF CYCLOPHILIN A/HIV-1 CA N-TERMINAL DOMAIN (1-146) M-TYPE COMPLEX.	ISOMERASE/VIRAL PROTEIN
1M9D	X-RAY CRYSTAL STRUCTURE OF CYCLOPHILIN A/HIV-1 CA N-TERMINAL DOMAIN (1-146) O-TYPE CHIMERA COMPLEX.	ISOMERASE/VIRAL PROTEIN
1M9E	X-RAY CRYSTAL STRUCTURE OF CYCLOPHILIN A/HIV-1 CA N-TERMINAL DOMAIN (1-146) M-TYPE H87A COMPLEX.	ISOMERASE/VIRAL PROTEIN
1M9F	X-RAY CRYSTAL STRUCTURE OF CYCLOPHILIN A/HIV-1 CA N-TERMINAL DOMAIN (1-146) M-TYPE H87A,A88M COMPLEX.	ISOMERASE/VIRAL PROTEIN
1M9P	RYSTALLINE HUMAN CARBONMONOXY HEMOGLOBIN C EXHIBITS THE R2 QUATERNARY STATE AT NEUTRAL PH IN THE PRESENCE OF POLYETHYLENE GLYCOL: THE 2.1 ANGSTROM RESOLUTION CRYSTAL STRUCTURE	OXYGEN STORAGE/TRANSPORT
1M9X	X-RAY CRYSTAL STRUCTURE OF CYCLOPHILIN A/HIV-1 CA N-TERMINAL DOMAIN (1-146) M-TYPE H87A,A88M,G89A COMPLEX.	ISOMERASE/VIRAL PROTEIN
1M9Y	X-RAY CRYSTAL STRUCTURE OF CYCLOPHILIN A/HIV-1 CA N-TERMINAL DOMAIN (1-146) M-TYPE H87A,G89A COMPLEX.	ISOMERASE/VIRAL PROTEIN
1MA3	STRUCTURE OF A SIR2 ENZYME BOUND TO AN ACETYLATED P53 PEPTIDE	PROTEIN BINDING, TRANSCRIPTION
1MA9	CRYSTAL STRUCTURE OF THE COMPLEX OF HUMAN VITAMIN D BINDING PROTEIN AND RABBIT MUSCLE ACTIN	TRANSPORT PROTEIN/CONTRACTILE PROTEIN
1MAB	RAT LIVER F1-ATPASE	HYDROLASE
1MAH	FASCICULIN2-MOUSE ACETYLCHOLINESTERASE COMPLEX	COMPLEX (HYDROLASE/TOXIN)
1MAM	CRYSTAL STRUCTURE TO 2.45 A RESOLUTION OF A MONOCLONAL FAB SPECIFIC FOR THE BRUCELLA A CELL WALL POLYSACCHARIDE ANTIGEN	IMMUNOGLOBULIN
1MBU	CRYSTAL STRUCTURE ANALYSIS OF CLPSN HETERODIMER	PROTEIN BINDING
1MBV	RYSTAL STRUCTURE ANALYSIS OF CLPSN HETERODIMER TETRAGONAL FORM	PROTEIN BINDING
1MBX	CRYSTAL STRUCTURE ANALYSIS OF CLPSN WITH TRANSITION METAL ION BOUND	PROTEIN BINDING
1MCB	PRINCIPLES AND PITFALLS IN DESIGNING SITE DIRECTED PEPTIDE LIGANDS	IMMUNOGLOBULIN
1MCC	PRINCIPLES AND PITFALLS IN DESIGNING SITE DIRECTED PEPTIDE LIGANDS	IMMUNOGLOBULIN
1MCD	PRINCIPLES AND PITFALLS IN DESIGNING SITE DIRECTED PEPTIDE LIGANDS	IMMUNOGLOBULIN
1MCE	PRINCIPLES AND PITFALLS IN DESIGNING SITE DIRECTED PEPTIDE	IMMUNOGLOBULIN

	LIGANDS	
1MCF	PRINCIPLES AND PITFALLS IN DESIGNING SITE DIRECTED PEPTIDE LIGANDS	IMMUNOGLOBULIN
1MCH	PRINCIPLES AND PITFALLS IN DESIGNING SITE DIRECTED PEPTIDE LIGANDS	IMMUNOGLOBULIN
1MCI	PRINCIPLES AND PITFALLS IN DESIGNING SITE DIRECTED PEPTIDE LIGANDS	IMMUNOGLOBULIN
1MCJ	PRINCIPLES AND PITFALLS IN DESIGNING SITE DIRECTED PEPTIDE LIGANDS	IMMUNOGLOBULIN
1MCK	PRINCIPLES AND PITFALLS IN DESIGNING SITE DIRECTED PEPTIDE LIGANDS	IMMUNOGLOBULIN
1MCL	PRINCIPLES AND PITFALLS IN DESIGNING SITE DIRECTED PEPTIDE LIGANDS	IMMUNOGLOBULIN
1MCN	PRINCIPLES AND PITFALLS IN DESIGNING SITE DIRECTED PEPTIDE LIGANDS	IMMUNOGLOBULIN
1MCO	HREE-DIMENSIONAL STRUCTURE OF A HUMAN IMMUNOGLOBULIN WITH A HINGE DELETION	IMMUNOGLOBULIN
1MCP	PHOSPHOCHOLINE BINDING IMMUNOGLOBULIN FAB MC/PC603. AN X-RAY DIFFRACTION STUDY AT 2.7 ANGSTROMS	IMMUNOGLOBULIN
1MCQ	PRINCIPLES AND PITFALLS IN DESIGNING SITE DIRECTED PEPTIDE LIGANDS	IMMUNOGLOBULIN
1MCR	PRINCIPLES AND PITFALLS IN DESIGNING SITE DIRECTED PEPTIDE LIGANDS	IMMUNOGLOBULIN
1MCS	PRINCIPLES AND PITFALLS IN DESIGNING SITE DIRECTED PEPTIDE LIGANDS	IMMUNOGLOBULIN
1MCT	THE REFINED 1.6 ANGSTROMS RESOLUTION CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN PORCINE BETA-TRYPSIN AND MCTI-A, A TRYPSIN INHIBITOR OF SQUASH FAMILY	COMPLEX(PROTEINASE/INHIBITOR)
1MCW	THREE-DIMENSIONAL STRUCTURE OF A HYBRID LIGHT CHAIN DIMER. PROTEIN ENGINEERING OF A BINDING CAVITY	IMMUNOGLOBULIN
1MDA	RYSTAL STRUCTURE OF AN ELECTRON-TRANSFER COMPLEX BETWEEN METHYLAMINE DEHYDROGENASE AND AMICYANIN	ELECTRON TRANSPORT
1MDI	HIGH RESOLUTION SOLUTION NMR STRUCTURE OF MIXED DISULFIDE INTERMEDIATE BETWEEN MUTANT HUMAN THIOREDOXIN AND A 13 RESIDUE PEPTIDE COMPRISING ITS TARGET SITE IN HUMAN NFKB	COMPLEX (ELECTRON TRANSPORT/PEPTIDE)
1MDM	INHIBITED FRAGMENT OF ETS-1 AND PAIRED DOMAIN OF PAX5 BOUND TO DNA	TRANSCRIPTION/DNA

1MDU	CRYSTAL STRUCTURE OF THE CHICKEN ACTIN TRIMER COMPLEXED WITH HUMAN GELSOLIN SEGMENT 1 (GS-1)	STRUCTURAL PROTEIN
1MDY	CRYSTAL STRUCTURE OF MYOD BHLH DOMAIN BOUND TO DNA: PERSPECTIVES ON DNA RECOGNITION AND IMPLICATIONS FOR TRANSCRIPTIONAL ACTIVATION	TRANSCRIPTION/DNA
1MEE	THE COMPLEX BETWEEN THE SUBTILISIN FROM A MESOPHILIC BACTERIUM AND THE LEECH INHIBITOR EGLIN-C	COMPLEX(SERINE PROTEINASE-INHIBITOR)
1MEL	CRYSTAL STRUCTURE OF A CAMEL SINGLE-DOMAIN VH ANTIBODY FRAGMENT IN COMPLEX WITH LYSOZYME	COMPLEX (ANTIBODY/ANTIGEN)
1MEX	ANTIBODY CATALYSIS OF A BIMOLECULAR CYCLOADDITION REACTION	IMMUNE SYSTEM
1MF2	ANTI HIV1 PROTEASE FAB COMPLEX	IMMUNOGLOBULIN
1MF4	STRUCTURE-BASED DESIGN OF POTENT AND SELECTIVE INHIBITORS OF PHOSPHOLIPASE A2: CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN PHOSHOLIPASE A2 FROM NAJA NAJA SAGITTIFERA AND A DESIGNED PEPTIDE INHIBITOR AT 1.9 A RESOLUTION	HYDROLASE
1MF8	CRYSTAL STRUCTURE OF HUMAN CALCINEURIN COMPLEXED WITH CYCLOSPORIN A AND HUMAN CYCLOPHILIN	HYDROLASE, LIGASE
1MFB	HIGH RESOLUTION STRUCTURES OF ANTIBODY FAB FRAGMENT COMPLEXED WITH CELL-SURFACE OLIGOSACCHARIDE OF PATHOGENIC SALMONELLA	IMMUNOGLOBULIN
1MFC	HIGH RESOLUTION STRUCTURES OF ANTIBODY FAB FRAGMENT COMPLEXED WITH CELL-SURFACE OLIGOSACCHARIDE OF PATHOGENIC SALMONELLA	IMMUNOGLOBULIN
1MFD	THE SOLUTION STRUCTURE OF A TRISACCHARIDE-ANTIBODY COMPLEX: COMPARISON OF NMR MEASUREMENTS WITH A CRYSTAL STRUCTURE	IMMUNOGLOBULIN
1MFE	RECOGNITION OF A CELL-SURFACE OLIGO-SACCHARIDE OF PATHOGENIC SALMONELLA BY AN ANTIBODY FAB FRAGMENT	IMMUNOGLOBULIN
1MFG	THE STRUCTURE OF ERBIN PDZ DOMAIN BOUND TO THE CARBOXY-TERMINAL TAIL OF THE ERBB2 RECEPTOR	SIGNALING PROTEIN
1MFL	THE STRUCTURE OF ERBIN PDZ DOMAIN BOUND TO THE CARBOXY-TERMINAL TAIL OF THE ERBB2 RECEPTOR	SIGNALING PROTEIN
1MFQ	CRYSTAL STRUCTURE ANALYSIS OF A TERNARY S-DOMAIN COMPLEX OF HUMAN SIGNAL RECOGNITION PARTICLE	SIGNALING PROTEIN/RNA
1MG2	MUTATION OF ALPHA PHE55 OF METHYLAMINE DEHYDROGENASE ALTERS THE REORGANIZATION ENERGY AND ELECTRONIC COUPLING FOR ITS ELECTRON TRANSFER REACTION WITH AMICYANIN	OXIDOREDUCTASE
1MG3	MUTATION OF ALPHA PHE55 OF METHYLAMINE DEHYDROGENASE ALTERS THE REORGANIZATION ENERGY AND ELECTRONIC COUPLING FOR ITS ELECTRON TRANSFER REACTION WITH AMICYANIN	OXIDOREDUCTASE

1MG9	THE STRUCTURAL BASIS OF CLPS-MEDIATED SWITCH IN CLPA SUBSTRATE RECOGNITION	CHAPERONE
1MH2	CRYSTAL STRUCTURE OF A ZINC CONTAINING DIMER OF PHOSPHOLIPASE A2 FROM THE VENOM OF INDIAN COBRA (NAJA NAJA SAGITTIFERA)	HYDROLASE
1MH5	THE STRUCTURE OF THE COMPLEX OF THE FAB FRAGMENT OF THE ESTEROLYTIC ANTIBODY MS6-164 AND A TRANSITION-STATE ANALOG	IMMUNE SYSTEM
1MHC	MODEL OF MHC CLASS I H2-M3 WITH NONAPEPTIDE FROM RAT ND1 REFINED AT 2.3 ANGSTROMS RESOLUTION	HISTOCOMPATIBILITY ANTIGEN/PEPTIDE
1MHE	THE HUMAN NON-CLASSICAL MAJOR HISTOCOMPATIBILITY COMPLEX MOLECULE HLA-E	MAJOR HISTOCOMPATIBILITY COMPLEX
1MHH	ANTIBODY-ANTIGEN COMPLEX	IMMUNE SYSTEM
1MHL	CRYSTAL STRUCTURE OF HUMAN MYELOPEROXIDASE ISOFORM C CRYSTALLIZED IN SPACE GROUP P2(1) AT PH 5.5 AND 20 DEG C	MYELOPEROXIDASE
1MHM	CRYSTAL STRUCTURE OF S-ADENOSYLMETHIONINE DECARBOXYLASE FROM POTATO	LYASE
1MHP	CRYSTAL STRUCTURE OF A CHIMERIC ALPHA1 INTEGRIN I-DOMAIN IN COMPLEX WITH THE FAB FRAGMENT OF A HUMANIZED NEUTRALIZING ANTIBODY	IMMUNE SYSTEM
1MHW	DESIGN OF NON-COVALENT INHIBITORS OF HUMAN CATHEPSIN L. FROM THE 96-RESIDUE PROREGION TO OPTIMIZED TRIPEPTIDES	HYDROLASE
1MHY	METHANE MONOOXYGENASE HYDROXYLASE	OXIDOREDUCTASE
1MHZ	METHANE MONOOXYGENASE HYDROXYLASE	OXIDOREDUCTASE
1MI5	THE CRYSTAL STRUCTURE OF LC13 TCR IN COMPLEX WITH HLAB8-EBV PEPTIDE COMPLEX	IMMUNE SYSTEM
1MIE	CRYSTAL STRUCTURE OF THE FAB FRAGMENT OF ESTEROLYTIC ANTIBODY MS5-393	IMMUNE SYSTEM
1MIM	IGG FAB FRAGMENT (CD25-BINDING)	IMMUNOGLOBULIN
1MIO	X-RAY CRYSTAL STRUCTURE OF THE NITROGENASE MOLYBDENUM-IRON PROTEIN FROM CLOSTRIDIUM PASTEURIANUM AT 3.0 ANGSTROMS RESOLUTION	MOLYBDENUM-IRON PROTEIN
1MIU	STRUCTURE OF A BRCA2-DSS1 COMPLEX	GENE REGULATION/ANTITUMOR PROTEIN
1MIZ	CRYSTAL STRUCTURE OF AN INTEGRIN BETA3-TALIN CHIMERA	STRUCTURAL PROTEIN
1MJ7	CRYSTAL STRUCTURE OF THE COMPLEX OF THE FAB FRAGMENT OF ESTEROLYTIC ANTIBODY MS5-393 AND A TRANSITION-STATE ANALOG	IMMUNE SYSTEM

1MJ8	HIGH RESOLUTION CRYSTAL STRUCTURE OF THE FAB FRAGMENT OF THE ESTEROLYTIC ANTIBODY MS6-126	IMMUNE SYSTEM
1MJE	STRUCTURE OF A BRCA2-DSS1-SSDNA COMPLEX	GENE REGULATION/ANTITUMOR PROTEIN/DNA
1MJG	CRYSTAL STRUCTURE OF BIFUNCTIONAL CARBON MONOXIDE DEHYDROGENASE/ACETYL-COA SYNTHASE(CODH/ACS) FROM MOORELLA THERMOACETICA (F. CLOSTRIDIUM THERMOACETICUM)	OXIDOREDUCTASE
1MJJ	HIGH RESOLUTION CRYSTAL STRUCTURE OF THE COMPLEX OF THE FAB FRAGMENT OF ESTEROLYTIC ANTIBODY MS6-12 AND A TRANSITION-STATE ANALOG	IMMUNE SYSTEM
1MJU	1.22 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE FAB FRAGMENT OF ESTEROLYTIC ANTIBODY MS6-12	IMMUNE SYSTEM
1MK2	SMAD3 SBD COMPLEX	TRANSCRIPTION
1MK7	CRYSTAL STRUCTURE OF AN INTEGRIN BETA3-TALIN CHIMERA	STRUCTURAL PROTEIN
1MK9	CRYSTAL STRUCTURE OF AN INTEGRIN BETA3-TALIN CHIMERA	STRUCTURAL PROTEIN
1MKO	A FOURTH QUATERNARY STRUCTURE OF HUMAN HEMOGLOBIN A AT 2.18 A RESOLUTION	OXYGEN STORAGE/TRANSPORT
1MKW	THE CO-CRYSTAL STRUCTURE OF UNLIGANDED BOVINE ALPHA-THROMBIN AND PRETHROMBIN-2: MOVEMENT OF THE YPPW SEGMENT AND ACTIVE SITE RESIDUES UPON LIGAND BINDING	COMPLEX (BLOOD COAGULATION/PROENZYME)
1MKX	THE CO-CRYSTAL STRUCTURE OF UNLIGANDED BOVINE ALPHA-THROMBIN AND PRETHROMBIN-2: MOVEMENT OF THE YPPW SEGMENT AND ACTIVE SITE RESIDUES UPON LIGAND BINDING	COMPLEX (BLOOD COAGULATION/PROENZYME)
1ML0	VIRAL CHEMOKINE BINDING PROTEIN M3 FROM MURINE GAMMAHERPESVIRUS68 IN COMPLEX WITH THE P8A VARIANT OF CC-CHEMOKINE MCP-1	IMMUNE SYSTEM
1MLB	MONOCLONAL ANTIBODY FAB D44.1 RAISED AGAINST CHICKEN EGG-WHITE LYSOZYME	IMMUNOGLOBULIN
1MLC	MONOCLONAL ANTIBODY FAB D44.1 RAISED AGAINST CHICKEN EGG-WHITE LYSOZYME COMPLEXED WITH LYSOZYME	COMPLEX (ANTIBODY/ANTIGEN)
1MMF	CRYSTAL STRUCTURE OF SUBSTRATE FREE FORM OF GLYCEROL DEHYDRATASE	LYASE
1MMO	CRYSTAL STRUCTURE OF A BACTERIAL NON-HAEM IRON HYDROXYLASE THAT CATALYSES THE BIOLOGICAL OXIDATION OF METHANE	OXIDOREDUCTASE (MONOOXYGENASE)
1MNF	DOMAIN MOTIONS IN GROEL UPON BINDING OF AN OLIGOPEPTIDE	CHAPERONE
1MNM	YEAST MATALPHA2/MCM1/DNA TERNARY TRANSCRIPTION COMPLEX CRYSTAL STRUCTURE	TRANSCRIPTION/DNA
1MO1	CRYSTAL STRUCTURE AT 1.8 ANGSTROMS OF SELENO METHIONYLED	TRANSPORT PROTEIN

	CRH, THE BACILLUS SUBTILIS CATABOLITE REPRESSION CONTAINING PROTEIN CRH REVEALS AN UNEXPECTED SWAPPING DOMAIN AS AN UNTERTWINNED DIMER	
1MOX	RYSTAL STRUCTURE OF HUMAN EPIDERMAL GROWTH FACTOR RECEPTOR (RESIDUES 1-501) IN COMPLEX WITH TGF-ALPHA	TRANSFERASE/GROWTH FACTOR
1MPA	BACTERICIDAL ANTIBODY AGAINST NEISSERIA MENINGITIDIS	COMPLEX (IMMUNOGLOBULIN/PEPTIDE)
1MPJ	X-RAY CRYSTALLOGRAPHIC STUDIES ON HEXAMERIC INSULINS IN THE PRESENCE OF HELIX-STABILIZING AGENTS, THIOCYANATE, METHYLPARABEN AND PHENOL	HORMONE
1MPS	PHOTOSYNTHETIC REACTION CENTER MUTANT WITH PHE M 197 REPLACED WITH ARG AND TYR M 177 REPLACED WITH PHE (CHAIN M, Y177F, F197R)	PHOTOSYNTHETIC REACTION CENTER
1MQ5	CRYSTAL STRUCTURE OF 3-CHLORO-N-[4-CHLORO-2-[[(4-CHLOROPHENYL)AMINO]CARBONYL]PHENYL]-4-[(4-METHYL-1-PIPERAZINYL)METHYL]-2-THIOPHENECARBOXAMIDE COMPLEXED WITH HUMAN FACTOR XA	BLOOD CLOTTING
1MQ6	CRYSTAL STRUCTURE OF 3-CHLORO-N-[4-CHLORO-2-[[(5-CHLORO-2-PYRIDINYL)AMINO]CARBONYL]-6-METHOXYPHENYL]-4-[[(4,5-DIHYDRO-2-OXAZOLYL)METHYLAMINO]METHYL]-2-THIOPHENECARBOXAMIDE COMPLEXED WITH HUMAN FACTOR XA	BLOOD CLOTTING
1MQ8	CRYSTAL STRUCTURE OF ALPHAL I DOMAIN IN COMPLEX WITH ICAM-1	IMMUNE SYSTEM
1MQL	BHA OF UKR/63	VIRAL PROTEIN
1MQM	BHA/LSTA	VIRAL PROTEIN
1MQN	BHA/LSTC	VIRAL PROTEIN
1MQS	CRYSTAL STRUCTURE OF SLY1P IN COMPLEX WITH AN N-TERMINAL PEPTIDE OF SED5P	ENDOCYTOSIS/EXOCYTOSIS
1MQT	SWINE VESICULAR DISEASE VIRUS COAT PROTEIN	VIRUS
1MR1	CRYSTAL STRUCTURE OF A SMAD4-SKI COMPLEX	SIGNALING PROTEIN
1MRC	PREPARATION, CHARACTERIZATION AND CRYSTALLIZATION OF AN ANTIBODY FAB FRAGMENT THAT RECOGNIZES RNA. CRYSTAL STRUCTURES OF NATIVE FAB AND THREE FAB-MONONUCLEOTIDE COMPLEXES	IMMUNOGLOBULIN
1MRD	PREPARATION, CHARACTERIZATION AND CRYSTALLIZATION OF AN ANTIBODY FAB FRAGMENT THAT RECOGNIZES RNA. CRYSTAL STRUCTURES OF NATIVE FAB AND THREE FAB-MONONUCLEOTIDE COMPLEXES	IMMUNOGLOBULIN
1MRE	PREPARATION, CHARACTERIZATION AND CRYSTALLIZATION OF AN ANTIBODY FAB FRAGMENT THAT RECOGNIZES RNA. CRYSTAL STRUCTURES OF NATIVE FAB AND THREE FAB-MONONUCLEOTIDE	IMMUNOGLOBULIN

	COMPLEXES	
1MRF	PREPARATION, CHARACTERIZATION AND CRYSTALLIZATION OF AN ANTIBODY FAB FRAGMENT THAT RECOGNIZES RNA. CRYSTAL STRUCTURES OF NATIVE FAB AND THREE FAB-MONONUCLEOTIDE COMPLEXES	IMMUNOGLOBULIN
1MRO	METHYL-COENZYME M REDUCTASE	METHANOGENESIS
1MSO	T6 HUMAN INSULIN AT 1.0 A RESOLUTION	HORMONE/GROWTH FACTOR
1MT1	THE CRYSTAL STRUCTURE OF PYRUVOYL-DEPENDENT ARGININE DECARBOXYLASE FROM METHANOCOCCUS JANNASCHII	LYASE
1MT7	VIABILITY OF A DRUG-RESISTANT HIV-1 PROTEASE MUTANT: STRUCTURAL INSIGHTS FOR BETTER ANTIVIRAL THERAPY	HYDROLASE/HYDROLASE INHIBITOR
1MT8	VIABILITY OF A DRUG-RESISTANT HIV-1 PROTEASE MUTANT: STRUCTURAL INSIGHTS FOR BETTER ANTIVIRAL THERAPY	HYDROLASE/HYDROLASE INHIBITOR
1MT9	VIABILITY OF A DRUG-RESISTANT HIV-1 PROTEASE MUTANT: STRUCTURAL INSIGHTS FOR BETTER ANTIVIRAL THERAPY	HYDROLASE
1MTN	BOVINE ALPHA-CHYMOTRYPSIN:BPTI CRYSTALLIZATION	COMPLEX (HYDROLASE/INHIBITOR)
1MTP	THE X-RAY CRYSTAL STRUCTURE OF A SERPIN FROM A THERMOPHILIC PROKARYOTE	STRUCTURAL GENOMICS
1MTY	ETHANE MONOOXYGENASE HYDROXYLASE FROM METHYLOCOCCUS CAPSULATUS (BATH)	MONOOXYGENASE
1MU2	CRYSTAL STRUCTURE OF HIV-2 REVERSE TRANSCRIPTASE	TRANSFERASE
1MU6	CRYSTAL STRUCTURE OF THROMBIN IN COMPLEX WITH L-378,622	HYDROLASE/BLOOD CLOTTING
1MU8	THROMBIN-HIRUGEN_L-378,650	HYDROLASE/BLOOD CLOTTING
1MUE	THROMBIN-HIRUGEN-L405,426	HYDROLASE/BLOOD CLOTTING
1MUJ	CRYSTAL STRUCTURE OF MURINE CLASS II MHC I-AB IN COMPLEX WITH A HUMAN CLIP PEPTIDE	IMMUNE SYSTEM
1MV9	CRYSTAL STRUCTURE OF THE HUMAN RXR ALPHA LIGAND BINDING DOMAIN BOUND TO THE EICOSANOID DHA (DOCOSA HEXAENOIC ACID) AND A COACTIVATOR PEPTIDE	TRANSCRIPTION
1MVC	CRYSTAL STRUCTURE OF THE HUMAN RXR ALPHA LIGAND BINDING DOMAIN BOUND TO THE SYNTHETIC AGONIST COMPOUND BMS 649 AND A COACTIVATOR PEPTIDE	TRANSCRIPTION
1MVF	MAZE ADDICTION ANTIDOTE	IMMUNE SYSTEM
1MVU	SINGLE CHAIN FV OF C219 HEAVY CHAIN V101L MUTANT IN COMPLEX WITH SYNTHETIC EPITOPE PEPTIDE	IMMUNE SYSTEM

1MVW	MOLECULAR MODELS OF AVERAGED RIGOR CROSSBRIDGES FROM TOMOGRAMS OF INSECT FLIGHT MUSCLE	CONTRACTILE PROTEIN
1MWA	2C/H-2KBM3/DEV8 ALLOGENEIC COMPLEX	IMMUNE SYSTEM
1MXE	STRUCTURE OF THE COMPLEX OF CALMODULIN WITH THE TARGET SEQUENCE OF CAMKI	METAL BINDING PROTEIN
1MYP	X-RAY CRYSTAL STRUCTURE OF CANINE MYELOPEROXIDASE AT 3 ANGSTROMS RESOLUTION	MYELOPEROXIDASE
1MZ8	CRYSTAL STRUCTURES OF THE NUCLEASE DOMAIN OF COLE7/IM7 IN COMPLEX WITH A PHOSPHATE ION AND A ZINC ION	TOXIN,HYDROLASE/PROTEIN BINDING
1MZC	CO-CRYSTAL STRUCTURE OF HUMAN FARNESYLTRANSFERASE WITH FARNESYLDIPHOSPHATE AND INHIBITOR COMPOUND 33A	TRANSFERASE
1MZN	CRYSTAL STRUCTURE AT 1.9 ANGSTROEMS RESOLUTION OF THE HOMODIMER OF HUMAN RXR ALPHA LIGAND BINDING DOMAIN BOUND TO THE SYNTHETIC AGONIST COMPOUND BMS 649 AND A COACTIVATOR PEPTIDE	TRANSCRIPTION
1MZW	CRYSTAL STRUCTURE OF A U4/U6 SNRNP COMPLEX BETWEEN HUMAN SPLICEOSOMAL CYCLOPHILIN H AND A U4/U6-60K PEPTIDE	ISOMERASE
1N0W	CRYSTAL STRUCTURE OF A RAD51-BRCA2 BRC REPEAT COMPLEX	GENE REGULATION/ANTITUMOR PROTEIN
1N0X	CRYSTAL STRUCTURE OF A BROADLY NEUTRALIZING ANTI-HIV-1 ANTIBODY IN COMPLEX WITH A PEPTIDE MIMOTOPE	IMMUNE SYSTEM
1N13	THE CRYSTAL STRUCTURE OF PYRUVOYL-DEPENDENT ARGININE DECARBOXYLASE FROM METHANOCOCCUS JANNASHII	LYASE
1N1J	CRYSTAL STRUCTURE OF THE NF-YB/NF-YC HISTONE PAIR	DNA BINDING PROTEIN
1N1L	CRYSTAL STRUCTURE OF HCV NS3 PROTEASE DOMAIN:NS4A PEPTIDE COMPLEX WITH COVALENTLY BOUND INHIBITOR (GW472467X)	VIRAL PROTEIN
1N2C	NITROGENASE COMPLEX FROM AZOTOBACTER VINELANDII STABILIZED BY ADP-TETRAFLUOROALUMINATE	COMPLEX OF NITROGENASE PROTEINS
1N2D	TERNARY COMPLEX OF MLC1P BOUND TO IQ2 AND IQ3 OF MYO2P, A CLASS V MYOSIN	CELL CYCLE
1N2R	A NATURAL SELECTED DIMORPHISM IN HLA B*44 ALTERS SELF, PEPTIDE REPORTOIRE AND T CELL RECOGNITION.	IMMUNE SYSTEM
1N32	TRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT BOUND TO CODON AND NEAR-COGNATE TRANSFER RNA ANTICODON STEM-LOOP MISMATCHED AT THE FIRST CODON POSITION AT THE A SITE WITH PAROMOMYCIN	RIBOSOME
1N33	TRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT BOUND TO CODON AND NEAR-COGNATE TRANSFER RNA ANTICODON STEM-LOOP MISMATCHED AT THE SECOND CODON POSITION AT THE A	RIBOSOME

	SITE WITH PAROMOMYCIN	
1N34	TRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT IN THE PRESENCE OF CODON AND CRYSTALLOGRAPHICALLY DISORDERED NEAR-COGNATE TRANSFER RNA ANTICODON STEM-LOOP MISMATCHED AT THE FIRST CODON POSITION	RIBOSOME
1N36	TRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT IN THE PRESENCE OF CRYSTALLOGRAPHICALLY DISORDERED CODON AND NEAR-COGNATE TRANSFER RNA ANTICODON STEM-LOOP MISMATCHED AT THE SECOND CODON POSITION	RIBOSOME
1N3N	CRYSTAL STRUCTURE OF A MYCOBACTERIAL HSP60 EPITOPE WITH THE MURINE CLASS I MHC MOLECULE H-2DB	IMMUNE SYSTEM
1N4H	HARACTERIZATION OF LIGANDS FOR THE ORPHAN NUCLEAR RECEPTOR RORBETA	HORMONE/GROWTH FACTOR
1N4M	STRUCTURE OF RB TUMOR SUPPRESSOR BOUND TO THE TRANSACTIVATION DOMAIN OF E2F-2	CELL CYCLE
1N4P	ROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH GERANYLGERANYL DIPHOSPHATE	TRANSFERASE
1N4Q	ROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A KKKSKTKCVIL PEPTIDE	TRANSFERASE
1N4R	ROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GERANYLGERANYLATED KKKSKTKCVIL PEPTIDE PRODUCT	TRANSFERASE
1N4S	ROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH GGPP AND A GERANYLGERANYLATED KKKSKTKCVIL PEPTIDE PRODUCT	TRANSFERASE
1N52	CAP BINDING COMPLEX	RNA BINDING PROTEIN
1N54	CAP BINDING COMPLEX M7GPPPG FREE	RNA BINDING PROTEIN
1N59	CRYSTAL STRUCTURE OF THE MURINE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX OF H-2KB, B2-MICROGLOBULIN, AND A 9-RESIDUE IMMUNODOMINANT PEPTIDE EPITOPE GP33 DERIVED FROM LCMV	IMMUNE SYSTEM
1N5A	CRYSTAL STRUCTURE OF THE MURINE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX OF H-2DB, B2-MICROGLOBULIN, AND A 9-RESIDUE IMMUNODOMINANT PEPTIDE EPITOPE GP33 DERIVED FROM LCMV	IMMUNE SYSTEM
1N5W	CRYSTAL STRUCTURE OF THE CU,MO-CO DEHYDROGENASE (CODH); OXIDIZED FORM	OXIDOREDUCTASE
1N5Y	HIV-1 REVERSE TRANSCRIPTASE CROSSLINKED TO POST-TRANSLOCATION AZTMP-TERMINATED DNA (COMPLEX P)	TRANSFERASE/IMMUNE SYSTEM/DNA
1N60	CRYSTAL STRUCTURE OF THE CU,MO-CO DEHYDROGENASE (CODH); CYANIDE-INACTIVATED FORM	OXIDOREDUCTASE

1N61	CRYSTAL STRUCTURE OF THE CU,MO-CO DEHYDROGENASE (CODH); DITHIONITE REDUCED STATE	OXIDOREDUCTASE
1N62	CRYSTAL STRUCTURE OF THE MO,CU-CO DEHYDROGENASE (CODH), N-BUTYLISOCYANIDE-BOUND STATE	OXIDOREDUCTASE
1N63	CRYSTAL STRUCTURE OF THE CU,MO-CO DEHYDROGENASE (CODH); CARBON MONOXIDE REDUCED STATE	OXIDOREDUCTASE
1N64	CRYSTAL STRUCTURE ANALYSIS OF THE IMMUNODOMINANT ANTIGENIC SITE ON HEPATITIS C VIRUS PROTEIN BOUND TO MAB 19D9D6	IMMUNE SYSTEM
1N6D	TRICORN PROTEASE IN COMPLEX WITH TETRAPEPTIDE CHLOROMETHYL KETONE DERIVATIVE	HYDROLASE
1N6E	TRICORN PROTEASE IN COMPLEX WITH A TRIDECAPEPTIDE CHLOROMETHYL KETONE DERIVATIVE	HYDROLASE
1N6Q	HIV-1 REVERSE TRANSCRIPTASE CROSSLINKED TO PRE-TRANSLOCATION AZTMP-TERMINATED DNA (COMPLEX N)	TRANSFERASE/IMMUNE SYSTEM/DNA
1N73	FIBRIN D-DIMER, LAMPREY COMPLEXED WITH THE PEPTIDE LIGAND: GLY-HIS-ARG-PRO-AMIDE	BLOOD CLOTTING
1N7F	CRYSTAL STRUCTURE OF THE SIXTH PDZ DOMAIN OF GRIP1 IN COMPLEX WITH LIPRIN C-TERMINAL PEPTIDE	PROTEIN BINDING
1N7M	GERMLINE 7G12 WITH N-METHYLMESOPORPHYRIN	IMMUNE SYSTEM
1N7S	HIGH RESOLUTION STRUCTURE OF A TRUNCATED NEURONAL SNARE COMPLEX	TRANSPORT PROTEIN
1N86	CRYSTAL STRUCTURE OF HUMAN D-DIMER FROM CROSS-LINKED FIBRIN COMPLEXED WITH GPR AND GHRPLDK PEPTIDE LIGANDS.	BLOOD CLOTTING
1N8O	CRYSTAL STRUCTURE OF A COMPLEX BETWEEN BOVINE CHYMOTRYPSIN AND ECOTIN	HYDROLASE
1N8R	STRUCTURE OF LARGE RIBOSOMAL SUBUNIT IN COMPLEX WITH VIRGINIAMYCIN M	RIBOSOME
1N8Z	CRYSTAL STRUCTURE OF EXTRACELLULAR DOMAIN OF HUMAN HER2 COMPLEXED WITH HERCEPTIN FAB	TRANSFERASE
1N94	ARYL TETRAHYDROPYRIDINE INHBITORS OF FARNESYLTRANSFERASE: GLYCINE, PHENYLALANINE AND HISTIDINE DERIVATES	TRANSFERASE
1N95	ARYL TETRAHYDROPHYRIDINE INHBITORS OF FARNESYLTRANFERASE: GLYCINE, PHENYLALANINE AND HISTIDINE DERIVATIVES	TRANSFERASE
1N9A	FARNESYLTRANSFERASE COMPLEX WITH TETRAHYDROPYRIDINE INHIBITORS	TRANSFERASE
1N9G	MITOCHONDRIAL 2-ENOYL THIOESTER REDUCTASE ETR1P/ETR2P	HYDROLASE

	HETERODIMER FROM CANDIDA TROPICALIS	
1NA1	THE STRUCTURE OF HRV14 WHEN COMPLEXED WITH PLECONARIL	VIRUS
1NAK	IGG1 FAB FRAGMENT (83.1) COMPLEX WITH 16-RESIDUE PEPTIDE (RESIDUES 304-321 OF HIV-1 GP120 (MN ISOLATE))	IMMUNE SYSTEM
1NAM	MURINE ALLOREACTIVE SCFV TCR-PEPTIDE-MHC CLASS I MOLECULE COMPLEX	IMMUNE SYSTEM
1NAN	MCH CLASS I H-2KB MOLECULE COMPLEXED WITH PBM1 PEPTIDE	IMMUNE SYSTEM
1NB3	CRYSTAL STRUCTURE OF STEFIN A IN COMPLEX WITH CATHEPSIN H: N-TERMINAL RESIDUES OF INHIBITORS CAN ADAPT TO THE ACTIVE SITES OF ENDO-AND EXOPEPTIDASES	HYDROLASE
1NB5	CRYSTAL STRUCTURE OF STEFIN A IN COMPLEX WITH CATHEPSIN H	HYDROLASE
1NBE	ASPARTATE TRANSCARBOMYLASE REGULATORY CHAIN MUTANT (T82A)	TRANSFERASE
1NBF	CRYSTAL STRUCTURE OF A UBP-FAMILY DEUBIQUITINATING ENZYME IN ISOLATION AND IN COMPLEX WITH UBIQUITIN ALDEHYDE	HYDROLASE
1NBM	THE STRUCTURE OF BOVINE F1-ATPASE COVALENTLY INHIBITED WITH 4-CHLORO-7-NITROBENZOFURAZAN	ATP SYNTHASE
1NBU	7,8-DIHYDRONEOPTERIN ALDOLASE COMPLEXED WITH PRODUCT FROM MYCOBACTERIUM TUBERCULOSIS	LYASE
1NBV	AN AUTOANTIBODY TO SINGLE-STRANDED DNA: COMPARISON OF THE THREE-DIMENSIONAL STRUCTURES OF THE UNLIGANDED FAB AND A DEOXYNUCLEOTIDE-FAB COMPLEX	IMMUNOGLOBULIN
1NBW	GLYCEROL DEHYDRATASE REACTIVASE	HYDROLASE
1NBY	CRYSTAL STRUCTURE OF HYHEL-63 COMPLEXED WITH HEL MUTANT K96A	IMMUNE SYSTEM/HYDROLASE
1NC2	CRYSTAL STRUCTURE OF MONOCLONAL ANTIBODY 2D12.5 FAB COMPLEXED WITH Y-DOTA	IMMUNE SYSTEM
1NC4	CRYSTAL STRUCTURE OF MONOCLONAL ANTIBODY 2D12.5 FAB COMPLEXED WITH GD-DOTA	IMMUNE SYSTEM
1NCA	REFINED CRYSTAL STRUCTURE OF THE INFLUENZA VIRUS N9 NEURAMINIDASE-NC41 FAB COMPLEX	HYDROLASE(O-GLYCOSYL)
1NCB	CRYSTAL STRUCTURES OF TWO MUTANT NEURAMINIDASE-ANTIBODY COMPLEXES WITH AMINO ACID SUBSTITUTIONS IN THE INTERFACE	HYDROLASE(O-GLYCOSYL)
1NCC	CRYSTAL STRUCTURES OF TWO MUTANT NEURAMINIDASE-ANTIBODY COMPLEXES WITH AMINO ACID SUBSTITUTIONS IN THE INTERFACE	HYDROLASE(O-GLYCOSYL)
1NCD	REFINED CRYSTAL STRUCTURE OF THE INFLUENZA VIRUS N9 NEURAMINIDASE-NC41 FAB COMPLEX	HYDROLASE(O-GLYCOSYL)

1NCQ	THE STRUCTURE OF HRV14 WHEN COMPLEXED WITH PLECONARIL, AN ANTIVIRAL COMPOUND	VIRUS
1NCR	THE STRUCTURE OF RHINOVIRUS 16 WHEN COMPLEXED WITH PLECONARIL, AN ANTIVIRAL COMPOUND	VIRUS
1NCW	CATIONIC CYCLIZATION ANTIBODY 4C6 IN COMPLEX WITH BENZOIC ACID	IMMUNE SYSTEM
1ND0	CATIONIC CYCLIZATION ANTIBODY 4C6 COMPLEX WITH TRANSITION STATE ANALOG	IMMUNE SYSTEM
1ND2	THE STRUCTURE OF RHINOVIRUS 16	VIRUS
1ND3	THE STRUCTURE OF HRV16, WHEN COMPLEXED WITH PLECONARIL, AN ANTIVIRAL COMPOUND	VIRUS
1NDM	CRYSTAL STRUCTURE OF FAB FRAGMENT OF ANTIBODY HYHEL-26 COMPLEXED WITH LYSOZYME	IMMUNE SYSTEM/HYDROLASE
1NDO	NAPTHALENE 1,2-DIOXYGENASE	NON-HEME IRON DIOXYGENASE
1NEJ	CRYSTALLINE HUMAN CARBONMONOXY HEMOGLOBIN S (LIGANDED SICKLE CELL HEMOGLOBIN) EXHIBITS THE R2 QUATERNARY STATE AT NEUTRAL PH IN THE PRESENCE OF POLYETHYLENE GLYCOL: THE 2.1 ANGSTROM RESOLUTION CRYSTAL STRUCTURE	OXYGEN STORAGE/TRANSPORT
1NEK	COMPLEX II (SUCCINATE DEHYDROGENASE) FROM E. COLI WITH UBIQUINONE BOUND	OXIDOREDUCTASE/ELECTRON TRANSPORT
1NEN	COMPLEX II (SUCCINATE DEHYDROGENASE) FROM E. COLI WITH DINITROPHENOL-17 INHIBITOR CO-CRYSTALLIZED AT THE UBIQUINONE BINDING SITE	OXIDOREDUCTASE/ELECTRON TRANSPORT
1NEX	CRYSTAL STRUCTURE OF SCSKP1-SCCDC4-CPD PEPTIDE COMPLEX	LIGASE, CELL CYCLE
1NF3	STRUCTURE OF CDC42 IN A COMPLEX WITH THE GTPASE-BINDING DOMAIN OF THE CELL POLARITY PROTEIN, PAR6	SIGNALING PROTEIN
1NF5	RYSTAL STRUCTURE OF LACTOSE SYNTHASE, COMPLEX WITH GLUCOSE	TRANSFERASE/TRANSFERASE
1NFD	AN ALPHA-BETA T CELL RECEPTOR (TCR) HETERODIMER IN COMPLEX WITH AN ANTI-TCR FAB FRAGMENT DERIVED FROM A MITOGENIC ANTIBODY	COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN)
1NFU	RYSTAL STRUCTURE OF HUMAN COAGULATION FACTOR XA COMPLEXED WITH RPR132747	HYDROLASE
1NFW	RYSTAL STRUCTURE OF HUMAN COAGULATION FACTOR XA COMPLEXED WITH RPR209685	HYDROLASE
1NFX	RYSTAL STRUCTURE OF HUMAN COAGULATION FACTOR XA COMPLEXED WITH RPR208944	HYDROLASE
1NFY	RYSTAL STRUCTURE OF HUMAN COAGULATION FACTOR XA COMPLEXED	HYDROLASE

	WITH RPR200095	
1NGM	CRYSTAL STRUCTURE OF A YEAST BRF1-TBP-DNA TERNARY COMPLEX	TRANSCRIPTION/DNA
1NGW	CHIMERIC AFFINITY MATURED FAB 7G12 COMPLEXED WITH MESOPORPHYRIN	IMMUNE SYSTEM
1NGX	CHIMERIC GERMLINE FAB 7G12 WITH JEFFAMINE FRAGMENT BOUND	IMMUNE SYSTEM
1NGY	CHIMERIC MATURE FAB 7G12-APO	IMMUNE SYSTEM
1NGZ	CHIMERIC GERMLINE FAB 7G12-APO	IMMUNE SYSTEM
1NH0	1.03 A STRUCTURE OF HIV-1 PROTEASE: INHIBITOR BINDING INSIDE AND OUTSIDE THE ACTIVE SITE	HYDROLASE/HYDROLASE INHIBITOR
1NH2	CRYSTAL STRUCTURE OF A YEAST TFIIA/TBP/DNA COMPLEX	TRANSCRIPTION/DNA
1NHE	CRYSTAL STRUCTURE OF LACTOSE SYNTHASE COMPLEX WITH UDP	TRANSFERASE ACTIVATOR/TRANSFERASE
1NHG	CRYSTAL STRUCTURE ANALYSIS OF PLASMODIUM FALCIPARUM ENOYL-ACYL-CARRIER-PROTEIN REDUCTASE WITH TRICLOSAN	OXIDOREDUCTASE
1NHW	CRYSTAL STRUCTURE ANALYSIS OF PLASMODIUM FALCIPARUM ENOYL-ACYL-CARRIER-PROTEIN REDUCTASE	OXIDOREDUCTASE
1NI1	IMIDAZOLE AND CYANOPHENYL FARNESYL TRANSFERASE INHIBITORS	TRANSFERASE
1NI4	HUMAN PYRUVATE DEHYDROGENASE	OXIDOREDUCTASE
1NIH	STRUCTURE OF DEOXY-QUATERNARY HAEMOGLOBIN WITH LIGANDED BETA SUBUNITS	OXYGEN TRANSPORT
1NIK	WILD TYPE RNA POLYMERASE II	TRANSCRIPTION
1NIW	CRYSTAL STRUCTURE OF ENDOTHELIAL NITRIC OXIDE SYNTHASE PEPTIDE BOUND TO CALMODULIN	SIGNALING PROTEIN/OXIDOREDUCTASE
1NJ9	COCAINE HYDROLYTIC ANTIBODY 15A10	IMMUNE SYSTEM
1NJI	STRUCTURE OF CHLORAMPHENICOL BOUND TO THE 50S RIBOSOMAL SUBUNIT	RIBOSOME
1NJT	COMPLEX STRUCTURE OF HCMV PROTEASE AND A PEPTIDOMIMETIC INHIBITOR	HYDROLASE
1NJU	COMPLEX STRUCTURE OF HCMV PROTEASE AND A PEPTIDOMIMETIC INHIBITOR	HYDROLASE
1NKK	COMPLEX STRUCTURE OF HCMV PROTEASE AND A PEPTIDOMIMETIC INHIBITOR	HYDROLASE
1NKM	COMPLEX STRUCTURE OF HCMV PROTEASE AND A PEPTIDOMIMETIC INHIBITOR	HYDROLASE

1NKP	CRYSTAL STRUCTURE OF MYC-MAX RECOGNIZING DNA	TRANSCRIPTION/DNA
1NKZ	CRYSTAL STRUCTURE OF LH2 B800-850 FROM RPS. ACIDOPHILA AT 2.0 ANGSTROM RESOLUTION	MEMBRANE PROTEIN
1NL0	CRYSTAL STRUCTURE OF HUMAN FACTOR IX GLA DOMAIN IN COMPLEX OF AN INHIBITORY ANTIBODY, 10C12	IMMUNE SYSTEM
1NL4	CRYSTAL STRUCTURE OF RAT FARNESYL TRANSFERASE IN COMPLEX WITH A POTENT BIPHENYL INHIBITOR	TRANSFERASE
1NLB	CRYSTAL STRUCTURE OF ANTI-HCV MONOCLONAL ANTIBODY 19D9D6	IMMUNE SYSTEM
1NLD	FAB FRAGMENT OF A NEUTRALIZING ANTIBODY DIRECTED AGAINST AN EPITOPE OF GP41 FROM HIV-1	IMMUNOGLOBULIN
1NLN	CRYSTAL STRUCTURE OF HUMAN ADENOVIRUS 2 PROTEINASE WITH ITS 11 AMINO ACID COFACTOR AT 1.6 ANGSTROM RESOLUTION	HYDROLASE
1NLV	CRYSTAL STRUCTURE OF DICTYOSTELIUM DISCOIDEUM ACTIN COMPLEXED WITH CA ATP AND HUMAN GELSOLIN SEGMENT 1	STRUCTURAL PROTEIN
1NLW	CRYSTAL STRUCTURE OF MAD-MAX RECOGNIZING DNA	TRANSCRIPTION/DNA
1NM1	CRYSTAL STRUCTURE OF D. DICSOIDEUM ACTIN COMPLEXED WITH GELSOLIN SEGMENT 1 AND MG ATP AT 1.8 A RESOLUTION	STRUCTURAL PROTEIN
1NMD	CRYSTAL STRUCTURE OF D. DISCOIDEUM ACTIN-GELSOLIN SEGMENT 1 COMPLEX CRYSTALLIZED IN PRESENCE OF LITHIUM ATP	STRUCTURAL PROTEIN
1NME	STRUCTURE OF CASP-3 WITH TETHERED SALICYLATE	APOPTOSIS, HYDROLASE
1NMM	BETA-1,4-GALACTOSYLTRANSFERASE MUTANT CYS342THR COMPLEX WITH ALPHA-LACTALBUMIN AND GLCNAC	TRANSFERASE ACTIVATOR/TRANSFERASE
1NMU	MBP-L30	SUGAR BINDING PROTEIN/RIBOSOME
1NNU	CRYSTAL STRUCTURE ANALYSIS OF PLASMODIUM FALCIPARUM ENOYL-ACYL-CARRIER-PROTEIN REDUCTASE WITH TRICLOSAN ANALOG	OXIDOREDUCTASE
1NOC	MURINE INDUCIBLE NITRIC OXIDE SYNTHASE OXYGENASE DOMAIN (DELTA 114) COMPLEXED WITH TYPE I E. COLI CHLORAMPHENICOL ACETYL TRANSFERASE AND IMIDAZOLE	COMPLEX (OXIDOREDUCTASE/TRANSFERASE)
1NOP	CRYSTAL STRUCTURE OF HUMAN TYROSYL-DNA PHOSPHODIESTERASE (TDP1) IN COMPLEX WITH VANADATE, DNA AND A HUMAN TOPOISOMERASE I-DERIVED PEPTIDE	HYDROLASE/DNA
1-Nov	NODAMURA VIRUS	VIRUS
1NPO	BOVINE NEUROPHYSIN II COMPLEX WITH OXYTOCIN	COMPLEX (HORMONE TRANSPORT/HORMONE)
1NQ7	HARACTERIZATION OF LIGANDS FOR THE ORPHAN NUCLEAR RECEPTOR RORBETA	TRANSCRIPTION

1NQI	CRYSTAL STRUCTURE OF LACTOSE SYNTHASE, A 1:1 COMPLEX BETWEEN BETA1,4-GALACTOSYLTRANSFERASE AND ALPHA-LACTALBUMIN IN THE PRESENCE OF GLCNAC	TRANSFERASE ACTIVATOR/TRANSFERASE
1NQL	STRUCTURE OF THE EXTRACELLULAR DOMAIN OF HUMAN EPIDERMAL GROWTH FACTOR (EGF) RECEPTOR IN AN INACTIVE (LOW PH) COMPLEX WITH EGF.	HORMONE/GROWTH FACTOR RECEPTOR
1NRJ	SIGNAL RECOGNITION PARTICLE RECEPTOR BETA-SUBUNIT IN COMPLEX WITH THE SRX DOMAIN FROM THE ALPHA-SUBUNIT	PROTEIN TRANSPORT
1NRL	CRYSTAL STRUCTURE OF THE HUMAN PXR-LBD IN COMPLEX WITH AN SRC-1 COACTIVATOR PEPTIDE AND SR12813	TRANSCRIPTION
1NRN	CRYSTALLOGRAPHIC STRUCTURES OF THROMBIN COMPLEXED WITH THROMBIN RECEPTOR PEPTIDES: EXISTENCE OF EXPECTED AND NOVEL BINDING MODES	SERINE PROTEINASE/RECEPTOR
1NRO	CRYSTALLOGRAPHIC STRUCTURES OF THROMBIN COMPLEXED WITH THROMBIN RECEPTOR PEPTIDES: EXISTENCE OF EXPECTED AND NOVEL BINDING MODES	SERINE PROTEINASE/RECEPTOR
1NRP	CRYSTALLOGRAPHIC STRUCTURES OF THROMBIN COMPLEXED WITH THROMBIN RECEPTOR PEPTIDES: EXISTENCE OF EXPECTED AND NOVEL BINDING MODES	SERINE PROTEINASE/RECEPTOR
1NRQ	CRYSTALLOGRAPHIC STRUCTURES OF THROMBIN COMPLEXED WITH THROMBIN RECEPTOR PEPTIDES: EXISTENCE OF EXPECTED AND NOVEL BINDING MODES	SERINE PROTEINASE/RECEPTOR
1NRR	CRYSTALLOGRAPHIC STRUCTURES OF THROMBIN COMPLEXED WITH THROMBIN RECEPTOR PEPTIDES: EXISTENCE OF EXPECTED AND NOVEL BINDING MODES	SERINE PROTEINASE/RECEPTOR
1NRS	CRYSTALLOGRAPHIC STRUCTURES OF THROMBIN COMPLEXED WITH THROMBIN RECEPTOR PEPTIDES: EXISTENCE OF EXPECTED AND NOVEL BINDING MODES	SERINE PROTEINASE/RECEPTOR
1NS3	STRUCTURE OF HCV PROTEASE (BK STRAIN)	COMPLEX (HYDROLASE/PEPTIDE)
1NS6	THE 2.1A STRUCTURE OF HORSE (ALPHA HEMICHROME/BETA MET) HEMOGLOBIN AT PH 5.4	OXYGEN STORAGE/TRANSPORT
1NSG	HE STRUCTURE OF THE IMMUNOPHILIN-IMMUNOSUPPRESSANT FKBP12-RAPAMYCIN COMPLEX INTERACTING WITH HUMAN FRAP	COMPLEX (ISOMERASE/KINASE)
1NSN	THE CRYSTAL STRUCTURE OF ANTIBODY N10-STAPHYLOCOCCAL NUCLEASE COMPLEX AT 2.9 ANGSTROMS RESOLUTION	COMPLEX (IMMUNOGLOBULIN/HYDROLASE)
1NT2	CRYSTAL STRUCTURE OF FIBRILLARIN/NOP5P COMPLEX	RNA BINDING PROTEIN
1NTK	CRYSTAL STRUCTURE OF MITOCHONDRIAL CYTOCHROME BC1 IN COMPLEX WITH ANTIMYCIN A1	OXIDOREDUCTASE
1NTM	RYSTAL STRUCTURE OF MITOCHONDRIAL CYTOCHROME BC1 COMPLEX	OXIDOREDUCTASE

	AT 2.4 ANGSTROM	
1NTV	CRYSTAL STRUCTURE OF THE DISABLED-1 (DAB1) PTB DOMAIN-APOER2 PEPTIDE COMPLEX	SIGNALING PROTEIN
1NTZ	RYSTAL STRUCTURE OF MITOCHONDRIAL CYTOCHROME BC1 COMPLEX BOUND WITH UBIQUINONE	OXIDOREDUCTASE
1NU1	RYSTAL STRUCTURE OF MITOCHONDRIAL CYTOCHROME BC1 COMPLEXED WITH 2-NONYL-4-HYDROXYQUINOLINE N-OXIDE (NQNO)	OXIDOREDUCTASE
1NU2	CRYSTAL STRUCTURE OF THE MURINE DISABLED-1 (DAB1) PTB DOMAIN-APOER2 PEPTIDE-PI-4,5P2 TERNARY COMPLEX	SIGNALING PROTEIN
1NU7	STAPHYLOCOAGULASE-THROMBIN COMPLEX	HYDROLASE/PROTEIN BINDING
1NU8	CRYSTAL STRUCTURE OF HUMAN DIPEPTIDYL PEPTIDASE IV (DPP-IV) IN COMPLEX WITH DIPROTIN A (ILI)	HYDROLASE
1NU9	STAPHYLOCOAGULASE-PRETHROMBIN-2 COMPLEX	HYDROLASE/PROTEIN BINDING
1NVI	ORTHORHOMBIC CRYSTAL FORM OF MOLYBDOPTERIN SYNTHASE	TRANSFERASE
1NVM	RYSTAL STRUCTURE OF A BIFUNCTIONAL ALDOLASE-DEHYDROGENASE : SEQUESTERING A REACTIVE AND VOLATILE INTERMEDIATE	LYASE/OXIDOREDUCTASE
1NVP	HUMAN TFIIA/TBP/DNA COMPLEX	TRANSCRIPTION/DNA
1NVU	STRUCTURAL EVIDENCE FOR FEEDBACK ACTIVATION BY RASGTP OF THE RAS-SPECIFIC NUCLEOTIDE EXCHANGE FACTOR SOS	SIGNALING PROTEIN
1NVV	STRUCTURAL EVIDENCE FOR FEEDBACK ACTIVATION BY RASGTP OF THE RAS-SPECIFIC NUCLEOTIDE EXCHANGE FACTOR SOS	SIGNALING PROTEIN
1NVW	STRUCTURAL EVIDENCE FOR FEEDBACK ACTIVATION BY RASGTP OF THE RAS-SPECIFIC NUCLEOTIDE EXCHANGE FACTOR SOS	SIGNALING PROTEIN
1NW9	STRUCTURE OF CASPASE-9 IN AN INHIBITORY COMPLEX WITH XIAP-BIR3	APOPTOSIS
1NWG	BETA-1,4-GALACTOSYLTRANSFERASE COMPLEX WITH ALPHA-LACTALBUMIN AND N-BUTANOYL-GLUCOAMINE	TRANSFERASE ACTIVATOR/TRANSFERASE
1NX0	STRUCTURE OF CALPAIN DOMAIN 6 IN COMPLEX WITH CALPASTATIN DIC	HYDROLASE
1NX1	CALPAIN DOMAIN VI COMPLEXED WITH CALPASTATIN INHIBITORY DOMAIN C (DIC)	HYDROLASE
1NYS	CRYSTAL STRUCTURE OF ACTIVIN A BOUND TO THE ECD OF ACTRIIB P41	MEMBRANE PROTEIN/HORMONE/GROWTH FACTOR
1NZL	CRYSTAL STRUCTURE OF SRC SH2 DOMAIN BOUND TO DOUBLY PHOSPHORYLATED PEPTIDE PQPYEPYIPI	TRANSFERASE

1NZQ	D-PHE-PRO-ARG-TYPE THROMBIN INHIBITOR	BLOOD CLOTTING/HYDROLASE INHIBITOR
1NZV	CRYSTAL STRUCTURE OF SRC SH2 DOMAIN BOUND TO DOUBLY PHOSPHORYLATED PEPTIDE PQPYIPYVPA	TRANSFERASE
1NZY	CHLOROBENZOYL COENZYME A DEHALOGENASE FROM PSEUDOMONAS SP. STRAIN CBS-3	LYASE
1O0D	HUMAN THROMBIN COMPLEXED WITH A D-PHE-PRO-ARG-TYPE INHIBITOR AND A C-TERMINAL HIRUDIN DERIVED EXO-SITE INHIBITOR	BLOOD CLOTTING/HYDROLASE INHIBITOR
1O1B	MOLECULAR MODELS OF AVERAGED RIGOR CROSSBRIDGES FROM TOMOGRAMS OF INSECT FLIGHT MUSCLE	CONTRACTILE PROTEIN
1O1C	MOLECULAR MODELS OF AVERAGED RIGOR CROSSBRIDGES FROM TOMOGRAMS OF INSECT FLIGHT MUSCLE	CONTRACTILE PROTEIN
1O1D	MOLECULAR MODELS OF AVERAGED RIGOR CROSSBRIDGES FROM TOMOGRAMS OF INSECT FLIGHT MUSCLE	CONTRACTILE PROTEIN
1O1E	MOLECULAR MODELS OF AVERAGED RIGOR CROSSBRIDGES FROM TOMOGRAMS OF INSECT FLIGHT MUSCLE	CONTRACTILE PROTEIN
1O1F	MOLECULAR MODELS OF AVERAGED RIGOR CROSSBRIDGES FROM TOMOGRAMS OF INSECT FLIGHT MUSCLE	CONTRACTILE PROTEIN
1O1G	MOLECULAR MODELS OF AVERAGED RIGOR CROSSBRIDGES FROM TOMOGRAMS OF INSECT FLIGHT MUSCLE	CONTRACTILE PROTEIN
1O1K	DEOXY HEMOGLOBIN (A,C:V1M; B,D:V1M,V67W)	OXYGEN STORAGE/TRANSPORT
1O1L	DEOXY HEMOGLOBIN (A-GLY-C:V1M,L29W,H58Q; B,D:V1M)	OXYGEN STORAGE/TRANSPORT
1O1M	DEOXY HEMOGLOBIN (A-GLYGLYGLY-C:V1M,L29F,H58Q B,D:V1M,V67W)	OXYGEN STORAGE/TRANSPORT
1O1N	DEOXY HEMOGLOBIN (A-GLYGLYGLY-C:V1M,L29W; B,D:V1M)	OXYGEN STORAGE/TRANSPORT
1O1O	DEOXY HEMOGLOBIN (A,C:V1M,V62L; B,D:V1M,V67L)	OXYGEN STORAGE/TRANSPORT
1O1P	DEOXY HEMOGLOBIN (A-GLY-C:V1M; B,D:V1M,C93A,N108K)	OXYGEN STORAGE/TRANSPORT
1O1R	STRUCTURE OF FPT BOUND TO GGPP	TRANSFERASE
1O1S	STRUCTURE OF FPT BOUND TO ISOPRENOID ANALOG 3B	TRANSFERASE
1O1T	STRUCTURE OF FPT BOUND TO THE CVIM-FPP PRODUCT	TRANSFERASE
1O23	CRYSTAL STRUCTURE OF LACTOSE SYNTHASE IN THE PRESENCE OF UDP-GLUCOSE	TRANSFERASE ACTIVATOR/TRANSFERASE
1O2G	ELABORATE MANIFOLD OF SHORT HYDROGEN BOND ARRAYS MEDIATING BINDING OF ACTIVE SITE-DIRECTED SERINE PROTEASE INHIBITORS	BLOOD CLOTTING, HYDROLASE
1O4X	TERNARY COMPLEX OF THE DNA BINDING DOMAINS OF THE OCT1 AND	TRANSCRIPTION/DNA

	SOX2 TRANSCRIPTION FACTORS WITH A 19MER OLIGONUCLEOTIDE FROM THE HOXB1 REGULATORY ELEMENT	
1O5D	DISSECTING AND DESIGNING INHIBITOR SELECTIVITY DETERMINANTS AT THE S1 SITE USING AN ARTIFICIAL ALA190 PROTEASE (ALA190 UPA)	BLOOD CLOTTING, HYDROLASE
1O5E	DISSECTING AND DESIGNING INHIBITOR SELECTIVITY DETERMINANTS AT THE S1 SITE USING AN ARTIFICIAL ALA190 PROTEASE (ALA190 UPA)	SERINE PROTEASE, HYDROLASE
1O5F	DISSECTING AND DESIGNING INHIBITOR SELECTIVITY DETERMINANTS AT THE S1 SITE USING AN ARTIFICIAL ALA190 PROTEASE (ALA190 UPA)	SERINE PROTEASE, HYDROLASE
1O5G	DISSECTING AND DESIGNING INHIBITOR SELECTIVITY DETERMINANTS AT THE S1 SITE USING AN ARTIFICIAL ALA190 PROTEASE (ALA190 UPA)	BLOOD CLOTTING, HYDROLASE
1O5M	STRUCTURE OF FPT BOUND TO THE INHIBITOR SCH66336	TRANSFERASE/TRANSFERASE INHIBITOR
1O6K	STRUCTURE OF ACTIVATED FORM OF PKB KINASE DOMAIN S474D WITH GSK3 PEPTIDE AND AMP-PNP	TRANSFERASE
1O6L	CRYSTAL STRUCTURE OF AN ACTIVATED AKT/PROTEIN KINASE B (PKB-PIF CHIMERA) TERNARY COMPLEX WITH AMP-PNP AND GSK3 PEPTIDE	TRANSFERASE
1O7D	THE STRUCTURE OF THE BOVINE LYSOSOMAL A-MANNOSIDASE SUGGESTS A NOVEL MECHANISM FOR LOW PH ACTIVATION	HYDROLASE
1O7G	NAPHTHALENE 1,2-DIOXYGENASE WITH NAPHTHALENE BOUND IN THE ACTIVE SITE.	OXIDOREDUCTASE
1O7H	NAPHTHALENE 1,2-DIOXYGENASE WITH OXIDIZED RIESKE IRON SULPHUR CENTER SITE.	OXIDOREDUCTASE
1O7M	NAPHTHALENE 1,2-DIOXYGENASE, BINARY COMPLEX WITH DIOXYGEN	OXIDOREDUCTASE
1O7N	NAPHTHALENE 1,2-DIOXYGENASE, TERNARY COMPLEX WITH DIOXYGEN AND INDOLE	OXIDOREDUCTASE
1O7P	NAPHTHALENE 1,2-DIOXYGENASE, PRODUCT COMPLEX	OXIDOREDUCTASE
1O7W	NAPHTHALENE 1,2-DIOXYGENASE, FULLY REDUCED FORM	OXIDOREDUCTASE
1O94	ERNARY COMPLEX BETWEEN TRIMETHYLAMINE DEHYDROGENASE AND ELECTRON TRANSFERRING FLAVOPROTEIN	ELECTRON TRANSPORT
1O95	ERNARY COMPLEX BETWEEN TRIMETHYLAMINE DEHYDROGENASE AND ELECTRON TRANSFERRING FLAVOPROTEIN	ELECTRON TRANSPORT/COMPLEX
1O96	STRUCTURE OF ELECTRON TRANSFERRING FLAVOPROTEIN FOR METHYLOPHILUS METHYLOTROPHUS.	ELECTRON TRANSFER
1O97	STRUCTURE OF ELECTRON TRANSFERRING FLAVOPROTEIN FROM	ELECTRON TRANSFER

	METHYLOPHILUS METHYLOTROPHUS, RECOGNITION LOOP REMOVED BY LIMITED PROTEOLYSIS	
1O9D	STRUCTURAL VIEW OF A FUNGAL TOXIN ACTING ON A 14-3-3 REGULATORY COMPLEX	PROTEIN BINDING
1O9F	STRUCTURAL VIEW OF A FUNGAL TOXIN ACTING ON A 14-3-3 REGULATORY COMPLEX	PROTEIN BINDING
1O9S	RYSTAL STRUCTURE OF A TERNARY COMPLEX OF THE HUMAN HISTONE METHYLTRANSFERASE SET7/9	TRANSFERASE
1O9U	GLYCOGEN SYNTHASE KINASE 3 BETA COMPLEXED WITH AXIN PEPTIDE	KINASE
1OAI	OMPLEX BETWEEN TAP UBA DOMAIN AND FXFG NUCLEOPORIN PEPTIDE	NUCLEAR TRANSPORT
1OAK	CRYSTAL STRUCTURE OF THE VON WILLEBRAND FACTOR (VWF) A1 DOMAIN IN COMPLEX WITH THE FUNCTION BLOCKING NMC-4 FAB	COMPLEX (WILLEBRAND/IMMUNOGLOBULIN)
1OAO	NIZN[FE4S4] AND NINI[FE4S4] CLUSTERS IN CLOSED AND OPEN ALPHA SUBUNITS OF ACETYL-COA SYNTHASE/CARBON MONOXIDE DEHYDROGENASE	OXIDOREDUCTASE
1OAZ	IGE FV SPE7 COMPLEXED WITH A RECOMBINANT THIOREDOXIN	ANTIBODY/COMPLEX
1OBX	CRYSTAL STRUCTURE OF THE COMPLEX OF PDZ2 OF SYNTENIN WITH AN INTERLEUKIN 5 RECEPTOR ALPHA PEPTIDE.	ADHESION/COMPLEX
1OBY	CRYSTAL STRUCTURE OF THE COMPLEX OF PDZ2 OF SYNTENIN WITH A SYNDECAN-4 PEPTIDE.	ADHESION/COMPLEX
1OBZ	CRYSTAL STRUCTURE OF THE COMPLEX OF THE PDZ TANDEM OF SYNTENIN WITH AN INTERLEUKIN 5 RECEPTOR ALPHA PEPTIDE.	ADHESION/COMPLEX
1OC0	PLASMINOGEN ACTIVATOR INHIBITOR-1 COMPLEX WITH SOMATOMEDIN B DOMAIN OF VITRONECTIN	SERINE PROTEASE INHIBITOR/COMPLEX
1OCC	TRUCTURE OF BOVINE HEART CYTOCHROME C OXIDASE AT THE FULLY OXIDIZED STATE	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)
1OCO	OVINE HEART CYTOCHROME C OXIDASE IN CARBON MONOXIDE-BOUND STATE	OXIDOREDUCTASE
1OCR	OVINE HEART CYTOCHROME C OXIDASE IN THE FULLY REDUCED STATE	OXIDOREDUCTASE
1OCW	FREE CONFORMATION AB2 OF THE IGE SPE-7	ANTIBODY
1OCZ	BOVINE HEART CYTOCHROME C OXIDASE IN AZIDE-BOUND STATE	OXIDOREDUCTASE
1OE9	CRYSTAL STRUCTURE OF MYOSIN V MOTOR WITH ESSENTIAL LIGHT CHAIN- NUCLEOTIDE-FREE	ATPASE/MYOSIN
1OED	TRUCTURE OF ACETYLCHOLINE RECEPTOR PORE FROM ELECTRON IMAGES	ION CHANNEL/RECEPTOR

1OEX	ATOMIC RESOLUTION STRUCTURE OF ENDOTHIAPEPSIN IN COMPLEX WITH A HYDROXYETHYLENE TRANSITION STATE ANALOGUE INHIBITOR H261	HYDROLASE
1OEY	HETERODIMER OF P40PHOX AND P67PHOX PB1 DOMAINS FROM HUMAN NADPH OXIDASE	PB1 HETERODIMER/COMPLEX
1OF2	CRYSTAL STRUCTURE OF HLA-B*2709 COMPLEXED WITH THE VASOACTIVE INTESTINAL PEPTIDE TYPE 1 RECEPTOR (VIPR) PEPTIDE (RESIDUES 400-408)	IMMUNE SYSTEM
1OFH	ASYMMETRIC COMPLEX BETWEEN HSLV AND I-DOMAIN DELETED HSLU (H. INFLUENZAE)	HYDROLASE
1OFI	ASYMMETRIC COMPLEX BETWEEN HSLV AND I-DOMAIN DELETED HSLU (H. INFLUENZAE)	HYDROLASE
1OFU	RYSTAL STRUCTURE OF SULA:FTSZ FROM PSEUDOMONAS AERUGINOSA	BACTERIAL CELL DIVISION INHIBITOR
1OGA	A STRUCTURAL BASIS FOR IMMUNODOMINANT HUMAN T-CELL RECEPTOR RECOGNITION.	IMMUNE SYSTEM/RECEPTOR/COMPLEX
1OGT	CRYSTAL STRUCTURE OF HLA-B*2705 COMPLEXED WITH THE VASOACTIVE INTESTINAL PEPTIDE TYPE 1 RECEPTOR (VIPR) PEPTIDE (RESIDUES 400-408)	IMMUNE SYSTEM/COMPLEX
1OGU	STRUCTURE OF HUMAN THR160-PHOSPHO CDK2/CYCLIN A COMPLEXED WITH A 2-ARYLAMINO-4-CYCLOHEXYLMETHYL-5-NITROSO-6-AMINOPYRIMIDINE INHIBITOR	TRANSFERASE
1OGV	LIPIDIC CUBIC PHASE CRYSTAL STRUCTURE OF THE PHOTOSYNTHETIC REACTION CENTRE FROM RHODOBACTER SPHAEROIDES	REACTION CENTRE
1OHE	STRUCTURE OF CDC14B PHOSPHATASE WITH A PEPTIDE LIGAND	HYDROLASE
1OHH	BOVINE MITOCHONDRIAL F1-ATPASE COMPLEXED WITH THE INHIBITOR PROTEIN IF1	SYNTHASE
1OHZ	COHESIN-DOCKERIN COMPLEX FROM THE CELLULOSOME OF CLOSTRIDIUM THERMOCELLUM	COHESIN/DOCKERIN COMPLEX
1OI9	STRUCTURE OF HUMAN THR160-PHOSPHO CDK2/CYCLIN A COMPLEXED WITH A 6-CYCLOHEXYLMETHYLOXY-2-ANILINO-PURINE INHIBITOR	KINASE
1OIJ	CRYSTAL STRUCTURE OF THE ALKYLSULFATASE ATSK, A NON-HEME FE (II) ALPHAKETOGLUTARATE DEPENDENT DIOXYGENASE IN COMPLEX WITH ALPHAKETOGLUTARATE	OXIDOREDUCTASE
1OIU	STRUCTURE OF HUMAN THR160-PHOSPHO CDK2/CYCLIN A COMPLEXED WITH A 6-CYCLOHEXYLMETHYLOXY-2-ANILINO-PURINE INHIBITOR	KINASE
1OIY	STRUCTURE OF HUMAN THR160-PHOSPHO CDK2/CYCLIN A COMPLEXED WITH A 6-CYCLOHEXYLMETHYLOXY-2-ANILINO-PURINE INHIBITOR	KINASE
1OJ5	CRYSTAL STRUCTURE OF THE NCO-A1 PAS-B DOMAIN BOUND TO THE	TRANSCRIPTIONAL COACTIVATOR

	STAT6 TRANSACTIVATION DOMAIN LXXLL MOTIF	
1OK7	A CONSERVED PROTEIN BINDING-SITE ON BACTERIAL SLIDING CLAMPS	TRANSFERASE
1OKK	HOMO-HETERODIMERIC COMPLEX OF THE SRP GTPASES	SIGNAL RECOGNITION/COMPLEX
1OKV	CYCLIN A BINDING GROOVE INHIBITOR H-ARG-ARG-LEU-ILE-PHE-NH2	COMPLEX (KINASE/CYCLIN)
1OKW	CYCLIN A BINDING GROOVE INHIBITOR AC-ARG-ARG-LEU-ASN-(M-CL-PHE)-NH2	COMPLEX(KINASE/CYCLIN)
1OL1	CYCLIN A BINDING GROOVE INHIBITOR H-CIT-CIT-LEU-ILE-(P-F-PHE)-NH2	COMPLEX(KINASE/CYCLIN)
1OL2	CYCLIN A BINDING GROOVE INHIBITOR H-ARG-ARG-LEU-ASN-(P-F-PHE)-NH2	COMPLEX(KINASE/CYCLIN)
1OL5	STRUCTURE OF AURORA-A 122-403, PHOSPHORYLATED ON THR287, THR288 AND BOUND TO TPX2 1-43	COMPLEX(KINASE/CELL DIVISION PROTEIN)
1OLA	THE STRUCTURAL BASIS OF MULTISPECIFICITY IN THE OLIGOPEPTIDE-BINDING PROTEIN OPPA	BINDING PROTEIN
1OLC	OLIGO-PEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH LYS-LYS-LYS-ALA	COMPLEX (BINDING PROTEIN/PEPTIDE)
1OLM	SUPERNATANT PROTEIN FACTOR IN COMPLEX WITH RRR-ALPHA-TOCOPHERYLQUINONE: A LINK BETWEEN OXIDIZED VITAMIN E AND CHOLESTEROL BIOSYNTHESIS	LIPID-BINDING PROTEIN
1OLS	ROLES OF HIS291-ALPHA AND HIS146-BETA' IN THE REDUCTIVE ACYLATION REACTION CATALYZED BY HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE	OXIDOREDUCTASE
1OLU	ROLES OF HIS291-ALPHA AND HIS146-BETA' IN THE REDUCTIVE ACYLATION REACTION CATALYZED BY HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE	OXIDOREDUCTASE
1OLX	ROLES OF HIS291-ALPHA AND HIS146-BETA' IN THE REDUCTIVE ACYLATION REACTION CATALYZED BY HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE	OXIDOREDUCTASE
1OM3	FAB 2G12 UNLIGANDED	IMMUNE SYSTEM
1OMW	RYSTAL STRUCTURE OF THE COMPLEX BETWEEN G PROTEIN-COUPLED RECEPTOR KINASE 2 AND HETEROTRIMERIC G PROTEIN BETA 1 AND GAMMA 2 SUBUNITS	TRANSFERASE
1ONK	MISTLETOE LECTIN I FROM VISCUM ALBUM	HYDROLASE/SUGER BINDING PROTEIN
1ONQ	CRYSTAL STRUCTURE OF CD1A IN COMPLEX WITH A SULFATIDE	IMMUNE SYSTEM
1OO0	CRYSTAL STRUCTURE OF THE DROSOPHILA MAGO NASHI-Y14 COMPLEX	SIGNALING PROTEIN
1OO4	P395S MUTANT OF THE P85 REGULATORY SUBUNIT OF THE N-	PROTEIN BINDING

	TERMINAL SRC HOMOLOGY 2 DOMAIN OF PI3-KINASE COMPLEXED TO A PEPTIDE DERIVED FROM PDGFR	
1OO9	ORIENTATION IN SOLUTION OF MMP-3 CATALYTIC DOMAIN AND N-TIMP-1 FROM RESIDUAL DIPOLAR COUPLINGS	HYDROLASE
1OOK	CRYSTAL STRUCTURE OF THE COMPLEX OF PLATELET RECEPTOR GPIB-ALPHA AND HUMAN ALPHA-THROMBIN	HYDROLASE
1OOP	THE CRYSTAL STRUCTURE OF SWINE VESICULAR DISEASE VIRUS	VIRUS
1OP3	CRYSTAL STRUCTURE OF FAB 2G12 BOUND TO MAN1->2MAN	IMMUNE SYSTEM
1OP5	CRYSTAL STRUCTURE OF FAB 2G12 BOUND TO MAN9GLCNAC2	IMMUNE SYSTEM
1OP9	COMPLEX OF HUMAN LYSOZYME WITH CAMELID VHH HL6 ANTIBODY FRAGMENT	HYDROLASE
1OPG	OPG2 FAB FRAGMENT	IMMUNOGLOBULIN
1OPH	NON-COVALENT COMPLEX BETWEEN ALPHA-1-PI-PITTSBURGH AND S195A TRYPSIN	HYDROLASE/HYDROLASE INHIBITOR
1OQD	CRYSTAL STRUCTURE OF STALL-1 AND BCMA	IMMUNE RESPONSE
1OQL	MISTLETOE LECTIN I FROM VISCUM ALBUM COMPLEXED WITH GALACTOSE	HYDROLASE/SUGER BINDING PROTEIN
1OQM	A 1:1 COMPLEX BETWEEN ALPHA-LACTALBUMIN AND BETA1,4-GALACTOSYLTRANSFERASE IN THE PRESENCE OF UDP-N-ACETYL-GALACTOSAMINE	TRANSFERASE, BIOSYNTHETIC PROTEIN
1OQN	CRYSTAL STRUCTURE OF THE PHOSPHOTYROSINE BINDING DOMAIN (PTB) OF MOUSE DISABLED 1 (DAB1)	SIGNALING PROTEIN
1OQO	COMPLEX BETWEEN G0 VERSION OF AN FC BOUND TO A MINIMIZED VERSION OF PROTEIN A CALLED MINI-Z	IMMUNE SYSTEM
1OQS	CRYSTAL STRUCTURE OF RV4/RV7 COMPLEX	HYDROLASE
1OQX	G-2 GLYCOVARIANT OF HUMAN IGG FC BOUND TO MINIMIZED VERSION OF PROTEIN A CALLED Z34C	IMMUNE SYSTEM
1OR0	CRYSTAL STRUCTURES OF GLUTARYL 7-AMINOCEPHALOSPORANIC ACID ACYLASE: INSIGHT INTO AUTOPROTEOLYTIC ACTIVATION	HYDROLASE
1OR7	CRYSTAL STRUCTURE OF ESCHERICHIA COLI SIGMAE WITH THE CYTOPLASMIC DOMAIN OF ITS ANTI-SIGMA RSEA	TRANSCRIPTION
1ORS	X-RAY STRUCTURE OF THE KVAP POTASSIUM CHANNEL VOLTAGE SENSOR IN COMPLEX WITH AN FAB	MEMBRANE PROTEIN
1OS3	DEHYDRATED T6 HUMAN INSULIN AT 100 K	HORMONE/GROWTH FACTOR
1OS4	DEHYDRATED T6 HUMAN INSULIN AT 295 K	HORMONE/GROWTH FACTOR

1OSP	CRYSTAL STRUCTURE OF OUTER SURFACE PROTEIN A OF BORRELIA BURGDORFERI COMPLEXED WITH A MURINE MONOCLONAL ANTIBODY FAB	COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN)
1OSV	STRUCTURAL BASIS FOR BILE ACID BINDING AND ACTIVATION OF THE NUCLEAR RECEPTOR FXR	DNA BINDING PROTEIN
1OSZ	MHC CLASS I H-2KB HEAVY CHAIN COMPLEXED WITH BETA-2 MICROGLOBULIN AND AN (L4V) MUTANT OF THE VESICULAR STOMATITIS VIRUS NUCLEOPROTEIN	COMPLEX (MHC I/PEPTIDE)
1OT5	THE 2.4 ANGSTROM CRYSTAL SRUCTURE OF KEX2 IN COMPLEX WITH A PEPTIDYL-BORONIC ACID INHIBITOR	HYDROLASE
1OT7	STRUCTURAL BASIS FOR 3-DEOXY-CDCA BINDING AND ACTIVATION OF FXR	HORMONE/GROWTH FACTOR RECEPTOR
1OTC	THE O. NOVA TELOMERE END BINDING PROTEIN COMPLEXED WITH SINGLE STRAND DNA	PROTEIN/DNA
1OTS	STRUCTURE OF THE ESCHERICHIA COLI CLC CHLORIDE CHANNEL AND FAB COMPLEX	MEMBRANE PROTEIN
1OTT	STRUCTURE OF THE ESCHERICHIA COLI CLC CHLORIDE CHANNEL E148A MUTANT AND FAB COMPLEX	MEMBRANE PROTEIN
1OUT	TROUT HEMOGLOBIN I	OXYGEN TRANSPORT
1OUU	CARBONMONOXY TROUT HEMOGLOBIN I	OXYGEN TRANSPORT
1OUZ	CRYSTAL STRUCTURE OF A MUTANT IHF (BETAE44A) COMPLEXED WITH A VARIANT H' SITE (T44A)	TRANSCRIPTION/DNA
1OVL	CRYSTAL STRUCTURE OF NURR1 LBD	TRANSCRIPTION
1OW0	CRYSTAL STRUCTURE OF HUMAN FCARI BOUND TO IGA1-FC	IMMUNE SYSTEM
1OW3	CRYSTAL STRUCTURE OF RHOA.GDP.MGF3-IN COMPLEX WITH RHOGAP	GENE REGULATION/SIGNALING PROTEIN
1OW6	PAXILLIN LD4 MOTIF BOUND TO THE FOCAL ADHESION TARGETING (FAT) DOMAIN OF THE FOCAL ADHESION KINASE	TRANSFERASE
1OW7	PAXILLIN LD4 MOTIF BOUND TO THE FOCAL ADHESION TARGETING (FAT) DOMAIN OF THE FOCAL ADHESION KINASE	TRANSFERASE
1OW8	PAXILLIN LD2 MOTIF BOUND TO THE FOCAL ADHESION TARGETING (FAT) DOMAIN OF THE FOCAL ADHESION KINASE	TRANSFERASE
1OWF	CRYSTAL STRUCTURE OF A MUTANT IHF (BETAE44A) COMPLEXED WITH THE NATIVE H' SITE	TRANSCRIPTION/DNA
1OWG	CRYSTAL STRUCTURE OF WT IHF COMPLEXED WITH AN ALTERED H' SITE (T44A)	TRANSCRIPTION/DNA
1OWS	CRYSTAL STRUCTURE OF A C49 PHOSPHOLIPASE A2 FROM INDIAN	HYDROLASE

	COBRA REVEALS CARBOHYDRATE BINDING IN THE HYDROPHOBIC CHANNEL	
1OX1	CRYSTAL STRUCTURE OF THE BOVINE TRYPSIN COMPLEX WITH A SYNTHETIC 11 PEPTIDE INHIBITOR	HYDROLASE
1OX4	TOWARDS UNDERSTANDING THE MECHANISM OF THE COMPLEX CYCLIZATION REACTION CATALYZED BY IMIDAZOLE GLYCEROPHOSPHATE SYNTHASE	TRANSFERASE, LYASE
1OX9	CRYSTAL STRUCTURE OF SSPB-SSRA COMPLEX	HYDROLASE ACTIVATOR
1OXB	COMPLEX BETWEEN YPD1 AND SLN1 RESPONSE REGULATOR DOMAIN IN SPACE GROUP P2(1)2(1)2(1)	SIGNALING PROTEIN
1OXG	CRYSTAL STRUCTURE OF A COMPLEX FORMED BETWEEN ORGANIC SOLVENT TREATED BOVINE ALPHA-CHYMOTRYPSIN AND ITS AUTOCATALYTICALLY PRODUCED HIGHLY POTENT 14-RESIDUE PEPTIDE AT 2.2 RESOLUTION	HYDROLASE
1OXK	COMPLEX BETWEEN YPD1 AND SLN1 RESPONSE REGULATOR DOMAIN IN SPACE GROUP P3(2)	SIGNALING PROTEIN
1OXN	STRUCTURE AND FUNCTION ANALYSIS OF PEPTIDE ANTAGONISTS OF MELANOMA INHIBITOR OF APOPTOSIS (ML-IAP)	APOPTOSIS
1OXQ	STRUCTURE AND FUNCTION ANALYSIS OF PEPTIDE ANTAGONISTS OF MELANOMA INHIBITOR OF APOPTOSIS (ML-IAP)	APOPTOSIS
1OY3	CRYSTAL STRUCTURE OF AN IKBBETA/NF-KB P65 HOMODIMER COMPLEX	DNA BINDING PROTEIN
1OY7	STRUCTURE AND FUNCTION ANALYSIS OF PEPTIDE ANTAGONISTS OF MELANOMA INHIBITOR OF APOPTOSIS (ML-IAP)	APOPTOSIS
1OYF	CRYSTAL STRUCTURE OF RUSSELLES VIPER (DABOIA RUSSELLII PULCHELLA) PHOSPHOLIPASE A2 IN A COMPLEX WITH VENOM 6-METHYL HEPTANOL	HYDROLASE
1OYT	COMPLEX OF RECOMBINANT HUMAN THROMBIN WITH A DESIGNED FLUORINATED INHIBITOR	HYDROLASE
1OYV	CRYSTAL STRUCTURE OF TOMATO INHIBITOR-II IN A TERNARY COMPLEX WITH SUBTILISIN CARLSBERG	HYDROLASE
1OZ7	CRYSTAL STRUCTURE OF ECHICETIN FROM THE VENOM OF INDIAN SAW-SCALED VIPER (ECHIS CARINATUS) AT 2.4 RESOLUTION	TOXIN
1OZB	CRYSTAL STRUCTURE OF SECB COMPLEXED WITH SECA C-TERMINUS	PROTEIN TRANSPORT
1P0S	CRYSTAL STRUCTURE OF BLOOD COAGULATION FACTOR XA IN COMPLEX WITH ECOTIN M84R	HYDROLASE
1P13	CRYSTAL STRUCTURE OF THE SRC SH2 DOMAIN COMPLEXED WITH PEPTIDE (SDPYANFK)	TRANSFERASE

1P16	STRUCTURE OF AN MRNA CAPPING ENZYME BOUND TO THE PHOSPHORYLATED CARBOXYL-TERMINAL DOMAIN OF RNA POLYMERASE II	TRANSFERASE
1P1Z	X-RAY CRYSTAL STRUCTURE OF THE LECTIN-LIKE NATURAL KILLER CELL RECEPTOR LY-49C BOUND TO ITS MHC CLASS I LIGAND H-2KB	IMMUNE SYSTEM
1P22	STRUCTURE OF A BETA-TRCP1-SKP1-BETA-CATENIN COMPLEX: DESTRUCTION MOTIF BINDING AND LYSINE SPECIFICITY ON THE SCFBETA-TRCP1 UBIQUITIN LIGASE	SIGNALING PROTEIN
1P27	CRYSTAL STRUCTURE OF THE HUMAN Y14/MAGOH COMPLEX	RNA BINDING PROTEIN
1P2C	CRYSTAL STRUCTURE ANALYSIS OF AN ANTI-LYSOZYME ANTIBODY	IMMUNE SYSTEM/HYDROLASE
1P2M	STRUCTURAL CONSEQUENCES OF ACCOMMODATION OF FOUR NON-COGNATE AMINO-ACID RESIDUES IN THE S1 POCKET OF BOVINE TRYPSIN AND CHYMOTRYPSIN	HYDROLASE/HYDROLASE INHIBITOR
1P2N	STRUCTURAL CONSEQUENCES OF ACCOMMODATION OF FOUR NON-COGNATE AMINO-ACID RESIDUES IN THE S1 POCKET OF BOVINE TRYPSIN AND CHYMOTRYPSIN	HYDROLASE/HYDROLASE INHIBITOR
1P2O	STRUCTURAL CONSEQUENCES OF ACCOMMODATION OF FOUR NON-COGNATE AMINO-ACID RESIDUES IN THE S1 POCKET OF BOVINE TRYPSIN AND CHYMOTRYPSIN	HYDROLASE/HYDROLASE INHIBITOR
1P2Q	STRUCTURAL CONSEQUENCES OF ACCOMMODATION OF FOUR NON-COGNATE AMINO-ACID RESIDUES IN THE S1 POCKET OF BOVINE TRYPSIN AND CHYMOTRYPSIN	HYDROLASE/HYDROLASE INHIBITOR
1P34	CRYSTALLOGRAPHIC STUDIES OF NUCLEOSOME CORE PARTICLES CONTAINING HISTONE 'SIN' MUTANTS	STRUCTURAL PROTEIN/DNA
1P3A	CRYSTALLOGRAPHIC STUDIES OF NUCLEOSOME CORE PARTICLES CONTAINING HISTONE 'SIN' MUTANTS	STRUCTURAL PROTEIN/DNA
1P3B	CRYSTALLOGRAPHIC STUDIES OF NUCLEOSOME CORE PARTICLES CONTAINING HISTONE 'SIN' MUTANTS	STRUCTURAL PROTEIN/DNA
1P3F	CRYSTALLOGRAPHIC STUDIES OF NUCLEOSOME CORE PARTICLES CONTAINING HISTONE 'SIN' MUTANTS	STRUCTURAL PROTEIN/DNA
1P3G	CRYSTALLOGRAPHIC STUDIES OF NUCLEOSOME CORE PARTICLES CONTAINING HISTONE 'SIN' MUTANTS	STRUCTURAL PROTEIN/DNA
1P3I	CRYSTALLOGRAPHIC STUDIES OF NUCLEOSOME CORE PARTICLES CONTAINING HISTONE 'SIN' MUTANTS	STRUCTURAL PROTEIN/DNA
1P3K	CRYSTALLOGRAPHIC STUDIES OF NUCLEOSOME CORE PARTICLES CONTAINING HISTONE 'SIN' MUTANTS	STRUCTURAL PROTEIN/DNA
1P3L	CRYSTALLOGRAPHIC STUDIES OF NUCLEOSOME CORE PARTICLES CONTAINING HISTONE 'SIN' MUTANTS	STRUCTURAL PROTEIN/DNA

1P3M	CRYSTALLOGRAPHIC STUDIES OF NUCLEOSOME CORE PARTICLES CONTAINING HISTONE 'SIN' MUTANTS	STRUCTURAL PROTEIN/DNA
1P3O	CRYSTALLOGRAPHIC STUDIES OF NUCLEOSOME CORE PARTICLES CONTAINING HISTONE 'SIN' MUTANTS	STRUCTURAL PROTEIN/DNA
1P3P	CRYSTALLOGRAPHIC STUDIES OF NUCLEOSOME CORE PARTICLES CONTAINING HISTONE 'SIN' MUTANTS	STRUCTURAL PROTEIN/DNA
1P3Q	MECHANISM OF UBIQUITIN RECOGNITION BY THE CUE DOMAIN OF VPS9	TRANSLATION
1P4B	THREE-DIMENSIONAL STRUCTURE OF A SINGLE CHAIN FV FRAGMENT COMPLEXED WITH THE PEPTIDE GCN4(7P-14P).	IMMUNE SYSTEM
1P4E	FLPE W330F MUTANT-DNA HOLLIDAY JUNCTION COMPLEX	DNA BINDING PROTEIN/RECOMBINATION/DNA
1P4L	CRYSTAL STRUCTURE OF NK RECEPTOR LY49C MUTANT WITH ITS MHC CLASS I LIGAND H-2KB	IMMUNE SYSTEM
1P57	EXTRACELLULAR DOMAIN OF HUMAN HEPSIN	HYDROLASE
1P5E	THE STRUCURE OF PHOSPHO-CDK2/CYCLIN A IN COMPLEX WITH THE INHIBITOR 4,5,6,7-TETRABROMOBENZOTRIAZOLE (TBS)	CELL CYCLE
1P7Q	CRYSTAL STRUCTURE OF HLA-A2 BOUND TO LIR-1, A HOST AND VIRAL MHC RECEPTOR	IMMUNE SYSTEM
1P7T	STRUCTURE OF ESCHERICHIA COLI MALATE SYNTHASE G:PYRUVATE:ACETYL-COENZYME A ABORTIVE TERNARY COMPLEX AT 1.95 ANGSTROM RESOLUTION	LYASE
1P7V	STRUCTURE OF A COMPLEX FORMED BETWEEN PROTEINASE K AND A DESIGNED HEPTAPEPTIDE INHIBITOR PRO-ALA-PRO-PHE-ALA-ALA-ALA AT ATOMIC RESOLUTION	HYDROLASE
1P7W	CRYSTAL STRUCTURE OF THE COMPLEX OF PROTEINASE K WITH A DESIGNED HEPTAPEPTIDE INHIBITOR PRO-ALA-PRO-PHE-ALA-SER-ALA AT ATOMIC RESOLUTION	HYDROLASE
1P84	HDBT INHIBITED YEAST CYTOCHROME BC1 COMPLEX	OXIDOREDUCTASE
1P8D	X-RAY CRYSTAL STRUCTURE OF LXR LIGAND BINDING DOMAIN WITH 24(S),25-EPOXYCHOLESTEROL	MEMBRANE PROTEIN/PROTEIN BINDING
1P8J	CRYSTAL STRUCTURE OF THE PROPROTEIN CONVERTASE FURIN	HYDROLASE
1P8V	CRYSTAL STRUCTURE OF THE COMPLEX OF PLATELET RECEPTOR GPIB-ALPHA AND ALPHA-THROMBIN AT 2.6A	MEMBRANE PROTEIN/HYDROLASE
1P8Z	COMPLEX BETWEEN RABBIT MUSCLE ALPHA-ACTIN: HUMAN GELSOLIN RESIDUES VAL26-GLU156	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN
1P93	CRYSTAL STRUCTURE OF THE AGONIST FORM OF GLUCOCORTICOID RECEPTOR	HORMONE RECEPTOR

1P9U	CORONAVIRUS MAIN PROTEINASE (3CLPRO) STRUCTURE: BASIS FOR DESIGN OF ANTI-SARS DRUGS	HYDROLASE
1PA6	CRYSTAL STRUCTURE OF THE OXYTRICHA NOVA TELOMERE END-BINDING PROTEIN COMPLEXED WITH NONCOGNATE SSDNA GGGGTTTTGAGG	DNA BINDING PROTEIN/DNA
1PAD	BINDING OF CHLOROMETHYL KETONE SUBSTRATE ANALOGUES TO CRYSTALLINE PAPAIN	HYDROLASE (SULFHYDRYL PROTEINASE)
1PAU	CRYSTAL STRUCTURE OF THE COMPLEX OF APOPAIN WITH THE TETRAPEPTIDE ALDEHYDE INHIBITOR AC-DEVD-CHO	COMPLEX (PROTEASE/INHIBITOR)
1PBX	HAEMOGLOBIN OF THE ANTARCTIC FISH PAGOTHENIA BERNACCHII: AMINO ACID SEQUENCE, OXYGEN EQUILIBRIA AND CRYSTAL STRUCTURE OF ITS CARBONMONOXY DERIVATIVE	OXYGEN TRANSPORT
1PBY	STRUCTURE OF THE PHENYLHYDRAZINE ADDUCT OF THE QUINOHEMOPROTEIN AMINE DEHYDROGENASE FROM PARACOCCUS DENITRIFICANS AT 1.7 A RESOLUTION	OXIDOREDUCTASE
1PC8	CRYSTAL STRUCTURE OF A NOVEL FORM OF MISTLETOE LECTIN FROM HIMALAYAN VISCUM ALBUM L. AT 3.8A RESOLUTION	HYDROLASE
1PCA	THREE DIMENSIONAL STRUCTURE OF PORCINE PANCREATIC PROCARBOXYPEPTIDASE A. A COMPARISON OF THE A AND B ZYMOGENS AND THEIR DETERMINANTS FOR INHIBITION AND ACTIVATION	HYDROLASE(C-TERMINAL PEPTIDASE)
1PCG	HELIX-STABILIZED CYCLIC PEPTIDES AS SELECTIVE INHIBITORS OF STEROID RECEPTOR-COACTIVATOR INTERACTIONS	TRANSCRIPTION
1PCQ	CRYSTAL STRUCTURE OF GROEL-GROES	CHAPERONE
1PCR	STRUCTURE OF THE PHOTOSYNTHETIC REACTION CENTRE FROM RHODOBACTER SPHAEROIDES AT 2.65 ANGSTROMS RESOLUTION: COFACTORS AND PROTEIN-COFACTOR INTERACTIONS	PHOTOSYNTHETIC REACTION CENTER
1PCX	CRYSTAL STRUCTURE OF THE COPII COAT SUBUNIT, SEC24, COMPLEXED WITH A PEPTIDE FROM THE SNARE PROTEIN BET1	TRANSPORT PROTEIN
1PD0	CRYSTAL STRUCTURE OF THE COPII COAT SUBUNIT, SEC24, COMPLEXED WITH A PEPTIDE FROM THE SNARE PROTEIN SED5 (YEAST SYNTAXIN-5)	TRANSPORT PROTEIN
1PDK	PAPD-PAPK CHAPERONE-PILUS SUBUNIT COMPLEX FROM E.COLI P PILUS	CHAPERONE
1PDQ	POLYCOMB CHROMODOMAIN COMPLEXED WITH THE HISTONE H3 TAIL CONTAINING TRIMETHYLLYSINE 27.	STRUCTURAL PROTEIN
1PEG	STRUCTURAL BASIS FOR THE PRODUCT SPECIFICITY OF HISTONE LYSINE METHYLTRANSFERASES	TRANSFERASE
1PEK	STRUCTURE OF THE COMPLEX OF PROTEINASE K WITH A SUBSTRATE-	HYDROLASE

	ANALOGUE HEXA-PEPTIDE INHIBITOR AT 2.2 ANGSTROMS RESOLUTION	
1PF9	GROEL-GROES-ADP	CHAPERONE
1PFB	STRUCTURAL BASIS FOR SPECIFIC BINDING OF POLYCOMB CHROMODOMAIN TO HISTONE H3 METHYLATED AT K27	PEPTIDE BINDING PROTEIN
1PFG	STRATEGY TO DESIGN INHIBITORS: STRUCTURE OF A COMPLEX OF PROTEINASE K WITH A DESIGNED OCTAPEPTIDE INHIBITOR N-AC-PRO-ALA-PRO-PHE-DALA-ALA-ALA-ALA-NH2 AT 2.5A RESOLUTION	HYDROLASE
1PG5	CRYSTAL STRUCTURE OF THE UNLIGATED (T-STATE) ASPARTATE TRANSCARBAMOYLASE FROM THE EXTREMELY THERMOPHILIC ARCHAEON SULFOLOBUS ACIDOCALDARIUS	TRANSFERASE
1PG7	MURINE 6A6 FAB IN COMPLEX WITH HUMANIZED ANTI-TISSUE FACTOR D3H44 FAB	IMMUNE SYSTEM
1PGR	2:2 COMPLEX OF G-CSF WITH ITS RECEPTOR	CYTOKINE
1PH1	CRYSTAL STRUCTURE OF THE OXYTRICHA NOVA TELOMERE END-BINDING PROTEIN COMPLEXED WITH NONCOGNATE SSDNA GGGGTTTTGGGGT	DNA BINDING PROTEIN/DNA
1PH2	CRYSTAL STRUCTURE OF THE OXYTRICHA NOVA TELOMERE END-BINDING PROTEIN COMPLEXED WITH NONCOGNATE SSDNA GGGGTTTTG	DNA BINDING PROTEIN/DNA
1PH3	CRYSTAL STRUCTURE OF THE OXYTRICHA NOVA TELOMERE END-BINDING PROTEIN COMPLEXED WITH NONCOGNATE SSDNA GGGGTTTTGGTG	DNA BINDING PROTEIN/DNA
1PH4	CRYSTAL STRUCTURE OF THE OXYTRICHA NOVA TELOMERE END-BINDING PROTEIN COMPLEXED WITH NONCOGNATE SSDNA GGGGTTTTGGCG	DNA BINDING PROTEIN/DNA
1PH5	CRYSTAL STRUCTURE OF THE OXYTRICHA NOVA TELOMERE END-BINDING PROTEIN COMPLEXED WITH NONCOGNATE SSDNA GGGGTTTTG(3DR)GG	DNA BINDING PROTEIN/DNA
1PH6	CRYSTAL STRUCTURE OF THE OXYTRICHA NOVA TELOMERE END-BINDING PROTEIN COMPLEXED WITH NONCOGNATE SSDNA GGGGTTTTGTGG	DNA BINDING PROTEIN/DNA
1PH7	CRYSTAL STRUCTURE OF THE OXYTRICHA NOVA TELOMERE END-BINDING PROTEIN COMPLEXED WITH NONCOGNATE SSDNA GGGGTTTTGIGG	DNA BINDING PROTEIN/DNA
1PH8	CRYSTAL STRUCTURE OF THE OXYTRICHA NOVA TELOMERE END-BINDING PROTEIN COMPLEXED WITH NONCOGNATE SSDNA GGGGTTTTGCGG	DNA BINDING PROTEIN/DNA
1PH9	CRYSTAL STRUCTURE OF THE OXYTRICHA NOVA TELOMERE END-BINDING PROTEIN COMPLEXED WITH NONCOGNATE SSDNA GGGGTTTTGAGG	DNA BINDING PROTEIN/DNA

1PHJ	CRYSTAL STRUCTURE OF THE OXYTRICHA NOVA TELOMERE END-BINDING PROTEIN COMPLEXED WITH NONCOGNATE SSDNA GG(3DR) GTTTTGGGG	DNA BINDING PROTEIN/DNA
1PHN	STRUCTURE OF PHYCOCYANIN FROM CYANIDIUM CALDARIUM AT 1.65A RESOLUTION	ELECTRON TRANSPORT
1PIC	PHOSPHATIDYLINOSITOL 3-KINASE, P85-ALPHA SUBUNIT: C-TERMINAL SH2 DOMAIN COMPLEXED WITH A TYR751 PHOSPHOPEPTIDE FROM THE PDGF RECEPTOR, NMR, MINIMIZED MEAN STRUCTURE	COMPLEX (PHOSPHOTRANSFERASE/RECEPTOR)
1PID	BOVINE DESPENTAPEPTIDE INSULIN	HORMONE
1PIN	PIN1 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE FROM HOMO SAPIENS	COMPLEX (ISOMERASE/DIPEPTIDE)
1PIP	CRYSTAL STRUCTURE OF PAPAIN-SUCCINYL-GLN-VAL-VAL-ALA-ALA-P-NITROANILIDE COMPLEX AT 1.7 ANGSTROMS RESOLUTION: NONCOVALENT BINDING MODE OF A COMMON SEQUENCE OF ENDOGENOUS THIOL PROTEASE INHIBITORS	HYDROLASE(THIOL PROTEASE)
1PJ8	STRUCTURE OF A TERNARY COMPLEX OF PROTEINASE K, MERCURY AND A SUBSTRATE-ANALOGUE HEXAPEPTIDE AT 2.2 A RESOLUTION	HYDROLASE
1PJM	MOUSE IMPORTIN ALPHA-BIPARTITE NLS FROM HUMAN RETINOBLASTOMA PROTEIN COMPLEX	PROTEIN TRANSPORT
1PJN	MOUSE IMPORTIN ALPHA-BIPARTITE NLS N1N2 FROM XENOPUS LAEVIS PHOSPHOPROTEIN COMPLEX	PROTEIN TRANSPORT
1PK0	CRYSTAL STRUCTURE OF THE EF3-CAM COMPLEXED WITH PMEAPP	LYASE/METAL BINDING PROTEIN
1PK1	HETERO SAM DOMAIN STRUCTURE OF PH AND SCM.	TRANSCRIPTION REPRESSION
1PKD	THE CRYSTAL STRUCTURE OF UCN-01 IN COMPLEX WITH PHOSPHO-CDK2/CYCLIN A	TRANSFERASE/CELL CYCLE
1PKQ	MYELIN OLIGODENDROCYTE GLYCOPROTEIN-(8-18C5) FAB-COMPLEX	IMMUNE SYSTEM
1PLG	EVIDENCE FOR THE EXTENDED HELICAL NATURE OF POLYSACCHARIDE EPITOPES. THE 2.8 ANGSTROMS RESOLUTION STRUCTURE AND THERMODYNAMICS OF LIGAND BINDING OF AN ANTIGEN BINDING FRAGMENT SPECIFIC FOR ALPHA-(2->8)-POLYSIALIC ACID	IMMUNOGLOBULIN
1PMA	PROTEASOME FROM THERMOPLASMA ACIDOPHILUM	PROTEASE
1PNK	PENICILLIN ACYLASE HAS A SINGLE-AMINO-ACID CATALYTIC CENTRE	ANTIBIOTIC RESISTANCE
1PNL	PENICILLIN ACYLASE HAS A SINGLE-AMINO-ACID CATALYTIC CENTRE	ANTIBIOTIC RESISTANCE
1PNM	PENICILLIN ACYLASE HAS A SINGLE-AMINO-ACID CATALYTIC CENTRE	ANTIBIOTIC RESISTANCE
1PNS	RYSTAL STRUCTURE OF A STREPTOMYCIN DEPENDENT RIBOSOME FROM E. COLI, 30S SUBUNIT OF 70S RIBOSOME. THIS FILE, 1PNS, CONTAINS THE 30S SUBUNIT, TWO TRNAS, AND ONE MRNA MOLECULE. THE 50S RIBOSOMAL SUBUNIT IS IN FILE 1PNU.	RIBOSOME

1PNX	CRYSTAL STRUCTURE OF THE WILD TYPE RIBOSOME FROM E. COLI, 30S SUBUNIT OF 70S RIBOSOME. THIS FILE, 1PNX, CONTAINS ONLY MOLECULES OF THE 30S RIBOSOMAL SUBUNIT. THE 50S SUBUNIT IS IN THE PDB FILE 1PNY.	RIBOSOME
1POI	CRYSTAL STRUCTURE OF GLUTACONATE COENZYME A-TRANSFERASE FROM ACIDAMINOCOCCUS FERMENTANS TO 2.55 ANGSTOMS RESOLUTION	TRANSFERASE
1POP	X-RAY CRYSTALLOGRAPHIC STRUCTURE OF A PAPAIN-LEUPEPTIN COMPLEX	HYDROLASE(THIOL PROTEASE)
1PP9	BOVINE CYTOCHROME BC1 COMPLEX WITH STIGMATELLIN BOUND	OXIDOREDUCTASE
1PPB	THE REFINED 1.9 ANGSTROMS CRYSTAL STRUCTURE OF HUMAN ALPHA-THROMBIN: INTERACTION WITH D-PHE-PRO-ARG CHLOROMETHYLKETONE AND SIGNIFICANCE OF THE TYR-PRO-PRO-TRP INSERTION SEGMENT	HYDROLASE(SERINE PROTEINASE)
1PPE	THE REFINED 2.0 ANGSTROMS X-RAY CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN BOVINE BETA-TRYPSIN AND CMTI-I, A TRYPSIN INHIBITOR FROM SQUASH SEEDS (CUCURBITA MAXIMA): TOPOLOGICAL SIMILARITY OF THE SQUASH SEED INHIBITORS WITH THE CARBOXYPEPTIDASE A INHIBITOR FROM POTATOES	HYDROLASE(SERINE PROTEINASE)
1PPF	X-RAY CRYSTAL STRUCTURE OF THE COMPLEX OF HUMAN LEUKOCYTE ELASTASE (PMN ELASTASE) AND THE THIRD DOMAIN OF THE TURKEY OVOMUCOID INHIBITOR	HYDROLASE(SERINE PROTEINASE)
1PPJ	BOVINE CYTOCHROME BC1 COMPLEX WITH STIGMATELLIN AND ANTIMYCIN	OXIDOREDUCTASE
1PPK	CRYSTALLOGRAPHIC ANALYSIS OF TRANSITION STATE MIMICS BOUND TO PENICILLOPEPSIN: PHOSPHOROUS-CONTAINING PEPTIDE ANALOGUES	HYDROLASE(ACID PROTEINASE)
1PPL	CRYSTALLOGRAPHIC ANALYSIS OF TRANSITION-STATE MIMICS BOUND TO PENICILLOPEPSIN: PHOSPHORUS-CONTAINING PEPTIDE ANALOGUES	HYDROLASE(ACID PROTEINASE)
1PPM	CRYSTALLOGRAPHIC ANALYSIS OF TRANSITION-STATE MIMICS BOUND TO PENICILLOPEPSIN: PHOSPHORUS-CONTAINING PEPTIDE ANALOGUES	HYDROLASE(ACID PROTEINASE)
1PQ1	CRYSTAL STRUCTURE OF BCL-XL/BIM	APOPTOSIS
1PQ8	TRYPSIN AT PH 4 AT ATOMIC RESOLUTION	HYDROLASE
1PRC	CRYSTALLOGRAPHIC REFINEMENT AT 2.3 ANGSTROMS RESOLUTION AND REFINED MODEL OF THE PHOTOSYNTHETIC REACTION CENTER FROM RHODOPSEUDOMONAS VIRIDIS	PHOTOSYNTHETIC REACTION CENTER
1PRT	THE CRYSTAL STRUCTURE OF PERTUSSIS TOXIN	TOXIN
1PSA	STRUCTURE OF A PEPSIN(SLASH)RENIN INHIBITOR COMPLEX REVEALS A NOVEL CRYSTAL PACKING INDUCED BY MINOR CHEMICAL ALTERATIONS IN THE INHIBITOR	HYDROLASE(ACID PROTEINASE)

1PSK	THE CRYSTAL STRUCTURE OF AN FAB FRAGMENT THAT BINDS TO THE MELANOMA-ASSOCIATED GD2 GANGLIOSIDE	IMMUNOGLOBULIN
1PSO	THE CRYSTAL STRUCTURE OF HUMAN PEPSIN AND ITS COMPLEX WITH PEPSTATIN	HYDROLASE (ACID PROTEINASE)
1PSS	CRYSTALLOGRAPHIC ANALYSES OF SITE-DIRECTED MUTANTS OF THE PHOTOSYNTHETIC REACTION CENTER FROM RHODOBACTER SPHAEROIDES	PHOTOSYNTHETIC REACTION CENTER
1PST	CRYSTALLOGRAPHIC ANALYSES OF SITE-DIRECTED MUTANTS OF THE PHOTOSYNTHETIC REACTION CENTER FROM RHODOBACTER SPHAEROIDES	PHOTOSYNTHETIC REACTION CENTER
1PTJ	CRYSTAL STRUCTURE ANALYSIS OF THE DI AND DIII COMPLEX OF TRANSHYDROGENASE WITH A THIO-NICOTINAMIDE NUCLEOTIDE ANALOGUE	OXIDOREDUCTASE
1PTO	THE STRUCTURE OF A PERTUSSIS TOXIN-SUGAR COMPLEX AS A MODEL FOR RECEPTOR BINDING	TOXIN
1PTT	CRYSTAL STRUCTURE OF PROTEIN TYROSINE PHOSPHATASE 1B COMPLEXED WITH PHOSPHOTYROSINE-CONTAINING TETRA-PEPTIDE (AC-DEPYL-NH2)	COMPLEX (HYDROLASE/PEPTIDE)
1PTU	CRYSTAL STRUCTURE OF PROTEIN TYROSINE PHOSPHATASE 1B COMPLEXED WITH PHOSPHOTYROSINE-CONTAINING HEXA-PEPTIDE (DADEPYL-NH2)	COMPLEX (HYDROLASE/PEPTIDE)
1PU9	RYSTAL STRUCTURE OF TETRAHYMENA GCN5 WITH BOUND COENZYME A AND A 19-RESIDUE HISTONE H3 PEPTIDE	TRANSFERASE/STRUCTURAL PROTEIN
1PUA	RYSTAL STRUCTURE OF TETRAHYMENA GCN5 WITH BOUND COENZYME A AND A PHOSPHORYLATED, 19-RESIDUE HISTONE H3 PEPTIDE	TRANSFERASE/STRUCTURAL PROTEIN
1PUF	RYSTAL STRUCTURE OF HOXA9 AND PBX1 HOMEODOMAINS BOUND TO DNA	TRANSCRIPTION/DNA
1PUM	MISTLETOE LECTIN I IN COMPLEX WITH GALACTOSE	SUGAR BINDING PROTEIN
1PUU	MISTLETOE LECTIN I IN COMPLEX WITH LACTOSE	SUGAR BINDING PROTEIN
1PVH	CRYSTAL STRUCTURE OF LEUKEMIA INHIBITORY FACTOR IN COMPLEX WITH GP130	SIGNALING PROTEIN/CYTOKINE
1PWW	CRYSTAL STRUCTURE OF ANTHRAX LETHAL FACTOR ACTIVE SITE MUTANT PROTEIN COMPLEXED WITH AN OPTIMISED PEPTIDE SUBSTRATE IN THE PRESENCE OF ZINC.	HYDROLASE
1PXV	THE STAPHOSTATIN-STAPHOPAIN COMPLEX: A FORWARD BINDING INHIBITOR IN COMPLEX WITH ITS TARGET CYSTEINE PROTEASE	HYDROLASE
1PY1	COMPLEX OF GGA1-VHS DOMAIN AND BETA-SECRETASE C-TERMINAL PHOSPHOPEPTIDE	PROTEIN TRANSPORT
1PYA	REFINED STRUCTURE OF THE PYRUVOYL-DEPENDENT HISTIDINE	CARBOXY-LYASE

	DECARBOXYLASE FROM LACTOBACILLUS 30A	
1PYO	RYSTAL STRUCTURE OF HUMAN CASPASE-2 IN COMPLEX WITH ACETYL-LEU-ASP-GLU-SER-ASP-CHO	HYDROLASE
1PYT	ERNARY COMPLEX OF PROCARBOXYPEPTIDASE A, PROPROTEINASE E, AND CHYMOTRYPSINOGEN C	TERNARY COMPLEX (ZYMOGEN)
1PYU	ROCESSED ASPARTATE DECARBOXYLASE MUTANT WITH SER25 MUTATED TO CYS	LYASE
1PYW	HUMAN CLASS II MHC PROTEIN HLA-DR1 BOUND TO A DESIGNED PEPTIDE RELATED TO INFLUENZA VIRUS HEMAGGLUTININ, FVKQNA(MAA)AL, IN COMPLEX WITH STAPHYLOCOCCAL ENTEROTOXIN C3 VARIANT 3B2 (SEC3-3B2)	IMMUNE SYSTEM/PROTEIN BINDING/TOXIN
1PZ5	STRUCTURAL BASIS OF PEPTIDE-CARBOHYDRATE MIMICRY IN AN ANTIBODY COMBINING SITE	IMMUNE SYSTEM
1PZL	CRYSTAL STRUCTURE OF HNF4A LBD IN COMPLEX WITH THE LIGAND AND THE COACTIVATOR SRC-1 PEPTIDE	TRANSCRIPTION
1PZY	V314A-BETA1,4-GALACTOSYLTRANSFERASE-I COMPLEXED WITH ALPHA-LACTALBUMIN IN THE PRESENCE OF N-ACETYLGLUCOSAMINE, UDP AND MANGANESE	TRANSFERASE ACTIVATOR/TRANSFERASE
1Q0X	ANTI-MORPHINE ANTIBODY 9B1 UNLIGANDED FORM	IMMUNE SYSTEM
1Q0Y	ANTI-MORPHINE ANTIBODY 9B1 COMPLEXED WITH MORPHINE	IMMUNE SYSTEM
1Q16	CRYSTAL STRUCTURE OF NITRATE REDUCTASE A, NARGHI, FROM ESCHERICHIA COLI	OXIDOREDUCTASE
1Q1A	STRUCTURE OF THE YEAST HST2 PROTEIN DEACETYLASE IN TERNARY COMPLEX WITH 2'-O-ACETYL ADP RIBOSE AND HISTONE PEPTIDE	GENE REGULATION
1Q1J	CRYSTAL STRUCTURE ANALYSIS OF ANTI-HIV-1 FAB 447-52D IN COMPLEX WITH V3 PEPTIDE	IMMUNE SYSTEM
1Q1S	IOUSE IMPORTIN ALPHA- PHOSPHORYLATED SV40 CN PEPTIDE COMPLEX	PROTEIN TRANSPORT
1Q1T	MOUSE IMPORTIN ALPHA: NON-PHOSPHORYLATED SV40 CN PEPTIDE COMPLEX	PROTEIN TRANSPORT
1Q2C	RYSTAL STRUCTURE OF TETRAHYMENA GCN5 WITH BOUND COENZYME A AND A 19-RESIDUE HISTONE H4 PEPTIDE	TRANSFERASE/STRUCTURAL PROTEIN
1Q2D	RYSTAL STRUCTURE OF TETRAHYMENA GCN5 WITH BOUND COENZYME A AND A 19-RESIDUE P53 PEPTIDE	TRANSFERASE/STRUCTURAL PROTEIN
1Q3L	CHROMODOMAIN OF HP1 COMPLEXED WITH HISTONE H3 TAIL CONTAINING MONOMETHYLLYSINE 9.	STRUCTURAL PROTEIN
1Q3P	RYSTAL STRUCTURE OF THE SHANK PDZ-LIGAND COMPLEX REVEALS A CLASS I PDZ INTERACTION AND A NOVEL PDZ-PDZ DIMERIZATION	PEPTIDE BINDING PROTEIN

1Q40	CRYSTAL STRUCTURE OF THE C. ALBICANS MTR2-MEX67 M DOMAIN COMPLEX	TRANSLATION
1Q4K	THE POLO-BOX DOMAIN OF PLK1 IN COMPLEX WITH A PHOSPHO-PEPTIDE	TRANSFERASE
1Q4Q	CRYSTAL STRUCTURE OF A DIAP1-DRONC COMPLEX	APOPTOSIS INHIBITOR
1Q4V	CRYSTAL STRUCTURE OF ALLO-ILEA2-INSULIN, AN INACTIVE CHIRAL ANALOGUE: IMPLICATIONS FOR THE MECHANISM OF RECEPTOR	HORMONE/GROWTH FACTOR
1Q5Q	THE RHODOCOCCUS 20S PROTEASOME	HYDROLASE
1Q5R	E RHODOCOCCUS 20S PROTEASOME WITH UNPROCESSED PRO-PEPTIDES	HYDROLASE
1Q61	PKA TRIPLE MUTANT MODEL OF PKB	TRANSFERASE/TRANSFERASE INHIBITOR
1Q72	ANTI-COCAINE ANTIBODY M82G2 COMPLEXED WITH COCAINE	IMMUNE SYSTEM
1Q7L	ZN-BINDING DOMAIN OF THE T347G MUTANT OF HUMAN AMINOACYLASE-I	HYDROLASE
1Q7Y	CRYSTAL STRUCTURE OF CCDAP-PUROMYCIN BOUND AT THE PEPTIDYL TRANSFERASE CENTER OF THE 50S RIBOSOMAL SUBUNIT	RIBOSOME
1Q81	CRYSTAL STRUCTURE OF MINIHELIX WITH 3' PUROMYCIN BOUND TO A-SITE OF THE 50S RIBOSOMAL SUBUNIT.	RIBOSOME
1Q82	CRYSTAL STRUCTURE OF CC-PUROMYCIN BOUND TO THE A-SITE OF THE 50S RIBOSOMAL SUBUNIT	RIBOSOME
1Q86	CRYSTAL STRUCTURE OF CCA-PHE-CAP-BIOTIN BOUND SIMULTANEOUSLY AT HALF OCCUPANCY TO BOTH THE A-SITE AND P-SITE OF THE THE 50S RIBOSOMAL SUBUNIT.	RIBOSOME
1Q8T	THE CATALYTIC SUBUNIT OF CAMP-DEPENDENT PROTEIN KINASE (PKA) IN COMPLEX WITH RHO-KINASE INHIBITOR Y-27632	TRANSFERASE/TRANSFERASE INHIBITOR
1Q8U	THE CATALYTIC SUBUNIT OF CAMP-DEPENDENT PROTEIN KINASE IN COMPLEX WITH RHO-KINASE INHIBITOR H-1152P	TRANSFERASE/TRANSFERASE INHIBITOR
1Q90	STRUCTURE OF THE CYTOCHROME B6F (PLASTOHYDROQUINONE : PLASTOCYANIN OXIDOREDUCTASE) FROM CHLAMYDOMONAS REINHARDTII	PHOTOSYNTHESIS
1Q94	STRUCTURES OF HLA-A*1101 IN COMPLEX WITH IMMUNODOMINANT NONAMER AND DECAMER HIV-1 EPITOPES CLEARLY REVEAL THE PRESENCE OF A MIDDLE ANCHOR RESIDUE	IMMUNE SYSTEM
1Q95	ASPARTATE TRANSCARBAMYLASE (ATCASE) OF ESCHERICHIA COLI: A NEW CRYSTALLINE R STATE BOUND TO PALA, OR TO PRODUCT ANALOGUES PHOSPHATE AND CITRATE	TRANSFERASE
1Q9K	S25-2 FAB UNLIGANDED 1	IMMUNE SYSTEM

1Q9L	S25-2 FAB UNLIGANDED 2	IMMUNE SYSTEM
1Q9O	S45-18 FAB UNLIGANDED	IMMUNE SYSTEM
1Q9Q	S25-2- A(2-8)-A(2-4)KDO TRISACCHARIDE COMPLEX	IMMUNE SYSTEM
1Q9R	S25-2- A(2-8)KDO DISACCHARIDE COMPLEX	IMMUNE SYSTEM
1Q9T	S25-2- A(2-4)KDO DISACCHARIDE COMPLEX	IMMUNE SYSTEM
1Q9V	S25-2- KDO MONOSACCHARIDE COMPLEX	IMMUNE SYSTEM
1Q9W	S45-18 FAB PENTASACCHARIDE BISPHOSPHATE COMPLEX	IMMUNE SYSTEM
1QAB	THE STRUCTURE OF HUMAN RETINOL BINDING PROTEIN WITH ITS CARRIER PROTEIN TRANSTHYRETIN REVEALS INTERACTION WITH THE CARBOXY TERMINUS OF RBP	TRANSPORT PROTEIN
1QAV	UNEXPECTED MODES OF PDZ DOMAIN SCAFFOLDING REVEALED BY STRUCTURE OF NNOS-SYNTROPHIN COMPLEX	MEMBRANE PROTEIN/OXIDOREDUCTASE
1QBK	STRUCTURE OF THE KARYOPHERIN BETA2-RAN GPPNHP NUCLEAR TRANSPORT COMPLEX	NUCLEAR TRANSPORT PROTEIN COMPLEX
1QBL	FAB E8 (FABE8A) X-RAY STRUCTURE AT 2.26 ANGSTROM RESOLUTION	IMMUNOGLOBULIN
1QBM	FAB E8B ANTIBODY, X-RAY STRUCTURE AT 2.37 ANGSTROMS RESOLUTION	IMMUNOGLOBULIN
1QBQ	STRUCTURE OF RAT FARNESYL PROTEIN TRANSFERASE COMPLEXED WITH A CVIM PEPTIDE AND ALPHA-HYDROXYFARNESYLPHOSPHONIC ACID.	TRANSFERASE
1QBV	CRYSTAL STRUCTURE OF THROMBIN COMPLEXED WITH AN GUANIDINE-MIMETIC INHIBITOR	HYDROLASE
1QC5	I DOMAIN FROM INTEGRIN ALPHA1-BETA1	CELL ADHESION
1QD6	OUTER MEMBRANE PHOSPHOLIPASE A FROM ESCHERICHIA COLI	MEMBRANE PROTEIN
1QDL	THE CRYSTAL STRUCTURE OF ANTHRANILATE SYNTHASE FROM SULFOLOBUS SOLFATARICUS	LYASE
1QDU	CRYSTAL STRUCTURE OF THE COMPLEX OF CASPASE-8 WITH THE TRIPEPTIDE KETONE INHIBITOR ZEVD-DCBMK	HYDROLASE
1QE1	CRYSTAL STRUCTURE OF 3TC-RESISTANT M184I MUTANT OF HIV-1 REVERSE TRANSCRIPTASE	TRANSFERASE
1QEW	HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN (HLA-A 0201) COMPLEX WITH A NONAMERIC PEPTIDE FROM MELANOMA-ASSOCIATED ANTIGEN 3 (RESIDUES 271-279)	COMPLEX (MHC PROTEINTIGEN)
1QFK	STRUCTURE OF HUMAN FACTOR VIIA AND ITS IMPLICATIONS FOR THE TRIGGERING OF BLOOD COAGULATION	SERINE PROTEASE

1QFU	INFLUENZA VIRUS HEMAGGLUTININ COMPLEXED WITH A NEUTRALIZING ANTIBODY	VIRAL PROTEIN/IMMUNE SYSTEM
1QGE	NEW CRYSTAL FORM OF PSEUDOMONAS GLUMAE (FORMERLY CHROMOBACTERIUM VISCOSUM ATCC 6918) LIPASE	HYDROLASE
1QGK	STRUCTURE OF IMPORTIN BETA BOUND TO THE IBB DOMAIN OF IMPORTIN ALPHA	TRANSPORT RECEPTOR
1QGR	STRUCTURE OF IMPORTIN BETA BOUND TO THE IBB DOMAIN OF IMPORTIN ALPHA (II CRYSTAL FORM, GROWN AT LOW PH)	TRANSPORT RECEPTOR
1QGU	NITROGENASE MO-FE PROTEIN FROM KLEBSIELLA PNEUMONIAE, DITHIONITE-REDUCED STATE	OXIDOREDUCTASE
1QGW	CRYSTAL STRUCTURE OF PHYCOERYTHRIN 545 FROM THE MARINE CRYPTOPHYTE RHODOMONAS CS24	PHOTOSYNTHESIS
1QH1	NITROGENASE MOFE PROTEIN FROM KLEBSIELLA PNEUMONIAE, PHENOSAFRANIN OXIDIZED STATE	OXIDOREDUCTASE
1QH8	NITROGENASE MOFE PROTEIN FROM KLEBSIELLA PNEUMONIAE, AS-CRYSTALLIZED (MIXED OXIDATION) STATE	OXIDOREDUCTASE
1QHH	STRUCTURE OF DNA HELICASE WITH ADPNP	HYDROLASE
1QHR	NOVEL COVALENT ACTIVE SITE THROMBIN INHIBITORS	BLOOD CLOTTING
1QI8	EOXYGENATED STRUCTURE OF A DISTAL POCKET HEMOGLOBIN MUTANT	OXYGEN STORAGE/TRANSPORT
1QIY	HUMAN INSULIN HEXAMERS WITH CHAIN B HIS MUTATED TO TYR COMPLEXED WITH PHENOL	HORMONE
1QIZ	HUMAN INSULIN HEXAMERS WITH CHAIN B HIS MUTATED TO TYR COMPLEXED WITH RESORCINOL	HORMONE
1QJ0	HUMAN INSULIN HEXAMERS WITH CHAIN B HIS MUTATED TO TYR	HORMONE
1QJ1	NOVEL COVALENT ACTIVE SITE THROMBIN INHIBITORS	COMPLEX (BLOOD COAGULATION/INHIBITOR)
1QJ6	NOVEL COVALENT ACTIVE SITE THROMBIN INHIBITORS	COMPLEX (BLOOD COAGULATION/INHIBITOR)
1QJ7	NOVEL COVALENT ACTIVE SITE THROMBIN INHIBITORS	COMPLEX (BLOOD COAGULATION/INHIBITOR)
1QJA	14-3-3 ZETA/PHOSPHOPEPTIDE COMPLEX (MODE 2)	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)
1QJB	14-3-3 ZETA/PHOSPHOPEPTIDE COMPLEX (MODE 1)	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)
1QJJ	STRUCTURE OF ASTACIN WITH A HYDROXAMIC ACID INHIBITOR	HYDROLASE(METALLOPROTEINASE)
1QKA	OLIGO-PEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH KRK	COMPLEX (PEPTIDE TRANSPORT/PEPTIDE)
1QKB	OLIGO-PEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH KVK	COMPLEX (PEPTIDE TRANSPORT/PEPTIDE)

1QKZ	FAB FRAGMENT (MN14C11.6) IN COMPLEX WITH A PEPTIDE ANTIGEN DERIVED FROM NEISSERIA MENINGITIDIS P1.7 SEROSUBTYPE ANTIGEN AND DOMAIN II FROM STREPTOCOCCAL PROTEIN G	IMMUNE SYSTEM
1QLB	RESPIRATORY COMPLEX II-LIKE FUMARATE REDUCTASE FROM WOLINELLA SUCCINOGENES	OXIDOREDUCTASE
1QLE	RYO-STRUCTURE OF THE PARACOCCUS DENITRIFICANS FOUR-SUBUNIT CYTOCHROME C OXIDASE IN THE COMPLETELY OXIDIZED STATE COMPLEXED WITH AN ANTIBODY FV FRAGMENT	COMPLEX (OXIDOREDUCTASE/ANTIBODY)
1QLF	MHC CLASS I H-2DB COMPLEXED WITH GLYCOPEPTIDE K3G	MURINE CLASS I MHC/PEPTIDE COMPLEX
1QLR	RYSTAL STRUCTURE OF THE FAB FRAGMENT OF A HUMAN MONOCLONAL IGM COLD AGGLUTININ	IMMUNOGLOBULIN
1QLS	S100C (S100A11),OR CALGIZZARIN, IN COMPLEX WITH ANNEXIN I N-TERMINUS	COMPLEX (LIGAND/ANNEXIN)
1QMB	CLEAVED ALPHA-1-ANTITRYPSIN POLYMER	SERINE PROTEASE INHIBITOR
1QMZ	PHOSPHORYLATED CDK2-CYCLYIN A-SUBSTRATE PEPTIDE COMPLEX	COMPLEX (PROTEIN KINASE/CYCLIN)
1QNH	LASMODIUM FALCIPARUM CYCLOPHILIN (DOUBLE MUTANT) COMPLEXED WITH CYCLOSPORIN A	COMPLEX (ISOMERASE/IMMUNOSUPPRESSANT)
1QO0	AMIDE RECEPTOR OF THE AMIDASE OPERON OF PSEUDOMONAS AERUGINOSA (AMIC) COMPLEXED WITH THE NEGATIVE REGULATOR AMIR.	BINDING PROTEIN
1QO3	COMPLEX BETWEEN NK CELL RECEPTOR LY49A AND ITS MHC CLASS I LIGAND H-2DD	COMPLEX (NK RECEPTOR/MHC CLASS I)
1QOP	CRYSTAL STRUCTURE OF WILD-TYPE TRYPTOPHAN SYNTHASE COMPLEXED WITH INDOLE PROPANOL PHOSPHATE	LYASE
1QOQ	CRYSTAL STRUCTURE OF WILD-TYPE TRYPTOPHAN SYNTHASE COMPLEXED WITH INDOLE GLYCEROL PHOSPHATE	LYASE
1QOV	PHOTOSYNTHETIC REACTION CENTER MUTANT WITH ALA M260 REPLACED WITH TRP (CHAIN M, A260W)	PHOTOSYNTHETIC REACTION CENTER
1QPW	CRYSTAL STRUCTURE DETERMINATION OF PORCINE HEMOGLOBIN AT 1.8A RESOLUTION	OXYGEN TRANSPORT
1QQD	CRYSTAL STRUCTURE OF HLA-CW4, A LIGAND FOR THE KIR2D NATURAL KILLER CELL INHIBITORY RECEPTOR	IMMUNE SYSTEM
1QR1	POOR BINDING OF A HER-2/NEU EPITOPE (GP2) TO HLA-A2.1 IS DUE TO A LACK OF INTERACTIONS IN THE CENTER OF THE PEPTIDE	IMMUNE SYSTEM
1QRJ	SOLUTION STRUCTURE OF HTLV-I CAPSID PROTEIN	VIRAL PROTEIN
1QRN	CRYSTAL STRUCTURE OF HUMAN A6 TCR COMPLEXED WITH HLA-A2 BOUND TO ALTERED HTLV-1 TAX PEPTIDE P6A	IMMUNE SYSTEM

1QRP	HUMAN PEPSIN 3A IN COMPLEX WITH A PHOSPHONATE INHIBITOR IVA-VAL-VAL-LEU(P)-(O) PHE-ALA-ALA-OME	HYDROLASE/HYDROLASE INHIBITOR
1QS0	CRYSTAL STRUCTURE OF PSEUDOMONAS PUTIDA 2-OXOISOVALERATE DEHYDROGENASE (BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE, E1B)	OXIDOREDUCTASE
1QS7	THE 1.8 ANGSTROM STRUCTURE OF CALMODULIN RS20 PEPTIDE COMPLEX	METAL BINDING PROTEIN/PEPTIDE
1QS8	CRYSTAL STRUCTURE OF THE P. VIVAX ASPARTIC PROTEINASE PLASMEPSIN COMPLEXED WITH THE INHIBITOR PEPSTATIN A	HYDROLASE
1QSC	CRYSTAL STRUCTURE OF THE TRAF DOMAIN OF TRAF2 IN A COMPLEX WITH A PEPTIDE FROM THE CD40 RECEPTOR	SIGNALING PROTEIN
1QSE	STRUCTURE OF HUMAN A6-TCR BOUND TO HLA-A2 COMPLEXED WITH ALTERED HTLV-1 TAX PEPTIDE V7R	IMMUNE SYSTEM
1QSF	STRUCTURE OF A6-TCR BOUND TO HLA-A2 COMPLEXED WITH ALTERED HTLV-1 TAX PEPTIDE Y8A	IMMUNE SYSTEM
1QSH	MAGNESIUM(II)-AND ZINC(II)-PROTOPORPHYRIN IX'S STABILIZE THE LOWEST OXYGEN AFFINITY STATE OF HUMAN HEMOGLOBIN EVEN MORE STRONGLY THAN DEOXYHEME	OXYGEN STORAGE/TRANSPORT
1QSI	MAGNESIUM(II)-AND ZINC(II)-PROTOPORPHYRIN IX'S STABILIZE THE LOWEST OXYGEN AFFINITY STATE OF HUMAN HEMOGLOBIN EVEN MORE STRONGLY THAN DEOXYHEME	OXYGEN STORAGE/TRANSPORT
1QSN	RYSTAL STRUCTURE OF TETRAHYMENA GCN5 WITH BOUND COENZYME A AND HISTONE H3 PEPTIDE	TRANSFERASE
1QTN	CRYSTAL STRUCTURE OF THE COMPLEX OF CASPASE-8 WITH THE TETRAPEPTIDE INHIBITOR ACE-IETD-ALDEHYDE	APOPTOSIS
1QTX	THE 1.65 ANGSTROM STRUCTURE OF CALMODULIN RS20 PEPTIDE COMPLEX	SIGNALING PROTEIN
1QTY	VASCULAR ENDOTHELIAL GROWTH FACTOR IN COMPLEX WITH DOMAIN 2 OF THE FLT-1 RECEPTOR	HORMONE/GROWTH FACTOR RECEPTOR
1QUN	X-RAY STRUCTURE OF THE FIMC-FIMH CHAPERONE ADHESIN COMPLEX FROM UROPATHOGENIC E.COLI	CHAPERONE/STRUCTURAL PROTEIN
1QUQ	COMPLEX OF REPLICATION PROTEIN A SUBUNITS RPA14 AND RPA32	DNA-BINDING PROTEIN
1QUR	HUMAN ALPHA-THROMBIN IN COMPLEX WITH BIVALENT, BENZAMIDINE-BASED SYNTHETIC INHIBITOR	HYDROLASE/HYDROLASE INHIBITOR
1QVF	STRUCTURE OF A DEACYLATED TRNA MINIHELIX BOUND TO THE E SITE OF THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME

1QVG	STRUCTURE OF CCA OLIGONUCLEOTIDE BOUND TO THE TRNA BINDING SITES OF THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1QVI	CRYSTAL STRUCTURE OF SCALLOP MYOSIN S1 IN THE PRE-POWER STROKE STATE TO 2.6 ANGSTROM RESOLUTION: FLEXIBILITY AND FUNCTION IN THE HEAD	CONTRACTILE PROTEIN
1QVO	STRUCTURES OF HLA-A*1101 IN COMPLEX WITH IMMUNODOMINANT NONAMER AND DECAMER HIV-1 EPITOPES CLEARLY REVEAL THE PRESENCE OF A MIDDLE ANCHOR RESIDUE	IMMUNE SYSTEM
1QX7	CRYSTAL STRUCTURE OF APOCAM BOUND TO THE GATING DOMAIN OF SMALL CONDUCTANCE CA2+-ACTIVATED POTASSIUM CHANNEL	SIGNALING PROTEIN
1QXD	STRUCTURAL BASIS FOR THE POTENT ANTISICKLING EFFECT OF A NOVEL CLASS OF 5-MEMBERED HETEROCYCLIC ALDEHYDIC COMPOUNDS	OXYGEN STORAGE/TRANSPORT
1QXE	STRUCTURAL BASIS FOR THE POTENT ANTISICKLING EFFECT OF A NOVEL CLASS OF 5-MEMBERED HETEROCYCLIC ALDEHYDIC COMPOUNDS	OXYGEN STORAGE/TRANSPORT
1QYG	ANTI-COCAINE ANTIBODY M82G2 COMPLEXED WITH BENZOYLECGONINE	IMMUNE SYSTEM
1QZ0	CRYSTAL STRUCTURE OF THE YERSINIA PESTIS PHOSPHATASE YOPH IN COMPLEX WITH A PHOSPHOTYROSYL MIMETIC-CONTAINING HEXAPEPTIDE	HYDROLASE
1QZ2	CRYSTAL STRUCTURE OF FKBP52 C-TERMINAL DOMAIN COMPLEX WITH THE C-TERMINAL PEPTIDE MEEVD OF HSP90	ISOMERASE/CHAPERONE
1QZ7	BETA-CATENIN BINDING DOMAIN OF AXIN IN COMPLEX WITH BETA-CATENIN	CELL ADHESION
1R0A	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE COVALENTLY TETHERED TO DNA TEMPLATE-PRIMER SOLVED TO 2.8 ANGSTROMS	TRANSFERASE/IMMUNE SYSTEM/DNA
1R0B	ASPARTATE TRANSCARBAMYLASE (ATCASE) OF ESCHERICHIA COLI: A NEW CRYSTALLINE R STATE BOUND TO PALA, OR TO PRODUCT ANALOGUES PHOSPHATE AND CITRATE	TRANSFERASE
1R0C	PRODUCTS IN THE T STATE OF ASPARTATE TRANSCARBAMYLASE: CRYSTAL STRUCTURE OF THE PHOSPHATE AND N-CARBAMYL-L-ASPARTATE LIGATED ENZYME	TRANSFERASE
1R0N	CRYSTAL STRUCTURE OF HETERODIMERIC ECDSYONE RECEPTOR DNA BINDING COMPLEX	TRANSCRIPTION/DNA
1R0O	CRYSTAL STRUCTURE OF THE HETERODIMERIC ECDYSONE RECEPTOR DNA-BINDING COMPLEX	TRANSCRIPTION/DNA
1R0R	1.1 ANGSTROM RESOLUTION STRUCTURE OF THE COMPLEX BETWEEN THE PROTEIN INHIBITOR, OMTKY3, AND THE SERINE PROTEASE, SUBTILISIN CARLSBERG	HYDROLASE
1R1K	CRYSTAL STRUCTURE OF THE LIGAND-BINDING DOMAINS OF THE	HORMONE/GROWTH FACTOR RECEPTOR

	HETERODIMER ECR/USP BOUND TO PONASTERONE A	
1R1L	STRUCTURE OF DIMERIC ANTITHROMBIN COMPLEXED WITH A P14-P9 REACTIVE LOOP PEPTIDE AND AN EXOGENOUS TRIPEPTIDE (FORMYL-NORLEUCINE-LF)	HYDROLASE INHIBITOR
1R1P	STRUCTURAL BASIS FOR DIFFERENTIAL RECOGNITION OF TYROSINE PHOSPHORYLATED SITES IN THE LINKER FOR ACTIVATION OF T CELLS (LAT) BY THE ADAPTOR PROTEIN GADS	PEPTIDE BINDING PROTEIN
1R1Q	STRUCTURAL BASIS FOR DIFFERENTIAL RECOGNITION OF TYROSINE PHOSPHORYLATED SITES IN THE LINKER FOR ACTIVATION OF T CELLS (LAT) BY THE ADAPTOR PROTEIN GADS	PEPTIDE BINDING PROTEIN
1R1R	RIBONUCLEOTIDE REDUCTASE R1 PROTEIN MUTANT Y730F WITH A REDUCED ACTIVE SITE FROM ESCHERICHIA COLI	OXIDOREDUCTASE
1R1X	CRYSTAL STRUCTURE OF OXY-HUMAN HEMOGLOBIN BASSETT AT 2.15 ANGSTROM	OXYGEN TRANSPORT
1R1Y	CRYSTAL STRUCTURE OF DEOXY-HUMAN HEMOGLOBIN BASSETT AT 1.8 ANGSTROM	OXYGEN TRANSPORT
1R20	CRYSTAL STRUCTURE OF THE LIGAND-BINDING DOMAINS OF THE HETERODIMER ECR/USP BOUND TO THE SYNTHETIC AGONIST BYI06830	HORMONE/GROWTH FACTOR RECEPTOR
1R24	FAB FROM MURINE IGG3 KAPPA	IMMUNE SYSTEM
1R27	CRYSTAL STRUCTURE OF NARGH COMPLEX	OXIDOREDUCTASE
1R2B	CRYSTAL STRUCTURE OF THE BCL6 BTB DOMAIN COMPLEXED WITH A SMRT CO-REPRESSOR PEPTIDE	TRANSCRIPTION
1R2C	PHOTOSYNTHETIC REACTION CENTER BLASTOCHLORIS VIRIDIS (ATCC)	PHOTOSYNTHESIS
1R3I	POTASSIUM CHANNEL KCSA-FAB COMPLEX IN RB+	MEMBRANE PROTEIN
1R3J	POTASSIUM CHANNEL KCSA-FAB COMPLEX IN HIGH CONCENTRATION OF TL+	MEMBRANE PROTEIN
1R3K	POTASSIUM CHANNEL KCSA-FAB COMPLEX IN LOW CONCENTRATION OF TL+	MEMBRANE PROTEIN
1R3L	POTASSIUM CHANNEL KCSA-FAB COMPLEX IN CS+	MEMBRANE PROTEIN
1R4A	CRYSTAL STRUCTURE OF GTP-BOUND ADP-RIBOSYLATION FACTOR LIKE PROTEIN 1 (ARL1) AND GRIP DOMAIN OF GOLGIN245 COMPLEX	PROTEIN TRANSPORT
1R4M	APPBP1-UBA3-NEDD8, AN E1-UBIQUITIN-LIKE PROTEIN COMPLEX	CELL CYCLE
1R4N	APPBP1-UBA3-NEDD8, AN E1-UBIQUITIN-LIKE PROTEIN COMPLEX WITH ATP	CELL CYCLE
1R4P	SHIGA TOXIN TYPE 2	TOXIN

1R4Q	SHIGA TOXIN	TOXIN
1R5I	CRYSTAL STRUCTURE OF THE MAM-MHC COMPLEX	IMMUNE SYSTEM
1R5U	RNA POLYMERASE II TFIIB COMPLEX	TRANSCRIPTION
1R5V	EVIDENCE THAT STRUCTURAL REARRANGEMENTS AND/OR FLEXIBILITY DURING TCR BINDING CAN CONTRIBUTE TO T-CELL ACTIVATION	SIGNALING PROTEIN
1R5W	EVIDENCE THAT STRUCTURAL REARRANGEMENTS AND/OR FLEXIBILITY DURING TCR BINDING CAN CONTRIBUTE TO T-CELL ACTIVATION	SIGNALING PROTEIN
1R64	THE 2.2 A CRYSTAL STRUCTURE OF KEX2 PROTEASE IN COMPLEX WITH AC-ARG-GLU-LYS-BOROARG PEPTIDYL BORONIC ACID INHIBITOR	HYDROLASE
1R6O	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA/ATP-DEPENDENT CLP PROTEASE ADAPTOR PROTEIN CLPS	HYDROLASE
1R6Q	CLPNS WITH FRAGMENTS	CHAPERONE/PROTEIN BINDING
1R8Q	FULL-LENGTH ARF1-GDP-MG IN COMPLEX WITH BREFELDIN A AND A SEC7 DOMAIN	PROTEIN TRANSPORT/EXCHANGE FACTOR
1R8S	ARF1[DELTA1-17]-GDP IN COMPLEX WITH A SEC7 DOMAIN CARRYING THE MUTATION OF THE CATALYTIC GLUTAMATE TO LYSINE	PROTEIN TRANSPORT/EXCHANGE FACTOR
1R9N	CRYSTAL STRUCTURE OF HUMAN DIPEPTIDYL PEPTIDASE IV IN COMPLEX WITH A DECAPEPTIDE (TNPY) AT 2.3 ANG. RESOLUTION	HYDROLASE
1R9S	RNA POLYMERASE II STRAND SEPARATED ELONGATION COMPLEX, MATCHED NUCLEOTIDE	TRANSCRIPTION/DNA/RNA
1R9T	RNA POLYMERASE II STRAND SEPARATED ELONGATION COMPLEX, MISMATCHED NUCLEOTIDE	TRANSCRIPTION/DNA/RNA
1RAA	CRYSTAL STRUCTURE OF CTP-LIGATED T STATE ASPARTATE TRANSCARBAMOYLASE AT 2.5 ANGSTROMS RESOLUTION: IMPLICATIONS FOR ATCASE MUTANTS AND THE MECHANISM OF NEGATIVE COOPERATIVITY	TRANSFERASE
1RAB	CRYSTAL STRUCTURE OF CTP-LIGATED T STATE ASPARTATE TRANSCARBAMOYLASE AT 2.5 ANGSTROMS RESOLUTION: IMPLICATIONS FOR ATCASE MUTANTS AND THE MECHANISM OF NEGATIVE COOPERATIVITY	TRANSFERASE
1RAC	CRYSTAL STRUCTURE OF CTP-LIGATED T STATE ASPARTATE TRANSCARBAMOYLASE AT 2.5 ANGSTROMS RESOLUTION: IMPLICATIONS FOR ATCASE MUTANTS AND THE MECHANISM OF NEGATIVE COOPERATIVITY	TRANSFERASE
1RAD	CRYSTAL STRUCTURE OF CTP-LIGATED T STATE ASPARTATE TRANSCARBAMOYLASE AT 2.5 ANGSTROMS RESOLUTION: IMPLICATIONS FOR ATCASE MUTANTS AND THE MECHANISM OF NEGATIVE COOPERATIVITY	TRANSFERASE

1RAE	CRYSTAL STRUCTURE OF CTP-LIGATED T STATE ASPARTATE TRANSCARBAMOYLASE AT 2.5 ANGSTROMS RESOLUTION: IMPLICATIONS FOR ATCASE MUTANTS AND THE MECHANISM OF NEGATIVE COOPERATIVITY	TRANSFERASE
1RAF	CRYSTAL STRUCTURE OF CTP-LIGATED T STATE ASPARTATE TRANSCARBAMOYLASE AT 2.5 ANGSTROMS RESOLUTION: IMPLICATIONS FOR ATCASE MUTANTS AND THE MECHANISM OF NEGATIVE COOPERATIVITY	TRANSFERASE
1RAG	CRYSTAL STRUCTURE OF CTP-LIGATED T STATE ASPARTATE TRANSCARBAMOYLASE AT 2.5 ANGSTROMS RESOLUTION: IMPLICATIONS FOR ATCASE MUTANTS AND THE MECHANISM OF NEGATIVE COOPERATIVITY	TRANSFERASE
1RAH	CRYSTAL STRUCTURE OF CTP-LIGATED T STATE ASPARTATE TRANSCARBAMOYLASE AT 2.5 ANGSTROMS RESOLUTION: IMPLICATIONS FOR ATCASE MUTANTS AND THE MECHANISM OF NEGATIVE COOPERATIVITY	TRANSFERASE
1RAI	CRYSTAL STRUCTURE OF CTP-LIGATED T STATE ASPARTATE TRANSCARBAMOYLASE AT 2.5 ANGSTROMS RESOLUTION: IMPLICATIONS FOR ATCASE MUTANTS AND THE MECHANISM OF NEGATIVE COOPERATIVITY	TRANSFERASE
1RB8	THE PHIX174 DNA BINDING PROTEIN J IN TWO DIFFERENT CAPSID ENVIRONMENTS.	VIRUS/DNA
1RBC	CRYSTALLOGRAPHIC STRUCTURES OF RIBONUCLEASE S VARIANTS WITH NONPOLAR SUBSTITUTION AT POSITION 13: PACKING AND CAVITIES	HYDROLASE(PHOSPHORIC DIESTER,RNA)
1RBD	CRYSTALLOGRAPHIC STRUCTURES OF RIBONUCLEASE S VARIANTS WITH NONPOLAR SUBSTITUTION AT POSITION 13: PACKING AND CAVITIES	HYDROLASE(PHOSPHORIC DIESTER,RNA)
1RBE	CRYSTALLOGRAPHIC STRUCTURES OF RIBONUCLEASE S VARIANTS WITH NONPOLAR SUBSTITUTION AT POSITION 13: PACKING AND CAVITIES	HYDROLASE(PHOSPHORIC DIESTER,RNA)
1RBF	CRYSTALLOGRAPHIC STRUCTURES OF RIBONUCLEASE S VARIANTS WITH NONPOLAR SUBSTITUTION AT POSITION 13: PACKING AND CAVITIES	HYDROLASE(PHOSPHORIC DIESTER,RNA)
1RBG	CRYSTALLOGRAPHIC STRUCTURES OF RIBONUCLEASE S VARIANTS WITH NONPOLAR SUBSTITUTION AT POSITION 13: PACKING AND CAVITIES	HYDROLASE(PHOSPHORIC DIESTER,RNA)
1RBH	CRYSTALLOGRAPHIC STRUCTURES OF RIBONUCLEASE S VARIANTS WITH NONPOLAR SUBSTITUTION AT POSITION 13: PACKING AND CAVITIES	HYDROLASE(PHOSPHORIC DIESTER,RNA)
1RBI	CRYSTALLOGRAPHIC STRUCTURES OF RIBONUCLEASE S VARIANTS WITH NONPOLAR SUBSTITUTION AT POSITION 13: PACKING AND CAVITIES	HYDROLASE(PHOSPHORIC DIESTER,RNA)
1RBL	STRUCTURE DETERMINATION AND REFINEMENT OF RIBULOSE 1,5 BISPHOSPHATE CARBOXYLASE(SLASH)OXYGENASE FROM SYNECHOCOCCUS PCC6301	LYASE(CARBON-CARBON)
1RBO	SPINACH RUBISCO IN COMPLEX WITH THE INHIBITOR 2-CARBOXYARABINITOL-1,5-DIPHOSPHATE	LYASE

1RCO	SPINACH RUBISCO IN COMPLEX WITH THE INHIBITOR D-XYLULOSE-2, 2-DIOL-1,5-BISPHOSPHATE	LYASE
1RCX	NON-ACTIVATED SPINACH RUBISCO IN COMPLEX WITH ITS SUBSTRATE RIBULOSE-1,5-BISPHOSPHATE	LYASE (CARBON-CARBON)
1RD3	2.5A STRUCTURE OF ANTICOAGULANT THROMBIN VARIANT E217K	HYDROLASE
1RD8	CRYSTAL SRUCTURE OF THE 1918 HUMAN H1 HEMAGGLUTININ PRECURSOR (HA0)	VIRAL PROTEIN
1RDQ	HYDROLYSIS OF ATP IN THE CRYSTAL OF Y204A MUTANT OF CAMP-DEPENDENT PROTEIN KINASE	TRANSFERASE/TRANSFERASE INHIBITOR
1RDT	CRYSTAL STRUCTURE OF A NEW REXINOID BOUND TO THE RXRALPHA LIGAND BINDING DOAMIN IN THE RXRALPHA/PPARGAMMA HETERODIMER	HORMONE/GROWTH FACTOR
1RE0	STRUCTURE OF ARF1-GDP BOUND TO SEC7 DOMAIN COMPLEXED WITH BREFELDIN A	PROTEIN TRANSPORT
1RE1	CRYSTAL STRUCTURE OF CASPASE-3 WITH A NICOTINIC ACID ALDEHYDE INHIBITOR	HYDROLASE
1RE3	CRYSTAL STRUCTURE OF FRAGMENT D OF BBETAD398A FIBRINOGEN WITH THE PEPTIDE LIGAND GLY-HIS-ARG-PRO-AMIDE	BLOOD CLOTTING
1REQ	METHYLMALONYL-COA MUTASE	ISOMERASE
1REV	HIV-1 REVERSE TRANSCRIPTASE	NUCLEOTIDYLTRANSFERASE
1REW	TRUCTURAL REFINEMENT OF THE COMPLEX OF BONE MORPHOGENETIC PROTEIN 2 AND ITS TYPE IA RECEPTOR	HORMONE/GROWTH FACTOR/SIGNALING PROTEIN
1RF0	CRYSTAL STRUCTURE OF FRAGMENT D OF GAMMAE132A FIBRINOGEN	BLOOD CLOTTING
1RF1	CRYSTAL STRUCTURE OF FRAGMENT D OF GAMMAE132A FIBRINOGEN WITH THE PEPTIDE LIGAND GLY-HIS-ARG-PRO-AMIDE	BLOOD CLOTTING
1RFD	ANTI-COCAINE ANTIBODY M82G2	IMMUNE SYSTEM
1RFF	CRYSTAL STRUCTURE OF HUMAN TYROSYL-DNA PHOSPHODIESTERASE COMPLEXED WITH VANADATE, OCTAPEPTIDE KLNYYDPR, AND TETRANUCLEOTIDE AGTT.	HYDROLASE/DNA
1RFI	CRYSTAL STRUCTURE OF HUMAN TYROSYL-DNA PHOSPHODIESTERASE COMPLEXED WITH VANADATE, PENTAPEPTIDE KLNYK, AND TETRANUCLEOTIDE AGTC	HYDROLASE/DNA
1RFN	HUMAN COAGULATION FACTOR IXA IN COMPLEX WITH P-AMINO BENZAMIDINE	COAGULATION FACTOR
1RG5	STRUCTURE OF THE PHOTOSYNTHETIC REACTION CENTRE FROM RHODOBACTER SPHAEROIDES CAROTENOIDLESS STRAIN R-26.1	PHOTOSYNTHESIS

1RGI	CRYSTAL STRUCTURE OF GELSOLIN DOMAINS G1-G3 BOUND TO ACTIN	CONTRACTILE PROTEIN
1RGN	STRUCTURE OF THE REACTION CENTRE FROM RHODOBACTER SPHAEROIDES CAROTENOIDLESS STRAIN R-26.1 RECONSTITUTED WITH SPHEROIDENE	PHOTOSYNTHESIS
1RGQ	M9A HCV PROTEASE COMPLEX WITH PENTAPEPTIDE KETO-AMIDE INHIBITOR	VIRAL PROTEIN, HYDROLASE
1RH5	THE STRUCTURE OF A PROTEIN CONDUCTING CHANNEL	PROTEIN TRANSPORT
1RHH	CRYSTAL STRUCTURE OF THE BROADLY HIV-1 NEUTRALIZING FAB X5 AT 1.90 ANGSTROM RESOLUTION	IMMUNE SYSTEM
1RHJ	CRYSTAL STRUCTURE OF THE COMPLEX OF CASPASE-3 WITH A PRYAZINONE INHIBITOR	HYDROLASE
1RHK	CRYSTAL STRUCTURE OF THE COMPLEX OF CASPASE-3 WITH A PHENYL-PROPYL-KETONE INHIBITOR	HYDROLASE
1RHM	CRYSTAL STRUCTURE OF THE COMPLEX OF CASPASE-3 WITH A NICOTINIC ACID ALDEHYDE INHIBITOR	HYDROLASE
1RHQ	CRYSTAL STRUCTURE OF THE COMPLEX OF CASPASE-3 WITH A BROMOMETHOXYPHENYL INHIBITOR	HYDROLASE
1RHR	CRYSTAL STRUCTURE OF THE COMPLEX OF CASPASE-3 WITH A CINNAMIC ACID METHYL ESTER INHIBITOR	HYDROLASE
1RHU	CRYSTAL STRUCTURE OF THE COMPLEX OF CASPASE-3 WITH A 5,6,7 TRICYCLIC PEPTIDOMIMETIC INHIBITOR	HYDROLASE
1RHZ	THE STRUCTURE OF A PROTEIN CONDUCTING CHANNEL	PROTEIN TRANSPORT
1RI8	CRYSTAL STRUCTURE OF THE CAMELID SINGLE DOMAIN ANTIBODY 1D2L19 IN COMPLEX WITH HEN EGG WHITE LYSOZYME	IMMUNE SYSTEM/HYDROLASE
1RIH	CRYSTAL STRUCTURE OF FAB 14F7, A UNIQUE ANTI-TUMOR ANTIBODY SPECIFIC FOR N-GLYCOLYL GM3	IMMUNE SYSTEM
1RIO	STRUCTURE OF BACTERIOPHAGE LAMBDA CI-NTD IN COMPLEX WITH SIGMA-REGION4 OF THERMUS AQUATICUS BOUND TO DNA	TRANSCRIPTION/DNA
1RIU	ANTI-COCAINE ANTIBODY M82G2 COMPLEXED WITH NORBENZOYLECGONINE	IMMUNE SYSTEM
1RIV	ANTI-COCAINE ANTIBODY M82G2 COMPLEXED WITH META-OXYBENZOYLECGONINE	IMMUNE SYSTEM
1RIW	THROMBIN IN COMPLEX WITH NATURAL PRODUCT INHIBITOR OSCILLARIN	HYDROLASE/BLOOD CLOTTING
1RJ9	STRUCTURE OF THE HETERODIMER OF THE CONSERVED GTPASE DOMAINS OF THE SIGNAL RECOGNITION PARTICLE (FFH) AND ITS RECEPTOR (FTSY)	PROTEIN TRANSPORT

1RJC	CRYSTAL STRUCTURE OF THE CAMELID SINGLE DOMAIN ANTIBODY CAB-LYS2 IN COMPLEX WITH HEN EGG WHITE LYSOZYME	IMMUNE SYSTEM/HYDROLASE
1RJK	CRYSTAL STRUCTURE OF THE RAT VITAMIN D RECEPTOR LIGAND BINDING DOMAIN COMPLEXED WITH 2MD AND A SYNTHETIC PEPTIDE CONTAINING THE NR2 BOX OF DRIP 205	HORMONE/GROWTH FACTOR RECEPTOR
1RJL	STRUCTURE OF THE COMPLEX BETWEEN OSPB-CT AND BACTERICIDAL FAB-H6831	IMMUNE SYSTEM
1RJY	MHC CLASS I NATURAL MUTANT H-2KBM8 HEAVY CHAIN COMPLEXED WITH BETA-2 MICROGLOBULIN AND HERPES SIMPLEX VIRUS GLYCOPROTEIN B PEPTIDE	IMMUNE SYSTEM
1RJZ	MHC CLASS I NATURAL MUTANT H-2KBM8 HEAVY CHAIN COMPLEXED WITH BETA-2 MICROGLOBULIN AND HERPIES SIMPLEX VIRUS MUTANT GLYCOPROTEIN B PEPTIDE	IMMUNE SYSTEM
1RK0	MHC CLASS I H-2KB HEAVY CHAIN COMPLEXED WITH BETA-2 MICROGLOBULIN AND HERPES SIMPLEX VIRUS GLYCOPROTEIN B PEPTIDE	IMMUNE SYSTEM
1RK1	MHC CLASS I NATURAL H-2KB HEAVY CHAIN COMPLEXED WITH BETA-2 MICROGLOBULIN AND HERPES SIMPLEX VIRUS MUTANT GLYCOPROTEIN B PEPTIDE	IMMUNE SYSTEM
1RK3	CRYSTAL STRUCTURE OF THE RAT VITAMIN D RECEPTOR LIGAND BINDING DOMAIN COMPLEXED WITH 1,25-DIHYDROXYVITAMIN D3 AND A SYNTHETIC PEPTIDE CONTAINING THE NR2 BOX OF DRIP 205	HORMONE/GROWTH FACTOR RECEPTOR
1RK8	STRUCTURE OF THE CYTOSOLIC PROTEIN PYM BOUND TO THE MAGO-Y14 CORE OF THE EXON JUNCTION COMPLEX	TRANSLATION
1RKC	HUMAN VINCULIN HEAD (1-258) IN COMPLEX WITH TALIN'S VINCULIN BINDING SITE 3 (RESIDUES 1944-1969)	CELL ADHESION, STRUCTURAL PROTEIN
1RKE	HUMAN VINCULIN HEAD (1-258) IN COMPLEX WITH HUMAN VINCULIN TAIL (879-1066)	CELL ADHESION, STRUCTURAL PROTEIN
1RKG	CRYSTAL STRUCTURE OF THE RAT VITAMIN D RECEPTOR LIGAND BINDING DOMAIN COMPLEXED WITH 2MBISP AND A SYNTHETIC PEPTIDE CONTAINING THE NR2 BOX OF DRIP 205	HORMONE/GROWTH FACTOR RECEPTOR
1RKH	CRYSTAL STRUCTURE OF THE RAT VITAMIN D RECEPTOR LIGAND BINDING DOMAIN COMPLEXED WITH 2AM20R AND A SYNTHETIC PEPTIDE CONTAINING THE NR2 BOX OF DRIP 205	HORMONE/GROWTH FACTOR RECEPTOR
1RLB	RETINOL BINDING PROTEIN COMPLEXED WITH TRANSTHYRETIN	COMPLEX (PROTEIN/PROTEIN)
1RLC	CRYSTAL STRUCTURE OF THE UNACTIVATED RIBULOSE 1, 5-BISPHOSPHATE CARBOXYLASE(SLASH)OXYGENASE COMPLEXED WITH A TRANSITION STATE ANALOG, 2-CARBOXY-D-ARABINITOL 1,5-BISPHOSPHATE	LYASE(CARBON-CARBON)

1RLD	SOLID-STATE PHASE TRANSITION IN THE CRYSTAL STRUCTURE OF RIBULOSE 1,5-BIPHOSPHATE CARBOXYLASE(SLASH)OXYGENASE	LYASE(CARBON-CARBON)
1RM1	STRUCTURE OF A YEAST TFIIA/TBP/TATA-BOX DNA COMPLEX	TRANSCRIPTION/DNA
1RM6	TRUCTURE OF 4-HYDROXYBENZOYL-COA REDUCTASE FROM THAUERA AROMATICA	OXIDOREDUCTASE
1RMF	STRUCTURES OF A MONOCLONAL ANTI-ICAM-1 ANTIBODY R6.5 FRAGMENT AT 2.8 ANGSTROMS RESOLUTION	IMMUNOGLOBULIN
1RP3	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM	TRANSCRIPTION
1RPS	CRYSTALLOGRAPHIC ANALYSIS OF THE INTERACTION OF NITRIC OXIDE WITH QUATERNARY-T HUMAN HEMOGLOBIN. HEMOGLOBIN EXPOSED TO NO UNDER ANEROBIC CONDITIONS	OXYGEN STORAGE/TRANSPORT
1RQ3	CRYSTALLOGRAPHIC ANALYSIS OF THE INTERACTION OF NITRIC OXIDE WITH QUATERNARY-T HUMAN DEOXYHEMOGLOBIN, DEOXYHEMOGLOBIN	OXYGEN STORAGE/TRANSPORT
1RQ4	CRYSTALLOGRAPHIC ANALYSIS OF THE INTERACTION OF NITRIC OXIDE WITH QUATERNARY-T HUMAN HEMOGLOBIN, HEMOGLOBIN EXPOSED TO NO UNDER AEROBIC CONDITIONS	OXYGEN STORAGE/TRANSPORT
1RQA	CRYSTALLOGRAPHIC ANALYSIS OF THE INTERACTION OF NITRIC OXIDE WITH QUATERNARY-T HUMAN HEMOGLOBIN. BETA W73E HEMOGLOBIN EXPOSED TO NO UNDER ANAEROBIC CONDITIONS	OXYGEN STORAGE/TRANSPORT
1RQF	STRUCTURE OF CK2 BETA SUBUNIT CRYSTALLIZED IN THE PRESENCE OF A P21WAF1 PEPTIDE	TRANSFERASE
1RQK	STRUCTURE OF THE REACTION CENTRE FROM RHODOBACTER SPHAEROIDES CAROTENOIDLESS STRAIN R-26.1 RECONSTITUTED WITH 3,4-DIHYDROSPHEROIDENE	PHOTOSYNTHESIS
1RQQ	CRYSTAL STRUCTURE OF THE INSULIN RECEPTOR KINASE IN COMPLEX WITH THE SH2 DOMAIN OF APS	TRANSFERASE/SIGNALING PROTEIN
1RRP	STRUCTURE OF THE RAN-GPPNHP-RANBD1 COMPLEX	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN)
1RSC	STRUCTURE OF AN EFFECTOR INDUCED INACTIVATED STATE OF RIBULOSE BISPHOSPHATE CARBOXYLASE(SLASH)OXYGENASE: THE BINARY COMPLEX BETWEEN ENZYME AND XYLULOSE BISPHOSPHATE	LYASE (CARBON-CARBON)
1RT1	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE COMPLEXED WITH MKC-442	NUCLEOTIDYLTRANSFERASE
1RT2	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE COMPLEXED WITH TNK-651	NUCLEOTIDYLTRANSFERASE
1RT3	AZT DRUG RESISTANT HIV-1 REVERSE TRANSCRIPTASE COMPLEXED WITH 1051U91	NUCLEOTIDYLTRANSFERASE

1RT4	HIV-1 REVERSE TRANSCRIPTASE COMPLEXED WITH UC781	NUCLEOTIDYLTRANSFERASE
1RT5	HIV-1 REVERSE TRANSCRIPTASE COMPLEXED WITH UC10	NUCLEOTIDYLTRANSFERASE
1RT6	HIV-1 REVERSE TRANSCRIPTASE COMPLEXED WITH UC38	NUCLEOTIDYLTRANSFERASE
1RT7	HIV-1 REVERSE TRANSCRIPTASE COMPLEXED WITH UC84	NUCLEOTIDYLTRANSFERASE
1RTD	STRUCTURE OF A CATALYTIC COMPLEX OF HIV-1 REVERSE TRANSCRIPTASE: IMPLICATIONS FOR NUCLEOSIDE ANALOG DRUG RESISTANCE	TRANSFERASE/DNA
1RTH	HIGH RESOLUTION STRUCTURES OF HIV-1 RT FROM FOUR RT-INHIBITOR COMPLEXES	NUCLEOTIDYLTRANSFERASE
1RTI	HIGH RESOLUTION STRUCTURES OF HIV-1 RT FROM FOUR RT-INHIBITOR COMPLEXES	NUCLEOTIDYLTRANSFERASE
1RTJ	MECHANISM OF INHIBITION OF HIV-1 REVERSE TRANSCRIPTASE BY NON-NUCLEOSIDE INHIBITORS	NUCLEOTIDYLTRANSFERASE
1RTL	CRYSTAL STRUCTURE OF HCV NS3 PROTEASE DOMAIN: NS4A PEPTIDE COMPLEX WITH COVALENTLY BOUND PYRROLIDINE-5,5-TRANSLACTAM INHIBITOR	VIRAL PROTEIN COMPLEX
1RU7	1934 HUMAN H1 HEMAGGLUTININ	VIRAL PROTEIN
1RU9	CRYSTAL STRUCTURE (A) OF U.V.-IRRADIATED CATIONIC CYCLIZATION ANTIBODY 4C6 FAB AT PH 4.6 WITH A DATA SET COLLECTED IN-HOUSE.	IMMUNE SYSTEM
1RUA	CRYSTAL STRUCTURE (B) OF U.V.-IRRADIATED CATIONIC CYCLIZATION ANTIBODY 4C6 FAB AT PH 4.6 WITH A DATA SET COLLECTED AT SSRL BEAMLINE 11-1.	IMMUNE SYSTEM
1RUK	CRYSTAL STRUCTURE (C) OF NATIVE CATIONIC CYCLIZATION ANTIBODY 4C6 FAB AT PH 4.6 WITH A DATA SET COLLECTED AT SSRL BEAMLINE 9-1	IMMUNE SYSTEM
1RUL	CRYSTAL STRUCTURE (D) OF U.V.-IRRADIATED CATIONIC CYCLIZATION ANTIBODY 4C6 FAB AT PH 5.6 WITH A DATA SET COLLECTED AT SSRL BEAMLINE 11-1.	IMMUNE SYSTEM
1RUM	CRYSTAL STRUCTURE (F) OF H2O2-SOAKED CATIONIC CYCLIZATION ANTIBODY 4C6 FAB AT PH 8.5 WITH A DATA SET COLLECTED AT SSRL BEAMLINE 9-1.	IMMUNE SYSTEM
1RUP	CRYSTAL STRUCTURE (G) OF NATIVE CATIONIC CYCLIZATION ANTIBODY 4C6 FAB AT PH 8.5 WITH A DATA SET COLLECTED AT APS BEAMLINE 19-ID	IMMUNE SYSTEM
1RUQ	CRYSTAL STRUCTURE (H) OF U.V.-IRRADIATED DIELS-ALDER ANTIBODY 13G5 FAB AT PH 8.0 WITH A DATA SET COLLECTED IN HOUSE.	IMMUNE SYSTEM

1RUR	CRYSTAL STRUCTURE (I) OF NATIVE DIELS-ALDER ANTIBODY 13G5 FAB AT PH 8.0 WITH A DATA SET COLLECTED AT SSRL BEAMLINE 9-1	IMMUNE SYSTEM
1RUZ	1918 H1 HEMAGGLUTININ	VIRAL PROTEIN
1RV0	1930 SWINE H1 HEMAGGLUTININ COMPLEXED WITH LSTA	VIRAL PROTEIN
1RV6	CRYSTAL STRUCTURE OF PLGF IN COMPLEX WITH DOMAIN 2 OF VEGFR1	HORMONE/GROWTH FACTOR/RECEPTOR
1RVJ	PHOTOSYNTHETIC REACTION CENTER DOUBLE MUTANT FROM RHODOBACTER SPHAEROIDES WITH ASP L213 REPLACED WITH ASN AND ARG H177 REPLACED WITH HIS	PHOTOSYNTHESIS
1RVT	1930 H1 HEMAGGLUTININ IN COMPLEX WITH LSTC	VIRAL PROTEIN
1RVW	R STATE HUMAN HEMOGLOBIN [ALPHA V96W], CARBONMONOXY	OXYGEN TRANSPORT
1RVX	1934 H1 HEMAGGLUTININ IN COMPLEX WITH LSTA	VIRAL PROTEIN
1RVZ	1934 H1 HEMAGGLUTININ IN COMPLEX WITH LSTC	VIRAL PROTEIN
1RWE	ENHANCING THE ACTIVITY OF INSULIN AT RECEPTOR EDGE: CRYSTAL STRUCTURE AND PHOTO-CROSS-LINKING OF A8 ANALOGUES	HORMONE/GROWTH FACTOR
1RWK	CRYSTAL STRUCTURE OF HUMAN CASPASE-1 IN COMPLEX WITH 3-(2-MERCAPTO-ACETYLAMINO)-4-OXO-PENTANOIC ACID	HYDROLASE
1RWM	CRYSTAL STRUCTURE OF HUMAN CASPASE-1 IN COMPLEX WITH 4-OXO-3-[2-(5-{[4-(QUINOXALIN-2-YLAMINO)-BENZOYLAMINO]-METHYL}-THIOPHEN-2-YL)-ACETYLAMINO]-PENTANOIC ACID	HYDROLASE
1RWN	CRYSTAL STRUCTURE OF HUMAN CASPASE-1 IN COMPLEX WITH 3-{2-ETHYL-6-[4-(QUINOXALIN-2-YLAMINO)-BENZOYLAMINO]-HEXANOYLAMINO}-4-OXO-BUTYRIC ACID	HYDROLASE
1RWO	CRYSTAL STRUCTURE OF HUMAN CASPASE-1 IN COMPLEX WITH 4-OXO-3-{6-[4-(QUINOXALIN-2-YLAMINO)-BENZOYLAMINO]-2-THIOPHEN-2-YL-HEXANOYLAMINO}-PENTANOIC ACID	HYDROLASE
1RWP	CRYSTAL STRUCTURE OF HUMAN CASPASE-1 IN COMPLEX WITH 3-{6-[(8-HYDROXY-QUINOLINE-2-CARBONYL)-AMINO]-2-THIOPHEN-2-YL-HEXANOYLAMINO}-4-OXO-BUTYRIC ACID	HYDROLASE
1RWV	CRYSTAL STRUCTURE OF HUMAN CASPASE-1 IN COMPLEX WITH 5-[5-(1-CARBOXYMETHYL-2-OXO-PROPYLCARBAMOYL)-5-PHENYL-PENTYLSULFAMOYL]-2-HYDROXY-BENZOIC ACID	HYDROLASE
1RWW	CRYSTAL STRUCTURE OF HUMAN CASPASE-1 IN COMPLEX WITH 4-OXO-3-[(6-{[4-(QUINOXALIN-2-YLAMINO)-BENZOYLAMINO]-METHYL}-PYRIDINE-3-CARBONYL)-AMINO]-BUTYRIC ACID	HYDROLASE
1RWX	CRYSTAL STRUCTURE OF HUMAN CASPASE-1 IN COMPLEX WITH 4-OXO-3-{6-[4-(QUINOXALIN-2-YLOXY)-BENZOYLAMINO]-2-THIOPHEN-2-YL-HEXANOYLAMINO}-BUTYRIC ACID	HYDROLASE

1RXO	ACTIVATED SPINACH RUBISCO IN COMPLEX WITH ITS SUBSTRATE RIBULOSE-1,5-BISPHOSPHATE AND CALCIUM	LYASE (CARBON-CARBON)
1RXZ	C-TERMINAL REGION OF A. FULGIDUS FEN-1 COMPLEXED WITH A. FULGIDUS PCNA	REPLICATION
1RY1	STRUCTURE OF THE SIGNAL RECOGNITION PARTICLE INTERACTING WITH THE ELONGATION-ARRESTED RIBOSOME	TRANSLATION
1RY5	PHOTOSYNTHETIC REACTION CENTER MUTANT FROM RHODOBACTER SPHAEROIDES WITH ASP L213 REPLACED WITH ASN	PHOTOSYNTHESIS
1RYP	CRYSTAL STRUCTURE OF THE 20S PROTEASOME FROM YEAST AT 2.4 ANGSTROMS RESOLUTION	MULTICATALYTIC PROTEINASE
1RZ7	CRYSTAL STRUCTURE OF HUMAN ANTI-HIV-1 GP120-REACTIVE ANTIBODY 48D	IMMUNE SYSTEM
1RZ8	CRYSTAL STRUCTURE OF HUMAN ANTI-HIV-1 GP120-REACTIVE ANTIBODY 17B	IMMUNE SYSTEM
1RZF	CRYSTAL STRUCTURE OF HUMAN ANTI-HIV-1 GP120-REACTIVE ANTIBODY E51	IMMUNE SYSTEM
1RZG	CRYSTAL STRUCTURE OF HUMAN ANTI-HIV-1 GP120 REACTIVE ANTIBODY 412D	IMMUNE SYSTEM
1RZH	PHOTOSYNTHETIC REACTION CENTER DOUBLE MUTANT FROM RHODOBACTER SPHAEROIDES WITH ASP L213 REPLACED WITH ASN AND ARG M233 REPLACED WITH CYS IN THE CHARGE-NEUTRAL DQAQB STATE (TRIGONAL FORM)	PHOTOSYNTHESIS
1RZI	CRYSTAL STRUCTURE OF HUMAN ANTI-HIV-1 GP120-REACTIVE ANTIBODY 47E FAB	IMMUNE SYSTEM
1RZJ	HIV-1 HXBC2 GP120 ENVELOPE GLYCOPROTEIN COMPLEXED WITH CD4 AND INDUCED NEUTRALIZING ANTIBODY 17B	VIRAL PROTEIN/IMMUNE SYSTEM
1RZK	HIV-1 YU2 GP120 ENVELOPE GLYCOPROTEIN COMPLEXED WITH CD4 AND INDUCED NEUTRALIZING ANTIBODY 17B	VIRAL PROTEIN/IMMUNE SYSTEM
1RZO	AGGLUTININ FROM RICINUS COMMUNIS WITH GALACTOAZA	HYDROLASE
1RZX	CRYSTAL STRUCTURE OF A PAR-6 PDZ-PEPTIDE COMPLEX	CELL CYCLE
1RZZ	PHOTOSYNTHETIC REACTION CENTER DOUBLE MUTANT FROM RHODOBACTER SPHAEROIDES WITH ASP L213 REPLACED WITH ASN AND ARG M233 REPLACED WITH CYS IN THE CHARGE-NEUTRAL DQAQB STATE (TETRAGONAL FORM)	PHOTOSYNTHESIS
1S00	PHOTOSYNTHETIC REACTION CENTER DOUBLE MUTANT FROM RHODOBACTER SPHAEROIDES WITH ASP L213 REPLACED WITH ASN AND ARG M233 REPLACED WITH CYS IN THE CHARGE-SEPARATED D+QAQB- STATE	PHOTOSYNTHESIS

1S0H	TRUCTURE DETERMINATION OF HAEMOGLOBIN FROM DONKEY(EQUUS ASINUS) AT 3.0 ANGSTROM RESOLUTION	OXYGEN STORAGE/TRANSPORT
1S0W	1B LACTAMSE/ B LACTAMASE INHIBITOR	HYDROLASE
1S0Y	THE STRUCTURE OF TRANS-3-CHLOROACRYLIC ACID DEHALOGENASE, COVALENTLY INACTIVATED BY THE MECHANISM-BASED INHIBITOR 3-BROMOPROPIOLATE AT 2.3 ANGSTROM RESOLUTION	LYASE
1S1C	RYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE HUMAN RHOA AND RHO-BINDING DOMAIN OF HUMAN ROCKI	SIGNALING PROTEIN
1S1H	STRUCTURE OF THE RIBOSOMAL 80S-EEF2-SORDARIN COMPLEX FROM YEAST OBTAINED BY DOCKING ATOMIC MODELS FOR RNA AND PROTEIN COMPONENTS INTO A 11.7 A CRYO-EM MAP. THIS FILE, 1S1H, CONTAINS 40S SUBUNIT. THE 60S RIBOSOMAL SUBUNIT IS IN FILE 1S1I.	RIBOSOME
1S1I	STRUCTURE OF THE RIBOSOMAL 80S-EEF2-SORDARIN COMPLEX FROM YEAST OBTAINED BY DOCKING ATOMIC MODELS FOR RNA AND PROTEIN COMPONENTS INTO A 11.7 A CRYO-EM MAP. THIS FILE, 1S1I, CONTAINS 60S SUBUNIT. THE 40S RIBOSOMAL SUBUNIT IS IN FILE 1S1H.	RIBOSOME
1S1T	CRYSTAL STRUCTURE OF L100I MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH UC-781	TRANSFERASE
1S1U	CRYSTAL STRUCTURE OF L100I MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH NEVIRAPINE	TRANSFERASE
1S1V	CRYSTAL STRUCTURE OF L100I MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH TNK-651	TRANSFERASE
1S1W	CRYSTAL STRUCTURE OF V106A MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH UC-781	TRANSFERASE
1S1X	CRYSTAL STRUCTURE OF V108I MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH NEVIRAPINE	TRANSFERASE
1S26	STRUCTURE OF ANTHRAX EDEMA FACTOR-CALMODULIN-ALPHA,BETA-METHYLENEADENOSINE 5'-TRIPHOSPHATE COMPLEX REVEALS AN ALTERNATIVE MODE OF ATP BINDING TO THE CATALYTIC SITE	TOXIN,LYASE/METAL BINDING PROTEIN
1S32	MOLECULAR RECOGNITION OF THE NUCLEOSOMAL 'SUPERGROOVE'	STRUCTURAL PROTEIN/DNA
1S3K	CRYSTAL STRUCTURE OF A HUMANIZED FAB (HU3S193) IN COMPLEX WITH THE LEWIS Y TETRASACCHARIDE	IMMUNE SYSTEM
1S3S	CRYSTAL STRUCTURE OF AAA ATPASE P97/VCP ND1 IN COMPLEX WITH P47 C	PROTEIN BINDING
1S3T	BORATE INHIBITED BACILLUS PASTEURII UREASE CRYSTAL STRUCTURE	HYDROLASE
1S4V	THE 2.0 A CRYSTAL STRUCTURE OF THE KDEL-TAILED CYSTEINE	HYDROLASE

	ENDOPEPTIDASE FUNCTIONING IN PROGRAMMED CELL DEATH OF RICINUS COMMUNIS ENDOSPERM	
1S4Y	CRYSTAL STRUCTURE OF THE ACTIVIN/ACTRIIB EXTRACELLULAR DOMAIN	TRANSFERASE
1S5C	CHOLERA HOLOTOXIN WITH AN A-SUBUNIT Y30S MUTATION, CRYSTAL FORM 1	TRANSERASE,TOXIN
1S5D	CHOLERA HOLOTOXIN WITH AN A-SUBUNIT Y30S MUTATION, CRYSTAL FORM 2	TRANSERASE,TOXIN
1S5E	CHOLERA HOLOTOXIN, CRYSTAL FORM 1	TRANSERASE,TOXIN
1S5F	CHOLERA HOLOTOXIN, CRYSTAL FORM 2	TRANSERASE,TOXIN
1S5G	STRUCTURE OF SCALLOP MYOSIN S1 REVEALS A NOVEL NUCLEOTIDE CONFORMATION	CONTRACTILE PROTEIN
1S5H	POTASSIUM CHANNEL KCSA-FAB COMPLEX T75C MUTANT IN K+	MEMBRANE PROTEIN
1S5I	FAB (LNKB-2) OF MONOCLONAL ANTIBODY TO HUMAN INTERLEUKIN-2, CRYSTAL STRUCTURE	IMMUNE SYSTEM
1S5L	RCHITECTURE OF THE PHOTOSYNTHETIC OXYGEN EVOLVING CENTER	PHOTOSYNTHESIS
1S5P	STRUCTURE AND SUBSTRATE BINDING PROPERTIES OF COBB, A SIR2 HOMOLOG PROTEIN DEACETYLASE FROM ESCHERICIA COLI.	HYDROLASE
1S5X	HE CRYSTAL STRUCTURE OF TREMATOMUS BERNACCHII HEMOGLOBIN OXIDIZED BY AIR	OXYGEN STORAGE/TRANSPORT
1S5Y	HE CRYSTAL STRUCTURE OF TREMATOMUS BERNACCHII HEMOGLOBIN OXIDIZED BY FERRICYANIDE	OXYGEN STORAGE/TRANSPORT
1S63	HUMAN PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH L-778,123 AND FPP	TRANSFERASE
1S64	AT PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH L-778,123 AND A SULFATE ANION	TRANSFERASE
1S6B	X-RAY CRYSTAL STRUCTURE OF A COMPLEX FORMED BETWEEN TWO HOMOLOGOUS ISOFORMS OF PHOSPHOLIPASE A2 FROM NAJA NAJA SAGITTIFERA: PRINCIPLE OF MOLECULAR ASSOCIATION AND INACTIVATION	HYDROLASE
1S6C	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN KCHIP1 AND KV4.2 N1-30	TRANSPORT PROTEIN
1S6P	CRYSTAL STRUCTURE OF HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 REVERSE TRANSCRIPTASE (RT) IN COMPLEX WITH JANSSEN-R100943	TRANSFERASE
1S6Q	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE (RT) IN COMPLEX WITH JANSSEN-R147681	TRANSFERASE

1S6V	STRUCTURE OF A CYTOCHROME C PEROXIDASE-CYTOCHROME C SITE SPECIFIC CROSS-LINK	OXIDOREDUCTASE/ELECTRON TRANSPORT
1S70	COMPLEX BETWEEN PROTEIN SER/THR PHOSPHATASE-1 (DELTA) AND THE MYOSIN PHOSPHATASE TARGETING SUBUNIT 1 (MYPT1)	HYDROLASE
1S72	REFINED CRYSTAL STRUCTURE OF THE HALOARCULA MARISMORTUI LARGE RIBOSOMAL SUBUNIT AT 2.4 ANGSTROM RESOLUTION	RIBOSOME
1S78	INSIGHTS INTO ERBB SIGNALING FROM THE STRUCTURE OF THE ERBB2-PERTUZUMAB COMPLEX	TRANSFERASE
1S7R	CRYSTAL STRUCTURES OF THE MURINE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX H-2KB IN COMPLEX WITH LCMV-DERIVED GP33 INDEX PEPTIDE AND THREE OF ITS ESCAPE VARIANTS	IMMUNE SYSTEM
1S7T	CRYSTAL STRUCTURES OF THE MURINE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX H-2KB IN COMPLEX WITH LCMV-DERIVED GP33 INDEX PEPTIDE AND THREE OF ITS ESCAPE VARIANTS	IMMUNE SYSTEM
1S7U	CRYSTAL STRUCTURES OF THE MURINE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX H-2DB IN COMPLEX WITH LCMV-DERIVED GP33 INDEX PEPTIDE AND THREE OF ITS ESCAPE VARIANTS	IMMUNE SYSTEM
1S7V	CRYSTAL STRUCTURES OF THE MURINE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX H-2DB IN COMPLEX WITH LCMV-DERIVED GP33 INDEX PEPTIDE AND THREE OF ITS ESCAPE VARIANTS	IMMUNE SYSTEM
1S7W	CRYSTAL STRUCTURES OF THE MURINE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX H-2DB IN COMPLEX WITH LCMV-DERIVED GP33 INDEX PEPTIDE AND THREE OF ITS ESCAPE VARIANTS	IMMUNE SYSTEM
1S7X	CRYSTAL STRUCTURES OF THE MURINE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX H-2DB IN COMPLEX WITH LCMV-DERIVED GP33 INDEX PEPTIDE AND THREE OF ITS ESCAPE VARIANTS	IMMUNE SYSTEM
1S8D	STRUCTURAL BASIS FOR DEGENERATE RECOGNITION OF HIV PEPTIDE VARIANTS BY CYTOTOXIC LYMPHOCYTE, VARIANT SL9-3A	IMMUNE SYSTEM
1S9D	ARF1[DELTA 1-17]-GDP-MG IN COMPLEX WITH BREFELDIN A AND A SEC7 DOMAIN	PROTEIN TRANSPORT/EXCHANGE FACTOR
1S9E	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE (RT) IN COMPLEX WITH JANSSEN-R129385	TRANSFERASE
1S9G	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE (RT) IN COMPLEX WITH JANSSEN-R120394.	TRANSFERASE
1S9K	CRYSTAL STRUCTURE OF HUMAN NFAT1 AND FOS-JUN ON THE IL-2 ARRE1 SITE	TRANSCRIPTION/DNA
1S9V	CRYSTAL STRUCTURE OF HLA-DQ2 COMPLEXED WITH DEAMIDATED GLIADIN PEPTIDE	IMMUNE SYSTEM
1S9W	CRYSTAL STRUCTURE ANALYSIS OF NY-ESO-1 EPITOPE, SLLMWITQC,	IMMUNE SYSTEM

	IN COMPLEX WITH HLA-A2	
1S9X	CRYSTAL STRUCTURE ANALYSIS OF NY-ESO-1 EPITOPE ANALOGUE, SLLMWITQA, IN COMPLEX WITH HLA-A2	IMMUNE SYSTEM
1S9Y	CRYSTAL STRUCTURE ANALYSIS OF NY-ESO-1 EPITOPE ANALOGUE, SLLMWITQS, IN COMPLEX WITH HLA-A2	IMMUNE SYSTEM
1SA0	TUBULIN-COLCHICINE: STATHMIN-LIKE DOMAIN COMPLEX	CELL CYCLE
1SA1	TUBULIN-PODOPHYLLOTOXIN: STATHMIN-LIKE DOMAIN COMPLEX	CELL CYCLE
1SA5	RAT PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH FPP AND BMS-214662	TRANSFERASE
1SB1	NOVEL NON-COVALENT THROMBIN INHIBITORS INCORPORATING P1 4,5,6,7-TETRAHYDROBENZOTHIAZOLE ARGININE SIDE CHAIN MIMETICS	BLOOD CLOTTING,HYDROLASE
1SB2	HIGH RESOLUTION STRUCTURE DETERMINATION OF RHODOCETIN	TOXIN
1SB3	TRUCTURE OF 4-HYDROXYBENZOYL-COA REDUCTASE FROM THAUERA AROMATICA	OXIDOREDUCTASE
1SBB	T-CELL RECEPTOR BETA CHAIN COMPLEXED WITH SUPERANTIGEN SEB	IMMUNE SYSTEM
1SBN	REFINED CRYSTAL STRUCTURES OF SUBTILISIN NOVO IN COMPLEX WITH WILD-TYPE AND TWO MUTANT EGLINS. COMPARISON WITH OTHER SERINE PROTEINASE INHIBITOR COMPLEXES	COMPLEX(PROTEINASE/INHIBITOR)
1SBS	CRYSTAL STRUCTURE OF AN ANTI-HCG FAB	MONOCLONAL ANTIBODY
1SC1	CRYSTAL STRUCTURE OF AN ACTIVE-SITE LIGAND-FREE FORM OF THE HUMAN CASPASE-1 C285A MUTANT	HYDROLASE
1SC3	CRYSTAL STRUCTURE OF THE HUMAN CASPASE-1 C285A MUTANT IN COMPLEX WITH MALONATE	HYDROLASE
1SC4	CRYSTAL STRUCTURE OF THE HUMAN CASPASE-1 C285A MUTANT AFTER REMOVAL OF MALONATE	HYDROLASE
1SC5	SIGMA-28(FLIA)/FLGM COMPLEX	TRANSCRIPTION
1SCJ	CRYSTAL STRUCTURE OF SUBTILISIN-PROPEPTIDE COMPLEX	HYDROLASE
1SCM	STRUCTURE OF THE REGULATORY DOMAIN OF SCALLOP MYOSIN AT 2.8 ANGSTROMS RESOLUTION	CALCIUM-BINDING PROTEIN
1SCN	INACTIVATION OF SUBTILISIN CARLSBERG BY N-(TERT-BUTOXYCARBONYL-ALANYL-PROLYL-PHENYLALANYL)-O-BENZOYL HYDROXYLAMINE: FORMATION OF COVALENT ENZYME-INHIBITOR LINKAGE IN THE FORM OF A CARBAMATE DERIVATIVE	COMPLEX(SERINE PROTEINASE/INHIBITOR)
1SCT	SCAPHARCA TETRAMERIC HEMOGLOBIN, CO-STATE	OXYGEN TRANSPORT
1SCU	THE CRYSTAL STRUCTURE OF SUCCINYL-COA SYNTHETASE FROM	LIGASE (ATP-BINDING)

	ESCHERICHIA COLI AT 2.5 ANGSTROMS RESOLUTION	
1SDB	PORCINE DESB1-2 DESPENTAPEPTIDE(B26-B30) INSULIN	HORMONE
1SDD	CRYSTAL STRUCTURE OF BOVINE FACTOR VAI	BLOOD CLOTTING
1SDK	CROSS-LINKED, CARBONMONOXY HEMOGLOBIN A	OXYGEN TRANSPORT
1SDL	CROSS-LINKED, CARBONMONOXY HEMOGLOBIN A	OXYGEN TRANSPORT
1SDX	CRYSTAL STRUCTURE OF THE ZINC SATURATED C-TERMINAL HALF OF BOVINE LACTOFERRIN AT 2.0 A RESOLUTION REVEALS TWO ADDITIONAL ZINC BINDING SITES	TRANSPORT PROTEIN
1SDZ	CRYSTAL STRUCTURE OF DIAP1 BIR1 BOUND TO A REAPER PEPTIDE	APOPTOSIS
1SE0	CRYSTAL STRUCTURE OF DIAP1 BIR1 BOUND TO A GRIM PEPTIDE	APOPTOSIS
1SEB	COMPLEX OF THE HUMAN MHC CLASS II GLYCOPROTEIN HLA-DR1 AND THE BACTERIAL SUPERANTIGEN SEB	COMPLEX (MHC II/PEPTIDE/TOXIN)
1SEQ	FAB MNAC13	IMMUNE SYSTEM
1SFC	NEURONAL SYNAPTIC FUSION COMPLEX	TRANSPORT PROTEIN
1SFI	HIGH RESOLUTION STRUCTURE OF A POTENT, CYCLIC PROTEASE INHIBITOR FROM SUNFLOWER SEEDS	COMPLEX (SERINE PROTEASE/INHIBITOR)
1SFO	RNA POLYMERASE II STRAND SEPARATED ELONGATION COMPLEX	TRANSCRIPTION/DNA/RNA
1SFQ	FAST FORM OF THROMBIN MUTANT R(77A)A BOUND TO PPACK	HYDROLASE
1SG8	RYSTAL STRUCTURE OF THE PROCOAGULANT FAST FORM OF THROMBIN	HYDROLASE
1SGD	ASP 18 VARIANT OF TURKEY OVOMUCOID INHIBITOR THIRD DOMAIN COMPLEXED WITH STREPTOMYCES GRISEUS PROTEINASE B AT PH 6.5	HYDROLASE/HYDROLASE INHIBITOR
1SGE	GLU 18 VARIANT OF TURKEY OVOMUCOID INHIBITOR THIRD DOMAIN COMPLEXED WITH STREPTOMYCES GRISEUS PROTEINASE B AT PH 6.5	HYDROLASE/HYDROLASE INHIBITOR
1SGF	CRYSTAL STRUCTURE OF 7S NGF: A COMPLEX OF NERVE GROWTH FACTOR WITH FOUR BINDING PROTEINS (SERINE PROTEINASES)	GROWTH FACTOR
1SGI	RYSTAL STRUCTURE OF THE ANTICOAGULANT SLOW FORM OF THROMBIN	HYDROLASE
1SGN	ASN 18 VARIANT OF TURKEY OVOMUCOID INHIBITOR THIRD DOMAIN COMPLEXED WITH STREPTOMYCES GRISEUS PROTEINASE B	HYDROLASE/HYDROLASE INHIBITOR
1SGP	ALA 18 VARIANT OF TURKEY OVOMUCOID INHIBITOR THIRD DOMAIN COMPLEXED WITH STREPTOMYCES GRISEUS PROTEINASE B	COMPLEX (SERINE PROTEASE/INHIBITOR)
1SGQ	GLY 18 VARIANT OF TURKEY OVOMUCOID INHIBITOR THIRD DOMAIN COMPLEXED WITH STREPTOMYCES GRISEUS PROTEINASE B	COMPLEX (SERINE PROTEASE/INHIBITOR)
1SGR	LEU 18 VARIANT OF TURKEY OVOMUCOID INHIBITOR THIRD DOMAIN	COMPLEX (SERINE PROTEASE/INHIBITOR)

	COMPLEXED WITH STREPTOMYCES GRISEUS PROTEINASE B	
1SGY	TYR 18 VARIANT OF TURKEY OVOMUCOID INHIBITOR THIRD DOMAIN COMPLEXED WITH STREPTOMYCES GRISEUS PROTEINASE B AT PH 6.5	HYDROLASE/HYDROLASE INHIBITOR
1SHB	RYSTAL STRUCTURE OF THE PHOSPHOTYROSINE RECOGNITION DOMAIN SH2 OF V-SRC COMPLEXED WITH TYROSINE-PHOSPHORYLATED PEPTIDES	PHOSPHOTRANSFERASE
1SHC	SHC PTB DOMAIN COMPLEXED WITH A TRKA RECEPTOR PHOSPHOPEPTIDE, NMR, MINIMIZED AVERAGE STRUCTURE	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)
1SHD	PEPTIDE INHIBITORS OF SRC SH3-SH2-PHOSPHOPROTEIN INTERACTIONS	COMPLEX(TRANSFERASE/PEPTIDE)
1SHH	SLOW FORM OF THROMBIN BOUND WITH PPACK	HYDROLASE
1SHR	RYSTAL STRUCTURE OF FERROCYANIDE BOUND HUMAN HEMOGLOBIN A2 AT 1.88A RESOLUTION	OXYGEN STORAGE/TRANSPORT
1SHZ	CRYSTAL STRUCTURE OF THE P115RHOGEF RGRGS DOMAIN IN A COMPLEX WITH GALPHA(13):GALPHA(I1) CHIMERA	SIGNALING PROTEIN
1SI4	CRYSTAL STRUCTURE OF HUMAN HEMOGLOBIN A2 (IN R2 STATE) AT 2.2 A RESOLUTION	OXYGEN STORAGE/TRANSPORT
1SIB	REFINED CRYSTAL STRUCTURES OF SUBTILISIN NOVO IN COMPLEX WITH WILD-TYPE AND TWO MUTANT EGLINS. COMPARISON WITH OTHER SERINE PROTEINASE INHIBITOR COMPLEXES	SERINE PROTEASE/INHIBITOR COMPLEX
1SIO	STRUCTURE OF KUMAMOLISIN-AS COMPLEXED WITH A COVALENTLY-BOUND INHIBITOR, ACIPF	HYDROLASE
1SIW	CRYSTAL STRUCTURE OF THE APOMOLYBDO-NARGHI	OXIDOREDUCTASE
1SJE	HLA-DR1 COMPLEXED WITH A 16 RESIDUE HIV CAPSID PEPTIDE BOUND IN A HAIRPIN CONFORMATION	IMMUNE SYSTEM
1SJH	HLA-DR1 COMPLEXED WITH A 13 RESIDUE HIV CAPSID PEPTIDE	IMMUNE SYSTEM
1SK6	CRYSTAL STRUCTURE OF THE ADENYLYL CYCLASE DOMAIN OF ANTHRAX EDEMA FACTOR (EF) IN COMPLEX WITH CALMODULIN, 3',5' CYCLIC AMP (CAMP), AND PYROPHOSPHATE	TOXIN, LYASE/METAL BINDING PROTEIN
1SKG	STRUCTURE-BASED RATIONAL DRUG DESIGN: CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN PHOSPHOLIPASE A2 AND A PENTAPEPTIDE VAL-ALA-PHE-ARG-SER	HYDROLASE
1SKO	MP1-P14 COMPLEX	SIGNALING PROTEIN
1SKR	7 DNA POLYMERASE COMPLEXED TO DNA PRIMER/TEMPLATE AND DDATP	TRANSFERASE/ELECTRON TRANSPORT/DNA
1SKS	BINARY 3' COMPLEX OF T7 DNA POLYMERASE WITH A DNA PRIMER/TEMPLATE CONTAINING A CIS-SYN THYMINE DIMER ON THE TEMPLATE	TRANSFERASE/ELECTRON TRANSPORT/DNA

1SKU	E. COLI ASPARTATE TRANSCARBAMYLASE 240'S LOOP MUTANT (K244N)	TRANSFERASE
1SKW	BINARY 3' COMPLEX OF T7 DNA POLYMERASE WITH A DNA PRIMER/TEMPLATE CONTAINING A DISORDERED CIS-SYN THYMINE DIMER ON THE TEMPLATE	TRANSFERASE/ELECTRON TRANSPORT/DNA
1SKY	CRYSTAL STRUCTURE OF THE NUCLEOTIDE FREE ALPHA3BETA3 SUB-COMPLEX OF F1-ATPASE FROM THE THERMOPHILIC BACILLUS PS3	ATP SYNTHASE
1SL0	TERNARY 3' COMPLEX OF T7 DNA POLYMERASE WITH A DNA PRIMER/TEMPLATE CONTAINING A DISORDERED CIS-SYN THYMINE DIMER ON THE TEMPLATE AND AN INCOMING NUCLEOTIDE	TRANSFERASE/ELECTRON TRANSPORT/DNA
1SL1	BINARY 5' COMPLEX OF T7 DNA POLYMERASE WITH A DNA PRIMER/TEMPLATE CONTAINING A CIS-SYN THYMINE DIMER ON THE TEMPLATE	TRANSFERASE/ELECTRON TRANSPORT/DNA
1SL2	TERNARY 5' COMPLEX OF T7 DNA POLYMERASE WITH A DNA PRIMER/TEMPLATE CONTAINING A CIS-SYN THYMINE DIMER ON THE TEMPLATE AND AN INCOMING NUCLEOTIDE	TRANSFERASE/ELECTRON TRANSPORT/DNA
1SLU	RAT ANIONIC N143H, E151H TRYPSIN COMPLEXED TO A86H ECOTIN	COMPLEX (SERINE PROTEASE/INHIBITOR)
1SLV	RAT ANIONIC N143H, E151H TRYPSIN COMPLEXED TO A86H ECOTIN; COPPER-BOUND	COMPLEX (SERINE PROTEASE/INHIBITOR)
1SLW	RAT ANIONIC N143H, E151H TRYPSIN COMPLEXED TO A86H ECOTIN; NICKEL-BOUND	COMPLEX (SERINE PROTEASE/INHIBITOR)
1SLX	RAT ANIONIC N143H, E151H TRYPSIN COMPLEXED TO A86H ECOTIN; ZINC-BOUND	COMPLEX (SERINE PROTEASE/INHIBITOR)
1SM3	CRYSTAL STRUCTURE OF THE TUMOR SPECIFIC ANTIBODY SM3 COMPLEX WITH ITS PEPTIDE EPITOPE	COMPLEX (ANTIBODY/PEPTIDE EPITOPE)
1SMH	PROTEIN KINASE A VARIANT COMPLEX WITH COMPLETELY ORDERED N-TERMINAL HELIX	SIGNALING PROTEIN,TRANSFERASE/INHIBITOR
1SMP	RYSTAL STRUCTURE OF A COMPLEX BETWEEN SERRATIA MARCESCENS METALLO-PROTEASE AND AN INHIBITOR FROM ERWINIA CHRYSANTHEMI	COMPLEX (METALLOPROTEASE/INHIBITOR)
1SMY	STRUCTURAL BASIS FOR TRANSCRIPTION REGULATION BY ALARMONE PPGPP	TRANSFERASE
1SOZ	CRYSTAL STRUCTURE OF DEGS PROTEASE IN COMPLEX WITH AN ACTIVATING PEPTIDE	HYDROLASE
1SP4	CRYSTAL STRUCTURE OF NS-134 IN COMPLEX WITH BOVINE CATHEPSIN B: A TWO HEADED EPOXYSUCCINYL INHIBITOR EXTENDS ALONG THE WHOLE ACTIVE SITE CLEFT	HYDROLASE
1SP5	CRYSTAL STRUCTURE OF HIV-1 PROTEASE COMPLEXED WITH A PRODUCT OF AUTOPROTEOLYSIS	HYDROLASE

1SPB	SUBTILISIN BPN' PROSEGMENT (77 RESIDUES) COMPLEXED WITH A MUTANT SUBTILISIN BPN' (266 RESIDUES). CRYSTAL PH 4.6. CRYSTALLIZATION TEMPERATURE 20 C DIFFRACTION TEMPERATURE-160 C	COMPLEX (SERINE PROTEINASE/PROSEGMENT)
1SPS	BINDING OF A HIGH AFFINITY PHOSPHOTYROSYL PEPTIDE TO THE SRC SH2 DOMAIN: CRYSTAL STRUCTURES OF THE COMPLEXED AND PEPTIDE-FREE FORMS	TRANSFERASE(PHOSPHOTRANSFERASE)
1SQ0	CRYSTAL STRUCTURE OF THE COMPLEX OF THE WILD-TYPE VON WILLEBRAND FACTOR A1 DOMAIN AND GLYCOPROTEIN IB ALPHA AT 2.6 ANGSTROM RESOLUTION	BLOOD CLOTTING
1SQ2	CRYSTAL STRUCTURE ANALYSIS OF THE NURSE SHARK NEW ANTIGEN RECEPTOR (NAR) VARIABLE DOMAIN IN COMPLEX WITH LYXOZYME	HYDROLASE/IMMUNE SYSTEM
1SQB	CRYSTAL STRUCTURE ANALYSIS OF BOVINE BC1 WITH AZOXYSTROBIN	OXIDOREDUCTASE
1SQK	CRYSTAL STRUCTURE OF CIBOULOT IN COMPLEX WITH SKELETAL ACTIN	STRUCTURAL PROTEIN/PROTEIN BINDING
1SQP	CRYSTAL STRUCTURE ANALYSIS OF BOVINE BC1 WITH MYXOTHIAZOL	OXIDOREDUCTASE
1SQQ	CRYSTAL STRUCTURE ANALYSIS OF BOVINE BC1 WITH METHOXY ACRYLATE STILBENE (MOAS)	OXIDOREDUCTASE
1SQV	CRYSTAL STRUCTURE ANALYSIS OF BOVINE BC1 WITH UHDBT	OXIDOREDUCTASE
1SQX	CRYSTAL STRUCTURE ANALYSIS OF BOVINE BC1 WITH STIGMATELLIN A	OXIDOREDUCTASE
1SQZ	DESIGN OF SPECIFIC INHIBITORS OF PHOPHOLIPASE A2: CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN GROUPII PHOPHOLIPASE A2 AND A DESIGNED PEPTIDE DEHYDRO-ILE-ALA-ARG-SER AT 1.2A RESOLUTION	TOXIN
1SR4	CRYSTAL STRUCTURE OF THE HAEMOPHILUS DUCREYI CYTOLETHAL DISTENDING TOXIN	TOXIN
1SR5	ANTITHROMBIN-ANHYDROTHROMBIN-HEPARIN TERNARY COMPLEX STRUCTURE	HYDROLASE/HYDROLASE INHIBITOR
1SR6	STRUCTURE OF NUCLEOTIDE-FREE SCALLOP MYOSIN S1	CONTRACTILE PROTEIN
1SRN	THE REFINED CRYSTAL STRUCTURE OF A FULLY ACTIVE SEMISYNTHETIC RIBONUCLEASE AT 1.8 ANGSTROMS RESOLUTION	HYDROLASE (NUCLEIC ACID,RNA)
1SSA	A STRUCTURAL INVESTIGATION OF CATALYTICALLY MODIFIED F12OL AND F12OY SEMISYNTHETIC RIBONUCLEASES	HYDROLASE(ENDORIBONUCLEASE)
1SSB	A STRUCTURAL INVESTIGATION OF CATALYTICALLY MODIFIED F12OL AND F12OY SEMISYNTHETIC RIBONUCLEASES	HYDROLASE(ENDORIBONUCLEASE)
1SSC	THE 1.6 ANGSTROMS STRUCTURE OF A SEMISYNTHETIC RIBONUCLEASE CRYSTALLIZED FROM AQUEOUS ETHANOL. COMPARISON WITH CRYSTALS FROM SALT SOLUTIONS AND WITH RNASE A FROM AQUEOUS ALCOHOL SOLUTIONS	ENDONUCLEASE

1STC	CAMP-DEPENDENT PROTEIN KINASE, ALPHA-CATALYTIC SUBUNIT IN COMPLEX WITH STAUROSPORINE	COMPLEX (TRANSFERASE/INHIBITOR)
1STF	THE REFINED 2.4 ANGSTROMS X-RAY CRYSTAL STRUCTURE OF RECOMBINANT HUMAN STEFIN B IN COMPLEX WITH THE CYSTEINE PROTEINASE PAPAIN: A NOVEL TYPE OF PROTEINASE INHIBITOR INTERACTION	HYDROLASE(SULFHYDRYL PROTEINASE)
1SUA	SUBTILISIN BPN'	COMPLEX (HYDROLASE/PEPTIDE)
1SUQ	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE (RT) IN COMPLEX WITH JANSSEN-R185545	TRANSFERASE
1SUV	RUCTURE OF HUMAN TRANSFERRIN RECEPTOR-TRANSFERRIN COMPLEX	METAL TRANSPORT
1SUY	NMR STRUCTURE OF THE THKAIA180C-CIIABD COMPLEX (AVERAGE MINIMIZED STRUCTURE)	CIRCADIAN CLOCK PROTEIN
1SV0	CRYSTAL STRUCTURE OF YAN-SAM/MAE-SAM COMPLEX	TRANSCRIPTION
1SV5	CRYSTAL STRUCTURE OF K103N MUTANT HIV-1 REVERSE TRANSCRIPTASE (RT) IN COMPLEX WITH JANSSEN-R165335	TRANSFERASE
1SVD	THE STRUCTURE OF HALOTHIOBACILLUS NEAPOLITANUS RUBISCO	LYASE
1SVF	PARAMYXOVIRUS SV5 FUSION PROTEIN CORE	VIRAL PROTEIN
1SVG	CRYSTAL STRUCTURE OF PROTEIN KINASE A IN COMPLEX WITH AZEPANE DERIVATIVE 4	TRANSFERASE
1SVH	CRYSTAL STRUCTURE OF PROTEIN KINASE A IN COMPLEX WITH AZEPANE DERIVATIVE 8	TRANSFERASE
1SVX	CRYSTAL STRUCTURE OF A DESIGNED SELECTED ANKYRIN REPEAT PROTEIN IN COMPLEX WITH THE MALTOSE BINDING PROTEIN	DE NOVO PROTEIN/SUGAR BINDING PROTEIN
1SX4	GROEL-GROES-ADP7	CHAPERONE
1SXJ	CRYSTAL STRUCTURE OF THE EUKARYOTIC CLAMP LOADER (REPLICATION FACTOR C, RFC) BOUND TO THE DNA SLIDING CLAMP (PROLIFERATING CELL NUCLEAR ANTIGEN, PCNA)	REPLICATION
1SY6	RYSTAL STRUCTURE OF CD3GAMMAEPSILON HETERODIMER IN COMPLEX WITH OKT3 FAB FRAGMENT	SIGNALING PROTEIN/ANTIBIOTIC
1SYQ	HUMAN VINCULIN HEAD DOMAIN VH1, RESIDUES 1-258, IN COMPLEX WITH HUMANTALIN'S VINCULIN BINDING SITE 1, RESIDUES 607-636	CELL ADHESION
1SYS	CRYSTAL STRUCTURE OF HLA, B*4403, AND PEPTIDE EEPTVIKKY	IMMUNE SYSTEM
1SYV	HLA-B*4405 COMPLEXED TO THE DOMINANT SELF LIGAND EEFGRAYGF	IMMUNE SYSTEM
1SYX	THE CRYSTAL STRUCTURE OF A BINARY U5 SNRNP COMPLEX	TRANSLATION/IMMUNE SYSTEM

1SZ6	MISTLETOE LECTIN I FROM VISCUM ALBUM. CRYSTAL STRUCTURE AT 2.05 A RESOLUTION	HYDROLASE INHIBITOR
1SZA	THE RNA POLYMERASE II CTD IN MRNA PROCESSING: BETA-TURN RECOGNITION AND BETA-SPIRAL MODEL	TRANSCRIPTION
1SZC	STRUCTURAL BASIS FOR NICOTINAMIDE CLEAVAGE AND ADP-RIBOSE TRANSFER BY NAD+-DEPENDENT SIR2 HISTONE/PROTEIN DEACETYLASES	GENE REGULATION
1SZD	STRUCTURAL BASIS FOR NICOTINAMIDE CLEAVAGE AND ADP-RIBOSE TRANSFER BY NAD+-DEPENDENT SIR2 HISTONE/PROTEIN DEACETYLASES	GENE REGULATION
1T01	VINCULIN COMPLEXED WITH THE VBS1 HELIX FROM TALIN	CELL ADHESION, STRUCTURAL PROTEIN
1T03	HIV-1 REVERSE TRANSCRIPTASE CROSSLINKED TO TENOFOVIR TERMINATED TEMPLATE-PRIMER (COMPLEX P)	TRANSFERASE/ANTIBODY/DNA
1T04	THREE DIMENSIONAL STRUCTURE OF A HUMANIZED ANTI-IFN-GAMMA FAB IN C2 SPACE GROUP	IMMUNE SYSTEM
1T05	HIV-1 REVERSE TRANSCRIPTASE CROSSLINKED TO TEMPLATE-PRIMER WITH TENOFOVIR-DIPHOSPHATE BOUND AS THE INCOMING NUCLEOTIDE SUBSTRATE	TRANSFERASE/DNA
1T08	CRYSTAL STRUCTURE OF BETA-CATENIN/ICAT HELICAL DOMAIN/UNPHOSPHORYLATED APC R3	CELL ADHESION/CELL CYCLE
1T0F	CRYSTAL STRUCTURE OF THE TNSA/TNSC(504-555) COMPLEX	DNA BINDING PROTEIN
1T0H	CRYSTAL STRUCTURE OF THE RATTUS NORVEGICUS VOLTAGE GATED CALCIUM CHANNEL BETA SUBUNIT ISOFORM 2A	SIGNALING PROTEIN
1T0J	CRYSTAL STRUCTURE OF A COMPLEX BETWEEN VOLTAGE-GATED CALCIUM CHANNEL BETA2A SUBUNIT AND A PEPTIDE OF THE ALPHA1C SUBUNIT	SIGNALING PROTEIN
1T0K	JOINT X-RAY AND NMR REFINEMENT OF YEAST L30E-MRNA COMPLEX	RIBOSOME
1T0M	CONFORMATIONAL SWITCH IN POLYMORPHIC H-2K MOLECULES CONTAINING AN HSV PEPTIDE	IMMUNE SYSTEM
1T0N	CONFORMATIONAL SWITCH IN POLYMORPHIC H-2K MOLECULES CONTAINING AN HSV PEPTIDE	IMMUNE SYSTEM
1T0P	STRUCTURAL BASIS OF ICAM RECOGNITION BY INTEGRIN ALPAHLBETA2 REVEALED IN THE COMPLEX STRUCTURE OF BINDING DOMAINS OF ICAM-3 AND ALPHALBETA2 AT 1.65 A	IMMUNE SYSTEM
1T0Q	RUCTURE OF THE TOLUENE/O-XYLENE MONOOXYGENASE HYDROXYLASE	OXIDOREDUCTASE
1T0R	CRYSTAL STRUCTURE OF THE TOLUENE/O-XYLENE MONOOXYGENASE HYDROXUYLASE FROM PSEUDOMONAS STUTZERI-AZIDE BOUND	OXIDOREDUCTASE

1T0S	RUCTURE OF THE TOLUENE/O-XYLENE MONOOXYGENASE HYDROXYLASE WITH 4-BROMOPHENOL BOUND	OXIDOREDUCTASE
1T15	RYSTAL STRUCTURE OF THE BRCA1 BRCT DOMAINS IN COMPLEX WITH THE PHOSPHORYLATED INTERACTING REGION FROM BACH1 HELICASE	ANTITUMOR PROTEIN
1T1N	CRYSTAL STRUCTURE OF CARBONMONOXY HEMOGLOBIN	OXYGEN TRANSPORT
1T1W	STRUCTURAL BASIS FOR DEGENERATE RECOGNITION OF HIV PEPTIDE VARIANTS BY CYTOTOXIC LYMPHOCYTE, VARIANT SL9-3F6I8V	IMMUNE SYSTEM
1T1X	STRUCTURAL BASIS FOR DEGENERATE RECOGNITION OF HIV PEPTIDE VARIANTS BY CYTOTOXIC LYMPHOCYTE, VARIANT SL9-4L	IMMUNE SYSTEM
1T1Y	STRUCTURAL BASIS FOR DEGENERATE RECOGNITION OF HIV PEPTIDE VARIANTS BY CYTOTOXIC LYMPHOCYTE, VARIANT SL9-5V	IMMUNE SYSTEM
1T1Z	STRUCTURAL BASIS FOR DEGENERATE RECOGNITION OF HIV PEPTIDE VARIANTS BY CYTOTOXIC LYMPHOCYTE, VARIANT SL9-6A	IMMUNE SYSTEM
1T20	STRUCTURAL BASIS FOR DEGENERATE RECOGNITION OF HIV PEPTIDE VARIANTS BY CYTOTOXIC LYMPHOCYTE, VARIANT SL9-6I	IMMUNE SYSTEM
1T21	STRUCTURAL BASIS FOR DEGENERATE RECOGNITION OF HIV PEPTIDE VARIANTS BY CYTOTOXIC LYMPHOCYTE, VARIANT SL9, MONOCLINIC CRYSTAL	IMMUNE SYSTEM
1T22	STRUCTURAL BASIS FOR DEGENERATE RECOGNITION OF HIV PEPTIDE VARIANTS BY CYTOTOXIC LYMPHOCYTE, VARIANT SL9, ORTHORHOMBIC CRYSTAL	IMMUNE SYSTEM
1T29	CRYSTAL STRUCTURE OF THE BRCA1 BRCT REPEATS BOUND TO A PHOSPHORYLATED BACH1 PEPTIDE	SIGNALING PROTEIN
1T2K	STRUCTURE OF THE DNA BINDING DOMAINS OF IRF3, ATF-2 AND JUN BOUND TO DNA	TRANSCRIPTION/DNA
1T2Q	THE CRYSTAL STRUCTURE OF AN NNA7 FAB THAT RECOGNIZES AN N-TYPE BLOOD GROUP ANTIGEN	IMMUNE SYSTEM
1T2V	STRUCTURAL BASIS OF PHOSPHO-PEPTIDE RECOGNITION BY THE BRCT DOMAIN OF BRCA1, STRUCTURE WITH PHOSPHOPEPTIDE	ANTITUMOR PROTEIN
1T34	ROTATION MECHANISM FOR TRANSMEMBRANE SIGNALING BY THE ATRIAL NATRIURETIC PEPTIDE RECEPTOR	SIGNALING PROTEIN,MEMBRANE PROTEIN
1T36	RYSTAL STRUCTURE OF E. COLI CARBAMOYL PHOSPHATE SYNTHETASE SMALL SUBUNIT MUTANT C248D COMPLEXED WITH URIDINE 5'-MONOPHOSPHATE	LIGASE
1T37	DESIGN OF SPECIFIC INHIBITORS OF PHOSPHOLIPASE A2: CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN GROUP I PHOSPHOLIPASE A2 AND A DESIGNED PENTAPEPTIDE LEU-ALA-ILE-TYR-SER AT 2.6A RESOLUTION	HYDROLASE

1T3E	STRUCTURAL BASIS OF DYNAMIC GLYCINE RECEPTOR CLUSTERING	STRUCTURAL PROTEIN/SIGNALING PROTEIN
1T3F	THREE DIMENSIONAL STRUCTURE OF A HUMANIZED ANTI-IFN-GAMMA FAB (HUZAF) IN P21 21 21 SPACE GROUP	IMMUNE SYSTEM
1T3L	STRUCTURAL ANALYSIS OF THE VOLTAGE-DEPENDENT CALCIUM CHANNEL BETA SUBUNIT FUNCTIONAL CORE IN COMPLEX WITH ALPHA1 INTERACTION DOMAIN	TRANSPORT PROTEIN
1T3M	STRUCTURE OF THE ISOASPARTYL PEPTIDASE WITH L-ASPARAGINASE ACTIVITY FROM E. COLI	HYDROLASE
1T3Q	CRYSTAL STRUCTURE OF QUINOLINE 2-OXIDOREDUCTASE FROM PSEUDOMONAS PUTIDA 86	OXIDOREDUCTASE
1T44	STRUCTURAL BASIS OF ACTIN SEQUESTRATION BY THYMOSIN-B4: IMPLICATIONS FOR ARP2/3 ACTIVATION	STRUCTURAL PROTEIN
1T4C	FORMYL-COA TRANSFERASE IN COMPLEX WITH OXALYL-COA	TRASNFERASE
1T4F	STRUCTURE OF HUMAN MDM2 IN COMPLEX WITH AN OPTIMIZED P53 PEPTIDE	LIGASE
1T4K	CRYSTAL STRUCTURE OF UNLIGANDED ALDOLASE ANTIBODY 93F3 FAB	IMMUNE SYSTEM
1T4U	CRYSTAL STRUCTURE ANALYSIS OF A NOVEL OXYGUANIDINE BOUND TO THROMBIN	HYDROLASE
1T4V	CRYSTAL STRUCTURE ANALYSIS OF A NOVEL OXYGUANIDINE BOUND TO THROMBIN	HYDROLASE
1T5W	HLA-DR1 IN COMPLEX WITH A SYNTHETIC PEPTIDE (AAYSDQATPLLLSPR)	IMMUNE SYSTEM
1T5X	HLA-DR1 IN COMPLEX WITH A SYNTHETIC PEPTIDE (AAYSDQATPLLLSPR) AND THE SUPERANTIGEN SEC3-3B2	IMMUNE SYSTEM
1T5Z	CRYSTAL STRUCTURE OF THE ANDROGEN RECEPTOR LIGAND BINDING DOMAIN (LBD) WITH DHT AND A PEPTIDE DERIVED FROM ITS PHYSIOLOGICAL COACTIVATOR ARA70	HORMONE/GROWTH FACTOR
1T60	CRYSTAL STRUCTURE OF TYPE IV COLLAGEN NC1 DOMAIN FROM BOVINE LENS CAPSULE	STRUCTURAL PROTEIN
1T61	CRYSTAL STRUCTURE OF COLLAGEN IV NC1 DOMAIN FROM PLACENTA BASEMENT MEMBRANE	STRUCTURAL PROTEIN
1T63	CRYSTAL STRUCTURE OF THE ANDROGEN RECEPTOR LIGAND BINDING DOMAIN WITH DHT AND A PEPTIDE DERIVED FROM ITS PHYSIOLOGICAL COACTIVATOR GRIP1 NR BOX3	HORMONE/GROWTH FACTOR
1T65	CRYSTAL STRUCTURE OF THE ANDROGEN RECEPTOR LIGAND BINDING DOMAIN WITH DHT AND A PEPTIDE DERIVED FORM ITS PHYSIOLOGICAL COACTIVATOR GRIP1 NR BOX 2 BOUND IN A NON-HELICAL CONFORMATION	HORMONE/GROWTH FACTOR

1T66	THE STRUCTURE OF FAB WITH INTERMEDIATE AFFINITY FOR FLUORESCEIN.	IMMUNE SYSTEM
1T6B	CRYSTAL STRUCTURE OF B. ANTHRACIS PROTECTIVE ANTIGEN COMPLEXED WITH HUMAN ANTHRAX TOXIN RECEPTOR	MEMBRANE PROTEIN/TOXIN
1T6O	NUCLEOCAPSID-BINDING DOMAIN OF THE MEASLES VIRUS P PROTEIN (AMINO ACIDS 457-507) IN COMPLEX WITH AMINO ACIDS 486-505 OF THE MEASLES VIRUS N PROTEIN	VIRAL PROTEIN
1T6V	CRYSTAL STRUCTURE ANALYSIS OF THE NURSE SHARK NEW ANTIGEN RECEPTOR (NAR) VARIABLE DOMAIN IN COMPLEX WITH LYSOZYME	HYDROLASE/IMMUNE SYSTEM
1T73	CRYSTAL STRUCTURE OF THE ANDROGEN RECEPTOR LIGAND BINDING DOMAIN IN COMPLEX WITH A FXXFF MOTIF	HORMONE/GROWTH FACTOR RECEPTOR
1T74	CRYSTAL STRUCTURE OF THE ANDROGEN RECEPTOR LIGAND BINDING DOMAIN IN COMPLEX WITH A WXXLF MOTIF	HORMONE/GROWTH FACTOR RECEPTOR
1T76	CRYSTAL STRUCTURE OF THE ANDROGEN RECEPTOR LIGAND BINDING DOMAIN IN COMPLEX WITH A WXXVW MOTIF	HORMONE/GROWTH FACTOR RECEPTOR
1T79	CRYSTAL STRUCTURE OF THE ANDROGEN RECEPTOR LIGAND BINDING DOMAIN IN COMPLEX WITH A FXXLW MOTIF	HORMONE/GROWTH FACTOR RECEPTOR
1T7C	CRYSTAL STRUCTURE OF THE P1 GLU BPTI MUTANT- BOVINE CHYMOTRYPSIN COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
1T7F	CRYSTAL STRUCTURE OF THE ANDROGEN RECEPTOR LIGAND BINDING DOMAIN IN COMPLEX WITH A LXXLL MOTIF	HORMONE/GROWTH FACTOR RECEPTOR
1T7M	CRYSTAL STRUCTURE OF THE ANDROGEN RECEPTOR LIGAND BINDING DOMAIN IN COMPLEX WITH A FXXYF MOTIF	HORMONE/GROWTH FACTOR RECEPTOR
1T7P	T7 DNA POLYMERASE COMPLEXED TO DNA PRIMER/TEMPLATE,A NUCLEOSIDE TRIPHOSPHATE, AND ITS PROCESSIVITY FACTOR THIOREDOXIN	TRANSFERASE/DNA
1T7R	CRYSTAL STRUCTURE OF THE ANDROGEN RECEPTOR LIGAND BINDING DOMAIN IN COMPLEX WITH A FXXLF MOTIF	HORMONE/GROWTH FACTOR RECEPTOR
1T83	CRYSTAL STRUCTURE OF A HUMAN TYPE III FC GAMMA RECEPTOR IN COMPLEX WITH AN FC FRAGMENT OF IGG1 (ORTHORHOMBIC)	IMMUNE SYSTEM
1T89	CRYSTAL STRUCTURE OF A HUMAN TYPE III FC GAMMA RECEPTOR IN COMPLEX WITH AN FC FRAGMENT OF IGG1 (HEXAGONAL)	IMMUNE SYSTEM
1T8E	T7 DNA POLYMERASE TERNARY COMPLEX WITH DCTP AT THE INSERTION SITE.	TRANSFERASE/ELECTRON TRANSPORT/DNA
1T8L	CRYSTAL STRUCTURE OF THE P1 MET BPTI MUTANT- BOVINE CHYMOTRYPSIN COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
1T8M	CRYSTAL STRUCTURE OF THE P1 HIS BPTI MUTANT- BOVINE	HYDROLASE/HYDROLASE INHIBITOR

	CHYMOTRYPSIN COMPLEX	
1T8N	CRYSTAL STRUCTURE OF THE P1 THR BPTI MUTANT- BOVINE CHYMOTRYPSIN COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
1T8O	CRYSTAL STRUCTURE OF THE P1 TRP BPTI MUTANT- BOVINE CHYMOTRYPSIN COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
1T9G	STRUCTURE OF THE HUMAN MCAD:ETF COMPLEX	OXIDOREDUCTASE, ELECTRON TRANSPORT
1TA3	CRYSTAL STRUCTURE OF XYLANASE (GH10) IN COMPLEX WITH INHIBITOR (XIP)	HYDROLASE INHIBITOR/HYDROLASE
1TAB	STRUCTURE OF THE TRYPSIN-BINDING DOMAIN OF BOWMAN-BIRK TYPE PROTEASE INHIBITOR AND ITS INTERACTION WITH TRYPSIN	HYDROLASE (SERINE PROTEINASE)
1TAW	BOVINE TRYPSIN COMPLEXED TO APPI	COMPLEX (SERINE PROTEASE/INHIBITOR)
1TB6	2.5A CRYSTAL STRUCTURE OF THE ANTITHROMBIN-THROMBIN-HEPARIN TERNARY COMPLEX	HYDROLASE/BLOOD CLOTTING
1TBG	BETA-GAMMA DIMER OF THE HETEROTRIMERIC G-PROTEIN TRANSDUCIN	COMPLEX (GTP-BINDING/TRANSDUCER)
1TBQ	CRYSTAL STRUCTURE OF INSECT DERIVED DOUBLE DOMAIN KAZAL INHIBITOR RHODNIIN IN COMPLEX WITH THROMBIN	COMPLEX (SERINE PROTEASE/INHIBITOR)
1TBR	CRYSTAL STRUCTURE OF INSECT DERIVED DOUBLE DOMAIN KAZAL INHIBITOR RHODNIIN IN COMPLEX WITH THROMBIN	COMPLEX (SERINE PROTEASE/INHIBITOR)
1TBZ	HUMAN THROMBIN WITH ACTIVE SITE N-METHYL-D PHENYLALANYL-N-[5-(AMINOIMINOMETHYL)AMINO]-1-{{BENZOTHIAZOLYL)CARBONYL] BUTYL]-L-PROLINAMIDE TRIFLUROACETATE AND EXOSITE-HIRUGEN	COMPLEX (SERINE PROTEASE/INHIBITOR)
1TCE	SOLUTION NMR STRUCTURE OF THE SHC SH2 DOMAIN COMPLEXED WITH A TYROSINE-PHOSPHORYLATED PEPTIDE FROM THE T-CELL RECEPTOR, MINIMIZED AVERAGE STRUCTURE	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)
1TCO	TERNARY COMPLEX OF A CALCINEURIN A FRAGMENT, CALCINEURIN B, FKBP12 AND THE IMMUNOSUPPRESSANT DRUG FK506 (TACROLIMUS)	COMPLEX (HYDROLASE/ISOMERASE)
1TCR	MURINE T-CELL ANTIGEN RECEPTOR 2C CLONE	RECEPTOR
1TDQ	STRUCTURAL BASIS FOR THE INTERACTIONS BETWEEN TENASCINS AND THE C-TYPE LECTIN DOMAINS FROM LECTICANS: EVIDENCE FOR A CROSS-LINKING ROLE FOR TENASCINS	EXTRACELLULAR MATRIX
1TDV	NON-SPECIFIC BINDING TO PHOSPHOLIPASE A2:CRYSTAL STRUCTURE OF THE COMPLEX OF PLA2 WITH A DESIGNED PEPTIDE TYR-TRP-ALA-ALA-ALA-ALA AT 1.7A RESOLUTION	HYDROLASE
1TE1	CRYSTAL STRUCTURE OF FAMILY 11 XYLANASE IN COMPLEX WITH INHIBITOR (XIP-I)	HYDROLASE INHIBITOR/HYDROLASE
1TEC	CRYSTALLOGRAPHIC REFINEMENT BY INCORPORATION OF MOLECULAR DYNAMICS. THE THERMOSTABLE SERINE PROTEASE THERMITASE	COMPLEX(SERINE PROTEINASE-INHIBITOR)

	COMPLEXED WITH EGLIN-C	
1TET	CRYSTAL STRUCTURE OF AN ANTICHOLERA TOXIN PEPTIDE COMPLEX AT 2.3 ANGSTROMS	IMMUNOGLOBULIN
1TF0	CRYSTAL STRUCTURE OF THE GA MODULE COMPLEXED WITH HUMAN SERUM ALBUMIN	PROTEIN BINDING
1TFC	CRYSTAL STRUCTURE OF THE LIGAND-BINDING DOMAIN OF THE ESTROGEN-RELATED RECEPTOR GAMMA IN COMPLEX WITH A STEROID RECEPTOR COACTIVATOR-1 PEPTIDE	TRANSCRIPTION
1TFK	RIBONUCLEASE FROM ESCHERICHIA COLI COMPLEXED WITH ITS INHIBTOR PROTEIN	TOXIN/TOXIN INHIBITOR
1TFM	CRYSTAL STRUCTURE OF A RIBOSOME INACTIVATING PROTEIN IN ITS NATURALLY INHIBITED FORM	TOXIN
1TFO	RIBONUCLEASE FROM ESCHERICHIA COLI COMPLEXED WITH ITS INHIBITOR PROTEIN	TOXIN/TOXIN INHIBITOR
1TG1	CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN RUSSELLS VIPER PHOSPHOLIPASE A2 AND A DESIGNED PEPTIDE INHIBITOR CBZ-DEHYDRO-LEU-VAL-ARG-TYR AT 1.2A RESOLUTION	HYDROLASE
1TG4	DESIGN OF SPECIFIC INHIBITORS OF GROUPII PHOSPHOLIPASE A2(PLA2): CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN RUSSELLS VIPER PLA2 AND DESIGNED PEPTIDE PHE-LEU-ALA-TYR-LYS AT 1.7A RESOLUTION	HYDROLASE
1TGS	THREE-DIMENSIONAL STRUCTURE OF THE COMPLEX BETWEEN PANCREATIC SECRETORY INHIBITOR (KAZAL TYPE) AND TRYPSINOGEN AT 1.8 ANGSTROMS RESOLUTION. STRUCTURE SOLUTION, CRYSTALLOGRAPHIC REFINEMENT AND PRELIMINARY STRUCTURAL INTERPRETATION	COMPLEX (PROTEINASE/INHIBITOR)
1TGZ	STRUCTURE OF HUMAN SENP2 IN COMPLEX WITH SUMO-1	CELL CYCLE, HYDROLASE
1TH1	BETA-CATENIN IN COMPLEX WITH A PHOSPHORYLATED APC 20AA REPEAT FRAGMENT	CELL ADHESION/ANTITUMOR PROTEIN
1TH8	CRYSTAL STRUCTURES OF THE ADP AND ATP BOUND FORMS OF THE BACILLUS ANTI-SIGMA FACTOR SPOIIAB IN COMPLEX WITH THE ANTI-ANTI-SIGMA SPOIIAA: INHIBITORY COMPLEX WITH ADP, CRYSTAL FORM II	TRANSCRIPTION
1THB	REFINEMENT OF A PARTIALLY OXYGENATED T STATE HAEMOGLOBIN AT 1.5 ANGSTROMS RESOLUTION	OXYGEN TRANSPORT
1THN	CRYSTAL STRUCTURES OF THE ADP AND ATP BOUND FORMS OF THE BACILLUS ANTI-SIGMA FACTOR SPOIIAB IN COMPLEX WITH THE ANTI-ANTI-SIGMA SPOIIAA: INHIBITORY COMPLEX WITH ADP, CRYSTAL FORM I	TRANSCRIPTION
1THP	STRUCTURE OF HUMAN ALPHA-THROMBIN Y225P MUTANT BOUND TO D-	SERINE PROTEASE

	PHE-PRO-ARG-CHLOROMETHYLKETONE	
1THR	STRUCTURES OF THROMBIN COMPLEXES WITH A DESIGNED AND A NATURAL EXOSITE INHIBITOR	HYDROLASE(SERINE PROTEINASE)
1THS	STRUCTURES OF THROMBIN COMPLEXES WITH A DESIGNED AND A NATURAL EXOSITE INHIBITOR	HYDROLASE(SERINE PROTEINASE)
1TI2	CRYSTAL STRUCTURE OF PYROGALLOL-PHLOROGLUCINOL TRANSHYDROXYLASE FROM PELOBACTER ACIDIGALLICI	OXIDOREDUCTASE
1TI4	CRYSTAL STRUCTURE OF PYROGALLOL-PHLOROGLUCINOL TRANSHYDROXYLASE FROM PELOBACTER ACIDIGALLICI COMPLEXED WITH PYROGALLOL	OXIDOREDUCTASE
1TI6	CRYSTAL STRUCTURE OF PYROGALLOL-PHLOROGLUCINOL TRANSHYDROXYLASE FROM PELOBACTER ACIDIGALLICI COMPLEXED WITH INHIBITOR 1,2,4,5-TETRAHYDROXY-BENZENE	OXIDOREDUCTASE
1TI8	H7 HAEMAGGLUTININ	VIRAL PROTEIN
1TID	CRYSTAL STRUCTURES OF THE ADP AND ATP BOUND FORMS OF THE BACILLUS ANTI-SIGMA FACTOR SPOIIAB IN COMPLEX WITH THE ANTI-ANTI-SIGMA SPOIIAA: POISED FOR PHOSPHORYLATION COMPLEX WITH ATP, CRYSTAL FORM I	TRANSCRIPTION
1TII	ESCHERICHIA COLI HEAT LABILE ENTEROTOXIN TYPE IIB	ENTEROTOXIN
1TIL	CRYSTAL STRUCTURES OF THE ADP AND ATP BOUND FORMS OF THE BACILLUS ANTI-SIGMA FACTOR SPOIIAB IN COMPLEX WITH THE ANTI-ANTI-SIGMA SPOIIAA:POISED FOR PHOSPHORYLATION COMPLEX WITH ATP, CRYSTAL FORM II	TRANSCRIPTION
1TJ9	STRUCTURE OF THE COMPLEXED FORMED BETWEEN GROUP II PHOSPHOLIPASE A2 AND A RATIONALLY DESIGNED TETRA PEPTIDE, VAL-ALA-ARG-SER AT 1.1A RESOLUTION	HYDROLASE
1TJG	CRYSTAL STRUCTURE OF THE BROADLY NEUTRALIZING ANTI-HIV-1 ANTIBODY 2F5 IN COMPLEX WITH A GP41 7MER EPITOPE	VIRAL PROTEIN/IMMUNE SYSTEM
1TJH	CRYSTAL STRUCTURE OF THE BROADLY NEUTRALIZING ANTI-HIV-1 ANTIBODY 2F5 IN COMPLEX WITH A GP41 11MER EPITOPE	VIRAL PROTEIN/IMMUNE SYSTEM
1TJI	CRYSTAL STRUCTURE OF THE BROADLY NEUTRALIZING ANTI-HIV-1 ANTIBODY 2F5 IN COMPLEX WITH A GP41 17MER EPITOPE	VIRAL PROTEIN/IMMUNE SYSTEM
1TJK	CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN GROUP II PHOSPHOLIPASE A2 WITH A DESIGNED PENTAPEPTIDE, PHE- LEU- SER- THR- LYS AT 1.2 A RESOLUTION	HYDROLASE
1TJP	CRYSTAL STRUCTURE OF WILD-TYPE TRYPTOPHAN SYNTHASE COMPLEXED WITH 1-[(2-HYDROXYLPHENYL)AMINO]3-GLYCEROLPHOSPHATE	LYASE
1TJQ	CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN A GROUP II	HYDROLASE

	PHOSPHOLIPASE A2 AND DESIGNED PEPTIDE INHIBITOR CARBOBENZOXY-DEHYDRO-VAL-ALA-ARG-SER AT 1.2 A RESOLUTION	
1TK0	T7 DNA POLYMERASE TERNARY COMPLEX WITH 8 OXO GUANOSINE AND DDCTP AT THE INSERTION SITE	TRANSFERASE/ELECTRON TRANSPORT/DNA
1TK2	CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN ALKALINE PROTEINASE SAVINASE AND GRAMICIDIN S AT 1.5A RESOLUTION	HYDROLASE
1TK4	CRYSTAL STRUCTURE OF RUSSELLS VIPER PHOSPHOLIPASE A2 IN COMPLEX WITH A SPECIFICALLY DESIGNED TETRAPEPTIDE ALA-ILE-ARG-SER AT 1.1 A RESOLUTION	HYDROLASE
1TK5	T7 DNA POLYMERASE BINARY COMPLEX WITH 8 OXO GUANOSINE IN THE TEMPLATING STRAND	TRANSFERASE/ELECTRON TRANSPORT/DNA
1TK8	T7 DNA POLYMERASE TERNARY COMPLEX WITH 8 OXO GUANOSINE AND DAMP AT THE ELONGATION SITE	TRANSFERASE/ELECTRON TRANSPORT/DNA
1TKD	T7 DNA POLYMERASE TERNARY COMPLEX WITH 8 OXO GUANOSINE AND DCMP AT THE ELONGATION SITE	TRANSFERASE/ELECTRON TRANSPORT/DNA
1TKT	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH GW426318	TRANSFERASE
1TKX	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH GW490745	TRANSFERASE
1TKZ	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH GW429576	TRANSFERASE
1TL1	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH GW451211	TRANSFERASE
1TL3	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH GW450557	TRANSFERASE
1TL7	COMPLEX OF GS- WITH THE CATALYTIC DOMAINS OF MAMMALIAN ADENYLYL CYCLASE: COMPLEX WITH 2'(3')-O-(N-METHYLANTHRANILOYL)-GUANOSINE 5'-TRIPHOSPHATE AND MN	LYASE
1TL9	HIGH RESOLUTION CRYSTAL STRUCTURE OF CALPAIN I PROTEASE CORE IN COMPLEX WITH LEUPEPTIN	HYDROLASE
1TLP	RYSTALLOGRAPHIC STRUCTURAL ANALYSIS OF PHOSPHORAMIDATES AS INHIBITORS AND TRANSITION-STATE ANALOGS OF THERMOLYSIN	HYDROLASE (METALLOPROTEINASE)
1TLX	THERMOLYSIN (NATIVE)	HYDROLASE
1TM1	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' WITH CHYMOTRYPSIN INHIBITOR 2	HYDROLASE
1TM3	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' WITH CHYMOTRYPSIN INHIBITOR 2 M59K MUTANT	HYDROLASE

1TM4	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILSIN BPN'WITH CHYMOTRYPSIN INHIBITOR 2 M59G MUTANT	HYDROLASE
1TM5	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' WITH CHYMOTRYPSIN INHIBITOR 2 M59A MUTANT	HYDROLASE/HYDROLASE INHIBIITOR
1TM7	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' WITH CHYMOTRYPSIN INHIBITOR 2 M59Y MUTANT	HYDROLASE
1TMB	MOLECULAR BASIS FOR THE INHIBITION OF HUMAN ALPHA-THROMBIN BY THE MACROCYCLIC PEPTIDE CYCLOTHEONAMIDE A	HYDROLASE(SERINE PROTEINASE)
1TMC	THE THREE-DIMENSIONAL STRUCTURE OF A CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX MOLECULE MISSING THE ALPHA3 DOMAIN OF THE HEAVY CHAIN	HISTOCOMPATIBILITY ANTIGEN
1TMG	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' WITH CHYMOTRYPSIN INHIBITOR 2 M59F MUTANT	HYDROLASE
1TMN	BINDING OF N-CARBOXYMETHYL DIPEPETIDE INHIBITORS TO THERMOLYSIN DETERMINED BY X-RAY CRYSTALLOGRAPHY. A NOVEL CLASS OF TRANSITION-STATE ANALOGUES FOR ZINC PEPTIDASES	HYDROLASE (METALLOPROTEINASE)
1TMQ	STRUCTURE OF TENEBRIO MOLITOR LARVAL ALPHA-AMYLASE IN COMPLEX WITH RAGI BIFUNCTIONAL INHIBITOR	HYDROLASE/HYDROLASE INHIBITOR
1TMT	CHANGES IN INTERACTIONS IN COMPLEXES OF HIRUDIN DERIVATIVES AND HUMAN ALPHA-THROMBIN DUE TO DIFFERENT CRYSTAL FORMS	COMPLEX(SERINE PROTEASE/INHIBITOR)
1TMU	CHANGES IN INTERACTIONS IN COMPLEXES OF HIRUDIN DERIVATIVES AND HUMAN ALPHA-THROMBIN DUE TO DIFFERENT CRYSTAL FORMS	COMPLEX(SERINE PROTEASE/INHIBITOR)
1TN6	PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH A RAP2A PEPTIDE SUBSTRATE AND A FPP ANALOG AT 1.8A RESOLUTION	TRANSFERASE
1TN7	PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH A TC21 PEPTIDE SUBSTRATE AND A FPP ANALOG AT 2.3A RESOLUTION	TRANSFERASE
1TN8	PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH A H-RAS PEPTIDE SUBSTRATE AND A FPP ANALOG AT 2.25A RESOLUTION	TRANSFERASE
1TNB	AT PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A SUBSTRATE KKSKTKCVIF PEPTIDE DERIVED FROM TC21	TRANSFERASE
1TNO	AT PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A KKKSKTKCVIM PEPTIDE DERIVED FROM K-RAS4B	TRANSFERASE
1TNU	AT PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A GCINCCKVL PEPTIDE DERIVED FROM RHOB	TRANSFERASE
1TNY	AT PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A FREKKFFCAIL PEPTIDE DERIVED FROM THE HETEROTRIMERIC G PROTEIN GAMMA-2 SUBUNIT	TRANSFERASE

1TNZ	AT PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A RRCVLL PEPTIDE DERIVED FROM CDC42 SPLICE ISOFORM-2	TRANSFERASE
1TO1	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' WITH CHYMOTRYPSIN INHIBITOR 2 Y61A MUTANT	HYDROLASE
1TO2	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' WITH CHYMOTRYPSIN INHIBITOR 2 M59K, IN PH 9 CRYOSOAK	HYDROLASE
1TO9	CRYSTAL STRUCTURE OF THI-4 PROTEIN FROM BACILLUS SUBTILIS	BIOSYNTHETIC PROTEIN
1TOC	STRUCTURE OF SERINE PROTEINASE	COMPLEX (HYDROLASE/INHIBITOR)
1TOM	ALPHA-THROMBIN COMPLEXED WITH HIRUGEN	COMPLEX (HYDROLASE/INHIBITOR)
1TP3	PDZ3 DOMAIN OF PSD-95 PROTEIN COMPLEXED WITH KKETPV PEPTIDE LIGAND	PROTEIN BINDING
1TP5	CRYSTAL STRUCTURE OF PDZ3 DOMAIN OF PSD-95 PROTEIN COMPLEXED WITH A PEPTIDE LIGAND KKETWV	PEPTIDE BINDING PROTEIN
1TPX	OVINE RECOMBINANT PRP(114-234), ARQ VARIANT IN COMPLEX WITH THE FAB OF THE VRQ14 ANTIBODY	UNKNOWN FUNCTION
1TQ0	CRYSTAL STRUCTURE OF THE POTENT ANTICOAGULANT THROMBIN MUTANT W215A/E217A IN FREE FORM	BLOOD CLOTTING
1TQB	OVINE RECOMBINANT PRP(114-234), VRQ VARIANT IN COMPLEX WITH THE FAB OF THE VRQ14 ANTIBODY	UNKNOWN FUNCTION/IMMUNE SYSTEM
1TQC	OVINE RECOMBINANT PRP(114-234), ARR VARIANT IN COMPLEX WITH THE VRQ14 FAB FRAGMENT (IGG2A)	UNKNOWN FUNCTION/IMMUNE SYSTEM
1TQE	MECHANISM OF RECRUITMENT OF CLASS II HISTONE DEACETYLASES BY MYOCYTE ENHANCER FACTOR-2	TRANSCRIPTION/PROTEIN BINDING/DNA
1TQY	THE ACTINORHODIN KETOSYNTHASE/CHAIN LENGTH FACTOR	TRANSFERASE
1TRZ	CRYSTALLOGRAPHIC EVIDENCE FOR DUAL COORDINATION AROUND ZINC IN THE T3R3 HUMAN INSULIN HEXAMER	HORMONE
1TSQ	CRYSTAL STRUCTURE OF AP2V SUBSTRATE VARIANT OF NC-P1 DECAMER PEPTIDE IN COMPLEX WITH V82A/D25N HIV-1 PROTEASE MUTANT	HYDROLASE/VIRAL PROTEIN
1TSU	CRYSTAL STRUCTURE OF DECAMER NCP1 SUBSTRATE PEPTIDE IN COMPLEX WITH WILD-TYPE D25N HIV-1 PROTEASE VARIANT	VIRAL PROTEIN/HYDROLASE
1TT5	STRUCTURE OF APPBP1-UBA3-UBC12N26: A UNIQUE E1-E2 INTERACTION REQUIRED FOR OPTIMAL CONJUGATION OF THE UBIQUITIN-LIKE PROTEIN NEDD8	CELL CYCLE, LIGASE
1TTH	ASPARTATE TRANSCARBAMOYLASE CATALYTIC CHAIN MUTANT GLU50ALA	HYDROLASE/HYDROLASE REGULATOR

	COMPLEXED WITH N-(PHOSPHONACETYL-L-ASPARTATE) (PALA)	
1TTP	TRYPTOPHAN SYNTHASE (E.C.4.2.1.20) IN THE PRESENCE OF CESIUM, ROOM TEMPERATURE	CARBON-OXYGEN LYASE
1TTQ	TRYPTOPHAN SYNTHASE (E.C.4.2.1.20) IN THE PRESENCE OF POTASSIUM AT ROOM TEMPERATURE	CARBON-OXYGEN LYASE
1TTW	CRYSTAL STRUCTURE OF THE YERSINIA PESTIS TYPE III SECRETION CHAPERONE SYCH IN COMPLEX WITH A STABLE FRAGMENT OF YSCM2	CHAPERONE
1TU0	ASPARTATE TRANSCARBAMOYLASE CATALYTIC CHAIN MUTANT E50A COMPLEX WITH PHOSPHONOACETAMIDE	HYDROLASE/HYDROLASE REGULATOR
1TU3	CRYSTAL STRUCTURE OF RAB5 COMPLEX WITH RABAPTIN5 C-TERMINAL DOMAIN	PROTEIN TRANSPORT
1TUB	TUBULIN ALPHA-BETA DIMER, ELECTRON DIFFRACTION	MICROTUBULES
1TUE	THE X-RAY STRUCTURE OF THE PAPILLOMAVIRUS HELICASE IN COMPLEX WITH ITS MOLECULAR MATCHMAKER E2	REPLICATION
1TUG	ASPARTATE TRANSCARBAMOYLASE CATALYTIC CHAIN MUTANT E50A COMPLEX WITH PHOSPHONOACETAMIDE, MALONATE, AND CYTIDINE-5-PRIME-TRIPHOSPHATE (CTP)	HYDROLASE/HYDROLASE REGULATOR
1TV6	HIV-1 REVERSE TRANSCRIPTASE COMPLEXED WITH CP-94,707	TRANSFERASE
1TVB	CRYSTAL STRUCTURE OF MELANOMA ANTIGEN GP100(209-217) BOUND TO HUMAN CLASS I MHC HLA-A2	IMMUNE SYSTEM
1TVH	CRYSTAL STRUCTURE OF MODIFIED MELANOMA ANTIGEN GP100(209-T2M) BOUND TO HUMAN CLASS I MHC HLA-A2	IMMUNE SYSTEM
1TVK	THE BINDING MODE OF EPOTHILONE A ON A,B-TUBULIN BY ELECTRON CRYSTALLOGRAPHY	CELL CYCLE, STRUCTURAL PROTEIN
1TVR	HIV-1 RT/9-CL TIBO	ASPARTYL PROTEASE
1TW6	STRUCTURE OF AN ML-IAP/XIAP CHIMERA BOUND TO A 9MER PEPTIDE DERIVED FROM SMAC	INHIBITOR/APOPTOSIS
1TWA	RNA POLYMERASE II COMPLEXED WITH ATP	TRANSCRIPTION
1TWC	RNA POLYMERASE II COMPLEXED WITH GTP	TRANSCRIPTION
1TWF	RNA POLYMERASE II COMPLEXED WITH UTP AT 2.3 A RESOLUTION	TRANSCRIPTION
1TWG	RNA POLYMERASE II COMPLEXED WITH CTP	TRANSCRIPTION
1TWH	RNA POLYMERASE II COMPLEXED WITH 2'DATP	TRANSCRIPTION
1TWQ	CRYSTAL STRUCTURE OF THE C-TERMINAL PGN-BINDING DOMAIN OF HUMAN PGRP-IALPHA IN COMPLEX WITH PGN ANALOG MURAMYL TRIPEPTIDE	IMMUNE SYSTEM, MEMBRANE PROTEIN

1TWX	CRYSTAL STRUCTURE OF THE THROMBIN MUTANT D221A/D222K	HYDROLASE
1TX4	RHO/RHOGAP/GDP(DOT)ALF4 COMPLEX	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE)
1TX6	TRYPSIN:BBI COMPLEX	HYDROLASE/PROTEIN BINDING
1TXQ	CRYSTAL STRUCTURE OF THE EB1 C-TERMINAL DOMAIN COMPLEXED WITH THE CAP-GLY DOMAIN OF P150GLUED	STRUCTURAL PROTEIN/PROTEIN BINDING
1TY4	CRYSTAL STRUCTURE OF A CED-9/EGL-1 COMPLEX	APOPTOSIS
1TYE	STRUCTURAL BASIS FOR ALLOSTERY IN INTEGRINS AND BINDING OF LIGAND-MIMETIC THERAPEUTICS TO THE PLATELET RECEPTOR FOR FIBRINOGEN	CELL ADHESION
1TYG	STRUCTURE OF THE THIAZOLE SYNTHASE/THIS COMPLEX	BIOSYNTHETIC PROTEIN
1TYL	THE STRUCTURE OF A COMPLEX OF HEXAMERIC INSULIN AND 4'-HYDROXYACETANILIDE	HORMONE
1TYQ	CRYSTAL STRUCTURE OF ARP2/3 COMPLEX WITH BOUND ATP AND CALCIUM	STRUCTURAL PROTEIN
1TZE	SIGNAL TRANSDUCTION ADAPTOR GROWTH FACTOR, GRB2 SH2 DOMAIN COMPLEXED WITH PHOSPHOTYROSYL HEPTAPEPTIDE LYS-PRO-PHE-PTYR-VAL-ASN-VAL-NH2 (KFPPYVNC-NH2)	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)
1TZG	CRYSTAL STRUCTURE OF HIV-1 NEUTRALIZING HUMAN FAB 4E10 IN COMPLEX WITH A 13-RESIDUE PEPTIDE CONTAINING THE 4E10 EPITOPE ON GP41	IMMUNE SYSTEM
1TZH	CRYSTAL STRUCTURE OF THE FAB YADS1 COMPLEXED WITH H-VEGF	IMMUNE SYSTEM
1TZI	CRYSTAL STRUCTURE OF THE FAB YADS2 COMPLEXED WITH H-VEGF	IMMUNE SYSTEM
1TZY	CRYSTAL STRUCTURE OF THE CORE-HISTONE OCTAMER TO 1.90 ANGSTROM RESOLUTION	DNA BINDING PROTEIN
1U00	HSCA SUBSTRATE BINDING DOMAIN COMPLEXED WITH THE ISCU RECOGNITION PEPTIDE ELPPVKIHC	CHAPERONE
1U0N	THE TERNARY VON WILLEBRAND FACTOR A1-GLYCOPROTEIN IBALPHA-BOTROCETIN COMPLEX	BLOOD CLOTTING
1U0O	THE MOUSE VON WILLEBRAND FACTOR A1-BOTROCETIN COMPLEX	BLOOD CLOTTING
1U0S	CHEMOTAXIS KINASE CHEA P2 DOMAIN IN COMPLEX WITH RESPONSE REGULATOR CHEY FROM THE THERMOPHILE THERMOTOGA MARITIMA	SIGNALING PROTEIN
1U28	R. RUBRUM TRANSHYDROGENASE ASYMMETRIC COMPLEX (DI.NAD+) 2(DIII.NADP+)1	OXIDOREDUCTASE
1U2D	STRUCTRE OF TRANSHYDROGENAES (DI.NADH)2(DIII.NADPH)1 ASYMMETRIC COMPLEX	OXIDOREDUCTASE

1U2G	TRANSHYDROGENASE (DI.ADPR)2(DIII.NADPH)1 ASYMMETRIC COMPLEX	OXIDOREDUCTASE
1U2V	CRYSTAL STRUCTURE OF ARP2/3 COMPLEX WITH BOUND ADP AND CALCIUM	STRUCTURAL PROTEIN
1U35	CRYSTAL STRUCTURE OF THE NUCLEOSOME CORE PARTICLE CONTAINING THE HISTONE DOMAIN OF MACROH2A	STRUCTURAL PROTEIN/DNA
1U3H	CRYSTAL STRUCTURE OF MOUSE TCR 172.10 COMPLEXED WITH MHC CLASS II I-AU MOLECULE AT 2.4 A	IMMUNE SYSTEM
1U3R	RYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH WAY-338	TRANSCRIPTION
1U3S	RYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH WAY-797	TRANSCRIPTION
1U54	CRYSTAL STRUCTURES OF THE PHOSPHORYLATED AND UNPHOSPHORYLATED KINASE DOMAINS OF THE CDC42-ASSOCIATED TYROSINE KINASE ACK1 BOUND TO AMP-PCP	TRANSFERASE
1U5B	RYSTAL STRUCTURE OF THE HUMAN MITOCHONDRIAL BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE	OXIDOREDUCTASE
1U5I	CRYSTAL STRUCTURE ANALYSIS OF RAT M-CALPAIN MUTANT LYS10 THR	HYDROLASE
1U5T	STRUCTURE OF THE ESCRT-II ENDOSOMAL TRAFFICKING COMPLEX	TRANSPORT PROTEIN
1U6A	CRYSTAL STRUCTURE OF THE BROADLY NEUTRALIZING ANTI-HIV FAB F105	IMMUNE SYSTEM
1U6G	CRYSTAL STRUCTURE OF THE CAND1-CUL1-ROC1 COMPLEX	LIGASE
1U6H	VINCULIN HEAD (0-258) IN COMPLEX WITH THE TALIN VINCULIN BINDING SITE 2 (849-879)	CELL ADHESION
1U74	ELECTRON TRANSFER COMPLEX BETWEEN CYTOCHROME C AND CYTOCHROME C PEROXIDASE	OXIDOREDUCTASE
1U75	ECTRON TRANSFER COMPLEX BETWEEN HORSE HEART CYTOCHROME C AND ZINC-PORPHYRIN SUBSTITUTED CYTOCHROME C PEROXIDASE	OXIDOREDUCTASE
1U76	CRYSTAL STRUCTURE OF HPCNA BOUND TO RESIDUES 452-466 OF THE DNA POLYMERASE-DELTA-P66 SUBUNIT	REPLICATION
1U7B	CRYSTAL STRUCTURE OF HPCNA BOUND TO RESIDUES 331-350 OF THE FLAP ENDONUCLEASE-1 (FEN1)	REPLICATION
1U7E	THE CRYSTAL STRUCTURE OF A PROTEIN KINASE A COMPLEX	TRANSFERASE
1U7F	CRYSTAL STRUCTURE OF THE PHOSPHORYLATED SMAD3/SMAD4 HETEROTRIMERIC COMPLEX	SIGNALING PROTEIN
1U7V	CRYSTAL STRUCTURE OF THE PHOSPHORYLATED SMAD2/SMAD4	SIGNALING PROTEIN

	HETEROTRIMERIC COMPLEX	
1U8C	A NOVEL ADAPTATION OF THE INTEGRIN PSI DOMAIN REVEALED FROM ITS CRYSTAL STRUCTURE	CELL ADHESION
1U8G	CRYSTAL STRUCTURE OF A HIV-1 PROTEASE IN COMPLEX WITH PEPTIDOMIMETIC INHIBITOR KI2-PHE-GLU-GLU-NH2	HYDROLASE
1U8H	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE ALDKWAS	IMMUNE SYSTEM
1U8I	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE ELDKWAN	IMMUNE SYSTEM
1U8J	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE ELDKWAG	IMMUNE SYSTEM
1U8K	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE LELDKWASL	IMMUNE SYSTEM
1U8L	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE DLDRWAS	IMMUNE SYSTEM
1U8M	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE ELDKYAS	IMMUNE SYSTEM
1U8N	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE ELDKFAS	IMMUNE SYSTEM
1U8O	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE ELDKHAS	IMMUNE SYSTEM
1U8P	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE ECDKWCS	IMMUNE SYSTEM
1U8Q	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE ELEKWAS	IMMUNE SYSTEM
1U8T	CRYSTAL STRUCTURE OF CHEY D13K Y106W ALONE AND IN COMPLEX WITH A FLIM PEPTIDE	SIGNALING PROTEIN
1U91	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE ANALOG ENDKW-[DAP]-S (CYCLIC)	IMMUNE SYSTEM

1U92	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE ANALOG E-[DAP]-DKWQS (CYCLIC)	IMMUNE SYSTEM
1U93	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE ANALOG EQDKW-[DAP]-S (CYCLIC)	IMMUNE SYSTEM
1U95	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE ELDHWAS	IMMUNE SYSTEM
1U9E	RYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH WAY-397	TRANSCRIPTION
1U9I	CRYSTAL STRUCTURE OF CIRCADIAN CLOCK PROTEIN KAIC WITH PHOSPHORYLATION SITES	CIRCADIAN CLOCK PROTEIN
1U9L	STRUCTURAL BASIS FOR A NUSA- PROTEIN N INTERACTION	RNA BINDING PROTEIN
1UA6	CRYSTAL STRUCTURE OF HYHEL-10 FV MUTANT SFSF COMPLEXED WITH HEN EGG WHITE LYSOZYME COMPLEX	IMMUNE SYSTEM/HYDROLASE
1UAD	CRYSTAL STRUCTURE OF THE RALA-GPPNHP-SEC5 RAL-BINDING DOMAIN COMPLEX	ENDOCYTOSIS/EXOCYTOSIS
1UB4	CRYSTAL STRUCTURE OF MAZEF COMPLEX	DNA BINDING PROTEIN
1UB5	CRYSTAL STRUCTURE OF ANTIBODY 19G2 WITH HAPTEN AT 100K	IMMUNE SYSTEM
1UB6	CRYSTAL STRUCTURE OF ANTIBODY 19G2 WITH SERA LIGAND	IMMUNE SYSTEM
1UBH	HREE-DIMENSIONAL STRUCTURE OF THE CARBON MONOXIDE COMPLEX OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE
1UBJ	HREE-DIMENSIONAL STRUCTURE OF THE CARBON MONOXIDE COMPLEX OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE
1UBK	HREE-DIMENSIONAL STRUCTURE OF THE CARBON MONOXIDE COMPLEX OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE
1UBL	HREE-DIMENSIONAL STRUCTURE OF THE CARBON MONOXIDE COMPLEX OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE
1UBM	HREE-DIMENSIONAL STRUCTURE OF THE CARBON MONOXIDE COMPLEX OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE
1UBO	HREE-DIMENSIONAL STRUCTURE OF THE CARBON MONOXIDE COMPLEX OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE

1UBP	CRYSTAL STRUCTURE OF UREASE FROM BACILLUS PASTEURII INHIBITED WITH BETA-MERCAPTOETHANOL AT 1.65 ANGSTROMS RESOLUTION	HYDROLASE
1UBR	HREE-DIMENSIONAL STRUCTURE OF THE CARBON MONOXIDE COMPLEX OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE
1UBS	TRYPTOPHAN SYNTHASE (E.C.4.2.1.20) WITH A MUTATION OF LYS 87->THR IN THE B SUBUNIT AND IN THE PRESENCE OF LIGAND L-SERINE	COMPLEX (LYASE/PEPTIDE)
1UBT	HREE-DIMENSIONAL STRUCTURE OF THE CARBON MONOXIDE COMPLEX OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE
1UBU	HREE-DIMENSIONAL STRUCTURE OF THE CARBON MONOXIDE COMPLEX OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE
1UC4	STRUCTURE OF DIOL DEHYDRATASE COMPLEXED WITH (S)-1,2-PROPANEDIOL	LYASE
1UC5	STRUCTURE OF DIOL DEHYDRATASE COMPLEXED WITH (R)-1,2-PROPANEDIOL	LYASE
1UCB	STRUCTURE OF UNCOMPLEXED FAB COMPARED TO COMPLEX (1CLY, 1CLZ)	IMMUNOGLOBULIN
1UCY	THROMBIN COMPLEXED WITH FIBRINOPEPTIDE A ALPHA (RESIDUES 7-19). THREE COMPLEXES, ONE WITH EPSILON-THROMBIN AND TWO WITH ALPHA-THROMBIN	COMPLEX (SERINE PROTEASE/COAGULATION)
1UDI	NUCLEOTIDE MIMICRY IN THE CRYSTAL STRUCTURE OF THE URACIL-DNA GLYCOSYLASE-URACIL GLYCOSYLASE INHIBITOR PROTEIN COMPLEX	COMPLEX (HYDROLASE/INHIBITOR)
1UEA	MMP-3/TIMP-1 COMPLEX	COMPLEX (METALLOPROTEASE/INHIBITOR)
1UEF	CRYSTAL STRUCTURE OF DOK1 PTB DOMAIN COMPLEX	PROTEIN BINDING/TRANSFERASE
1UEX	CRYSTAL STRUCTURE OF VON WILLEBRAND FACTOR A1 DOMAIN COMPLEXED WITH SNAKE VENOM BITISCETIN	TOXIN/BLOOD CLOTTING
1UF2	THE ATOMIC STRUCTURE OF RICE DWARF VIRUS (RDV)	VIRUS
1UGH	CRYSTAL STRUCTURE OF HUMAN URACIL-DNA GLYCOSYLASE IN COMPLEX WITH A PROTEIN INHIBITOR: PROTEIN MIMICRY OF DNA	GLYCOSYLASE
1UGP	CRYSTAL STRUCTURE OF CO-TYPE NITRILE HYDRATASE COMPLEXED WITH N-BUTYRIC ACID	LYASE
1UGQ	CRYSTAL STRUCTURE OF APOENZYME OF CO-TYPE NITRILE HYDRATASE	LYASE

1UGR	CRYSTAL STRUCTURE OF AT109S MUTANT OF CO-TYPE NITRILE HYDRATASE	LYASE
1UGS	CRYSTAL STRUCTURE OF AY114T MUTANT OF CO-TYPE NITRILE HYDRATASE	LYASE
1UHB	CRYSTAL STRUCTURE OF PORCINE ALPHA TRYPSIN BOUND WITH AUTO CATALYTICALY PRODUCED NATIVE PEPTIDE AT 2.15 A RESOLUTION	HYDROLASE
1UHD	CRYSTAL STRUCTURE OF ASPARTATE DECARBOXYLASE, PYRUVOLY GROUP BOUND FORM	LYASE
1UHE	CRYSTAL STRUCTURE OF ASPARTATE DECARBOXYLASE, ISOASPARGINE COMPLEX	LYASE
1UHL	CRYSTAL STRUCTURE OF THE LXRALFA-RXRBETA LBD HETERODIMER	DNA BINDING PROTEIN
1UIW	CRYSTAL STRUCTURES OF UNLIGANDED AND HALF-LIGANDED HUMAN HEMOGLOBIN DERIVATIVES CROSS-LINKED BETWEEN LYS 82BETA1 AND LYS 82BETA2	OXYGEN STORAGE/TRANSPORT
1UJ3	CRYSTAL STRUCTURE OF A HUMANIZED FAB FRAGMENT OF ANTI-TISSUE-FACTOR ANTIBODY IN COMPLEX WITH TISSUE FACTOR	IMMUNE SYSTEM/BLOOD CLOTTING
1UJJ	VHS DOMAIN OF HUMAN GGA1 COMPLEXED WITH C-TERMINAL PEPTIDE FROM BACE	PROTEIN TRANSPORT/HYDROLASE
1UJK	VHS DOMAIN OF HUMAN GGA1 COMPLEXED WITH C-TERMINAL PHOSPHOPEPTIDE FROM BACE	PROTEIN TRANSPORT/HYDROLASE
1UJW	STRUCTURE OF THE COMPLEX BETWEEN BTUB AND COLICIN E3 RECEPTOR BINDING DOMAIN	TRANSPORT PROTEIN/HYDROLASE
1UJZ	CRYSTAL STRUCTURE OF THE E7_C/IM7_C COMPLEX; A COMPUTATIONALLY DESIGNED INTERFACE BETWEEN THE COLICIN E7 DNASE AND THE IM7 IMMUNITY PROTEIN	IMMUNE SYSTEM
1UK4	CRYSTAL STRUCTURE OF SARS CORONAVIRUS MAIN PROTEINASE (3CLPRO) COMPLEXED WITH AN INHIBITOR	HYDROLASE
1UKH	STRUCTURAL BASIS FOR THE SELECTIVE INHIBITION OF JNK1 BY THE SCAFFOLDING PROTEIN JIP1 AND SP600125	TRANSFERASE
1UKI	STRUCTURAL BASIS FOR THE SELECTIVE INHIBITION OF JNK1 BY THE SCAFFOLDING PROTEIN JIP1 AND SP600125	TRANSFERASE
1UKL	CRYSTAL STRUCTURE OF IMPORTIN-BETA AND SREBP-2 COMPLEX	PROTEIN TRANSPORT/DNA BINDING PROTEIN
1UKM	CRYSTAL STRUCTURE OF EMS16, AN ANTAGONIST OF COLLAGEN RECEPTOR INTEGRIN ALPHA2BETA1 (GPIA/IIA)	TOXIN
1UKV	STRUCTURE OF RABGDP-DISSOCIATION INHIBITOR IN COMPLEX WITH PRENYLATED YPT1 GTPASE	PROTEIN TRANSPORT
1UL1	CRYSTAL STRUCTURE OF THE HUMAN FEN1-PCNA COMPLEX	HYDROLASE/DNA BINDING PROTEIN

1ULI	BIPHENYL DIOXYGENASE (BPHA1A2) DERIVED FROM RHODOCOCCUS SP. STRAIN RHA1	OXIDOREDUCTASE
1ULJ	BIPHENYL DIOXYGENASE (BPHA1A2) IN COMPLEX WITH THE SUBSTRATE	OXIDOREDUCTASE
1UM2	CRYSTAL STRUCTURE OF THE VMA1-DERIVED ENDONUCLEASE WITH THE LIGATED EXTEIN SEGMENT	HYDROLASE
1UM4	CATALYTIC ANTIBODY 21H3 WITH HAPTEN	IMMUNE SYSTEM
1UM5	CATALYTIC ANTIBODY 21H3 WITH ALCOHOL SUBSTRATE	IMMUNE SYSTEM
1UM6	CATALYTIC ANTIBODY 21H3	IMMUNE SYSTEM
1UM9	BRANCHED-CHAIN 2-OXO ACID DEHYDROGENASE (E1) FROM THERMUS THERMOPHILUS HB8 IN APO-FORM	OXIDOREDUCTASE
1UMB	BRANCHED-CHAIN 2-OXO ACID DEHYDROGENASE (E1) FROM THERMUS THERMOPHILUS HB8 IN HOLO-FORM	OXIDOREDUCTASE
1UMC	BRANCHED-CHAIN 2-OXO ACID DEHYDROGENASE (E1) FROM THERMUS THERMOPHILUS HB8 WITH 4-METHYLPENTANOATE	OXIDOREDUCTASE
1UMD	BRANCHED-CHAIN 2-OXO ACID DEHYDROGENASE (E1) FROM THERMUS THERMOPHILUS HB8 WITH 4-METHYL-2-OXOPENTANOATE AS AN INTERMEDIATE	OXIDOREDUCTASE
1UMR	CRYSTAL STRUCTURE OF THE PLATELET ACTIVATOR CONVULXIN, A DISULFIDE LINKED A4B4 CYCLIC TETRAMER FROM THE VENOM OF CROTALUS DURISSUS TERRIFICUS	LECTIN
1UMW	STRUCTURE OF A HUMAN PLK1 POLO-BOX DOMAIN/PHOSPHOPEPTIDE COMPLEX	KINASE
1UMX	PHOTOSYNTHETIC REACTION CENTER MUTANT WITH ARG M267 REPLACED WITH LEU (CHAIN M, R267L)	PHOTOSYNTHETIC REACTION CENTER
1UN0	CRYSTAL STRUCTURE OF YEAST KARYOPHERIN (IMPORTIN) ALPHA IN COMPLEX WITH A NUP2P N-TERMINAL FRAGMENT	NUCLEAR IMPORT
1UNN	COMPLEX OF BETA-CLAMP PROCESSIVITY FACTOR AND LITTLE FINGER DOMAIN OF POLIV	BETA-CLAMP
1UOO	PROLYL OLIGOPEPTIDASE FROM PORCINE BRAIN, S554A MUTANT WITH BOUND PEPTIDE LIGAND GLY-PHE-ARG-PRO	HYDROLASE
1UOP	PROLYL OLIGOPEPTIDASE FROM PORCINE BRAIN, S554A MUTANT WITH BOUND PEPTIDE LIGAND GLY-PHE-GLU-PRO	HYDROLASE
1UOQ	PROLYL OLIGOPEPTIDASE FROM PORCINE BRAIN, S554A MUTANT WITH BOUND PEPTIDE LIGAND GLU-PHE-SER-PRO	HYDROLASE
1UOS	THE CRYSTAL STRUCTURE OF THE SNAKE VENOM TOXIN CONVULXIN	LECTIN

1UPK	CRYSTAL STRUCTURE OF MO25 IN COMPLEX WITH A C-TERMINAL PEPTIDE OF STRAD	TRANSFERASE
1UPM	ACTIVATED SPINACH RUBISCO COMPLEXED WITH 2-CARBOXYARABINITOL 2 BISPHOSPHAT AND CA2+.	LYASE
1UPN	COMPLEX OF ECHOVIRUS TYPE 12 WITH DOMAINS 3 AND 4 OF ITS RECEPTOR DECAY ACCELERATING FACTOR (CD55) BY CRYO ELECTRON MICROSCOPY AT 16 A	VIRUS/RECEPTOR
1UPP	SPINACH RUBISCO IN COMPLEX WITH 2-CARBOXYARABINITOL 2 BISPHOSPHATE AND CALCIUM.	LYASE
1UPT	STRUCTURE OF A COMPLEX OF THE GOLGIN-245 GRIP DOMAIN WITH ARL1	COMPLEX (GTPASE/GOLGIN)
1URC	CYCLIN A BINDING GROOVE INHIBITOR ACE-ARG-LYS-LEU-PHE-GLY	KINASE
1URQ	CRYSTAL STRUCTURE OF NEURONAL Q-SNARES IN COMPLEX WITH R-SNARE MOTIF OF TOMOSYN	TRANSPORT PROTEIN
1US8	THE RAD50 SIGNATURE MOTIF: ESSENTIAL TO ATP BINDING AND BIOLOGICAL FUNCTION	DNA REPAIR
1USP	ORGANIC HYDROPEROXIDE RESISTANCE PROTEIN FROM DEINOCOCCUS RADIODURANS	OXIDOREDUCTASE
1USU	THE STRUCTURE OF THE COMPLEX BETWEEN AHA1 AND HSP90	CHAPERONE/COMPLEX
1USV	THE STRUCTURE OF THE COMPLEX BETWEEN AHA1 AND HSP90	CHAPERONE/COMPLEX
1USY	ATP PHOSPHORIBOSYL TRANSFERASE (HISG:HISZ) COMPLEX FROM THERMOTOGA MARITIMA	TRANSFERASE
1UTB	DNTR FROM BURKHOLDERIA SP. STRAIN DNT	TRANSCRIPTION REGULATION
1UTH	DNTR FROM BURKHOLDERIA SP. STRAIN DNT IN COMPLEX WITH THIOCYANATE	TRANSCRIPTION REGULATION
1UUG	ESCHERICHIA COLI URACIL-DNA GLYCOSYLASE:INHIBITOR COMPLEX WITH WILD-TYPE UDG AND WILD-TYPE UGI	REPLICATION, HYDROLASE
1UUV	NAPHTHALENE 1,2-DIOXYGENASE WITH NITRIC OXIDE AND INDOLE BOUND IN THE ACTIVE SITE.	OXIDOREDUCTASE
1UUW	NAPHTHALENE 1,2-DIOXYGENASE WITH NITRIC OXIDE BOUND IN THE ACTIVE SITE.	OXIDOREDUCTASE
1UUZ	IVY:A NEW FAMILY OF PROTEIN	LYSOZYME/INHIBITOR COMPLEX
1UVQ	CRYSTAL STRUCTURE OF HLA-DQ0602 IN COMPLEX WITH A HYPOCRETIN PEPTIDE	IMMUNOLOGY
1UVS	BOVINE THROMBIN--BM51.1011 COMPLEX	SERINE PROTEASE

1UVT	BOVINE THROMBIN--BM14.1248 COMPLEX	SERINE PROTEASE
1UVU	BOVINE THROMBIN--BM12.1700 COMPLEX	SERINE PROTEASE
1UW4	THE STRUCTURAL BASIS OF THE INTERACTION BETWEEN NONSENSE MEDIATED DECAY FACTORS UPF2 AND UPF3	RNA-BINDING PROTEIN
1UW9	L290F-A222T CHLAMYDOMONAS RUBISCO MUTANT	LYASE
1UWA	L290F MUTANT RUBISCO FROM CHLAMYDOMONAS	LYASE
1UWB	TYR 181 CYS HIV-1 RT/8-CL TIBO	ASPARTYL PROTEASE
1UWE	OLECULAR MECHANISM OF ENANTIOSELECTIVE PROTON TRANSFER TO CARBON IN CATALYTIC ANTIBODY 14D9	ANTIBODY
1UWX	P1.2 SEROSUBTYPE ANTIGEN DERIVED FROM N. MENINGITIDIS PORA IN COMPLEX WITH FAB FRAGMENT	ANTIBODY/COMPLEX
1UXS	CRYSTAL STRUCTURE OF HLA-B*2705 COMPLEXED WITH THE LATENT MEMBRANE PROTEIN 2 PEPTIDE (LMP2)OF EPSTEIN-BARR VIRUS	COMPLEX (HLA/PEPTIDE)
1UXW	CRYSTAL STRUCTURE OF HLA-B*2709 COMPLEXED WITH THE LATENT MEMBRANE PROTEIN 2 PEPTIDE (LMP2) OF EPSTEIN-BARR VIRUS	COMPLEX (ANTIGEN/PEPTIDE)
1UYW	CRYSTAL STRUCTURE OF THE ANTIFLAVIVIRUS FAB4G2	IMMUNE SYSTEM
1UZ6	ANTI-LEWIS X FAB FRAGMENT UNCOMPLEXED	ANTIBODY/COMPLEX
1UZ8	ANTI-LEWIS X FAB FRAGMENT IN COMPLEX WITH LEWIS X	ANTIBODY/COMPLEX
1UZ9	CRYSTALLOGRAPHIC AND SOLUTION STUDIES OF N-LITHOCHOLYL INSULIN: A NEW GENERATION OF PROLONGED-ACTING INSULINS.	INSULIN
1UZD	CHLAMYDOMONAS,SPINACH CHIMERIC RUBISCO	LYASE
1UZH	CHIMERIC CHLAMYDOMONAS, SYNECHOCOCCUS RUBISCO ENZYME	LYASE
1V02	CRYSTAL STRUCTURE OF THE SORGHUM BICOLOR DHURRINASE 1	HYDROLASE
1V11	ROSSTALK BETWEEN COFACTOR BINDING AND THE PHOSPHORYLATION LOOP CONFORMATION IN THE BCKD MACHINE	OXIDOREDUCTASE
1V16	ROSSTALK BETWEEN COFACTOR BINDING AND THE PHOSPHORYLATION LOOP CONFORMATION IN THE BCKD MACHINE	OXIDOREDUCTASE
1V18	THE CRYSTAL STRUCTURE OF BETA-CATENIN ARMADILLO REPEAT COMPLEXED WITH A PHOSPHORYLATED APC 20MER REPEAT.	SIGNALLING COMPLEX
1V1M	ROSSTALK BETWEEN COFACTOR BINDING AND THE PHOSPHORYLATION LOOP CONFORMATION IN THE BCKD MACHINE	OXIDOREDUCTASE
1V1R	ROSSTALK BETWEEN COFACTOR BINDING AND THE PHOSPHORYLATION LOOP CONFORMATION IN THE BCKD MACHINE	OXIDOREDUCTASE

1V1T	CRYSTAL STRUCTURE OF THE PDZ TANDEM OF HUMAN SYNTENIN IN COMPLEX WITH TNEYKV PEPTIDE	ADHESION/COMPLEX
1V29	CRYSTAL STRUCTURE OF NITRILE HYDRATASE FROM A THERMOPHILE BACILLUS SMITHII	LYASE
1V3X	FACTOR XA IN COMPLEX WITH THE INHIBITOR 1-[6-METHYL-4,5,6,7-TETRAHYDROTHIAZOLO(5,4-C)PYRIDIN-2-YL] CARBONYL-2-CARBAMOYL-4-(6-CHLORONAPHTH-2-YLSULPHONYL)PIPERAZINE	HYDROLASE
1V4L	CRYSTAL STRUCTURE OF A PLATELET AGGLUTINATION FACTOR ISOLATED FROM THE VENOM OF TAIWAN HABU (TRIMERESURUS MUCROSQUAMATUS)	BLOOD CLOTTING
1V4U	RYSTAL STRUCTURE OF BLUEFIN TUNA CARBONMONOXY-HEMOGLOBIN	OXYGEN STORAGE/TRANSPORT
1V4W	CRYSTAL STRUCTURE OF BLUEFIN TUNA HEMOGLOBIN DEOXY FORM AT PH7.5	OXYGEN STORAGE/TRANSPORT
1V4X	CRYSTAL STRUCTURE OF BLUEFIN TUNA HEMOGLOBIN DEOXY FORM AT PH5.0	OXYGEN STORAGE/TRANSPORT
1V54	BOVINE HEART CYTOCHROME C OXIDASE AT THE FULLY OXIDIZED STATE	OXIDOREDUCTASE
1V55	BOVINE HEART CYTOCHROME C OXIDASE AT THE FULLY REDUCED STATE	OXIDOREDUCTASE
1V5I	CRYSTAL STRUCTURE OF SERINE PROTEASE INHIBITOR POIA1 IN COMPLEX WITH SUBTILISIN BPN'	HYDROLASE/PROTEIN BINDING
1V74	RIBONUCLEASE-INHIBITOR COMPLEX	ANTIBIOTIC/IMMUNE SYSTEM
1V75	CRYSTAL STRUCTURE OF HEMOGLOBIN D FROM THE ALDABRA GIANT TORTOISE (GEOCHELONE GIGANTEA) AT 2.0 A RESOLUTION	OXYGEN STORAGE/TRANSPORT
1V7M	HUMAN THROMBOPOIETIN FUNCTIONAL DOMAIN COMPLEXED TO NEUTRALIZING ANTIBODY TN1 FAB	IMMUNE SYSTEM/CYTOKINE
1V7N	HUMAN THROMBOPOIETIN FUNCTIONAL DOMAIN COMPLEXED TO NEUTRALIZING ANTIBODY TN1 FAB	IMMUNE SYSTEM/CYTOKINE
1V7P	STRUCTURE OF EMS16-ALPHA2-I DOMAIN COMPLEX	TOXIN/CELL ADHESION
1V9T	STRUCTURE OF E. COLI CYCLOPHILIN B K163T MUTANT BOUND TO SUCCINYL-ALA-PRO-ALA-P-NITROANILIDE	ISOMERASE
1VAC	MHC CLASS I H-2KB HEAVY CHAIN COMPLEXED WITH BETA-2 MICROGLOBULIN AND CHICKEN OVALBUMIN	COMPLEX (MHC I/PEPTIDE)
1VAD	MHC CLASS I H-2KB HEAVY CHAIN COMPLEXED WITH BETA-2 MICROGLOBULIN AND YEAST ALPHA-GLUCOSIDASE	COMPLEX (MHC I/PEPTIDE)
1VC3	CRYSTAL STRUCTURE OF L-ASPARTATE-ALPHA-DECARBOXYLASE	LYASE
1VCB	THE VHL-ELONGINC-ELONGINB STRUCTURE	TRANSCRIPTION

1VET	CRYSTAL STRUCTURE OF P14/MP1 AT 1.9 A RESOLUTION	SIGNALING PROTEIN/PROTEIN BINDING
1VEU	CRYSTAL STRUCTURE OF THE P14/MP1 COMPLEX AT 2.15 A RESOLUTION	SIGNALING PROTEIN/PROTEIN BINDING
1VF5	CRYSTAL STRUCTURE OF CYTOCHROME B6F COMPLEX FROM M.LAMINOSUS	PHOTOSYNTHESIS
1VF6	2.1 ANGSTROM CRYSTAL STRUCTURE OF THE PALS-1-L27N AND PATJ L27 HETERODIMER COMPLEX	PROTEIN BINDING/PROTEIN TRANSPORT
1VFB	BOUND WATER MOLECULES AND CONFORMATIONAL STABILIZATION HELP MEDIATE AN ANTIGEN-ANTIBODY ASSOCIATION	IMMUNOGLOBULIN/HYDROLASE(O-GLYCOSYL)
1VG0	THE CRYSTAL STRUCTURES OF THE REP-1 PROTEIN IN COMPLEX WITH MONOPRENYLATED RAB7 PROTEIN	PROTEIN BINDING/PROTEIN TRANSPORT
1VG9	THE CRYSTAL STRUCTURES OF THE REP-1 PROTEIN IN COMPLEX WITH C-TERMINALLY TRUNCATED RAB7 PROTEIN	PROTEIN BINDING/PROTEIN TRANSPORT
1VGC	GAMMA-CHYMOTRYPSIN L-PARA-CHLORO-1-ACETAMIDO BORONIC ACID INHIBITOR COMPLEX	SERINE PROTEASE
1VGE	TR1.9 FAB FRAGMENT OF A HUMAN IGG1 KAPPA AUTOANTIBODY	IMMUNOGLOBULIN
1VGK	THE CRYSTAL STRUCTURE OF CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX, H-2KD AT 2.0 A RESOLUTION	IMMUNE SYSTEM
1VIT	THROMBIN:HIRUDIN 51-65 COMPLEX	COMPLEX (SERINE PROTEASE/INHIBITOR)
1VIW	TENEBRIO MOLITOR ALPHA-AMYLASE-INHIBITOR COMPLEX	COMPLEX (GLYCOSIDASE/INHIBITOR)
1VLD	CRYSTAL STRUCTURE OF PYROGALLOL-PHLOROGLUCINOL TRANSHYDROXYLASE FROM PELOBACTER ACIDIGALLICI	OXIDOREDUCTASE
1VLE	CRYSTAL STRUCTURE OF PYROGALLOL-PHLOROGLUCINOL TRANSHYDROXYLASE FROM PELOBACTER ACIDIGALLICI COMPLEXED WITH PYROGALLOL	OXIDOREDUCTASE
1VLF	CRYSTAL STRUCTURE OF PYROGALLOL-PHLOROGLUCINOL TRANSHYDROXYLASE FROM PELOBACTER ACIDIGALLICI COMPLEXED WITH INHIBITOR 1,2,4,5-TETRAHYDROXY-BENZENE	OXIDOREDUCTASE
1VOQ	CRYSTAL STRUCTURE OF FIVE 70S RIBOSOMES FROM ESCHERICHIA COLI IN COMPLEX WITH PROTEIN Y. THIS FILE CONTAINS THE 30S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS FIVE 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
1VOS	CRYSTAL STRUCTURE OF FIVE 70S RIBOSOMES FROM ESCHERICHIA COLI IN COMPLEX WITH PROTEIN Y. THIS FILE CONTAINS THE 30S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS FIVE 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
1VOU	CRYSTAL STRUCTURE OF FIVE 70S RIBOSOMES FROM ESCHERICHIA COLI IN COMPLEX WITH PROTEIN Y. THIS FILE CONTAINS THE 50S	RIBOSOME

	SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS FIVE 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	
1VOV	CRYSTAL STRUCTURE OF FIVE 70S RIBOSOMES FROM ESCHERICHIA COLI IN COMPLEX WITH PROTEIN Y. THIS FILE CONTAINS THE 30S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS FIVE 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
1VOW	CRYSTAL STRUCTURE OF FIVE 70S RIBOSOMES FROM ESCHERICHIA COLI IN COMPLEX WITH PROTEIN Y. THIS FILE CONTAINS THE 50S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS FIVE 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
1VOX	CRYSTAL STRUCTURE OF FIVE 70S RIBOSOMES FROM ESCHERICHIA COLI IN COMPLEX WITH PROTEIN Y. THIS FILE CONTAINS THE 30S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS FIVE 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
1VOY	CRYSTAL STRUCTURE OF FIVE 70S RIBOSOMES FROM ESCHERICHIA COLI IN COMPLEX WITH PROTEIN Y. THIS FILE CONTAINS THE 50S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS FIVE 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
1VOZ	CRYSTAL STRUCTURE OF FIVE 70S RIBOSOMES FROM ESCHERICHIA COLI IN COMPLEX WITH PROTEIN Y. THIS FILE CONTAINS THE 30S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS FIVE 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
1VP0	CRYSTAL STRUCTURE OF FIVE 70S RIBOSOMES FROM ESCHERICHIA COLI IN COMPLEX WITH PROTEIN Y. THIS FILE CONTAINS THE 50S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS FIVE 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
1VPO	CRYSTAL STRUCTURE ANALYSIS OF THE ANTI-TESTOSTERONE FAB IN COMPLEX WITH TESTOSTERONE	IMMUNE SYSTEM
1VPP	COMPLEX BETWEEN VEGF AND A RECEPTOR BLOCKING PEPTIDE	GROWTH FACTOR/GROWTH FACTOR INHIBITOR
1VQ4	THE STRUCTURE OF THE TRANSITION STATE ANALOGUE "DAA" BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1VQ5	THE STRUCTURE OF THE TRANSITION STATE ANALOGUE "RAA" BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1VQ6	THE STRUCTURE OF C-HPMN AND CCA-PHE-CAP-BIO BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1VQ7	THE STRUCTURE OF THE TRANSITION STATE ANALOGUE "DCA" BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1VQ8	THE STRUCTURE OF CCDA-PHE-CAP-BIO AND THE ANTIBIOTIC SPARSOMYCIN BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1VQ9	THE STRUCTURE OF CCA-PHE-CAP-BIO AND THE ANTIBIOTIC	RIBOSOME

	SPARSOMYCIN BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	
1VQK	THE STRUCTURE OF CCDA-PHE-CAP-BIO BOUND TO THE A SITE OF THE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1VQL	THE STRUCTURE OF THE TRANSITION STATE ANALOGUE "DCSN" BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1VQM	THE STRUCTURE OF THE TRANSITION STATE ANALOGUE "DAN" BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1VQN	THE STRUCTURE OF CC-HPMN AND CCA-PHE-CAP-BIO BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1VQO	HE STRUCTURE OF CCPMN BOUND TO THE LARGE RIBOSOMAL SUBUNIT HALOARCULA MARISMORTUI	RIBOSOME
1VQP	THE STRUCTURE OF THE TRANSITION STATE ANALOGUE "RAP" BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1VRA	CRYSTAL STRUCTURE OF ARGININE BIOSYNTHESIS BIFUNCTIONAL PROTEIN ARGJ (10175521) FROM BACILLUS HALODURANS AT 2.00 A RESOLUTION	TRANSFERASE
1VRK	THE 1.9 ANGSTROM STRUCTURE OF E84K-CALMODULIN RS20 PEPTIDE COMPLEX	COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1VRQ	CRYSTAL STRUCTURE OF HETEROTETRAMERIC SARCOSINE OXIDASE FROM CORYNEBACTERIUM SP. U-96 IN COMPLEX WITH FOLINIC ACID	OXIDOREDUCTASE
1VRS	CRYSTAL STRUCTURE OF THE DISULFIDE-LINKED COMPLEX BETWEEN THE N-TERMINAL AND C-TERMINAL DOMAIN OF THE ELECTRON TRANSFER CATALYST DSBD	OXIDOREDUCTASE
1VRT	HIGH RESOLUTION STRUCTURES OF HIV-1 RT FROM FOUR RT-INHIBITOR COMPLEXES	NUCLEOTIDYLTRANSFERASE
1VRU	HIGH RESOLUTION STRUCTURES OF HIV-1 RT FROM FOUR RT-INHIBITOR COMPLEXES	NUCLEOTIDYLTRANSFERASE
1VS5	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH THE ANTIBIOTIC KASUGAMYIN AT 3.5A RESOLUTION. THIS FILE CONTAINS THE 30S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
1VS6	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH THE ANTIBIOTIC KASUGAMYIN AT 3.5A RESOLUTION. THIS FILE CONTAINS THE 50S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
1VS7	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH THE ANTIBIOTIC KASUGAMYIN	RIBOSOME

	AT 3.5A RESOLUTION. THIS FILE CONTAINS THE 30S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	
1VS8	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH THE ANTIBIOTIC KASUGAMYIN AT 3.5A RESOLUTION. THIS FILE CONTAINS THE 30S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
1VSA	CRYSTAL STRUCTURE OF A 70S RIBOSOME-TRNA COMPLEX REVEALS FUNCTIONAL INTERACTIONS AND REARRANGEMENTS. THIS FILE, 1VSA, CONTAINS THE 50S RIBOSOME SUBUNIT. 30S RIBOSOME SUBUNIT IS IN THE FILE 2OW8	RIBOSOME
1VSQ	SOLUTION NMR STRUCTURE OF THE PRODUCTIVE COMPLEX BETWEEN IIAMANNOSE AND IIBMANNOSE OF THE MANNOSE TRANSPORTER OF THE E. COLI PHOSPHOTRANSFERASE SYSTEM	TRANSFERASE
1VWT	T STATE HUMAN HEMOGLOBIN [ALPHA V96W], ALPHA AQUOMET, BETA DEOXY	OXYGEN TRANSPORT
1VYH	PAF-AH HOLOENZYME: LIS1/ALFA2	HYDROLASE
1VYJ	STRUCTURAL AND BIOCHEMICAL STUDIES OF HUMAN PCNA COMPLEXES PROVIDE THE BASIS FOR ASSOCIATION WITH CDK/CYCLIN AND RATIONALE FOR INHIBITOR DESIGN	DNA-BINDING PROTEIN
1VYT	BETA3 SUBUNIT COMPLEXED WITH AID	ION TRANSPORT/COMPLEX
1VYW	STRUCTURE OF CDK2/CYCLIN A WITH PNU-292137	PROTEIN KINASE/COMPLEX
1VZJ	STRUCTURE OF THE TETRAMERIZATION DOMAIN OF ACETYLCHOLINESTERASE: FOUR-FOLD INTERACTION OF A WWW MOTIF WITH A LEFT-HANDED POLYPROLINE HELIX	HYDROLASE
1VZQ	COMPLEX OF THROMBIN WITH DESIGNED INHIBITOR 7165	HYDROLASE
1W0J	BERYLLIUM FLUORIDE INHIBITED BOVINE F1-ATPASE	HYDROLASE
1W0K	BERYLLIUM FLUORIDE INHIBITED BOVINE F1-ATPASE	HYDROLASE
1W0V	CRYSTAL STRUCTURE OF HLA-B*2705 COMPLEXED WITH THE SELF-PEPTIDE TIS FROM EGF-RESPONSE FACTOR 1	IMMUNE SYSTEM
1W0W	CRYSTAL STRUCTURE OF HLA-B*2709 COMPLEXED WITH THE SELF-PEPTIDE TIS FROM EGF-RESPONSE FACTOR 1	IMMUNE SYSTEM
1W0Y	TF7A_3771 COMPLEX	HYDROLASE
1W1I	CRYSTAL STRUCTURE OF DIPEPTIDYL PEPTIDASE IV (DPPIV OR CD26) IN COMPLEX WITH ADENOSINE DEAMINASE	HYDROLASE/COMPLEX
1W2B	TRIGGER FACTOR RIBOSOME BINDING DOMAIN IN COMPLEX WITH 50S	RIBOSOME

1W2K	TF7A_4380 COMPLEX	HYDROLASE
1W2W	CRYSTAL STRUCTURE OF YEAST YPR118W, A METHYLTHIORIBOSE-1-PHOSPHATE ISOMERASE RELATED TO REGULATORY EIF2B SUBUNITS	ISOMERASE
1W3C	CRYSTAL STRUCTURE OF THE HEPATITIS C VIRUS NS3 PROTEASE IN COMPLEX WITH A PEPTIDOMIMETIC INHIBITOR	HYDROLASE
1W5C	PHOTOSYSTEM II FROM THERMOSYNECHOCOCCUS ELONGATUS	PHOTOSYNTHESIS
1W72	CRYSTAL STRUCTURE OF HLA-A1:MAGE-A1 IN COMPLEX WITH FAB-HYB3	COMPLEX, HLA/FAB FRAGMENT
1W7I	CRYSTAL STRUCTURE OF MYOSIN V MOTOR WITHOUT NUCLEOTIDE SOAKED IN 10 MM MGADP	MOTOR PROTEIN
1W7J	CRYSTAL STRUCTURE OF MYOSIN V MOTOR WITH ESSENTIAL LIGHT CHAIN + ADP-BEFX- NEAR RIGOR	MOTOR PROTEIN
1W7P	THE CRYSTAL STRUCTURE OF ENDOSOMAL COMPLEX ESCRT-II (VPS22/VPS25/VPS36)	PROTEIN TRANSPORT
1W7V	ZNMG SUBSTITUTED AMINOPEPTIDASE P FROM E. COLI	HYDROLASE
1W7X	FACTOR7- 413 COMPLEX	HYDROLASE
1W80	CRYSTAL STRUCTURE OF THE ALPHA-ADAPTIN APPENDAGE DOMAIN, FROM THE AP2 ADAPTOR COMPLEX, BOUND TO 2 PEPTIDES FROM SYNAPTOJANIN170	ENDOCYTOSIS/EXOCYTOSIS
1W85	HE CRYSTAL STRUCTURE OF PYRUVATE DEHYDROGENASE E1 BOUND TO THE PERIPHERAL SUBUNIT BINDING DOMAIN OF E2	OXIDOREDUCTASE
1W88	THE CRYSTAL STRUCTURE OF PYRUVATE DEHYDROGENASE E1(D180N, E183Q) BOUND TO THE PERIPHERAL SUBUNIT BINDING DOMAIN OF E2	OXIDOREDUCTASE
1W8P	STRUCTURAL PROPERTIES OF THE B25TYR-NME-B26PHE INSULIN MUTANT.	HORMONE/GROWTH FACTOR
1W8X	STRUCTURAL ANALYSIS OF PRD1	VIRUS
1W98	THE STRUCTURAL BASIS OF CDK2 ACTIVATION BY CYCLIN E	TRANSFERASE
1W9E	CRYSTAL STRUCTURE OF THE PDZ TANDEM OF HUMAN SYNTENIN IN COMPLEX WITH TNEFYF PEPTIDE	ADHESION/COMPLEX
1W9O	CRYSTAL STRUCTURE OF THE PDZ TANDEM OF HUMAN SYNTENIN IN COMPLEX WITH TNEYYV PEPTIDE	ADHESION/COMPLEX
1W9Q	CRYSTAL STRUCTURE OF THE PDZ TANDEM OF HUMAN SYNTENIN IN COMPLEX WITH TNEFAF PEPTIDE	ADHESION/COMPLEX
1WA8	SOLUTION STRUCTURE OF THE CFP-10.ESAT-6 COMPLEX. MAJOR VIRULENCE DETERMINANTS OF PATHOGENIC MYCOBACTERIA	TUBERCULOSIS
1WAV	CRYSTAL STRUCTURE OF FORM B MONOCLINIC CRYSTAL OF INSULIN	HORMONE

1WAY	ACTIVE SITE THROMBIN INHIBITORS	HYDROLASE
1WBG	ACTIVE SITE THROMBIN INHIBITORS	COMPLEX (BLOOD COAGULATION/INHIBITOR)
1WBJ	WILDTYPE TRYPTOPHAN SYNTHASE COMPLEXED WITH GLYCEROL PHOSPHATE	LYASE
1WBP	SRPK1 BOUND TO 9MER DOCKING MOTIF PEPTIDE	TRANSFERASE
1WBX	CRYSTAL STRUCTURES OF MURINE MHC CLASS I H-2 DB AND KB MOLECULES IN COMPLEX WITH CTL EPITOPES FROM INFLUENZA A VIRUS: IMPLICATIONS FOR TCR REPERTOIRE SELECTION AND IMMUNODOMINANCE	IMMUNE SYSTEM
1WBY	CRYSTAL STRUCTURES OF MURINE MHC CLASS I H-2 DB AND KB MOLECULES IN COMPLEX WITH CTL EPITOPES FROM INFLUENZA A VIRUS: IMPLICATIONS FOR TCR REPERTOIRE SELECTION AND IMMUNODOMINANCE	IMMUNE SYSTEM
1WBZ	CRYSTAL STRUCTURES OF MURINE MHC CLASS I H-2 DB AND KB MOLECULES IN COMPLEX WITH CTL EPITOPES FROM INFLUENZA A VIRUS: IMPLICATIONS FOR TCR REPERTOIRE SELECTION AND IMMUNODOMINANCE	IMMUNE SYSTEM
1WCB	PLP-DEPENDENT CATALYTIC ANTIBODY 15A9 IN COMPLEX WITH ITS HAPTEN	IMMUNE SYSTEM
1WCI	REACTIVITY MODULATION OF HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE BY AN INTERNAL MOLECULAR SWITCH	OXIDOREDUCTASE
1WCM	COMPLETE 12-SUBUNIT RNA POLYMERASE II AT 3.8 ANG	TRANSCRIPTION
1WCY	CRYSTAL STRUCTURE OF HUMAN DIPEPTIDYL PEPTIDASE IV (DPPIV) COMPLEX WITH DIPROTIN A	HYDROLASE
1WDC	SCALLOP MYOSIN REGULATORY DOMAIN	MUSCLE PROTEIN
1WDD	CRYSTAL STRUCTURE OF ACTIVATED RICE RUBISCO COMPLEXED WITH 2-CARBOXYARABINITOL-1,5-BISPHOSPHATE	LYASE
1WDK	FATTY ACID BETA-OXIDATION MULTIENZYME COMPLEX FROM PSEUDOMONAS FRAGI, FORM I (NATIVE2)	LYASE,OXIDOREDUCTASE/TRANSFERASE
1WDL	FATTY ACID BETA-OXIDATION MULTIENZYME COMPLEX FROM PSEUDOMONAS FRAGI, FORM II (NATIVE4)	LYASE,OXIDOREDUCTASE/TRANSFERASE
1WDM	FATTY ACID BETA-OXIDATION MULTIENZYME COMPLEX FROM PSEUDOMONAS FRAGI, FORM I (NATIVE3)	LYASE,OXIDOREDUCTASE/TRANSFERASE
1WDW	STRUCTURAL BASIS OF MUTUAL ACTIVATION OF THE TRYPTOPHAN SYNTHASE A2B2 COMPLEX FROM A HYPERTHERMOPHILE, PYROCOCCUS FURIOSUS	LYASE
1WE3	CRYSTAL STRUCTURE OF THE CHAPERONIN COMPLEX	CHAPERONE

	CPN60/CPN10/(ADP)7 FROM THERMUS THERMOPHILUS	
1WEJ	IGG1 FAB FRAGMENT (OF E8 ANTIBODY) COMPLEXED WITH HORSE CYTOCHROME C AT 1.8 A RESOLUTION	COMPLEX (ANTIBODY/ELECTRON TRANSPORT)
1WHS	STRUCTURE OF THE COMPLEX OF L-BENZYLSUCCINATE WITH WHEAT SERINE CARBOXYPEPTIDASE II AT 2.0 ANGSTROMS RESOLUTION	SERINE CARBOXYPEPTIDASE
1WHT	STRUCTURE OF THE COMPLEX OF L-BENZYLSUCCINATE WITH WHEAT SERINE CARBOXYPEPTIDASE II AT 2.0 ANGSTROMS RESOLUTION	SERINE CARBOXYPEPTIDASE
1WKR	CRYSTAL STRUCTURE OF ASPARTIC PROTEINASE FROM IRPEX LACTEUS	HYDROLASE
1WKW	CRYSTAL STRUCTURE OF THE TERNARY COMPLEX OF EIF4E-M7GPPPA-4EBP1 PEPTIDE	TRANSLATION/PROTEIN BINDING
1WLP	SOLUTION STRUCTURE OF THE P22PHOX-P47PHOX COMPLEX	OXIDOREDUCTASE/SIGNALING PROTEIN
1WLQ	STRUCURE OF GEMININ-CDT1 COMPLEX	CELL CYCLE
1WM0	PPARGAMMA IN COMPLEX WITH A 2-BABA COMPOUND	TRANSCRIPTION/SIGNALING PROTEIN
1WMH	CRYSTAL STRUCTURE OF A PB1 DOMAIN COMPLEX OF PROTEIN KINASE C IOTA AND PAR6 ALPHA	TRANSFERASE/CELL CYCLE
1WMI	CRYSTAL STRUCTURE OF ARCHAEAL RELE-RELB COMPLEX FROM PYROCOCCUS HORIKOSHII OT3	HYDROLASE/HYDROLASE INHIBITOR
1WMU	CRYSTAL STRUCTURE OF HEMOGLOBIN D FROM THE ALDABRA GIANT TORTOISE, GEOCHELONE GIGANTEA, AT 1.65 A RESOLUTION	OXYGEN STORAGE/TRANSPORT
1WPL	CRYSTAL STRUCTURE OF THE INHIBITORY FORM OF RAT GTP CYCLOHYDROLASE I/GFRP COMPLEX	HYDROLASE/PROTEIN BINDING
1WPX	CRYSTAL STRUCTURE OF CARBOXYPEPTIDASE Y INHIBITOR COMPLEXED WITH THE COGNATE PROTEINASE	HYDROLASE
1WQ1	RAS-RASGAP COMPLEX	COMPLEX (GTP-BINDING/GTPASE ACTIVATION)
1WQ9	CRYSTAL STRUCTURE OF VR-1, A VEGF-F FROM A SNAKE VENOM	TOXIN
1WQJ	STRUCTURAL BASIS FOR THE REGULATION OF INSULIN-LIKE GROWTH FACTORS (IGFS) BY IGF BINDING PROTEINS (IGFBPS)	PROTEIN BINDING/HORMONE/GROWTH FACTOR
1WQL	UMENE DIOXYGENASE (CUMA1A2) FROM PSEUDOMONAS FLUORESCENS IP01	OXIDOREDUCTASE
1WQV	HUMAN FACTOR VIIA-TISSUE FACTOR COMPLEXED WITH PROPYLSULFONAMIDE-D-THR-MET-P-AMINOBENZAMIDINE	HYDROLASE
1WR6	CRYSTAL STRUCTURE OF GGA3 GAT DOMAIN IN COMPLEX WITH UBIQUITIN	PROTEIN TRANSPORT/SIGNALING PROTEIN
1WRD	CRYSTAL STRUCTURE OF TOM1 GAT DOMAIN IN COMPLEX WITH UBIQUITIN	PROTEIN TRANSPORT/SIGNALING PROTEIN

1WRZ	CALMODULIN COMPLEXED WITH A PEPTIDE FROM A HUMAN DEATH-ASSOCIATED PROTEIN KINASE	METAL BINDING PROTEIN/TRANSFERASE
1WSS	HUMAN FACTOR VIIA-TISSUE FACTOR IN COMPLEX WITH PEPRID MIMETIC INHIBITOR THAT HAS TWO CHARGE GROUPS IN P2 AND P4	HYDROLASE/BLOOD CLOTTING
1WT9	CRYSTAL STRUCTURE OF AA-X-BP-I, A SNAKE VENOM PROTEIN WITH THE ACTIVITY OF BINDING TO COAGULATION FACTOR X FROM AGKISTRODON ACUTUS	BLOOD CLOTTING
1WTG	HUMAN FACTOR VIIA-TISSUE FACTOR COMPLEXED WITH ETHYLSULFONAMIDE-D-BIPHENYLALANINE-GLN-P-AMINOBENZAMIDINE	HYDROLASE/BLOOD CLOTTING
1WTH	CRYSTAL STRUCTURE OF GP5-S351L MUTANT AND GP27 COMPLEX	HYDROLASE/STRUCTURAL PROTEIN
1WU1	FACTOR XA IN COMPLEX WITH THE INHIBITOR 4-[(5-CHLOROINDOL-2-YL)SULFONYL]-2-(2-METHYLPROPYL)-1-[[5-(PYRIDIN-4-YL) PYRIMIDIN-2-YL]CARBONYL]PIPERAZINE	HYDROLASE
1WUH	THREE-DIMENSIONAL STRUCTURE OF THE NI-A STATE OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE
1WUI	ULTRA-HIGH RESOLUTION STRUCTURE OF THE NI-A STATE OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE
1WUJ	THREE-DIMENSIONAL STRUCTURE OF THE NI-B STATE OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE
1WUK	HIGH RESOLUTION STRUCTURE OF THE OXIDIZED STATE OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE
1WUL	HIGH RESOLUTION STRUCTURE OF THE REDUCED STATE OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE
1WUN	HUMAN FACTOR VIIA-TISSUE FACTOR COMPLEXED WITH ETHYLSULFONAMIDE-D-TRP-GLN-P-AMINOBENZAMIDINE	HYDROLASE/BLOOD CLOTTING
1WV7	HUMAN FACTOR VIIA-TISSUE FACTOR COMPLEXED WITH ETHYLSULFONAMIDE-D-5-PROPOXY-TRP-GLN-P-AMINOBENZAMIDINE	HYDROLASE/BLOOD CLOTTING
1WVE	P-CRESOL METHYLHYDROXYLASE: ALTERATION OF THE STRUCTURE OF THE FLAVOPROTEIN SUBUNIT UPON ITS BINDING TO THE CYTOCHROME SUBUNIT	OXIDOREDUCTASE
1WWW	NGF IN COMPLEX WITH DOMAIN 5 OF THE TRKA RECEPTOR	NERVE GROWTH FACTOR/TRKA COMPLEX
1WX2	CRYSTAL STRUCTURE OF THE OXY-FORM OF THE COPPER-BOUND STREPTOMYCES CASTANEOGLOBISPORUS TYROSINASE COMPLEXED WITH A CADDIE PROTEIN PREPARED BY THE ADDITION OF HYDROGENPEROXIDE	OXIDOREDUCTASE/METAL TRANSPORT
1WX3	CRYSTAL STRUCTURE OF THE MET-FORM OF THE COPPER-BOUND STREPTOMYCES CASTANEOGLOBISPORUS TYROSINASE COMPLEXED WITH A CADDIE PROTEIN	OXIDOREDUCTASE/METAL TRANSPORT

1WX4	CRYSTAL STRUCTURE OF THE OXY-FORM OF THE COPPER-BOUND STREPTOMYCES CASTANEOGLOBISPORUS TYROSINASE COMPLEXED WITH A CADDIE PROTEIN PREPARED BY THE ADDITION OF DITHIOTHREITOL	OXIDOREDUCTASE/METAL TRANSPORT
1WX5	CRYSTAL STRUCTURE OF THE COPPER-FREE STREPTOMYCES CASTANEOGLOBISPORUS TYROSINASE COMPLEXED WITH A CADDIE PROTEIN IN THE MONOCLINIC CRYSTAL	OXIDOREDUCTASE/METAL TRANSPORT
1WXC	CRYSTAL STRUCTURE OF THE COPPER-FREE STREPTOMYCES CASTANEOGLOBISPORUS TYROSINASE COMPLEXED WITH A CADDIE PROTEIN	OXIDOREDUCTASE/METAL TRANSPORT
1WYT	CRYSTAL STRUCTURE OF GLYCINE DECARBOXYLASE (P-PROTEIN) OF THE GLYCINE CLEAVAGE SYSTEM, IN APO FORM	OXIDOREDUCTASE
1WYU	CRYSTAL STRUCTURE OF GLYCINE DECARBOXYLASE (P-PROTEIN) OF THE GLYCINE CLEAVAGE SYSTEM, IN HOLO FORM	OXIDOREDUCTASE
1WYV	CRYSTAL STRUCTURE OF GLYCINE DECARBOXYLASE (P-PROTEIN) OF THE GLYCINE CLEAVAGE SYSTEM, IN INHIBITOR-BOUND FORM	OXIDOREDUCTASE
1WYW	CRYSTAL STRUCTURE OF SUMO1-CONJUGATED THYMINE DNA GLYCOSYLASE	HYDROLASE
1X11	X11 PTB DOMAIN	COMPLEX (PEPTIDE BINDING MODULE/PEPTIDE)
1X1U	WATER-MEDIATE INTERACTION AT APROTEIN-PROTEIN INTERFACE	HYDROLASE/PROTEIN BINDING
1X1W	WATER-MEDIATE INTERACTION AT APROTEIN-PROTEIN INTERFACE	HYDROLASE/PROTEIN BINDING
1X1X	WATER-MEDIATE INTERACTION AT APROTEIN-PROTEIN INTERFACE	HYDROLASE/PROTEIN BINDING
1X1Y	WATER-MEDIATE INTERACTION AT APROTEIN-PROTEIN INTERFACE	HYDROLASE/PROTEIN BINDING
1X27	CRYSTAL STRUCTURE OF LCK SH2-SH3 WITH SH2 BINDING SITE OF P130CAS	SIGNALING PROTEIN
1X2T	CRYSTAL STRUCTURE OF HABU IX-BP AT PH 6.5	PROTEIN BINDING
1X2W	CRYSTAL STRUCTURE OF APO-HABU IX-BP AT PH 4.6	PROTEIN BINDING
1X31	CRYSTAL STRUCTURE OF HETEROTETRAMERIC SARCOSINE OXIDASE FROM CORYNEBACTERIUM SP. U-96	OXIDOREDUCTASE
1X3W	STRUCTURE OF A PEPTIDE:N-GLYCANASE-RAD23 COMPLEX	HYDROLASE
1X3Z	STRUCTURE OF A PEPTIDE:N-GLYCANASE-RAD23 COMPLEX	HYDROLASE
1X75	CCDB:GYRA14 COMPLEX	ISOMERASE/SIGNALING PROTEIN
1X76	RYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH WAY-697	TRANSCRIPTION
1X78	RYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH	TRANSCRIPTION

	WAY-244	
1X79	RYSTAL STRUCTURE OF HUMAN GGA1 GAT DOMAIN COMPLEXED WITH THE GAT-BINDING DOMAIN OF RABAPTIN5	PROTEIN TRANSPORT
1X7B	RYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH ERB-041	TRANSCRIPTION
1X7E	RYSTAL STRUCTURE OF ESTROGEN RECEPTOR ALPHA COMPLEXED WITH WAY-244	TRANSCRIPTION
1X7J	RYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH GENISTEIN	TRANSCRIPTION
1X7Q	CRYSTAL STRUCTURE OF HLA-A*1101 WITH SARS NUCLEOCAPSID PEPTIDE	IMMUNE SYSTEM
1X7R	RYSTAL STRUCTURE OF ESTROGEN RECEPTOR ALPHA COMPLEXED WITH GENISTEIN	TRANSCRIPTION
1X7W	RYSTAL STRUCTURE OF THE HUMAN MITOCHONDRIAL BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE	OXIDOREDUCTASE
1X7X	RYSTAL STRUCTURE OF THE HUMAN MITOCHONDRIAL BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE	OXIDOREDUCTASE
1X7Y	RYSTAL STRUCTURE OF THE HUMAN MITOCHONDRIAL BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE	OXIDOREDUCTASE
1X7Z	RYSTAL STRUCTURE OF THE HUMAN MITOCHONDRIAL BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE	OXIDOREDUCTASE
1X80	RYSTAL STRUCTURE OF THE HUMAN MITOCHONDRIAL BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE	OXIDOREDUCTASE
1X81	FARNESYL TRANSFERASE STRUCTURE OF JANSEN COMPOUND	TRANSFERASE
1X86	CRYSTAL STRUCTURE OF THE DH/PH DOMAINS OF LEUKEMIA-ASSOCIATED RHOGEF IN COMPLEX WITH RHOA	SIGNALING PROTEIN/MEMBRANE PROTEIN
1X8S	STRUCTURE OF THE PAR-6 PDZ DOMAIN WITH A PALS1 INTERNAL LIGAND	CELL CYCLE
1X9F	HEMOGLOBIN DODECAMER FROM LUMBRICUS ERYTHROCRUORIN	OXYGEN STORAGE/TRANSPORT
1X9M	T7 DNA POLYMERASE IN COMPLEX WITH AN N-2-ACETYLAMINOFLUORENE-ADDUCTED DNA	TRANSFERASE/ELECTRON TRANSPORT/DNA
1X9S	T7 DNA POLYMERASE IN COMPLEX WITH A PRIMER/TEMPLATE DNA CONTAINING A DISORDERED N-2 AMINOFLUORENE ON THE TEMPLATE, CRYSTALLIZED WITH DIDEOXY-CTP AS THE INCOMING NUCLEOTIDE.	TRANSFERASE/ELECTRON TRANSPORT/DNA
1X9T	THE CRYSTAL STRUCTURE OF HUMAN ADENOVIRUS 2 PENTON BASE IN COMPLEX WITH AN AD2 N-TERMINAL FIBRE PEPTIDE	VIRUS LIKE PARTICLE/PEPTIDE

1X9W	T7 DNA POLYMERASE IN COMPLEX WITH A PRIMER/TEMPLATE DNA CONTAINING A DISORDERED N-2 AMINOFLUORENE ON THE TEMPLATE, CRYSTALLIZED WITH DIDEOXY-ATP AS THE INCOMING NUCLEOTIDE.	TRANSFERASE/ELECTRON TRANSPORT/DNA
1XB1	THE STRUCTURE OF THE BIR DOMAIN OF IAP-LIKE PROTEIN 2	APOPTOSIS
1XB2	CRYSTAL STRUCTURE OF BOS TAURUS MITOCHONDRIAL ELONGATION FACTOR TU/TS COMPLEX	TRANSLATION
1XB7	X-RAY STRUCTURE OF ERRALPHA LBD IN COMPLEX WITH A PGC-1ALPHA PEPTIDE AT 2.5A RESOLUTION	TRANSCRIPTION
1XCG	CRYSTAL STRUCTURE OF HUMAN RHOA IN COMPLEX WITH DH/PH FRAGMENT OF PDZRHOGEF	SIGNALING PROTEIN ACTIVATOR/SIGNALING PR
1XCQ	COMPLEX HCV CORE-FAB 19D9D6-PROTEIN L MUTANT (D55A,L57H, Y64W) IN SPACE GROUP P21	IMMUNE SYSTEM
1XCT	COMPLEX HCV CORE-FAB 19D9D6-PROTEIN L MUTANT (D55A, L57H, Y64W) IN SPACE GROUP P21212	IMMUNE SYSTEM
1XD2	CRYSTAL STRUCTURE OF A TERNARY RAS:SOS:RAS*GDP COMPLEX	SIGNALING PROTEIN
1XD3	CRYSTAL STRUCTURE OF UCHL3-UBVME COMPLEX	HYDROLASE
1XDA	STRUCTURE OF INSULIN	HORMONE
1XDK	CRYSTAL STRUCTURE OF THE RARBETA/RXRALPHA LIGAND BINDING DOMAIN HETERODIMER IN COMPLEX WITH 9-CIS RETINOIC ACID AND A FRAGMENT OF THE TRAP220 COACTIVATOR	HORMONE/GROWTH FACTOR RECEPTOR
1XEW	STRUCTURAL BIOCHEMISTRY OF ATP-DRIVEN DIMERIZATION AND DNA STIMULATED ACTIVATION OF SMC ATPASES.	CELL CYCLE
1XF2	STRUCTURE OF FAB DNA-1 COMPLEXED WITH DT3	IMMUNE SYSTEM/DNA
1XF3	STRUCTURE OF LIGAND-FREE FAB DNA-1 IN SPACE GROUP P65	IMMUNE SYSTEM
1XF4	STRUCTURE OF LIGAND-FREE FAB DNA-1 IN SPACE GROUP P321 SOLVED FROM CRYSTALS WITH PERFECT HEMIHEDRAL TWINNING	IMMUNE SYSTEM
1XF5	COMPLEX HCV CORE-FAB 19D9D6-PROTEIN L MUTANT (H74C, Y64W)IN SPACE GROUP P21212	IMMUNE SYSTEM
1XF6	HIGH RESOLUTION CRYSTAL STRUCTURE OF PHYCOERYTHRIN 545 FROM THE MARINE CRYPTOPHYTE RHODOMONAS CS24	PHOTOSYNTHESIS
1XFP	CRYSTAL STRUCTURE OF THE CDR2 GERMLINE REVERSION MUTANT OF CAB-LYS3 IN COMPLEX WITH HEN EGG WHITE LYSOZYME	IMMUNE SYSTEM/HYDROLASE
1XFU	CRYSTAL STRUCTURE OF ANTHRAX EDEMA FACTOR (EF) TRUNCATION MUTANT, EF-DELTA 64 IN COMPLEX WITH CALMODULIN	LYASE/METAL BINDING PROTEIN
1XFV	CRYSTAL STRUCTURE OF ANTHRAX EDEMA FACTOR (EF) IN COMPLEX WITH CALMODULIN AND 3' DEOXY-ATP	LYASE/METAL BINDING PROTEIN

1XFW	CRYSTAL STRUCTURE OF ANTHRAX EDEMA FACTOR (EF) IN COMPLEX WITH CALMODULIN AND 3'5' CYCLIC AMP (CAMP)	LYASE/METAL BINDING PROTEIN
1XFX	CRYSTAL STRUCTURE OF ANTHRAX EDEMA FACTOR (EF) IN COMPLEX WITH CALMODULIN IN THE PRESENCE OF 10 MILLIMOLAR EXOGENOUSLY ADDED CALCIUM CHLORIDE	LYASE/METAL BINDING PROTEIN
1XFY	CRYSTAL STRUCTURE OF ANTHRAX EDEMA FACTOR (EF) IN COMPLEX WITH CALMODULIN	LYASE/METAL BINDING PROTEIN
1XFZ	CRYSTAL STRUCTURE OF ANTHRAX EDEMA FACTOR (EF) IN COMPLEX WITH CALMODULIN IN THE PRESENCE OF 1 MILLIMOLAR EXOGENOUSLY ADDED CALCIUM CHLORIDE	LYASE/METAL BINDING PROTEIN
1XG0	HIGH RESOLUTION CRYSTAL STRUCTURE OF PHYCOERYTHRIN 545 FROM THE MARINE CRYPTOPHYTE RHODOMONAS CS24	PHOTOSYNTHESIS
1XG2	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN PECTIN METHYLESTERASE AND ITS INHIBITOR PROTEIN	HYDROLASE/HYDROLASE INHIBITOR
1XGP	STRUCTURE FOR ANTIBODY HYHEL-63 Y33A MUTANT COMPLEXED WITH HEN EGG LYSOZYME	IMMUNE SYSTEM
1XGQ	STRUCTURE FOR ANTIBODY HYHEL-63 Y33V MUTANT COMPLEXED WITH HEN EGG LYSOZYME	IMMUNE SYSTEM
1XGR	STRUCTURE FOR ANTIBODY HYHEL-63 Y33I MUTANT COMPLEXED WITH HEN EGG LYSOZYME	IMMUNE SYSTEM
1XGT	STRUCTURE FOR ANTIBODY HYHEL-63 Y33L MUTANT COMPLEXED WITH HEN EGG LYSOZYME	IMMUNE SYSTEM
1XGU	STRUCTURE FOR ANTIBODY HYHEL-63 Y33F MUTANT COMPLEXED WITH HEN EGG LYSOZYME	IMMUNE SYSTEM
1XGY	CRYSTAL STRUCTURE OF ANTI-META I RHODOPSIN FAB FRAGMENT K42-41L	IMMUNE SYSTEM
1XH3	CONFORMATIONAL RESTRAINTS AND FLEXIBILITY OF 14-MERIC PEPTIDES IN COMPLEX WITH HLA-B*3501	IMMUNE SYSTEM
1XH4	CRYSTAL STRUCTURES OF PROTEIN KINASE B SELECTIVE INHIBITORS IN COMPLEX WITH PROTEIN KINASE A AND MUTANTS	TRANSFERASE/TRANSFERASE INHIBITOR
1XH5	CRYSTAL STRUCTURES OF PROTEIN KINASE B SELECTIVE INHIBITORS IN COMPLEX WITH PROTEIN KINASE A AND MUTANTS	TRANSFERASE/TRANSFERASE INHIBITOR
1XH6	CRYSTAL STRUCTURES OF PROTEIN KINASE B SELECTIVE INHIBITORS IN COMPLEX WITH PROTEIN KINASE A AND MUTANTS	TRANSFERASE/TRANSFERASE INHIBITOR
1XH7	CRYSTAL STRUCTURES OF PROTEIN KINASE B SELECTIVE INHIBITORS IN COMPLEX WITH PROTEIN KINASE A AND MUTANTS	TRANSFERASE/TRANSFERASE INHIBITOR
1XH8	CRYSTAL STRUCTURES OF PROTEIN KINASE B SELECTIVE INHIBITORS	TRANSFERASE/TRANSFERASE INHIBITOR

	IN COMPLEX WITH PROTEIN KINASE A AND MUTANTS	
1XH9	CRYSTAL STRUCTURES OF PROTEIN KINASE B SELECTIVE INHIBITORS IN COMPLEX WITH PROTEIN KINASE A AND MUTANTS	TRANSFERASE/TRANSFERASE INHIBITOR
1XHA	CRYSTAL STRUCTURES OF PROTEIN KINASE B SELECTIVE INHIBITORS IN COMPLEX WITH PROTEIN KINASE A AND MUTANTS	TRANSFERASE/TRANSFERASE INHIBITOR
1XHM	THE CRYSTAL STRUCTURE OF A BIOLOGICALLY ACTIVE PEPTIDE (SIGK) BOUND TO A G PROTEIN BETA:GAMMA HETERODIMER	SIGNALING PROTEIN
1XIU	CRYSTAL STRUCTURE OF THE AGONIST-BOUND LIGAND-BINDING DOMAIN OF BIOMPHALARIA GLABRATA RXR	TRANSCRIPTION/TRANSFERASE
1XJ7	COMPLEX ANDROGEN RECEPTOR LBD AND RAC3 PEPTIDE	HORMONE/GROWTH FACTOR
1XJW	THE STRUCTURE OF E. COLI ASPARTATE TRANSCARBAMOYLASE Q137A MUTANT IN THE R-STATE	TRANSFERASE/TRANSFERASE REGULATOR
1XK4	CRYSTAL STRUCTURE OF HUMAN CALPROTECTIN(S100A8/S100A9)	METAL BINDING PROTEIN
1XKA	FACTOR XA COMPLEXED WITH A SYNTHETIC INHIBITOR FX-2212A, (2S)-(3'-AMIDINO-3-BIPHENYLYL)-5-(4-PYRIDYLAMINO)PENTANOIC ACID	BLOOD COAGULATION FACTOR
1XKB	FACTOR XA COMPLEXED WITH A SYNTHETIC INHIBITOR FX-2212A, (2S)-(3'-AMIDINO-3-BIPHENYLYL)-5-(4-PYRIDYLAMINO)PENTANOIC ACID	BLOOD COAGULATION FACTOR
1XKP	CRYSTAL STRUCTURE OF THE VIRULENCE FACTOR YOPN IN COMPLEX WITH ITS HETERODIMERIC CHAPERONE SYCN-YSCB	MEMBRANE PROTEIN/CHAPERON
1XL3	COMPLEX STRUCTURE OF Y.PESTIS VIRULENCE FACTORS YOPN AND TYEA	CELL INVASION
1XLS	CRYSTAL STRUCTURE OF THE MOUSE CAR/RXR LBD HETERODIMER BOUND TO TCPOBOP AND 9CRA AND A TIF2 PEPTIDE CONTAING THE THIRD LXXLL MOTIFS	TRANSCRIPTION
1XLT	CRYSTAL STRUCTURE OF TRANSHYDROGENASE [(DOMAIN I)2:DOMAIN III] HETEROTRIMER COMPLEX	OXIDOREDUCTASE
1XM4	CATALYTIC DOMAIN OF HUMAN PHOSPHODIESTERASE 4B IN COMPLEX WITH PICLAMILAST	HYDROLASE
1XME	STRUCTURE OF RECOMBINANT CYTOCHROME BA3 OXIDASE FROM THERMUS THERMOPHILUS	OXIDOREDUCTASE
1XMF	STRUCTURE OF MN(II)-SOAKED APO METHANE MONOOXYGENASE HYDROXYLASE CRYSTALS FROM M. CAPSULATUS (BATH)	OXIDOREDUCTASE
1XMG	YSTAL STRUCTURE OF APO METHANE MONOOXYGENASE HYDROXYLASE FROM M. CAPSULATUS (BATH)	OXIDOREDUCTASE
1XMH	STRUCTURE OF CO(II) RECONSTITUTED METHANE MONOOXYGENASE	OXIDOREDUCTASE

	HYDROXYLASE FROM M. CAPSULATUS (BATH)	
1XMN	CRYSTAL STRUCTURE OF THROMBIN BOUND TO HEPARIN	BLOOD CLOTTING
1XMO	RYSTAL STRUCTURE OF MNM5U34T6A37-TRNALYSUUU COMPLEXED WITH AAG-MRNA IN THE DECODING CENTER	RIBOSOME
1XMQ	CRYSTAL STRUCTURE OF T6A37-ASLLYSUUU AAA-MRNA BOUND TO THE DECODING CENTER	RIBOSOME
1XMU	CATALYTIC DOMAIN OF HUMAN PHOSPHODIESTERASE 4B IN COMPLEX WITH ROFLUMILAST	HYDROLASE
1XMY	CATALYTIC DOMAIN OF HUMAN PHOSPHODIESTERASE 4B IN COMPLEX WITH (R)-ROLIPRAM	HYDROLASE
1XN2	NEW SUBSTRATE BINDING POCKETS FOR BETA-SECRETASE.	HYDROLASE
1XN3	CRYSTAL STRUCTURE OF BETA-SECRETASE BOUND TO A LONG INHIBITOR WITH ADDITIONAL UPSTREAM RESIDUES.	HYDROLASE
1XNQ	STRUCTURE OF AN INOSINE-ADENINE WOBBLE BASE PAIR COMPLEX IN THE CONTEXT OF THE DECODING CENTER	RIBOSOME
1XNR	CRYSTAL STRUCTURE OF AN INOSINE-CYTOSINE WOBBLE BASE PAIR IN THE CONTEXT OF THE DECODING CENTER	RIBOSOME
1XO2	CRYSTAL STRUCTURE OF A HUMAN CYCLIN-DEPENDENT KINASE 6 COMPLEX WITH A FLAVONOL INHIBITOR, FISETIN	CELL CYCLE/TRANSFERASE
1XOF	HETEROOLIGOMERIC BETA BETA ALPHA MINIPROTEIN	DE NOVO PROTEIN
1XOU	CRYSTAL STRUCTURE OF THE CESA-ESPA COMPLEX	STRUCTURAL PROTEIN/CHAPERONE
1XOW	CRYSTAL STRUCTURE OF THE HUMAN ANDROGEN RECEPTOR LIGAND BINDING DOMAIN BOUND WITH AN ANDROGEN RECEPTOR NH2-TERMINAL PEPTIDE, AR20-30, AND R1881	TRANSCRIPTION
1XPK	RYSTAL STRUCTURE OF STAPHYLOCOCCUS AUREUS HMG-COA SYNTHASE WITH HMG-COA AND WITH ACETOACETYL-COA AND ACETYLATED CYSTEINE	TRANSFERASE
1XQ5	MET-PERCH HEMOGLOBIN AT 1.9A	OXYGEN STORAGE/TRANSPORT
1XQ7	CYCLOPHILIN FROM TRYPANOSOMA CRUZI BOUND TO CYCLOSPORIN A	ISOMERASE
1XQH	CRYSTAL STRUCTURE OF A TERNARY COMPLEX OF THE METHYLTRANSFERASE SET9 (ALSO KNOWN AS SET7/9) WITH A P53 PEPTIDE AND SAH	TRANSFERASE
1XQS	CRYSTAL STRUCTURE OF THE HSPBP1 CORE DOMAIN COMPLEXED WITH THE FRAGMENT OF HSP70 ATPASE DOMAIN	CHAPERONE
1XQY	CRYSTAL STRUCTURE OF F1-MUTANT S105A COMPLEX WITH PRO-LEU-GLY-GLY	HYDROLASE

1XR0	STRUCTURAL BASIS OF SNT PTB DOMAIN INTERACTIONS WITH DISTINCT NEUROTROPHIC RECEPTORS	SIGNALING PROTEIN/GROWTH FACTOR RECEPTOR
1XR8	CRYSTAL STRUCTURES OF HLA-B*1501 IN COMPLEX WITH PEPTIDES FROM HUMAN UBCH6 AND EPSTEIN-BARR VIRUS EBNA-3	IMMUNE SYSTEM
1XRP	CRYSTAL STRUCTURE OF ACTIVE SITE F1-MUTANT E213Q SOAKED WITH PEPTIDE PRO-LEU-GLY-GLY	HYDROLASE
1XRS	CRYSTAL STRUCTURE OF LYSINE 5,6-AMINOMUTASE IN COMPLEX WITH PLP, COBALAMIN, AND 5'-DEOXYADENOSINE	ISOMERASE
1XS9	A MODEL OF THE TERNARY COMPLEX FORMED BETWEEN MARA, THE ALPHA-CTD OF RNA POLYMERASE AND DNA	TRANSCRIPTION/DNA
1XT9	CRYSTAL STRUCTURE OF DEN1 IN COMPLEX WITH NEDD8	HYDROLASE/HYDROLASE INHIBITOR
1XTC	CHOLERA TOXIN	TOXIN
1XTG	CRYSTAL STRUCTURE OF NEUROTOXIN BONT/A COMPLEXED WITH SYNAPTOSOMAL-ASSOCIATED PROTEIN 25	TOXIN
1XU2	THE CRYSTAL STRUCTURE OF APRIL BOUND TO BCMA	CYTOKINE, HORMONE/GROWTH FACTOR RECEPTOR
1XU3	SOLUBLE METHANE MONOOXYGENASE HYDROXYLASE-SOAKED WITH BROMOPHENOL	OXIDOREDUCTASE
1XU5	OLUBLE METHANE MONOOXYGENASE HYDROXYLASE-PHENOL SOAKED	OXIDOREDUCTASE
1XV9	CRYSTAL STRUCTURE OF CAR/RXR HETERODIMER BOUND WITH SRC1 PEPTIDE, FATTY ACID, AND 5B-PREGNANE-3,20-DIONE.	DNA BINDING PROTEIN
1XVB	OLUBLE METHANE MONOOXYGENASE HYDROXYLASE: 6-BROMOHEXANOL SOAKED STRUCTURE	OXIDOREDUCTASE
1XVC	OLUBLE METHANE MONOOXYGENASE HYDROXYLASE: 8-BROMOOCTANOL SOAKED STRUCTURE	OXIDOREDUCTASE
1XVD	OLUBLE METHANE MONOOXYGENASE HYDROXYLASE: 4-FLUOROPHENOL SOAKED STRUCTURE	OXIDOREDUCTASE
1XVE	SOLUBLE METHANE MONOOXYGENASE HYDROXYLASE: 3-BROMO-3-BUTENOL SOAKED STRUCTURE	OXIDOREDUCTASE
1XVF	LUBLE METHANE MONOOXYGENASE HYDROXYLASE: CHLOROPROPANOL SOAKED STRUCTURE	OXIDOREDUCTASE
1XVG	OLUBLE METHANE MONOOXYGENASE HYDROXYLASE: BROMOETHANOL SOAKED STRUCTURE	OXIDOREDUCTASE
1XVM	RYPSIN FROM FUSARIUM OXYSPORUM- ROOM TEMPERATURE TO ATOMIC RESOLUTION	HYDROLASE
1XVP	CRYSTAL STRUCTURE OF CAR/RXR HETERODIMER BOUND WITH SRC1	DNA BINDING PROTEIN

	PEPTIDE, FATTY ACID AND CITCO	
1XW7	DIABETES-ASSOCIATED MUTATIONS IN HUMAN INSULIN: CRYSTAL STRUCTURE AND PHOTO-CROSS-LINKING STUDIES OF A-CHAIN VARIANT INSULIN WAKAYAMA	HORMONE/GROWTH FACTOR
1XWD	CRYSTAL STRUCTURE OF HUMAN FOLLICLE STIMULATING HORMONE COMPLEXED WITH ITS RECEPTOR	HORMONE/GROWTH FACTOR
1XWJ	VINCULIN HEAD (1-258) IN COMPLEX WITH THE TALIN VINCULIN BINDING SITE 3 (1945-1969)	CELL ADHESION/PROTEIN BINDING
1XX9	CRYSTAL STRUCTURE OF THE FXIA CATALYTIC DOMAIN IN COMPLEX WITH ECOTINM84R	BLOOD CLOTTING/HYDROLASE INHIBITOR
1XXD	CRYSTAL STRUCTURE OF THE FXIA CATALYTIC DOMAIN IN COMPLEX WITH MUTATED ECOTIN	BLOOD CLOTTING/HYDROLASE INHIBITOR
1XXF	CRYSTAL STRUCTURE OF THE FXIA CATALYTIC DOMAIN IN COMPLEX WITH ECOTIN MUTANT (ECOTINP)	BLOOD CLOTTING/HYDROLASE INHIBITOR
1XXH	ATPGS BOUND E. COLI CLAMP LOADER COMPLEX	TRANSFERASE
1XXI	ADP BOUND E. COLI CLAMP LOADER COMPLEX	TRANSFERASE
1XXM	THE MODULAR ARCHITECTURE OF PROTEIN-PROTEIN BINDING SITE	HYDROLASE/HYDROLASE INHIBITOR
1XXP	YERSINIA YOPH (RESIDUES 163-468) C403S BINDS PHOSPHOTYROSYL PEPTIDE AT TWO SITES	HYDROLASE
1XXT	THE T-TO-T HIGH TRANSITIONS IN HUMAN HEMOGLOBIN: WILD-TYPE DEOXY HB A (LOW SALT, ONE TEST SET)	TRANSPORT PROTEIN
1XXV	YERSINIA YOPH (RESIDUES 163-468) BINDS PHOSPHONODIFLUOROMETHYL-PHE CONTAINING HEXAPEPTIDE AT TWO SITES	HYDROLASE
1XXW	STRUCTURE OF ZINC INDUCED HETERODIMER OF TWO CALCIUM FREE ISOFORMS OF PHOSPHOLIPASE A2 FROM NAJA NAJA SAGITTIFERA AT 2.7A RESOLUTION	HYDROLASE
1XY0	T-TO-THIGH TRANSITIONS IN HUMAN HEMOGLOBIN: ALPHAK40G DEOXY LOW-SALT	TRANSPORT PROTEIN
1XYE	T-TO-THIGH TRANSITIONS IN HUMAN HEMOGLOBIN: ALPHA Y42A DEOXY LOW SALT	TRANSPORT PROTEIN
1XZ0	CRYSTAL STRUCTURE OF CD1A IN COMPLEX WITH A SYNTHETIC MYCOBACTIN LIPOPEPTIDE	IMMUNE SYSTEM
1XZ2	WILD-TYPE HEMOGLOBIN DEOXY NO-SALT	TRANSPORT PROTEIN
1XZ4	INTERSUBUNIT INTERACTIONS ASSOCIATED WITH TYR42ALPHA STABILIZE THE QUATERNARY-T TETRAMER BUT ARE NOT MAJOR QUATERNARY CONSTRAINTS IN DEOXYHEMOGLOBIN: ALPHAY42A	TRANSPORT PROTEIN

	DEOXYHEMOGLOBIN NO-SALT	
1XZ5	T-TO-THIGH QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: ALPHAL91A DEOXY LOW-SALT	TRANSPORT PROTEIN
1XZ7	T-TO-THIGH QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: ALPHAR92A DEOXY LOW-SALT	TRANSPORT PROTEIN
1XZP	STRUCTURE OF THE GTP-BINDING PROTEIN TRME FROM THERMOTOGA MARITIMA	HYDROLASE
1XZQ	STRUCTURE OF THE GTP-BINDING PROTEIN TRME FROM THERMOTOGA MARITIMA COMPLEXED WITH 5-FORMYL-THF	HYDROLASE
1XZU	T-TO-THIGH QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: ALPHAD94G DEOXY LOW-SALT	TRANSPORT PROTEIN
1XZV	T-TO-THIGH QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: ALPHAP95A DEOXY LOW-SALT	TRANSPORT PROTEIN
1Y01	CRYSTAL STRUCTURE OF AHSP BOUND TO FE(II) ALPHA-HEMOGLOBIN	OXYGEN STORAGE/TRANSPORT
1Y09	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: ALPHAN97A DEOXY LOW-SALT	TRANSPORT PROTEIN
1Y0A	T-TO-THIGH QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: ALPHAY140A DEOXY LOW-SALT	TRANSPORT PROTEIN
1Y0C	T-TO-THIGH QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: ALPHAY140F DEOXY LOW-SALT	TRANSPORT PROTEIN
1Y0D	T-TO-THIGH QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: DESARG141ALPHA DEOXY LOW-SALT	TRANSPORT PROTEIN
1Y0L	CATALYTIC ELIMINATION ANTIBODY 34E4 IN COMPLEX WITH HAPTEN	IMMUNE SYSTEM
1Y0T	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAV1M DEOXY LOW-SALT (1 TEST SET)	TRANSPORT PROTEIN
1Y0V	CRYSTAL STRUCTURE OF ANTHRAX EDEMA FACTOR (EF) IN COMPLEX WITH CALMODULIN AND PYROPHOSPHATE	LYASE
1Y0W	T-TO-THIGH QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAV1M DEOXY LOW-SALT (10 TEST SETS)	TRANSPORT PROTEIN
1Y14	CRYSTAL STRUCTURE OF YEAST SUBCOMPLEX OF RPB4 AND RPB7	TRANSFERASE
1Y17	CRYSTAL STRUCTURE OF AA-X-BP-II, A SNAKE VENOM PROTEIN WITH THE ACTIVITY OF BINDING TO COAGULATION FACTOR X FROM AGKISTRODON ACUTUS	BLOOD CLOTTING
1Y18	FAB FRAGMENT OF CATALYTIC ELIMINATION ANTIBODY 34E4 E(H50)D MUTANT IN COMPLEX WITH HAPTEN	IMMUNE SYSTEM
1Y19	STRUCTURAL BASIS FOR PHOSPHATIDYLINOSITOL PHOSPHATE KINASE	STRUCTURAL PROTEIN, SIGNALING PROTEIN

	TYPE I-GAMMA BINDING TO TALIN AT FOCAL ADHESIONS	
1Y1K	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' WITH CHYMOTRYPSIN INHIBITOR 2 T58A MUTANT	HYDROLASE/HYDROLASE INHIBITOR
1Y1V	REFINED RNA POLYMERASE II-TFIIS COMPLEX	TRANSFERASE/TRANSCRIPTION
1Y1W	COMPLETE RNA POLYMERASE II ELONGATION COMPLEX	TRANSFERASE/DNA/RNA
1Y22	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAV33A DEOXY LOW-SALT (1 TEST SET)	TRANSPORT PROTEIN
1Y2A	STRUCTURE OF MAMMALIAN IMPORTIN BOUND TO THE NON-CLASSICAL PLSCR1-NLS	PROTEIN TRANSPORT
1Y2Z	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAV34G DEOXY LOW-SALT (1 TEST SET)	TRANSPORT PROTEIN
1Y31	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAY35A DEOXY LOW-SALT (1 TEST SET)	TRANSPORT PROTEIN
1Y33	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' WITH CHYMOTRYPSIN INHIBITOR 2 T58P MUTANT	HYDROLASE/HYDROLASE INHIBITOR
1Y34	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' WITH CHYMOTRYPSIN INHIBITOR 2 E60A MUTANT	HYDROLASE/HYDROLASE INHIBITOR
1Y35	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAY35F DEOXY LOW-SALT (1 TEST SET)	TRANSPORT PROTEIN
1Y3A	STRUCTURE OF G-ALPHA-I1 BOUND TO A GDP-SELECTIVE PEPTIDE PROVIDES INSIGHT INTO GUANINE NUCLEOTIDE EXCHANGE	SIGNALING PROTEIN
1Y3B	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' WITH CHYMOTRYPSIN INHIBITOR 2 E60S MUTANT	HYDROLASE/HYDROLASE INHIBITOR
1Y3C	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' WITH CHYMOTRYPSIN INHIBITOR 2 R62A MUTANT	HYDROLASE/HYDROLASE INHIBITOR
1Y3D	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' WITH CHYMOTRYPSIN INHIBITOR 2 R67A MUTANT	HYDROLASE/HYDROLASE INHIBITOR
1Y3F	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' WITH CHYMOTRYPSIN INHIBITOR 2 F69A MUTANT	HYDROLASE/HYDROLASE INHIBITOR
1Y45	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAP36A DEOXY LOW-SALT (10 TEST SETS)	TRANSPORT PROTEIN
1Y46	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAW37Y DEOXY LOW-SALT (10 TEST SETS)	TRANSPORT PROTEIN
1Y48	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' WITH CHYMOTRYPSIN INHIBITOR 2 R65A MUTANT	HYDROLASE/HYDROLASE INHIBITOR
1Y4A	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' WITH	HYDROLASE/HYDROLASE INHIBITOR

	CHYMOTRYPSIN INHIBITOR 2 M59R/E60S MUTANT	
1Y4B	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAW37H DEOXY LOW-SALT (10 TEST SETS)	TRANSPORT PROTEIN
1Y4D	CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' WITH CHYMOTRYPSIN INHIBITOR 2 M59R/E60S MUTANT	HYDROLASE/HYDROLASE INHIBITOR
1Y4F	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAW37A DEOXY LOW-SALT (10 TEST SETS)	TRANSPORT PROTEIN
1Y4G	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAW37G DEOXY LOW-SALT (10 TEST SETS)	TRANSPORT PROTEIN
1Y4H	WILD TYPE STAPHOPAIN-STAPHOSTATIN COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
1Y4P	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAW37E DEOXY LOW-SALT (10 TEST SETS)	TRANSPORT PROTEIN
1Y4Q	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAF42A DEOXY LOW-SALT (1 TEST SET)	TRANSPORT PROTEIN
1Y4R	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAF45A DEOXY LOW-SALT (1 TEST SET)	TRANSPORT PROTEIN
1Y4V	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAC93A DEOXY LOW-SALT (1 TEST SET)	TRANSPORT PROTEIN
1Y4Z	THE CRYSTAL STRUCTURE OF NITRATE REDUCTASE A, NARGHI, IN COMPLEX WITH THE Q-SITE INHIBITOR PENTACHLOROPHENOL	OXIDOREDUCTASE
1Y56	CRYSTAL STRUCTURE OF L-PROLINE DEHYDROGENASE FROM P.HORIKOSHII	OXIDOREDUCTASE
1Y5F	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAL96A DEOXY LOW-SALT (1 TEST SET)	TRANSPORT PROTEIN
1Y5I	THE CRYSTAL STRUCTURE OF THE NARGHI MUTANT NARI-K86A	OXIDOREDUCTASE
1Y5J	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAH97A DEOXY LOW-SALT (1 TEST SET)	TRANSPORT PROTEIN
1Y5K	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAD99A DEOXY LOW-SALT (10 TEST SETS)	TRANSPORT PROTEIN
1Y5L	THE CRYSTAL STRUCTURE OF THE NARGHI MUTANT NARI-H66Y	OXIDOREDUCTASE
1Y5N	THE CRYSTAL STRUCTURE OF THE NARGHI MUTANT NARI-K86A IN COMPLEX WITH PENTACHLOROPHENOL	OXIDOREDUCTASE
1Y64	BNI1P FORMIN HOMOLOGY 2 DOMAIN COMPLEXED WITH ATP-ACTIN	STRUCTURAL PROTEIN
1Y6K	CRYSTAL STRUCTURE OF HUMAN IL-10 COMPLEXED WITH THE SOLUBLE IL-10R1 CHAIN	IMMUNE SYSTEM

1Y6M	CRYSTAL STRUCTURE OF EPSTEIN-BARR VIRUS IL-10 COMPLEXED WITH THE SOLUBLE IL-10R1 CHAIN	IMMUNE SYSTEM
1Y6N	CRYSTAL STRUCTURE OF EPSTEIN-BARR VIRUS IL-10 MUTANT (A87I) COMPLEXED WITH THE SOLUBLE IL-10R1 CHAIN	IMMUNE SYSTEM
1Y75	A NEW FORM OF CATALYTICALLY INACTIVE PHOSPHOLIPASE A2 WITH AN UNUSUAL DISULPHIDE BRIDGE CYS 32- CYS 49 REVEALS RECOGNITION FOR N-ACETYLGLUCOSMINE	HYDROLASE
1Y77	COMPLETE RNA POLYMERASE II ELONGATION COMPLEX WITH SUBSTRATE ANALOGUE GMPCPP	TRANSFERASE/DNA/RNA
1Y7C	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAP100A DEOXY LOW-SALT (1 TEST SET)	TRANSPORT PROTEIN
1Y7D	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAP100G DEOXY LOW-SALT (1 TEST SET)	TRANSPORT PROTEIN
1Y7G	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAN102A DEOXY LOW-SALT (1 TEST SET)	TRANSPORT PROTEIN
1Y7L	O-ACETYLSERINE SULFHYDRYLASE COMPLEX	TRANSFERASE
1Y7Z	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAN108A DEOXY LOW-SALT (1 TEST SET)	TRANSPORT PROTEIN
1Y83	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAY145G DEOXY LOW-SALT (1 TEST SET)	TRANSPORT PROTEIN
1Y85	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: DESHIS146BETA DEOXY LOW-SALT	TRANSPORT PROTEIN
1Y8H	HORSE METHEMOGLOBIN LOW SALT, PH 7.0	OXYGEN STORAGE/TRANSPORT
1Y8I	HORSE METHEMOGLOBIN LOW SALT, PH 7.0 (98% RELATIVE HUMIDITY)	OXYGEN STORAGE/TRANSPORT
1Y8K	HORSE METHEMOGLOBIN LOW SALT, PH 7.0 (88% RELATIVE HUMIDITY)	OXYGEN STORAGE/TRANSPORT
1Y8N	CRYSTAL STRUCTURE OF THE PDK3-L2 COMPLEX	TRANSFERASE
1Y8O	CRYSTAL STRUCTURE OF THE PDK3-L2 COMPLEX	TRANSFERASE
1Y8P	CRYSTAL STRUCTURE OF THE PDK3-L2 COMPLEX	TRANSFERASE
1Y8Q	SUMO E1 ACTIVATING ENZYME SAE1-SAE2-MG-ATP COMPLEX	LIGASE
1Y8R	SUMO E1 ACTIVATING ENZYME SAE1-SAE2-SUMO1-MG-ATP COMPLEX	LIGASE
1Y8W	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: ALPHAR92A OXY (2MM IHP, 20% PEG) (10 TEST SETS)	TRANSPORT PROTEIN
1Y8X	STRUCTURAL BASIS FOR RECRUITMENT OF UBC12 BY AN E2-BINDING DOMAIN IN NEDD8'S E1	LIGASE

1Y96	CRYSTAL STRUCTURE OF THE GEMIN6/GEMIN7 HETERODIMER FROM THE HUMAN SMN COMPLEX	RNA BINDING PROTEIN
1Y98	STRUCTURE OF THE BRCT REPEATS OF BRCA1 BOUND TO A CTIP PHOSPHOPEPTIDE.	ANTITUMOR PROTEIN
1YA7	IMPLICATIONS FOR INTERACTIONS OF PROTEASOME WITH PAN AND PA700 FROM THE 1.9 A STRUCTURE OF A PROTEASOME-11S ACTIVATOR COMPLEX	HYDROLASE/HYDROLASE ACTIVATOR
1YAG	STRUCTURE OF THE YEAST ACTIN-HUMAN GELSOLIN SEGMENT 1 COMPLEX	CONTRACTILE PROTEIN
1YAR	STRUCTURE OF ARCHEABACTERIAL 20S PROTEASOME MUTANT D9S-PA26 COMPLEX	HYDROLASE/HYDROLASE ACTIVATOR
1YAU	STRUCTURE OF ARCHEABACTERIAL 20S PROTEASOME- PA26 COMPLEX	HYDROLASE/HYDROLASE ACTIVATOR
1YBO	CRYSTAL STRUCTURE OF THE PDZ TANDEM OF HUMAN SYNTENIN WITH SYNDECAN PEPTIDE	STRUCTURAL PROTEIN
1YBQ	CRYSTAL STRUCTURE OF ESCHERICHIA COLI ISOASPARTYL DIPEPTIDASE MUTANT D285N COMPLEXED WITH BETA-ASPARTYLHISTIDINE	HYDROLASE
1YC5	SIR2-P53 PEPTIDE-NICOTINAMIDE	HYDROLASE
1YCP	THE CRYSTAL STRUCTURE OF FIBRINOGEN-AA PEPTIDE 1-23 (F8Y) BOUND TO BOVINE THROMBIN EXPLAINS WHY THE MUTATION OF PHE-8 TO TYROSINE STRONGLY INHIBITS NORMAL CLEAVAGE AT ARGININE-16	COMPLEX (SERINE PROTEASE/PEPTIDE)
1YCQ	XENOPUS LAEVIS MDM2 BOUND TO THE TRANSACTIVATION DOMAIN OF HUMAN P53	COMPLEX (ONCOGENE PROTEIN/PEPTIDE)
1YCR	MDM2 BOUND TO THE TRANSACTIVATION DOMAIN OF P53	COMPLEX (ONCOGENE PROTEIN/PEPTIDE)
1YCS	P53-53BP2 COMPLEX	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1YD8	COMPLEX OF HUMAN GGA3 GAT DOMAIN AND UBIQUITIN	PROTEIN TRANSPORT, CHROMOSOMAL PROTEIN
1YDI	HUMAN VINCULIN HEAD DOMAIN (VH1, 1-258) IN COMPLEX WITH HUMAN ALPHA-ACTININ'S VINCULIN-BINDING SITE (RESIDUES 731-760)	CELL ADHESION, STRUCTURAL PROTEIN
1YDP	1.9A CRYSTAL STRUCTURE OF HLA-G	IMMUNE SYSTEM
1YDR	STRUCTURE OF CAMP-DEPENDENT PROTEIN KINASE, ALPHA-CATALYTIC SUBUNIT IN COMPLEX WITH H7 PROTEIN KINASE INHIBITOR 1-(5-ISOQUINOLINESULFONYL)-2-METHYLPIPERAZINE	COMPLEX (PHOSPHOTRANSFERASE/INHIBITOR)
1YDS	STRUCTURE OF CAMP-DEPENDENT PROTEIN KINASE, ALPHA-CATALYTIC SUBUNIT IN COMPLEX WITH H8 PROTEIN KINASE INHIBITOR [N-(2-METHYLAMINO)ETHYL]-5-ISOQUINOLINESULFONAMIDE	COMPLEX (PHOSPHOTRANSFERASE/INHIBITOR)

1YDT	STRUCTURE OF CAMP-DEPENDENT PROTEIN KINASE, ALPHA-CATALYTIC SUBUNIT IN COMPLEX WITH H89 PROTEIN KINASE INHIBITOR N-[2-(4-BROMOCINNAMYLAMINO)ETHYL]-5-ISOQUINOLINE	COMPLEX (PHOSPHOTRANSFERASE/INHIBITOR)
1YDZ	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: ALPHAY140F OXY (2MM IHP, 20% PEG) (1 TEST SET)	TRANSPORT PROTEIN
1YE0	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAV33A OXY (2MM IHP, 20% PEG) (1 TEST SET)	TRANSPORT PROTEIN
1YE1	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAY35A OXY (2MM IHP, 20% PEG) (1 TEST SET)	TRANSPORT PROTEIN
1YE2	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAY35F OXY (2MM IHP, 20% PEG) (1 TEST SET)	TRANSPORT PROTEIN
1YE9	CRYSTAL STRUCTURE OF PROTEOLYTICALLY TRUNCATED CATALASE HPII FROM E. COLI	OXIDOREDUCTASE
1YEC	STRUCTURE OF A CATALYTIC ANTIBODY IGG2A FAB FRAGMENT (D2.3)	CATALYTIC ANTIBODY
1YED	STRUCTURE OF A CATALYTIC ANTIBODY IGG2A FAB FRAGMENT (D2.4)	CATALYTIC ANTIBODY
1YEE	STRUCTURE OF A CATALYTIC ANTIBODY, IGG2A FAB FRAGMENT (D2.5)	CATALYTIC ANTIBODY
1YEF	STRUCTURE OF IGG2A FAB FRAGMENT (D2.3) COMPLEXED WITH SUBSTRATE ANALOGUE	CATALYTIC ANTIBODY
1YEG	STRUCTURE OF IGG2A FAB FRAGMENT (D2.3) COMPLEXED WITH REACTION PRODUCT	CATALYTIC ANTIBODY
1YEH	STRUCTURE OF IGG2A FAB FRAGMENT	CATALYTIC ANTIBODY
1YEI	CATALYTIC ANTIBODY D2.3 COMPLEX	IMMUNE SYSTEM
1YEJ	CATALYTIC ANTIBODY COMPLEX	IMMUNE SYSTEM
1YEK	CATALYTIC ANTIBODY D2.3 COMPLEX	IMMUNE SYSTEM
1YEN	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAP36A OXY (2MM IHP, 20% PEG) (10 TEST SETS)	TRANSPORT PROTEIN
1YEO	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAW37A OXY (10 TEST SETS)	TRANSPORT PROTEIN
1YEQ	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAW37Y OXY (10 TEST SETS)	TRANSPORT PROTEIN
1YEU	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAW37G OXY (10 TEST SETS)	TRANSPORT PROTEIN
1YEV	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAW37E OXY (10 TEST SETS)	TRANSPORT PROTEIN
1YEW	CRYSTAL STRUCTURE OF PARTICULATE METHANE MONOOXYGENASE	OXIDOREDUCTASE, MEMBRANE PROTEIN

1YF4	CRYSTAL STRUCTURE OF TRYPSIN-VASOPRESSIN COMPLEX	HYDROLASE/HORMONE/GROWTH FACTOR
1YF6	STRUCTURE OF A QUINTUPLE MUTANT OF PHOTOSYNTHETIC REACTION CENTER FROM RHODOBACTER SPHAEROIDES	PHOTOSYNTHESIS
1YF8	CRYSTAL STRUCTURE OF HIMALAYAN MISTLETOE RIP REVEALS THE PRESENCE OF A NATURAL INHIBITOR AND A NEW FUNCTIONALLY ACTIVE SUGAR-BINDING SITE	HYDROLASE
1YFF	TRUCTURE OF HUMAN CARBONMONOXYHEMOGLOBIN C (BETA E6K): TWO QUATERNARY STATES (R2 AND R3) IN ONE CRYSTAL	OXYGEN STORAGE/TRANSPORT
1YFN	VERSATILE MODES OF PEPTIDE RECOGNITION BY THE AAA+ ADAPTOR PROTEIN SSPB- THE CRYSTAL STRUCTURE OF A SSPB-RSEA COMPLEX	PROTEIN BINDING
1YG5	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAW37H OXY (2MM IHP, 20% PEG) (10 TEST SETS)	TRANSPORT PROTEIN
1YGC	SHORT FACTOR VIIA WITH A SMALL MOLECULE INHIBITOR	HYDROLASE
1YGD	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAW37E ALPHA ZINC BETA OXY (10 TEST SETS)	TRANSPORT PROTEIN
1YGF	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAH97A OXY (2MM IHP, 20% PEG) (1 TEST SET)	TRANSPORT PROTEIN
1YGU	CRYSTAL STRUCTURE OF THE TANDEM PHOSPHATASE DOMAINS OF RPTP CD45 WITH A PTYR PEPTIDE	HYDROLASE
1YH9	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: HBA OXY (2MM IHP, 20% PEG) (10 TEST SETS)	TRANSPORT PROTEIN
1YHE	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: HBA OXY (5.0MM IHP, 20% PEG) (10 TEST SETS)	TRANSPORT PROTEIN
1YHN	STRUCTURE BASIS OF RILP RECRUITMENT BY RAB7	PROTEIN TRANSPORT
1YHQ	CRYSTAL STRUCTURE OF AZITHROMYCIN BOUND TO THE G2099A MUTANT 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1YHR	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: HBA OXY (10.0MM IHP, 20% PEG) (10 TEST SETS)	OXYGEN STORAGE/TRANSPORT
1YHU	CRYSTAL STRUCTURE OF RIFTIA PACHYPTILA C1 HEMOGLOBIN REVEALS NOVEL ASSEMBLY OF 24 SUBUNITS.	OXYGEN STORAGE/TRANSPORT
1YI2	CRYSTAL STRUCTURE OF ERYTHROMYCIN BOUND TO THE G2099A MUTANT 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1YI5	CRYSTAL STRUCTURE OF THE A-COBRATOXIN-ACHBP COMPLEX	TOXIN
1YIE	T-TO-THIGH QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAW37A OXY (2.2MM IHP, 13% PEG) (1 TEST SET)	OXYGEN STORAGE/TRANSPORT

1YIH	T-TO-T(HIGH) QUATERNARY TRANSITIONS IN HUMAN HEMOGLOBIN: BETAP100A OXY (2.2MM IHP, 20% PEG) (1 TEST SET)	OXYGEN STORAGE/TRANSPORT
1YIJ	CRYSTAL STRUCTURE OF TELITHROMYCIN BOUND TO THE G2099A MUTANT 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1YIT	CRYSTAL STRUCTURE OF VIRGINIAMYCIN M AND S BOUND TO THE 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1YJ5	OLECULAR ARCHITECTURE OF MAMMALIAN POLYNUCLEOTIDE KINASE, A DNA REPAIR ENZYME	TRANSFERASE
1YJ9	CRYSTAL STRUCTURE OF THE MUTANT 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI CONTAINING A THREE RESIDUE DELETION IN L22	RIBOSOME
1YJD	CRYSTAL STRUCTURE OF HUMAN CD28 IN COMPLEX WITH THE FAB FRAGMENT OF A MITOGENIC ANTIBODY (5.11A1)	IMMUNE SYSTEM/SIGNALING PROTEIN
1YJN	RYSTAL STRUCTURE OF CLINDAMYCIN BOUND TO THE G2099A MUTANT 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1YJW	CRYSTAL STRUCTURE OF QUINUPRISTIN BOUND TO THE G2099A MUTANT 50S RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
1YK0	TRUCTURE OF NATRIURETIC PEPTIDE RECEPTOR-C COMPLEXED WITH ATRIAL NATRIURETIC PEPTIDE	HORMONE/GROWTH FACTOR RECEPTOR
1YK1	TRUCTURE OF NATRIURETIC PEPTIDE RECEPTOR-C COMPLEXED WITH BRAIN NATRIURETIC PEPTIDE	HORMONE/GROWTH FACTOR RECEPTOR
1YKE	STRUCTURE OF THE MEDIATOR MED7/MED21 SUBCOMPLEX	GENE REGULATION
1YKH	TRUCTURE OF THE MEDIATOR MED7/MED21 (MED7/SRB7) SUBCOMPLEX	GENE REGULATION
1YKK	PROTOCATECHUATE 3,4-DIOXYGENASE Y408C MUTANT	OXIDOREDUCTASE
1YKL	PROTOCATECHUATE 3,4-DIOXYGENASE Y408C MUTANT BOUND TO DHB	OXIDOREDUCTASE
1YKM	PROTOCATECHUATE 3,4-DIOXYGENASE Y408E MUTANT	OXIDOREDUCTASE
1YKN	PROTOCATECHUATE 3,4-DIOXYGENASE Y408E MUTANT BOUND TO DHB	OXIDOREDUCTASE
1YKO	PROTOCATECHUATE 3,4-DIOXYGENASE Y408H MUTANT	OXIDOREDUCTASE
1YKP	PROTOCATECHUATE 3,4-DIOXYGENASE Y408H MUTANT BOUND TO DHB	OXIDOREDUCTASE
1YL3	CRYSTAL STRUCTURE OF 70S RIBOSOME WITH THRS OPERATOR AND TRNAS. LARGE SUBUNIT. THE COORDINATES FOR THE SMALL SUBUNIT ARE IN THE PDB ENTRY 1YL4.	RIBOSOME
1YL4	CRYSTAL STRUCTURE OF 70S RIBOSOME WITH THRS OPERATOR AND TRNAS. 30S SUBUNIT. THE COORDINATES FOR THE 50S SUBUNIT ARE IN THE PDB ENTRY 1YL3	RIBOSOME

1YM0	CRYSTAL STRUCTURE OF EARTHWORM FIBRINOLYTIC ENZYME COMPONENT B: A NOVEL, GLYCOSYLATED TWO-CHAINED TRYPSIN	HYDROLASE
1YMH	ANTI-HCV FAB 19D9D6 COMPLEXED WITH PROTEIN L (PPL) MUTANT A66W	IMMUNE SYSTEM
1YMM	TCR/HLA-DR2B/MBP-PEPTIDE COMPLEX	IMMUNE SYSTEM
1YMT	MOUSE SF-1 LBD	TRANSCRIPTION
1YN6	CRYSTAL STRUCTURE OF A MOUSE MHC CLASS I PROTEIN, H2-DB, IN COMPLEX WITH A PEPTIDE FROM THE INFLUENZA A ACID POLYMERASE	IMMUNE SYSTEM
1YN7	CRYSTAL STRUCTURE OF A MOUSE MHC CLASS I PROTEIN, H2-DB, IN COMPLEX WITH A MUTATED PEPTIDE (R7A) OF THE INFLUENZA A ACID POLYMERASE	IMMUNE SYSTEM
1YNJ	TAQ RNA POLYMERASE-SORANGICIN COMPLEX	TRANSFERASE
1YNK	IDENTIFICATION OF KEY RESIDUES OF THE NC6.8 FAB ANTIBODY FRAGMENT BINDING TO SYNTHETIC SWEETENERS: CRYSTAL STRUCTURE OF NC6.8 CO-CRYSTALIZED WITH HIGH POTENCY SWEETENER COMPOUND SC45647	IMMUNE SYSTEM
1YNL	IDENTIFICATION OF KEY RESIDUES OF THE NC6.8 FAB ANTIBODY FRAGMENT BINDING TO SYNTHETIC SWEETERNERS: CRYSTAL STRUCTURE OF NC6.8 CO-CRYSTALIZED WITH HIGH POTENCY SWEETENER COMPOUND SC45647	IMMUNE SYSTEM
1YNN	TAQ RNA POLYMERASE-RIFAMPICIN COMPLEX	TRANSFERASE
1YNT	STRUCTURE OF THE IMMUNODOMINANT EPITOPE DISPLAYED BY THE SURFACE ANTIGEN 1 (SAG1) OF TOXOPLASMA GONDII COMPLEXED TO A MONOCLONAL ANTIBODY	IMMUNE SYSTEM
1YOK	CRYSTAL STRUCTURE OF HUMAN LRH-1 BOUND WITH TIF-2 PEPTIDE AND PHOSPHATIDYLGLYCEROL	TRANSCRIPTION
1YOV	INSIGHTS INTO THE UBIQUITIN TRANSFER CASCADE FROM THE REFINED STRUCTURE OF THE ACTIVATING ENZYME FOR NEDD8	SIGNALING PROTEIN
1YOW	HUMAN STEROIDOGENIC FACTOR 1 LBD WITH BOUND CO-FACTOR PEPTIDE	TRANSCRIPTION
1YP0	STRUCTURE OF THE STEROIDOGENIC FACTOR-1 LIGAND BINDING DOMAIN BOUND TO PHOSPHOLIPID AND A SHP PEPTIDE MOTIF	TRANSCRIPTION
1YPE	THROMBIN INHIBITOR COMPLEX	BLOOD CLOTTING/HYDROLASE INHIBITOR
1YPG	THROMBIN INHIBITOR COMPLEX	BLOOD CLOTTING/HYDROLASE INHIBITOR
1YPH	HIGH RESOLUTION STRUCTURE OF BOVINE ALPHA-CHYMOTRYPSIN	HYDROLASE
1YPJ	THROMBIN INHIBITOR COMPLEX	BLOOD CLOTTING/HYDROLASE INHIBITOR

1YPK	THROMBIN INHIBITOR COMPLEX	HYDROLASE
1YPL	X-RAY CRYSTAL STRUCTURE OF THROMBIN INHIBITED BY SYNTHETIC CYANOPEPTIDE ANALOGUE RA-1008	BLOOD CLOTTING/HYDROLASE INHIBITOR
1YPM	X-RAY CRYSTAL STRUCTURE OF THROMBIN INHIBITED BY SYNTHETIC CYANOPEPTIDE ANALOGUE RA-1014	BLOOD CLOTTING/HYDROLASE INHIBITOR
1YPZ	IMMUNE RECEPTOR	IMMUNE SYSTEM
1YQ3	AVIAN RESPIRATORY COMPLEX II WITH OXALOACETATE AND UBIQUINONE	OXIDOREDUCTASE
1YQ4	AVIAN RESPIRATORY COMPLEX II WITH 3-NITROPROPIONATE AND UBIQUINONE	OXIDOREDUCTASE
1YQ9	STRUCTURE OF THE UNREADY OXIDIZED FORM OF [NIFE] HYDROGENASE	OXIDOREDUCTASE
1YQV	THE CRYSTAL STRUCTURE OF THE ANTIBODY FAB HYHEL5 COMPLEX WITH LYSOZYME AT 1.7A RESOLUTION	IMMUNE SYSTEM
1YQW	STRUCTURE OF THE OXIDIZED UNREADY FORM OF NI-FE HYDROGENASE	OXIDOREDUCTASE
1YR5	1.7-A STRUCTURE OF CALMODULIN BOUND TO A PEPTIDE FROM DAP KINASE	METAL BINDING PROTEIN/TRANSFERASE
1YRN	CRYSTAL STRUCTURE OF THE MATA1/MATALPHA2 HOMEODOMAIN HETERODIMER BOUND TO DNA	DNA BINDING PROTEIN/DNA
1YRO	CRYSTAL STRUCTURE OF BETA14,-GALACTOSYLTRANSFERASE MUTANT ARG228LYS IN COMPLEX WITH ALPHA-LACTALBUMIN IN THE PRESENCE OF UDP-GALACTOSE AND MN	TRANSFERASE ACTIVATOR/TRANSFERASE
1YRQ	STRUCTURE OF THE READY OXIDIZED FORM OF [NIFE]-HYDROGENASE	OXIDOREDUCTASE
1YRT	CRYSTAL STRUCTURE ANALYSIS OF THE ADENYLYL CYCLAES CATALYTIC DOMAIN OF ADENYLYL CYCLASE TOXIN OF BORDETELLA PERTUSSIS IN PRESENCE OF C-TERMINAL CALMODULIN	LAYSE, TOXIN
1YRU	CRYSTAL STRUCTURE ANALYSIS OF THE ADENYLYL CYCLAES CATALYTIC DOMAIN OF ADENYLYL CYCLASE TOXIN OF BORDETELLA PERTUSSIS IN PRESENCE OF C-TERMINAL CALMODULIN AND 1MM CALCIUM CHLORIDE	LAYSE, TOXIN
1YSH	LOCALIZATION AND DYNAMIC BEHAVIOR OF RIBOSOMAL PROTEIN L30E	STRUCTURAL PROTEIN/RNA
1YST	STRUCTURE OF THE PHOTOCHEMICAL REACTION CENTER OF A SPHEROIDENE CONTAINING PURPLE BACTERIUM, RHODOBACTER SPHAEROIDES Y, AT 3 ANGSTROMS RESOLUTION	PHOTOSYNTHETIC REACTION CENTER
1YTF	YEAST TFIIA/TBP/DNA COMPLEX	TRANSCRIPTION/DNA
1YTG	SIV PROTEASE CRYSTALLIZED WITH PEPTIDE PRODUCT	COMPLEX (HYDROLASE/PEPTIDE)
1YTH	SIV PROTEASE CRYSTALLIZED WITH PEPTIDE PRODUCT	COMPLEX (HYDROLASE/PEPTIDE)

1YTV	MALTOSE-BINDING PROTEIN FUSION TO A C-TERMINAL FRAGMENT OF THE V1A VASOPRESSIN RECEPTOR	SUGAR BINDING PROTEIN, HORMONE RECEPTOR
1YTZ	CRYSTAL STRUCTURE OF SKELETAL MUSCLE TROPONIN IN THE CA2+-ACTIVATED STATE	CONTRACTILE PROTEIN
1YU6	RYSTAL STRUCTURE OF THE SUBTILISIN CARLSBERG:OMTKY3 COMPLEX	HYDROLASE
1YUC	UMAN NUCLEAR RECEPTOR LIVER RECEPTOR HOMOLOGUE-1, LRH-1, BOUND TO PHOSPHOLIPID AND A FRAGMENT OF HUMAN SHP	TRANSCRIPTION REGULATION
1YUH	FAB FRAGMENT	IMMUNOGLOBULIN
1YUK	THE CRYSTAL STRUCTURE OF THE PSI/HYBRID DOMAIN/ I-EGF1 SEGMENT FROM THE HUMAN INTEGRIN BETA2 AT 1.8 RESOLUTION	CELL ADHESION
1YV0	CRYSTAL STRUCTURE OF SKELETAL MUSCLE TROPONIN IN THE CA2+-FREE STATE	CONTRACTILE PROTEIN
1YVH	CRYSTAL STRUCTURE OF THE C-CBL TKB DOMAIN IN COMPLEX WITH THE APS PTYR-618 PHOSPHOPEPTIDE	LIGASE,SIGNALING PROTEIN,IMMUNE SYSTEM
1YVL	STRUCTURE OF UNPHOSPHORYLATED STAT1	SIGNALING PROTEIN
1YVN	THE YEAST ACTIN VAL 159 ASN MUTANT COMPLEX WITH HUMAN GELSOLIN SEGMENT 1.	STRUCTURAL PROTEIN
1YVQ	THE LOW SALT (PEG) CRYSTAL STRUCTURE OF CO HEMOGLOBIN E (BETAE26K) APPROACHING PHYSIOLOGICAL PH (PH 7.5)	TRANSPORT PROTEIN
1YVT	THE HIGH SALT (PHOSPHATE) CRYSTAL STRUCTURE OF CO HEMOGLOBIN E (GLU26LYS) AT PHYSIOLOGICAL PH (PH 7.35)	TRANSPORT PROTEIN
1YWH	CRYSTAL STRUCTURE OF UROKINASE PLASMINOGEN ACTIVATOR RECEPTOR	HYDROLASE RECEPTOR
1YWT	CRYSTAL STRUCTURE OF THE HUMAN SIGMA ISOFORM OF 14-3-3 IN COMPLEX WITH A MODE-1 PHOSPHOPEPTIDE	SIGNALING PROTEIN/DE NOVO PROTEIN
1YY4	RYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH 1-CHLORO-6-(4-HYDROXY-PHENYL)-NAPHTHALEN-2-OL	TRANSCRIPTION
1YY8	RYSTAL STRUCTURE OF THE FAB FRAGMENT FROM THE MONOCLONAL ANTIBODY CETUXIMAB/ERBITUX/IMC-C225	IMMUNE SYSTEM
1YY9	STRUCTURE OF THE EXTRACELLULAR DOMAIN OF THE EPIDERMAL GROWTH FACTOR RECEPTOR IN COMPLEX WITH THE FAB FRAGMENT OF CETUXIMAB/ERBITUX/IMC-C225	IMMUNE SYSTEM/SIGANLING PROTEIN
1YYE	RYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH WAY-202196	TRANSCRIPTION
1YYF	CORRECTION OF X-RAY INTENSITIES FROM AN HSLV-HSLU CO-CRYSTAL CONTAINING LATTICE TRANSLOCATION DEFECTS	CHAPERONE/HYDROLASE

1YYL	CRYSTAL STRUCTURE OF CD4M33, A SCORPION-TOXIN MIMIC OF CD4, IN COMPLEX WITH HIV-1 YU2 GP120 ENVELOPE GLYCOPROTEIN AND ANTI-HIV-1 ANTIBODY 17B	VIRAL PROTEIN/IMMUNE SYSTEM
1YYM	CRYSTAL STRUCTURE OF F23, A SCORPION-TOXIN MIMIC OF CD4, IN COMPLEX WITH HIV-1 YU2 GP120 ENVELOPE GLYCOPROTEIN AND ANTI-HIV-1 ANTIBODY 17B	VIRAL PROTEIN/IMMUNE SYSTEM
1YYP	CRYSTAL STRUCTURE OF CYTOMEGALOVIRUS UL44 BOUND TO C-TERMINAL PEPTIDE FROM CMV UL54	REPLICATION/TRANSFERASE
1YZI	A NOVEL QUATERNARY STRUCTURE OF HUMAN CARBONMONOXY HEMOGLOBIN	OXYGEN STORAGE/TRANSPORT
1Z0J	STRUCTURE OF GTP-BOUND RAB22Q64L GTPASE IN COMPLEX WITH THE MINIMAL RAB BINDING DOMAIN OF RABENOSYN-5	PROTEIN TRANSPORT
1Z0K	STRUCTURE OF GTP-BOUND RAB4Q67L GTPASE IN COMPLEX WITH THE CENTRAL RAB BINDING DOMAIN OF RABENOSYN-5	PROTEIN TRANSPORT
1Z2B	TUBULIN-COLCHICINE-VINBLASTINE: STATHMIN-LIKE DOMAIN COMPLEX	CELL CYCLE
1Z2C	CRYSTAL STRUCTURE OF MDIA1 GBD-FH3 IN COMPLEX WITH RHOC-GMPPNP	SIGNALING PROTEIN
1Z3E	CRYSTAL STRUCTURE OF SPX IN COMPLEX WITH THE C-TERMINAL DOMAIN OF THE RNA POLYMERASE ALPHA SUBUNIT	TRANSCRIPTION
1Z3G	RYSTAL STRUCTURE OF COMPLEX BETWEEN PVS25 AND FAB FRAGMENT OF MALARIA TRANSMISSION BLOCKING ANTIBODY 2A8	IMMUNE SYSTEM/CELL ADHESION
1Z3L	X-RAY CRYSTAL STRUCTURE OF A MUTANT RIBONUCLEASE S (F8ANB)	HYDROLASE
1Z3M	CRYSTAL STRUCTURE OF MUTANT RIBONUCLEASE S (F8NVA)	HYDROLASE
1Z3P	X-RAY CRYSTAL STRUCTURE OF A MUTANT RIBONUCLEASE S (M13NVA)	HYDROLASE
1Z56	CO-CRYSTAL STRUCTURE OF LIF1P-LIG4P	LIGASE
1Z5L	STRUCTURE OF A HIGHLY POTENT SHORT-CHAIN GALACTOSYL CERAMIDE AGONIST BOUND TO CD1D	IMMUNE SYSTEM
1Z5S	CRYSTAL STRUCTURE OF A COMPLEX BETWEEN UBC9, SUMO-1, RANGAP1 AND NUP358/RANBP2	LIGASE
1Z5X	HEMIPTERAN ECDYSONE RECEPTOR LIGAND-BINDING DOMAIN COMPLEXED WITH PONASTERONE A	HORMONE/GROWTH FACTOR RECEPTOR
1Z5Y	CRYSTAL STRUCTURE OF THE DISULFIDE-LINKED COMPLEX BETWEEN THE N-TERMINAL DOMAIN OF THE ELECTRON TRANSFER CATALYST DSBD AND THE CYTOCHROME C BIOGENESIS PROTEIN CCMG	OXIDOREDUCTASE/BIOSYNTHETIC PROTEIN
1Z6E	CRYSTAL STRUCTURE OF FACTOR XA COMPLEXED TO RAZAXABAN	HYDROLASE

1Z6J	CRYSTAL STRUCTURE OF A TERNARY COMPLEX OF FACTOR VIIA/TISSUE FACTOR/PYRAZINONE INHIBITOR	HYDROLASE
1Z6O	CRYSTAL STRUCTURE OF TRICHOPLUSIA NI SECRETED FERRITIN	METAL BINDING PROTEIN
1Z7M	ATP PHOSPHORIBOSYL TRANSFERASE (HISZG ATP-PRTASE) FROM LACTOCOCCUS LACTIS	TRANSFERASE
1Z7N	ATP PHOSPHORIBOSYL TRANSFERASE (HISZG ATP-PRTASE) FROM LACTOCOCCUS LACTIS WITH BOUND PRPP SUBSTRATE	TRANSFERASE
1Z7Q	CRYSTAL STRUCTURE OF THE 20S PROTEASOME FROM YEAST IN COMPLEX WITH THE PROTEASOME ACTIVATOR PA26 FROM TRYPANOSOME BRUCEI AT 3.2 ANGSTROMS RESOLUTION	HYDROLASE/HYDROLASE ACTIVATOR
1Z7X	X-RAY STRUCTURE OF HUMAN RIBONUCLEASE INHIBITOR COMPLEXED WITH RIBONUCLEASE I	HYDROLASE/HYDROLASE INHIBITOR
1Z8C	CRYSTAL STRUCTURE OF THE COMPLEX OF MUTANT HIV-1 PROTEASE (L63P, A71V, V82T, I84V) WITH A HYDROXYETHYLAMINE PEPTIDOMIMETIC INHIBITOR BOC-PHE-PSI[R-CH(OH)CH2NH]-PHE-GLU-PHE-NH2	HYDROLASE/HYDROLASE INHIBITOR
1Z8I	CRYSTAL STRUCTURE OF THE THROMBIN MUTANT G193A BOUND TO PPACK	HYDROLASE
1Z8J	CRYSTAL STRUCTURE OF THE THROMBIN MUTANT G193P BOUND TO PPACK	HYDROLASE
1Z8U	RYSTAL STRUCTURE OF OXIDIZED ALPHA HEMOGLOBIN BOUND TO AHSP	ELECTRON TRANSPORT
1Z8Y	MAPPING THE E2 GLYCOPROTEIN OF ALPHAVIRUSES	VIRUS
1Z92	STRUCTURE OF INTERLEUKIN-2 WITH ITS ALPHA RECEPTOR	IMMUNE SYSTEM
1Z9J	OTOSYNTHETIC REACTION CENTER FROM RHODOBACTER SPHAEROIDES	PHOTOSYNTHESIS
1Z9K	OTOSYNTHETIC REACTION CENTER FROM RHODOBACTER SPHAEROIDES	PHOTOSYNTHESIS
1Z9O	1.9 ANGSTROM CRYSTAL STRUCTURE OF THE RAT VAP-A MSP HOMOLOGY DOMAIN IN COMPLEX WITH THE RAT ORP1 FFAT MOTIF	PROTEIN BINDING/LIPID BINDING PROTEIN
1ZA1	STRUCTURE OF WILD-TYPE E. COLI ASPARTATE TRANSCARBAMOYLASE IN THE PRESENCE OF CTP AT 2.20 A RESOLUTION	TRANSFERASE
1ZA2	STRUCTURE OF WILD-TYPE E. COLI ASPARTATE TRANSCARBAMOYLASE IN THE PRESENCE OF CTP, CARBAMOYL PHOSPHATE AT 2.50 A RESOLUTION	TRANSFERASE
1ZA3	THE CRYSTAL STRUCTURE OF THE YSD1 FAB BOUND TO DR5	IMMUNE SYSTEM/SIGNALING PROTEIN
1ZA6	HE STRUCTURE OF AN ANTITUMOR CH2-DOMAIN-DELETED HUMANIZED ANTIBODY	IMMUNE SYSTEM
1ZAF	RYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH	TRANSCRIPTION/TRANSFERASE

	3-BROMO-6-HYDROXY-2-(4-HYDROXY-PHENYL)-INDEN-1-ONE	
1ZAN	CRYSTAL STRUCTURE OF ANTI-NGF AD11 FAB	IMMUNE SYSTEM
1ZAV	RIBOSOMAL PROTEIN L10-L12(NTD) COMPLEX, SPACE GROUP P21	STRUCTURAL PROTEIN
1ZAW	RIBOSOMAL PROTEIN L10-L12(NTD) COMPLEX, SPACE GROUP P212121, FORM A	STRUCTURAL PROTEIN
1ZAX	RIBOSOMAL PROTEIN L10-L12(NTD) COMPLEX, SPACE GROUP P212121, FORM B	STRUCTURAL PROTEIN
1ZB5	RECOGNITION OF PEPTIDE LIGANDS BY SIGNALLING PROTEIN FROM PORCINE MAMMARY GLAND (SPP-40): CRYSTAL STRUCTURE OF THE COMPLEX OF SPP-40 WITH A PEPTIDE TRP-PRO-TRP AT 2.45A RESOLUTION	SIGNALING PROTEIN
1ZBB	STRUCTURE OF THE 4_601_167 TETRANUCLEOSOME	STRUCTURAL PROTEIN/DNA
1ZBD	STRUCTURAL BASIS OF RAB EFFECTOR SPECIFICITY: CRYSTAL STRUCTURE OF THE SMALL G PROTEIN RAB3A COMPLEXED WITH THE EFFECTOR DOMAIN OF RABPHILIN-3A	G PROTEIN
1ZBG	CRYSTAL STRUCTURE OF A COMPLEX OF MUTANT HIV-1 PROTEASE (A71V, V82T, I84V) WITH A HYDROXYETHYLAMINE PEPTIDOMIMETIC INHIBITOR BOC-PHE-PSI[R-CH(OH)CH2NH]-PHE-GLU-PHE-NH2	HYDROLASE/HYDROLASE INHIBITOR
1ZBX	CRYSTAL STRUCTURE OF A ORC1P-SIR1P COMPLEX	TRANSCRIPTION
1ZC3	CRYSTAL STRUCTURE OF THE RAL-BINDING DOMAIN OF EXO84 IN COMPLEX WITH THE ACTIVE RALA	SIGNALING PROTEIN
1ZC4	CRYSTAL STRUCTURE OF THE RAL-BINDING DOMAIN OF EXO84 IN COMPLEX WITH THE ACTIVE RALA	SIGNALING PROTEIN
1ZDT	THE CRYSTAL STRUCTURE OF HUMAN STEROIDOGENIC FACTOR-1	TRANSCRIPTION
1ZDU	HE CRYSTAL STRUCTURE OF HUMAN LIVER RECEPTOR HOMOLOGUE-1	TRANSCRIPTION
1ZE3	CRYSTAL STRUCTURE OF THE TERNARY COMPLEX OF FIMD (N-TERMINAL DOMAIN) WITH FIMC AND THE PILIN DOMAIN OF FIMH	CHAPERONE/STRUCTURAL/MEMBRANE PROTEIN
1ZEA	STRUCTURE OF THE ANTI-CHOLERA TOXIN ANTIBODY FAB FRAGMENT TE33 IN COMPLEX WITH A D-PEPTIDE	IMMUNE SYSTEM
1ZEG	STRUCTURE OF B28 ASP INSULIN IN COMPLEX WITH PHENOL	HORMONE
1ZEH	STRUCTURE OF INSULIN	HORMONE
1ZFP	ROWTH FACTOR RECEPTOR BINDING PROTEIN SH2 DOMAIN COMPLEXED WITH A PHOSPHOTYROSYL PENTAPEPTIDE	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)
1ZGL	CRYSTAL STRUCTURE OF 3A6 TCR BOUND TO MBP/HLA-DR2A	IMMUNE SYSTEM
1ZGX	CRYSTAL STRUCTURE OF RIBONUCLEASE MUTANT	HYDROLASE

1ZGY	STRUCTURAL AND BIOCHEMICAL BASIS FOR SELECTIVE REPRESSION OF THE ORPHAN NUCLEAR RECEPTOR LRH-1 BY SHP	TRANSCRIPTION
1ZH7	STRUCTURAL AND BIOCHEMICAL BASIS FOR SELECTIVE REPRESSION OF THE ORPHAN NUCLEAR RECEPTOR LRH-1 BY SHP	TRANSCRIPTION
1ZHB	CRYSTAL STRUCTURE OF THE MURINE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX OF H-2DB, B2-MICROGLOBULIN, AND A 9-RESIDUE PEPTIDE DERIVED FROM RAT DOPAMINE BETA-MONOOXIGENASE	IMMUNE SYSTEM
1ZHH	CRYSTAL STRUCTURE OF THE APO FORM OF VIBRIO HARVEYI LUXP COMPLEXED WITH THE PERIPLASMIC DOMAIN OF LUXQ	SIGNALING PROTEIN
1ZHI	COMPLEX OF THE S. CEREVISIAE ORC1 AND SIR1 INTERACTING DOMAINS	TRANSCRIPTION/REPLICATION
1ZHK	CRYSTAL STRUCTURE OF HLA-B*3501 PRESENTING 13-MER EBV ANTIGEN LPEPLPQGQLTAY	IMMUNE SYSTEM
1ZHL	CRYSTAL STRUCTURE OF HLA-B*3508 PRESENTING 13-MER EBV ANTIGEN LPEPLPQGQLTAY	IMMUNE SYSTEM
1ZKY	HUMAN ESTROGEN RECEPTOR ALPHA LIGAND-BINDING DOMAIN IN COMPLEX WITH OBCP-3M AND A GLUCOCORTICOID RECEPTOR INTERACTING PROTEIN 1 NR BOX II PEPTIDE	HORMONE/GROWTH FACTOR RECEPTOR
1ZLA	X-RAY STRUCTURE OF A KAPOSI'S SARCOMA HERPESVIRUS LANA PEPTIDE BOUND TO THE NUCLEOSOMAL CORE	PROTEIN BINDING/VIRUS/DNA
1ZLF	CRYSTAL STRUCTURE OF A COMPLEX OF MUTANT HIV-1 PROTEASE (A71V, V82T, I84V) WITH A HYDROXYETHYLAMINE PEPTIDOMIMETIC INHIBITOR	HYDROLASE/HYDROLASE INHIBITOR
1ZLH	CRYSTAL STRUCTURE OF THE TICK CARBOXYPEPTIDASE INHIBITOR IN COMPLEX WITH BOVINE CARBOXYPEPTIDASE A	HYDROLASE/HYDROLASE INHIBITOR
1ZLI	CRYSTAL STRUCTURE OF THE TICK CARBOXYPEPTIDASE INHIBITOR IN COMPLEX WITH HUMAN CARBOXYPEPTIDASE B	HYDROLASE/HYDROLASE INHIBITOR
1ZLU	FAB 2G12 + MAN5	IMMUNE SYSTEM
1ZLW	FAB 2G12 + MAN8	IMMUNE SYSTEM
1ZM2	STRUCTURE OF ADP-RIBOSYLATED EEF2 IN COMPLEX WITH CATALYTIC FRAGMENT OF ETA	BIOSYNTHETIC PROTEIN/TRANSFERASE
1ZM3	STRUCTURE OF THE APO EEF2-ETA COMPLEX	BIOSYNTHETIC PROTEIN/TRANSFERASE
1ZM4	STRUCTURE OF THE EEF2-ETA-BTAD COMPLEX	BIOSYNTHETIC PROTEIN/TRANSFERASE
1ZM6	CRYSTAL STRUCTURE OF THE COMPLEX FORMED BEWEEN A GROUP I PHOSPHOLIPASE A2 AND DESIGNED PENTA PEPTIDE LEU-ALA-ILE-TYR-SER AT 2.6A RESOLUTION	HYDROLASE

1ZM9	STRUCTURE OF EEF2-ETA IN COMPLEX WITH PJ34	BIOSYNTHETIC PROTEIN/TRANSFERASE
1ZMY	CABBCII-10 VHH FRAMEWORK WITH CDR LOOPS OF CABLYS3 GRAFTED ON IT AND IN COMPLEX WITH HEN EGG WHITE LYSOZYME	IMMUNE SYSTEM/HYDROLASE
1ZNI	INSULIN	HORMONE
1ZNJ	INSULIN, MONOCLINIC CRYSTAL FORM	HORMONE
1ZNV	HOW A HIS-METAL FINGER ENDONUCLEASE COLE7 BINDS AND CLEAVES DNA WITH A TRANSITION METAL ION COFACTOR	HYDROLASE/PROTEIN BINDING
1ZO1	IF2, IF1, AND TRNA FITTED TO CRYO-EM DATA OF E. COLI 70S INITIATION COMPLEX	TRANSLATION/RNA
1ZOQ	IRF3-CBP COMPLEX	TRANSCRIPTION/TRANSFERASE
1ZOT	CRYSTAL STRUCTURE ANALYSIS OF THE CYAA/C-CAM WITH PMEAPP	LYASE
1ZOY	CRYSTAL STRUCTURE OF MITOCHONDRIAL RESPIRATORY COMPLEX II FROM PORCINE HEART AT 2.4 ANGSTROMS	OXIDOREDUCTASE
1ZP0	CRYSTAL STRUCTURE OF MITOCHONDRIAL RESPIRATORY COMPLEX II BOUND WITH 3-NITROPROPIONATE AND 2-THENOYLTRIFLUOROACETONE	OXIDOREDUCTASE
1ZPK	CRYSTAL STRUCTURE OF THE COMPLEX OF MUTANT HIV-1 PROTEASE (A71V, V82T, I84V) WITH A HYDROXYETHYLAMINE PEPTIDOMIMETIC INHIBITOR BOC-PHE-PSI[R-CH(OH)CH2NH]-PHE-GLU-PHE-NH2	HYDROLASE/HYDROLASE INHIBITOR
1ZQ1	STRUCTURE OF GATDE TRNA-DEPENDENT AMIDOTRANSFERASE FROM PYROCOCCUS ABYSSI	LYASE
1ZR0	CRYSTAL STRUCTURE OF KUNITZ DOMAIN 1 OF TISSUE FACTOR PATHWAY INHIBITOR-2 WITH BOVINE TRYPSIN	HYDROLASE/BLOOD CLOTTING
1ZRT	RHODOBACTER CAPSULATUS CYTOCHROME BC1 COMPLEX WITH STIGMATELLIN BOUND	OXIDOREDUCTASE/METAL TRANSPORT
1ZS8	CRYSTAL STRUCTURE OF THE MURINE MHC CLASS IB MOLECULE M10.5	IMMUNE SYSTEM
1ZSD	CRYSTAL STRUCTURE OF HLA-B*3501 PRESENTING AN 11-MER EBV ANTIGEN EPLPQGQLTAY	IMMUNE SYSTEM
1ZSF	CRYSTAL STRUCTURE OF COMPLEX OF A HYDROXYETHYLAMINE INHIBITOR WITH HIV-1 PROTEASE AT 2.0A RESOLUTION	HYDROLASE/HYDROLASE INHIBITOR
1ZSR	CRYSTAL STRUCTURE OF WILD TYPE HIV-1 PROTEASE (BRU ISOLATE) WITH A HYDROXYETHYLAMINE PEPTIDOMIMETIC INHIBITOR BOC-PHE-PSI[S-CH(OH)CH2NH]-PHE-GLU-PHE-NH2	HYDROLASE/HYDROLASE INHIBITOR
1ZSZ	CRYSTAL STRUCTURE OF A COMPUTATIONALLY DESIGNED SSPB HETERODIMER	DE NOVO PROTEIN
1ZT1	CRYSTAL STRUCTURE OF CLASS I MHC H-2KK IN COMPLEX WITH AN	IMMUNE SYSTEM

	OCTAPEPTIDE	
1ZT2	HETERODIMERIC STRUCTURE OF THE CORE PRIMASE.	REPLICATION, TRANSFERASE
1ZT4	THE CRYSTAL STRUCTURE OF HUMAN CD1D WITH AND WITHOUT ALPHA-GALACTOSYLCERAMIDE	IMMUNE SYSTEM
1ZT7	CRYSTAL STRUCTURE OF CLASS I MHC H-2KK IN COMPLEX WITH A NONAPEPTIDE	IMMUNE SYSTEM
1ZTX	WEST NILE VIRUS ENVELOPE PROTEIN DIII IN COMPLEX WITH NEUTRALIZING E16 ANTIBODY FAB	VIRAL PROTEIN/IMMUNE SYSTEM
1ZTZ	RYSTAL STRUCTURE OF HIV PROTEASE- METALLACARBORANE COMPLEX	HYDROLASE
1ZUN	CRYSTAL STRUCTURE OF A GTP-REGULATED ATP SULFURYLASE HETERODIMER FROM PSEUDOMONAS SYRINGAE	TRANSFERASE
1ZUZ	CALMODULIN IN COMPLEX WITH A MUTANT PEPTIDE FROM HUMAN DRP-1 KINASE	METAL BINDING PROTEIN/TRANSFERASE
1ZV5	CRYSTAL STRUCTURE OF THE VARIABLE DOMAIN OF THE CAMELID HEAVY-CHAIN ANTIBODY D2-L29 IN COMPLEX WITH HEN EGG WHITE LYSOZYME	HYDROLASE/IMMUNE SYSTEM
1ZV8	STRUCTURE-BASED MECHANISM OF SARS VIRUS MEMBRANE FUSION	VIRUS/VIRAL PROTEIN
1ZVS	CRYSTAL STRUCTURE OF THE FIRST CLASS MHC MAMU AND TAT-TL8 COMPLEX	IMMUNE SYSTEM
1ZVV	CRYSTAL STRUCTURE OF A CCPA-CRH-DNA COMPLEX	TRANSCRIPTION/DNA
1ZVY	CRYSTAL STRUCTURE OF THE VHH D3-L11 IN COMPLEX WITH HEN EGG WHITE LYSOZYME	HYDROLASE/IMMUNE SYSTEM
1ZVZ	VINCULIN HEAD (0-258) IN COMPLEX WITH THE TALIN ROD RESIDUE 820-844	PROTEIN BINDING
1ZW2	VINCULIN HEAD (0-258) IN COMPLEX WITH THE TALIN ROD RESIDUES 2345-2369	PROTEIN BINDING
1ZW3	VINCULIN HEAD (0-258) IN COMPLEX WITH THE TALIN ROD RESIDUES 1630-1652	PROTEIN BINDING
1ZWI	STRUCTURE OF MUTANT KCSA POTASSIUM CHANNEL	IMMUNE SYSTEM/ION TRANSPORT
1ZXI	RECONSTITUTED CO DEHYDROGENASE FROM OLIGOTROPHA CARBOXIDOVORANS	OXIDOREDUCTASE
1ZY1	X-RAY STRUCTURE OF PEPTIDE DEFORMYLASE FROM ARABIDOPSIS THALIANA (ATPDF1A) IN COMPLEX WITH MET-ALA-SER	HYDROLASE
1ZY3	STRUCTURAL MODEL OF COMPLEX OF BCL-W PROTEIN WITH BID BH3-PEPTIDE	APOPTOSIS

1ZY8	HE CRYSTAL STRUCTURE OF DIHYDROLIPOAMIDE DEHYDROGENASE AND DIHYDROLIPOAMIDE DEHYDROGENASE-BINDING PROTEIN (DIDOMAIN) SUBCOMPLEX OF HUMAN PYRUVATE DEHYDROGENASE COMPLEX.	OXIDOREDUCTASE
1ZYQ	T7 DNA POLYMERASE IN COMPLEX WITH 8OG AND INCOMING DDATP	TRANSFERASE/ELECTRON TRANSPORT/DNA
1ZYR	RUCTURE OF THERMUS THERMOPHILUS RNA POLYMERASE HOLOENZYME IN COMPLEX WITH THE ANTIBIOTIC STREPTOLYDIGIN	TRANSCRIPTION,TRANSFERASE
1ZZD	STRUCTURES OF YEAST RIBONUCLEOTIDE REDUCTASE I	OXIDOREDUCTASE
207L	MUTANT HUMAN LYSOZYME C77A	COMPLEX (HYDROLASE (O-GLYCOSYL)/CYS)
25C8	CATALYTIC ANTIBODY 5C8, FAB-HAPTEN COMPLEX	CATALYTIC ANTIBODY
2A06	BOVINE CYTOCHROME BC1 COMPLEX WITH STIGMATELLIN BOUND	OXIDOREDUCTASE
2A0F	STRUCTURE OF D236A MUTANT E. COLI ASPARTATE TRANSCARBAMOYLASE IN PRESENCE OF PHOSPHONOACETAMIDE AT 2.90 A RESOLUTION	TRANSFERASE/TRANSFERASE REGULATOR
2A0L	CRYSTAL STRUCTURE OF KVAP-33H1 FV COMPLEX	MEMBRANE PROTEIN
2A0Q	STRUCTURE OF THROMBIN IN 400 MM POTASSIUM CHLORIDE	HYDROLASE
2A19	PKR KINASE DOMAIN- EIF2ALPHA- AMP-PNP COMPLEX.	PROTEIN SYNTHESIS/TRANSFERASE
2A1A	PKR KINASE DOMAIN-EIF2ALPHA COMPLEX	PROTEIN SYNTHESIS/TRANSFERASE
2A1D	STAPHYLOCOAGULASE BOUND TO BOVINE THROMBIN	HYDROLASE
2A1J	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE C-TERMINAL DOMAINS OF HUMAN XPF AND ERCC1	DNA BINDING PROTEIN
2A1T	STRUCTURE OF THE HUMAN MCAD:ETF E165BETAA COMPLEX	OXIDOREDUCTASE/ELECTRON TRANSPORT
2A1U	CRYSTAL STRUCTURE OF THE HUMAN ETF E165BETAA MUTANT	ELECTRON TRANSPORT
2A1W	ANTI-COCAINE ANTIBODY 7.5.21, CRYSTAL FORM I	IMMUNE SYSTEM
2A2Q	COMPLEX OF ACTIVE-SITE INHIBITED HUMAN COAGULATION FACTOR VIIA WITH HUMAN SOLUBLE TISSUE FACTOR IN THE PRESENCE OF CA2+, MG2+, NA+, AND ZN2+	HYDROLASE/BLOOD CLOTTING
2A2X	ORALLY ACTIVE THROMBIN INHIBITORS IN COMPLEX WITH THROMBIN INH12	HYDROLASE/HYDROLASE INHIBITOR
2A3G	THE STRUCTURE OF T6 BOVINE INSULIN	HORMONE/GROWTH FACTOR
2A3I	STRUCTURAL AND BIOCHEMICAL MECHANISMS FOR THE SPECIFICITY OF HORMONE BINDING AND COACTIVATOR ASSEMBLY BY MINERALOCORTICOID RECEPTOR	TRANSFERASE
2A3Z	TERNARY COMPLEX OF THE WH2 DOMAIN OF WASP WITH ACTIN-DNASE I	STRUCTURAL PROTEIN

2A40	TERNARY COMPLEX OF THE WH2 DOMAIN OF WAVE WITH ACTIN-DNASE I	STRUCTURAL PROTEIN
2A41	TERNARY COMPLEX OF THE WH2 DOMAIN OF WIP WITH ACTIN-DNASE I	STRUCTURAL PROTEIN
2A42	ACTIN-DNASE I COMPLEX	STRUCTURAL PROTEIN
2A45	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THROMBIN AND THE CENTRAL "E" REGION OF FIBRIN	BLOOD CLOTTING
2A4G	HEPATITIS C PROTEASE NS3-4A SERINE PROTEASE WITH KETOAMIDE INHIBITOR SCH225724 BOUND	VIRUS/VIRAL PROTEIN
2A4Q	HCV NS3 PROTEASE WITH NS4A PEPTIDE AND A COVALENTLY BOUND MACROCYCLIC KETOAMIDE COMPOUND.	VIRUS/VIRAL PROTEIN
2A4R	HCV NS3 PROTEASE DOMAIN WITH A KETOAMIDE INHIBITOR COVALENTLY BOUND.	VIRUS/VIRAL PROTEIN
2A50	FLUORESCENT PROTEIN ASFP595, WT, OFF-STATE	LUMINESCENT PROTEIN
2A52	FLUORESCENT PROTEIN ASFP595, S158V, ON-STATE	LUMINESCENT PROTEIN
2A53	FLUORESCENT PROTEIN ASFP595, A143S, OFF-STATE	LUMINESCENT PROTEIN
2A54	FLUORESCENT PROTEIN ASFP595, A143S, ON-STATE, 1MIN IRRADIATION	LUMINESCENT PROTEIN
2A56	FLUORESCENT PROTEIN ASFP595, A143S, ON-STATE, 5MIN IRRADIATION	LUMINESCENT PROTEIN
2A5D	STRUCTURAL BASIS FOR THE ACTIVATION OF CHOLERA TOXIN BY HUMAN ARF6-GTP	PROTEIN TRANSPORT/TRANSFERASE
2A5F	CHOLERA TOXIN A1 SUBUNIT BOUND TO ITS SUBSTRATE, NAD+, AND ITS HUMAN PROTEIN ACTIVATOR, ARF6	PROTEIN TRANSPORT/TRANSFERASE
2A5G	CHOLERA TOXIN A1 SUBUNIT BOUND TO ARF6(Q67L)	PROTEIN TRANSPORT/TRANSFERASE
2A5T	CRYSTAL STRUCTURE OF THE NR1/NR2A LIGAND-BINDING CORES COMPLEX	METAL TRANSPORT,MEMBRANE PROTEIN
2A5Y	STRUCTURE OF A CED-4/CED-9 COMPLEX	APOPTOSIS
2A68	CRYSTAL STRUCTURE OF THE T. THERMOPHILUS RNA POLYMERASE HOLOENZYME IN COMPLEX WITH ANTIBIOTIC RIFABUTIN	TRANSFERASE
2A69	CRYSTAL STRUCTURE OF THE T. THERMOPHILUS RNA POLYMERASE HOLOENZYME IN COMPLEX WITH ANTIBIOTIC RIFAPENTIN	TRANSFERASE
2A6D	CRYSTAL STRUCTURE ANALYSIS OF THE ANTI-ARSONATE GERMLINE ANTIBODY 36-65 IN COMPLEX WITH A PHAGE DISPLAY DERIVED DODECAPEPTIDE RLLIADPPSPRE	IMMUNE SYSTEM
2A6E	CRYSTAL STRUCTURE OF THE T. THERMOPHILUS RNA POLYMERASE HOLOENZYME	TRANSFERASE

2A6H	CRYSTAL STRUCTURE OF THE T. THERMOPHILUS RNA POLYMERASE HOLOENZYME IN COMPLEX WITH ANTIBIOTIC STERPTOLYDIGIN	TRANSFERASE
2A6I	CRYSTAL STRUCTURE ANALYSIS OF THE ANTI-ARSONATE GERMLINE ANTIBODY 36-65 IN COMPLEX WITH A PHAGE DISPLAY DERIVED DODECAPEPTIDE KLASIPTHTSPL	IMMUNE SYSTEM
2A6J	CRYSTAL STRUCTURE ANALYSIS OF THE ANTI-ARSONATE GERMLINE ANTIBODY 36-65	IMMUNE SYSTEM
2A6K	CRYSTAL STRUCTURE ANALYSIS OF THE GERMLINE ANTIBODY 36-65 FAB IN COMPLEX WITH THE DODECAPEPTIDE SLGDNLTNHNLR	IMMUNE SYSTEM
2A6Q	CRYSTAL STRUCTURE OF YEFM-YOEB COMPLEX	TOXIN INHIBITOR/TOXIN
2A74	HUMAN COMPLEMENT COMPONENT C3C	IMMUNE SYSTEM
2A77	ANTI-COCAINE ANTIBODY 7.5.21, CRYSTAL FORM II	IMMUNE SYSTEM
2A78	CRYSTAL STRUCTURE OF THE C3BOT-RALA COMPLEX REVEALS A NOVEL TYPE OF ACTION OF A BACTERIAL EXOENZYME	PROTEIN BINDING/TRANSFERASE
2A79	MAMMALIAN SHAKER KV1.2 POTASSIUM CHANNEL- BETA SUBUNIT COMPLEX	MEMBRANE PROTEIN
2A7U	NMR SOLUTION STRUCTURE OF THE E.COLI F-ATPASE DELTA SUBUNIT N-TERMINAL DOMAIN IN COMPLEX WITH ALPHA SUBUNIT N-TERMINAL 22 RESIDUES	HYDROLASE
2A83	CRYSTAL STRUCTURE OF HLA-B*2705 COMPLEXED WITH THE GLUCAGON RECEPTOR (GR) PEPTIDE (RESIDUES 412-420)	IMMUNE SYSTEM
2A9H	NMR STRUCTURAL STUDIES OF A POTASSIUM CHANNEL / CHARYBDOTOXIN COMPLEX	METAL TRANSPORT, MEMBRANE PROTEIN
2A9K	CRYSTAL STRUCTURE OF THE C3BOT-NAD-RALA COMPLEX REVEALS A NOVEL TYPE OF ACTION OF A BACTERIAL EXOENZYME	PROTEIN BINDING/TRANSFERASE
2A9M	STRUCTURAL ANALYSIS OF A TIGHT-BINDING FLUORESCEIN-SCFV; APO FORM	IMMUNE SYSTEM
2AA1	CRYSTAL STRUCTURE OF THE CATHODIC HEMOGLOBIN ISOLATED FROM THE ANTARCTIC FISH TREMATOMUS NEWNESI	OXYGEN STORAGE/TRANSPORT
2AAB	STRUCTURAL BASIS OF ANTIGEN MIMICRY IN A CLINICALLY RELEVANT MELANOMA ANTIGEN SYSTEM	IMMUNE SYSTEM
2AAI	CRYSTALLOGRAPHIC REFINEMENT OF RICIN TO 2.5 ANGSTROMS	GLYCOSIDASE
2ABZ	CRYSTAL STRUCTURE OF C19A/C43A MUTANT OF LEECH CARBOXYPEPTIDASE INHIBITOR IN COMPLEX WITH BOVINE CARBOXYPEPTIDASE A	HYDROLASE/HYDROLASE INHIBITOR
2ACH	CRYSTAL STRUCTURE OF CLEAVED HUMAN ALPHA1-ANTICHYMOTRYPSIN	PROTEINASE INHIBITOR

	AT 2.7 ANGSTROMS RESOLUTION AND ITS COMPARISON WITH OTHER SERPINS	
2ACL	LIVER X-RECEPTOR ALPHA LIGAND BINDING DOMAIN WITH SB313987	TRANSCRIPTION
2ACZ	COMPLEX II (SUCCINATE DEHYDROGENASE) FROM E. COLI WITH ATPENIN A5 INHIBITOR CO-CRYSTALLIZED AT THE UBIQUINONE BINDING SITE	OXIDOREDUCTASE/ELECTRON TRANSPORT
2AD6	CRYSTAL STRUCTURE OF METHANOL DEHYDROGENASE FROM M. W3A1 (FORM C)	OXIDOREDUCTASE
2AD7	CRYSTAL STRUCTURE OF METHANOL DEHYDROGENASE FROM M. W3A1 (FORM C) IN THE PRESENCE OF METHANOL	OXIDOREDUCTASE
2AD8	CRYSTAL STRUCTURE OF METHANOL DEHYDROGENASE FROM M. W3A1 (FORM C) IN THE PRESENCE OF ETHANOL	OXIDOREDUCTASE
2ADF	CRYSTAL STRUCTURE AND PARATOPE DETERMINATION OF 82D6A3, AN ANTITHROMBOTIC ANTIBODY DIRECTED AGAINST THE VON WILLEBRAND FACTOR A3-DOMAIN	BLOOD CLOTTING/IMMUNE SYSTEM
2ADG	CRYSTAL STRUCTURE OF MONOCLONAL ANTI-CD4 ANTIBODY Q425	IMMUNE SYSTEM
2ADI	CRYSTAL STRUCTURE OF MONOCLONAL ANTI-CD4 ANTIBODY Q425 IN COMPLEX WITH BARIUM	IMMUNE SYSTEM
2ADJ	CRYSTAL STRUCTURE OF MONOCLONAL ANTI-CD4 ANTIBODY Q425 IN COMPLEX WITH CALCIUM	IMMUNE SYSTEM
2ADV	CRYSTAL STRUCTURES OF GLUTARYL 7-AMINOCEPHALOSPORANIC ACID ACYLASE: MUTATIONAL STUDY OF ACTIVATION MECHANISM	HYDROLASE
2AE3	GLUTARYL 7-AMINOCEPHALOSPORANIC ACID ACYLASE: MUTATIONAL STUDY OF ACTIVATION MECHANISM	HYDROLASE
2AE4	GLUTARYL 7-AMINOCEPHALOSPORANIC ACID ACYLASE: MUTATIONAL STUDY OF ACTIVATION MECHANISM	HYDROLASE
2AE5	GLUTARYL 7-AMINOCEPHALOSPORANIC ACID ACYLASE: MUTATIONAL STUDY OF ACTIVATION MECHANISM	HYDROLASE
2AEI	CRYSTAL STRUCTURE OF A TERNARY COMPLEX OF FACTOR VIIA/TISSUE FACTOR AND 2-[[6-[3-(AMINOIMINOMETHYL)PHENOXY]-3,5-DIFLURO-4-[(1-METHYL-3-PHENYLPROPYL)AMINO]-2-PYRIDINYL]OXY]-BENZOIC ACID	HYDROLASE
2AER	CRYSTAL STRUCTURE OF BENZAMIDINE-FACTOR VIIA/SOLUBLE TISSUE FACTOR COMPLEX.	BLOOD CLOTTING
2AFH	CRYSTAL STRUCTURE OF NUCLEOTIDE-FREE AV2-AV1 COMPLEX	OXIDOREDUCTASE
2AFI	CRYSTAL STRUCTURE OF MGADP BOUND AV2-AV1 COMPLEX	OXIDOREDUCTASE
2AFK	CRYSTAL STRUCTURE OF MGAMPPCP-BOUND AV2-AV1 COMPLEX	OXIDOREDUCTASE

2AFQ	1.9 ANGSTROM CRYTAL STRUCTURE OF WILD-TYPE HUMAN THROMBIN IN THE SODIUM FREE STATE	BLOOD CLOTTING,HYDROLASE
2AGE	SUCCINYL-AAPR-TRYPSIN ACYL-ENZYME AT 1.15 A RESOLUTION	HYDROLASE
2AGG	SUCCINYL-AAPK-TRYPSIN ACYL-ENZYME AT 1.28 A RESOLUTION	HYDROLASE
2AGI	THE LEUPEPTIN-TRYPSIN COVALENT COMPLEX AT 1.14 A RESOLUTION	HYDROLASE
2AGJ	CRYSTAL STRUCTURE OF A GLYCOSYLATED FAB FROM AN IGM CRYOGLOBULIN WITH PROPERTIES OF A NATURAL PROTEOLYTIC ANTIBODY	IMMUNE SYSTEM
2AGL	CRYSTAL STRUCTURE OF THE PHENYLHYDRAZINE ADDUCT OF AROMATIC AMINE DEHYDROGENASE FROM ALCALIGENES FAECALIS	OXIDOREDUCTASE
2AGW	CRYSTAL STRUCTURE OF TRYPTAMINE-REDUCED AROMATIC AMINE DEHYDROGENASE (AADH) FROM ALCALIGENES FAECALIS IN COMPLEX WITH TRYPTAMINE	OXIDOREDUCTASE
2AGX	CRYSTAL STRUCTURE OF THE SCHIFF BASE INTERMEDIATE IN THE REDUCTIVE HALF-REACTION OF AROMATIC AMINE DEHYDROGENASE (AADH) WITH TRYPTAMINE. P212121 FORM	OXIDOREDUCTASE
2AGZ	CRYSTAL STRUCTURE OF THE CARBINOLAMINE INTERMEDIATE IN THE REDUCTIVE HALF-REACTION OF AROMATIC AMINE DEHYDROGENASE (AADH) WITH TRYPTAMINE. F222 FORM	OXIDOREDUCTASE
2AHJ	NITRILE HYDRATASE COMPLEXED WITH NITRIC OXIDE	LYASE
2AHK	CRYSTAL STRUCTURE OF THE MET-FORM OF THE COPPER-BOUND STREPTOMYCES CASTANEOGLOBISPORUS TYROSINASE IN COMPLEX WITH A CADDIE PROTEIN OBTAINED BY SOKING IN CUPRIC SULFATE FOR 6 MONTHS	OXIDOREDUCTASE/METAL TRANSPORT
2AHL	CRYSTAL STRUCTURE OF THE HYDROXYLAMINE-INDUCED DEOXY-FORM OF THE COPPER-BOUND STREPTOMYCES CASTANEOGLOBISPORUS TYROSINASE IN COMPLEX WITH A CADDIE PROTEIN	OXIDOREDUCTASE/METAL TRANSPORT
2AHM	CRYSTAL STRUCTURE OF SARS-COV SUPER COMPLEX OF NON-STRUCTURAL PROTEINS: THE HEXADECAMER	VIRAL PROTEIN, REPLICATION
2AHO	STRUCTURE OF THE ARCHAEAL INITIATION FACTOR EIF2 ALPHA-GAMMA HETERODIMER FROM SULFOLOBUS SOLFATARICUS COMPLEXED WITH GDPNP	TRANSLATION
2AI0	ANTI-COCAINE ANTIBODY 7.5.21, CRYSTAL FORM III	IMMUNE SYSTEM
2AIG	ADAMALYSIN II WITH PEPTIDOMIMETIC INHIBITOR POL647	COMPLEX (METALLOPROTEASE/INHIBITOR)
2AIJ	FORMYLGLYCINE GENERATING ENZYME C336S MUTANT COVALENTLY BOUND TO SUBSTRATE PEPTIDE CTPSR	HYDROLASE ACTIVATOR,PROTEIN BINDING
2AIR	T-STATE ACTIVE SITE OF ASPARTATE TRANSCARBAMYLASE:CRYSTAL	TRANSFERASE

	STRUCTURE OF THE CARBAMYL PHOSPHATE AND L-ALANOSINE LIGATED ENZYME	
2AUH	CRYSTAL STRUCTURE OF THE GRB14 BPS REGION IN COMPLEX WITH THE INSULIN RECEPTOR TYROSINE KINASE	TRANSFERASE/SIGNALING PROTEIN
2B05	CRYSTAL STRUCTURE OF 14-3-3 GAMMA IN COMPLEX WITH A PHOSPHOSERINE PEPTIDE	CELL CYCLE
2B0S	CRYSTAL STRUCTURE ANALYSIS OF ANTI-HIV-1 V3 FAB 2219 IN COMPLEX WITH MN PEPTIDE	IMMMUNE SYSTEM
2B0U	THE STRUCTURE OF THE FOLLISTATIN:ACTIVIN COMPLEX	SIGNALING PROTEIN
2B0Z	CRYSTAL STRUCTURE OF THE PROTEIN-PROTEIN COMPLEX BETWEEN F82I CYTOCHROME C AND CYTOCHROME C PEROXIDASE	OXIDOREDUCTASE/ELECTRON TRANSPORT
2B10	CRYSTAL STRUCTURE OF THE PROTEIN-PROTEIN COMPLEX BETWEEN F82S CYTOCHROME C AND CYTOCHROME C PEROXIDASE	OXIDOREDUCTASE/ELECTRON TRANSPORT
2B11	CRYSTAL STRUCTURE OF THE PROTEIN-PROTEIN COMPLEX BETWEEN F82W CYTOCHROME C AND CYTOCHROME C PEROXIDASE	OXIDOREDUCTASE/ELECTRON TRANSPORT
2B12	CRYSTAL STRUCTURE OF THE PROTEIN-PROTEIN COMPLEX BETWEEN F82Y CYTOCHROME C AND CYTOCHROME C PEROXIDASE	OXIDOREDUCTASE/ELECTRON TRANSPORT
2B1A	CRYSTAL STRUCTURE ANALYSIS OF ANTI-HIV-1 V3 FAB 2219 IN COMPLEX WITH UG1033 PEPTIDE	IMMMUNE SYSTEM
2B1H	CRYSTAL STRUCTURE ANALYSIS OF ANTI-HIV-1 V3 FAB 2219 IN COMPLEX WITH UG29 PEPTIDE	IMMMUNE SYSTEM
2B1J	CRYSTAL STRUCTURE OF UNPHOSPHORYLATED CHEY BOUND TO THE N-TERMINUS OF FLIM	SIGNALING PROTEIN
2B1N	CRYSTAL STRUCTURE OF A PAPAIN-FOLD PROTEIN WITHOUT THE CATALYTIC CYSTEINE FROM SEEDS OF PACHYRHIZUS EROSUS	SUGAR BINDING PROTEIN
2B1V	HUMAN ESTROGEN RECEPTOR ALPHA LIGAND-BINDING DOMAIN IN COMPLEX WITH OBCP-1M AND A GLUCOCORTICOID RECEPTOR INTERACTING PROTEIN 1 NR BOX II PEPTIDE	HORMONE/GROWTH FACTOR RECEPTOR
2B1X	CRYSTAL STRUCTURE OF NAPHTHALENE 1,2-DIOXYGENASE FROM RHODOCOCCUS SP.	OXIDOREDUCTASE
2B1Z	HUMAN ESTROGEN RECEPTOR ALPHA LIGAND-BINDING DOMAIN IN COMPLEX WITH 17METHYL-17ALPHA-DIHYDROEQUILENIN AND A GLUCOC INTERACTING PROTEIN 1 NR BOX II PEPTIDE	HORMONE/GROWTH FACTOR RECEPTOR
2B23	HUMAN ESTROGEN RECEPTOR ALPHA LIGAND-BINDING DOMAIN AND A GLUCOCORTICOID RECEPTOR-INTERACTING PROTEIN 1 NR BOX II PEPTIDE	HORMONE/GROWTH FACTOR RECEPTOR
2B24	CRYSTAL STRUCTURE OF NAPHTHALENE 1,2-DIOXYGENASE FROM RHODOCOCCUS SP. BOUND TO INDOLE	OXIDOREDUCTASE

2B26	THE CRYSTAL STRUCTURE OF THE PROTEIN COMPLEX OF YEAST HSP40 SIS1 AND HSP70 SSA1	CHAPERONE/PROTEIN TRANSPORT
2B2T	ANDEM CHROMODOMAINS OF HUMAN CHD1 COMPLEXED WITH HISTONE H3 TAIL CONTAINING TRIMETHYLLYSINE 4 AND PHOSPHOTHREONINE 3	PEPTIDE BINDING PROTEIN
2B2U	ANDEM CHROMODOMAINS OF HUMAN CHD1 COMPLEXED WITH HISTONE H3 TAIL CONTAINING TRIMETHYLLYSINE 4 AND DIMETHYLARGININE 2	PEPTIDE BINDING PROTEIN
2B2V	CRYSTAL STRUCTURE ANALYSIS OF HUMAN CHD1 CHROMODOMAINS 1 AND 2 BOUND TO HISTONE H3 RESI 1-15 MEK4	PEPTIDE BINDING PROTEIN
2B2W	ANDEM CHROMODOMAINS OF HUMAN CHD1 COMPLEXED WITH HISTONE H3 TAIL CONTAINING TRIMETHYLLYSINE 4	PEPTIDE BINDING PROTEIN
2B2X	VLA1 RDELTAH I-DOMAIN COMPLEXED WITH A QUADRUPLE MUTANT OF THE AQC2 FAB	IMMUNE SYSTEM
2B2Y	TANDEM CHROMODOMAINS OF HUMAN CHD1	PEPTIDE BINDING PROTEIN
2B3G	P53N (FRAGMENT 33-60) BOUND TO RPA70N	REPLICATION
2B3T	MOLECULAR BASIS FOR BACTERIAL CLASS 1 RELEASE FACTOR METHYLATION BY PRMC	TRANSLATION
2B42	CRYSTAL STRUCTURE OF THE TRITICUM XYLANSE INHIBITOR-I IN COMPLEX WITH BACILLUS SUBTILIS XYLANASE	HYDROLASE INHIBITOR/HYDROLASE
2B4C	CRYSTAL STRUCTURE OF HIV-1 JR-FL GP120 CORE PROTEIN CONTAINING THE THIRD VARIABLE REGION (V3) COMPLEXED WITH CD4 AND THE X5 ANTIBODY	VIRAL PROTEIN/IMMUNE SYSTEM
2B4D	SSAT+COA+SP- SP DISORDERED	TRANSFERASE
2B4J	STRUCTURAL BASIS FOR THE RECOGNITION BETWEEN HIV-1 INTEGRASE AND LEDGF/P75	VIRAL PROTEIN, RECOMBINATION
2B4S	CRYSTAL STRUCTURE OF A COMPLEX BETWEEN PTP1B AND THE INSULIN RECEPTOR TYROSINE KINASE	HYDROLASE/TRANSFERASE
2B59	THE TYPE II COHESIN DOCKERIN COMPLEX	HYDROLASE/STRUCTURAL PROTEIN
2B5G	WILD TYPE SSAT- 1.7A STRUCTURE	TRANSFERASE
2B5I	CYTOKINE RECEPTOR COMPLEX	CYTOKINE/CYTOKINE RECEPTOR
2B5J	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE (RT) IN COMPLEX WITH JANSSEN-R165481	TRANSFERASE
2B5L	CRYSTAL STRUCTURE OF DDB1 IN COMPLEX WITH SIMIAN VIRUS 5 V PROTEIN	PROTEIN BINDING/VIRAL PROTEIN
2B5R	1B LACTAMASE / B LACTAMASE INHIBITOR	HYDROLASE/HYDROLASE INHIBITOR

2B5T	.1 ANGSTROM STRUCTURE OF A NONPRODUCTIVE COMPLEX BETWEEN ANTITHROMBIN, SYNTHETIC HEPARIN MIMETIC SR123781 AND TWO S195A THROMBIN MOLECULES	BLOOD CLOTTING
2B5U	CRYSTAL STRUCTURE OF COLICIN E3 V206C MUTANT IN COMPLEX WITH ITS IMMUNITY PROTEIN	RIBOSOME INHIBITOR, HYDROLASE
2B63	COMPLETE RNA POLYMERASE II-RNA INHIBITOR COMPLEX	TRANSFERASE/RNA
2B64	30S RIBOSOMAL SUBUNIT, TRNAS, MRNA AND RELEASE FACTOR RF1 FROM A CRYSTAL STRUCTURE OF THE WHOLE RIBOSOMAL COMPLEX. THIS FILE CONTAINS THE 30S SUBUNIT, TRNAS, MRNA AND RELEASE FACTOR RF1 FROM A CRYSTAL STRUCTURE OF THE WHOLE RIBOSOMAL COMPLEX". THE ENTIRE CRYSTAL STRUCTURE CONTAINS ONE 70S RIBOSOME, TRNAS, MRNA AND RELEASE FACTOR RF1 AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2B66	50S RIBOSOMAL SUBUNIT FROM A CRYSTAL STRUCTURE OF RELEASE FACTOR RF1, TRNAS AND MRNA BOUND TO THE RIBOSOME. THIS FILE CONTAINS THE 50S SUBUNIT FROM A CRYSTAL STRUCTURE OF RELEASE FACTOR RF1, TRNAS AND MRNA BOUND TO THE RIBOSOME AND IS DESCRIBED IN REMARK 400	RIBOSOME
2B6A	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE (RT) IN COMPLEX WITH THR-50	TRANSFERASE
2B6N	THE 1.8 A CRYSTAL STRUCTURE OF A PROTEINASE K LIKE ENZYME FROM A PSYCHROTROPH SERRATIA SPECIES	HYDROLASE
2B76	E. COLI QUINOL FUMARATE REDUCTASE FRDA E49Q MUTATION	OXIDOREDUCTASE
2B7B	YEAST GUANINE NUCLEOTIDE EXCHANGE FACTOR EEF1BALPHA K205A MUTANT IN COMPLEX WITH EEF1A AND GDP	TRANSLATION
2B7C	YEAST GUANINE NUCLEOTIDE EXCHANGE FACTOR EEF1BALPHA K205A MUTANT IN COMPLEX WITH EEF1A	TRANSLATION
2B7F	CRYSTAL STRUCTURE OF HUMAN T-CELL LEUKEMIA VIRUS PROTEASE, A NOVEL TARGET FOR ANTI-CANCER DESIGN	HYDROLASE
2B7H	HEMOGLOBIN FROM CERDOCYON THOUS, A CANIDAE FROM BRAZIL, AT 2.2 ANGSTROMS RESOLUTION	OXYGEN STORAGE/TRANSPORT
2B7Y	FAVA BEAN LECTIN-GLUCOSE COMPLEX	LECTIN
2B8K	12-SUBUNIT RNA POLYMERASE II	TRANSFERASE
2B8O	RYSTAL STRUCTURE OF GLU-GLY-ARG-CHLOROMETHYL KETONE-FACTOR VIIA/SOLUBLE TISSUE FACTOR COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
2B9H	CRYSTAL STRUCTURE OF FUS3 WITH A DOCKING MOTIF FROM STE7	TRANSFERASE
2B9I	CRYSTAL STRUCTURE OF FUS3 WITH A DOCKING MOTIF FROM MSG5	TRANSFERASE
2B9J	CRYSTAL STRUCTURE OF FUS3 WITH A DOCKING MOTIF FROM FAR1	TRANSFERASE

2B9M	30S RIBOSOMAL SUBUNIT, TRNAS, MRNA AND RELEASE FACTOR RF2 FROM A CRYSTAL STRUCTURE OF THE WHOLE RIBOSOMAL COMPLEX. THIS FILE CONTAINS THE 30S RIBOSOMAL SUBUNIT, TRNAS, MRNA AND RELEASE FACTOR RF2 FROM A CRYSTAL STRUCTURE OF THE WHOLE RIBOSOMAL COMPLEX". THE ENTIRE CRYSTAL STRUCTURE CONTAINS ONE 70S RIBOSOME, TRNAS, MRNA AND RELEASE FACTOR RF2 AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2B9N	50S RIBOSOMAL SUBUNIT FROM A CRYSTAL STRUCTURE OF RELEASE FACTOR RF2, TRNAS AND MRNA BOUND TO THE RIBOSOME. THIS FILE CONTAINS THE 50S SUBUNIT FROM A CRYSTAL STRUCTURE OF RELEASE FACTOR RF1, TRNAS AND MRNA BOUND TO THE RIBOSOME AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2B9O	30S RIBOSOMAL SUBUNIT, TRNAS AND MRNA FROM A CRYSTAL STRUCTURE OF THE WHOLE RIBOSOMAL COMPLEX WITH A STOP CODON IN THE A-SITE. THIS FILE CONTAINS THE 30S SUBUNIT, TRNAS AND MRNA FROM A CRYSTAL STRUCTURE OF THE WHOLE RIBOSOMAL COMPLEX WITH A STOP CODON IN THE A-SITE AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2B9P	50S RIBOSOMAL SUBUNIT FROM A CRYSTAL STRUCTURE OF THE RIBOSOME IN COMPLEX WITH TRNAS AND MRNA WITH A STOP CODON IN THE A-SITE. THIS FILE CONTAINS THE 50S SUBUNIT FROM A CRYSTAL STRUCTURE OF THE RIBOSOME IN COMPLEX WITH TRNAS AND MRNA WITH A STOP CODON IN THE A-SITE AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2B9S	CRYSTAL STRUCTURE OF HETERODIMERIC L. DONOVANI TOPOISOMERASE I-VANADATE-DNA COMPLEX	ISOMERASE/DNA
2BA0	ARCHAEAL EXOSOME CORE	RNA BINDING PROTEIN
2BA1	ARCHAEAL EXOSOME CORE	RNA BINDING PROTEIN
2BAN	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE (RT) IN COMPLEX WITH JANSSEN-R157208	TRANSFERASE
2BAP	CRYSTAL STRUCTURE OF THE N-TERMINAL MDIA1 ARMADILLO REPEAT REGION AND DIMERISATION DOMAIN IN COMPLEX WITH THE MDIA1 AUTOREGULATORY DOMAIN (DAD)	SIGNALING PROTEIN
2BBA	RYSTAL STRUCTURE AND THERMODYNAMIC CHARACTERIZATION OF THE EPHB4 RECEPTOR IN COMPLEX WITH AN EPHRIN-B2 ANTAGONIST PEPTIDE REVEALS THE DETERMINANTS FOR RECEPTOR SPECIFICITY	SIGNALING PROTEIN
2BBM	SOLUTION STRUCTURE OF A CALMODULIN-TARGET PEPTIDE COMPLEX BY MULTIDIMENSIONAL NMR	CALCIUM-BINDING PROTEIN
2BBV	THE REFINED THREE-DIMENSIONAL STRUCTURE OF AN INSECT VIRUS AT 2.8 ANGSTROMS RESOLUTION	VIRUS/RNA
2BC4	CRYSTAL STRUCTURE OF HLA-DM	IMMUNE SYSTEM

2BCC	STIGMATELLIN-BOUND CYTOCHROME BC1 COMPLEX FROM CHICKEN	OXIDOREDUCTASE
2BCG	STRUCTURE OF DOUBLY PRENYLATED YPT1:GDI COMPLEX	PROTEIN TRANSPORT
2BCJ	CRYSTAL STRUCTURE OF G PROTEIN-COUPLED RECEPTOR KINASE 2 IN COMPLEX WITH GALPHA-Q AND GBETAGAMMA SUBUNITS	TRANSFERASE/HYDROLASE
2BCN	SOLVENT ISOTOPE EFFECTS ON INTERFACIAL PROTEIN ELECTRON TRANSFER BETWEEN CYTOCHROME C AND CYTOCHROME C PEROXIDASE	OXIDOREDUCTASE/ELECTRON TRANSFER
2BCX	CRYSTAL STRUCTURE OF CALMODULIN IN COMPLEX WITH A RYANODINE RECEPTOR PEPTIDE	CALCIUM BINDING PROTEIN
2BDN	CRYSTAL STRUCTURE OF HUMAN MCP-1 BOUND TO A BLOCKING ANTIBODY, 11K2	IMMUNE SYSTEM
2BE1	STRUCTURE OF THE COMPACT LUMENAL DOMAIN OF YEAST IRE1	TRANSCRIPTION
2BE2	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE (RT) IN COMPLEX WITH R221239	TRANSFERASE
2BE5	CRYSTAL STRUCTURE OF THE T. THERMOPHILUS RNA POLYMERASE HOLOENZYME IN COMPLEX WITH INHIBITOR TAGETITOXIN	TRANSFERASE
2BE6	2.0 A CRYSTAL STRUCTURE OF THE CAV1.2 IQ DOMAIN-CA/CAM COMPLEX	MEMBRANE PROTEIN
2BE7	CRYSTAL STRUCTURE OF THE UNLIGANDED (T-STATE) ASPARTATE TRANSCARBAMOYLASE OF THE PSYCHROPHILIC BACTERIUM MORITELLA PROFUNDA	TRANSFERASE
2BE9	CRYSTAL STRUCTURE OF THE CTP-LIGANDED (T-STATE) ASPARTATE TRANSCARBAMOYLASE FROM THE EXTREMELY THERMOPHILIC ARCHAEON SULFOLOBUS ACIDOCALDARIUS	TRANSFERASE
2BEC	CRYSTAL STRUCTURE OF CHP2 IN COMPLEX WITH ITS BINDING REGION IN NHE1 AND INSIGHTS INTO THE MECHANISM OF PH REGULATION	METAL BINDING PROTEIN/TRANSPORT PROTEIN
2BED	STRUCTURE OF FPT BOUND TO INHIBITOR SCH207736	TRANSFERASE
2BEQ	STRUCTURE OF A PROTEOLYTICALLY RESISTANT CORE FROM THE SEVERE ACUTE RESPIRATORY SYNDROME CORONAVIRUS S2 FUSION PROTEIN	VIRAL PROTEIN
2BEU	REACTIVITY MODULATION OF HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE BY AN INTERNAL MOLECULAR SWITCH	OXIDOREDUCTASE
2BEV	REACTIVITY MODULATION OF HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE BY AN INTERNAL MOLECULAR SWITCH	OXIDOREDUCTASE
2BEW	REACTIVITY MODULATION OF HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE BY AN INTERNAL MOLECULAR SWITCH	OXIDOREDUCTASE
2BEX	CRYSTAL STRUCTURE OF PLACENTAL RIBONUCLEASE INHIBITOR IN	COMPLEX (INHIBITOR/NUCLEASE)

	COMPLEX WITH HUMAN EOSINOPHIL DERIVED NEUROTOXIN AT 2A RESOLUTION	
2BEZ	STRUCTURE OF A PROTEOLITICALLY RESISTANT CORE FROM THE SEVERE ACUTE RESPIRATORY SYNDROME CORONAVIRUS S2 FUSION PROTEIN	VIRAL PROTEIN
2BF3	CRYSTAL STRUCTURE OF A TOLUENE 4-MONOOXYGENASE CATALYTIC EFFECTOR PROTEIN VARIANT MISSING TEN N-TERMINAL RESIDUES (DELTA-N10 T4MOD)	OXIDOREDUCTASE
2BF8	CRYSTAL STRUCTURE OF SUMO MODIFIED UBIQUITIN CONJUGATING ENZYME E2-25K	LIGASE/COMPLEX
2BFB	REACTIVITY MODULATION OF HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE BY AN INTERNAL MOLECULAR SWITCH	OXIDOREDUCTASE
2BFC	REACTIVITY MODULATION OF HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE BY AN INTERNAL MOLECULAR SWITCH	OXIDOREDUCTASE
2BFD	REACTIVITY MODULATION OF HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE BY AN INTERNAL MOLECULAR SWITCH	OXIDOREDUCTASE
2BFE	REACTIVITY MODULATION OF HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE BY AN INTERNAL MOLECULAR SWITCH	OXIDOREDUCTASE
2BFF	REACTIVITY MODULATION OF HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE BY AN INTERNAL MOLECULAR SWITCH	OXIDOREDUCTASE
2BFU	X-RAY STRUCTURE OF CPMV TOP COMPONENT	VIRUS
2BFX	MECHANISM OF AURORA-B ACTIVATION BY INCENP AND INHIBITION BY HESPERIDIN.	TRANSFERASE COMPLEX
2BFZ	BACILLUS CEREUS METALLO-BETA-LACTAMASE (BCII) ARG (121) CYS MUTANT. SOLVED AT PH4.5 USING 20MM ZNSO4 IN BUFFER. 1MM DTT WAS USED AS A REDUCING AGENT. CYS221 IS OXIDIZED.	HYDROLASE
2BG8	BACILLUS CEREUS METALLO-BETA-LACTAMASE (BCII) ARG (121) CYS MUTANT. SOLVED AT PH4.5 USING 20 MICROMOLAR ZNSO4 IN THE BUFFER. 1MM DTT AND 1MM TCEP-HCL WERE USED AS REDUCING AGENTS.	HYDROLASE
2BG9	REFINED STRUCTURE OF THE NICOTINIC ACETYLCHOLINE RECEPTOR AT 4A RESOLUTION.	ION CHANNEL/RECEPTOR
2BGN	HIV-1 TAT PROTEIN DERIVED N-TERMINAL NONAPEPTIDE TRP2-TAT (1-9) BOUND TO THE ACTIVE SITE OF DIPEPTIDYL PEPTIDASE IV (CD26)	HYDROLASE/COMPLEX
2BGR	CRYSTAL STRUCTURE OF HIV-1 TAT DERIVED NONAPEPTIDES TAT(1-9) BOUND TO THE ACTIVE SITE OF DIPEPTIDYL PEPTIDASE IV (CD26)	HYDROLASE/COMPLEX
2BH1	X-RAY STRUCTURE OF THE GENERAL SECRETION PATHWAY COMPLEX OF	TRANSPORT PROTEIN

	THE N-TERMINAL DOMAIN OF EPSE AND THE CYTOSOLIC DOMAIN OF EPSL OF VIBRIO CHOLERAE	
2BIL	THE HUMAN PROTEIN KINASE PIM1 IN COMPLEX WITH ITS CONSENSUS PEPTIDE PIMTIDE	TRANSFERASE
2BJ4	ESTROGEN RECEPTOR ALPHA LBD IN COMPLEX WITH A PHAGE-DISPLAY DERIVED PEPTIDE ANTAGONIST	NUCLEAR RECEPTOR
2BKH	MYOSIN VI NUCLEOTIDE-FREE (MDINSERT2) CRYSTAL STRUCTURE	COMPLEX (MOTOR PROTEIN/CALMODULIN)
2BKI	MYOSIN VI NUCLEOTIDE-FREE (MDINSERT2-IQ) CRYSTAL STRUCTURE	COMPLEX (MOTOR PROTEIN/CALMODULIN)
2BKK	RYSTAL STRUCTURE OF AMINOGLYCOSIDE PHOSPHOTRANSFERASE APH (3')-IIIA IN COMPLEX WITH THE INHIBITOR AR_3A	TRANSFERASE/DESIGNED PROTEIN COMPLEX
2BKR	NEDD8 NEDP1 COMPLEX	UBIQUITIN/HYDROLASE COMPLEX
2BKU	KAP95P:RANGTP COMPLEX	NUCLEAR TRANSPORT
2BKY	CRYSTAL STRUCTURE OF THE ALBA1:ALBA2 HETERODIMER FROM SULFOLOBUS SOLFATARICUS	DNA BINDING PROTEIN
2BKZ	STRUCTURE OF CDK2-CYCLIN A WITH PHA-404611	TRANSFERASE/COMPLEX
2BL0	PHYSARUM POLYCEPHALUM MYOSIN II REGULATORY DOMAIN	MUSCLE PROTEIN
2BLD	THE QUASI-ATOMIC MODEL OF HUMAN ADENOVIRUS TYPE 5 CAPSID (PART 1)	ADENOVIRUS
2BLF	SULFITE DEHYDROGENASE FROM STARKEYA NOVELLA	OXIDOREDUCTASE
2BMG	CRYSTAL STRUCTURE OF FACTOR XA IN COMPLEX WITH 50	HYDROLASE
2BMK	FAB FRAGMENT OF PLP-DEPENDENT CATALYTIC ANTIBODY 15A9 IN COMPLEX WITH PHOSPHOPYRIDOXYL-D-ALANINE	IMMUNE SYSTEM
2BMO	THE CRYSTAL STRUCTURE OF NITROBENZENE DIOXYGENASE	OXIDOREDUCTASE
2BMQ	THE CRYSTAL STRUCTURE OF NITROBENZENE DIOXYGENASE IN COMPLEX WITH NITROBENZENE	OXIDOREDUCTASE
2BMR	THE CRYSTAL STRUCTURE OF NITROBENZENE DIOXYGENASE IN COMPLEX WITH 3-NITROTOLUENE	OXIDOREDUCTASE
2BN1	INSULIN AFTER A HIGH DOSE X-RAY BURN	RADIATION DAMAGE
2BN2	CRYSTAL STRUCTURE OF BOVINE NEUROPHYSIN II COMPLEXED WITH THE VASOPRESSIN ANALOGUE PHE-TYR AMIDE	COMPLEX (PROTEIN/PEPTIDE)
2BN3	INSULIN BEFORE A HIGH DOSE X-RAY BURN	RADIATION DAMAGE
2BNP	IPIDIC CUBIC PHASE GROWN REACTION CENTRE FROM RHODOBACTER SPHAEROIDES, GROUND STATE	REACTION CENTRE

2BNQ	STRUCTURAL AND KINETIC BASIS FOR HEIGHTENED IMMUNOGENICITY OF T CELL VACCINES	IMMUNE SYSTEM/RECEPTOR/COMPLEX
2BNR	STRUCTURAL AND KINETIC BASIS FOR HEIGHTENED IMMUNOGENICITY OF T CELL VACCINES	IMMUNE SYSTEM/RECEPTOR/COMPLEX
2BNS	IPIDIC CUBIC PHASE GROWN REACTION CENTRE FROM RHODOBACTER SPHAEROIDES, EXCITED STATE	REACTION CENTRE
2BNU	STRUCTURAL AND KINETIC BASIS FOR HEIGHTENED IMMUNOGENICITY OF T CELL VACCINES	IMMUNE SYSTEM/RECEPTOR
2BO9	HUMAN CARBOXYPEPTIDASE A4 IN COMPLEX WITH HUMAN LATEXIN.	HYDROLASE
2BOB	POTASSIUM CHANNEL KCSA-FAB COMPLEX IN THALLIUM WITH TETRABUTYLAMMONIUM (TBA)	COMPLEX (ANTIBODY/ION CHANNEL)
2BOC	POTASSIUM CHANNEL KCSA-FAB COMPLEX IN THALLIUM WITH TETRAETHYLARSONIUM (TEAS)	COMPLEX (ANTIBODY/ION CHANNEL)
2BOV	MOLECULAR RECOGNITION OF AN ADP-RIBOSYLATING CLOSTRIDIUM BOTULINUM C3 EXOENZYME BY RALA GTPASE	TRANSFERASE
2BOZ	PHOTOSYNTHETIC REACTION CENTER MUTANT WITH GLY M203 REPLACED WITH LEU	REACTION CENTER
2BP0	M168L MUTANT OF NITRITE REDUCTASE FROM ALCALIGENES XYLOSOXIDANS	OXIDOREDUCTASE
2BP7	IEW CRYSTAL FORM OF THE PSEUDOMONAS PUTIDA BRANCHED-CHAIN DEHYDROGENASE (E1)	OXIDOREDUCTASE
2BP8	M168Q STRUCTURE OF NITRITE REDUCTASE FROM ALCALIGENES XYLOSOXIDANS	OXIDOREDUCTASE
2BPB	SULFITE DEHYDROGENASE FROM STARKEYA NOVELLA	OXIDOREDUCTASE
2BPM	STRUCTURE OF CDK2-CYCLIN A WITH PHA-630529	TRANSFERASE
2BPT	STRUCTURE OF THE NUP1P:KAP95P COMPLEX	NUCLEAR TRANSPORT
2BQ1	IBONUCLEOTIDE REDUCTASE CLASS 1B HOLOCOMPLEX R1E,R2F FROM SALMONELLA TYPHIMURIUM	OXIDOREDUCTASE
2BQ6	CRYSTAL STRUCTURE OF FACTOR XA IN COMPLEX WITH 21	HYDROLASE
2BQ7	CRYSTAL STRUCTURE OF FACTOR XA IN COMPLEX WITH 43	HYDROLASE
2BQW	RYSTAL STRUCTURE OF FACTOR XA IN COMPLEX WITH COMPOUND 45	HYDROLASE
2BQZ	RYSTAL STRUCTURE OF A TERNARY COMPLEX OF THE HUMAN HISTONE METHYLTRANSFERASE PR-SET7 (ALSO KNOWN AS SET8)	TRANSFERASE
2BR2	RNASE PH CORE OF THE ARCHAEAL EXOSOME	HYDROLASE

2BR8	CRYSTAL STRUCTURE OF ACETYLCHOLINE-BINDING PROTEIN (ACHBP) FROM APLYSIA CALIFORNICA IN COMPLEX WITH AN ALPHA-CONOTOXIN PNIA VARIANT	RECEPTOR/INHIBITOR COMPLEX
2BR9	14-3-3 PROTEIN EPSILON (HUMAN) COMPLEXED TO PEPTIDE	CELL REGULATOR PROTEIN
2BRR	COMPLEX OF THE NEISSERIAL PORA P1.4 EPITOPE PEPTIDE AND TWO FAB-FRAGMENTS (ANTIBODY MN20B9.34)	ANTIBODY/ANTIGEN COMPLEX
2BS3	GLU C180-> GLN VARIANT QUINOL:FUMARATE REDUCTASE FROM WOLINELLA SUCCINOGENES	OXIDOREDUCTASE
2BS4	GLU C180-> ILE VARIANT QUINOL:FUMARATE REDUCTASE FROM WOLINELLA SUCCINOGENES	OXIDOREDUCTASE
2BSK	CRYSTAL STRUCTURE OF THE TIM9 TIM10 HEXAMERIC COMPLEX	PROTEIN TRANSPORT
2BSQ	FITAB BOUND TO DNA	TRANSCRIPTION REGULATION COMPLEX
2BSR	CRYSTAL STRUCTURES AND KIR3DL1 RECOGNITION OF THREE IMMUNODOMINANT VIRAL PEPTIDES COMPLEXED TO HLA-B2705	COMPLEX (ANTIGEN/PEPTIDE)
2BSS	CRYSTAL STRUCTURES AND KIR3DL1 RECOGNITION OF THREE IMMUNODOMINANT VIRAL PEPTIDES COMPLEXED TO HLA-B2705	COMPLEX (ANTIGEN/PEPTIDE)
2BST	CRYSTAL STRUCTURES AND KIR3DL1 RECOGNITION OF THREE IMMUNODOMINANT VIRAL PEPTIDES COMPLEXED TO HLA-B2705	COMPLEX (ANTIGEN/PEPTIDE)
2BTF	THE STRUCTURE OF CRYSTALLINE PROFILIN-BETA-ACTIN	ACETYLATION AND ACTIN-BINDING
2BTO	STRUCTURE OF BTUBA FROM PROSTHECOBACTER DEJONGEII	CYTOSKELETAL PROTEIN
2BTP	14-3-3 PROTEIN THETA (HUMAN) COMPLEXED TO PEPTIDE	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)
2BTQ	STRUCTURE OF BTUBAB HETERODIMER FROM PROSTHECOBACTER DEJONGEII	CYTOSKELETAL PROTEIN/COMPLEX
2BTV	ATOMIC MODEL FOR BLUETONGUE VIRUS (BTV) CORE	VIRUS
2BTW	CRYSTAL STRUCTURE OF ALR0975	TRANSFERASE
2BUM	CRYSTAL STRUCTURE OF WILD-TYPE PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1	OXIDOREDUCTASE
2BUO	HIV-1 CAPSID C-TERMINAL DOMAIN IN COMPLEX WITH AN INHIBITOR OF PARTICLE ASSEMBLY	VIRAL PROTEIN/PEPTIDE
2BUQ	CRYSTAL STRUCTURE OF WILD-TYPE PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 IN COMPLEX WITH CATECHOL	OXIDOREDUCTASE
2BUR	CRYSTAL STRUCTURE OF WILD-TYPE PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 IN COMPLEX WITH 4-HYDROXYBENZOATE	OXIDOREDUCTASE

2BUT	CRYSTAL STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 MUTANT R457S- APO	OXIDOREDUCTASE
2BUU	CRYSTAL STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 MUTANT R457S IN COMPLEX WITH 4-NITROCATECHOL	OXIDOREDUCTASE
2BUV	CRYSTAL STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 MUTANT R457S IN COMPLEX WITH PROTOCATECHUATE	OXIDOREDUCTASE
2BUW	CRYSTAL STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 MUTANT R457S IN COMPLEX WITH 4-HYDROXYBENZOATE	OXIDOREDUCTASE
2BUX	CRYSTAL STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 MUTANT R133H	OXIDOREDUCTASE
2BUY	CRYSTAL STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 MUTANT R133H IN COMPLEX WITH CATECHOL	OXIDOREDUCTASE
2BUZ	CRYSTAL STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 MUTANT R133H IN COMPLEX WITH 4-NITROCATECHOL	OXIDOREDUCTASE
2BV0	CRYSTAL STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 MUTANT R133H IN COMPLEX WITH PROTOCATECHUATE.	OXIDOREDUCTASE
2BV8	THE CRYSTAL STRUCTURE OF PHYCOCYANIN FROM GRACILARIA CHILENSIS.	PHOTOSYNTHESIS
2BVO	STRUCTURES OF THREE HIV-1 HLA-B5703-PEPTIDE COMPLEXES AND IDENTIFICATION OF RELATED HLAS POTENTIALLY ASSOCIATED WITH LONG-TERM NON-PROGRESSION	GLYCOPROTEIN/PEPTIDE COMPLEX
2BVP	STRUCTURES OF THREE HIV-1 HLA-B5703-PEPTIDE COMPLEXES AND IDENTIFICATION OF RELATED HLAS POTENTIALLY ASSOCIATED WITH LONG-TERM NON-PROGRESSION	GLYCOPROTEIN/PEPTIDE COMPLEX
2BW3	THREE-DIMENSIONAL STRUCTURE OF THE HERMES DNA TRANSPOSASE	DNA RECOMBINATION
2BWE	THE CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE UBA AND UBL DOMAINS OF DSK2	SIGNALING PROTEIN
2BWO	5-AMINOLEVULINATE SYNTHASE FROM RHODOBACTER CAPSULATUS IN COMPLEX WITH SUCCINYL-COA	TRANSFERASE
2BYK	HISTONE FOLD HETERODIMER OF THE CHROMATIN ACCESSIBILITY COMPLEX	DNA-BINDING PROTEIN
2BYM	HISTONE FOLD HETERODIMER OF THE CHROMATIN ACCESSIBILITY COMPLEX	DNA-BINDING PROTEIN

2BYP	CRYSTAL STRUCTURE OF APLYSIA CALIFORNICA ACHBP IN COMPLEX WITH ALPHA-CONOTOXIN IMI	RECEPTOR COMPLEX
2BZ6	ORALLY AVAILABLE FACTOR7A INHIBITOR	HYDROLASE
2BZK	CRYSTAL STRUCTURE OF THE HUMAN PIM1 IN COMPLEX WITH AMPPNP AND PIMTIDE	COMPLEX TRANSFERASE/PEPTIDE
2BZW	THE CRYSTAL STRUCTURE OF BCL-XL IN COMPLEX WITH FULL-LENGTH BAD	TRANSCRIPTION COMPLEX
2B05	CRYSTAL STRUCTURE OF 14-3-3 GAMMA IN COMPLEX WITH A PHOSPHOSERINE PEPTIDE	CELL CYCLE
2B0S	CRYSTAL STRUCTURE ANALYSIS OF ANTI-HIV-1 V3 FAB 2219 IN COMPLEX WITH MN PEPTIDE	IMMMUNE SYSTEM
2B0U	THE STRUCTURE OF THE FOLLISTATIN:ACTIVIN COMPLEX	SIGNALING PROTEIN
2B0Z	CRYSTAL STRUCTURE OF THE PROTEIN-PROTEIN COMPLEX BETWEEN F82I CYTOCHROME C AND CYTOCHROME C PEROXIDASE	OXIDOREDUCTASE/ELECTRON TRANSPORT
2B10	CRYSTAL STRUCTURE OF THE PROTEIN-PROTEIN COMPLEX BETWEEN F82S CYTOCHROME C AND CYTOCHROME C PEROXIDASE	OXIDOREDUCTASE/ELECTRON TRANSPORT
2B11	CRYSTAL STRUCTURE OF THE PROTEIN-PROTEIN COMPLEX BETWEEN F82W CYTOCHROME C AND CYTOCHROME C PEROXIDASE	OXIDOREDUCTASE/ELECTRON TRANSPORT
2B12	CRYSTAL STRUCTURE OF THE PROTEIN-PROTEIN COMPLEX BETWEEN F82Y CYTOCHROME C AND CYTOCHROME C PEROXIDASE	OXIDOREDUCTASE/ELECTRON TRANSPORT
2B1A	CRYSTAL STRUCTURE ANALYSIS OF ANTI-HIV-1 V3 FAB 2219 IN COMPLEX WITH UG1033 PEPTIDE	IMMMUNE SYSTEM
2B1H	CRYSTAL STRUCTURE ANALYSIS OF ANTI-HIV-1 V3 FAB 2219 IN COMPLEX WITH UG29 PEPTIDE	IMMMUNE SYSTEM
2B1J	CRYSTAL STRUCTURE OF UNPHOSPHORYLATED CHEY BOUND TO THE N-TERMINUS OF FLIM	SIGNALING PROTEIN
2B1N	CRYSTAL STRUCTURE OF A PAPAIN-FOLD PROTEIN WITHOUT THE CATALYTIC CYSTEINE FROM SEEDS OF PACHYRHIZUS EROSUS	SUGAR BINDING PROTEIN
2B1V	HUMAN ESTROGEN RECEPTOR ALPHA LIGAND-BINDING DOMAIN IN COMPLEX WITH OBCP-1M AND A GLUCOCORTICOID RECEPTOR INTERACTING PROTEIN 1 NR BOX II PEPTIDE	HORMONE/GROWTH FACTOR RECEPTOR
2B1X	CRYSTAL STRUCTURE OF NAPHTHALENE 1,2-DIOXYGENASE FROM RHODOCOCCUS SP.	OXIDOREDUCTASE
2B1Z	HUMAN ESTROGEN RECEPTOR ALPHA LIGAND-BINDING DOMAIN IN COMPLEX WITH 17METHYL-17ALPHA-DIHYDROEQUILENIN AND A GLUCOC INTERACTING PROTEIN 1 NR BOX II PEPTIDE	HORMONE/GROWTH FACTOR RECEPTOR
2B23	HUMAN ESTROGEN RECEPTOR ALPHA LIGAND-BINDING DOMAIN AND A	HORMONE/GROWTH FACTOR RECEPTOR

	GLUCOCORTICOID RECEPTOR-INTERACTING PROTEIN 1 NR BOX II PEPTIDE	
2B24	CRYSTAL STRUCTURE OF NAPHTHALENE 1,2-DIOXYGENASE FROM RHODOCOCCUS SP. BOUND TO INDOLE	OXIDOREDUCTASE
2B26	THE CRYSTAL STRUCTURE OF THE PROTEIN COMPLEX OF YEAST HSP40 SIS1 AND HSP70 SSA1	CHAPERONE/PROTEIN TRANSPORT
2B2T	ANDEM CHROMODOMAINS OF HUMAN CHD1 COMPLEXED WITH HISTONE H3 TAIL CONTAINING TRIMETHYLLYSINE 4 AND PHOSPHOTHREONINE 3	PEPTIDE BINDING PROTEIN
2B2U	ANDEM CHROMODOMAINS OF HUMAN CHD1 COMPLEXED WITH HISTONE H3 TAIL CONTAINING TRIMETHYLLYSINE 4 AND DIMETHYLARGININE 2	PEPTIDE BINDING PROTEIN
2B2V	CRYSTAL STRUCTURE ANALYSIS OF HUMAN CHD1 CHROMODOMAINS 1 AND 2 BOUND TO HISTONE H3 RESI 1-15 MEK4	PEPTIDE BINDING PROTEIN
2B2W	ANDEM CHROMODOMAINS OF HUMAN CHD1 COMPLEXED WITH HISTONE H3 TAIL CONTAINING TRIMETHYLLYSINE 4	PEPTIDE BINDING PROTEIN
2B2X	VLA1 RDELTAH I-DOMAIN COMPLEXED WITH A QUADRUPLE MUTANT OF THE AQC2 FAB	IMMUNE SYSTEM
2B2Y	TANDEM CHROMODOMAINS OF HUMAN CHD1	PEPTIDE BINDING PROTEIN
2B3G	P53N (FRAGMENT 33-60) BOUND TO RPA70N	REPLICATION
2B3T	MOLECULAR BASIS FOR BACTERIAL CLASS 1 RELEASE FACTOR METHYLATION BY PRMC	TRANSLATION
2B42	CRYSTAL STRUCTURE OF THE TRITICUM XYLANSE INHIBITOR-I IN COMPLEX WITH BACILLUS SUBTILIS XYLANASE	HYDROLASE INHIBITOR/HYDROLASE
2B4C	CRYSTAL STRUCTURE OF HIV-1 JR-FL GP120 CORE PROTEIN CONTAINING THE THIRD VARIABLE REGION (V3) COMPLEXED WITH CD4 AND THE X5 ANTIBODY	VIRAL PROTEIN/IMMUNE SYSTEM
2B4D	SSAT+COA+SP- SP DISORDERED	TRANSFERASE
2B4J	STRUCTURAL BASIS FOR THE RECOGNITION BETWEEN HIV-1 INTEGRASE AND LEDGF/P75	VIRAL PROTEIN, RECOMBINATION
2B4S	CRYSTAL STRUCTURE OF A COMPLEX BETWEEN PTP1B AND THE INSULIN RECEPTOR TYROSINE KINASE	HYDROLASE/TRANSFERASE
2B59	THE TYPE II COHESIN DOCKERIN COMPLEX	HYDROLASE/STRUCTURAL PROTEIN
2B5G	WILD TYPE SSAT- 1.7A STRUCTURE	TRANSFERASE
2B5I	CYTOKINE RECEPTOR COMPLEX	CYTOKINE/CYTOKINE RECEPTOR
2B5J	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE (RT) IN COMPLEX WITH JANSSEN-R165481	TRANSFERASE

2B5L	CRYSTAL STRUCTURE OF DDB1 IN COMPLEX WITH SIMIAN VIRUS 5 V PROTEIN	PROTEIN BINDING/VIRAL PROTEIN
2B5R	1B LACTAMASE / B LACTAMASE INHIBITOR	HYDROLASE/HYDROLASE INHIBITOR
2B5T	.1 ANGSTROM STRUCTURE OF A NONPRODUCTIVE COMPLEX BETWEEN ANTITHROMBIN, SYNTHETIC HEPARIN MIMETIC SR123781 AND TWO S195A THROMBIN MOLECULES	BLOOD CLOTTING
2B5U	CRYSTAL STRUCTURE OF COLICIN E3 V206C MUTANT IN COMPLEX WITH ITS IMMUNITY PROTEIN	RIBOSOME INHIBITOR, HYDROLASE
2B63	COMPLETE RNA POLYMERASE II-RNA INHIBITOR COMPLEX	TRANSFERASE/RNA
2B64	30S RIBOSOMAL SUBUNIT, TRNAS, MRNA AND RELEASE FACTOR RF1 FROM A CRYSTAL STRUCTURE OF THE WHOLE RIBOSOMAL COMPLEX. THIS FILE CONTAINS THE 30S SUBUNIT, TRNAS, MRNA AND RELEASE FACTOR RF1 FROM A CRYSTAL STRUCTURE OF THE WHOLE RIBOSOMAL COMPLEX". THE ENTIRE CRYSTAL STRUCTURE CONTAINS ONE 70S RIBOSOME, TRNAS, MRNA AND RELEASE FACTOR RF1 AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2B66	50S RIBOSOMAL SUBUNIT FROM A CRYSTAL STRUCTURE OF RELEASE FACTOR RF1, TRNAS AND MRNA BOUND TO THE RIBOSOME. THIS FILE CONTAINS THE 50S SUBUNIT FROM A CRYSTAL STRUCTURE OF RELEASE FACTOR RF1, TRNAS AND MRNA BOUND TO THE RIBOSOME AND IS DESCRIBED IN REMARK 400	RIBOSOME
2B6A	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE (RT) IN COMPLEX WITH THR-50	TRANSFERASE
2B6N	THE 1.8 A CRYSTAL STRUCTURE OF A PROTEINASE K LIKE ENZYME FROM A PSYCHROTROPH SERRATIA SPECIES	HYDROLASE
2B76	E. COLI QUINOL FUMARATE REDUCTASE FRDA E49Q MUTATION	OXIDOREDUCTASE
2B7B	YEAST GUANINE NUCLEOTIDE EXCHANGE FACTOR EEF1BALPHA K205A MUTANT IN COMPLEX WITH EEF1A AND GDP	TRANSLATION
2B7C	YEAST GUANINE NUCLEOTIDE EXCHANGE FACTOR EEF1BALPHA K205A MUTANT IN COMPLEX WITH EEF1A	TRANSLATION
2B7F	CRYSTAL STRUCTURE OF HUMAN T-CELL LEUKEMIA VIRUS PROTEASE, A NOVEL TARGET FOR ANTI-CANCER DESIGN	HYDROLASE
2B7H	HEMOGLOBIN FROM CERDOCYON THOUS, A CANIDAE FROM BRAZIL, AT 2.2 ANGSTROMS RESOLUTION	OXYGEN STORAGE/TRANSPORT
2B7Y	FAVA BEAN LECTIN-GLUCOSE COMPLEX	LECTIN
2B8K	12-SUBUNIT RNA POLYMERASE II	TRANSFERASE
2B8O	RYSTAL STRUCTURE OF GLU-GLY-ARG-CHLOROMETHYL KETONE-FACTOR VIIA/SOLUBLE TISSUE FACTOR COMPLEX	HYDROLASE/HYDROLASE INHIBITOR

2B9H	CRYSTAL STRUCTURE OF FUS3 WITH A DOCKING MOTIF FROM STE7	TRANSFERASE
2B9I	CRYSTAL STRUCTURE OF FUS3 WITH A DOCKING MOTIF FROM MSG5	TRANSFERASE
2B9J	CRYSTAL STRUCTURE OF FUS3 WITH A DOCKING MOTIF FROM FAR1	TRANSFERASE
2B9M	30S RIBOSOMAL SUBUNIT, TRNAS, MRNA AND RELEASE FACTOR RF2 FROM A CRYSTAL STRUCTURE OF THE WHOLE RIBOSOMAL COMPLEX. THIS FILE CONTAINS THE 30S RIBOSOMAL SUBUNIT, TRNAS, MRNA AND RELEASE FACTOR RF2 FROM A CRYSTAL STRUCTURE OF THE WHOLE RIBOSOMAL COMPLEX". THE ENTIRE CRYSTAL STRUCTURE CONTAINS ONE 70S RIBOSOME, TRNAS, MRNA AND RELEASE FACTOR RF2 AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2B9N	50S RIBOSOMAL SUBUNIT FROM A CRYSTAL STRUCTURE OF RELEASE FACTOR RF2, TRNAS AND MRNA BOUND TO THE RIBOSOME. THIS FILE CONTAINS THE 50S SUBUNIT FROM A CRYSTAL STRUCTURE OF RELEASE FACTOR RF1, TRNAS AND MRNA BOUND TO THE RIBOSOME AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2B9O	30S RIBOSOMAL SUBUNIT, TRNAS AND MRNA FROM A CRYSTAL STRUCTURE OF THE WHOLE RIBOSOMAL COMPLEX WITH A STOP CODON IN THE A-SITE. THIS FILE CONTAINS THE 30S SUBUNIT, TRNAS AND MRNA FROM A CRYSTAL STRUCTURE OF THE WHOLE RIBOSOMAL COMPLEX WITH A STOP CODON IN THE A-SITE AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2B9P	50S RIBOSOMAL SUBUNIT FROM A CRYSTAL STRUCTURE OF THE RIBOSOME IN COMPLEX WITH TRNAS AND MRNA WITH A STOP CODON IN THE A-SITE. THIS FILE CONTAINS THE 50S SUBUNIT FROM A CRYSTAL STRUCTURE OF THE RIBOSOME IN COMPLEX WITH TRNAS AND MRNA WITH A STOP CODON IN THE A-SITE AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2B9S	CRYSTAL STRUCTURE OF HETERODIMERIC L. DONOVANI TOPOISOMERASE I-VANADATE-DNA COMPLEX	ISOMERASE/DNA
2BA0	ARCHAEAL EXOSOME CORE	RNA BINDING PROTEIN
2BA1	ARCHAEAL EXOSOME CORE	RNA BINDING PROTEIN
2BAN	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE (RT) IN COMPLEX WITH JANSSEN-R157208	TRANSFERASE
2BAP	CRYSTAL STRUCTURE OF THE N-TERMINAL MDIA1 ARMADILLO REPEAT REGION AND DIMERISATION DOMAIN IN COMPLEX WITH THE MDIA1 AUTOREGULATORY DOMAIN (DAD)	SIGNALING PROTEIN
2BBA	RYSTAL STRUCTURE AND THERMODYNAMIC CHARACTERIZATION OF THE EPHB4 RECEPTOR IN COMPLEX WITH AN EPHRIN-B2 ANTAGONIST PEPTIDE REVEALS THE DETERMINANTS FOR RECEPTOR SPECIFICITY	SIGNALING PROTEIN
2BBM	SOLUTION STRUCTURE OF A CALMODULIN-TARGET PEPTIDE COMPLEX BY MULTIDIMENSIONAL NMR	CALCIUM-BINDING PROTEIN

2BBV	THE REFINED THREE-DIMENSIONAL STRUCTURE OF AN INSECT VIRUS AT 2.8 ANGSTROMS RESOLUTION	VIRUS/RNA
2BC4	CRYSTAL STRUCTURE OF HLA-DM	IMMUNE SYSTEM
2BCC	STIGMATELLIN-BOUND CYTOCHROME BC1 COMPLEX FROM CHICKEN	OXIDOREDUCTASE
2BCG	STRUCTURE OF DOUBLY PRENYLATED YPT1:GDI COMPLEX	PROTEIN TRANSPORT
2BCJ	CRYSTAL STRUCTURE OF G PROTEIN-COUPLED RECEPTOR KINASE 2 IN COMPLEX WITH GALPHA-Q AND GBETAGAMMA SUBUNITS	TRANSFERASE/HYDROLASE
2BCN	SOLVENT ISOTOPE EFFECTS ON INTERFACIAL PROTEIN ELECTRON TRANSFER BETWEEN CYTOCHROME C AND CYTOCHROME C PEROXIDASE	OXIDOREDUCTASE/ELECTRON TRANSFER
2BCX	CRYSTAL STRUCTURE OF CALMODULIN IN COMPLEX WITH A RYANODINE RECEPTOR PEPTIDE	CALCIUM BINDING PROTEIN
2BDN	CRYSTAL STRUCTURE OF HUMAN MCP-1 BOUND TO A BLOCKING ANTIBODY, 11K2	IMMUNE SYSTEM
2BE1	STRUCTURE OF THE COMPACT LUMENAL DOMAIN OF YEAST IRE1	TRANSCRIPTION
2BE2	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE (RT) IN COMPLEX WITH R221239	TRANSFERASE
2BE5	CRYSTAL STRUCTURE OF THE T. THERMOPHILUS RNA POLYMERASE HOLOENZYME IN COMPLEX WITH INHIBITOR TAGETITOXIN	TRANSFERASE
2BE6	2.0 A CRYSTAL STRUCTURE OF THE CAV1.2 IQ DOMAIN-CA/CAM COMPLEX	MEMBRANE PROTEIN
2BE7	CRYSTAL STRUCTURE OF THE UNLIGANDED (T-STATE) ASPARTATE TRANSCARBAMOYLASE OF THE PSYCHROPHILIC BACTERIUM MORITELLA PROFUNDA	TRANSFERASE
2BE9	CRYSTAL STRUCTURE OF THE CTP-LIGANDED (T-STATE) ASPARTATE TRANSCARBAMOYLASE FROM THE EXTREMELY THERMOPHILIC ARCHAEON SULFOLOBUS ACIDOCALDARIUS	TRANSFERASE
2BEC	CRYSTAL STRUCTURE OF CHP2 IN COMPLEX WITH ITS BINDING REGION IN NHE1 AND INSIGHTS INTO THE MECHANISM OF PH REGULATION	METAL BINDING PROTEIN/TRANSPORT PROTEIN
2BED	STRUCTURE OF FPT BOUND TO INHIBITOR SCH207736	TRANSFERASE
2BEQ	STRUCTURE OF A PROTEOLYTICALLY RESISTANT CORE FROM THE SEVERE ACUTE RESPIRATORY SYNDROME CORONAVIRUS S2 FUSION PROTEIN	VIRAL PROTEIN
2BEU	REACTIVITY MODULATION OF HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE BY AN INTERNAL MOLECULAR SWITCH	OXIDOREDUCTASE
2BEV	REACTIVITY MODULATION OF HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE BY AN INTERNAL MOLECULAR SWITCH	OXIDOREDUCTASE

2BEW	REACTIVITY MODULATION OF HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE BY AN INTERNAL MOLECULAR SWITCH	OXIDOREDUCTASE
2BEX	CRYSTAL STRUCTURE OF PLACENTAL RIBONUCLEASE INHIBITOR IN COMPLEX WITH HUMAN EOSINOPHIL DERIVED NEUROTOXIN AT 2A RESOLUTION	COMPLEX (INHIBITOR/NUCLEASE)
2BEZ	STRUCTURE OF A PROTEOLITICALLY RESISTANT CORE FROM THE SEVERE ACUTE RESPIRATORY SYNDROME CORONAVIRUS S2 FUSION PROTEIN	VIRAL PROTEIN
2BF3	CRYSTAL STRUCTURE OF A TOLUENE 4-MONOOXYGENASE CATALYTIC EFFECTOR PROTEIN VARIANT MISSING TEN N-TERMINAL RESIDUES (DELTA-N10 T4MOD)	OXIDOREDUCTASE
2BF8	CRYSTAL STRUCTURE OF SUMO MODIFIED UBIQUITIN CONJUGATING ENZYME E2-25K	LIGASE/COMPLEX
2BFB	REACTIVITY MODULATION OF HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE BY AN INTERNAL MOLECULAR SWITCH	OXIDOREDUCTASE
2BFC	REACTIVITY MODULATION OF HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE BY AN INTERNAL MOLECULAR SWITCH	OXIDOREDUCTASE
2BFD	REACTIVITY MODULATION OF HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE BY AN INTERNAL MOLECULAR SWITCH	OXIDOREDUCTASE
2BFE	REACTIVITY MODULATION OF HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE BY AN INTERNAL MOLECULAR SWITCH	OXIDOREDUCTASE
2BFF	REACTIVITY MODULATION OF HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE BY AN INTERNAL MOLECULAR SWITCH	OXIDOREDUCTASE
2BFU	X-RAY STRUCTURE OF CPMV TOP COMPONENT	VIRUS
2BFX	MECHANISM OF AURORA-B ACTIVATION BY INCENP AND INHIBITION BY HESPERIDIN.	TRANSFERASE COMPLEX
2BFZ	BACILLUS CEREUS METALLO-BETA-LACTAMASE (BCII) ARG (121) CYS MUTANT. SOLVED AT PH4.5 USING 20MM ZNSO4 IN BUFFER. 1MM DTT WAS USED AS A REDUCING AGENT. CYS221 IS OXIDIZED.	HYDROLASE
2BG8	BACILLUS CEREUS METALLO-BETA-LACTAMASE (BCII) ARG (121) CYS MUTANT. SOLVED AT PH4.5 USING 20 MICROMOLAR ZNSO4 IN THE BUFFER. 1MM DTT AND 1MM TCEP-HCL WERE USED AS REDUCING AGENTS.	HYDROLASE
2BG9	REFINED STRUCTURE OF THE NICOTINIC ACETYLCHOLINE RECEPTOR AT 4A RESOLUTION.	ION CHANNEL/RECEPTOR
2BGN	HIV-1 TAT PROTEIN DERIVED N-TERMINAL NONAPEPTIDE TRP2-TAT (1-9) BOUND TO THE ACTIVE SITE OF DIPEPTIDYL PEPTIDASE IV (CD26)	HYDROLASE/COMPLEX

2BGR	CRYSTAL STRUCTURE OF HIV-1 TAT DERIVED NONAPEPTIDES TAT(1-9) BOUND TO THE ACTIVE SITE OF DIPEPTIDYL PEPTIDASE IV (CD26)	HYDROLASE/COMPLEX
2BH1	-RAY STRUCTURE OF THE GENERAL SECRETION PATHWAY COMPLEX OF THE N-TERMINAL DOMAIN OF EPSE AND THE CYTOSOLIC DOMAIN OF EPSL OF VIBRIO CHOLERAE	TRANSPORT PROTEIN
2BIL	THE HUMAN PROTEIN KINASE PIM1 IN COMPLEX WITH ITS CONSENSUS PEPTIDE PIMTIDE	TRANSFERASE
2BJ4	ESTROGEN RECEPTOR ALPHA LBD IN COMPLEX WITH A PHAGE-DISPLAY DERIVED PEPTIDE ANTAGONIST	NUCLEAR RECEPTOR
2BKH	MYOSIN VI NUCLEOTIDE-FREE (MDINSERT2) CRYSTAL STRUCTURE	COMPLEX (MOTOR PROTEIN/CALMODULIN)
2BKI	MYOSIN VI NUCLEOTIDE-FREE (MDINSERT2-IQ) CRYSTAL STRUCTURE	COMPLEX (MOTOR PROTEIN/CALMODULIN)
2BKK	RYSTAL STRUCTURE OF AMINOGLYCOSIDE PHOSPHOTRANSFERASE APH (3')-IIIA IN COMPLEX WITH THE INHIBITOR AR_3A	TRANSFERASE/DESIGNED PROTEIN COMPLEX
2BKR	NEDD8 NEDP1 COMPLEX	UBIQUITIN/HYDROLASE COMPLEX
2BKU	KAP95P:RANGTP COMPLEX	NUCLEAR TRANSPORT
2BKY	CRYSTAL STRUCTURE OF THE ALBA1:ALBA2 HETERODIMER FROM SULFOLOBUS SOLFATARICUS	DNA BINDING PROTEIN
2BKZ	STRUCTURE OF CDK2-CYCLIN A WITH PHA-404611	TRANSFERASE/COMPLEX
2BL0	PHYSARUM POLYCEPHALUM MYOSIN II REGULATORY DOMAIN	MUSCLE PROTEIN
2BLD	THE QUASI-ATOMIC MODEL OF HUMAN ADENOVIRUS TYPE 5 CAPSID (PART 1)	ADENOVIRUS
2BLF	SULFITE DEHYDROGENASE FROM STARKEYA NOVELLA	OXIDOREDUCTASE
2BMG	CRYSTAL STRUCTURE OF FACTOR XA IN COMPLEX WITH 50	HYDROLASE
2BMK	FAB FRAGMENT OF PLP-DEPENDENT CATALYTIC ANTIBODY 15A9 IN COMPLEX WITH PHOSPHOPYRIDOXYL-D-ALANINE	IMMUNE SYSTEM
2BMO	THE CRYSTAL STRUCTURE OF NITROBENZENE DIOXYGENASE	OXIDOREDUCTASE
2BMQ	THE CRYSTAL STRUCTURE OF NITROBENZENE DIOXYGENASE IN COMPLEX WITH NITROBENZENE	OXIDOREDUCTASE
2BMR	THE CRYSTAL STRUCTURE OF NITROBENZENE DIOXYGENASE IN COMPLEX WITH 3-NITROTOLUENE	OXIDOREDUCTASE
2BN1	INSULIN AFTER A HIGH DOSE X-RAY BURN	RADIATION DAMAGE
2BN2	CRYSTAL STRUCTURE OF BOVINE NEUROPHYSIN II COMPLEXED WITH THE VASOPRESSIN ANALOGUE PHE-TYR AMIDE	COMPLEX (PROTEIN/PEPTIDE)

2BN3	INSULIN BEFORE A HIGH DOSE X-RAY BURN	RADIATION DAMAGE
2BNP	IPIDIC CUBIC PHASE GROWN REACTION CENTRE FROM RHODOBACTER SPHAEROIDES, GROUND STATE	REACTION CENTRE
2BNQ	STRUCTURAL AND KINETIC BASIS FOR HEIGHTENED IMMUNOGENICITY OF T CELL VACCINES	IMMUNE SYSTEM/RECEPTOR/COMPLEX
2BNR	STRUCTURAL AND KINETIC BASIS FOR HEIGHTENED IMMUNOGENICITY OF T CELL VACCINES	IMMUNE SYSTEM/RECEPTOR/COMPLEX
2BNS	IPIDIC CUBIC PHASE GROWN REACTION CENTRE FROM RHODOBACTER SPHAEROIDES, EXCITED STATE	REACTION CENTRE
2BNU	STRUCTURAL AND KINETIC BASIS FOR HEIGHTENED IMMUNOGENICITY OF T CELL VACCINES	IMMUNE SYSTEM/RECEPTOR
2BO9	HUMAN CARBOXYPEPTIDASE A4 IN COMPLEX WITH HUMAN LATEXIN.	HYDROLASE
2BOB	POTASSIUM CHANNEL KCSA-FAB COMPLEX IN THALLIUM WITH TETRABUTYLAMMONIUM (TBA)	COMPLEX (ANTIBODY/ION CHANNEL)
2BOC	POTASSIUM CHANNEL KCSA-FAB COMPLEX IN THALLIUM WITH TETRAETHYLARSONIUM (TEAS)	COMPLEX (ANTIBODY/ION CHANNEL)
2BOV	MOLECULAR RECOGNITION OF AN ADP-RIBOSYLATING CLOSTRIDIUM BOTULINUM C3 EXOENZYME BY RALA GTPASE	TRANSFERASE
2BOZ	PHOTOSYNTHETIC REACTION CENTER MUTANT WITH GLY M203 REPLACED WITH LEU	REACTION CENTER
2BP0	M168L MUTANT OF NITRITE REDUCTASE FROM ALCALIGENES XYLOSOXIDANS	OXIDOREDUCTASE
2BP7	IEW CRYSTAL FORM OF THE PSEUDOMONAS PUTIDA BRANCHED-CHAIN DEHYDROGENASE (E1)	OXIDOREDUCTASE
2BP8	M168Q STRUCTURE OF NITRITE REDUCTASE FROM ALCALIGENES XYLOSOXIDANS	OXIDOREDUCTASE
2BPB	SULFITE DEHYDROGENASE FROM STARKEYA NOVELLA	OXIDOREDUCTASE
2BPM	STRUCTURE OF CDK2-CYCLIN A WITH PHA-630529	TRANSFERASE
2BPT	STRUCTURE OF THE NUP1P:KAP95P COMPLEX	NUCLEAR TRANSPORT
2BQ1	RIBONUCLEOTIDE REDUCTASE CLASS 1B HOLOCOMPLEX R1E,R2F FROM SALMONELLA TYPHIMURIUM	OXIDOREDUCTASE
2BQ6	CRYSTAL STRUCTURE OF FACTOR XA IN COMPLEX WITH 21	HYDROLASE
2BQ7	CRYSTAL STRUCTURE OF FACTOR XA IN COMPLEX WITH 43	HYDROLASE
2BQW	CRYSTAL STRUCTURE OF FACTOR XA IN COMPLEX WITH COMPOUND 45	HYDROLASE

2BQZ	CRYSTAL STRUCTURE OF A TERNARY COMPLEX OF THE HUMAN HISTONE METHYLTRANSFERASE PR-SET7 (ALSO KNOWN AS SET8)	TRANSFERASE
2BR2	RNASE PH CORE OF THE ARCHAEAL EXOSOME	HYDROLASE
2BR8	CRYSTAL STRUCTURE OF ACETYLCHOLINE-BINDING PROTEIN (ACHBP) FROM APLYSIA CALIFORNICA IN COMPLEX WITH AN ALPHA-CONOTOXIN PNIA VARIANT	RECEPTOR/INHIBITOR COMPLEX
2BR9	14-3-3 PROTEIN EPSILON (HUMAN) COMPLEXED TO PEPTIDE	CELL REGULATOR PROTEIN
2BRR	COMPLEX OF THE NEISSERIAL PORA P1.4 EPITOPE PEPTIDE AND TWO FAB-FRAGMENTS (ANTIBODY MN20B9.34)	ANTIBODY/ANTIGEN COMPLEX
2BS3	GLU C180-> GLN VARIANT QUINOL:FUMARATE REDUCTASE FROM WOLINELLA SUCCINOGENES	OXIDOREDUCTASE
2BS4	GLU C180-> ILE VARIANT QUINOL:FUMARATE REDUCTASE FROM WOLINELLA SUCCINOGENES	OXIDOREDUCTASE
2BSK	CRYSTAL STRUCTURE OF THE TIM9 TIM10 HEXAMERIC COMPLEX	PROTEIN TRANSPORT
2BSQ	FITAB BOUND TO DNA	TRANSCRIPTION REGULATION COMPLEX
2BSR	CRYSTAL STRUCTURES AND KIR3DL1 RECOGNITION OF THREE IMMUNODOMINANT VIRAL PEPTIDES COMPLEXED TO HLA-B2705	COMPLEX (ANTIGEN/PEPTIDE)
2BSS	CRYSTAL STRUCTURES AND KIR3DL1 RECOGNITION OF THREE IMMUNODOMINANT VIRAL PEPTIDES COMPLEXED TO HLA-B2705	COMPLEX (ANTIGEN/PEPTIDE)
2BST	CRYSTAL STRUCTURES AND KIR3DL1 RECOGNITION OF THREE IMMUNODOMINANT VIRAL PEPTIDES COMPLEXED TO HLA-B2705	COMPLEX (ANTIGEN/PEPTIDE)
2BTF	THE STRUCTURE OF CRYSTALLINE PROFILIN-BETA-ACTIN	ACETYLATION AND ACTIN-BINDING
2BTO	STRUCTURE OF BTUBA FROM PROSTHECOBACTER DEJONGEII	CYTOSKELETAL PROTEIN
2BTP	14-3-3 PROTEIN THETA (HUMAN) COMPLEXED TO PEPTIDE	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE)
2BTQ	STRUCTURE OF BTUBAB HETERODIMER FROM PROSTHECOBACTER DEJONGEII	CYTOSKELETAL PROTEIN/COMPLEX
2BTV	ATOMIC MODEL FOR BLUETONGUE VIRUS (BTV) CORE	VIRUS
2BTW	CRYSTAL STRUCTURE OF ALR0975	TRANSFERASE
2BUM	CRYSTAL STRUCTURE OF WILD-TYPE PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1	OXIDOREDUCTASE
2BUO	HIV-1 CAPSID C-TERMINAL DOMAIN IN COMPLEX WITH AN INHIBITOR OF PARTICLE ASSEMBLY	VIRAL PROTEIN/PEPTIDE
2BUQ	CRYSTAL STRUCTURE OF WILD-TYPE PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 IN COMPLEX WITH CATECHOL	OXIDOREDUCTASE

2BUR	CRYSTAL STRUCTURE OF WILD-TYPE PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 IN COMPLEX WITH 4-HYDROXYBENZOATE	OXIDOREDUCTASE
2BUT	CRYSTAL STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 MUTANT R457S- APO	OXIDOREDUCTASE
2BUU	CRYSTAL STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 MUTANT R457S IN COMPLEX WITH 4-NITROCATECHOL	OXIDOREDUCTASE
2BUV	CRYSTAL STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 MUTANT R457S IN COMPLEX WITH PROTOCATECHUATE	OXIDOREDUCTASE
2BUW	CRYSTAL STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 MUTANT R457S IN COMPLEX WITH 4-HYDROXYBENZOATE	OXIDOREDUCTASE
2BUX	CRYSTAL STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 MUTANT R133H	OXIDOREDUCTASE
2BUY	CRYSTAL STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 MUTANT R133H IN COMPLEX WITH CATECHOL	OXIDOREDUCTASE
2BUZ	CRYSTAL STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 MUTANT R133H IN COMPLEX WITH 4-NITROCATECHOL	OXIDOREDUCTASE
2BV0	CRYSTAL STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE FROM ACINETOBACTER SP. ADP1 MUTANT R133H IN COMPLEX WITH PROTOCATECHUATE.	OXIDOREDUCTASE
2BV8	THE CRYSTAL STRUCTURE OF PHYCOCYANIN FROM GRACILARIA CHILENSIS.	PHOTOSYNTHESIS
2BVO	STRUCTURES OF THREE HIV-1 HLA-B5703-PEPTIDE COMPLEXES AND IDENTIFICATION OF RELATED HLAS POTENTIALLY ASSOCIATED WITH LONG-TERM NON-PROGRESSION	GLYCOPROTEIN/PEPTIDE COMPLEX
2BVP	STRUCTURES OF THREE HIV-1 HLA-B5703-PEPTIDE COMPLEXES AND IDENTIFICATION OF RELATED HLAS POTENTIALLY ASSOCIATED WITH LONG-TERM NON-PROGRESSION	GLYCOPROTEIN/PEPTIDE COMPLEX
2BW3	THREE-DIMENSIONAL STRUCTURE OF THE HERMES DNA TRANSPOSASE	DNA RECOMBINATION
2BWE	THE CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE UBA AND UBL DOMAINS OF DSK2	SIGNALING PROTEIN
2BWO	5-AMINOLEVULINATE SYNTHASE FROM RHODOBACTER CAPSULATUS IN COMPLEX WITH SUCCINYL-COA	TRANSFERASE
2BYK	HISTONE FOLD HETERODIMER OF THE CHROMATIN ACCESSIBILITY	DNA-BINDING PROTEIN

	COMPLEX	
2BYM	HISTONE FOLD HETERODIMER OF THE CHROMATIN ACCESSIBILITY COMPLEX	DNA-BINDING PROTEIN
2BYP	CRYSTAL STRUCTURE OF APLYSIA CALIFORNICA ACHBP IN COMPLEX WITH ALPHA-CONOTOXIN IMI	RECEPTOR COMPLEX
2BZ6	ORALLY AVAILABLE FACTOR7A INHIBITOR	HYDROLASE
2BZK	CRYSTAL STRUCTURE OF THE HUMAN PIM1 IN COMPLEX WITH AMPPNP AND PIMTIDE	COMPLEX TRANSFERASE/PEPTIDE
2BZW	THE CRYSTAL STRUCTURE OF BCL-XL IN COMPLEX WITH FULL-LENGTH BAD	TRANSCRIPTION COMPLEX
2C0L	TPR DOMAIN OF HUMAN PEX5P IN COMPLEX WITH HUMAN MSCP2	TRANSPORT PROTEIN/RECEPTOR COMPLEX
2C1D	CRYSTAL STRUCTURE OF SOXXA FROM P. PANTOTROPHUS	OXIDOREDUCTASE
2C1E	CRYSTAL STRUCTURES OF CASPASE-3 IN COMPLEX WITH AZA-PEPTIDE MICHAEL ACCEPTOR INHIBITORS.	HYDROLASE
2C1J	MOLECULAR BASIS FOR THE RECOGNITION OF PHOSPHORYLATED AND PHOSPHOACETYLATED HISTONE H3 BY 14-3-3	SIGNALING PROTEIN/COMPLEX
2C1M	NUP50:IMPORTIN-ALPHA COMPLEX	NUCLEAR TRANSPORT/COMPLEX
2C1N	MOLECULAR BASIS FOR THE RECOGNITION OF PHOSPHORYLATED AND PHOSPHOACETYLATED HISTONE H3 BY 14-3-3	SIGNALING PROTEIN/COMPLEX
2C1O	ENAIIHIS FAB FRAGMENT IN THE FREE FORM	IMMUNE SYSTEM
2C1P	FAB-FRAGMENT OF ENANTIOSELECTIVE ANTIBODY COMPLEXED WITH FINROZOLE	IMMUNE SYSTEM
2C1T	STRUCTURE OF THE KAP60P:NUP2 COMPLEX	NUCLEAR TRANSPORT/COMPLEX
2C23	14-3-3 PROTEIN BETA (HUMAN) IN COMPLEX WITH EXOENZYME S PEPTIDE	SIGNALING PROTEIN/COMPLEX
2C2K	CRYSTAL STRUCTURES OF CASPASE-3 IN COMPLEX WITH AZA-PEPTIDE MICHAEL ACCEPTOR INHIBITORS.	HYDROLASE
2C2L	CRYSTAL STRUCTURE OF THE CHIP U-BOX E3 UBIQUITIN LIGASE	HEAT-SHOCK PROTEIN COMPLEX
2C2M	CRYSTAL STRUCTURES OF CASPASE-3 IN COMPLEX WITH AZA-PEPTIDE MICHAEL ACCEPTOR INHIBITORS.	HYDROLASE
2C2O	CRYSTAL STRUCTURES OF CASPASE-3 IN COMPLEX WITH AZA-PEPTIDE MICHAEL ACCEPTOR INHIBITORS.	HYDROLASE
2C2Z	CRYSTAL STRUCTURE OF CASPASE-8 IN COMPLEX WITH AZA-PEPTIDE MICHAEL ACCEPTOR INHIBITOR	HYDROLASE

2C35	SUBUNITS RPB4 AND RPB7 OF HUMAN RNA POLYMERASE II	POLYMERASE
2C37	RNASE PH CORE OF THE ARCHAEAL EXOSOME IN COMPLEX WITH U8 RNA	HYDROLASE
2C38	RNASE PH CORE OF THE ARCHAEAL EXOSOME IN COMPLEX WITH A5 RNA	HYDROLASE
2C3I	CRYSTAL STRUCTURE OF HUMAN PIM1 IN COMPLEX WITH IMIDAZOPYRIDAZIN I	COMPLEX TRANSFERASE/PEPTIDE
2C4F	CRYSTAL STRUCTURE OF FACTOR VII.STF COMPLEXED WITH PD0297121	HYDROLASE
2C4G	STRUCTURE OF CDK2-CYCLIN A WITH PHA-533514	TRANSFERASE
2C4O	CRYSTAL STRUCTURE OF HUMAN UBIQUITIN-CONJUGATING ENZYME UBCH5B	LIGASE
2C5I	N-TERMINAL DOMAIN OF TLG1 COMPLEXED WITH N-TERMINUS OF VPS51 IN DISTORTED CONFORMATION	PROTEIN TRANSPORT/COMPLEX
2C5K	N-TERMINAL DOMAIN OF TLG1 COMPLEXED WITH N-TERMINUS OF VPS51	PROTEIN TRANSPORT/COMPLEX
2C5L	STRUCTURE OF PLC EPSILON RAS ASSOCIATION DOMAIN WITH HRAS	SIGNALING PROTEIN/COMPLEX
2C5N	DIFFERENTIAL BINDING OF INHIBITORS TO ACTIVE AND INACTIVE CDK2 PROVIDES INSIGHTS FOR DRUG DESIGN	TRANSFERASE
2C5P	DIFFERENTIAL BINDING OF INHIBITORS TO ACTIVE AND INACTIVE CDK2 PROVIDES INSIGHTS FOR DRUG DESIGN	TRANSFERASE
2C5V	DIFFERENTIAL BINDING OF INHIBITORS TO ACTIVE AND INACTIVE CDK2 PROVIDES INSIGHTS FOR DRUG DESIGN	COMPLEX (TRANSFERASE/CYCLIN)
2C5W	PENICILLIN-BINDING PROTEIN 1A (PBP-1A) ACYL-ENZYME COMPLEX (CEFOTAXIME) FROM STREPTOCOCCUS PNEUMONIAE	PEPTIDOGLYCAN SYNTHESIS
2C5X	DIFFERENTIAL BINDING OF INHIBITORS TO ACTIVE AND INACTIVE CDK2 PROVIDES INSIGHTS FOR DRUG DESIGN	COMPLEX (TRANSFERASE/INHIBITOR)
2C63	14-3-3 PROTEIN ETA (HUMAN) COMPLEXED TO PEPTIDE	SIGNALING PROTEIN/PEPTIDE COMPLEX
2C6T	CRYSTAL STRUCTURE OF THE HUMAN CDK2 COMPLEXED WITH THE TRIAZOLOPYRIMIDINE INHIBITOR	COMPLEX (TRANSFERASE/CYCLIN2)
2C6W	PENICILLIN-BINDING PROTEIN 1A (PBP-1A) FROM STREPTOCOCCUS PNEUMONIAE	PEPTIDOGLYCAN SYNTHESIS
2C74	14-3-3 PROTEIN ETA (HUMAN) COMPLEXED TO PEPTIDE	SIGNALING PROTEIN/PEPTIDE COMPLEX
2C7J	PHYCOERYTHROCYANIN FROM MASTIGOCLADUS LAMINOSUS, 295 K, 3.0 A	ELECTRON TRANSPORT
2C7K	AUE STRUCTURE OF PHYCOERYTHROCYANIN FROM MASTIGOCLADUS LAMINOSUS	ELECTRON TRANSPORT
2C7L	LOW TEMPERATURE STRUCTURE OF PHYCOERYTHROCYANIN FROM	ELECTRON TRANSPORT

	MASTIGOCLADUS LAMINOSUS	
2C7M	HUMAN RABEX-5 RESIDUES 1-74 IN COMPLEX WITH UBIQUITIN	UBIQUITIN COMPLEX
2C7N	HUMAN RABEX-5 RESIDUES 1-74 IN COMPLEX WITH UBIQUITIN	UBIQUITIN COMPLEX
2C7U	CONFLICTING SELECTIVE FORCES AFFECT CD8 T-CELL RECEPTOR CONTACT SITES IN AN HLA-A2 IMMUNODOMINANT HIV EPITOPE.	GLYCOPROTEIN/PEPTIDE COMPLEX
2C8Q	INSULINE(1SEC) AND UV LASER EXCITED FLUORESCENCE	HORMONE
2C8R	INSULINE(60SEC) AND UV LASER EXCITED FLUORESCENCE	HORMONE
2C8W	THROMBIN INHIBITORS	HYDROLASE
2C8X	THROMBIN INHIBITORS	HYDROLASE
2C8Y	THROMBIN INHIBITORS	HYDROLASE
2C8Z	THROMBIN INHIBITORS	HYDROLASE
2C90	THROMBIN INHIBITORS	HYDROLASE
2C93	THROMBIN INHIBITORS	HYDROLASE
2C9F	THE QUASI-ATOMIC MODEL OF THE ADENOVIRUS TYPE 3 PENTON DODECAHEDRON	VIRUS LIKE PARTICLE
2C9T	CRYSTAL STRUCTURE OF ACETYLCHOLINE BINDING PROTEIN (ACHBP) FROM APLYSIA CALIFORNICA IN COMPLEX WITH ALPHA-CONOTOXIN IMI	RECEPTOR/TOXIN COMPLEX
2C9W	CRYSTAL STRUCTURE OF SOCS-2 IN COMPLEX WITH ELONGIN-B AND ELONGIN-C AT 1.9A RESOLUTION	TRANSCRIPTION REGULATION
2C9X	SULFITE DEHYDROGENASE FROM STARKEYA NOVELLA Y236F MUTANT	OXIDOREDUCTASE
2CA3	SULFITE DEHYDROGENASE FROM STARKEYA NOVELLA R55M MUTANT	OXIDOREDUCTASE
2CA4	SULFITE DEHYDROGENASE FROM STARKEYA NOVELLA MUTANT	OXIDOREDUCTASE
2CAZ	ESCRT-I CORE	PROTEIN TRANSPORT
2CBL	N-TERMINAL DOMAIN OF CBL IN COMPLEX WITH ITS BINDING SITE ON ZAP-70	COMPLEX (PROTO-ONCOGENE/PEPTIDE)
2CCH	THE CRYSTAL STRUCTURE OF CDK2 CYCLIN A IN COMPLEX WITH A SUBSTRATE PEPTIDE DERIVED FROM CDC MODIFIED WITH A GAMMA-LINKED ATP ANALOGUE	COMPLEX(TRANSFERASE/CELL DIVISION)
2CCI	CRYSTAL STRUCTURE OF PHOSPHO-CDK2 CYCLIN A IN COMPLEX WITH A PEPTIDE CONTAINING BOTH THE SUBSTRATE AND RECRUITMENT SITES OF CDC6	COMPLEX (TRANSFERASE/CELL DIVISION)
2CDE	STRUCTURE AND BINDING KINETICS OF THREE DIFFERENT HUMAN	CELL RECEPTOR

	CD1D-ALPHA-GALACTOSYLCERAMIDE SPECIFIC T CELL RECEPTORS-INKT-TCR	
2CDF	STRUCTURE AND BINDING KINETICS OF THREE DIFFERENT HUMAN CD1D-ALPHA-GALACTOSYLCERAMIDE-SPECIFIC T CELL RECEPTORS (TCR 5E)	CELL RECEPTOR
2CDG	STRUCTURE AND BINDING KINETICS OF THREE DIFFERENT HUMAN CD1D-ALPHA-GALACTOSYLCERAMIDE-SPECIFIC T CELL RECEPTORS (TCR 5B)	CELL RECEPTOR
2CDR	CRYSTAL STRUCTURES OF CASPASE-3 IN COMPLEX WITH AZA-PEPTIDE EPOXIDE INHIBITORS.	HYDROLASE/INHIBITOR COMPLEX
2CE8	AN EH1 PEPTIDE BOUND TO THE GROUCHO-TLE WD40 DOMAIN.	TRANSCRIPTION REGULATION
2CEU	DESPENTAPEPTIDE INSULIN IN ACETIC ACID (PH 2)	HORMONE
2CF8	THROMBIN-METHOXY	COMPLEX HYDROLASE/INHIBITOR
2CF9	THROMBIN-METHOXY2	COMPLEX HYDROLASE/INHIBITOR
2CFA	STRUCTURE OF VIRAL FLAVIN-DEPENDANT THYMIDYLATE SYNTHASE THYX	TRANSFERASE
2CG5	STRUCTURE OF AMINOADIPATE-SEMIALDEHYDE DEHYDROGENASE-PHOSPHOPANTETHEINYL TRANSFERASE IN COMPLEX WITH CYTOSOLIC ACYL CARRIER PROTEIN AND COENZYME A	TRANSFERASE/HYDROLASE (COMPLEX)
2CG9	RYSTAL STRUCTURE OF AN HSP90-SBA1 CLOSED CHAPERONE COMPLEX	CHAPERONE COMPLEX
2CGR	LOCAL AND TRANSMITTED CONFORMATIONAL CHANGES ON COMPLEXATION OF AN ANTI-SWEETENER FAB	IMMUNOGLOBULIN
2CGT	GROEL-ADP-GP31 COMPLEX	CHAPERONE
2CH4	COMPLEX BETWEEN BACTERIAL CHEMOTAXIS HISTIDINE KINASE CHEA DOMAINS P4 AND P5 AND RECEPTOR-ADAPTOR PROTEIN CHEW	TRANSFERASE/CHEMOTAXIS
2CHA	THE STRUCTURE OF CRYSTALLINE ALPHA-CHYMOTRYPSIN, $V.THE ATOMIC STRUCTURE OF TOSYL-ALPHA-CHYMOTRYPSIN AT 2 ANGSTROMS RESOLUTION	HYDROLASE (SERINE PROTEINASE)
2CHN	BACTEROIDES THETAIOTAOMICRON HEXOSAMINIDASE WITH O-GLCNACASE ACTIVITY- NAG-THIAZOLINE COMPLEX	HYDROLASE
2CHO	BACTEROIDES THETAIOTAOMICRON HEXOSAMINIDASE WITH O-GLCNACASE ACTIVITY	HYDROLASE
2CI9	ICK1 SH2-DOMAIN IN COMPLEX WITH A DODECAPHOSPHOPEPTIDE FROM EPEC PROTEIN TIR	SH2-DOMAIN/COMPLEX
2CII	THE CRYSTAL STRUCTURE OF H-2DB COMPLEXED WITH A PARTIAL PEPTIDE EPITOPE SUGGESTS AN MHC CLASS I ASSEMBLY-INTERMEDIATE	COMPLEX (ANTIGEN/PEPTIDE)

2CIK	INSIGHTS INTO CROSSREACTIVITY IN HUMAN ALLORECOGNITION: THE STRUCTURE OF HLA-B35011 PRESENTING AN EPITOPE DERIVED FROM CYTOCHROME P450.	ANTIGEN/PEPTIDE COMPLEX
2CJI	CRYSTAL STRUCTURE OF A HUMAN FACTOR XA INHIBITOR COMPLEX	HYDROLASE
2CJM	MECHANISM OF CDK INHIBITION BY ACTIVE SITE PHOSPHORYLATION: CDK2 Y15P T160P IN COMPLEX WITH CYCLIN A STRUCTURE	COMPLEX (TRANSFERASE/CELL DIVISION)
2CJS	STRUCTURAL BASIS FOR A MUNC13-1 HOMODIMER- MUNC13-1- RIM HETERODIMER SWITCH: C2-DOMAINS AS VERSATILE PROTEIN-PROTEIN INTERACTION MODULES	EXOCYTOSIS
2CJW	CRYSTAL STRUCTURE OF THE SMALL GTPASE GEM (GEMDNDCAM) IN COMPLEX TO MG.GDP	G-PROTEIN
2CJX	EXTENDED SUBSTRATE RECOGNITION IN CASPASE-3 REVEALED BY HIGH RESOLUTION X-RAY STRUCTURE ANALYSIS	COMPLEX (HYDROLASE-INHIBITOR)
2CJY	EXTENDED SUBSTRATE RECOGNITION IN CASPASE-3 REVEALED BY HIGH RESOLUTION X-RAY STRUCTURE ANALYSIS	COMPLEX (HYDROLASE-INHIBITOR)
2CK0	ANTI-ANTI-IDIOTYPIC ANTIBODY AGAINST HUMAN ANGIOTENSIN II, COMPLEX WITH A SYNTHETIC CYCLIC PEPTIDE	IMMUNOGLOBULIN
2CK3	AZIDE INHIBITED BOVINE F1-ATPASE	HYDROLASE
2CKB	STRUCTURE OF THE 2C/KB/DEV8 COMPLEX	MAJOR HISTOCOMPATIBILITY COMPLEX
2CKF	CRYSTAL STRUCTURE OF THE TERMINAL COMPONENT OF THE PAH-HYDROXYLATING DIOXYGENASE FROM SPHINGOMONAS SP CHY-1	OXIDOREDUCTASE
2CKH	SENP1-SUMO2 COMPLEX	HYDROLASE
2CKL	RING1B-BMI1 E3 CATALYTIC DOMAIN STRUCTURE	TRANSCRIPTION REGULATION COMPLEX
2CLK	TRYPTOPHAN SYNTHASE IN COMPLEX WITH D-GLYCERALDEHYDE 3-PHOSPHATE (G3P)	LYASE
2CLR	THREE DIMENSIONAL STRUCTURE OF A PEPTIDE EXTENDING OUT ONE END OF A CLASS I MHC BINDING SITE	HISTOCOMPATIBILITY ANTIGEN
2CLV	MHC CLASS I NATURAL MUTANT H-2KBM8 HEAVY CHAIN COMPLEXED WITH BETA-2 MICROGLOBULIN AND PBM8 PEPTIDE	IMMUNE SYSTEM
2CLW	CRYSTAL STRUCTURE OF HUMAN UBIQUITIN-CONJUGATING ENZYME UBCH5B	LIGASE
2CLY	SUBCOMPLEX OF THE STATOR OF BOVINE MITOCHONDRIAL ATP SYNTHASE	HYDROLASE
2CLZ	MHC CLASS I NATURAL MUTANT H-2KBM8 HEAVY CHAIN COMPLEXED WITH BETA-2 MICROGLOBULIN AND PBM1 PEPTIDE	IMMUNE SYSTEM

2CMR	CRYSTAL STRUCTURE OF THE HIV-1 NEUTRALIZING ANTIBODY D5 FAB BOUND TO THE GP41 INNER-CORE MIMETIC 5-HELIX	IMMUNOGLOBULIN COMPLEX
2CMY	CRYSTAL COMPLEX BETWEEN BOVINE TRYPSIN AND VERONICA HEDERIFOLIA TRYPSIN INHIBITOR	HYDROLASE
2CN0	COMPLEX OF RECOMBINANT HUMAN THROMBIN WITH A DESIGNED INHIBITOR	HYDROLASE
2CNK	CRYSTAL STRUCTURES OF CASPASE-3 IN COMPLEX WITH AZA-PEPTIDE EPOXIDE INHIBITORS.	HYDROLASE
2CNL	CRYSTAL STRUCTURES OF CASPASE-3 IN COMPLEX WITH AZA-PEPTIDE EPOXIDE INHIBITORS.	HYDROLASE
2CNM	RIMI - RIBOSOMAL S18 N-ALPHA-PROTEIN ACETYLTRANSFERASE IN COMPLEX WITH A BISUBSTRATE INHIBITOR (CTERM-ARG-ARG-PHE-TYR-ARG-ALA-N-ALPHA-ACETYL-S-COA).	TRANSFERASE
2CNN	CRYSTAL STRUCTURES OF CASPASE-3 IN COMPLEX WITH AZA-PEPTIDE EPOXIDE INHIBITORS.	HYDROLASE
2CNO	CRYSTAL STRUCTURES OF CASPASE-3 IN COMPLEX WITH AZA-PEPTIDE EPOXIDE INHIBITORS.	HYDROLASE
2CNW	GDPALF4 COMPLEX OF THE SRP GTPASES FFH AND FTSY	SIGNAL RECOGNITION
2COL	CRYSTAL STRUCTURE ANALYSIS OF CYAA/C-CAM WITH PYROPHOSPHATE	LYASE/METAL BINDING PROTEIN
2CPK	CRYSTAL STRUCTURE OF THE CATALYTIC SUBUNIT OF CYCLIC ADENOSINE MONOPHOSPHATE-DEPENDENT PROTEIN KINASE	TRANSFERASE(PHOSPHOTRANSFERASE)
2CV5	CRYSTAL STRUCTURE OF HUMAN NUCLEOSOME CORE PARTICLE	STRUCTURAL PROTEIN/DNA
2CVY	STRUCTURES OF YEAST RIBONUCLEOTIDE REDUCTASE I	OXIDOREDUCTASE
2CW0	CRYSTAL STRUCTURE OF THERMUS THERMOPHILUS RNA POLYMERASE HOLOENZYME AT 3.3 ANGSTROMS RESOLUTION	TRANSFERASE
2CWG	CRYSTALLOGRAPHIC REFINEMENT AND STRUCTURE ANALYSIS OF THE COMPLEX OF WHEAT GERM AGGLUTININ WITH A BIVALENT SIALOGLYCOPEPTIDE FROM GLYCOPHORIN A	LECTIN(AGGLUTININ)
2CYZ	PHOTO-ACTIVATION STATE OF FE-TYPE NHASE IN ANAEROBIC CONDITION	LYASE
2CZ0	PHOTO-ACTIVATION STATE OF FE-TYPE NHASE IN AEROBIC CONDITION	LYASE
2CZ1	PHOTO-ACTIVATION STATE OF FE-TYPE NHASE WITH N-BA IN ANAEROBIC CONDITION	LYASE
2CZ6	COMPLEX OF INACTIVE FE-TYPE NHASE WITH CYCLOHEXYL ISOCYANIDE	LYASE
2CZ7	FE-TYPE NHASE PHOTO-ACTIVATED FOR 75MIN AT 105K	LYASE

2CZV	CRYSTAL STRUCTURE OF ARCHEAL RNASE P PROTEIN PH1481P IN COMPLEX WITH PH1877P	HYDROLASE
2D03	CRYSTAL STRUCTURE OF THE G91S MUTANT OF THE NNA7 FAB	IMMUNE SYSTEM
2D07	RYSTAL STRUCTURE OF SUMO-3-MODIFIED THYMINE-DNA GLYCOSYLASE	HYDROLASE
2D0O	TRCUTURE OF DIOL DEHYDRATASE-REACTIVATING FACTOR COMPLEXED WITH ADP AND MG2+	CHAPERONE
2D0P	STRCUTURE OF DIOL DEHYDRATASE-REACTIVATING FACTOR IN NUCLEOTIDE FREE FORM	CHAPERONE
2D0Q	COMPLEX OF FE-TYPE NHASE WITH CYCLOHEXYL ISOCYANIDE, PHOTO-ACTIVATED FOR 1HR AT 277K	LYASE
2D0V	CRYSTAL STRUCTURE OF METHANOL DEHYDROGENASE FROM HYPHOMICROBIUM DENITRIFICANS	OXIDOREDUCTASE
2D10	RYSTAL STRUCTURE OF THE RADIXIN FERM DOMAIN COMPLEXED WITH THE NHERF-1 C-TERMINAL TAIL PEPTIDE	CELL ADHESION
2D11	RYSTAL STRUCTURE OF THE RADIXIN FERM DOMAIN COMPLEXED WITH THE NHERF-2 C-TERMINAL TAIL PEPTIDE	CELL ADHESION
2D1J	FACTOR XA IN COMPLEX WITH THE INHIBITOR 2-[[4-[(5-CHLOROINDOL-2-YL)SULFONYL]PIPERAZIN-1-YL] CARBONYL]THIENO[3,2-B]PYRIDINE N-OXIDE	HYDROLASE
2D1K	TERNARY COMPLEX OF THE WH2 DOMAIN OF MIM WITH ACTIN-DNASE I	STRUCTURAL PROTEIN
2D1P	RYSTAL STRUCTURE OF HETEROHEXAMERIC TUSBCD PROTEINS, WHICH ARE CRUCIAL FOR THE TRNA MODIFICATION	TRANSLATION
2D26	ACTIVE SITE DISTORTION IS SUFFICIENT FOR PROTEINASE INHIBIT SECOND CRYSTAL STRUCTURE OF COVALENT SERPIN-PROTEINASE COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
2D2C	RYSTAL STRUCTURE OF CYTOCHROME B6F COMPLEX WITH DBMIB FROM M. LAMINOSUS	PHOTOSYNTHESIS
2D2M	STRUCTURE OF AN EXTRACELLULAR GIANT HEMOGLOBIN OF THE GUTLESS BEARD WORM OLIGOBRACHIA MASHIKOI	OXYGEN STORAGE/TRANSPORT
2D2N	STRUCTURE OF AN EXTRACELLULAR GIANT HEMOGLOBIN OF THE GUTLESS BEARD WORM OLIGOBRACHIA MASHIKOI	OXYGEN STORAGE/TRANSPORT
2D31	CRYSTAL STRUCTURE OF DISULFIDE-LINKED HLA-G DIMER	IMMUNE SYSTEM/CELL CYCLE
2D3G	DOUBLE SIDED UBIQUITIN BINDING OF HRS-UIM	PROTEIN TRANSPORT
2D3O	STRUCTURE OF RIBOSOME BINDING DOMAIN OF THE TRIGGER FACTOR ON THE 50S RIBOSOMAL SUBUNIT FROM D. RADIODURANS	RIBOSOME
2D3T	FATTY ACID BETA-OXIDATION MULTIENZYME COMPLEX FROM	LYASE, OXIDOREDUCTASE/TRANSFERASE

	PSEUDOMONAS FRAGI, FORM V	
2D5R	CRYSTAL STRUCTURE OF A TOB-HCAF1 COMPLEX	TRANSCRIPTION
2D5W	THE CRYSTAL STRUCTURE OF OLIGOPEPTIDE BINDING PROTEIN FROM THERMUS THERMOPHILUS HB8 COMPLEXED WITH PENTAPEPTIDE	PEPTIDE BINDING PROTEIN
2D5X	CRYSTAL STRUCTURE OF CARBONMONOXY HORSE HEMOGLOBIN COMPLEXED WITH L35	OXYGEN STORAGE/TRANSPORT
2D5Z	CRYSTAL STRUCTURE OF T-STATE HUMAN HEMOGLOBIN COMPLEXED WITH THREE L35 MOLECULES	OXYGEN STORAGE/TRANSPORT
2D60	RYSTAL STRUCTURE OF DEOXY HUMAN HEMOGLOBIN COMPLEXED WITH TWO L35 MOLECULES	OXYGEN STORAGE/TRANSPORT
2D6F	CRYSTAL STRUCTURE OF GLU-TRNA(GLN) AMIDOTRANSFERASE IN THE COMPLEX WITH TRNA(GLN)	LIGASE/RNA
2D74	CRYSTAL STRUCTURE OF TRANSLATION INITIATION FACTOR AIF2BETAGAMMA HETERODIMER	TRANSLATION
2D7C	CRYSTAL STRUCTURE OF HUMAN RAB11 IN COMPLEX WITH FIP3 RAB-BINDING DOMAIN	PROTEIN TRANSPORT
2D7D	STRUCTURAL INSIGHTS INTO THE CRYPTIC DNA DEPENDENT ATP-ASE ACTIVITY OF UVRB	HYDROLASE/DNA
2D7S	FOOT AND MOUTH DISEASE VIRUS RNA-DEPENDENT RNA POLYMERASE IN COMPLEX WITH VPG PROTEIN	TRANSFERASE
2D9Q	CRYSTAL STRUCTURE OF THE HUMAN GCSF-RECEPTOR SIGNALING COMPLEX	SIGNALING PROTEIN/CYTOKINE
2DBU	CRYSTAL STRUCTURE OF GAMMA-GLUTAMYLTRANSPEPTIDASE FROM ESCHERICHIA COLI	TRANSFERASE
2DBW	CRYSTAL STRUCTURE OF GAMMA-GLUTAMYLTRANSPEPTIDASE FROM ESCHERICHIA COLI ACYL-ENZYME INTERMEDIATE	TRANSFERASE
2DBX	CRYSTAL STRUCTURE OF GAMMA-GLUTAMYLTRANSPEPTIDASE FROM ESCHERICHIA COLI COMPLEXED WITH L-GLUTAMATE	TRANSFERASE
2DCU	CRYSTAL STRUCTURE OF TRANSLATION INITIATION FACTOR AIF2BETAGAMMA HETERODIMER WITH GDP	TRANSLATION
2DD4	THIOCYANATE HYDROLASE (SCNASE) FROM THIOBACILLUS THIOPARUS RECOMBINANT APO-ENZYME	HYDROLASE
2DD5	THIOCYANATE HYDROLASE (SCNASE) FROM THIOBACILLUS THIOPARUS NATIVE HOLO-ENZYME	HYDROLASE
2DD8	CRYSTAL STRUCTURE OF SARS-COV SPIKE RECEPTOR-BINDING DOMAIN COMPLEXED WITH NEUTRALIZING ANTIBODY	IMMUNE SYSTEM/VIRAL PROTEIN

2DDQ	CRYSTAL STRUCTURE OF THE FAB FRAGMENT OF A R310 ANTIBODY COMPLEXED WITH (R)-HNE-HISTIDINE ADDUCT	IMMUNE SYSTEM
2DE5	RYSTAL STRUCTURE OF THE ELECTRON TRANSFER COMPLEX BETWEEN OXYGENASE AND FERREDOXIN IN CARBAZOLE 1,9A-DIOXYGENASE	OXIDOREDUCTASE
2DE6	THE REDUCED COMPLEX BETWEEN OXYGENASE AND FERREDOXIN IN CARBAZOLE 1,9A-DIOXYGENASE	OXIDOREDUCTASE
2DE7	THE SUBSTRATE-BOUND COMPLEX BETWEEN OXYGENASE AND FERREDOXIN IN CARBAZOLE 1,9A-DIOXYGENASE	OXIDOREDUCTASE
2DEW	CRYSTAL STRUCTURE OF HUMAN PEPTIDYLARGININE DEIMINASE 4 IN COMPLEX WITH HISTONE H3 N-TERMINAL TAIL INCLUDING ARG8	HYDROLASE
2DEX	CRYSTAL STRUCTURE OF HUMAN PEPTIDYLARGININE DEIMINASE 4 IN COMPLEX WITH HISTONE H3 N-TERMINAL PEPTIDE INCLUDING ARG17	HYDROLASE
2DEY	CRYSTAL STRUCTURE OF HUMAN PEPTIDYLARGININE DEIMINASE 4 IN COMPLEX WITH HISTONE H4 N-TERMINAL TAIL INCLUDING ARG3	HYDROLASE
2DF4	STRUCTURE OF TRNA-DEPENDENT AMIDOTRANSFERASE GATCAB COMPLEXED WITH MN2+	LIGASE
2DFK	CRYSTAL STRUCTURE OF THE CDC42-COLLYBISTIN II COMPLEX	CELL CYCLE
2DFS	3-D STRUCTURE OF MYOSIN-V INHIBITED STATE	CONTRACTILE PROTEIN/TRANSPORT PROTEIN
2DFX	CRYSTAL STRUCTURE OF THE CARBOXY TERMINAL DOMAIN OF COLICIN E5 COMPLEXED WITH ITS INHIBITOR	HYDROLASE
2DG5	CRYSTAL STRUCTURE OF GAMMA-GLUTAMYL TRANSPEPTIDASE FROM ESCHERICHIA COLI IN COMPLEX WITH HYDROLYZED GLUTATHIONE	TRANSFERASE
2DHB	THREE DIMENSIONAL FOURIER SYNTHESIS OF HORSE DEOXYHAEMOGLOBIN AT 2.8 ANGSTROMS RESOLUTION	OXYGEN TRANSPORT
2DJF	CRYSTAL STRUCTURE OF HUMAN DIPEPTIDYL PEPTIDASE I (CATHEPSIN C) IN COMPLEX WITH THE INHIBITOR GLY-PHE-CHN2	HYDROLASE
2DJG	RE-DETERMINATION OF THE NATIVE STRUCTURE OF HUMAN DIPEPTIDYL PEPTIDASE I (CATHEPSIN C)	HYDROLASE
2DKO	EXTENDED SUBSTRATE RECOGNITION IN CASPASE-3 REVEALED BY HIGH RESOLUTION X-RAY STRUCTURE ANALYSIS	HYDROLASE
2DN1	1.25A RESOLUTION CRYSTAL STRUCTURE OF HUMAN HEMOGLOBIN IN THE OXY FORM	OXYGEN STORAGE/TRANSPORT
2DN2	1.25A RESOLUTION CRYSTAL STRUCTURE OF HUMAN HEMOGLOBIN IN THE DEOXY FORM	OXYGEN STORAGE/TRANSPORT
2DN3	1.25A RESOLUTION CRYSTAL STRUCTURE OF HUMAN HEMOGLOBIN IN THE CARBONMONOXY FORM	OXYGEN STORAGE/TRANSPORT

2DO2	DESIGN OF SPECIFIC INHIBITORS OF PHOSPHOLIPASE A2: CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN A GROUP II CYS 49 PHOSPHOLIPASE A2 AND A DESIGNED PENTAPEPTIDE ALA-LEU-ALA-SER-LYS AT 2.6A RESOLUTION	HYDROLASE
2DOH	THE X-RAY CRYSTALLOGRAPHIC STRUCTURE OF THE ANGIOGENESIS INHIBITOR, ANGIOSTATIN, BOUND A TO A PEPTIDE FROM THE GROUP A STREPTOCOCCAL SURFACE PROTEIN PAM	HYDROLASE
2DOI	THE X-RAY CRYSTALLOGRAPHIC STRUCTURE OF THE ANGIOGENESIS INHIBITOR, ANGIOSTATIN, BOUND TO A PEPTIDE FROM THE GROUP A STREPTOCOCCUS PROTEIN PAM	HYDROLASE
2DOQ	CRYSTAL STRUCTURE OF SFI1P/CDC31P COMPLEX	CELL CYCLE
2DP4	RYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN PROTEINASE K AND A HUMAN LACTOFERRIN FRAGMENT AT 2.9 A RESOLUTION	HYDROLASE
2DPP	CRYSTAL STRUCTURE OF THERMOSTABLE BACILLUS SP. RAPC8 NITRILE HYDRATASE	LYASE
2DQC	CRYSTAL STRUCTURE OF HYHEL-10 FV MUTANT(HY33F) COMPLEXED WITH HEN EGG LYSOZYME	IMMUNE SYSTEM/HYDROLASE
2DQD	CRYSTAL STRUCTURE OF HYHEL-10 FV MUTANT (HY50F) COMPLEXED WITH HEN EGG LYSOZYME	IMMUNE SYSTEM/HYDROLASE
2DQE	CRYSTAL STRUCTURE OF HYHEL-10 FV MUTANT (HY53A) COMPLEXED WITH HEN EGG LYSOZYME	IMMUNE SYSTEM/HYDROLASE
2DQF	CRYSTAL STRUCTURE OF HYHEL-10 FV MUTANT (Y33AY53A) COMPLEXED WITH HEN EGG LYSOZYME	IMMUNE SYSTEM/HYDROLASE
2DQG	CRYSTAL STRUCTURE OF HYHEL-10 FV MUTANT (HY53F) COMPLEXED WITH HEN EGG LYSOZYME	IMMUNE SYSTEM/HYDROLASE
2DQH	CRYSTAL STRUCTURE OF HYHEL-10 FV MUTANT (HY58A) COMPLEXED WITH HEN EGG LYSOZYME	IMMUNE SYSTEM/HYDROLASE
2DQI	CRYSTAL STRUCTURE OF HYHEL-10 FV MUTANT (LY50A) COMPLEXED WITH HEN EGG LYSOZYME	IMMUNE SYSTEM/HYDROLASE
2DQJ	CRYSTAL STRUCTURE OF HYHEL-10 FV (WILD-TYPE) COMPLEXED WITH HEN EGG LYSOZYME AT 1.8A RESOLUTION	IMMUNE SYSTEM/HYDROLASE
2DQK	CRYSTAL STRUCTURE OF THE COMPLEX OF PROTEINASE K WITH A SPECIFIC LACTOFERRIN PEPTIDE VAL-LEU-LEU-HIS AT 1.93 A RESOLUTION	HYDROLASE
2DQN	STRUCTURE OF TRNA-DEPENDENT AMIDOTRANSFERASE GATCAB COMPLEXED WITH ASN	LIGASE
2DQT	HIGH RESOLUTION CRYSTAL STRUCTURE OF THE COMPLEX OF THE HYDROLYTIC ANTIBODY FAB 6D9 AND A TRANSITION-STATE ANALOG	IMMUNE SYSTEM

2DQU	CRYSTAL FORM II: HIGH RESOLUTION CRYSTAL STRUCTURE OF THE COMPLEX OF THE HYDROLYTIC ANTIBODY FAB 6D9 AND A TRANSITION-STATE ANALOG	IMMUNE SYSTEM
2DS2	CRYSTAL STRUCTURE OF MABINLIN II	PLANT PROTEIN
2DS8	STRUCTURE OF THE ZBD-XB COMPLEX	METAL BINDING PROTEIN, PROTEIN BINDING
2DSP	STRUCTURAL BASIS FOR THE INHIBITION OF INSULIN-LIKE GROWTH FACTORS BY IGF BINDING PROTEINS	PROTEIN BINDING/HORMONE/GROWTH FACTOR
2DSQ	STRUCTURAL BASIS FOR THE INHIBITION OF INSULIN-LIKE GROWTH FACTORS BY IGF BINDING PROTEINS	PROTEIN BINDING/HORMONE/GROWTH FACTOR
2DSR	STRUCTURAL BASIS FOR THE INHIBITION OF INSULIN-LIKE GROWTH FACTORS BY IGF BINDING PROTEINS	PROTEIN BINDING/HORMONE/GROWTH FACTOR
2DTG	INSULIN RECEPTOR (IR) ECTODOMAIN IN COMPLEX WITH FAB'S	HORMONE RECEPTOR/IMMUNE SYSTEM
2DTM	THERMODYNAMIC AND STRUCTURAL ANALYSES OF HYDROLYTIC MECHANISM BY CATALYTIC ANTIBODIES	IMMUNE SYSTEM
2DUJ	RYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN PROTEINASE K AND A SYNTHETIC PEPTIDE LEU-LEU-PHE-ASN-ASP AT 1.67 A RESOLUTION	HYDROLASE
2DVQ	CRYSTAL STRUCTURE ANALYSIS OF THE N-TERMINAL BROMODOMAIN OF HUMAN BRD2 COMPLEXED WITH ACETYLATED HISTONE H4 PEPTIDE	TRANSCRIPTION
2DVR	CRYSTAL STRUCTURE ANALYSIS OF THE N-TERMINAL BROMODOMAIN OF HUMAN BRD2 COMPLEXED WITH ACETYLATED HISTONE H4 PEPTIDE	TRANSCRIPTION
2DVS	CRYSTAL STRUCTURE ANALYSIS OF THE N-TERMINAL BROMODOMAIN OF HUMAN BRD2 COMPLEXED WITH ACETYLATED HISTONE H4 PEPTIDE	TRANSCRIPTION
2DVW	STRUCTURE OF THE ONCOPROTEIN GANKYRIN IN COMPLEX WITH S6 ATPASE OF THE 26S PROTEASOME	CELL CYCLE/PROTEIN-BINDING
2DWD	CRYSTAL STRUCTURE OF KCSA-FAB-TBA COMPLEX IN TL+	MEMBRANE PROTEIN
2DWE	CRYSTAL STRUCTURE OF KCSA-FAB-TBA COMPLEX IN RB+	MEMBRANE PROTEIN
2DWZ	STRUCTURE OF THE ONCOPROTEIN GANKYRIN IN COMPLEX WITH S6 ATPASE OF THE 26S PROTEASOME	ONCOPROTEIN
2DX5	THE COMPLEX STRUCTURE BETWEEN THE MOUSE EAP45-GLUE DOMAIN AND UBIQUITIN	PROTEIN TRANSPORT/SIGNALING PROTEIN
2DXB	RECOMBINANT THIOCYANATE HYDROLASE COMPRISING PARTIALLY-MODIFIED COBALT CENTERS	HYDROLASE
2DXC	RECOMBINANT THIOCYANATE HYDROLASE, FULLY-MATURED FORM	HYDROLASE
2DXM	NEUTRON STRUCTURE ANALYSIS OF DEOXY HUMAN HEMOGLOBIN	OXYGEN STORAGE/TRANSPORT

2DXP	RYSTAL STRUCTURE OF THE COMPLEX OF THE ARCHAEAL SULFOLOBUS PTP-FOLD PHOSPHATASE WITH PHOSPHOPEPTIDES A-(P)Y-R	HYDROLASE
2DYM	THE CRYSTAL STRUCTURE OF SACCHAROMYCES CEREVISIAE ATG5-ATG16(1-46) COMPLEX	PROTEIN TURNOVER/PROTEIN TURNOVER
2DYO	THE CRYSTAL STRUCTURE OF SACCHAROMYCES CEREVISIAE ATG5-ATG16(1-57) COMPLEX	PROTEIN TURNOVER/PROTEIN TURNOVER
2DYP	CRYSTAL STRUCTURE OF LILRB2(LIR2/ILT4/CD85D) COMPLEXED WITH HLA-G	IMMUNE SYSTEM
2DYR	BOVINE HEART CYTOCHROME C OXIDASE AT THE FULLY OXIDIZED STATE	OXIDOREDUCTASE
2DYS	BOVINE HEART CYTOCHROME C OXIDASE MODIFIED BY DCCD	OXIDOREDUCTASE
2DZN	CRYSTAL STRUCTURE ANALYSIS OF YEAST NAS6P COMPLEXED WITH THE PROTEASOME SUBUNIT, RPT3	PROTEIN BINDING
2DZO	CRYSTAL STRUCTURE ANALYSIS OF YEAST NAS6P COMPLEXED WITH THE PROTEASOME SUBUNIT, RPT3	PROTEIN BINDING
2E0X	:RYSTAL STRUCTURE OF GAMMA-GLUTAMYLTRANSPEPTIDASE FROM ESCHERICHIA COLI (MONOCLINIC FORM)	TRANSFERASE
2E0Y	CRYSTAL STRUCTURE OF THE SAMARIUM DERIVATIVE OF MATURE GAMMA-GLUTAMYLTRANSPEPTIDASE FROM ESCHERICHIA COLI	TRANSFERASE
2E1M	:RYSTAL STRUCTURE OF L-GLUTAMATE OXIDASE FROM STREPTOMYCES SP. X-119-6	OXIDOREDUCTASE
2E2D	FLEXIBILITY AND VARIABILITY OF TIMP BINDING: X-RAY STRUCTURE OF THE COMPLEX BETWEEN COLLAGENASE-3/MMP-13 AND TIMP-2	HYDROLASE/HYDROLASE INHIBITOR
2E2H	RNA POLYMERASE II ELONGATION COMPLEX AT 5 MM MG2+ WITH GTP	TRANSCRIPTION/DNA/RNA
2E2I	RNA POLYMERASE II ELONGATION COMPLEX IN 5 MM MG+2 WITH 2'-DGTP	TRANSCRIPTION/DNA/RNA
2E2J	RNA POLYMERASE II ELONGATION COMPLEX IN 5 MM MG+2 WITH GMPCPP	TRANSCRIPTION/DNA/RNA
2.00E+31	3TRUCTURAL BASIS FOR SELECTION OF GLYCOSYLATED SUBSTRATE BY SCFFBS1 UBIQUITIN LIGASE	LIGASE
2.00E+32	3TRUCTURAL BASIS FOR SELECTION OF GLYCOSYLATED SUBSTRATE BY SCFFBS1 UBIQUITIN LIGASE	LIGASE
2.00E+33	3TRUCTURAL BASIS FOR SELECTION OF GLYCOSYLATED SUBSTRATE BY SCFFBS1 UBIQUITIN LIGASE	LIGASE/HYDROLASE
2E3K	:RYSTAL STRUCTURE OF THE HUMAN BRD2 SECOND BROMODOMAIN IN COMPLEXED WITH THE ACETYLATED HISTONE H4 PEPTIDE	TRANSCRIPTION

2E3X	RYSTAL STRUCTURE OF RUSSELL'S VIPER VENOM METALLOPROTEINASE	HYDROLASE, BLOOD CLOTTING, TOXIN
2E5L	A SNAPSHOT OF THE 30S RIBOSOMAL SUBUNIT CAPTURING MRNA VIA THE SHINE- DALGARNO INTERACTION	RIBOSOME
2.00E+74	CRYSTAL STRUCTURE OF THE CYTOCHROME B6F COMPLEX FROM M.LAMINOSUS	PHOTOSYNTHESIS
2.00E+75	CRYSTAL STRUCTURE OF THE CYTOCHROME B6F COMPLEX WITH 2-NONYL-4-HYDROXYQUINOLINE N-OXIDE (NQNO) FROM M.LAMINOSUS	PHOTOSYNTHESIS
2.00E+76	CRYSTAL STRUCTURE OF THE CYTOCHROME B6F COMPLEX WITH TRIDECYL-STIGMATELLIN (TDS) FROM M.LAMINOSUS	PHOTOSYNTHESIS
2E7L	STRUCTURE OF A HIGH-AFFINITY MUTANT OF THE 2C TCR IN COMPLEX WITH LD/QL9	IMMUNE SYSTEM
2E9W	CRYSTAL STRUCTURE OF THE EXTRACELLULAR DOMAIN OF KIT IN COMPLEX WITH STEM CELL FACTOR (SCF)	TRANSFERASE/HORMONE
2E9X	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX	REPLICATION
2EAX	CRYSTAL STRUCTURE OF HUMAN PGRP-IBETAC IN COMPLEX WITH GLYCOSAMYL MURAMYL PENTAPEPTIDE	SUGAR BINDING PROTEIN
2EC6	PLACOPECTEN STRIATED MUSCLE MYOSIN II	CONTRACTILE PROTEIN
2EC9	CRYSTAL STRUCTURE ANALYSIS OF HUMAN FACTOR VIIA , SOULUBLE TISSUE FACTOR COMPLEXED WITH BCX-3607	BLOOD CLOTTING
2EEO	CRYSTAL STRUCTURE OF T.TH. HB8 L-ASPARTATE-ALPHA-DECARBOXYLASE COMPLEXED WITH FUMARATE	LYASE
2EFA	NEUTRON CRYSTAL STRUCTURE OF CUBIC INSULIN AT PD6.6	HORMONE/GROWTH FACTOR
2EFC	ARA7-GDP/ATVPS9A	TRANSPORT PROTEIN
2EFD	ARA7/ATVPS9A	TRANSPORT PROTEIN
2EFE	ARA7-GDPNH2/ATVPS9A	TRANSPORT PROTEIN
2EFH	ARA7-GDP/ATVPS9A(D185N)	TRANSPORT PROTEIN
2EG4	RYSTAL STRUCTURE OF PROBABLE THIOSULFATE SULFURTRANSFERASE	TRANSFERASE
2EH7	CRYSTAL STRUCTURE OF HUMANIZED KR127 FAB	IMMUNE SYSTEM
2EH8	CRYSTAL STRUCTURE OF THE COMPLEX OF HUMANIZED KR127 FAB AND PRES1 PEPTIDE EPITOPE	IMMUNE SYSTEM
2EHB	THE STRUCTURE OF THE C-TERMINAL DOMAIN OF THE PROTEIN KINASE ATSOS2 BOUND TO THE CALCIUM SENSOR ATSOS3	SIGNALLING PROTEIN/TRANSFERASE
2EHO	CRYSTAL STRUCTURE OF HUMAN GINS COMPLEX	REPLICATION

2EI6	FACTOR XA IN COMPLEX WITH THE INHIBITOR (-)-CIS-N1-[(5-CHLOROINDOL-2-YL)CARBONYL]-N2-[(5-METHYL-4,5,6,7-TETRAHYDROTHIAZOLO[5,4-C]PYRIDIN-2-YL)CARBONYL]-1,2-CYCLOHEXANEDIAMINE	HYDROLASE
2EI7	FACTOR XA IN COMPLEX WITH THE INHIBITOR TRANS-N1-[(5-CHLOROINDOL-2-YL)CARBONYL]-N2-[(5-METHYL-4,5,6,7-TETRAHYDROTHIAZOLO[5,4-C]PYRIDIN-2-YL)CARBONYL]-1,2-CYCLOHEXANEDIAMINE	HYDROLASE
2EI8	FACTOR XA IN COMPLEX WITH THE INHIBITOR (1S,2R,4S)-N1-[(5-CHLOROINDOL-2-YL)CARBONYL]-4-(N,N-DIMETHYLCARBAMOYL)-N2-[(5-METHYL-4,5,6,7-TETRAHYDROTHIAZOLO[5,4-C]PYRIDIN-2-YL) CARBONYL]-1,2-CYCLOHEXANEDIAMINE	HYDROLASE
2EIJ	BOVINE HEART CYTOCHROME C OXIDASE IN THE FULLY REDUCED STATE	OXIDOREDUCTASE
2EIK	CADMIUM ION BINDING STRUCTURE OF BOVINE HEART CYTOCHROME C OXIDASE IN THE FULLY REDUCED STATE	OXIDOREDUCTASE
2EIL	CADMIUM ION BINDING STRUCTURE OF BOVINE HEART CYTOCHROME C OXIDASE IN THE FULLY OXIDIZED STATE	OXIDOREDUCTASE
2EIM	ZINC ION BINDING STRUCTURE OF BOVINE HEART CYTOCHROME C OXIDASE IN THE FULLY REDUCED STATE	OXIDOREDUCTASE
2EIN	ZINC ION BINDING STRUCTURE OF BOVINE HEART CYTOCHROME C OXIDASE IN THE FULLY OXIDIZED STATE	OXIDOREDUCTASE
2EIZ	CRYSTAL STRUCTURE OF HUMANIZED HYHEL-10 FV MUTANT(HW47Y)-HEN LYSOZYME COMPLEX	IMMUNE SYSTEM/HYDROLASE
2EJF	CRYSTAL STRUCTURE OF THE BIOTIN PROTEIN LIGASE (MUTATIONS R48A AND K111A) AND BIOTIN CARBOXYL CARRIER PROTEIN COMPLEX FROM PYROCOCCUS HORIKOSHII OT3	LIGASE
2EJG	CRYSTAL STRUCTURE OF THE BIOTIN PROTEIN LIGASE (MUTATION R48A) AND BIOTIN CARBOXYL CARRIER PROTEIN COMPLEX FROM PYROCOCCUS HORIKOSHII OT3	LIGASE
2EKE	STRUCTURE OF A SUMO-BINDING-MOTIF MIMIC BOUND TO SMT3P-UBC9P: CONSERVATION OF A NONCOVALENT UBIQUITIN-LIKE PROTEIN-E2 COMPLEX AS A PLATFORM FOR SELECTIVE INTERACTIONS WITHIN A SUMO PATHWAY	LIGASE/PROTEIN BINDING
2EKS	CRYSTAL STRUCTURE OF HUMANIZED HYHEL-10 FV-HEN LYSOZYME COMPLEX	IMMUNE SYSTEM/HYDROLASE
2EKV	THE CRYSTAL STRUCTURE OF RIGOR LIKE SQUID MYOSIN S1 IN THE ABSENCE OF NUCLEOTIDE	CONTRACTILE PROTEIN
2EKW	THE CRYSTAL STRUCTURE OF SQUID MYOSIN S1 IN THE PRESENCE OF SO4 2-	CONTRACTILE PROTEIN

2EMS	CRYSTAL STRUCTURE ANALYSIS OF THE RADIXIN FERM DOMAIN COMPLEXED WITH ADHESION MOLECULE CD43	CELL ADHESION
2EMT	CRYSTAL STRUCTURE ANALYSIS OF THE RADIXIN FERM DOMAIN COMPLEXED WITH ADHESION MOLECULE PSGL-1	CELL ADHESION
2EPH	CRYSTAL STRUCTURE OF FRUCTOSE-BISPHOSPHATE ALDOLASE FROM PLASMODIUM FALCIPARUM IN COMPLEX WITH TRAP-TAIL DETERMINED AT 2.7 ANGSTROM RESOLUTION	LYASE
2EQ7	RYSTAL STRUCTURE OF LIPOAMIDE DEHYDROGENASE FROM THERMUS THERMOPHILUS HB8 WITH PSBDO	OXIDOREDUCTASE
2EZ0	CRYSTAL STRUCTURE OF THE S107A/E148Q/Y445A MUTANT OF ECCLC, IN COMPLEX WITH A FAB FRAGMENT	MEMBRANE PROTEIN
2F0Y	CRYSTAL STRUCTURE OF HUMAN PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH FARNESYL DIPHOSPHATE AND HYDANTOIN DERIVATIVE	TRANSFERASE
2F16	CRYSTAL STRUCTURE OF THE YEAST 20S PROTEASOME IN COMPLEX WITH BORTEZOMIB	HYDROLASE
2F19	THREE-DIMENSIONAL STRUCTURE OF TWO CRYSTAL FORMS OF FAB R19.9, FROM A MONOCLONAL ANTI-ARSONATE ANTIBODY	IMMUNOGLOBULIN
2F2A	STRUCTURE OF TRNA-DEPENDENT AMIDOTRANSFERASE GATCAB COMPLEXED WITH GLN	LIGASE
2F2C	X-RAY STRUCTURE OF HUMAN CDK6-VCYCLINWITH THE INHIBITOR AMINOPURVALANOL	CELL CYCLE/TRANSFERASE
2F2F	CRYSTAL STRUCTURE OF CYTOLETHAL DISTENDING TOXIN (CDT) FROM ACTINOBACILLUS ACTINOMYCETEMCOMITANS	TOXIN
2F2L	CRYSTAL STRUCTURE OF TRACHEAL CYTOTOXIN (TCT) BOUND TO THE ECTODOMAIN COMPLEX OF PEPTIDOGLYCAN RECOGNITION PROTEINS LCA (PGRP-LCA) AND LCX (PGRP-LCX)	MEMBRANE PROTEIN, IMMUNE SYSTEM, TOXIN
2F31	CRYSTAL STRUCTURE OF THE AUTOINHIBITORY SWITCH IN FORMIN MDIA1; THE DID/DAD COMPLEX	STRUCTURAL PROTEIN
2F3C	CRYSTAL STRUCTURE OF INFESTIN 1, A KAZAL-TYPE SERINEPROTEASE INHIBITOR, IN COMPLEX WITH TRYPSIN	HYDROLASE/HYDROLASE INHIBITOR
2F3Y	CALMODULIN/IQ DOMAIN COMPLEX	METAL BINDING PROTEIN
2F3Z	CALMODULIN/IQ-AA DOMAIN COMPLEX	METAL BINDING PROTEIN
2F43	RAT LIVER F1-ATPASE	HYDROLASE
2F49	CRYSTAL STRUCTURE OF FUS3 IN COMPLEX WITH A STE5 PEPTIDE	TRANSFERASE
2F4M	THE MOUSE PNGASE-HR23 COMPLEX REVEALS A COMPLETE REMODULATION OF THE PROTEIN-PROTEIN INTERFACE COMPARED TO	HYDROLASE

	ITS YEAST ORTHOLOGS	
2F4O	THE MOUSE PNGASE-HR23 COMPLEX REVEALS A COMPLETE REMODULATION OF THE PROTEIN-PROTEIN INTERFACE COMPARED TO ITS YEAST ORTHOLOGS	HYDROLASE
2F4V	30S RIBOSOME + DESIGNER ANTIBIOTIC	RIBOSOME
2F53	DIRECTED EVOLUTION OF HUMAN T-CELL RECEPTOR CDR2 RESIDUES BY PHAGE DISPLAY DRAMATICALLY ENHANCES AFFINITY FOR COGNATE PEPTIDE-MHC WITHOUT APPARENT CROSS-REACTIVITY	IMMUNE SYSTEM
2F54	DIRECTED EVOLUTION OF HUMAN T CELL RECEPTOR CDR2 RESIDUES BY PHAGE DISPLAY DRAMATICALLY ENHANCES AFFINITY FOR COGNATE PEPTIDE-MHC WITHOUT INCREASING APPARENT CROSS-REACTIVITY	IMMUNE SYSTEM
2F58	IGG1 FAB FRAGMENT (58.2) COMPLEX WITH 12-RESIDUE CYCLIC PEPTIDE (INCLUDING RESIDUES 315-324 OF HIV-1 GP120) (MN ISOLATE)	IMMUNE SYSTEM
2F5A	CRYSTAL STRUCTURE OF FAB' FROM THE HIV-1 NEUTRALIZING ANTIBODY 2F5	IMMUNOGLOBULIN
2F5B	CRYSTAL STRUCTURE OF FAB' FROM THE HIV-1 NEUTRALIZING ANTIBODY 2F5 IN COMPLEX WITH ITS GP41 EPITOPE	IMMUNOGLOBULIN
2F5Z	RYSTAL STRUCTURE OF HUMAN DIHYDROLIPOAMIDE DEHYDROGENASE (E3) COMPLEXED TO THE E3-BINDING DOMAIN OF HUMAN E3-BINDING PROTEIN	OXIDOREDUCTASE/PROTEIN BINDING
2F66	STRUCTURE OF THE ESCRT-I ENDOSOMAL TRAFFICKING COMPLEX	TRANSPORT PROTEIN
2F69	TERNARY COMPLEX OF SET7/9 BOUND TO ADOHCY AND A TAF10 PEPTIDE	TRANSFERASE
2F6A	COLLAGEN ADHESIN AND COLLAGEN COMPLEX STRUCTURE	CELL ADHESION/STRUCTURAL PROTEIN
2F6J	RYSTAL STRUCTURE OF PHD FINGER-LINKER-BROMODOMAIN FRAGMENT OF HUMAN BPTF IN THE H3(1-15)K4ME3 BOUND STATE	TRANSCRIPTION
2F6M	STRUCTURE OF A VPS23-C:VPS28-N SUBCOMPLEX	TRANSPORT PROTEIN
2F74	MURINE MHC CLASS I H-2DB IN COMPLEX WITH HUMAN B2-MICROGLOBULIN AND LCMV-DERIVED IMMUNODMINANT PEPTIDE GP33	IMMUNE SYSTEM
2F7E	PKA COMPLEXED WITH (S)-2-(1H-INDOL-3-YL)-1-(5-ISOQUINOLIN-6-YL-PYRIDIN-3-YLOXYMETHYL-ETYLAMINE	TRANSFERASE
2F7X	PROTEIN KINASE A BOUND TO (S)-2-(1H-INDOL-3-YL)-1-[5-((E)-2-PYRIDIN-4-YL-VINYL)-PYRIDIN-3-YLOXYMETHYL]-ETHYLAMINE	TRANSFERASE
2F7Z	PROTEIN KINASE A BOUND TO (R)-1-(1H-INDOL-3-YLMETHYL)-2-(2-PYRIDIN-4-YL-[1,7]NAPHTYRIDIN-5-YLOXY)-EHYLAMINE	TRANSFERASE

2F8E	FOOT AND MOUTH DISEASE VIRUS RNA-DEPENDENT RNA POLYMERASE IN COMPLEX WITH URIDYLYLATED VPG PROTEIN	TRANSFERASE
2F8N	9 ANGSTROM X-RAY STRUCTURE OF HYBRID MACROH2A NUCLEOSOMES	STRUCTURAL PROTEIN/DNA
2F8X	CRYSTAL STRUCTURE OF ACTIVATED NOTCH, CSL AND MAML ON HES-1 PROMOTER DNA SEQUENCE	TRANSCRIPTION/DNA
2F93	K INTERMEDIATE STRUCTURE OF SENSORY RHODOPSIN II/TRANSDUCER COMPLEX IN COMBINATION WITH THE GROUND STATE STRUCTURE	MEMBRANE PROTEIN
2F95	M INTERMEDIATE STRUCTURE OF SENSORY RHODOPSIN II/TRANSDUCER COMPLEX IN COMBINATION WITH THE GROUND STATE STRUCTURE	MEMBRANE PROTEIN
2F9B	DISCOVERY OF NOVEL HETEROCYCLIC FACTOR VIIA INHIBITORS	HYDROLASE/BLOOD CLOTTING
2F9D	2.5 ANGSTROM RESOLUTION STRUCTURE OF THE SPLICEOSOMAL PROTEIN P14 BOUND TO REGION OF SF3B155	RNA BINDING PROTEIN
2F9I	RYSTAL STRUCTURE OF THE CARBOXYLTRANSFERASE SUBUNIT OF ACC FROM STAPHYLOCOCCUS AUREUS	TRANSFERASE
2F9J	3.0 ANGSTROM RESOLUTION STRUCTURE OF A Y22M MUTANT OF THE SPLICEOSOMAL PROTEIN P14 BOUND TO A REGION OF SF3B155	RNA BINDING PROTEIN
2F9N	CRYSTAL STRUCTURE OF THE RECOMBINANT HUMAN ALPHA I TRYPTASE MUTANT K192Q/D216G IN COMPLEX WITH LEUPEPTIN	HYDROLASE
2F9P	CRYSTAL STRUCTURE OF THE RECOMBINANT HUMAN ALPHA I TRYPTASE MUTANT D216G IN COMPLEX WITH LEUPEPTIN	HYDROLASE
2F9U	HCV NS3 PROTEASE DOMAIN WITH NS4A PEPTIDE AND A KETOAMIDE INHIBITOR WITH A P2 NORBORANE	VIRUS/VIRAL PROTEIN
2F9Y	HE CRYSTAL STRUCTURE OF THE CARBOXYLTRANSFERASE SUBUNIT OF ACC FROM ESCHERICHIA COLI	LIGASE
2F9Z	COMPLEX BETWEEN THE CHEMOTAXIS DEAMIDASE CHED AND THE CHEMOTAXIS PHOSPHATASE CHEC FROM THERMOTOGA MARITIMA	SIGNALING PROTEIN
2FAI	HUMAN ESTROGEN RECEPTOR ALPHA LIGAND-BINDING DOMAIN IN COMPLEX WITH OBCP-2M AND A GLUCOCORTICOID RECEPTOR INTERACTING PROTEIN 1 NR BOX II PEPTIDE	HORMONE/GROWTH FACTOR RECEPTOR
2FAK	CRYSTAL STRUCTURE OF SALINOSPORAMIDE A IN COMPLEX WITH THE YEAST 20S PROTEASOME	HYDROLASE
2FAP	HE STRUCTURE OF THE IMMUNOPHILIN-IMMUNOSUPPRESSANT FKBP12-(C16)-ETHOXY RAPAMYCIN COMPLEX INTERACTING WITH HUMA	COMPLEX (ISOMERASE/KINASE)
2FAT	AN ANTI-UROKINASE PLASMINOGEN ACTIVATOR RECEPTOR (UPAR) ANTIBODY: CRYSTAL STRUCTURE AND BINDING EPITOPE	IMMUNE SYSTEM
2FBJ	REFINED CRYSTAL STRUCTURE OF THE GALACTAN-BINDING IMMUNOGLOBULIN FAB J539 AT 1.95-ANGSTROMS RESOLUTION	IMMUNOGLOBULIN

2FBW	AVIAN RESPIRATORY COMPLEX II WITH CARBOXIN BOUND	OXIDOREDUCTASE
2FCW	STRUCTURE OF A COMPLEX BETWEEN THE PAIR OF THE LDL RECEPTOR LIGAND-BINDING MODULES 3-4 AND THE RECEPTOR ASSOCIATED PROTEIN (RAP).	LIPID TRANSPORT/ENDOCYTOSIS/CHAPERONE
2FD6	STRUCTURE OF HUMAN UROKINASE PLASMINOGEN ACTIVATOR IN COMPLEX WITH UROKINASE RECEPTOR AND AN ANTI-UPAR ANTIBODY AT 1.9 A	IMMUNE SYSTEM, HYDROLASE
2FDB	CRYSTAL STRUCTURE OF FIBROBLAST GROWTH FACTOR (FGF)8B IN COMPLEX WITH FGF RECEPTOR (FGFR) 2C	HORMONE/GROWTH FACTOR/TRANSFERASE
2FEC	STRUCTURE OF THE E203Q MUTANT OF THE CL-/H+ EXCHANGER CLC-EC1 FROM E.COLI	PROTON TRANSPORT,MEMBRANE PROTEIN
2FED	STRUCTURE OF THE E203Q MUTANT OF THE CL-/H+ EXCHANGER CLC-EC1 FROM E.COLI	PROTON TRANSPORT,MEMBRANE PROTEIN
2FEE	STRUCTURE OF THE CL-/H+ EXCHANGER CLC-EC1 FROM E.COLI IN NABR	PROTON TRANSPORT,MEMBRANE PROTEIN
2FEP	STRUCTURE OF TRUNCATED CCPA IN COMPLEX WITH P-SER-HPR AND SULFATE IONS	TRANSCRIPTION
2FEQ	ORALLY ACTIVE THROMBIN INHIBITORS	HYDROLASE/HYDROLASE INHIBITOR
2FES	ORALLY ACTIVE THROMBIN INHIBITORS	HYDROLASE/HYDROLASE INHIBITOR
2FEW	COMPLEX OF ENZYME IIAMTL AND PHOSPHORYLATED ENZYME IIBMTL FROM ESCHERICHIA COLI NMR, RESTRAINED REGULARIZED MEAN STRUCTURE	TRANSFERASE
2FF3	CRYSTAL STRUCTURE OF GELSOLIN DOMAIN 1:N-WASP V2 MOTIF HYBRID IN COMPLEX WITH ACTIN	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN
2FF4	MYCOBACTERIUM TUBERCULOSIS EMBR IN COMPLEX WITH LOW AFFINITY PHOSPHOPEPTIDE	TRANSCRIPTION
2FF6	CRYSTAL STRUCTURE OF GELSOLIN DOMAIN 1:CIBOULOT DOMAIN 2 HYBRID IN COMPLEX WITH ACTIN	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN
2FFD	FIBRINOGEN FRAGMENT D WITH "A" KNOB PEPTIDE MIMIC GPRVVE	BLOOD CLOTTING
2FFF	OPEN FORM OF A CLASS A TRANSPEPTIDASE DOMAIN	MEMBRANE PROTEIN, TRANSFERASE
2FFK	SOLUTION STRUCTURE OF THE COMPLEX BETWEEN POXVIRUS-ENCODED CC CHEMOKINE INHIBITOR VCCI AND HUMAN MIP-1BETA, MINIMIZED AVERAGE STRUCTURE	VIRUS/VIRAL PROTEIN/CYTOKINE
2FFU	CRYSTAL STRUCTURE OF HUMAN PPGALNACT-2 COMPLEXED WITH UDP AND EA2	TRANSFERASE
2FGE	CRYSTAL STRUCTURE OF PRESEQUENCE PROTEASE PREP FROM	HYDROLASE, PLANT PROTEIN

	ARABIDOPSIS THALIANA	
2FGW	X-RAY STRUCTURES OF FRAGMENTS FROM BINDING AND NONBINDING VERSIONS OF A HUMANIZED ANTI-CD18 ANTIBODY: STRUCTURAL INDICATIONS OF THE KEY ROLE OF VH RESIDUES 59 TO 65	IMMUNOGLOBULIN
2FH5	THE STRUCTURE OF THE MAMMALIAN SRP RECEPTOR	TRANSPORT PROTEIN
2FHE	FASCIOLA HEPATICA GLUTATHIONE S-TRANSFERASE ISOFORM 1 IN COMPLEX WITH GLUTATHIONE	TRANSFERASE
2FHG	RYSTAL STRUCTURE OF MYCOBACTERIAL TUBERCULOSIS PROTEASOME	HYDROLASE
2FHH	RYSTAL STRUCTURE OF MYCOBACTERIUM TUBERCULOSIS PROTEASOME IN COMPLEX WITH A PEPTIDYL BORONATE INHIBITOR MLN-273	HYDROLASE
2FHJ	CRYSTAL STRUCTURE OF FORMYLMETHANOFURAN: TETRAHYDROMETHANOPTERIN FORMYLTRANSFERASE IN COMPLEX WITH ITS COENZYMES	TRANSFERASE
2FHS	STRUCTURE OF ACYL CARRIER PROTEIN BOUND TO FABI, THE ENOYL REDUCTASE FROM ESCHERICHIA COLI	OXIDOREDUCTASE/BIOSYNTHETIC PROTEIN
2FHX	PSEUDOMONAS AERUGINOSA SPM-1 METALLO-BETA-LACTAMASE	HYDROLASE, METAL BINDING PROTEIN
2FHZ	MOLECULAR BASIS OF INHIBITION OF THE RIBONUCLEASE ACTIVITY IN COLICIN E5 BY ITS COGNATE IMMUNITY PROTEIN	IMMUNE SYSTEM, HYDROLASE
2FIB	RECOMBINANT HUMAN GAMMA-FIBRINOGEN CARBOXYL TERMINAL FRAGMENT (RESIDUES 143-411) COMPLEXED TO THE PEPTIDE GLY-PRO-ARG-PRO AT PH 6.0	COMPLEX (BLOOD COAGULATION/PEPTIDE)
2FID	CRYSTAL STRUCTURE OF A BOVINE RABEX-5 FRAGMENT COMPLEXED WITH UBIQUITIN	PROTEIN TURNOVER/ENDOCYTOSIS
2FIF	CRYSTAL STRUCTURE OF A BOVINE RABEX-5 FRAGMENT COMPLEXED WITH UBIQUITIN	PROTEIN TURNOVER/ENDOCYTOSIS
2FIR	CRYSTAL STRUCTURE OF DFPR-VIIA/STF	BLOOD CLOTTING
2FIV	CRYSTAL STRUCTURE OF FELINE IMMUNODEFICIENCY VIRUS PROTEASE COMPLEXED WITH A SUBSTRATE	COMPLEX (ACID PROTEINASE/SUBSTRATE)
2FJ7	CRYSTAL STRUCTURE OF NUCLEOSOME CORE PARTICLE CONTAINING A POLY (DA.DT) SEQUENCE ELEMENT	STRUCTURAL PROTEIN/DNA
2FJA	ADENOSINE 5'-PHOSPHOSULFATE REDUCTASE IN COMPLEX WITH SUBSTRATE	OXIDOREDUCTASE
2FJB	ADENOSINE-5'-PHOSPHOSULFATE REDUCTASE IM COMPLEX WITH PRODUCTS	OXIDOREDUCTASE
2FJD	ADENOSINE-5-PHOSPHOSULFATE REDUCTASE IN COMPLEX WITH SULFITE (COVALENT ADDUCT)	OXIDOREDUCTASE

2FJE	ADENOSINE-5-PHOSPHOSULFATE REDUCTASE OXIDIZED STATE	OXIDOREDUCTASE
2FJF	STRUCTURE OF THE G6 FAB, A PHAGE DERIVED VEGF BINDING FAB	IMMUNE SYSTEM
2FJG	STRUCTURE OF THE G6 FAB, A PHAGE DERIVED FAB FRAGMENT, IN COMPLEX WITH VEGF	HORMONE/GROWTH FACTOR/IMMUNE SYSTEM
2FJH	STRUCTURE OF THE B20-4 FAB, A PHAGE DERIVED FAB FRAGMENT, IN COMPLEX WITH VEGF	HORMONE/GROWTH FACTOR/IMMUNE SYSTEM
2FJU	ACTIVATED RAC1 BOUND TO ITS EFFECTOR PHOSPHOLIPASE C BETA 2	SIGNALING PROTEIN,APOPTOSIS/HYDROLASE
2FK0	CRYSTAL STRUCTURE OF A H5N1 INFLUENZA VIRUS HEMAGGLUTININ.	VIRUS/VIRAL PROTEIN
2FKA	CRYSTAL STRUCTURE OF MG(2+) AND BEF(3)(-)-BOUND CHEY IN COMPLEX WITH CHEZ(200-214) SOLVED FROM A F432 CRYSTAL GROWN IN CAPS (PH 10.5)	SIGNALING PROTEIN
2FKW	STRUCTURE OF LH2 FROM RPS. ACIDOPHILA CRYSTALLIZED IN LIPIDIC MESOPHASES	MEMBRANE PROTEIN, PHOTOSYNTHESIS
2FL5	COFACTOR-CONTAINING ANTIBODIES: CRYSTAL STRUCTURE OF THE ORIGINAL YELLOW ANTIBODY	IMMUNE SYSTEM
2FLB	DISCOVERY OF A NOVEL HYDROXY PYRAZOLE BASED FACTOR IXA INHIBITOR	HYDROLASE/BLOOD CLOTTING
2FLK	CRYSTAL STRUCTURE OF CHEY IN COMPLEX WITH CHEZ(200-214) SOLVED FROM A F432 CRYSTAL GROWN IN CAPS (PH 10.5)	SIGNALING PROTEIN
2FLR	NOVEL 5-AZAINDOLE FACTOR VIIA INHIBITORS	HYDROLASE/BLOOD CLOTTING
2FLW	CRYSTAL STRUCTURE OF MG2+ AND BEF3- OUND CHEY IN COMPLEX WITH CHEZ 200-214 SOLVED FROM A F432 CRYSTAL GROWN IN HEPES (PH 7.5)	SIGNALING PROTEIN
2FM2	HCV NS3-4A PROTEASE DOMAIN COMPLEXED WITH A KETOAMIDE INHIBITOR, SCH446211	HYDROLASE
2FM8	CRYSTAL STRUCTURE OF THE SALMONELLA SECRETION CHAPERONE INVB IN COMPLEX WITH SIPA	CHAPERONE/CELL INVASION
2FMF	CRYSTAL STRUCTURE OF CHEY IN COMPLEX WITH CHEZ 200-214 SOLVED FROM A F432 CRYSTAL GROWN IN HEPES (PH 7.5)	SIGNALING PROTEIN
2FMH	CRYSTAL STRUCTURE OF MG2+ AND BEF3- BOUND CHEY IN COMPLEX WITH CHEZ 200-214 SOLVED FROM A F432 CRYSTAL GROWN IN TRIS (PH 8.4)	SIGNALING PROTEIN
2FMI	CRYSTAL STRUCTURE OF CHEY IN COMPLEX WITH CHEZ 200-214 SOLVED FROM A F432 CRYSTAL GROWN IN TRIS (PH 8.4)	SIGNALING PROTEIN
2FMK	CRYSTAL STRUCTURE OF MG2+ AND BEF3- BOUND CHEY IN COMPLEX WITH CHEZ 200-214 SOLVED FROM A P2(1)2(1)2 CRYSTAL GROWN IN MES (PH 6.0)	SIGNALING PROTEIN

2FMM	CRYSTAL STRUCTURE OF EMSY-HP1 COMPLEX	TRANSCRIPTION
2FNJ	CRYSTAL STRUCTURE OF A B30.2/SPRY DOMAIN-CONTAINING PROTEIN GUSTAVUS IN COMPLEX WITH ELONGIN B AND ELONGIN C	PROTEIN TRANSPORT/SIGNALING PROTEIN
2FNS	CRYSTAL STRUCTURE OF WILD-TYPE INACTIVE (D25N) HIV-1 PROTEASE COMPLEXED WITH WILD-TYPE HIV-1 NC-P1 SUBSTRATE.	HYDROLASE
2FNT	CRYSTAL STRUCTURE OF A DRUG-RESISTANT (V82A) INACTIVE (D25N) HIV-1 PROTEASE COMPLEXED WITH AP2V VARIANT OF HIV-1 NC-P1 SUBSTRATE.	HYDROLASE
2FNX	DESIGN OF SPECIFIC PEPTIDE INHIBITORS OF PHOSPHOLIPASE A2 (PLA2): CRYSTAL STRUCTURE OF THE COMPLEX OF PLA2 WITH A HIGHLY POTENT PEPTIDE VAL-ILE-ALA-LYS AT 2.7A RESOLUTION	HYDROLASE
2FO1	CRYSTAL STRUCTURE OF THE CSL-NOTCH-MASTERMIND TERNARY COMPLEX BOUND TO DNA	GENE REGULATION/SIGNALLING PROTEIN/DNA
2FO4	ENHANCED MHC CLASS I BINDING AND IMMUNE RESPONSES THROUGH ANCHOR MODIFICATION OF THE NON-CANONICAL TUMOR ASSOCIATED MUC1-8 PEPTIDE	IMMUNE SYSTEM
2FO5	CRYSTAL STRUCTURE OF RECOMBINANT BARLEY CYSTEINE ENDOPROTEASE B ISOFORM 2 (EP-B2) IN COMPLEX WITH LEUPEPTIN	HYDROLASE
2FOI	SYNTHESIS, BIOLOGICAL ACTIVITY, AND X-RAY CRYSTAL STRUCTURAL ANALYSIS OF DIARYL ETHER INHIBITORS OF MALARIAL ENOYL ACP REDUCTASE.	OXIDOREDUCTASE
2FOM	DENGUE VIRUS NS2B/NS3 PROTEASE	VIRAL PROTEIN/PROTEASE
2FOT	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN CALMODULIN AND ALPHAII-SPECTRIN	METAL BINDING, STRUCTURAL PROTEIN
2FP4	CRYSTAL STRUCTURE OF PIG GTP-SPECIFIC SUCCINYL-COA SYNTHETASE IN COMPLEX WITH GTP	LIGASE
2FP7	WEST NILE VIRUS NS2B/NS3PROTEASE IN COMPLEX WITH BZ-NLE-LYS-ARG-ARG-H	VIRAL PROTEIN/PROTEASE
2FPG	CRYSTAL STRUCTURE OF PIG GTP-SPECIFIC SUCCINYL-COA SYNTHETASE IN COMPLEX WITH GDP	LIGASE
2FPI	CRYSTAL STRUCTURE OF PIG GTP-SPECIFIC SUCCINYL-COA SYNTHETASE FROM POLYETHYLENE GLYCOL	LIGASE
2FPP	CRYSTAL STRUCTURE OF PIG GTP-SPECIFIC SUCCINYL-COA SYNTHETASE FROM POLYETHYLENE GLYCOL WITH CHLORIDE IONS	LIGASE
2FQQ	CRYSTAL STRUCTURE OF HUMAN CASPASE-1 (CYS285->ALA, CYS362->ALA, CYS364->ALA, CYS397->ALA) IN COMPLEX WITH 1-METHYL-3-TRIFLUOROMETHYL-1H-THIENO[2,3-C]PYRAZOLE-5-CARBOXYLIC ACID (2-MERCAPTO-ETHYL)-AMIDE	HYDROLASE

2FR4	STRUCTURE OF FAB DNA-1 COMPLEXED WITH A STEM-LOOP DNA LIGAND	IMMUNE SYSTEM/DNA
2FR8	STRUCTURE OF TRANSHYDROGENASE (DI.R127A.NAD+)2(DIII.NADP+)1 ASYMMETRIC COMPLEX	OXIDOREDUCTASE
2FRD	STRUCTURE OF TRANSHYDROGENASE (DI.S138A.NADH)2(DIII.NADPH)1 ASYMMETRIC COMPLEX	OXIDOREDUCTASE
2FRV	CRYSTAL STRUCTURE OF THE OXIDIZED FORM OF NI-FE HYDROGENASE	OXIDOREDUCTASE
2FSA	RYSTAL STRUCTURE OF PHD FINGER-LINKER-BROMODOMAIN FRAGMENT OF HUMAN BPTF IN THE H3(1-15)K4ME2 BOUND STATE	TRANSCRIPTION
2FSE	CRYSTALLOGRAPHIC STRUCTURE OF A RHEUMATOID ARTHRITIS MHC SUSCEPTIBILITY ALLELE, HLA-DR1 (DRB1*0101), COMPLEXED WITH THE IMMUNODOMINANT DETERMINANT OF HUMAN TYPE II COLLAGEN	IMMUNE SYSTEM, STRUCTURAL PROTEIN
2FSV	STRUCTURE OF TRANSHYDROGENASE (DI.D135N.NAD+) 2(DIII.E155W.NADP+)1 ASYMMETRIC COMPLEX	OXIDOREDUCTASE
2FTK	BERYLLOFLOURIDE SPO0F COMPLEX WITH SPO0B	TRANSFERASE
2FTS	CRYSTAL STRUCTURE OF THE GLYCINE RECEPTOR-GEPHYRIN COMPLEX	STRUCTURAL PROTEIN
2FTX	CRYSTAL STRUCTURE OF THE YEAST KINETOCHORE SPC24/SPC25 GLOBULAR DOMAIN	STRUCTURAL PROTEIN, PROTEIN BINDING
2FU5	STRUCTURE OF RAB8 IN COMPLEX WITH MSS4	SIGNALING PROTEIN
2FUG	CRYSTAL STRUCTURE OF THE HYDROPHILIC DOMAIN OF RESPIRATORY COMPLEX I FROM THERMUS THERMOPHILUS	OXIDOREDUCTASE
2FUN	ALTERNATIVE P35-CASPASE-8 COMPLEX	APOPTOSIS/HYDROLASE
2FVJ	A NOVEL ANTI-ADIPOGENIC PARTIAL AGONIST OF PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR-GAMMA (PPARG) RECRUITS PPARG-COACTIVATOR-1 ALPHA (PGC1A) BUT POTENTIATES INSULIN SIGNALING IN VITRO	SIGNALING PROTEIN
2FWO	MHC CLASS I H-2KD HEAVY CHAIN IN COMPLEX WITH BETA-2MICROGLOBULIN AND PEPTIDE DERIVED FROM INFLUENZA NUCLEOPROTEIN	IMMUNE SYSTEM/VIRAL PROTEIN
2FX7	CRYSTAL STRUCTURE OF HIV-1 NEUTRALIZING HUMAN FAB 4E10 IN COMPLEX WITH A 16-RESIDUE PEPTIDE ENCOMPASSING THE 4E10 EPITOPE ON GP41	IMMUNE SYSTEM
2FX8	CRYSTAL STRUCTURE OF HIV-1 NEUTRALIZING HUMAN FAB 4E10 IN COMPLEX WITH AN AIB-INDUCED PEPTIDE ENCOMPASSING THE 4E10 EPITOPE ON GP41	IMMUNE SYSTEM
2FX9	CRYSTAL STRUCTURE OF HIV-1 NEUTRALIZING HUMAN FAB 4E10 IN COMPLEX WITH A THIOETHER-LINKED PEPTIDE ENCOMPASSING THE 4E10 EPITOPE ON GP41	IMMUNE SYSTEM

2FYC	CRYSTAL STRUCTURE OF THE CATALYTIC DOMAIN OF BOVINE BETA1,4-GALACTOSYLTRANSFERASE-I IN COMPLEX WITH ALPHA-LACTALBUMIN, CA AND UDP-GALACTOSE	TRANSFERASE
2FYD	CATALYTIC DOMAIN OF BOVINE BETA 1, 4-GALACTOSYLTRANSFERASE IN COMPLEX WITH ALPHA-LACTALBUMIN, GLUCOSE, MN, AND UDP-N-ACETYLGALACTOSAMINE	TRANSFERASE
2FYL	IADDOCK MODEL OF THE COMPLEX BETWEEN DOUBLE MODULE OF LRP, CR56, AND FIRST DOMAIN OF RECEPTOR ASSOCIATED PROTEIN, RAP-D1.	SURFACE ACTIVE PROTEIN
2FYM	CRYSTAL STRUCTURE OF E. COLI ENOLASE COMPLEXED WITH THE MINIMAL BINDING SEGMENT OF RNASE E.	LYASE
2FYN	RYSTAL STRUCTURE ANALYSIS OF THE DOUBLE MUTANT RHODOBACTER SPHAEROIDES BC1 COMPLEX	OXIDOREDUCTASE
2FYS	CRYSTAL STRUCTURE OF ERK2 COMPLEX WITH KIM PEPTIDE DERIVED FROM MKP3	TRANSFERASE
2FYU	CRYSTAL STRUCTURE OF BOVINE HEART MITOCHONDRIAL BC1 WITH JG144 INHIBITOR	OXIDOREDUCTASE
2FYY	THE ROLE OF T CELL RECEPTOR ALPHA GENES IN DIRECTING HUMAN MHC RESTRICTION	IMMUNE SYSTEM
2FYZ	STRUCTURAL OF MUMPS VIRUS FUSION PROTEIN CORE	PROTEIN BINDING
2FZ3	THE ROLE OF T CELL RECEPTOR ALPHA GENES IN DIRECTING HUMAN MHC RESTRICTION	IMMUNE SYSTEM
2FZC	THE STRUCTURE OF WILD-TYPE E. COLI ASPARTATE TRANSCARBAMOYLASE IN COMPLEX WITH NOVEL T STATE INHIBITORS AT 2.10 RESOLUTION	TRANSFERASE
2FZG	THE STRUCTURE OF WILD-TYPE E. COLI ASPARTATE TRANSCARBAMOYLASE IN COMPLEX WITH NOVEL T STATE INHIBITORS AT 2.25 RESOLUTION	TRANSFERASE
2FZK	THE STRUCTURE OF WILD-TYPE E. COLI ASPARTATE TRANSCARBAMOYLASE IN COMPLEX WITH NOVEL T STATE INHIBITORS AT 2.50 RESOLUTION	TRANSFERASE
2FZZ	FACTOR XA IN COMPLEX WITH THE INHIBITOR 1-(3-AMINO-1,2-BENZISOXAZOL-5-YL)-6-(2'-(((3R)-3-HYDROXY-1-PYRROLIDINYL) METHYL)-4-BIPHENYLYL)-3-(TRIFLUOROMETHYL)-1,4,5,6-TETRAHYDRO-7H-PYRAZOLO[3,4-C]PYRIDIN-7-ONE	HYDROLASE
2G00	FACTOR XA IN COMPLEX WITH THE INHIBITOR 3-(6-(2'-((DIMETHYLAMINO)METHYL)-4-BIPHENYLYL)-7-OXO-3-(TRIFLUOROMETHYL)-4,5,6,7-TETRAHYDRO-1H-PYRAZOLO[3,4-C]PYRIDIN-1-YL)BENZAMIDE	HYDROLASE

2G16	STRUCTURE OF S65A Y66S GFP VARIANT AFTER BACKBONE FRAGMENTATION	LUMINESCENT PROTEIN
2G1T	A SRC-LIKE INACTIVE CONFORMATION IN THE ABL TYROSINE KINASE DOMAIN	TRANSFERASE
2G2F	A SRC-LIKE INACTIVE CONFORMATION IN THE ABL TYROSINE KINASE DOMAIN	TRANSFERASE
2G2I	A SRC-LIKE INACTIVE CONFORMATION IN THE ABL TYROSINE KINASE DOMAIN	TRANSFERASE
2G2L	CRYSTAL STRUCTURE OF THE SECOND PDZ DOMAIN OF SAP97 IN COMPLEX WITH A GLUR-A C-TERMINAL PEPTIDE	MEMBRANE PROTEIN
2G2R	GREEN-FLUORESCENT ANTIBODY 11G10 IN COMPLEX WITH ITS HAPTEN (NITRO-STILBENE DERIVATIVE)	IMMUNE SYSTEM
2G2S	STRUCTURE OF S65G Y66S GFP VARIANT AFTER SPONTANEOUS PEPTIDE HYDROLYSIS	LUMINESCENT PROTEIN
2G2U	CRYSTAL STRUCTURE OF THE SHV-1 BETA-LACTAMASE/BETA-LACTAMASE INHIBITOR PROTEIN (BLIP) COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
2G2W	CRYSTAL STRUCTURE OF THE SHV D104K BETA-LACTAMASE/BETA-LACTAMASE INHIBITOR PROTEIN (BLIP) COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
2G30	BETA APPENDAGE OF AP2 COMPLEXED WITH ARH PEPTIDE	ENDOCYTOSIS/EXOCYTOSIS
2G38	A PE/PPE PROTEIN COMPLEX FROM MYCOBACTERIUM TUBERCULOSIS	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
2G3D	STRUCTURE OF S65G Y66A GFP VARIANT AFTER SPONTANEOUS PEPTIDE HYDROLYSIS	LUMINESCENT PROTEIN
2G3V	CRYSTAL STRUCTURE OF CAGS (HP0534, CAG13) FROM HELICOBACTER PYLORI	UNKNOWN FUNCTION
2G44	HUMAN ESTROGEN RECEPTOR ALPHA LIGAND-BINDING DOMAIN IN COMPLEX WITH OBCP-1M-G AND A GLUCOCORTICOID RECEPTOR INTERACTING PROTEIN 1 NR BOX II PEPTIDE	HORMONE/GROWTH FACTOR RECEPTOR
2G45	CO-CRYSTAL STRUCTURE OF ZNF UBP DOMAIN FROM THE DEUBIQUITINATING ENZYME ISOPEPTIDASE T (ISOT) IN COMPLEX WITH UBIQUITIN	HYDROLASE
2G47	CRYSTAL STRUCTURE OF HUMAN INSULIN-DEGRADING ENZYME IN COMPLEX WITH AMYLOID-BETA (1-40)	HYDROLASE
2G48	CRYSTAL STRUCTURE OF HUMAN INSULIN-DEGRADING ENZYME IN COMPLEX WITH AMYLIN	HYDROLASE
2G49	CRYSTAL STRUCTURE OF HUMAN INSULIN-DEGRADING ENZYME IN COMPLEX WITH GLUCAGON	HYDROLASE
2G4D	CRYSTAL STRUCTURE OF HUMAN SENP1 MUTANT (C603S) IN COMPLEX	HYDROLASE/PROTEIN BINDING

	WITH SUMO-1	
2G4M	INSULIN COLLECTED AT 2.0 A WAVELENGTH	HORMONE/GROWTH FACTOR
2G54	CRYSTAL STRUCTURE OF ZN-BOUND HUMAN INSULIN-DEGRADING ENZYME IN COMPLEX WITH INSULIN B CHAIN	HYDROLASE
2G56	CRYSTAL STRUCTURE OF HUMAN INSULIN-DEGRADING ENZYME IN COMPLEX WITH INSULIN B CHAIN	HYDROLASE
2G58	CRYSTAL STRUCTURE OF A COMPLEX OF PHOSPHOLIPASE A2 WITH A DESIGNED PEPTIDE INHIBITOR DEHYDRO-ILE-ALA-ARG-SER AT 0.98 A RESOLUTION	HYDROLASE
2G5B	CRYSTAL STRUCTURE OF THE ANTI-BAX MONOCLONAL ANTIBODY 6A7 AND A BAX PEPTIDE.	APOPTOSIS
2G5H	STRUCTURE OF TRNA-DEPENDENT AMIDOTRANSFERASE GATCAB	LIGASE
2G5I	STRUCTURE OF TRNA-DEPENDENT AMIDOTRANSFERASE GATCAB COMPLEXED WITH ADP-ALF4	LIGASE
2G5L	STREPTAVIDIN IN COMPLEX WITH NANOTAG	PEPTIDE BINDING PROTEIN
2G5O	HUMAN ESTROGEN RECEPTOR ALPHA LIGAND-BINDING DOMAIN IN COMPLEX WITH 2-(BUT-1-ENYL)-17BETA-ESTRADIOL AND A GLUCOCORTICOID RECEPTOR INTERACTING PROTEIN 1 NR BOX II PEPTIDE	HORMONE/GROWTH FACTOR RECEPTOR
2G5Z	STRUCTURE OF S65G Y66S GFP VARIANT AFTER SPONTANEOUS PEPTIDE HYDROLYSIS AND DECARBOXYLATION	LUMINESCENT PROTEIN
2G60	STRUCTURE OF ANTI-FLAG M2 FAB DOMAIN	IMMUNE SYSTEM
2G75	CRYSTAL STRUCTURE OF ANTI-SARS M396 ANTIBODY	IMMUNE SYSTEM
2G77	CRYSTAL STRUCTURE OF GYP1 TBC DOMAIN IN COMPLEX WITH RAB33 GTPASE BOUND TO GDP AND ALF3	HYDROLASE ACTIVATOR/PROTEIN TRANSPORT
2G81	CRYSTAL STRUCTURE OF THE BOWMAN-BIRK INHIBITOR FROM VIGNA UNGUICULATA SEEDS IN COMPLEX WITH BETA-TRYPSIN AT 1.55 ANGSTRONS RESOLUTION	HYDROLASE/HYDROLASE INHIBITOR
2G83	STRUCTURE OF ACTIVATED G-ALPHA-I1 BOUND TO A NUCLEOTIDE-STATE-SELECTIVE PEPTIDE: MINIMAL DETERMINANTS FOR RECOGNIZING THE ACTIVE FORM OF A G PROTEIN ALPHA SUBUNIT	SIGNALING PROTEIN
2G9H	CRYSTAL STRUCTURE OF STAPHYLOCOCCAL ENTEROTOXIN I (SEI) IN COMPLEX WITH A HUMAN MHC CLASS II MOLECULE	IMMUNE SYSTEM
2G9X	STRUCTURE OF THR 160 PHOSPHORYLATED CDK2/CYCLIN A IN COMPLEX WITH THE INHIBITOR NU6271	TRANSFERASE/CELL CYCLE
2GA4	STX2 WITH ADENINE	TOXIN

2GA9	CRYSTAL STRUCTURE OF THE HETERODIMERIC VACCINIA VIRUS POLYADENYLATE POLYMERASE WITH BOUND ATP-GAMMA-S	TRANSFERASE
2GAC	T152C MUTANT GLYCOSYLASPARAGINASE FROM FLAVOBACTERIUM MENINGOSEPTICUM	HYDROLASE
2GAF	CRYSTAL STRUCTURE OF THE VACCINIA POLYADENYLATE POLYMERASE HETERODIMER (APO FORM)	TRANSFERASE
2GAG	HETEROTETERAMERIC SARCOSINE: STRUCTURE OF A DIFLAVIN METALOENZYME AT 1.85 A RESOLUTION	OXIDOREDUCTASE
2GAH	HETEROTETRAMERIC SARCOSINE: STRUCTURE OF A DIFLAVIN METALOENZYME AT 1.85 A RESOLUTION	OXIDOREDUCTASE
2GAW	WILD TYPE GLYCOSYLASPARAGINASE FROM FLAVOBACTERIUM MENINGOSEPTICUM	HYDROLASE
2GBL	CRYSTAL STRUCTURE OF FULL LENGTH CIRCADIAN CLOCK PROTEIN KAIC WITH PHOSPHORYLATION SITES	CIRCADIAN CLOCK PROTEIN, TRANSFERASE
2GBW	CRYSTAL STRUCTURE OF BIPHENYL 2,3-DIOXYGENASE FROM SPHINGOMONAS YANOIKUYAE B1	OXIDOREDUCTASE
2GBX	CRYSTAL STRUCTURE OF BIPHENYL 2,3-DIOXYGENASE FROM SPHINGOMONAS YANOIKUYAE B1 BOUND TO BIPHENYL	OXIDOREDUCTASE
2GC4	STRUCTURAL COMPARISON OF THE OXIDIZED TERNARY ELECTRON TRANSFER COMPLEX OF METHYLAMINE DEHYDROGENASE, AMICYANIN AND CYTOCHROME C551I FROM PARACOCCUS DENITRIFICANS WITH THE SUBSTRATE-REDUCED, COPPER FREE COMPLEX AT 1.9 A RESOLUTION.	OXIDOREDUCTASE, ELECTRON TRANSPORT
2GC7	SUBSTRATE REDUCED, COPPER FREE COMPLEX OF METHYLAMINE DEHYDROGENASE, AMICYANIN AND CYTOCHROME C551I FROM PARACOCCUS DENITRIFICANS.	OXIDOREDUCTASE, ELECTRON TRANSPORT
2GCH	REFINED CRYSTAL STRUCTURE OF GAMMA-CHYMOTRYPSIN AT 1.9 ANGSTROMS RESOLUTION	HYDROLASE (SERINE PROTEINASE)
2GCO	CRYSTAL STRUCTURE OF THE HUMAN RHOC-GPPNHP COMPLEX	SIGNALING PROTEIN
2GCY	HUMANIZED ANTIBODY C25 FAB FRAGMENT	IMMUNE SYSTEM
2GD4	CRYSTAL STRUCTURE OF THE ANTITHROMBIN-S195A FACTOR XA-PENTASACCHARIDE COMPLEX	HYDROLASE
2GDE	THROMBIN IN COMPLEX WITH INHIBITOR	BLOOD CLOTTING
2GEZ	CRYSTAL STRUCTURE OF POTASSIUM-INDEPENDENT PLANT ASPARAGINASE	HYDROLASE
2GFB	CRYSTAL STRUCTURE OF A CATALYTIC FAB HAVING ESTERASE-LIKE ACTIVITY	IMMUNOGLOBULIN

2GFC	CAMP-DEPENDENT PROTEIN KINASE PKA CATALYTIC SUBUNIT WITH PKI-5-24	TRANSFERASE
2GGM	HUMAN CENTRIN 2 XERODERMA PIGMENTOSUM GROUP C PROTEIN COMPLEX	CELL CYCLE
2GGV	CRYSTAL STRUCTURE OF THE WEST NILE VIRUS NS2B-NS3 PROTEASE, HIS51ALA MUTANT	HYDROLASE
2GH0	GROWTH FACTOR/RECEPTOR COMPLEX	HORMONE/GROWTH FACTOR
2GHO	ECOMBINANT THERMUS AQUATICUS RNA POLYMERASE FOR STRUCTURAL STUDIES	TRANSFERASE
2GHQ	CTD-SPECIFIC PHOSPHATASE SCP1 IN COMPLEX WITH PEPTIDE C-TERMINAL DOMAIN OF RNA POLYMERASE II	HYDROLASE
2GHT	CTD-SPECIFIC PHOSPHATASE SCP1 IN COMPLEX WITH PEPTIDE FROM C-TERMINAL DOMAIN OF RNA POLYMERASE II	HYDROLASE
2GHW	CRYSTAL STRUCTURE OF SARS SPIKE PROTEIN RECEPTOR BINDING DOMAIN IN COMPLEX WITH A NEUTRALIZING ANTIBODY, 80R	VIRUS/VIRAL PROTEIN/ANTIBIOTIC
2GIA	CRYSTAL STRUCTURES OF TRYPANOSOMA BRUCIEI MRP1/MRP2	TRANSLATION
2GID	CRYSTAL STRUCTURES OF TRYPANOSOMA BRUCIEI MRP1/MRP2	TRANSLATION
2GIT	HUMAN CLASS I MHC HLA-A2 IN COMPLEX WITH THE MODIFIED HTLV-1 TAX (Y5K-4-[3-INDOLYL]-BUTYRIC ACID) PEPTIDE	IMMUNE SYSTEM
2GJ6	THE COMPLEX BETWEEN TCR A6 AND HUMAN CLASS I MHC HLA-A2 WITH THE MODIFIED HTLV-1 TAX (Y5K-4-[3-INDOLYL]-BUTYRIC ACID) PEPTIDE	IMMUNE SYSTEM
2GJ7	CRYSTAL STRUCTURE OF A GE-GI/FC COMPLEX	IMMUNE SYSTEM/VIRUS/VIRAL PROTEIN
2GJE	STRUCTURE OF A GUIDERNA-BINDING PROTEIN COMPLEX BOUND TO A GRNA	TRANSLATION/RNA
2GJX	RYSTALLOGRAPHIC STRUCTURE OF HUMAN BETA-HEXOSAMINIDASE A	HYDROLASE
2GJZ	STRUCTURE OF CATALYTIC ELIMINATION ANTIBODY 13G5 FROM A CRYSTAL IN SPACE GROUP P2(1)	IMMUNE SYSTEM
2GK0	STRUCTURE OF CATALYTIC ELIMINATION ANTIBODY 13G5 FROM A TWINNED CRYSTAL IN SPACE GROUP C2	IMMUNE SYSTEM
2GK1	X-RAY CRYSTAL STRUCTURE OF NGT-BOUND HEXA	HYDROLASE
2GKV	CRYSTAL STRUCTURE OF THE SGPB:P14'-ALA32 OMTKY3-DEL(1-5) COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
2GKW	KEY CONTACTS PROMOTE RECONGNITO OF BAFF-R BY TRAF3	APOPTOSIS
2GL7	CRYSTAL STRUCTURE OF A BETA-CATENIN/BCL9/TCF4 COMPLEX	TRANSCRIPTION

2GL9	RYSTAL STRUCTURE OF GLYCOSYLASPARAGINASE-SUBSTRATE COMPLEX	HYDROLASE
2GMI	MMS2/UBC13~UBIQUITIN	LIGASE, HUMAN PROTEIN
2GMR	PHOTOSYNTHETIC REACTION CENTER MUTANT FROM RHODOBACTER SPHAEROIDES WITH ASP L210 REPLACED WITH ASN	PHOTOSYNTHESIS
2GMX	SELECTIVE AMINOPYRIDINE-BASED C-JUN N-TERMINAL KINASE INHIBITORS WITH CELLULAR ACTIVITY	TRANSCRIPTION
2GNF	PROTEIN KINASE A FIVEFOLD MUTANT MODEL OF RHO-KINASE WITH Y-27632	TRANSFERASE/TRANSFERASE INHIBITOR
2GNG	PROTEIN KINASE A FIVEFOLD MUTANT MODEL OF RHO-KINASE	TRANSFERASE/TRANSFERASE INHIBITOR
2GNH	PKA FIVE FOLD MUTANT MODEL OF RHO-KINASE WITH H1152P	TRANSFERASE/TRANSFERASE INHIBITOR
2GNI	PKA FIVEFOLD MUTANT MODEL OF RHO-KINASE WITH INHIBITOR FASUDIL (HA1077)	TRANSFERASE/TRANSFERASE INHIBITOR
2GNJ	PKA THREE FOLD MUTANT MODEL OF RHO-KINASE WITH Y-27632	TRANSFERASE/TRANSFERASE INHIBITOR
2GNL	PKA THREEFOLD MUTANT MODEL OF RHO-KINASE WITH INHIBITOR H-1152P	TRANSFERASE/TRANSFERASE INHIBITOR
2GNS	DESIGN OF SPECIFIC PEPTIDE INHIBITORS OF PHOSPHOLIPASE A2: CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN A GROUP II PHOSPHOLIPASE A2 AND A DESIGNED PENTAPEPTIDE ALA- LEU- VAL- TYR- LYS AT 2.3 A RESOLUTION	HYDROLASE
2GNU	THE CRYSTALLIZATION OF REACTION CENTER FROM RHODOBACTER SPHAEROIDES OCCURS VIA A NEW ROUTE	PHOTOSYNTHESIS
2GO5	STRUCTURE OF SIGNAL RECOGNITION PARTICLE RECEPTOR (SR) IN COMPLEX WITH SIGNAL RECOGNITION PARTICLE (SRP) AND RIBOSOME NASCENT CHAIN COMPLEX	TRANSLATION/RNA
2GOL	XRAY STRUCTURE OF GAG278	VIRUS/VIRAL PROTEIN
2GOO	TERNARY COMPLEX OF BMP-2 BOUND TO BMPR-IA-ECD AND ACTRII-ECD	TRANSFERASE
2GOX	CRYSTAL STRUCTURE OF EFB-C / C3D COMPLEX	CELL ADHESION/TOXIN
2GP9	CRYSTAL STRUCTURE OF THE SLOW FORM OF THROMBIN IN A SELF-INHIBITED CONFORMATION	HYDROLASE
2GPH	DOCKING MOTIF INTERACTIONS IN THE MAP KINASE ERK2	TRANSFERASE
2GPL	TMC-95 BASED BIPHENYL-ETHER MACROCYCLES: SPECIFIC PROTEASOME INHIBITORS	HYDROLASE
2GPO	ESTROGEN RELATED RECEPTOR-GAMMA LIGAND BINDING DOMAIN COMPLEXED WITH A SYNTHETIC PEPTIDE FROM RIP140	TRANSCRIPTION

2GPP	ESTROGEN RELATED RECEPTOR-GAMMA LIGAND BINDING DOMAIN COMPLEXED WITH A RIP140 PEPTIDE AND SYNTHETIC LIGAND GSK4716	TRANSCRIPTION
2GPV	ESTROGEN RELATED RECEPTOR-GAMMA LIGAND BINDING DOMAIN COMPLEXED WITH 4-HYDROXY-TAMOXIFEN AND A SMRT PEPTIDE	TRANSCRIPTION
2GRL	CRYSTAL STRUCTURE OF DCT/ICF10 COMPLEX	TRANSCRIPTION
2GRM	CRYSTAL STRUCTURE OF PRGX/ICF10 COMPLEX	TRANSCRIPTION
2GRN	CRYSTAL STRUCTURE OF HUMAN RANGAP1-UBC9	LIGASE
2GRO	CRYSTAL STRUCTURE OF HUMAN RANGAP1-UBC9-N85Q	LIGASE
2GRP	CRYSTAL STRUCTURE OF HUMAN RANGAP1-UBC9-Y87A	LIGASE
2GRQ	CRYSTAL STRUCTURE OF HUMAN RANGAP1-UBC9-D127A	LIGASE
2GRR	CRYSTAL STRUCTURE OF HUMAN RANGAP1-UBC9-D127S	LIGASE
2GRX	CRYSTAL STRUCTURE OF TONB IN COMPLEX WITH FHUA, E. COLI OUTER MEMBRANE RECEPTOR FOR FERRICHROME	METAL TRANSPORT
2GS6	CRYSTAL STRUCTURE OF THE ACTIVE EGFR KINASE DOMAIN IN COMPLEX WITH AN ATP ANALOG-PEPTIDE CONJUGATE	TRANSFERASE
2GSI	CRYSTAL STRUCTURE OF A MURINE FAB IN COMPLEX WITH AN 11 RESIDUE PEPTIDE DERIVED FROM STAPHYLOCOCCAL NUCLEASE	IMMUNE SYSTEM
2GSK	STRUCTURE OF THE BTUB:TONB COMPLEX	SIGNALING PROTEIN/MEMBRANE PROTEIN
2GSM	CATALYTIC CORE (SUBUNITS I AND II) OF CYTOCHROME C OXIDASE FROM RHODOBACTER SPHAEROIDES	OXIDOREDUCTASE
2GSR	STRUCTURE OF PORCINE CLASS PI GLUTATHIONE S-TRANSFERASE	COMPLEX (TRANSFERASE/INHIBITOR)
2GT9	HUMAN CLASS I MHC HLA-A2 IN COMPLEX WITH THE DECAMERIC MELAN-A/MART-1(26-35) PEPTIDE	IMMUNE SYSTEM
2GTK	STRUCTURE-BASED DESIGN OF INDOLE PROPIONIC ACIDS AS NOVEL PPARAG CO-AGONISTS	TRANSCRIPTION REGULATOR
2GTL	LUMBRICUS ERYTHROCRUORIN AT 3.5A RESOLUTION	OXYGEN STORAGE/TRANSPORT
2GTP	CRYSTAL STRUCTURE OF THE HETERODIMERIC COMPLEX OF HUMAN RGS1 AND ACTIVATED GI ALPHA 1	SIGNALING PROTEIN
2GTW	HUMAN CLASS I MHC HLA-A2 IN COMPLEX WITH THE NONAMERIC MELAN-A/MART-1(27-35) PEPTIDE HAVING A27L SUBSTITUTION	IMMUNE SYSTEM
2GTZ	HUMAN CLASS I MHC HLA-A2 IN COMPLEX WITH THE NONAMERIC MELAN-A/MART-1(27-35) PEPTIDE HAVING A28L SUBSTITUTION	IMMUNE SYSTEM
2GU8	DISCOVERY OF 2-PYRIMIDYL-5-AMIDOTHIOPHENES AS NOVEL AND	SIGNALING PROTEIN,TRANSFERASE/INHIBITOR

	POTENT INHIBITORS FOR AKT: SYNTHESIS AND SAR STUDIES	
2GUO	HUMAN CLASS I MHC HLA-A2 IN COMPLEX WITH THE NATIVE NONAMERIC MELAN-A/MART-1(27-35) PEPTIDE	IMMUNE SYSTEM
2GUZ	STRUCTURE OF THE TIM14-TIM16 COMPLEX OF THE MITOCHONDRIAL PROTEIN IMPORT MOTOR	CHAPERONE, PROTEIN TRANSPORT
2GV2	MDM2 IN COMPLEX WITH AN 8-MER P53 PEPTIDE ANALOGUE	LIGASE
2GV5	CRYSTAL STRUCTURE OF SFI1P/CDC31P COMPLEX	CELL CYCLE
2GVD	COMPLEX OF GS- WITH THE CATALYTIC DOMAINS OF MAMMALIAN ADENYLYL CYCLASE: COMPLEX WITH TNP-ATP AND MN	LYASE
2GVF	HCV NS3-4A PROTEASE DOMAIN COMPLEXED WITH A MACROCYCLIC KETOAMIDE INHIBITOR, SCH419021	HYDROLASE
2GVZ	CRYSTAL STRUCTURE OF COMPLEX OF GS- WITH THE CATALYTIC DOMAINS OF MAMMALIAN ADENYLYL CYCLASE: COMPLEX WITH MANT-ATP AND MN	LYASE
2GW4	CRYSTAL STRUCTURE OF STONY CORAL FLUORESCENT PROTEIN KAEDE, RED FORM	LUMINESCENT PROTEIN
2GWF	STRUCTURE OF A USP8-NRDP1 COMPLEX	HYDROLASE/LIGASE
2GWW	HUMAN VINCULIN (HEAD DOMAIN, VH1, RESIDUES 1-258) IN COMPLEX WITH SHIGELLA'S IPAA VINCULIN BINDING SITE (RESIDUES 602-633)	CELL ADHESION, STRUCTURAL PROTEIN
2GY7	ANGIOPOIETIN-2/TIE2 COMPLEX CRYSTAL STRUCTURE	SIGNALING PROTEIN
2GY9	STRUCTURE OF THE 30S SUBUNIT OF A PRE-TRANSLOCATIONAL E. COLI RIBOSOME OBTAINED BY FITTING ATOMIC MODELS FOR RNA AND PROTEIN COMPONENTS INTO CRYO-EM MAP EMD-1056	RIBOSOME
2GYA	STRUCTURE OF THE 50S SUBUNIT OF A PRE-TRANSLOCATIONAL E. COLI RIBOSOME OBTAINED BY FITTING ATOMIC MODELS FOR RNA AND PROTEIN COMPONENTS INTO CRYO-EM MAP EMD-1056	RIBOSOME
2GYB	STRUCTURE OF THE 30S SUBUNIT OF A SECM-STALLED E. COLI RIBOSOME COMPLEX OBTAINED BY FITTING ATOMIC MODELS FOR RNA AND PROTEIN COMPONENTS INTO CRYO-EM MAP EMD-1143	RIBOSOME
2GYC	STRUCTURE OF THE 50S SUBUNIT OF A SECM-STALLED E. COLI RIBOSOME COMPLEX OBTAINED BY FITTING ATOMIC MODELS FOR RNA AND PROTEIN COMPONENTS INTO CRYO-EM MAP EMD-1143	RIBOSOME
2GYK	CRYSTAL STRUCTURE OF THE COMPLEX OF THE COLICIN E9 DNASE DOMAIN WITH A MUTANT IMMUNITY PROTEIN, IMME9 (D51A)	ANTIBIOTIC/ANTIBIOTIC INHIBITOR
2GZD	CRYSTAL STRUCTURE OF RAB11 IN COMPLEX WITH RAB11-FIP2	PROTEIN TRANSPORT
2GZE	CRYSTAL STRUCTURE OF THE E9 DNASE DOMAIN WITH A MUTANT	ANTIBIOTIC/ANTIBIOTIC INHIBITOR

	IMMUNITY PROTEIN IM9 (Y55A)	
2GZF	CRYSTAL STRUCTURE OF THE E9 DNASE DOMAIN WITH A MUTANT IMMUNITY PROTEIN IM9 (Y54F)	ANTIBIOTIC/ANTIBIOTIC INHIBITOR
2GZG	CRYSTAL STRUCTURE OF THE E9 DNASE DOMAIN WITH A MUTANT IMMUNITY PROTEIN IM9 (Y55F)	ANTIBIOTIC/ANTIBIOTIC INHIBITOR
2GZH	CRYSTAL STRUCTURE OF RAB11 IN COMPLEX WITH RAB11-FAMILY INTERACTING PROTEIN 2	PROTEIN TRANSPORT
2GZI	CRYSTAL STRUCTURE OF THE E9 DNASE DOMAIN WITH A MUTANT IMMUNITY PROTEIN IM9 (V34A)	ANTIBIOTIC/ANTIBIOTIC INHIBITOR
2GZJ	CRYSTAL STRUCTURE OF THE E9 DNASE DOMAIN WITH A MUTANT IMMUNITY PROTEIN IM9 (D51A)	ANTIBIOTIC/ANTIBIOTIC INHIBITOR
2H0D	STRUCTURE OF A BMI-1-RING1B POLYCOMB GROUP UBIQUITIN LIGASE COMPLEX	METAL BINDING PROTEIN/LIGASE
2H1C	CRYSTAL STRUCTURE OF FITACB FROM NEISSERIA GONORRHOEAE	GENE REGULATION
2H1L	THE STRUCTURE OF THE ONCOPROTEIN SV40 LARGE T ANTIGEN AND P53 TUMOR SUPPRESSOR COMPLEX	VIRUS/VIRAL PROTEIN
2H1O	STRUCTURE OF FITAB BOUND TO IR36 DNA FRAGMENT	GENE REGULATION/DNA COMPLEX
2H1P	THE THREE-DIMENSIONAL STRUCTURES OF A POLYSACCHARIDE BINDING ANTIBODY TO CRYPTOCOCCUS NEOFORMANS AND ITS COMPLEX WITH A PEPTIDE FROM A PHAGE DISPLAY LIBRARY: IMPLICATIONS FOR THE IDENTIFICATION OF PEPTIDE MIMOTOPES	COMPLEX (ANTIBODY/PEPTIDE)
2H2D	THE STRUCTURAL BASIS FOR SIRTUIN SUBSTRATE AFFINITY	HYDROLASE
2H2F	THE STRUCTURAL BASIS FOR SIRTUIN SUBSTRATE AFFINITY	HYDROLASE
2H2G	THE STRUCTURAL BASIS OF SIRTUIN SUBSTRATE AFFINITY	HYDROLASE
2H2H	THE STRUCTURAL BASIS OF SIRTUIN SUBSTRATE SPECIFICITY	HYDROLASE
2H2P	CRYSTAL STRUCTURE OF CLC-EC1 IN COMPLEX WITH FAB FRAGMENT IN SECN-	ION TRANSPORT
2H2S	CRYSTAL STRUCTURE OF E148A MUTANT OF CLC-EC1 IN SECN-	ION TRANSPORT
2H3E	STRUCTURE OF WILD-TYPE E. COLI ASPARTATE TRANSCARBAMOYLASE IN THE PRESENCE OF N-PHOSPHONACETYL-L-ISOASPARAGINE AT 2.3A RESOLUTION	TRANSFERASE
2H3N	CRYSTAL STRUCTURE OF A SURROGATE LIGHT CHAIN (LAMBDA5 AND VPREB) HOMODIMER	IMMUNE SYSTEM
2H3X	RYSTAL STRUCTURE OF AN ELECTRON TRANSFER COMPLEX BETWEEN AROMATIC AMINE DEHYDROGENASE AND AZURIN FROM ALCALIGENES FAECALIS (FORM 3)	OXIDOREDUCTASE/ELECTRON TRANSPORT

2H43	RYSTAL STRUCTURE OF HUMAN FRAGMENT D COMPLEXED WITH ALA-HIS-ARG-PRO-AMIDE	BLOOD CLOTTING
2H47	RYSTAL STRUCTURE OF AN ELECTRON TRANSFER COMPLEX BETWEEN AROMATIC AMINE DEPHYDROGENASE AND AZURIN FROM ALCALIGENES FAECALIS (FORM 1)	OXIDOREDUCTASE/ELECTRON TRANSPORT
2H48	CRYSTAL STRUCTURE OF HUMAN CASPASE-1 (CYS362->ALA, CYS364->ALA, CYS397->ALA) IN COMPLEX WITH 3-[2-(2-BENZYLOXYCARBONYLAMINO-3-METHYL-BUTYRYLAMINO)-PROPIONYLAMINO]-4-OXO-PENTANOIC ACID (Z-VAD-FMK)	HYDROLASE
2H4C	STRUCTURE OF DABOIATOXIN (HETERODIMERIC PLA2 VENOM)	HYDROLASE
2H4F	SIR2-P53 PEPTIDE-NAD+	HYDROLASE
2H4H	SIR2 H116Y MUTANT-P53 PEPTIDE-NAD	HYDROLASE
2H4J	SIR2-DEACETYLATED PEPTIDE (FROM ENZYMATIC TURNOVER IN CRYSTAL)	HYDROLASE
2H4M	KARYOPHERIN BETA2/TRANSPORTIN-M9NLS	PROTEIN TRANSPORT
2H4P	CRYSTAL STRUCTURE OF WILDTYPE MENT IN THE CLEAVED CONFORMATION	HYDROLASE INHIBITOR
2H4Q	CRYSTAL STRUCTURE OF A M-LOOP DELETION VARIANT OF MENT IN THE CLEAVED CONFORMATION	HYDROLASE INHIBITOR
2H4W	CRYSTAL STRUCTURE OF HUMAN CASPASE-1 (GLU390->ASP) IN COMPLEX WITH 3-[2-(2-BENZYLOXYCARBONYLAMINO-3-METHYL-BUTYRYLAMINO)-PROPIONYLAMINO]-4-OXO-PENTANOIC ACID (Z-VAD-FMK)	HYDROLASE
2H4Y	CRYSTAL STRUCTURE OF HUMAN CASPASE-1 (ARG286->LYS) IN COMPLEX WITH 3-[2-(2-BENZYLOXYCARBONYLAMINO-3-METHYL-BUTYRYLAMINO)-PROPIONYLAMINO]-4-OXO-PENTANOIC ACID (Z-VAD-FMK)	HYDROLASE
2H51	CRYSTAL STRUCTURE OF HUMAN CASPASE-1 (GLU390->ASP AND ARG286->LYS) IN COMPLEX WITH 3-[2-(2-BENZYLOXYCARBONYLAMINO-3-METHYL-BUTYRYLAMINO)-PROPIONYLAMINO]-4-OXO-PENTANOIC ACID (Z-VAD-FMK)	HYDROLASE
2H54	CRYSTAL STRUCTURE OF HUMAN CASPASE-1 (THR388->ALA) IN COMPLEX WITH 3-[2-(2-BENZYLOXYCARBONYLAMINO-3-METHYL-BUTYRYLAMINO)-PROPIONYLAMINO]-4-OXO-PENTANOIC ACID (Z-VAD-FMK)	HYDROLASE
2H59	SIR2 H116A-DEACETYLATED P53 PEPTIDE-3'-O-ACETYL ADP RIBOSE	HYDROLASE
2H5I	CRYSTAL STRUCTURE OF CASPASE-3 WITH INHIBITOR AC-DEVD-CHO	HYDROLASE
2H5J	CRYSTAL STRUSTURE OF CASPASE-3 WITH INHIBITOR AC-DMQD-CHO	HYDROLASE

2H61	X-RAY STRUCTURE OF HUMAN CA2+-LOADED S100B	METAL BINDING PROTEIN, SIGNALING PROTEIN
2H62	CRYSTAL STRUCTURE OF A TERNARY LIGAND-RECEPTOR COMPLEX OF BMP-2	HORMONE/GROWTH FACTOR
2H64	CRYSTAL STRUCTURE OF A TERNARY LIGAND-RECEPTOR COMPLEX OF BMP-2	HORMONE/GROWTH FACTOR
2H65	CRYSTAL STRUSTURE OF CASPASE-3 WITH INHIBITOR AC-VDVAD-CHO	HYDROLASE
2H6F	PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH A FARNESYLATED DDPTASACVLS PEPTIDE PRODUCT AT 1.5A RESOLUTION	TRANSFERASE
2H6G	W102T PROTEIN FARNESYLTRANSFERASE MUTANT COMPLEXED WITH A GERANYLGERANYLATED DDPTASACVLS PEPTIDE PRODUCT AT 1.85A RESOLUTION	TRANSFERASE
2H6H	Y365F PROTEIN FARNESYLTRANSFERASE MUTANT COMPLEXED WITH A FARNESYLATED DDPTASACVLS PEPTIDE PRODUCT AT 1.8A	TRANSFERASE
2H6I	W102T/Y365F PROTEIN FARNESYLTRANSFERASE DOUBLE MUTANT COMPLEXED WITH A GERANYLGERANYLATED DDPTASACVLS PEPTIDE PRODUCT AT 3.0A	TRANSFERASE
2H6J	RYSTAL STRUCTURE OF THE BETA F145A RHODOCOCCUS PROTEASOME (CASP TARGET)	HYDROLASE
2H6M	AN EPISULFIDE CATION (THIIRANIUM RING) TRAPPED IN THE ACTIVE SITE OF HAV 3C PROTEINASE INACTIVATED BY PEPTIDE-BASED KETONE INHIBITORS	HYDROLASE/HYDROLASE INHIBITOR
2H6P	CRYSTAL STRUCTURE OF HLA-B*3501 PRESENTING THE HUMAN CYTOCHROME P450 DERIVED PEPTIDE, KPIVVLHGY	IMMUNE SYSTEM
2H7E	SOLUTION STRUCTURE OF THE TALIN F3 DOMAIN IN COMPLEX WITH A CHIMERIC BETA3 INTEGRIN-PIP KINASE PEPTIDE- MINIMIZED AVERAGE STRUCTURE	STRUCTURAL PROTEIN
2H7V	CO-CRYSTAL STRUCTURE OF YPKA-RAC1	SIGNALING PROTEIN
2H88	AVIAN MITOCHONDRIAL RESPIRATORY COMPLEX II AT 1.8 ANGSTROM RESOLUTION	OXIDOREDUCTASE
2H89	AVIAN RESPIRATORY COMPLEX II WITH MALONATE BOUND	OXIDOREDUCTASE
2H8D	CRYSTAL STRUCTURE OF DEOXY HEMOGLOBIN FROM TREMATOMUS BERNACCHII AT PH 8.4	TRANSPORT PROTEIN
2H8F	CRYSTAL STRUCTURE OF DEOXY HEMOGLOBIN FROM TREMATOMUS BERNACCHII AT PH 6.2	TRANSPORT PROTEIN
2H8P	STRUCTURE OF A K CHANNEL WITH AN AMIDE TO ESTER SUBSTITUTION IN THE SELECTIVITY FILTER	MEMBRANE PROTEIN

2H96	DISCOVERY OF POTENT, HIGHLY SELECTIVE, AND ORALLY BIOAVAILABLE PYRIDINE CARBOXAMIDE C-JUN NH2-TERMINAL KINASE INHIBITORS	TRANSCRIPTION
2H9A	CORRINOID IRON-SULFUR PROTEIN	OXIDOREDUCTASE
2H9E	CRYSTAL STRUCTURE OF FXA/SELECTIDE/NAPC2 TERNARY COMPLEX	HYDROLASE, BLOOD CLOTTING
2H9G	CRYSTAL STRUCTURE OF PHAGE DERIVED FAB BDF1 WITH HUMAN DEATH RECEPTOR 5 (DR5)	IMMUNE SYSTEM/APOTOSIS
2H9H	AN EPISULFIDE CATION (THIIRANIUM RING) TRAPPED IN THE ACTIVE SITE OF HAV 3C PROTEINASE INACTIVATED BY PEPTIDE-BASED KETONE INHIBITORS	HYDROLASE
2H9T	CRYSTAL STRUCTURE OF HUMAN ALPHA-THROMBIN IN COMPLEX WITH SURAMIN	HYDROLASE
2HAL	AN EPISULFIDE CATION (THIIRANIUM RING) TRAPPED IN THE ACTIVE SITE OF HAV 3C PROTEINASE INACTIVATED BY PEPTIDE-BASED KETONE INHIBITORS	HYDROLASE
2HAN	STRUCTURAL BASIS OF HETERODIMERIC ECDYSTEROID RECEPTOR INTERACTION WITH NATURAL RESPONSE ELEMENT HSP27 GENE PROMOTER	TRANSCRIPTION/DNA
2HBC	HIGH RESOLUTION X-RAY STRUCTURES OF MYOGLOBIN-AND HEMOGLOBIN-ALKYL ISOCYANIDE COMPLEXES	OXYGEN TRANSPORT
2HBD	HIGH RESOLUTION X-RAY STRUCTURES OF MYOGLOBIN-AND HEMOGLOBIN-ALKYL ISOCYANIDE COMPLEXES	OXYGEN TRANSPORT
2HBE	HIGH RESOLUTION X-RAY STRUCTURES OF MYOGLOBIN-AND HEMOGLOBIN-ALKYL ISOCYANIDE COMPLEXES	OXYGEN TRANSPORT
2HBF	HIGH RESOLUTION X-RAY STRUCTURES OF MYOGLOBIN-AND HEMOGLOBIN-ALKYL ISOCYANIDE COMPLEXES	OXYGEN TRANSPORT
2HBH	CRYSTAL STRUCTURE OF VITAMIN D NUCLEAR RECEPTOR LIGAND BINDING DOMAIN BOUND TO A LOCKED SIDE-CHAIN ANALOG OF CALCITRIOL AND SRC-1 PEPTIDE	GENE REGULATION
2HBQ	CRYSTAL STRUCTURE OF WILDTYPE HUMAN CASPASE-1 IN COMPLEX WITH 3-[2-(2-BENZYLOXYCARBONYLAMINO-3-METHYL-BUTYRYLAMINO)-PROPIONYLAMINO]-4-OXO-PENTANOIC ACID (Z-VAD-FMK)	HYDROLASE
2HBR	CRYSTAL STRUCTURE OF HUMAN CASPASE-1 (ARG286->ALA) IN COMPLEX WITH 3-[2-(2-BENZYLOXYCARBONYLAMINO-3-METHYL-BUTYRYLAMINO)-PROPIONYLAMINO]-4-OXO-PENTANOIC ACID (Z-VAD-FMK)	HYDROLASE
2HBS	HE HIGH RESOLUTION CRYSTAL STRUCTURE OF DEOXYHEMOGLOBIN S	OXYGEN TRANSPORT
2HBY	CRYSTAL STRUCTURE OF HUMAN CASPASE-1 (GLU390->ALA) IN COMPLEX WITH 3-[2-(2-BENZYLOXYCARBONYLAMINO-3-METHYL-	HYDROLASE

	BUTYRYLAMINO)-PROPIONYLAMINO]-4-OXO-PENTANOIC ACID (Z-VAD-FMK)	
2HBZ	CRYSTAL STRUCTURE OF HUMAN CASPASE-1 (ARG286->ALA, GLU390->ALA) IN COMPLEX WITH 3-[2-(2-BENZYLOXYCARBONYLAMINO-3-METHYL-BUTYRYLAMINO)-PROPIONYLAMINO]-4-OXO-PENTANOIC ACID (Z-VAD-FMK)	HYDROLASE
2HC4	CRYSTAL STRUCTURE OF THE LBD OF VDR OF DANIO RERIO IN COMPLEX WITH CALCITRIOL	GENE REGULATION
2HCD	CRYSTAL STRUCTURE OF THE LIGAND BINDING DOMAIN OF THE VITAMIN D NUCLEAR RECEPTOR IN COMPLEX WITH GEMINI AND A COACTIVATOR PEPTIDE	GENE REGULATION
2HCJ	"TRYPSIN-MODIFIED ELONGATION FACTOR TU IN COMPLEX WITH TETRACYCLINE"	TRANSLATION
2HCO	THE STRUCTURE OF HUMAN CARBONMONOXY HAEMOGLOBIN AT 2.7 ANGSTROMS RESOLUTION	OXYGEN TRANSPORT
2HD4	CRYSTAL STRUCTURE OF PROTEINASE K INHIBITED BY A LACTOFERRIN OCTAPEPTIDE GLY-ASP-GLU-GLN-GLY-GLU-ASN-LYS AT 2.15 A RESOLUTION	HYDROLASE
2HD5	USP2 IN COMPLEX WITH UBIQUITIN	HYDROLASE
2HDI	CRYSTAL STRUCTURE OF THE COLICIN I RECEPTOR CIR FROM E.COLI IN COMPLEX WITH RECEPTOR BINDING DOMAIN OF COLICIN IA.	PROTEIN TRANSPORT,ANTIMICROBIAL PROTEIN
2HDN	TRYPSIN-MODIFIED ELONGATION FACTOR TU IN COMPLEX WITH TETRACYCLINE AT 2.8 ANGSTROM RESOLUTION	TRANSLATION
2HDX	CRYSTAL STRUCTURE OF THE SRC HOMOLOGY-2 DOMAIN OF SH2-B IN COMPLEX WITH JAK2 PTYR813 PHOSPHOPEPTIDE	SIGNALING PROTEIN
2HFE	RB+ COMPLEX OF A K CHANNEL WITH AN AMIDE TO ESTER SUBSTITUTION IN THE SELECTIVITY FILTER	MEMBRANE PROTEIN
2HFF	CRYSTAL STRUCTURE OF CB2 FAB	IMMUNE SYSTEM
2HFG	CRYSTAL STRUCTURE OF HBR3 BOUND TO CB3S-FAB	IMMUNE SYSTEM
2HFP	CRYSTAL STRUCTURE OF PPAR GAMMA WITH N-SULFONYL-2-INDOLE CARBOXAMIDE LIGANDS	TRANSCRIPTION
2HG3	REACTION CENTRE FROM RHODOBACTER SPHAEROIDES STRAIN R-26.1 COMPLEXED WITH BROMINATED PHOSPHATIDYLCHOLINE	PHOTOSYNTHESIS/MEMBRANE PROTEIN
2HG5	CS+ COMPLEX OF A K CHANNEL WITH AN AMIDE TO ESTER SUBSTITUTION IN THE SELECTIVITY FILTER	MEMBRANE PROTEIN
2HG9	REACTION CENTRE FROM RHODOBACTER SPHAEROIDES STRAIN R-26.1 COMPLEXED WITH TETRABROMINATED PHOSPHATIDYLCHOLINE	PHOTOSYNTHESIS/MEMBRANE PROTEIN

2HGI	CRYSTAL STRUCTURE OF THE 70S THERMUS THERMOPHILUS RIBOSOME SHOWING HOW THE 16S 3'-END MIMICKS MRNA E AND P CODONS. THIS ENTRY 2HGI CONTAINS 30S RIBOSOMAL SUBUNIT. THE 50S RIBOSOMAL SUBUNIT CAN BE FOUND IN PDB ENTRY 2HGJ.	RIBOSOME
2HGJ	CRYSTAL STRUCTURE OF THE 70S THERMUS THERMOPHILUS RIBOSOME SHOWING HOW THE 16S 3'-END MIMICKS MRNA E AND P CODONS. THIS ENTRY 2HGJ CONTAINS 50S RIBOSOMAL SUBUNIT. THE 30S RIBOSOMAL SUBUNIT CAN BE FOUND IN PDB ENTRY 2HGI.	RIBOSOME
2HGP	CRYSTAL STRUCTURE OF THE 70S THERMUS THERMOPHILUS RIBOSOME WITH TRANSLOCATED AND ROTATED SHINE-DALGARNO DUPLEX. THIS ENTRY 2HGP CONTAINS 30S RIBOSOMAL SUBUNIT. THE 50S RIBOSOMAL SUBUNIT CAN BE FOUND IN PDB ENTRY 2HGQ.	RIBOSOME
2HGQ	CRYSTAL STRUCTURE OF THE 70S THERMUS THERMOPHILUS RIBOSOME WITH TRANSLOCATED AND ROTATED SHINE-DALGARNO DUPLEX. THIS ENTRY 2HGQ CONTAINS 50S RIBOSOMAL SUBUNIT. THE 30S RIBOSOMAL SUBUNIT CAN BE FOUND IN PDB ENTRY 2HGP.	RIBOSOME
2HGR	70S T.TH. RIBOSOME FUNCTIONAL COMPLEX WITH MRNA AND E- AND P-SITE TRNAS AT 4.5A. THIS ENTRY 2HGR CONTAINS 30S RIBOSOMAL SUBUNIT. THE 50S RIBOSOMAL SUBUNIT CAN BE FOUND IN PDB ENTRY 2HGU.	RIBOSOME
2HGT	STRUCTURE OF THE HIRUGEN AND HIRULOG 1 COMPLEXES OF ALPHA-THROMBIN	HYDROLASE(SERINE PROTEASE)
2HGU	70S T.TH. RIBOSOME FUNCTIONAL COMPLEX WITH MRNA AND E- AND P-SITE TRNAS AT 4.5A. THIS ENTRY 2HGU CONTAINS 50S RIBOSOMAL SUBUNIT. THE 30S RIBOSOMAL SUBUNIT CAN BE FOUND IN PDB ENTRY 2HGR.	RIBOSOME
2HH0	STRUCTURE OF AN ANTI-PRP FAB, P-CLONE, IN COMPLEX WITH ITS COGNATE BOVINE PEPTIDE EPITOPE.	IMMUNE SYSTEM
2HH1	REACTION CENTRE FROM RHODOBACTER SPHAEROIDES STRAIN R-26.1 COMPLEXED WITH DIBROMINATED PHOSPHATIDYLCHOLINE	PHOTOSYNTHESIS/MEMBRANE PROTEIN
2HHB	THE CRYSTAL STRUCTURE OF HUMAN DEOXYHAEMOGLOBIN AT 1.74 ANGSTROMS RESOLUTION	OXYGEN TRANSPORT
2HHD	OXYGEN AFFINITY MODULATION BY THE N-TERMINI OF THE BETA-CHAINS IN HUMAN AND BOVINE HEMOGLOBIN	OXYGEN TRANSPORT
2HHE	OXYGEN AFFINITY MODULATION BY THE N-TERMINI OF THE BETA CHAINS IN HUMAN AND BOVINE HEMOGLOBIN	OXYGEN TRANSPORT
2HHF	X-RAY CRYSTAL STRUCTURE OF OXIDIZED HUMAN MITOCHONDRIAL BRANCHED CHAIN AMINOTRANSFERASE (HBCATM)	TRANSFERASE
2HHH	CRYSTAL STRUCTURE OF KASUGAMYCIN BOUND TO THE 30S RIBOSOMAL SUBUNIT	RIBOSOME
2HHK	REACTION CENTRE FROM RHODOBACTER SPHAEROIDES STRAIN R-26.1	PHOTOSYNTHESIS/MEMBRANE PROTEIN

	COMPLEXED WITH DIBROMINATED PHOSPHATIDYLGLYCEROL	
2HI7	CRYSTAL STRUCTURE OF DSBA-DSBB-UBIQUINONE COMPLEX	OXIDOREDUCTASE
2HI8	HUMAN FORMYLGLYCINE GENERATING ENZYME, C336S MUTANT, BROMIDE CO-CRYSTALLIZATION	HYDROLASE ACTIVATOR, PROTEIN BINDING
2HII	HETEROTRIMERIC PCNA SLIDING CLAMP	REPLICATION
2HIK	HETEROTRIMERIC PCNA SLIDING CLAMP	REPLICATION
2HIO	HISTONE OCTAMER (CHICKEN), CHROMOSOMAL PROTEIN	STRUCTURAL PROTEIN,DNA BINDING PROTEIN
2HIT	REACTION CENTRE FROM RHODOBACTER SPHAEROIDES STRAIN R-26.1 COMPLEXED WITH DIBROMINATED PHOSPHATIDYLETHANOLAMINE	PHOTOSYNTHESIS/MEMBRANE PROTEIN
2HJ4	CRYSTAL STRUCTURE OF ALCALIGENES FAECALIS AADH COMPLEX WITH P-NITROBENZYLAMINE	OXIDOREDUCTASE
2HJ6	REACTION CENTRE FROM RHODOBACTER SPHAEROIDES STRAIN R-26.1 COMPLEXED WITH DIBROMINATED PHOSPHATIDYLSERINE	PHOTOSYNTHESIS/MEMBRANE PROTEIN
2HJ9	CRYSTAL STRUCTURE OF THE AUTOINDUCER-2-BOUND FORM OF VIBRIO HARVEYI LUXP COMPLEXED WITH THE PERIPLASMIC DOMAIN OF LUXQ	SIGNALING PROTEIN
2HJB	CRYSTAL STRUCTURE OF ALCALIGENES FAECALIS AADH IN COMPLEX WITH P-METHOXYBENZYLAMINE	OXIDOREDUCTASE
2HJF	OTASSIUM CHANNEL KCSA-FAB COMPLEX WITH TETRABUTYLAMMONIUM (TBA)	METAL TRANSPORT
2HJK	CRYSTAL STRUCTURE OF HLA-B5703 AND HIV-1 PEPTIDE	IMMUNE SYSTEM
2HJL	CRYSTAL STRUCTURE OF HLA-B5703 AND HIV-1 PEPTIDE	IMMUNE SYSTEM
2HKF	CRYSTAL STRUCTURE OF THE COMPLEX FAB M75- PEPTIDE	IMMUNE SYSTEM
2HKH	CRYSTAL STRUCTURE OF THE FAB M75	IMMUNE SYSTEM
2HKM	CRYSTAL STRUCTURE OF THE SCHIFF BASE INTERMEDIATE IN THE REDUCTIVE HALF-REACTION OF AROMATIC AMINE DEHYDROGENASE (AADH) WITH PHENYLETHYLAMINE.	OXIDOREDUCTASE
2HKQ	CRYSTAL STRUCTURE OF THE C-TERMINAL DOMAIN OF HUMAN EB1 IN COMPLEX WITH THE CAP-GLY DOMAIN OF HUMAN DYNACTIN-1 (P150-GLUED)	STRUCTURAL PROTEIN
2HKR	STRUCTURES OF THE CARBINOLAMINE AND SCHIFF-BASE INTERMEDIATES IN THE REDUCTIVE HALF-REACTION OF AROMATIC AMINE DEHYDROGENASE (AADH) WITH P-METHOXYPHENYLETHYLAMINE	OXIDOREDUCTASE
2HL5	CRYSTAL STRUCTURE OF THE C-TERMINAL DOMAIN OF HUMAN EB1 IN COMPLEX WITH THE A49M MUTANT CAP-GLY DOMAIN OF HUMAN DYNACTIN-1 (P150-GLUED)	STRUCTURAL PROTEIN

2HLB	A STRUCTURAL BASIS FOR NUCLEOTIDE EXCHANGE ON G-ALPHA-I SUBUNITS AND RECEPTOR COUPLING SPECIFICITY	SIGNALING PROTEIN
2HLD	CRYSTAL STRUCTURE OF YEAST MITOCHONDRIAL F1-ATPASE	HYDROLASE
2HLF	STRUCTURE OF THE ESCHERICHIS COLI CLC CHLORIDE CHANNEL Y445E MUTANT AND FAB COMPLEX	PROTON TRANSPORT,MEMBRANE PROTEIN
2HLO	CRYSTAL STRUCTURE OF FRAGMENT D-DIMER FROM HUMAN FIBRIN COMPLEXED WITH GLY-HYDROXYPRO-ARG-PRO-AMIDE	BLOOD CLOTTING
2HMG	REFINEMENT OF THE INFLUENZA VIRUS HEMAGGLUTININ BY SIMULATED ANNEALING	VIRAL PROTEIN
2HMH	CRYSTAL STRUCTURE OF SOCS3 IN COMPLEX WITH GP130(PTYR757) PHOSPHOPEPTIDE.	CYTOKINE REGULATOR
2HMI	HIV-1 REVERSE TRANSCRIPTASE/FRAGMENT OF FAB 28/DNA COMPLEX	IMMUNE SYSTEM/DNA
2HMJ	CRYSTAL STRUCTURE OF THE NAPHTHALENE 1,2-DIOXYGENASE PHE-352-VAL MUTANT.	OXIDOREDUCTASE
2HMK	CRYSTAL STRUCTURE OF NAPHTHALENE 1,2-DIOXYGENASE BOUND TO PHENANTHRENE	OXIDOREDUCTASE
2HML	CRYSTAL STRUCTURE OF THE NAPHTHALENE 1,2-DIOXYGENASE F352V MUTANT BOUND TO PHENANTHRENE.	OXIOREDUCTASE
2HMM	CRYSTAL STRUCTURE OF NAPHTHALENE 1,2-DIOXYGENASE BOUND TO ANTHRACENE	OXIOREDUCTASE
2HMN	CRYSTAL STRUCTURE OF THE NAPHTHALENE 1,2-DIOXYGENASE F352V MUTANT BOUND TO ANTHRACENE.	OXIDOREDUCTASE
2HMO	CRYSTAL STRUCTURE OF NAPHTHALENE 1,2-DIOXYGENASE BOUND TO 3-NITROTOLUENE.	OXIDOREDUCTASE
2HN7	HLA-A*1101 IN COMPLEX WITH HBV PEPTIDE HOMOLOGUE	IMMUNE SYSTEM
2HND	CRYSTAL STRUCTURE OF K101E MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH NEVIRAPINE	TRANSFERASE
2HNT	CRYSTALLOGRAPHIC STRUCTURE OF HUMAN GAMMA-THROMBIN	SERINE PROTEASE
2HNY	CRYSTAL STRUCTURE OF E138K MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH NEVIRAPINE	TRANSFERASE
2HNZ	CRYSTAL STRUCTURE OF E138K MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH PETT-2	TRANSFERASE
2HOD	CRYSTAL STRUCTURE OF FRAGMENT D FROM HUMAN FIBRINOGEN COMPLEXED WITH GLY-HYDROXYPRO-ARG-PRO-AMIDE	BLOOD CLOTTING
2HP0	CRYSTAL STRUCTURE OF IMINODISUCCINATE EPIMERASE	ISOMERASE

2HPC	CRYSTAL STRUCTURE OF FRAGMENT D FROM HUMAN FIBRINOGEN COMPLEXED WITH GLY-PRO-ARG-PRO-AMIDE.	BLOOD CLOTTING
2HPE	COMPARISON OF THE STRUCTURES OF HIV-2 PROTEASE COMPLEXES IN THREE CRYSTAL SPACE GROUPS WITH AN HIV-1 PROTEASE COMPLEX STRUCTURE	HYDROLASE(ACID PROTEASE)
2HPF	COMPARISON OF THE STRUCTURES OF HIV-2 PROTEASE COMPLEXES IN THREE CRYSTAL SPACE GROUPS WITH AN HIV-1 PROTEASE COMPLEX STRUCTURE	HYDROLASE(ACID PROTEASE)
2HPL	CRYSTAL STRUCTURE OF THE MOUSE P97/PNGASE COMPLEX	HYDROLASE
2HPP	TRUCTURES OF THE NONCOVALENT COMPLEXES OF HUMAN AND BOVINE PROTHROMBIN FRAGMENT 2 WITH HUMAN PPACK-THROMBIN	HYDROLASE(SERINE PROTEINASE)
2HPQ	TRUCTURES OF THE NONCOVALENT COMPLEXES OF HUMAN AND BOVINE PROTHROMBIN FRAGMENT 2 WITH HUMAN PPACK-THROMBIN	HYDROLASE(SERINE PROTEINASE)
2HPZ	CRYSTAL STRUCTURE OF PROTEINASE K COMPLEX WITH A SYNTHETIC PEPTIDE KLKLLVVIRLK AT 1.69 A RESOLUTION	HYDROLASE
2HQS	CRYSTAL STRUCTURE OF TOLB/PAL COMPLEX	TRANSPORT PROTEIN/LIPOPROTEIN
2HQW	RYSTAL STRUCTURE OF CA2+/CALMODULIN BOUND TO NMDA RECEPTOR NR1C1 PEPTIDE	METAL BINDING PROTEIN
2HR0	STRUCTURE OF COMPLEMENT C3B: INSIGHTS INTO COMPLEMENT ACTIVATION AND REGULATION	IMMUNE SYSTEM
2HRK	TRUCTURAL BASIS OF YEAST AMINOACYL-TRNA SYNTHETASE COMPLEX FORMATION REVEALED BY CRYSTAL STRUCTURES OF TWO BINARY SUB-COMPLEXES	LIGASE/RNA BINDING PROTEIN
2HRP	ANTIGEN-ANTIBODY COMPLEX	COMPLEX (IMMUNOGLOBULIN/PEPTIDE)
2HSE	STRUCTURE OF D236A E. COLI ASPARTATE TRANSCARBAMOYLASE IN THE PRESENCE OF PHOSPHONOACETAMIDE AND L-ASPARTATE AT 2.60 A RESOLUTION	TRANSFERASE
2HSM	TRUCTURAL BASIS OF YEAST AMINOACYL-TRNA SYNTHETASE COMPLEX FORMATION REVEALED BY CRYSTAL STRUCTURES OF TWO BINARY SUB-COMPLEXES	LIGASE/RNA BINDING PROTEIN
2HSN	TRUCTURAL BASIS OF YEAST AMINOACYL-TRNA SYNTHETASE COMPLEX FORMATION REVEALED BY CRYSTAL STRUCTURES OF TWO BINARY SUB-COMPLEXES	LIGASE/RNA BINDING PROTEIN
2HSQ	HUMAN VINCULIN (HEAD DOMAIN, VH1, RESIDUES 1-258) IN COMPLEX WITH SHIGELLA'S IPAA VINCULIN BINDING SITE 2 (RESIDUES 565-587)	CELL ADHESION, STRUCTURAL PROTEIN
2HT0	IHF BOUND TO DOUBLY NICKED DNA	TRANSCRIPTION/DNA
2HT2	STRUCTURE OF THE ESCHERICHIA COLI CLC CHLORIDE CHANNEL	MEMBRANE PROTEIN

	Y445H MUTANT AND FAB COMPLEX	
2HT3	STRUCTURE OF THE ESCHERICHIA COLI CLC CHLORIDE CHANNEL Y445L MUTANT AND FAB COMPLEX	MEMBRANE PROTEIN
2HT4	STRUCTURE OF THE ESCHERICHIA COLI CLC CHLORIDE CHANNEL Y445W MUTANT AND FAB COMPLEX	MEMBRANE PROTEIN
2HT9	THE STRUCTURE OF DIMERIC HUMAN GLUTAREDOXIN 2	OXIDOREDUCTASE
2HTH	STRUCTURAL BASIS FOR UBIQUITIN RECOGNITION BY THE HUMAN EAP45/ESCRT-II GLUE DOMAIN	PROTEIN TRANSPORT
2HTK	STRUCTURE OF THE ESCHERICHIA COLI CLC CHLORIDE CHANNEL Y445A MUTANT AND FAB COMPLEX	MEMBRANE PROTEIN
2HTL	STRUCTURE OF THE ESCHERICHIA COLI CLC CHLORIDE CHANNEL Y445F MUTANT AND FAB COMPLEX	MEMBRANE PROTEIN
2HTM	RYSTAL STRUCTURE OF TTHA0676 FROM THERMUS THERMOPHILUS HB8	BIOSYNTHETIC PROTEIN
2HU2	CTBP/BARS IN TERNARY COMPLEX WITH NAD(H) AND RRTGAPPAL PEPTIDE	OXIDOREDUCTASE
2HUE	STRUCTURE OF THE H3-H4 CHAPERONE ASF1 BOUND TO HISTONES H3 AND H4	DNA BINDING PROTEIN
2HV8	CRYSTAL STRUCTURE OF GTP-BOUND RAB11 IN COMPLEX WITH FIP3	PROTEIN TRANSPORT
2HVY	CRYSTAL STRUCTURE OF AN H/ACA BOX RNP FROM PYROCOCCUS FURIOSUS	ISOMERASE/BIOSYNTHETIC PROTEIN/RNA
2HWL	CRYSTAL STRUCTURE OF THROMBIN IN COMPLEX WITH FIBRINOGEN GAMMA' PEPTIDE	HYDROLASE
2HWN	CRYSTAL STRUCTURE OF RII ALPHA DIMERIZATION/DOCKING DOMAIN OF PKA BOUND TO THE D-AKAP2 PEPTIDE	TRANSFERASE
2HWZ	FAB FRAGMENT OF HUMANIZED ANTI-VIRAL ANTIBODY MEDI-493 (SYNAGIS TM)	IMMUNE SYSTEM
2HXF	KIF1A HEAD-MICROTUBULE COMPLEX STRUCTURE IN AMPPNP-FORM	TRANSPORT PROTEIN
2HXH	KIF1A HEAD-MICROTUBULE COMPLEX STRUCTURE IN ADP-FORM	TRANSPORT PROTEIN
2HY5	CRYSTAL STRUCTURE OF DSREFH	TRANSFERASE
2HYB	CRYSTAL STRUCTURE OF HEXAMERIC DSREFH	TRANSFERASE
2HYE	CRYSTAL STRUCTURE OF THE DDB1-CUL4A-RBX1-SV5V COMPLEX	PROTEIN BINDING
2HYI	TRUCTURE OF THE HUMAN EXON JUNCTION COMPLEX WITH A TRAPPED DEAD-BOX HELICASE BOUND TO RNA	HYDROLASE/RNA BINDING PROTEIN/RNA
2HZE	CRYSTAL STRUCTURES OF A POXVIRAL GLUTAREDOXIN IN THE	ELECTRON TRANSPORT, OXIDOREDUCTASE

	OXIDIZED AND REDUCED STATES SHOW REDOX-CORRELATED STRUCTURAL CHANGES	
2HZM	STRUCTURE OF THE MEDIATOR HEAD SUBCOMPLEX MED18/20	TRANSCRIPTION
2HZS	STRUCTURE OF THE MEDIATOR HEAD SUBMODULE MED8C/18/20	TRANSCRIPTION
2I04	X-RAY CRYSTAL STRUCTURE OF MAGI-1 PDZ1 BOUND TO THE C-TERMINAL PEPTIDE OF HPV18 E6	PEPTIDE BINDING PROTEIN
2I07	HUMAN COMPLEMENT COMPONENT C3B	IMMUNE SYSTEM
2I0I	X-RAY CRYSTAL STRUCTURE OF SAP97 PDZ3 BOUND TO THE C-TERMINAL PEPTIDE OF HPV18 E6	PEPTIDE BINDING PROTEIN
2I0L	X-RAY CRYSTAL STRUCTURE OF SAP97 PDZ2 BOUND TO THE C-TERMINAL PEPTIDE OF HPV18 E6.	PEPTIDE BINDING PROTEIN
2I0Q	CRYSTAL STRUCTURE OF A TELOMERE SINGLE-STRAND DNA-PROTEIN COMPLEX FROM O. NOVA WITH FULL-LENGTH ALPHA AND BETA TELOMERE PROTEINS	STRUCTURAL PROTEIN/DNA
2I0R	CRYSTAL STRUCTURE OF AROMATIC AMINE DEHYDROGENASE TTQ-FORMAMIDE ADDUCT	OXIDOREDUCTASE
2I0S	CRYSTAL STRUCTURE OF AROMATIC AMINE DEHYDROGENASE TTQ-PHENYLACETALDEHYDE ADDUCT	OXIDOREDUCTASE
2I0T	CRYSTAL STRUCTURE OF PHENYLACETALDEHYDE DERIVED R-CARBINOLAMINE ADDUCT OF AROMATIC AMINE DEHYDROGENASE	OXIDOREDUCTASE
2I25	CRYSTAL STRUCTURE ANALYSIS OF THE NURSE SHARK NEW ANTIGEN RECEPTOR PBLA8 VARIABLE DOMAIN IN COMPLEX WITH LYSOZYME	IMMUNE SYSTEM
2I26	CRYSTAL STRUCTURE ANALYSIS OF THE NURSE SHARK NEW ANTIGEN RECEPTOR ANCESTRAL VARIABLE DOMAIN IN COMPLEX WITH LYSOZYME	IMMUNE SYSTEM
2I2P	CRYSTAL STRUCTURE OF RIBOSOME WITH MESSENGER RNA AND THE ANTICODON STEM-LOOP OF P-SITE TRNA. THIS FILE CONTAINS THE 30S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2I2R	CRYSTAL STRUCTURE OF THE KCHIP1/KV4.3 T1 COMPLEX	TRANSPORT PROTEIN
2I2T	CRYSTAL STRUCTURE OF RIBOSOME WITH MESSENGER RNA AND THE ANTICODON STEM-LOOP OF P-SITE TRNA. THIS FILE CONTAINS THE 50S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2I2U	CRYSTAL STRUCTURE OF RIBOSOME WITH MESSENGER RNA AND THE ANTICODON STEM-LOOP OF P-SITE TRNA. THIS FILE CONTAINS THE 30S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN	RIBOSOME

	REMARK 400.	
2I2V	CRYSTAL STRUCTURE OF RIBOSOME WITH MESSENGER RNA AND THE ANTICODON STEM-LOOP OF P-SITE TRNA. THIS FILE CONTAINS THE 50S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2I2X	RYSTAL STRUCTURE OF METHANOL:COBALAMIN METHYLTRANSFERASE COMPLEX MTABC FROM METHANOSARCINA BARKERI	TRANSFERASE
2I3H	STRUCTURE OF AN ML-IAP/XIAP CHIMERA BOUND TO A 4-MER PEPTIDE (AVPW)	INHIBITOR/APOPTOSIS
2I3S	BUB3 COMPLEX WITH BUB1 GLEBS MOTIF	CELL CYCLE
2I3T	BUB3 COMPLEX WITH MAD3 (BUBR1) GLEBS MOTIF	CELL CYCLE
2I40	CDK2/CYCLIN A COMPLEXED WITH A THIOPHENE CARBOXAMIDE INHIBITOR	TRANSFERASE/CELL CYCLE
2I5J	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE (RT) IN COMPLEX WITH DHBNH, AN RNASE H INHIBITOR	TRANSFERASE
2I5N	1.96 A X-RAY STRUCTURE OF PHOTOSYNTHETIC REACTION CENTER FROM RHODOPSEUDOMONAS VIRIDIS:CRYSTALS GROWN BY MICROFLUIDIC TECHNIQUE	PHOTOSYNTHESIS
2I5Y	CRYSTAL STRUCTURE OF CD4M47, A SCORPION-TOXIN MIMIC OF CD4, IN COMPLEX WITH HIV-1 YU2 GP120 ENVELOPE GLYCOPROTEIN AND ANTI-HIV-1 ANTIBODY 17B	VIRUS/VIRAL PROTEIN/IMMUNE SYSTEM
2I60	CRYSTAL STRUCTURE OF [PHE23]M47, A SCORPION-TOXIN MIMIC OF CD4, IN COMPLEX WITH HIV-1 YU2 GP120 ENVELOPE GLYCOPROTEIN AND ANTI-HIV-1 ANTIBODY 17B	VIRUS/VIRAL PROTEIN/IMMUNE SYSTEM
2I6O	RYSTAL STRUCTURE OF THE COMPLEX OF THE ARCHAEAL SULFOLOBUS PTP-FOLD PHOSPHATASE WITH PHOSPHOPEPTIDES N-G-(P)Y-K-N	HYDROLASE
2I9B	CRYSTAL STRUCTURE OF ATF-UROKINASE RECEPTOR COMPLEX	HYDROLASE
2I9L	STRUCTURE OF FAB 7D11 FROM A NEUTRALIZING ANTIBODY AGAINST THE POXVIRUS L1 PROTEIN	IMMUNE SYSTEM/VIRAL PROTEIN
2IAA	RYSTAL STRUCTURE OF AN ELECTRON TRANSFER COMPLEX BETWEEN AROMATIC AMINE DEPHYDROGENASE AND AZURIN FROM ALCALIGENES FAECALIS (FORM 2)	OXIDOREDUCTASE/ELECTRON TRANSPORT
2IAD	CLASS II MHC I-AD IN COMPLEX WITH AN INFLUENZA HEMAGGLUTININ PEPTIDE 126-138	MHC II
2IAE	CRYSTAL STRUCTURE OF A PROTEIN PHOSPHATASE 2A (PP2A) HOLOENZYME.	HYDROLASE
2IAJ	CRYSTAL STRUCTURE OF K103N/Y181C MUTANT HIV-1 REVERSE	TRANSFERASE

	TRANSCRIPTASE (RT) IN COMPLEX WITH ATP	
2IAL	STRUCTURAL BASIS FOR RECOGNITION OF MUTANT SELF BY A TUMOR-SPECIFIC, MHC CLASS II-RESTRICTED TCR	IMMUNE SYSTEM
2IAM	STRUCTURAL BASIS FOR RECOGNITION OF MUTANT SELF BY A TUMOR-SPECIFIC, MHC CLASS II-RESTRICTED TCR	IMMUNE SYSTEM
2IAN	STRUCTURAL BASIS FOR RECOGNITION OF MUTANT SELF BY A TUMOR-SPECIFIC, MHC CLASS II-RESTRICTED TCR	IMMUNE SYSTEM
2IBF	HUMAN VINCULIN'S HEAD DOMAIN (VH1, RESIDUES 1-258) IN COMPLEX WITH TWO VINCULIN BINDING SITES OF SHIGELLA FLEXNERI'S IPAA (RESIDUES 565-587)	CELL ADHESION, STRUCTURAL PROTEIN
2IBG	CRYSTAL STRUCTURE OF HEDGEHOG BOUND TO THE FNIII DOMAINS OF IHOG	PROTEIN BINDING
2IBI	COVALENT UBIQUITIN-USP2 COMPLEX	HYDROLASE
2IBX	INFLUENZA VIRUS (VN1194) H5 HA	VIRUS/VIRAL PROTEIN
2IBZ	YEAST CYTOCHROME BC1 COMPLEX WITH STIGMATELLIN	OXIDOREDUCTASE
2IC3	CRYSTAL STRUCTURE OF K103N/Y181C MUTANT HIV-1 REVERSE TRANSCRIPTASE (RT) IN COMPLEX WITH NONNUCLEOSIDE INHIBITOR HBY 097	TRANSFERASE
2ICE	CRIG BOUND TO C3C	IMMUNE SYSTEM
2ICF	CRIG BOUND TO C3B	IMMUNE SYSTEM
2ICW	RYSTAL STRUCTURE OF A COMPLETE TERNARY COMPLEX BETWEEN TCR, SUPERANTIGEN, AND PEPTIDE-MHC CLASS II MOLECULE	IMMUNE SYSTEM
2ID4	THE 1.9 A STRUCTURE OF KEX2 IN COMPLEX WITH AN AC-R-E-R-K-CHLOROMETHYL KETONE INHIBITOR.	HYDROLASE
2IDO	STRUCTURE OF THE E. COLI POL III EPSILON-HOT PROOFREADING COMPLEX	TRANSFERASE
2IE3	STRUCTURE OF THE PROTEIN PHOSPHATASE 2A CORE ENZYME BOUND TO TUMOR-INDUCING TOXINS	SIGNALING PROTEIN,HYDROLASE
2IE4	STRUCTURE OF THE PROTEIN PHOSPHATASE 2A CORE ENZYME BOUND TO OKADAIC ACID	SIGNALING PROTEIN,HYDROLASE
2IEJ	HUMAN PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH INHIBITOR COMPOUND STN-48 AND FPP ANALOG AT 1.8A RESOLUTION	TRANSFERASE
2IFF	STRUCTURE OF AN ANTIBODY-LYSOZYME COMPLEX: EFFECT OF A CONSERVATIVE MUTATION	IMMUNOGLOBULIN/HYDROLASE(O-GLYCOSYL)
2IFG	STRUCTURE OF THE EXTRACELLULAR SEGMENT OF HUMAN TRKA IN COMPLEX WITH NERVE GROWTH FACTOR	TRANSFERASE

2IFQ	CRYSTAL STRUCTURE OF S-NITROSO THIOREDOXIN	OXIDOREDUCTASE
2IGF	CRYSTAL STRUCTURES OF AN ANTIBODY TO A PEPTIDE AND ITS COMPLEX WITH PEPTIDE ANTIGEN AT 2.8 ANGSTROMS	IMMUNOGLOBULIN
2IH1	ION SELECTIVITY IN A SEMI-SYNTHETIC K+ CHANNEL LOCKED IN THE CONDUCTIVE CONFORMATION	MEMBRANE PROTEIN
2IH3	ION SELECTIVITY IN A SEMI-SYNTHETIC K+ CHANNEL LOCKED IN THE CONDUCTIVE CONFORMATION	MEMBRANE PROTEIN
2IHB	CRYSTAL STRUCTURE OF THE HETERODIMERIC COMPLEX OF HUMAN RGS10 AND ACTIVATED GI ALPHA 3	SIGNALING PROTEIN
2IHS	CRYSTAL STRUCTURE OF THE B30.2/SPRY DOMAIN OF GUSTAVUS IN COMPLEX WITH A 20-RESIDUE VASA PEPTIDE	PEPTIDE BINDING PROTEIN
2IJ0	STRUCTURAL BASIS OF T CELL SPECIFICITY AND ACTIVATION BY THE BACTERIAL SUPERANTIGEN TOXIC SHOCK SYNDROME TOXIN-1	PROTEIN BINDING
2IJO	CRYSTAL STRUCTURE OF THE WEST NILE VIRUS NS2B-NS3 PROTEASE COMPLEXED WITH BOVINE PANCREATIC TRYPSIN INHIBITOR	HYDROLASE/HYDROLASE INHIBITOR
2IK8	CRYSTAL STRUCTURE OF THE HETERODIMERIC COMPLEX OF HUMAN RGS16 AND ACTIVATED GI ALPHA 1	SIGNALING PROTEIN
2ILM	FACTOR INHIBITING HIF-1 ALPHA D201A MUTANT IN COMPLEX WITH FE(II), ALPHA-KETOGLUTARATE AND HIF-1 ALPHA 35MER	TRANSCRIPTION REGULATOR, OXIDOREDUCTASE
2ILN	CRYSTAL STRUCTURE OF THE BOWMAN-BIRK INHIBITOR FROM SNAIL MEDIC SEEDS IN COMPLEX WITH BOVINE TRYPSIN	HYDROLASE/HYDROLASE INHIBITOR
2INC	NATIVE TOLUENE/O-XYLENE MONOOXYGENASE HYDROXYLASE X-RAY CRYSTAL STRUCTURE	OXIDOREDUCTASE
2IND	MN(II) RECONSTITUTED TOLUENE/O-XYLENE MONOOXYGENASE HYDROXYLASE X-RAY CRYSTAL STRUCTURE	OXIDOREDUCTASE
2INN	STRUCTURE OF THE PHENOL HYDROXYALSE-REGULATORY PROTEIN COMPLEX	OXIDOREDUCTASE
2INP	STRUCTURE OF THE PHENOL HYDROXYLASE-REGULATORY PROTEIN COMPLEX	OXIDOREDUCTASE
2INS	THE STRUCTURE OF DES-PHE B1 BOVINE INSULIN	HORMONE
2IO0	CRYSTAL STRUCTURE OF HUMAN SENP2 IN COMPLEX WITH PRESUMO-2	PROTEIN BINDING, HYDROLASE
2IO1	CRYSTAL STRUCTURE OF HUMAN SENP2 IN COMPLEX WITH PRESUMO-3	PROTEIN BINDING, HYDROLASE
2IO2	CRYSTAL STRUCTURE OF HUMAN SENP2 IN COMPLEX WITH RANGAP1-SUMO-1	PROTEIN BINDING, HYDROLASE
2IO3	CRYSTAL STRUCTURE OF HUMAN SENP2 IN COMPLEX WITH RANGAP1-	PROTEIN BINDING, HYDROLASE

	SUMO-2	
2IO4	CRYSTAL STRUCTURE OF PCNA12 DIMER FROM SULFOLOBUS SOLFATARICUS.	DNA BINDING PROTEIN
2IO5	CRYSTAL STRUCTURE OF THE CIA- HISTONE H3-H4 COMPLEX	CHAPERONE/STRUCTURAL PROTEIN
2IOF	RYSTAL STRUCTURE OF PHOSPHONOACETALDEHYDE HYDROLASE WITH SODIUM BOROHYDRIDE-REDUCED SUBSTRATE INTERMEDIATE	HYDROLASE
2IOU	MAJOR TROPISM DETERMINANT P1 (MTD-P1) VARIANT COMPLEXED WITH BORDETELLA BROCHISEPTICA VIRULENCE FACTOR PERTACTIN EXTRACELLULAR DOMAIN (PRN-E).	VIRAL PROTEIN/MEMBRANE PROTEIN
2IPK	CRYSTAL STRUCTURE OF THE MHC CLASS II MOLECULE HLA-DR1 IN COMPLEX WITH THE FLUOROGENIC PEPTIDE, ACPKXVKQNTLKLAT (X=3-[5-(DIMETHYLAMINO)-1,3-DIOXO-1,3-DIHYDRO-2H-ISOINDOL-2-YL]-L-ALANINE) AND THE SUPERANTIGEN, SEC3 VARIANT 3B2	IMMUNE SYSTEM
2IPO	E. COLI ASPARTATE TRANSCARBAMOYLASE COMPLEXED WITH N-PHOSPHONACETYL-L-ASPARAGINE	TRANSFERASE
2IPP	CRYSTAL STRUCTURE OF THE TETRAGONAL FORM OF HUMAN LIVER CATHEPSIN B	HYDROLASE
2IPT	PFA1 FAB FRAGMENT	IMMUNE SYSTEM
2IPU	PFA1 FAB FRAGMENT COMPLEXED WITH ABETA 1-8 PEPTIDE	IMMUNE SYSTEM
2IQ6	CRYSTAL STRUCTURE OF THE AMINOPEPTIDASE FROM VIBRIO PROTEOLYTICUS IN COMPLEXATION WITH LEUCYL-LEUCYL-LEUCINE.	HYDROLASE
2IQ9	PFA2 FAB FRAGMENT, TRICLINIC APO FORM	IMMUNE SYSTEM
2IQA	PFA2 FAB FRAGMENT, MONOCLINIC APO FORM	IMMUNE SYSTEM
2ISQ	CRYSTAL STRUCTURE OF O-ACETYLSERINE SULFHYDRYLASE FROM ARABIDOPSIS THALIANA IN COMPLEX WITH C-TERMINAL PEPTIDE FROM ARABIDOPSIS SERINE ACETYLTRANSFERASE	TRANSFERASE
2ISS	TRUCTURE OF THE PLP SYNTHASE HOLOENZYME FROM THERMOTOGA MARITIMA	LYASE, TRANSFERASE
2ITC	POTASSIUM CHANNEL KCSA-FAB COMPLEX IN SODIUM CHLORIDE	MEMBRANE PROTEIN
2ITD	POTASSIUM CHANNEL KCSA-FAB COMPLEX IN BARIUM CHLORIDE	MEMBRANE PROTEIN
2ITK	HUMAN PIN1 BOUND TO D-PEPTIDE	ISOMERASE
2IUC	STRUCTURE OF ALKALINE PHOSPHATASE FROM THE ANTARCTIC BACTERIUM TAB5	HYDROLASE
2IUH	CRYSTAL STRUCTURE OF THE PI3-KINASE P85 N-TERMINAL SH2 DOMAIN IN COMPLEX WITH C-KIT PHOSPHOTYROSYL PEPTIDE	TRANSFERASE

2IUI	CRYSTAL STRUCTURE OF THE PI3-KINASE P85 N-TERMINAL SH2 DOMAIN IN COMPLEX WITH PDGFR PHOSPHOTYROSYL PEPTIDE	TRANSFERASE
2IUP	CRYSTAL STRUCTURE OF DITHIONITE-REDUCED AROMATIC AMINE DEHYDROGENASE (AADH) FROM ALCALIGENES FAECALIS	OXIDOREDUCTASE
2IUQ	CRYSTAL STRUCTURE OF DITHIONITE-REDUCED AROMATIC AMINE DEHYDROGENASE (AADH) FROM ALCALIGENES FAECALIS IN COMPLEX WITH TRYPTAMINE	OXIDOREDUCTASE
2IUR	CRYSTAL STRUCTURE OF N-QUINOL FORM OF AROMATIC AMINE DEHYDROGENASE (AADH) FROM ALCALIGENES FAECALIS, FORM A COCRYSTAL	OXIDOREDUCTASE
2IUV	CRYSTAL STRUCTURE OF N-QUINOL FORM OF AROMATIC AMINE DEHYDROGENASE (AADH) FROM ALCALIGENES FAECALIS, FORM B	OXIDOREDUCTASE
2IV8	BETA APPENDAGE IN COMPLEX WITH B-ARRESTIN PEPTIDE	ENDOCYTOSIS/REGULATOR
2IV9	B2-APPENDAGE FROM AP2 IN COMPLEX WITH EPS15 PEPTIDE	ENDOCYTOSIS/REGULATOR
2IVF	THYLBENZENE DEHYDROGENASE FROM AROMATOLEUM AROMATICUM	OXIDOREDUCTASE
2IVZ	STRUCTURE OF TOLB IN COMPLEX WITH A PEPTIDE OF THE COLICIN E9 T-DOMAIN	PROTEIN TRANSPORT/HYDROLASE COMPLEX
2IW5	STRUCTURAL BASIS FOR COREST-DEPENDENT DEMETHYLATION OF NUCLEOSOMES BY THE HUMAN LSD1 HISTONE DEMETHYLASE	OXIDOREDUCTASE/REPRESSOR COMPLEX
2IW6	STRUCTURE OF HUMAN THR160-PHOSPHO CDK2-CYCLIN A COMPLEXED WITH A BISANILINOPYRIMIDINE INHIBITOR	CELL CYCLE COMPLEX
2IW8	STRUCTURE OF HUMAN THR160-PHOSPHO CDK2-CYCLIN A F82H-L83V-H84D MUTANT WITH AN O6-CYCLOHEXYLMETHYLGUANINE INHIBITOR	CELL CYCLE COMPLEX
2IW9	STRUCTURE OF HUMAN THR160-PHOSPHO CDK2-CYCLIN A COMPLEXED WITH A BISANILINOPYRIMIDINE INHIBITOR	CELL CYCLE COMPLEX
2IWB	MECR1 UNBOUND EXTRACELLULAR ANTIBIOTIC-SENSOR DOMAIN.	ANTIBIOTIC RESISTANCE
2IWG	COMPLEX BETWEEN THE PRYSPRY DOMAIN OF TRIM21 AND IGG FC	IMMUNOGLOBULIN DOMAIN
2IX2	CRYSTAL STRUCTURE OF THE HETEROTRIMERIC PCNA FROM SULFOLOBUS SOLFATARICUS	REPLICATION
2IX7	TRUCTURE OF APO-CALMODULIN BOUND TO UNCONVENTIONAL MYOSIN V	CONTRACTILE PROTEIN/METAL BINDING
2IXP	CRYSTAL STRUCTURE OF THE PP2A PHOSPHATASE ACTIVATOR YPA1 PTPA1 IN COMPLEX WITH MODEL SUBSTRATE	ISOMERASE
2IY0	SENP1 (MUTANT) SUMO1 RANGAP	HYDROLASE/ACTIVATOR COMPLEX
2IY1	SENP1 (MUTANT) FULL LENGTH SUMO1	HYDROLASE/NUCLEAR PROTEIN COMPLEX
2IYB	STRUCTURE OF COMPLEX BETWEEN THE 3RD LIM DOMAIN OF TES AND	METAL-BINDING

	THE EVH1 DOMAIN OF MENA	
2IYD	SENP1 COVALENT COMPLEX WITH SUMO-2	HYDROLASE
2IZ2	CRYSTAL STRUCTURE OF THE LIGAND BINDING DOMAIN OF FUSHI TARAZU FACTOR 1 FROM DROSOPHILA MELANOGASTER	DNA BINDING PROTEIN
2IZO	STRUCTURE OF AN ARCHAEAL PCNA1-PCNA2-FEN1 COMPLEX	HYDROLASE
2IZV	CRYSTAL STRUCTURE OF SOCS-4 IN COMPLEX WITH ELONGIN-B AND ELONGIN-C AT 2.55A RESOLUTION	TRANSCRIPTION
2IZX	MOLECULAR BASIS OF AKAP SPECIFICITY FOR PKA REGULATORY SUBUNITS	KINASE
2J00	STRUCTURE OF THE THERMUS THERMOPHILUS 70S RIBOSOME COMPLEXED WITH MRNA, TRNA AND PAROMOMYCIN (PART 1 OF 4). THIS FILE CONTAINS THE 30S SUBUNIT, MRNA, A-, P- AND E-SITE TRNAS AND PAROMOMYCIN FOR MOLECULE I.	RIBOSOME
2J01	STRUCTURE OF THE THERMUS THERMOPHILUS 70S RIBOSOME COMPLEXED WITH MRNA, TRNA AND PAROMOMYCIN (PART 2 OF 4). THIS FILE CONTAINS THE 50S SUBUNIT FROM MOLECULE I.	RIBOSOME
2J02	STRUCTURE OF THE THERMUS THERMOPHILUS 70S RIBOSOME COMPLEXED WITH MRNA, TRNA AND PAROMOMYCIN (PART 3 OF 4) THIS FILE CONTAINS THE 30S SUBUNIT, MRNA, A-, P- AND E-SITE TRNAS AND PAROMOMYCIN FOR MOLECULE II.	RIBOSOME
2J03	STRUCTURE OF THE THERMUS THERMOPHILUS 70S RIBOSOME COMPLEXED WITH MRNA, TRNA AND PAROMOMYCIN (PART 4 OF 4). THIS FILE CONTAINS THE 50S SUBUNIT FROM MOLECULE II.	RIBOSOME
2J0M	CRYSTAL STRUCTURE A TWO-CHAIN COMPLEX BETWEEN THE FERM AND KINASE DOMAINS OF FOCAL ADHESION KINASE.	TRANSFERASE
2J0Q	THE CRYSTAL STRUCTURE OF THE EXON JUNCTION COMPLEX AT 3.2 A RESOLUTION	HYDROLASE/RNA
2J0S	THE CRYSTAL STRUCTURE OF THE EXON JUNCTION COMPLEX AT 2.2 A RESOLUTION	HYDROLASE/RNA
2J0T	CRYSTAL STRUCTURE OF THE CATALYTIC DOMAIN OF MMP-1 IN COMPLEX WITH THE INHIBITORY DOMAIN OF TIMP-1	HYDROLASE
2J0U	THE CRYSTAL STRUCTURE OF EIF4AIII-BARENTSZ COMPLEX AT 3.0 A RESOLUTION	HYDROLASE
2J1K	CAV-2 FIBRE HEAD IN COMPLEX WITH CAR D1	VIRUS/RECEPTOR COMPLEX
2J28	MODEL OF E. COLI SRP BOUND TO 70S RNCS	PROTEIN/RNA COMPLEX
2J2U	CRYSTAL STRUCTURE OF A HUMAN FACTOR XA INHIBITOR COMPLEX	HYDROLASE
2J2Z	X-RAY STRUCTURE OF THE CHAPERONE PAPD IN COMPLEX WITH THE	CHAPERONE/SURFACE ACTIVE PROTEIN

	PILUS TERMINATOR SUBUNIT PAPH AT 2.3 ANGSTROM RESOLUTION	
2J30	THE ROLE OF LOOP BUNDLE HYDROGEN BONDS IN THE MATURATION AND ACTIVITY OF (PRO)CASPASE-3	HYDROLASE
2J31	THE ROLE OF LOOP BUNDLE HYDROGEN BONDS IN THE MATURATION AND ACTIVITY OF(PRO)CASPASE-3	HYDROLASE
2J32	THE ROLE OF LOOP BUNDLE HYDROGEN BONDS IN THE MATURATION AND ACTIVITY OF(PRO)CASPASE-3	HYDROLASE
2J33	THE ROLE OF LOOP BUNDLE HYDROGEN BONDS IN THE MATURATION AND ACTIVITY OF (PRO)CASPASE-3	HYDROLASE
2J34	CRYSTAL STRUCTURE OF A HUMAN FACTOR XA INHIBITOR COMPLEX	HYDROLASE
2J37	MODEL OF MAMMALIAN SRP BOUND TO 80S RNCS	RIBOSOME
2J38	CRYSTAL STRUCTURE OF A HUMAN FACTOR XA INHIBITOR COMPLEX	HYDROLASE
2J3F	L-FICOLIN COMPLEXED TO N-ACETYL-D-GALACTOSAMINE	LECTIN
2J3R	THE CRYSTAL STRUCTURE OF THE BET3-TRS31 HETERODIMER.	VESICLE TRANSPORT
2J3W	THE CRYSTAL STRUCTURE OF THE BET3-TRS31-SEDLIN COMPLEX.	VESICLE TRANSPORT
2J4I	CRYSTAL STRUCTURE OF A HUMAN FACTOR XA INHIBITOR COMPLEX	HYDROLASE
2J4U	E.COLI OMPC- CAMEL LACTOFERRIN COMPLEX	MEMBRANE PROTEIN/HYDROLASE COMPLEX
2J4W	STRUCTURE OF A PLASMODIUM VIVAX APICAL MEMBRANE ANTIGEN 1-FAB F8.12.19 COMPLEX	IMMUNE SYSTEM
2J55	X-RAY REDUCED PARACCOCUS DENITRIFICANS METHYLAMINE DEHYDROGENASE O-QUINONE IN COMPLEX WITH AMICYANIN.	OXIDOREDUCTASE
2J56	X-RAY REDUCED PARACCOCUS DENITRIFICANS METHYLAMINE DEHYDROGENASE N-SEMIQUINONE IN COMPLEX WITH AMICYANIN.	OXIDOREDUCTASE
2J57	X-RAY REDUCED PARACCOCUS DENITRIFICANS METHYLAMINE DEHYDROGENASE N-QUINOL IN COMPLEX WITH AMICYANIN.	OXIDOREDUCTASE
2J59	CRYSTAL STRUCTURE OF THE ARF1:ARHGAP21-ARFBD COMPLEX	HYDROLASE
2J5G	THE NATIVE STRUCTURE OF A BETA-DIKETONE HYDROLASE FROM THE CYANOBACTERIUM ANABAENA SP. PCC 7120	HYDROLASE
2J5I	RYSTAL STRUCTURE OF HYDROXYCINNAMOYL-COA HYDRATASE-LYASE	LYASE
2J5L	STRUCTURE OF A PLASMODIUM FALCIPARUM APICAL MEMBRANE ANTIGEN 1-FAB F8.12.19 COMPLEX	IMMUNE SYSTEM
2J6E	RYSTAL STRUCTURE OF AN AUTOIMMUNE COMPLEX BETWEEN A HUMAN IGM RHEUMATOID FACTOR AND IGG1 FC REVEALS A NOVEL FC EPITOPE AND EVIDENCE FOR AFFINITY MATURATION	IMMUNE SYSTEM

2J7A	CRYSTAL STRUCTURE OF CYTOCHROME C NITRITE REDUCTASE NRFHA COMPLEX FROM DESULFOVIBRIO VULGARIS	OXIDOREDUCTASE
2J7P	GMPPNP-STABILIZED NG DOMAIN COMPLEX OF THE SRP GTPASES FFH AND FTSY	SIGNAL RECOGNITION
2J7Q	CRYSTAL STRUCTURE OF THE UBIQUITIN-SPECIFIC PROTEASE ENCODED BY MURINE CYTOMEGALOVIRUS TEGUMENT PROTEIN M48 IN COMPLEX WITH A UBQUITIN-BASED SUICIDE SUBSTRATE	HYDROLASE
2J7X	STRUCTURE OF ESTRADIOL-BOUND ESTROGEN RECEPTOR BETA LBD IN COMPLEX WITH LXXLL MOTIF FROM NCOA5	TRANSCRIPTION
2J7Y	STRUCTURE OF 17-EPIESTRIOL-BOUND ESTROGEN RECEPTOR BETA LBD IN COMPLEX WITH LXXLL MOTIF FROM NCOA5	TRANSCRIPTION
2J88	HYALURONIDASE IN COMPLEX WITH A MONOCLONAL IGG FAB FRAGMENT	HYDROLASE
2J8C	X-RAY HIGH RESOLUTION STRUCTURE OF THE PHOTOSYNTHETIC REACTION CENTER FROM RB. SPHAEROIDES AT PH 8 IN THE NEUTRAL STATE	ELECTRON TRANSPORT
2J8D	X-RAY HIGH RESOLUTION STRUCTURE OF THE PHOTOSYNTHETIC REACTION CENTER FROM RB. SPHAEROIDES AT PH 8 IN THE CHARGE-SEPARATED STATE	ELECTRON TRANSPORT
2J8S	DRUG EXPORT PATHWAY OF MULTIDRUG EXPORTER ACRB REVEALED BY DARPIN INHIBITORS	MEMBRANE PROTEIN/COMPLEX
2J8U	LARGE CDR3A LOOP ALTERATION AS A FUNCTION OF MHC MUTATION.	IMMUNE SYSTEM
2J8X	EPSTEIN-BARR VIRUS URACIL-DNA GLYCOSYLASE IN COMPLEX WITH UGI FROM PBS-2	HYDROLASE/INHIBITOR COMPLEX
2J94	CRYSTAL STRUCTURE OF A HUMAN FACTOR XA INHIBITOR COMPLEX	HYDROLASE
2J95	CRYSTAL STRUCTURE OF A HUMAN FACTOR XA INHIBITOR COMPLEX	HYDROLASE
2J98	HUMAN CORONAVIRUS 229E NON STRUCTURAL PROTEIN 9 CYS69ALA MUTANT (NSP9)	RNA-BINDING PROTEIN
2J9A	BLLAP IN COMPLEX WITH MICROGININ FR1	HYDROLASE
2J9D	STRUCTURE OF GLNK1 WITH BOUND EFFECTORS INDICATES REGULATORY MECHANISM FOR AMMONIA UPTAKE	MEMBRANE TRANSPORT
2J9F	HUMAN BRANCHED-CHAIN ALPHA-KETOACID DEHYDROGENASE-DECARBOXYLASE E1B	OXIDOREDUCTASE
2J9J	ATOMIC-RESOLUTION CRYSTAL STRUCTURE OF CHEMICALLY-SYNTHESIZED HIV-1 PROTEASE COMPLEXED WITH INHIBITOR JG-365	HYDROLASE
2J9K	ATOMIC-RESOLUTION CRYSTAL STRUCTURE OF CHEMICALLY-SYNTHESIZED HIV-1 PROTEASE COMPLEXED WITH INHIBITOR MVT-	HYDROLASE

2J9U	2 ANGSTROM X-RAY STRUCTURE OF THE YEAST ESCRT-I VPS28 C-TERMINUS IN COMPLEX WITH THE NZF-N DOMAIN FROM ESCRT-II	PROTEIN TRANSPORT
2JA5	CPD LESION CONTAINING RNA POLYMERASE II ELONGATION COMPLEX A	TRANSFERASE
2JA6	CPD LESION CONTAINING RNA POLYMERASE II ELONGATION COMPLEX B	TRANSFERASE
2JA7	CPD LESION CONTAINING RNA POLYMERASE II ELONGATION COMPLEX C	TRANSFERASE
2JA8	CPD LESION CONTAINING RNA POLYMERASE II ELONGATION COMPLEX D	TRANSFERASE
2JAC	GLUTAREDOXIN GRX1P C30S MUTANT FROM YEAST	GLUTAREDOXIN
2JAM	CRYSTAL STRUCTURE OF HUMAN CALMODULIN-DEPENDENT PROTEIN KINASE I G	TRANSFERASE
2JAZ	CRYSTAL STRUCTURE OF THE MUTANT N560D OF THE NUCLEASE DOMAIN OF COLE7 IN COMPLEX WITH IM7	HYDROLASE/INHIBITOR COMPLEX
2JB0	CRYSTAL STRUCTURE OF THE MUTANT H573A OF THE NUCLEASE DOMAIN OF COLE7 IN COMPLEX WITH IM7	HYDROLASE/INHIBITOR COMPLEX
2JBA	PHOB RESPONSE REGULATOR RECEIVER DOMAIN CONSTITUTIVELY-ACTIVE DOUBLE MUTANT D53A AND Y102C.	TRANSCRIPTION
2JBG	CRYSTAL STRUCTURE OF THE MUTANT N560A OF THE NUCLEASE DOMAIN OF COLE7 IN COMPLEX WITH IM7	HYDROLASE/INHIBITOR COMPLEX
2JBL	PHOTOSYNTHETIC REACTION CENTER FROM BLASTOCHLORIS VIRIDIS	ELECTRON TRANSPORT
2JBU	CRYSTAL STRUCTURE OF HUMAN INSULIN DEGRADING ENZYME COMPLEXED WITH CO-PURIFIED PEPTIDES.	HYDROLASE
2JBY	A VIRAL PROTEIN UNEXPECTEDLY MIMICS THE STRUCTURE AND FUNCTION OF PRO-SURVIVAL BCL-2	APOPTOSIS
2JCC	AH3 RECOGNITION OF MUTANT HLA-A2 W167A	IMMUNE SYSTEM
2JD5	SKY1P BOUND TO NPL3P-DERIVED SUBSTRATE PEPTIDE	TRANSFERASE
2JDI	GROUND STATE STRUCTURE OF F1-ATPASE FROM BOVINE HEART MITOCHONDRIA (BOVINE F1-ATPASE CRYSTALLISED IN THE ABSENCE OF AZIDE)	HYDROLASE
2JDL	STRUCTURE OF C-TERMINAL REGION OF ACIDIC P2 RIBOSOMAL PROTEIN COMPLEXED WITH TRICHOSANTHIN	HYDROLASE
2JDO	STRUCTURE OF PKB-BETA (AKT2) COMPLEXED WITH ISOQUINOLINE-5-SULFONIC ACID (2-(2-(4-CHLOROBENZYLOXY) ETHYLAMINO)ETHYL) AMIDE	TRANSFERASE
2JDQ	C-TERMINAL DOMAIN OF INFLUENZA A VIRUS POLYMERASE PB2 SUBUNIT IN COMPLEX WITH HUMAN IMPORTIN ALPHA5	PROTEIN TRANSPORT

2JDR	STRUCTURE OF PKB-BETA (AKT2) COMPLEXED WITH THE INHIBITOR A-443654	TRANSFERASE
2JDS	TRUCTURE OF CAMP-DEPENDENT PROTEIN KINASE COMPLEXED WITH A-443654	TRANSFERASE
2JDT	STRUCTURE OF PKA-PKB CHIMERA COMPLEXED WITH ISOQUINOLINE-5-SULFONIC ACID (2-(2-(4-CHLOROBENZYLOXY) ETHYLAMINO)ETHYL) AMIDE	TRANSFERASE
2JDV	STRUCTURE OF PKA-PKB CHIMERA COMPLEXED WITH A-443654	TRANSFERASE
2JE4	ATOMIC-RESOLUTION CRYSTAL STRUCTURE OF CHEMICALLY-SYNTHESIZED HIV-1 PROTEASE IN COMPLEX WITH JG-365	HYDROLASE
2JE6	STRUCTURE OF A 9-SUBUNIT ARCHAEAL EXOSOME	HYDROLASE
2JEA	STRUCTURE OF A 9-SUBUNIT ARCHAEAL EXOSOME BOUND TO RNA	HYDROLASE
2JEB	STRUCTURE OF A 9-SUBUNIT ARCHAEAL EXOSOME BOUND TO MN IONS	HYDROLASE
2JEL	JEL42 FAB/HPR COMPLEX	COMPLEX (ANTIBODY/ANTIGEN)
2JES	PORTAL PROTEIN FROM BACTERIOPHAGE SPP1	VIRAL PROTEIN
2JET	CRYSTAL STRUCTURE OF A TRYPSIN-LIKE MUTANT (S189D, A226G) CHYMOTRYPSIN.	HYDROLASE
2JF9	ESTROGEN RECEPTOR ALPHA LBD IN COMPLEX WITH A TAMOXIFEN-SPECIFIC PEPTIDE ANTAGONIST	TRANSCRIPTION
2JFA	ESTROGEN RECEPTOR ALPHA LBD IN COMPLEX WITH AN AFFINITY-SELECTED COREPRESSOR PEPTIDE	TRANSCRIPTION
2JGB	TRUCTURE OF HUMAN EIF4E HOMOLOGOUS PROTEIN 4EHP WITH M7GTP	TRANSLATION
2JGD	E. COLI 2-OXOGLUTARATE DEHYDROGENASE (E1O)	OXIDOREDUCTASE
2JGZ	CRYSTAL STRUCTURE OF PHOSPHO-CDK2 IN COMPLEX WITH CYCLIN B	TRANSFERASE
2JH0	HUMAN THROMBIN HIRUGEN INHIBITOR COMPLEX.	HYDROLASE
2JH5	HUMAN THROMBIN HIRUGEN INHIBITOR COMPLEX.	HYDROLASE
2JH6	HUMAN THROMBIN HIRUGEN INHIBITOR COMPLEX.	HYDROLASE
2JIX	CRYSTAL STRUCTURE OF ABT-007 FAB FRAGMENT WITH THE SOLUBLE DOMAIN OF EPO RECEPTOR	RECEPTOR/IMMUNE SYSTEM
2JIY	PHOTOSYNTHETIC REACTION CENTER MUTANT WITH ALA M149 REPLACED WITH TRP (CHAIN M, AM149W)	PHOTOSYNTHESIS
2JIZ	THE STRUCTURE OF F1-ATPASE INHIBITED BY RESVERATROL.	HYDROLASE

2JJ0	PHOTOSYNTHETIC REACTION CENTER MUTANT WITH ALA M248 REPLACED WITH TRP (CHAIN M, AM248W)	PHOTOSYNTHESIS
2JJ1	THE STRUCTURE OF F1-ATPASE INHIBITED BY PICEATANNOL.	HYDROLASE
2JJ2	THE STRUCTURE OF F1-ATPASE INHIBITED BY QUERCETIN.	HYDROLASE
2JJ4	THE COMPLEX OF PII AND ACETYLGLUTAMATE KINASE FROM SYNECHOCOCCUS ELONGATUS PCC7942	TRANSCRIPTION
2JKG	PLASMODIUM FALCIPARUM PROFILIN	PROTEIN-BINDING
2JKI	COMPLEX OF HSP90 N-TERMINAL AND SGT1 CS DOMAIN	CHAPERONE
2JKR	AP2 CLATHRIN ADAPTOR CORE WITH DILEUCINE PEPTIDE RM(PHOSPHOS)QIKRLLSE	ENDOCYTOSIS
2JKT	AP2 CLATHRIN ADAPTOR CORE WITH CD4 DILEUCINE PEPTIDE RM(PHOSPHOS)EIKRLLSE Q TO E MUTANT	ENDOCYTOSIS
2JL5	INSIGHTS INTO TRANSLATIONAL TERMINATION FROM THE STRUCTURE OF RF2 BOUND TO THE RIBOSOME (PART 1 OF 4). THIS FILE CONTAINS THE 30S SUBUNIT.	RIBOSOME
2JL6	INSIGHTS INTO TRANSLATIONAL TERMINATION FROM THE STRUCTURE OF RF2 BOUND TO THE RIBOSOME (PART 2 OF 4). THIS FILE CONTAINS THE 50S SUBUNIT.	RIBOSOME
2JL7	INSIGHTS INTO TRANSLATIONAL TERMINATION FROM THE STRUCTURE OF RF2 BOUND TO THE RIBOSOME (PART 3 OF 4). THIS FILE CONTAINS THE 30S SUBUNIT.	RIBOSOME
2JL8	INSIGHTS INTO TRANSLATIONAL TERMINATION FROM THE STRUCTURE OF RF2 BOUND TO THE RIBOSOME (PART 4 OF 4). THIS FILE CONTAINS THE 50S SUBUNIT.	RIBOSOME
2JM6	SOLUTION STRUCTURE OF MCL-1 COMPLEXED WITH NOXAB	APOPTOSIS
2JOD	PAC1-RSHORT N-TERMINAL EC DOMAIN PACAP(6-38) COMPLEX	SIGNALING PROTEIN
2JXR	STRUCTURE OF YEAST PROTEINASE A	COMPLEX (HYDROLASE/INHIBITOR)
2JZN	SOLUTION NMR STRUCTURE OF THE PRODUCTIVE COMPLEX BETWEEN IIAMANNOSE AND IIBMANNOSE OF THE MANNOSE TRANSPORTER OF THE E. COLI PHOSPHOTRANSFERASE SYSTEM	TRANSFERASE
2JZO	SOLUTION NMR STRUCTURE OF THE NON-PRODUCTIVE COMPLEX BETWEEN IIAMANNOSE AND IIBMANNOSE OF THE MANNOSE TRANSPORTER OF THE E. COLI PHOSPHOTRANSFERASE SYSTEM	TRANSFERASE
2K7V		HYDROLASE (UREA AMIDO)
2KAU	THE CRYSTAL STRUCTURE OF UREASE FROM KLEBSIELLA AEROGENES AT 2.2 ANGSTROMS RESOLUTION	
		MOTOR PROTEIN
2KIN	KINESIN (MONOMERIC) FROM RATTUS NORVEGICUS	

2MCP	REFINED CRYSTAL STRUCTURE OF THE MC/PC603 FAB-PHOSPHOCHOLINE COMPLEX AT 3.1 ANGSTROMS RESOLUTION	IMMUNOGLOBULIN
2MHA	CRYSTAL STRUCTURE OF THE MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I H-2KB MOLECULE CONTAINING A SINGLE VIRAL PEPTIDE: IMPLICATIONS FOR PEPTIDE BINDING AND T-CELL RECEPTOR RECOGNITION	HISTOCOMPATIBILITY ANTIGEN
2MHB	THE STRUCTURE OF HORSE METHAEMOGLOBIN AT 2.0 ANGSTROMS RESOLUTION	OXYGEN TRANSPORT
2MIN	NITROGENASE MOFE PROTEIN FROM AZOTOBACTER VINELANDII, OXIDIZED STATE	NITROGEN FIXATION
2MIP	CRYSTAL STRUCTURE OF HUMAN IMMUNODEFICIENCY VIRUS (HIV) TYPE 2 PROTEASE IN COMPLEX WITH A REDUCED AMIDE INHIBITOR AND COMPARISON WITH HIV-1 PROTEASE STRUCTURES	HYDROLASE(ACID PROTEINASE)
2MLL	MISTLETOE LECTIN I FROM VISCUM ALBUM	RIBOSOME
2MPA	BACTERICIDAL ANTIBODY AGAINST NEISSERIA MENINGITIDIS	IMMUNE SYSTEM
2NGR	TRANSITION STATE COMPLEX FOR GTP HYDROLYSIS BY CDC42: COMPARISONS OF THE HIGH RESOLUTION STRUCTURES FOR CDC42 BOUND TO THE ACTIVE AND CATALYTICALLY COMPROMISED FORMS OF THE CDC42-GAP.	HYDROLASE
2NL9	CRYSTAL STRUCTURE OF THE MCL-1:BIM BH3 COMPLEX	APOPTOSIS
2NLA	CRYSTAL STRUCTURE OF THE MCL-1:MNOXAB BH3 COMPLEX	APOPTOSIS
2NLJ	POTASSIUM CHANNEL KCSA(M96V)-FAB COMPLEX IN KCL	MEMBRANE PROTEIN
2NM1	STRUCTURE OF BONT/B IN COMPLEX WITH ITS PROTEIN RECEPTOR	TOXIN,HYDROLASE
2NMV	DAMAGE DETECTION BY THE UVRABC PATHWAY: CRYSTAL STRUCTURE OF UVRB BOUND TO FLUORESCEIN-ADDUCTED DNA	HYDROLASE/DNA
2NN6	TRUCTURE OF THE HUMAN RNA EXOSOME COMPOSED OF RRP41, RRP45, RRP46, RRP43, MTR3, RRP42, CSL4, RRP4, AND RRP40	HYDROLASE/TRANSFERASE
2NNA	STRUCTURE OF THE MHC CLASS II MOLECULE HLA-DQ8 BOUND WITH A DEAMIDATED GLUTEN PEPTIDE	IMMUNE SYSTEM
2NNU	CRYSTAL STRUCTURE OF THE PAPILLOMAVIRUS DNA TETHERING COMPLEX E2:BRD4	TRANSCRIPTION
2NNW	ALTERNATIVE CONFORMATIONS OF NOP56/58-FIBRILLARIN COMPLEX AND IMPLICATION FOR INDUCED-FIT ASSENLY OF BOX C/D RNPS	TRANSFERASE
2NO3	NOVEL 4-ANILINOPYRIMIDINES AS POTENT JNK1 INHIBITORS	SIGNALING PROTEIN/INHIBITOR
2NOJ	CRYSTAL STRUCTURE OF EHP / C3D COMPLEX	IMMUNE SYSTEM
		HYDROLASE

2NP0	CRYSTAL STRUCTURE OF THE BOTULINUM NEUROTOXIN TYPE B COMPLEXED WITH SYNAPTOTAGAMIN-II ECTODOMAIN	
2NPA	THE CRYSTAL STRUCTURE OF THE HUMAN PPARAPLPHA LIGAND BINDING DOMAIN IN COMPLEX WITH A A-HYDROXYIMINO PHENYLPROPANOIC ACID	TRANSCRIPTION
2NPH	CRYSTAL STRUCTURE OF HIV1 PROTEASE IN SITU PRODUCT COMPLEX	HYDROLASE
2NPI	CLP1-ATP-PCF11 COMPLEX	TRANSCRIPTION
2NPM	CRYSTAL STRUCTURE OF CRYPTOSPORIDIUM PARVUM 14-3-3 PROTEIN IN COMPLEX WITH PEPTIDE	PROTEIN BINDING
2NPP	STRUCTURE OF THE PROTEIN PHOSPHATASE 2A HOLOENZYME	SIGNALING PROTEIN,HYDROLASE
2NPS	CRYSTAL STRUCTURE OF THE EARLY ENDOSOMAL SNARE COMPLEX	TRANSPORT PROTEIN
2NPT	CRYSTAL STRUCTURE OF THE COMPLEX OF HUMAN MITOGEN ACTIVATED PROTEIN KINASE KINASE 5 PHOX DOMAIN (MAP2K5-PHOX) WITH HUMAN MITOGEN ACTIVATED PROTEIN KINASE KINASE KINASE 2 PHOX DOMAIN (MAP3K2-PHOX)	TRANSFERASE
2NQ8	MALARIAL ENOYL ACYL ACP REDUCTASE BOUND WITH INH-NAD ADDUCT	OXIDOREDUCTASE
2NQA	CATALYTIC DOMAIN OF HUMAN CALPAIN 8	HYDROLASE/HYDROLASE INHIBITOR
2NQB	DROSOPHILA NUCLEOSOME STRUCTURE	STRUCTURAL PROTEIN/DNA
2NQD	CRYSTAL STRUCTURE OF CYSTEINE PROTEASE INHIBITOR, CHAGASIN, IN COMPLEX WITH HUMAN CATHEPSIN L	HYDROLASE INHIBITOR/HYDROLASE
2NQO	CRYSTAL STRUCTURE OF HELICOBACTER PYLORI GAMMA-GLUTAMYLTRANSPEPTIDASE	TRANSFERASE
2NR6	CRYSTAL STRUCTURE OF THE COMPLEX OF ANTIBODY AND THE ALLERGEN BLA G 2	HYDROLASE/IMMUNE SYSTEM
2NS1	CRYSTAL STRUCTURE OF THE E. COLI AMMONIA CHANNEL AMTB COMPLEXED WITH THE SIGNAL TRANSDUCTION PROTEIN GLNK	TRANSPORT PROTEIN/SIGNALING PROTEIN
2NS8	HOW AN IN VITRO SELECTED PEPTIDE MIMICS THE ANTIBIOTIC TETRACYCLINE TO INDUCE TET REPRESSOR	TRANSCRIPTION
2NTF	CRYSTAL STRUCTURE OF A QUORUM-QUENCHING ANTIBODY IN COMPLEX WITH AN N-ACYL-L-HOMOSERINE LACTONE ANALOG	IMMUNE SYSTEM
2NTI	CRYSTAL STRUCTURE OF PCNA123 HETEROTRIMER.	DNA BINDING PROTEIN
2NTS	CRYSTAL STRUCTURE OF SEK-HVB5.1	TOXIN/IMMUNE SYSTEM
2NTY	ROP4-GDP-PRONE8	SIGNALING PROTEIN
2NU0	MOLECULAR STRUCTURES OF THE COMPLEXES OF SGPB WITH OMTKY3 AROMATIC P1 VARIANTS TRP18I, HIS18I, PHE18I, AND TYR18I	HYDROLASE

2NU1	OLECULAR STRUCTURES OF THE COMPLEXES OF SGPB WITH OMTKY3 AROMATIC P1 VARIANTS TRP18I, HIS18I, PHE18I AND TYR18I	HYDROLASE
2NU2	ACCOMMODATION OF POSITIVELY-CHARGED RESIDUES IN A HYDROPHOBIC SPECIFICITY POCKET: CRYSTAL STRUCTURES OF SGPB IN COMPLEX WITH OMTKY3 VARIANTS LYS18I AND ARG18I	HYDROLASE
2NU3	ACCOMMODATION OF POSITIVELY-CHARGED RESIDUES IN A HYDROPHOBIC SPECIFICITY POCKET: CRYSTAL STRUCTURES OF SGPB IN COMPLEX WITH OMTKY3 VARIANTS LYS18I AND ARG18I	HYDROLASE
2NU4	ACCOMMODATION OF POSITIVELY-CHARGED RESIDUES IN A HYDROPHOBIC SPECIFICITY POCKET: CRYSTAL STRUCTURES OF SGPB IN COMPLEX WITH OMTKY3 VARIANTS LYS18I AND ARG18I	HYDROLASE
2NU6	C123AA MUTANT OF E. COLI SUCCINYL-COA SYNTHETASE	LIGASE
2NU7	C123AS MUTANT OF E. COLI SUCCINYL-COA SYNTHETASE	LIGASE
2NU8	C123AT MUTANT OF E. COLI SUCCINYL-COA SYNTHETASE	LIGASE
2NU9	C123AT MUTANT OF E. COLI SUCCINYL-COA SYNTHETASE ORTHORHOMBIC CRYSTAL FORM	LIGASE
2NUA	C123AV MUTANT OF E. COLI SUCCINYL-COA SYNTHETASE	LIGASE
2NUD	THE STRUCTURE OF THE TYPE III EFFECTOR AVRB COMPLEXED WITH A HIGH-AFFINITY RIN4 PEPTIDE	TOXIN/PROTEIN BINDING
2NUP	CRYSTAL STRUCTURE OF THE HUMAN SEC23A/24A HETERODIMER, COMPLEXED WITH THE SNARE PROTEIN SEC22B	PROTEIN TRANSPORT
2NUT	CRYSTAL STRUCTURE OF THE HUMAN SEC23A/24A HETERODIMER, COMPLEXED WITH THE SNARE PROTEIN SEC22B	PROTEIN TRANSPORT
2NUU	REGULATING THE ESCHERICHIA COLI AMMONIA CHANNEL: THE CRYSTAL STRUCTURE OF THE AMTB-GLNK COMPLEX	TRANSPORT PROTEIN/SIGNALING PROTEIN
2NV2	STRUCTURE OF THE PLP SYNTHASE COMPLEX PDX1/2 (YAAD/E) FROM BACILLUS SUBTILIS	LYASE/TRANSFERASE
2NV7	RYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH WAY-555	TRANSCRIPTION
2NVQ	RNA POLYMERASE II ELONGATION COMPLEX IN 150 MM MG+2 WITH 2'DUTP	TRANSCRIPTION/DNA/RNA
2NVT	RNA POLYMERASE II ELONGATION COMPLEX IN 150 MM MG+2 WITH GMPCPP	TRANSCRIPTION/DNA/RNA
2NVU	STRUCTURE OF APPBP1-UBA3~NEDD8-NEDD8-MGATP-UBC12(C111A), A TRAPPED UBIQUITIN-LIKE PROTEIN ACTIVATION COMPLEX	PROTEIN TURNOVER, LIGASE
2NVX	RNA POLYMERASE II ELONGATION COMPLEX IN 5 MM MG+2 WITH 2'-	TRANSCRIPTION/DNA/RNA

	DUTP	
2NVY	RNA POLYMERASE II FORM II IN 150 MM MN+2	TRANSCRIPTION
2NVZ	RNA POLYMERASE II ELONGATION COMPLEX WITH UTP, UPDATED 11/2006	TRANSCRIPTION/DNA/RNA
2NW2	CRYSTAL STRUCTURE OF ELS4 TCR AT 1.4A	IMMUNE SYSTEM
2NW3	CRYSTAL STRUCTURE OF HLA-B*3508 PRESENTING EBV PEPTIDE EPLPQGQLTAY AT 1.7A	IMMUNE SYSTEM
2NWN	NEW PHARMACOPHORE FOR SERINE PROTEASE INHIBITION REVEALED BY CRYSTAL STRUCTURE OF HUMAN UROKINASE-TYPE PLASMINOGEN ACTIVATOR COMPLEXED WITH A CYCLIC PEPTIDYL INHIBITOR, UPAIN-1	HYDROLASE
2NX5	CRYSTAL STRUCTURE OF ELS4 TCR BOUND TO HLA-B*3508 PRESENTING EBV PEPTIDE EPLPQGQLTAY AT 1.7A	IMMUNE SYSTEM
2NXD	STRUCTURE OF HIV-1 PROTEASE D25N COMPLEXED WITH RT-RH ANALOGUE PEPTIDE GLY-ALA-ASP-ILE-PHE*TYR-LEU-ASP-GLY-ALA	HYDROLASE/HYDROLASE SUBSTRATE
2NXL	STRUCTURE OF HIV-1 PROTEASE D25N COMPLEXED WITH THE RT-RH ANALOGUE PEPTIDE GLY-ALA-GLU-VAL-PHE*TYR-VAL-ASP-GLY-ALA	HYDROLASE/HYDROLASE SUBSTRATE
2NXM	STRUCTURE OF HIV-1 PROTEASE D25N COMPLEXED WITH THE RT-RH ANALOGUE PEPTIDE GLY-ALA-GLN-THR-PHE*TYR-VAL-ASP-GLY-ALA	HYDROLASE/HYDROLASE SUBSTRATE
2NXN	T. THERMOPHILUS RIBOSOMAL PROTEIN L11 METHYLTRANSFERASE (PRMA) IN COMPLEX WITH RIBOSOMAL PROTEIN L11	TRANSFERASE
2NXX	CRYSTAL STRUCTURE OF THE LIGAND-BINDING DOMAINS OF THE T.CASTANEUM (COLEOPTERA) HETERODIMER ECRUSP BOUND TO PONASTERONE A	HORMONE/GROWTH FACTOR
2NXY	HIV-1 GP120 ENVELOPE GLYCOPROTEIN(S334A) COMPLEXED WITH CD4 AND ANTIBODY 17B	VIRAL PROTEIN/IMMUNE SYSTEM
2NXZ	HIV-1 GP120 ENVELOPE GLYCOPROTEIN (T257S, S334A, S375W) COMPLEXED WITH CD4 AND ANTIBODY 17B	VIRAL PROTEIN/IMMUNE SYSTEM
2NY0	HIV-1 GP120 ENVELOPE GLYCOPROTEIN (M95W, W96C, T257S, V275C, S334A, S375W, A433M) COMPLEXED WITH CD4 AND ANTIBODY 17B	VIRAL PROTEIN/IMMUNE SYSTEM
2NY1	HIV-1 GP120 ENVELOPE GLYCOPROTEIN (I109C, T257S, S334A, S375W, Q428C) COMPLEXED WITH CD4 AND ANTIBODY 17B	VIRAL PROTEIN/IMMUNE SYSTEM
2NY2	HIV-1 GP120 ENVELOPE GLYCOPROTEIN (T123C, T257S, S334A, S375W, G431C) COMPLEXED WITH CD4 AND ANTIBODY 17B	VIRAL PROTEIN/IMMUNE SYSTEM
2NY3	HIV-1 GP120 ENVELOPE GLYCOPROTEIN (K231C, T257S, E267C, S334A, S375W) COMPLEXED WITH CD4 AND ANTIBODY 17B	VIRAL PROTEIN/IMMUNE SYSTEM
2NY4	HIV-1 GP120 ENVELOPE GLYCOPROTEIN (K231C, T257S, E268C,	VIRAL PROTEIN/IMMUNE SYSTEM

	S334A, S375W) COMPLEXED WITH CD4 AND ANTIBODY 17B	
2NY5	HIV-1 GP120 ENVELOPE GLYCOPROTEIN (M95W, W96C, I109C, T257S, V275C, S334A, S375W, Q428C, A433M) COMPLEXED WITH CD4 AND ANTIBODY 17B	VIRAL PROTEIN/IMMUNE SYSTEM
2NY6	HIV-1 GP120 ENVELOPE GLYCOPROTEIN (M95W, W96C, I109C, T123C, T257S, V275C,S334A, S375W, Q428C, G431C) COMPLEXED WITH CD4 AND ANTIBODY 17B	VIRAL PROTEIN/IMMUNE SYSTEM
2NY7	HIV-1 GP120 ENVELOPE GLYCOPROTEIN COMPLEXED WITH THE BROADLY NEUTRALIZING CD4-BINDING-SITE ANTIBODY B12	VIRAL PROTEIN/IMMUNE SYSTEM
2NYL	CRYSTAL STRUCTURE OF PROTEIN PHOSPHATASE 2A (PP2A) HOLOENZYME WITH THE CATALYTIC SUBUNIT CARBOXYL TERMINUS TRUNCATED	HYDROLASE
2NYM	CRYSTAL STRUCTURE OF PROTEIN PHOSPHATASE 2A (PP2A) WITH C-TERMINUS TRUNCATED CATALYTIC SUBUNIT	HYDROLASE
2NYQ	STRUCTURE OF VIBRIO PROTEOLYTICUS AMINOPEPTIDASE WITH A BOUND TRP FRAGMENT OF DLWCF	HYDROLASE
2NYY	CRYSTAL STRUCTURE OF BOTULINUM NEUROTOXIN TYPE A COMPLEXED WITH MONOCLONAL ANTIBODY CR1	TOXIN/IMMUNE SYSTEM
2NYZ	VIRAL CHEMOKINE BINDING PROTEIN M3 FROM MURINE GAMMAHERPESVIRUS68 IN COMPLEX WITH THE C- CHEMOKINE XCL1	VIRAL PROTEIN/CYTOKINE
2NZ0	CRYSTAL STRUCTURE OF POTASSIUM CHANNEL KV4.3 IN COMPLEX WITH ITS REGULATORY SUBUNIT KCHIP1 (CASP TARGET)	MEMBRANE PROTEIN
2NZ1	VIRAL CHEMOKINE BINDING PROTEIN M3 FROM MURINE GAMMAHERPESVIRUS68 IN COMPLEX WITH THE CC-CHEMOKINE CCL2/MCP-1	VIRAL PROTEIN/CYTOKINE
2NZ8	N-TERMINAL DHPH CASSETTE OF TRIO IN COMPLEX WITH NUCLEOTIDE-FREE RAC1	SIGNALING PROTEIN,CELL CYCLE
2NZ9	CRYSTAL STRUCTURE OF BOTULINUM NEUROTOXIN TYPE A COMPLEXED WITH MONOCLONAL ANTIBODY AR2	TOXIN/IMMUNE SYSTEM
2NZD	NUCLEOSOME CORE PARTICLE CONTAINING 145 BP OF DNA	STRUCTURAL PROTEIN/DNA
2NZU	STRUCTURAL MECHANISM FOR THE FINE-TUNING OF CCPA FUNCTION BY THE SMALL MOLECULE EFFECTORS G6P AND FBP	TRANSCRIPTION
2NZV	STRUCTURAL MECHANISM FOR THE FINE-TUNING OF CCPA FUNCTION BY THE SMALL MOLECULE EFFECTORS G6P AND FBP	TRANSCRIPTION
2O01	THE STRUCTURE OF A PLANT PHOTOSYSTEM I SUPERCOMPLEX AT 3.4 ANGSTROM RESOLUTION	PHOTOSYNTHESIS
2O02	PHOSPHORYLATION INDEPENDENT INTERACTIONS BETWEEN 14-3-3 AND EXOENZYME S: FROM STRUCTURE TO PATHOGENESIS	PROTEIN BINDING/TOXIN

2O1N	CRYSTAL STRUCTURE OF A COMPLEX OF PHOSPHOLIPASE A2 WITH A PEPTIDE ALA-ILE-ALA-SER AT 2.8 A RESOLUTION	HYDROLASE
2O1R	STRUCTURAL GENOMICS, THE CRYSTAL STRUCTURE OF A CONSERVED PUTATIVE PROTEIN FROM HAEMOPHILUS INFLUENZAE RD KW20	MEMBRANE PROTEIN
2O25	UBIQUITIN-CONJUGATING ENZYME E2-25 KDA COMPLEXED WITH SUMO-1-CONJUGATING ENZYME UBC9	LIGASE
2O26	STRUCTURE OF A CLASS III RTK SIGNALING ASSEMBLY	CYTOKINE/SIGNALING PROTEIN
2O2V	CRYSTAL STRUCTURE OF THE COMPLEX OF HUMAN MITOGEN ACTIVATED PROTEIN KINASE KINASE 5 PHOX DOMAIN (MAP2K5-PHOX) WITH HUMAN MITOGEN ACTIVATED PROTEIN KINASE KINASE KINASE 3 (MAP3K3B-PHOX)	TRANSFERASE
2O3B	CRYSTAL STRUCTURE COMPLEX OF NUCLEASE A (NUCA) WITH INTRA-CELLULAR INHIBITOR NUIA	HYDROLASE/HYDROLASE INHIBITOR
2O4J	CRYSTAL STRUCTURE OF RAT VITAMIN D RECEPTOR LIGAND BINDING DOMAIN COMPLEXED WITH VITIII 17-20Z AND THE NR2 BOX OF DRIP 205	HORMONE/GROWTH FACTOR RECEPTOR
2O4R	CRYSTAL STRUCTURE OF RAT VITAMIN D RECEPTOR LIGAND BINDING DOMAIN COMPLEXED WITH VITIII 17-20E AND THE NR2 BOX OF DRIP 205	HORMONE/GROWTH FACTOR RECEPTOR
2O4X	CRYSTAL STRUCTURE OF HUMAN P100 TUDOR DOMAIN	HYDROLASE
2O5G	CALMODULIN-SMOOTH MUSCLE LIGHT CHAIN KINASE PEPTIDE COMPLEX	METAL BINDING PROTEIN
2O5I	CRYSTAL STRUCTURE OF THE T. THERMOPHILUS RNA POLYMERASE ELONGATION COMPLEX	TRANSFERASE/DNA/RNA
2O5J	CRYSTAL STRUCTURE OF THE T. THERMOPHILUS RNAP POLYMERASE ELONGATION COMPLEX WITH THE NTP SUBSTRATE ANALOG	TRANSFERASE/DNA/RNA
2O5X	CRYSTAL STRUCTURE OF 1E9 LEUH47TRP/ARGH100TRP, AN ENGINEERED DIELS-ALDERASE FAB WITH NM STEROID-BINDING AFFINITY	IMMUNE SYSTEM
2O5Y	CRYSTAL STRUCTURE OF THE 1E9 LEUH47TRP/ARGH100TRP FAB PROGESTERONE COMPLEX	IMMUNE SYSTEM
2O5Z	CRYSTAL STRUCTURE OF THE 1E9 LEUH47TRP/ARGH100TRP FAB 5-BETA-ANDROSTANE-3,17-DIONE COMPLEX	IMMUNE SYSTEM
2O60	CALMODULIN BOUND TO PEPTIDE FROM NEURONAL NITRIC OXIDE SYNTHASE	METAL BINDING PROTEIN
2O6V	CRYSTAL STRUCTURE AND SOLUTION NMR STUDIES OF LYS48-LINKED TETRAUBIQUITIN AT NEUTRAL PH	SIGNALING PROTEIN
2O8A	RAT PP1CGAMMA COMPLEXED WITH MOUSE INHIBITOR-2	HYDROLASE/INHIBITOR

2O8B	HUMAN MUTSALPHA (MSH2/MSH6) BOUND TO ADP AND A G T MISPAIR	DNA BINDING PROTEIN/DNA
2O8C	HUMAN MUTSALPHA (MSH2/MSH6) BOUND TO ADP AND AN O6-METHYL-GUANINE T MISPAIR	DNA BINDING PROTEIN/DNA
2O8D	HUMAN MUTSALPHA (MSH2/MSH6) BOUND TO ADP AND A G DU MISPAIR	DNA BINDING PROTEIN/DNA
2O8E	HUMAN MUTSALPHA (MSH2/MSH6) BOUND TO A G T MISPAIR, WITH ADP BOUND TO MSH2 ONLY	DNA BINDING PROTEIN/DNA
2O8F	HUMAN MUTSALPHA (MSH2/MSH6) BOUND TO DNA WITH A SINGLE BASE T INSERT	DNA BINDING PROTEIN/DNA
2O8G	RAT PP1C GAMMA COMPLEXED WITH MOUSE INHIBITOR-2	HYDROLASE/INHIBITOR
2O8M	CRYSTAL STRUCTURE OF THE S139A MUTANT OF HEPATITIS C VIRUS NS3/4A PROTEASE	VIRAL PROTEIN
2O8V	PAPS REDUCTASE IN A COVALENT COMPLEX WITH THIOREDOXIN C35A	OXIDOREDUCTASE
2O97	CRYSTAL STRUCTURE OF E. COLI HU HETERODIMER	DNA BINDING PROTEIN
2O98	STRUCTURE OF THE 14-3-3 / H+-ATPASE PLANT COMPLEX	PROTEIN BINDING
2O9I	CRYSTAL STRUCTURE OF THE HUMAN PREGNANE X RECEPTOR LBD IN COMPLEX WITH AN SRC-1 COACTIVATOR PEPTIDE AND T0901317	TRANSCRIPTION
2OBH	CENTRIN-XPC PEPTIDE	CELL CYCLE
2OBO	DISCOVERY OF THE HCV NS3/4A PROTEASE INHIBITOR SCH503034. KEY STEPS IN STRUCTURE-BASED OPTIMIZATION	VIRAL PROTEIN
2OBQ	DISCOVERY OF THE HCV NS3/4A PROTEASE INHIBITOR SCH503034. KEY STEPS IN STRUCTURE-BASED OPTIMIZATION	VIRAL PROTEIN
2OC0	STRUCTURE OF NS3 COMPLEXED WITH A KETOAMIDE INHIBITOR SCH491762	VIRAL PROTEIN
2OC1	STRUCTURE OF THE HCV NS3/4A PROTEASE INHIBITOR CVS4819	VIRAL PROTEIN
2OC7	STRUCTURE OF HEPATITIS C VIRAL NS3 PROTEASE DOMAIN COMPLEXED WITH NS4A PEPTIDE AND KETOAMIDE SCH571696	VIRAL PROTEIN
2OC8	STRUCTURE OF HEPATITIS C VIRAL NS3 PROTEASE DOMAIN COMPLEXED WITH NS4A PEPTIDE AND KETOAMIDE SCH503034	VIRAL PROTEIN
2OCC	BOVINE HEART CYTOCHROME C OXIDASE AT THE FULLY OXIDIZED STATE	OXIDOREDUCTASE
2OCF	HUMAN ESTROGEN RECEPTOR ALPHA LIGAND-BINDING DOMAIN IN COMPLEX WITH ESTRADIOL AND THE E2#23 FN3 MONOBODY	HORMONE/GROWTH FACTOR
2OCV	STRUCTURAL BASIS OF NA+ ACTIVATION MIMICRY IN MURINE THROMBIN	HYDROLASE

2OCY	COMPLEX OF THE GUANINE EXCHANGE FACTOR SEC2P AND THE RAB GTPASE SEC4P	ENDOCYTOSIS/EXOCYTOSIS
2OD2	CRYSTAL STRUCTURE OF YHST2 I117F MUTANT BOUND TO CARBA-NAD+ AND AN ACETYLATED H4 PEPTIDE	HYDROLASE
2OD3	HUMAN THROMBIN CHIMERA WITH HUMAN RESIDUES 184A, 186, 186A, 186B, 186C AND 222 REPLACED BY MURINE THROMBIN EQUIVALENTS.	HYDROLASE
2OD7	CRYSTAL STRUCTURE OF YHST2 BOUND TO THE INTERMEDIATE ANALOGUE ADP-HPD, AND AND ACEYLATED H4 PEPTIDE	HYDROLASE
2OD8	STRUCTURE OF A PEPTIDE DERIVED FROM CDC9 BOUND TO PCNA	PROTEIN BINDING
2OD9	STRUCTURAL BASIS FOR NICOTINAMIDE INHIBITION AND BASE EXCHANGE IN SIR2 ENZYMES	HYDROLASE
2ODB	THE CRYSTAL STRUCTURE OF HUMAN CDC42 IN COMPLEX WITH THE CRIB DOMAIN OF HUMAN P21-ACTIVATED KINASE 6 (PAK6)	PROTEIN BINDING
2ODE	CRYSTAL STRUCTURE OF THE HETERODIMERIC COMPLEX OF HUMAN RGS8 AND ACTIVATED GI ALPHA 3	SIGNALING PROTEIN
2ODG	COMPLEX OF BARRIER-TO-AUTOINTEGRATION FACTOR AND LEM-DOMAIN OF EMERIN	MEMBRANE PROTEIN, PROTEIN BINDING
2ODY	THROMBIN-BOUND BOOPHILIN DISPLAYS A FUNCTIONAL AND ACCESSIBLE REACTIVE-SITE LOOP	BLOOD CLOTTING/BLOOD CLOTTING INHIBITOR
2OEN	STRUCTURAL MECHANISM FOR THE FINE-TUNING OF CCPA FUNCTION BY THE SMALL MOLECULE EFFECTORS GLUCOSE-6-PHOSPHATE AND FRUCTOSE-1,6-BISPHOSPHATE	TRANSCRIPTION
2OF5	OLIGOMERIC DEATH DOMAIN COMPLEX	APOPTOSIS
2OGX	THE CRYSTAL STRUCTURE OF THE MOLYBDENUM STORAGE PROTEIN FROM AZOTOBACTER VINELANDII LOADED WITH POLYOXOTUNGSTATES (WSTO)	METAL BINDING PROTEIN
2OH0	CRYSTAL STRUCTURE OF PROTEIN KINASE A IN COMPLEX WITH PYRIDINE-PYRAZOLOPYRIDINE BASED INHIBITORS	TRANSFERASE
2OI9	STRUCTURE OF THE 2C/LD/QL9 ALLOGENEIC COMPLEX	IMMUNE SYSTEM
2OIN	CRYSTAL STRUCTURE OF HCV NS3-4A R155K MUNTANT	HYDROLASE
2OIZ	CRYSTAL STRUCTURE OF THE TRYPTAMINE-DERIVED (INDOL-3-ACETAMIDE)-TTQ ADDUCT OF AROMATIC AMINE DEHYDROGENASE	OXIDOREDUCTASE
2OJE	MYCOPLASMA ARTHRITIDIS-DERIVED MITOGEN COMPLEXED WITH CLASS II MHC MOLECULE HLA-DR1/HA COMPLEX IN THE PRESENCE OF EDTA	IMMUNE SYSTEM
2OJF	CRYSTAL STRUCTURE OF PROTEIN KINASE A IN COMPLEX WITH PYRIDINE-PYRAZOLOPYRIDINE BASED INHIBITORS	TRANSFERASE

2OJX	MOLECULAR AND STRUCTURAL BASIS OF POLO-LIKE KINASE 1 SUBSTRATE RECOGNITION: IMPLICATIONS IN CENTROSOMAL LOCALIZATION	TRANSFERASE
2OJY	CRYSTAL STRUCTURE OF INDOL-3-ACETALDEHYDE DERIVED TTQ-AMIDE ADDUCT OF AROMATIC AMINE DEHYDROGENASE	OXIDOREDUCTASE
2OJZ	ANTI-DNA ANTIBODY ED10	IMMUNE SYSTEM
2OK0	FAB ED10-DNA COMPLEX	IMMUNE SYSTEM/DNA
2OK4	CRYSTAL STRUCTURE OF AROMATIC AMINE DEHYDROGENASE TTQ-PHENYLACETALDEHYDE ADDUCT OXIDIZED WITH FERRICYANIDE	OXIDOREDUCTASE
2OK6	CRYSTAL STRUCTURE OF AROMATIC AMINE DEHYDROGENASE TTQ-FORMAMIDE ADDUCT OXIDIZED WITH FERRICYANIDE.	OXIDOREDUCTASE
2OKR	CRYSTAL STRUCTURE OF THE P38A-MAPKAP KINASE 2 HETERODIMER	TRANSFERASE
2OL3	CRYSTAL STRUCTURE OF BM3.3 SCFV TCR IN COMPLEX WITH PBM8-H-2KBM8 MHC CLASS I MOLECULE	IMMUNE SYSTEM
2OLB	OLIGOPEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH TRI-LYSINE	COMPLEX (BINDING PROTEIN/PEPTIDE)
2OLY	STRUCTURE OF HUMAN INSULIN IN PRESENCE OF UREA AT PH 7.0	HORMONE
2OLZ	STRUCTURE OF HUMAN INSULIN IN PRESENCE OF THIOCYANATE AT PH 7	HORMONE
2OM0	STRUCTURE OF HUMAN INSULIN IN PRESENCE OF UREA AT PH 6.5	HORMONE
2OM1	STRUCTURE OF HUMAN INSULIN IN PRESENCE OF THIOCYANATE AT PH 6.5	HORMONE
2OM2	CRYSTAL STRUCTURE OF HUMAN G[ALPHA]I1 BOUND TO THE GOLOCO MOTIF OF RGS14	SIGNALING PROTEIN
2OM7	STRUCTURAL BASIS FOR INTERACTION OF THE RIBOSOME WITH THE SWITCH REGIONS OF GTP-BOUND ELONGATION FACTORS	RIBOSOME
2OMG	STRUCTURE OF HUMAN INSULIN COCRYSTALLIZED WITH PROTAMINE AND UREA	HORMONE
2OMH	STRUCTURE OF HUMAN INSULIN COCRYSTALLIZED WITH ARG-12 PEPTIDE IN PRESENCE OF UREA	HORMONE
2OMI	STRUCTURE OF HUMAN INSULIN COCRYSTALLIZED WITH PROTAMINE	HORMONE
2ONK	ABC TRANSPORTER MODBC IN COMPLEX WITH ITS BINDING PROTEIN MODA	MEMBRANE PROTEIN
2ONL	CRYSTAL STRUCTURE OF THE P38A-MAPKAP KINASE 2 HETERODIMER	TRANSFERASE
		OXIDOREDUCTASE

2OO5 STRUCTURE OF TRANSHYDROGENASE (DI.H2NADH)2(DIII.NADP+)1 ASYMMETRIC COMPLEX

LIGASE

2OOB CRYSTAL STRUCTURE OF THE UBA DOMAIN FROM CBL-B UBIQUITIN LIGASE IN COMPLEX WITH UBIQUITIN

OXIDOREDUCTASE

2OOR STRUCTURE OF TRANSHYDROGENASE (DI.NAD+)2(DIII.H2NADPH)1 ASYMMETRIC COMPLEX

OXIDOREDUCTASE

2OOV CRYSTAL STRUCTURE OF HANSENULA POLYMORPHA AMINE OXIDASE TO 1.7 ANGSTROMS

TRANSFERASE

2OOX CRYSTAL STRUCTURE OF THE ADENYLATE SENSOR FROM AMP-ACTIVATED PROTEIN KINASE COMPLEXED WITH AMP

TRANSFERASE

2OOY CRYSTAL STRUCTURE OF THE ADENYLATE SENSOR FROM AMP-ACTIVATED PROTEIN KINASE COMPLEXED WITH ATP

IMMUNE SYSTEM

2OP4 CRYSTAL STRUCTURE OF QUORUM-QUENCHING ANTIBODY 1G9

STRUCTURAL GENOMICS, UNKNOWN FUNCTION

2OPL CRYSTAL STRUCTURE OF OSMC-LIKE PROTEIN FROM GEOBACTER SULFURREDUCENS AT 1.50 A RESOLUTION

TRANSFERASE

2OPP CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH GW420867X.

TRANSFERASE

2OPQ CRYSTAL STRUCTURE OF L100I MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH GW420867X.

TRANSFERASE

2OPR CRYSTAL STRUCTURE OF K101E MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH GW420867X.

APOPTOSIS INHIBITOR

2OPZ AVPF BOUND TO BIR3-XIAP

TRANSFERASE

2OQ1 TANDEM SH2 DOMAINS OF ZAP-70 WITH 19-MER ZETA1 PEPTIDE

OXIDOREDUCTASE

2OQ6 CRYSTAL STRUCTURE OF JMJD2A COMPLEXED WITH HISTONE H3 PEPTIDE TRIMETHYLATED AT LYS9

OXIDOREDUCTASE

2OQE CRYSTAL STRUCTURE OF HANSENULA POLYMORPHA AMINE OXIDASE IN COMPLEX WITH XE TO 1.6 ANGSTROMS

IMMUNE SYSTEM

2OQJ CRYSTAL STRUCTURE ANALYSIS OF FAB 2G12 IN COMPLEX WITH PEPTIDE 2G12.1

IMMUNE SYSTEM

2OR9 THE STRUCTURE OF THE ANTI-C-MYC ANTIBODY 9E10 FAB FRAGMENT/EPITOPE PEPTIDE COMPLEX REVEALS A NOVEL BINDING MODE DOMINATED BY THE HEAVY CHAIN HYPERVARIABLE LOOPS

IMMUNE SYSTEM

2ORB THE STRUCTURE OF THE ANTI-C-MYC ANTIBODY 9E10 FAB FRAGMENT

OXIDOREDUCTASE

2OS2 CRYSTAL STRUCTURE OF JMJD2A COMPLEXED WITH HISTONE H3 PEPTIDE TRIMETHYLATED AT LYS36

CONTRACTILE PROTEIN

2OS8 RIGOR-LIKE STRUCTURES OF MUSCLE MYOSINS REVEAL KEY

	MECHANICAL ELEMENTS IN THE TRANSDUCTION PATHWAYS OF THIS ALLOSTERIC MOTOR	
2OSL	CRYSTAL STRUCTURE OF RITUXIMAB FAB IN COMPLEX WITH AN EPITOPE PEPTIDE	IMMUNE SYSTEM
2OT0	FRUCTOSE-1,6-BISPHOSPHATE ALDOLASE FROM RABBIT MUSCLE IN COMPLEX WITH A C-TERMINAL PEPTIDE OF WISKOTT-ALDRICH SYNDROME PROTEIN	LYASE
2OT3	CRYSTAL STRUCTURE OF RABEX-5 VPS9 DOMAIN IN COMPLEX WITH NUCLEOTIDE FREE RAB21	PROTEIN TRANSPORT
2OT7	CRYSTAL STRUCTURE OF JMJD2A COMPLEXED WITH HISTONE H3 PEPTIDE MONOMETHYLATED AT LYS9	OXIDOREDUCTASE
2OT8	KARYOPHERIN BETA2/TRANSPORTIN-HNRNPM NLS COMPLEX	TRANSPORT PROTEIN
2OTG	RIGOR-LIKE STRUCTURES OF MUSCLE MYOSINS REVEAL KEY MECHANICAL ELEMENTS IN THE TRANSDUCTION PATHWAYS OF THIS ALLOSTERIC MOTOR	CONTRACTILE PROTEIN
2OTJ	3-DEOXYTEDANOLIDE BOUND TO THE LARGE SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
2OTL	GIRODAZOLE BOUND TO THE LARGE SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
2OUL	THE STRUCTURE OF CHAGASIN IN COMPLEX WITH A CYSTEINE PROTEASE CLARIFIES THE BINDING MODE AND EVOLUTION OF A NEW INHIBITOR FAMILY	HYDROLASE/HYDROLASE INHIBITOR
2OV2	THE CRYSTAL STRUCTURE OF THE HUMAN RAC3 IN COMPLEX WITH THE CRIB DOMAIN OF HUMAN P21-ACTIVATED KINASE 4 (PAK4)	PROTEIN BINDING/TRANSFERASE
2OVH	PROGESTERONE RECEPTOR WITH BOUND ASOPRISNIL AND A PEPTIDE FROM THE CO-REPRESSOR SMRT	TRANSCRIPTION
2OVK	CRYSTAL STRUCTURE OF RIGOR-LIKE SQUID MYOSIN S1	CONTRACTILE PROTEIN
2OVM	PROGESTERONE RECEPTOR WITH BOUND ASOPRISNIL AND A PEPTIDE FROM THE CO-REPRESSOR NCOR	TRANSCRIPTION
2OVP	STRUCTURE OF THE SKP1-FBW7 COMPLEX	TRANSCRIPTION/CELL CYCLE
2OVQ	STRUCTURE OF THE SKP1-FBW7-CYCLINEDEGC COMPLEX	TRANSCRIPTION/CELL CYCLE
2OVR	STRUCTURE OF THE SKP1-FBW7-CYCLINEDEGN COMPLEX	TRANSCRIPTION/CELL CYCLE
2OX0	CRYSTAL STRUCTURE OF JMJD2A COMPLEXED WITH HISTONE H3 PEPTIDE DIMETHYLATED AT LYS9	OXIDOREDUCTASE
2OX5	THE SOXYZ COMPLEX OF PARACOCCUS PANTOTROPHUS	TRANSPORT PROTEIN
2OXG	THE SOXYZ COMPLEX OF PARACOCCUS PANTOTROPHUS	TRANSPORT PROTEIN

2OXH	THE SOXYZ COMPLEX OF PARACOCCUS PANTOTROPHUS	TRANSPORT PROTEIN
2OXQ	STRUCTURE OF THE UBCH5 :CHIP U-BOX COMPLEX	LIGASE
2OXW	HUMAN MMP-12 COMPLEXED WITH THE PEPTIDE IAG	HYDROLASE
2OXZ	HUMAN MMP-12 IN COMPLEX WITH TWO PEPTIDES PQG AND IAG	HYDROLASE
2OY2	HUMAN MMP-8 IN COMPLEX WITH PEPTIDE IAG	HYDROLASE
2OY6	CRYSTAL STRUCTURE OF SQUID MG.ADP MYOSIN S1	CONTRACTILE PROTEIN
2OYH	CRYSTAL STRUCTURE OF FRAGMENT D OF GAMMAD298,301A FIBRINOGEN WITH THE PEPTIDE LIGAND GLY-HIS-ARG-PRO-AMIDE	BLOOD CLOTTING
2OYI	CRYSTAL STRUCTURE OF FRAGMENT D OF GAMMAD298,301A FIBRINOGEN WITH THE PEPTIDE LIGAND GLY-PRO-ARG-PRO-AMIDE	BLOOD CLOTTING
2OZ1	THE SOXAX COMPLEX OF RHODOVULUM SULFIDOPHILUM	ELECTRON TRANSPORT
2OZ4	STRUCTURAL PLASTICITY IN IGSF DOMAIN 4 OF ICAM-1 MEDIATES CELL SURFACE DIMERIZATION	CELL ADHESION
2OZA	STRUCTURE OF P38ALPHA COMPLEX	SIGNALING PROTEIN/TRANSFERASE
2OZB	STRUCTURE OF A HUMAN PRP31-15.5K-U4 SNRNA COMPLEX	RNA BINDING PROTEIN/RNA
2OZL	HUMAN PYRUVATE DEHYDROGENASE S264E VARIANT	OXIDOREDUCTASE
2OZN	THE COHESIN-DOCKERIN COMPLEX OF NAGJ AND NAGH FROM CLOSTRIDIUM PERFRINGENS	TOXIN
2P0R	STRUCTURE OF HUMAN CALPAIN 9 IN COMPLEX WITH LEUPEPTIN	HYDROLASE
2P0W	HUMAN HISTONE ACETYLTRANSFERASE 1 (HAT1)	TRANSFERASE
2P15	CRYSTAL STRUCTURE OF THE ER ALPHA LIGAND BINDING DOMAIN WITH THE AGONIST ORTHO-TRIFLUOROMETHYLPHENYLVINYL ESTRADIOL	HORMONE RECEPTOR
2P16	FACTOR XA IN COMPLEX WITH THE INHIBITOR APIXABAN (BMS-562247) AKA 1-(4-METHOXYPHENYL)-7-OXO-6-(4-(2-OXO-1-PIPERIDINYL)PHENYL)-4,5,6,7-TETRAHYDRO-1H-PYRAZOLO[3, 4-C]PYRIDINE-3-CARBOXAMIDE	HYDROLASE
2P1L	STRUCTURE OF THE BCL-XL:BECLIN 1 COMPLEX	APOPTOSIS
2P1M	TIR1-ASK1 COMPLEX STRUCTURE	SIGNALING PROTEIN
2P1N	MECHANISM OF AUXIN PERCEPTION BY THE TIR1 UBIQUTIN LIGASE	SIGNALING PROTEIN
2P1O	MECHANISM OF AUXIN PERCEPTION BY THE TIR1 UBIQUITIN LIGASE	SIGNALING PROTEIN
2P1P	MECHANISM OF AUXIN PERCEPTION BY THE TIR1 UBIQUITIN LIGASE	SIGNALING PROTEIN
		SIGNALING PROTEIN

2P1Q MECHANISM OF AUXIN PERCEPTION BY THE TIR1 UBIQUITIN LIGASE

HORMONE RECEPTOR

2P1T CRYSTAL STRUCTURE OF THE LIGAND BINDING DOMAIN OF THE RETINOID X RECEPTOR ALPHA IN COMPLEX WITH 3-(2'-METHOXY)-TETRAHYDRONAPHTYL CINNAMIC ACID AND A FRAGMENT OF THE COACTIVATOR TIF-2

HORMONE RECEPTOR

2P1U CRYSTAL STRUCTURE OF THE LIGAND BINDING DOMAIN OF THE RETINOID X RECEPTOR ALPHA IN COMPLEX WITH 3-(2'-ETHOXY)-TETRAHYDRONAPHTYL CINNAMIC ACID AND A FRAGMENT OF THE COACTIVATOR TIF-2

HORMONE RECEPTOR

2P1V CRYSTAL STRUCTURE OF THE LIGAND BINDING DOMAIN OF THE RETINOID X RECEPTOR ALPHA IN COMPLEX WITH 3-(2'-PROPOXY)-TETRAHYDRONAPHTYL CINNAMIC ACID AND A FRAGMENT OF THE COACTIVATOR TIF-2

TRANSPORT PROTEIN

2P22 STRUCTURE OF THE YEAST ESCRT-I HETEROTETRAMER CORE

IMMUNE SYSTEM

2P24 I-AU/MBP125-135

CELL ADHESION

2P28 STRUCTURE OF THE PHE2 AND PHE3 FRAGMENTS OF THE INTEGRIN BETA2 SUBUNIT

HYDROLASE

2P2C INHIBITION OF CASPASE-2 BY A DESIGNED ANKYRIN REPEAT PROTEIN (DARPIN)

HYDROLASE

2P3B CRYSTAL STRUCTURE OF THE SUBTYPE B WILD TYPE HIV PROTEASE COMPLEXED WITH TL-3 INHIBITOR

HYDROLASE

2P3F CRYSTAL STRUCTURE OF THE FACTOR XA/NAP5 COMPLEX

BLOOD CLOTTING

2P3T CRYSTAL STRUCTURE OF HUMAN FACTOR XA COMPLEXED WITH 3-CHLORO-4-(2-METHYLAMINO-IMIDAZOL-1-YLMETHYL)-THIOPHENE-2-CARBOXYLIC ACID [4-CHLORO-2-(5-CHLORO-PYRIDIN-2-YLCARBAMOYL)-6-METHOXY-PHENYL]-AMIDE

BLOOD CLOTTING

2P3U CRYSTAL STRUCTURE OF HUMAN FACTOR XA COMPLEXED WITH 3-CHLORO-N-(4-CHLORO-2-{[(5-CHLOROPYRIDIN-2-YL) AMINO]CARBONYL}-6-METHOXYPHENYL)-4-[(1-METHYL-1H-IMIDAZOL-2-YL)METHYL]THIOPHENE-2-CARBOXAMIDE {PFIZER 320663}

HYDROLASE/IMMUNE SYSTEM

2P42 COMPLEX OF A CAMELID SINGLE-DOMAIN VHH ANTIBODY FRAGMENT WITH RNASE A AT 1.8A RESOLUTION: SE3-MONO-2 CRYSTAL FORM WITH THREE SE-MET SITES (M34, M51, M83) IN VHH SCAFFOLD

HYDROLASE/IMMUNE SYSTEM

2P43 COMPLEX OF A CAMELID SINGLE-DOMAIN VHH ANTIBODY FRAGMENT WITH RNASE A AT 1.65A RESOLUTION: SE3-MONO-1 CRYSTAL FORM WITH THREE SE-MET SITES (M34, M51, M83) IN VHH SCAFFOLD

HYDROLASE/IMMUNE SYSTEM

2P44 COMPLEX OF A CAMELID SINGLE-DOMAIN VHH ANTIBODY FRAGMENT WITH RNASE A AT 1.8A RESOLUTION: SE5A-MONO-1 CRYSTAL FORM WITH FIVE SE-MET SITES (M34, M51, F68M, M83, L86M) IN VHH SCAFFOLD

HYDROLASE/IMMUNE SYSTEM

2P49	COMPLEX OF A CAMELID SINGLE-DOMAIN VHH ANTIBODY FRAGMENT WITH RNASE A AT 1.4A RESOLUTION: NATIVE MONO_1 CRYSTAL FORM	
2P4A	X-RAY STRUCTURE OF A CAMELID AFFINITY MATURED SINGLE-DOMAIN VHH ANTIBODY FRAGMENT IN COMPLEX WITH RNASE A	HYDROLASE/IMMUNE SYSTEM
2P4N	HUMAN MONOMERIC KINESIN (1BG2) AND BOVINE TUBULIN (1JFF) DOCKED INTO THE 9-ANGSTROM CRYO-EM MAP OF NUCLEOTIDE-FREE KINESIN COMPLEXED TO THE MICROTUBULE	TRANSPORT PROTEIN
2P54	A CRYSTAL STRUCTURE OF PPAR ALPHA BOUND WITH SRC1 PEPTIDE AND GW735	TRANSCRIPTION
2P58	STRUCTURE OF THE YERSINIA PESTIS TYPE III SECRETION SYSTEM NEEDLE PROTEIN YSCF IN COMPLEX WITH ITS CHAPERONES YSCE/YSCG	TRANSPORT PROTEIN/CHAPERONE
2P59	CRYSTAL STRUCTURE OF HEPATITIS C VIRUS NS3.4A PROTEASE	VIRAL PROTEIN
2P5B	THE COMPLEX STRUCTURE OF JMJD2A AND TRIMETHYLATED H3K36 PEPTIDE	METAL BINDING PROTEIN
2P5E	CRYSTAL STRUCTURES OF HIGH AFFINITY HUMAN T-CELL RECEPTORS BOUND TO PMHC REVEAL NATIVE DIAGONAL BINDING GEOMETRY	IMMUNE SYSTEM
2P5T	MOLECULAR AND STRUCTURAL CHARACTERIZATION OF THE PEZAT CHROMOSOMAL TOXIN-ANTITOXIN SYSTEM OF THE HUMAN PATHOGEN STREPTOCOCCUS PNEUMONIAE	TRANSCRIPTION REGULATOR
2P5W	CRYSTAL STRUCTURES OF HIGH AFFINITY HUMAN T-CELL RECEPTORS BOUND TO PMHC REVEAL NATIVE DIAGONAL BINDING GEOMETRY	IMMUNE SYSTEM
2P6A	THE STRUCTURE OF THE ACTIVIN:FOLLISTATIN 315 COMPLEX	SIGNALING PROTEIN
2P6B	CRYSTAL STRUCTURE OF HUMAN CALCINEURIN IN COMPLEX WITH PVIVIT PEPTIDE	HYDROLASE/HYDROLASE REGULATOR
2P7T	CRYSTAL STRUCTURE OF KCSA MUTANT	MEMBRANE PROTEIN
2P7V	CRYSTAL STRUCTURE OF THE ESCHERICHIA COLI REGULATOR OF SIGMA 70, RSD, IN COMPLEX WITH SIGMA 70 DOMAIN 4	TRANSCRIPTION
2P8L	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE ELLELDKWASLWN	VIRAL PROTEIN
2P8M	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE ELLELDKWASLWN IN NEW CRYSTAL FORM	VIRAL PROTEIN
2P8O	CRYSTAL STRUCTURE OF A BENZOHYDROXAMIC ACID/VANADATE COMPLEX BOUND TO CHYMOTRYPSIN A	HYDROLASE
2P8Q	CRYSTAL STRUCTURE OF HUMAN IMPORTIN BETA BOUND TO THE SNURPORTIN1 IBB-DOMAIN	PROTEIN TRANSPORT

2P8W	FITTED STRUCTURE OF EEF2 IN THE 80S:EEF2:GDPNP CRYO-EM RECONSTRUCTION	TRANSLATION
2P8X	FITTED STRUCTURE OF ADPR-EEF2 IN THE 80S:ADPR-EEF2:GDPNP CRYO-EM RECONSTRUCTION	TRANSLATION
2P8Z	FITTED STRUCTURE OF ADPR-EEF2 IN THE 80S:ADPR-EEF2:GDPNP:SORDARIN CRYO-EM RECONSTRUCTION	TRANSLATION
2P93	FACTOR XA IN COMPLEX WITH THE INHIBITOR 5-CHLORO-N-(2-(4-(2-OXOPYRIDIN-1(2H)-YL)BENZAMIDO)ETHYL)THIOPHENE-2-CARBOXAMIDE	HYDROLASE
2P94	FACTOR XA IN COMPLEX WITH THE INHIBITOR 3-CHLORO-N-((1R,2S)-2-(4-(2-OXOPYRIDIN-1(2H)-YL)BENZAMIDO)CYCLOHEXYL)-1H-INDOLE-6-CARBOXAMIDE	HYDROLASE
2P95	FACTOR XA IN COMPLEX WITH THE INHIBITOR 5-CHLORO-N-((1R,2S)-2-(4-(2-OXOPYRIDIN-1(2H)-YL)BENZAMIDO) CYCLOPENTYL) THIOPHENE-2-CARBOXAMIDE	HYDROLASE
2P9I	CRYSTAL STRUCTURE OF BOVINE ARP2/3 COMPLEX CO-CRYSTALLIZED WITH ADP AND CROSSLINKED WITH GLUTERALDEHYDE	STRUCTURAL PROTEIN
2P9K	CRYSTAL STRUCTURE OF BOVINE ARP2/3 COMPLEX CO-CRYSTALLIZED WITH ATP AND CROSSLINKED WITH GLUTARALDEHYDE	STRUCTURAL PROTEIN
2P9L	CRYSTAL STRUCTURE OF BOVINE ARP2/3 COMPLEX	STRUCTURAL PROTEIN
2P9N	CRYSTAL STRUCTURE OF BOVINE ARP2/3 COMPLEX CO-CRYSTALLIZED WITH ADP	STRUCTURAL PROTEIN
2P9P	CRYSTAL STRUCTURE OF BOVINE ARP2/3 COMPLEX CO-CRYSTALLIZED WITH ADP	STRUCTURAL PROTEIN
2P9S	STRUCTURE OF BOVINE ARP2/3 COMPLEX CO-CRYSTALLIZED WITH ATP/MG2+	STRUCTURAL PROTEIN
2P9U	CRYSTAL STRUCTURE OF BOVINE ARP2/3 COMPLEX CO-CRYSTALLIZED WITH AMP-PNP AND CALCIUM	STRUCTURAL PROTEIN
2P9V	STRUCTURE OF AMPC BETA-LACTAMASE WITH CROSS-LINKED ACTIVE SITE AFTER EXPOSURE TO SMALL MOLECULE INHIBITOR	HYDROLASE
2PA8	X-RAY CRYSTAL STRUCTURE OF THE D/L SUBCOMPLEX OF THE SULFOLOBUS SOLFATARICUS RNA POLYMERASE	TRANSFERASE
2PAV	TERNARY COMPLEX OF PROFILIN-ACTIN WITH THE LAST POLY-PRO OF HUMAN VASP	STRUCTURAL PROTEIN
2PB8	CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN PHOSPHOLIPASE A2 AND PEPTIDE ALA-VAL-TYR-SER AT 2.0 A RESOLUTION	HYDROLASE
2PBD	TERNARY COMPLEX OF PROFILIN-ACTIN WITH THE POLY-PRO-GAB	STRUCTURAL PROTEIN

	DOMAIN OF VASP*	
2PBI	THE MULTIFUNCTIONAL NATURE OF GBETA5/RGS9 REVEALED FROM ITS CRYSTAL STRUCTURE	SIGNALING PROTEIN
2PBK	CRYSTAL STRUCTURE OF KSHV PROTEASE IN COMPLEX WITH HEXAPEPTIDE PHOSPHONATE INHIBITOR	VIRAL PROTEIN
2PC4	CRYSTAL STRUCTURE OF FRUCTOSE-BISPHOSPHATE ALDOLASE FROM PLASMODIUM FALCIPARUM IN COMPLEX WITH TRAP-TAIL DETERMINED AT 2.4 ANGSTROM RESOLUTION	LYASE
2PCB	CRYSTAL STRUCTURE OF A COMPLEX BETWEEN ELECTRON TRANSFER PARTNERS, CYTOCHROME C PEROXIDASE AND CYTOCHROME C	OXIDOREDUCTASE/ELECTRON TRANSPORT
2PCC	CRYSTAL STRUCTURE OF A COMPLEX BETWEEN ELECTRON TRANSFER PARTNERS, CYTOCHROME C PEROXIDASE AND CYTOCHROME C	OXIDOREDUCTASE/ELECTRON TRANSPORT
2PCD	STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE FROM PSEUDOMONAS AERUGINOSA AT 2.15 ANGSTROMS RESOLUTION	DIOXYGENASE
2PCP	ANTIBODY FAB COMPLEXED WITH PHENCYCLIDINE	IMMUNOGLOBULIN
2PCU	HUMAN CARBOXYPEPTIDASE A4 IN COMPLEX WITH A CLEAVED HEXAPEPTIDE.	HYDROLASE
2PE6	ION-COVALENT COMPLEX BETWEEN HUMAN SUMO-1 AND HUMAN UBC9	PROTEIN BINDING, LIGASE
2PEG	CRYSTAL STRUCTURE OF TREMATOMUS BERNACCHII HEMOGLOBIN IN A PARTIAL HEMICHROME STATE	OXYGEN STORAGE/TRANSPORT
2PEH	CRYSTAL STRUCTURE OF THE UHM DOMAIN OF HUMAN SPF45 IN COMPLEX WITH SF3B155-ULM5	PROTEIN BINDING
2PEM	CRYSTAL STRUCTURE OF RBCX IN COMPLEX WITH SUBSTRATE	CHAPERONE
2PF4	CRYSTAL STRUCTURE OF THE FULL-LENGTH SIMIAN VIRUS 40 SMALL T ANTIGEN COMPLEXED WITH THE PROTEIN PHOSPHATASE 2A AALPHA SUBUNIT	HYDROLASE REGULATOR/VIRAL PROTEIN
2PG1	STRUCTURAL ANALYSIS OF A CYTOPLASMIC DYNEIN LIGHT CHAIN-INTERMEDIATE CHAIN COMPLEX	STRUCTURAL PROTEIN
2PGB	INHIBITOR-FREE HUMAN THROMBIN MUTANT C191A-C220A	HYDROLASE
2PGH	STRUCTURE DETERMINATION OF AQUOMET PORCINE HEMOGLOBIN AT 2.8 ANGSTROM RESOLUTION	OXYGEN TRANSPORT
2PGQ	HUMAN THROMBIN MUTANT C191A-C220A IN COMPLEX WITH THE INHIBITOR PPACK	HYDROLASE
2PHB	AN ORALLY EFFICACIOUS FACTOR XA INHIBITOR	BLOOD CLOTTING
2PHK	THE CRYSTAL STRUCTURE OF A PHOSPHORYLASE KINASE PEPTIDE SUBSTRATE COMPLEX: KINASE SUBSTRATE RECOGNITION	COMPLEX (TRANSFERASE/PEPTIDE)

2PI2	FULL-LENGTH REPLICATION PROTEIN A SUBUNITS RPA14 AND RPA32	REPLICATION, DNA BINDING PROTEIN
2PJR	HELICASE PRODUCT COMPLEX	HYDROLASE/DNA
2PJW	THE VPS27/HSE1 COMPLEX IS A GAT DOMAIN-BASED SCAFFOLD FOR UBIQUITIN-DEPENDENT SORTING	ENDOCYTOSIS/EXOCYTOSIS
2PJX	CRYSTAL STRUCTURE OF THE MUNC18C/SYNTAXIN4 N-PEPTIDE COMPLEX	ENDOCYTOSIS/EXOCYTOSIS
2PJY	STRUCTURAL BASIS FOR COOPERATIVE ASSEMBLY OF THE TGF-BETA SIGNALING COMPLEX	CYTOKINE/CYTOKINE RECEPTOR
2PK9	STRUCTURE OF THE PHO85-PHO80 CDK-CYCLIN COMPLEX OF THE PHOSPHATE-RESPONSIVE SIGNAL TRANSDUCTION PATHWAY	SIGNALING PROTEIN,TRANSFERASE/CELL CYCLE
2PKA	REFINED 2 ANGSTROMS X-RAY CRYSTAL STRUCTURE OF PORCINE PANCREATIC KALLIKREIN A, A SPECIFIC TRYPSIN-LIKE SERINE PROTEINASE. CRYSTALLIZATION, STRUCTURE DETERMINATION, CRYSTALLOGRAPHIC REFINEMENT, STRUCTURE AND ITS COMPARISON WITH BOVINE TRYPSIN	SERINE PROTEINASE
2PKG	STRUCTURE OF A COMPLEX BETWEEN THE A SUBUNIT OF PROTEIN PHOSPHATASE 2A AND THE SMALL T ANTIGEN OF SV40	HYDROLASE REGULATOR/VIRAL PROTEIN
2PKL	ANDROGEN RECEPTOR LBD WITH SMALL MOLECULE	HORMONE RECEPTOR
2PKQ	RYSTAL STRUCTURE OF THE PHOTOSYNTHETIC A2B2-GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE, COMPLEXED WITH NADP	OXIDOREDUCTASE
2PKS	THROMBIN IN COMPLEX WITH INHIBITOR	HYDROLASE
2PL9	CRYSTAL STRUCTURE OF CHEY-MG(2+)-BEF(3)(-) IN COMPLEX WITH CHEZ(C19) PEPTIDE SOLVED FROM A P2(1)2(1)2 CRYSTAL	SIGNALING PROTIEN
2PLD	NUCLEAR MAGNETIC RESONANCE STRUCTURE OF AN SH2 DOMAIN OF PHOSPHOLIPASE C-GAMMA1 COMPLEXED WITH A HIGH AFFINITY BINDING PEPTIDE	PHOSPHORIC DIESTER HYDROLASE
2PLX	TRYPSIN COMPLEXED TO A SYNTHETIC PEPTIDE FROM VERONICA HEDERIFOLIA	HYDROLASE
2PM6	CRYSTAL STRUCTURE OF YEAST SEC13/31 EDGE ELEMENT OF THE COPII VESICULAR COAT, NATIVE VERSION	PROTEIN TRANSPORT
2PM7	CRYSTAL STRUCTURE OF YEAST SEC13/31 EDGE ELEMENT OF THE COPII VESICULAR COAT, SELENOMETHIONINE VERSION	PROTEIN TRANSPORT
2PMC	CRYSTAL STRUCTURE OF CHEY-MG(2+) IN COMPLEX WITH CHEZ(C15) PEPTIDE SOLVED FROM A P1 CRYSTAL	SIGNALING PROTEIN
2PMI	STRUCTURE OF THE PHO85-PHO80 CDK-CYCLIN COMPLEX OF THE PHOSPHATE-RESPONSIVE SIGNAL TRANSDUCTION PATHWAY WITH BOUND ATP-GAMMA-S	SIGNALING PROTEIN,TRANSFERASE/CELL CYCLE
		METAL TRANSPORT, HYDROLASE

2PMS	CRYSTAL STRUCTURE OF THE COMPLEX OF HUMAN LACTOFERRIN N-LOBE AND LACTOFERRIN-BINDING DOMAIN OF PNEUMOCOCCAL SURFACE PROTEIN A	
2PMW	THE CRYSTAL STRUCTURE OF PROPROTEIN CONVERTASE SUBTILISIN KEXIN TYPE 9 (PCSK9)	HYDROLASE
2PMZ	ARCHAEAL RNA POLYMERASE FROM SULFOLOBUS SOLFATARICUS	TRANSLATION, TRANSFERASE
2PNR	CRYSTAL STRUCTURE OF THE ASYMMETRIC PDK3-L2 COMPLEX	TRANSFERASE
2PNZ	CRYSTAL STRUCTURE OF THE P. ABYSSI EXOSOME RNASE PH RING COMPLEXED WITH UDP AND GMP	HYDROLASE/HYDROLASE
2PO0	CRYSTAL STRUCTURE OF THE P. ABYSSI EXOSOME RNASE PH RING COMPLEXED WITH ADP IN DOUBLE CONFORMATION	HYDROLASE/HYDROLASE
2PO1	CRYSTAL STRUCTURE OF THE P. ABYSSI EXOSOME RNASE PH RING COMPLEXED WITH A SINGLE STRANDED 10-MER POLY(A) RNA	HYDROLASE/HYDROLASE/RNA
2PO2	CRYSTAL STRUCTURE OF THE P. ABYSSI EXOSOME RNASE PH RING COMPLEXED WITH CDP	HYDROLASE/HYDROLASE
2PO6	CRYSTAL STRUCTURE OF CD1D-LIPID-ANTIGEN COMPLEXED WITH BETA-2-MICROGLOBULIN, NKT15 ALPHA-CHAIN AND NKT15 BETA-CHAIN	LIPID BINDING PROTEIN/IMMUNE SYSTEM
2PON	SOLUTION STRUCTURE OF THE BCL-XL/BECLIN-1 COMPLEX	APOPTOSIS INHIBITOR
2POP	THE CRYSTAL STRUCTURE OF TAB1 AND BIR1 COMPLEX	SIGNALING PROTEIN/APOPTOSIS
2POY	CRYPTOSPORIDIUM PARVUM CYCLOPHILIN TYPE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE CGD2_4120 IN COMPLEX WITH CYCLOSPORIN A	ISOMERASE
2PPB	CRYSTAL STRUCTURE OF THE T. THERMOPHILUS RNAP POLYMERASE ELONGATION COMPLEX WITH THE NTP SUBSTRATE ANALOG AND ANTIBIOTIC STREPTOLYDIGIN	TRANSFERASE/DNA/RNA
2PQ2	STRUCTURE OF SERINE PROTEINASE K COMPLEX WITH A HIGHLY FLEXIBLE HYDROPHOBIC PEPTIDE AT 1.8A RESOLUTION	HYDROLASE
2PQA	CRYSTAL STRUCTURE OF FULL-LENGTH HUMAN RPA 14/32 HETERODIMER	REPLICATION
2PQK	X-RAY CRYSTAL STRUCTURE OF HUMAN MCL-1 IN COMPLEX WITH BIM BH3	APOPTOSIS
2PQN	CRYSTAL STRUCTURE OF YEAST FIS1 COMPLEXED WITH A FRAGMENT OF YEAST MDV1	APOPTOSIS
2PQR	CRYSTAL STRUCTURE OF YEAST FIS1 COMPLEXED WITH A FRAGMENT OF YEAST CAF4	APOPTOSIS
2PR3	FACTOR XA INHIBITOR	BLOOD CLOTTING
2PR4	CRYSTAL STRUCTURE OF FAB' FROM THE HIV-1 NEUTRALIZING ANTIBODY 2F5	VIRAL PROTEIN

		PHOTOSYNTHETIC REACTION CENTER
2PRC	HOTOSYNTHETIC REACTION CENTER FROM RHODOPSEUDOMONAS VIRIDIS (UBIQUINONE-2 COMPLEX)	COMPLEX (THIAZOLIDINEDIONE/RECEPTOR)
2PRG	IGAND-BINDING DOMAIN OF THE HUMAN PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR GAMMA	CYTOKINE
2PSM	CRYSTAL STRUCTURE OF INTERLEUKIN 15 IN COMPLEX WITH INTERLEUKIN 15 RECEPTOR ALPHA	HYDROLASE/PROTEIN BINDING
2PT7	CRYSTAL STRUCTURE OF CAG VIRB11 (HP0525) AND AN INHIBITORY PROTEIN (HP1451)	ELECTRON TRANSPORT
2PU9	RYSTAL SRTUCTURE OF THE BINARY COMPLEX BETWEEN FERREDOXIN: THIOREDOXIN REDUCTASE AND THIOREDOXIN F	ELECTRON TRANSPORT
2PUK	RYSTAL SRTUCTURE OF THE BINARY COMPLEX BETWEEN FERREDOXIN: THIOREDOXIN REDUCTASE AND THIOREDOXIN M	ELECTRON TRANSPORT
2PUO	CRYSTAL SRTUCTURE OF THE NEM MODIFIED FERREDOXIN:THIOREDOXIN REDUCTASE	BLOOD CLOTTING
2PUQ	CRYSTAL STRUCTURE OF ACTIVE SITE INHIBITED COAGULATION FACTOR VIIA IN COMPLEX WITH SOLUBLE TISSUE FACTOR	HYDROLASE
2PUX	CRYSTAL STRUCTURE OF MURINE THROMBIN IN COMPLEX WITH THE EXTRACELLULAR FRAGMENT OF MURINE PAR3	TRANSCRIPTION
2PUY	CRYSTAL STRUCTURE OF THE BHC80 PHD FINGER	ISOMERASE
2PV1	CRYSTALLOGRAPHIC STRUCTURE OF SURA FIRST PEPTIDYL-PROLYL ISOMERASE DOMAIN COMPLEXED WITH PEPTIDE WEYIPNV	ISOMERASE
2PV2	CRYSTALLOGRAPHIC STRUCTURE OF SURA FIRST PEPTIDYL-PROLYL ISOMERASE DOMAIN COMPLEXED WITH PEPTIDE NFTLKFWDIFRK	ISOMERASE
2PV3	CRYSTALLOGRAPHIC STRUCTURE OF SURA FRAGMENT LACKING THE SECOND PEPTIDYL-PROLYL ISOMERASE DOMAIN COMPLEXED WITH PEPTIDE NFTLKFWDIFRK	HYDROLASE
2PV9	CRYSTAL STRUCTURE OF MURINE THROMBIN IN COMPLEX WITH THE EXTRACELLULAR FRAGMENT OF MURINE PAR4	TRANSFERASE REGULATOR
2PVC	DNMT3L RECOGNIZES UNMETHYLATED HISTONE H3 LYSINE 4	ELECTRON TRANSPORT
2PVD	CRYSTAL SRTUCTURE OF THE REDUCED FERREDOXIN:THIOREDOXIN REDUCTASE	TRANSFERASE
2PVF	RYSTAL STRUCTURE OF TYROSINE PHOSPHORYLATED ACTIVATED FGF RECEPTOR 2 (FGFR2) KINASE DOMAIN IN COMPLEX WITH ATP ANALOG AND SUBSTRATE PEPTIDE	ELECTRON TRANSPORT
2PVG	RYSTAL SRTUCTURE OF THE BINARY COMPLEX BETWEEN FERREDOXIN AND FERREDOXIN:THIOREDOXIN REDUCTASE	ELECTRON TRANSPORT

2PVO	CRYSTAL SRTUCTURE OF THE TERNARY COMPLEX BETWEEN THIOREDOXIN F, FERREDOXIN, AND FERREDOXIN: THIOREDOXIN REDUCTASE	
2PW1	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE ELDKWNSL	IMMUNE SYSTEM
2PW2	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE ELDKWKSL	IMMUNE SYSTEM
2PW8	CRYSTAL STRUCTURE OF SULFO-HIRUDIN COMPLEXED TO THROMBIN	HYDROLASE
2PXJ	THE COMPLEX STRUCTURE OF JMJD2A AND MONOMETHYLATED H3K36 PEPTIDE	OXIDOREDUCTASE
2PXY	CRYSTAL STRUCTURES OF IMMUNE RECEPTOR COMPLEXES	IMMUNE SYSTEM
2PYE	CRYSTAL STRUCTURES OF HIGH AFFINITY HUMAN T-CELL RECEPTORS BOUND TO PMHC REVEALNATIVE DIAGONAL BINDING GEOMETRY TCR CLONE C5C1 COMPLEXED WITH MHC	IMMUNE SYSTEM
2PYF	CRYSTAL STRUCTURES OF HIGH AFFINITY HUMAN T-CELL RECEPTORS BOUND TO PMHC REVEALNATIVE DIAGONAL BINDING GEOMETRY UNBOUND TCR CLONE 5-1	IMMUNE SYSTEM
2PYO	DROSOPHILA NUCLEOSOME CORE	STRUCTURAL PROTEIN/DNA
2Q0N	STRUCTURE OF HUMAN P21 ACTIVATING KINASE 4 (PAK4) IN COMPLEX WITH A CONSENSUS PEPTIDE	TRANSFERASE
2Q0O	CRYSTAL STRUCTURE OF AN ANTI-ACTIVATION COMPLEX IN BACTERIAL QUORUM SENSING	TRANSCRIPTION
2Q1J	THE DISCOVERY OF GLYCINE AND RELATED AMINO ACID-BASED FACTOR XA INHIBITORS	HYDROLASE
2Q1Z	CRYSTAL STRUCTURE OF RHODOBACTER SPHAEROIDES SIGE IN COMPLEX WITH THE ANTI-SIGMA CHRR	TRANSCRIPTION
2Q26	FHV VIRUS LIKE PARTICLE	VIRUS/RNA
2Q2E	CRYSTAL STRUCTURE OF THE TOPOISOMERASE VI HOLOENZYME FROM METHANOSARCINA MAZEI	ISOMERASE
2Q3C	2.1 A RESOLUTION CRYSTAL STRUCTURE OF O-ACETYLSERINE SULFHYDRYLASE (OASS) HOLOENZYME FROM MYCOBACTERIUM TUBERCULOSIS IN COMPLEX WITH THE INHIBITORY PEPTIDE DFSI	TRANSFERASE
2Q3I	CRYSTAL STRUCTURE OF THE D10-P3/IQN17 COMPLEX: A D-PEPTIDE INHIBITOR OF HIV-1 ENTRY BOUND TO THE GP41 COILED-COIL POCKET	VIRAL PROTEIN/VIRAL PROTEIN INHIBITOR
2Q3N	AGGLUTININ FROM ABRUS PRECATORIUS (APA-I)	PLANT PROTEIN

2Q3Y	ANCESTRAL CORTICIOD RECEPTOR IN COMPLEX WITH DOC	TRANSCRIPTION
2Q3Z	RANSGLUTAMINASE 2 UNDERGOES LARGE CONFORMATIONAL CHANGE UPON ACTIVATION	TRANSFERASE
2Q59	CRYSTAL STRUCTURE OF PPARGAMMA LBD BOUND TO FULL AGONIST MRL20	LIGAND BINDING PROTEIN
2Q5A	HUMAN PIN1 BOUND TO L-PEPTIDE	ISOMERASE
2Q5D	CRYSTAL STRUCTURE OF HUMAN IMPORTIN BETA BOUND TO THE SNURPORTIN1 IBB-DOMAIN SECOND CRYSTAL FORM	PROTEIN TRANSPORT
2Q5W	HE X-RAY CRYSTAL STRUCTURE OF MOLYBDOPTERIN SYNTHASE FROM STAPHYLOCOCCUS AUREUS	TRANSFERASE
2Q5Y	CRYSTAL STRUCTURE OF THE C-TERMINAL DOMAIN OF HNUP98	PROTEIN TRANSPORT
2Q6G	CRYSTAL STRUCTURE OF SARS-COV MAIN PROTEASE H41A MUTANT IN COMPLEX WITH AN N-TERMINAL SUBSTRATE	HYDROLASE
2Q6J	RYSTAL STRUCTURE OF ESTROGEN RECEPTOR ALPHA COMPLEXED TO A B-N SUBSTITUTED LIGAND	TRANSCRIPTION
2Q6W	THE STRUCTURE OF HLA-DRA, DRB3*0101 (DR52A) WITH BOUND PLATELET INTEGRIN PEPTIDE ASSOCIATED WITH FETAL AND NEONATAL ALLOIMMUNE THROMBOCYTOPENIA	IMMUNE SYSTEM
2Q76	MOUSE ANTI-HEN EGG WHITE LYSOZYME ANTIBODY F10.6.6 FAB FRAGMENT	IMMUNE SYSTEM
2Q7I	HE WILD TYPE ANDROGEN RECEPTOR LIGAND BINDING DOMAIN BOUND WITH TESTOSTERONE AND AN AR 20-30 PEPTIDE	HORMONE
2Q7J	HE WILD TYPE ANDROGEN RECEPTOR LIGAND BINDING DOMAIN BOUND WITH TESTOSTERONE AND A TIF2 BOX 3 COACTIVATOR PEPTIDE 740-753	HORMONE
2Q7K	HE ANDROGEN RECEPTOR PROSTATE CANCER MUTANT H874Y LIGAND BINDING DOMAIN BOUND WITH TESTOSTERONE AND AN AR 20-30 PEPTIDE	HORMONE
2Q7L	HE ANDROGEN RECEPTOR PROSTATE CANCER MUTANT H874Y LIGAND BINDING DOMAIN BOUND WITH TESTOSTERONE AND A TIF2 BOX3 COACTIVATOR PEPTIDE 740-753	HORMONE
2Q7N	CRYSTAL STRUCTURE OF LEUKEMIA INHIBITORY FACTOR IN COMPLEX WITH LIF RECEPTOR (DOMAINS 1-5)	CYTOKINE RECEPTOR/CYTOKINE
2Q7Q	CRYSTAL STRUCTURE OF ALCALIGENES FAECALIS AADH IN COMPLEX WITH P-CHLOROBENZYLAMINE.	OXIDOREDUCTASE
2Q7Y	STRUCTURE OF THE ENDOGENOUS INKT CELL LIGAND IGB3 BOUND TO MCD1D	IMMUNE SYSTEM

2Q86	STRUCTURE OF THE MOUSE INVARIANT NKT CELL RECEPTOR VALPHA14	IMMUNE SYSTEM
2Q8A	STRUCTURE OF THE MALARIA ANTIGEN AMA1 IN COMPLEX WITH A GROWTH-INHIBITORY ANTIBODY	IMMUNE SYSTEM
2Q8B	STRUCTURE OF THE MALARIA ANTIGEN AMA1 IN COMPLEX WITH A GROWTH-INHIBITORY ANTIBODY	IMMUNE SYSTEM
2Q8C	CRYSTAL STRUCTURE OF JMJD2A IN TERNARY COMPLEX WITH AN HISTONE H3K9ME3 PEPTIDE AND 2-OXOGLUTARATE	OXIDOREDUCTASE
2Q8D	CRYSTAL STRUCTURE OF JMJ2D2A IN TERNARY COMPLEX WITH HISTONE H3-K36ME2 AND SUCCINATE	OXIDOREDUCTASE
2Q8E	SPECIFICITY AND MECHANISM OF JMJD2A, A TRIMETHYLLYSINE-SPECIFIC HISTONE DEMETHYLASE	OXIDOREDUCTASE
2Q8I	PYRUVATE DEHYDROGENASE KINASE ISOFORM 3 IN COMPLEX WITH ANTITUMOR DRUG RADICICOL	TRANSFERASE
2Q97	COMPLEX OF MAMMALIAN ACTIN WITH TOXOFILIN FROM TOXOPLASMA GONDII	STRUCTURAL PROTEIN/CELL INVASION
2Q9I	CRYSTAL STRUCTURE OF D-DIMER FROM HUMAN FIBRIN COMPLEXED WITH MET-HIS-ARG-PRO-TYR-AMIDE.	BLOOD CLOTTING
2Q9Q	THE CRYSTAL STRUCTURE OF FULL LENGTH HUMAN GINS COMPLEX	REPLICATION
2QA4	A MORE COMPLETE STRUCTURE OF THE THE L7/L12 STALK OF THE HALOARCULA MARISMORTUI 50S LARGE RIBOSOMAL SUBUNIT	RIBOSOME
2QA6	CRYSTAL STRUCTURE OF ESTROGEN RECEPTOR ALPHA MUTANT 537S COMPLEXED WITH 4-(6-HYDROXY-1H-INDAZOL-3-YL)BENZENE-1,3-DIOL	TRANSCRIPTION
2QA8	CRYSTAL STRUCTURE OF THE ESTROGEN RECEPTOR ALPHA LIGAND BINDING DOMAIN MUTANT 537S COMPLEXED WITH GENISTEIN	TRANSCRIPTION
2QAB	CRYSTAL STRUCTURE OF ESTROGEN RECEPTOR ALPHA LIGAND BINDING DOMAIN MUTANT 537S COMPLEXED WITH AN ETHYL INDAZOLE COMPOUND	TRANSCRIPTION
2QAC	THE CLOSED MTIP-MYOSINA-TAIL COMPLEX FROM THE MALARIA PARASITE INVASION MACHINERY	MEMBRANE PROTEIN
2QAD	STRUCTURE OF TYROSINE-SULFATED 412D ANTIBODY COMPLEXED WITH HIV-1 YU2 GP120 AND CD4	VIRAL PROTEIN/IMMUNE SYSTEM
2QAG	CRYSTAL STRUCTURE OF HUMAN SEPTIN TRIMER 2/6/7	CELL CYCLE, STRUCTURAL PROTEIN
2QAL	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH NEOMYCIN. THIS FILE CONTAINS THE 30S SUBUNIT OF THE FIRST 70S RIBOSOME, WITH NEOMYCIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO	RIBOSOME

	70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	
2QAM	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH NEOMYCIN. THIS FILE CONTAINS THE 50S SUBUNIT OF THE FIRST 70S RIBOSOME, WITH NEOMYCIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2QAN	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH NEOMYCIN. THIS FILE CONTAINS THE 30S SUBUNIT OF THE SECOND 70S RIBOSOME, WITH NEOMYCIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2QAO	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH NEOMYCIN. THIS FILE CONTAINS THE 50S SUBUNIT OF THE SECOND 70S RIBOSOME, WITH NEOMYCIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2QAR	STRUCTURE OF THE 2TEL CRYSTALLIZATION MODULE FUSED TO T4 LYSOZYME WITH A HELICAL LINKER.	HYDROLASE REGULATOR
2QAS	RYSTAL STRUCTURE OF CAULOBACTER CRESCENTUS SSPB ORTHOLOG	HYDROLASE ACTIVATOR
2QB0	STRUCTURE OF THE 2TEL CRYSTALLIZATION MODULE FUSED TO T4 LYSOZYME WITH AN ALA-GLY-PRO LINKER.	HYDROLASE REGULATOR
2QB9	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH GENTAMICIN. THIS FILE CONTAINS THE 30S SUBUNIT OF THE FIRST 70S RIBOSOME, WITH GENTAMICIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2QBA	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH GENTAMICIN. THIS FILE CONTAINS THE 50S SUBUNIT OF THE FIRST 70S RIBOSOME, WITH GENTAMICIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2QBB	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH GENTAMICIN. THIS FILE CONTAINS THE 30S SUBUNIT OF THE SECOND 70S RIBOSOME, WITH GENTAMICIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2QBC	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH GENTAMICIN. THIS FILE CONTAINS THE 50S SUBUNIT OF THE SECOND 70S RIBOSOME, WITH GENTAMICIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2QBD	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH RIBOSOME RECYCLING FACTOR (RRF). THIS FILE CONTAINS THE 30S SUBUNIT OF THE FIRST 70S	RIBOSOME

	RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	
2QBE	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH RIBOSOME RECYCLING FACTOR (RRF). THIS FILE CONTAINS THE 50S SUBUNIT OF THE FIRST 70S RIBOSOME, WITH RRF BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2QBF	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH RIBOSOME RECYCLING FACTOR (RRF). THIS FILE CONTAINS THE 30S SUBUNIT OF THE SECOND 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2QBG	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH RIBOSOME RECYCLING FACTOR (RRF). THIS FILE CONTAINS THE 50S SUBUNIT OF THE SECOND 70S RIBOSOME, WITH RRF BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2QBH	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH GENTAMICIN AND RIBOSOME RECYCLING FACTOR (RRF). THIS FILE CONTAINS THE 30S SUBUNIT OF THE FIRST 70S RIBOSOME, WITH GENTAMICIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2QBI	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH GENTAMICIN AND RIBOSOME RECYCLING FACTOR (RRF). THIS FILE CONTAINS THE 50S SUBUNIT OF THE FIRST 70S RIBOSOME, WITH GENTAMICIN AND RRF BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2QBJ	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH GENTAMICIN AND RIBOSOME RECYCLING FACTOR (RRF). THIS FILE CONTAINS THE 30S SUBUNIT OF THE SECOND 70S RIBOSOME, WITH GENTAMICIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2QBK	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH GENTAMICIN AND RIBOSOME RECYCLING FACTOR (RRF). THIS FILE CONTAINS THE 50S SUBUNIT OF THE SECOND 70S RIBOSOME, WITH GENTAMICIN AND RRF BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2QBW	THE CRYSTAL STRUCTURE OF PDZ-FIBRONECTIN FUSION PROTEIN	UNKNOWN FUNCTION
2QBY	CRYSTAL STRUCTURE OF A HETERODIMER OF CDC6/ORC1 INITIATORS BOUND TO ORIGIN DNA (FROM S. SOLFATARICUS)	REPLICATION/DNA
2QCS	A COMPLEX STRUCTURE BETWEEN THE CATALYTIC AND REGULATORY	TRANSFERASE/TRANSFERASE INHIBITOR

	SUBUNIT OF PROTEIN KINASE A THAT REPRESENTS THE INHIBITED STATE	
		LYASE
2QDY	CRYSTAL STRUCTURE OF FE-TYPE NHASE FROM RHODOCOCCUS ERYTHROPOLIS AJ270	
		HYDROLASE
2QE7	CRYSTAL STRUCTURE OF THE F1-ATPASE FROM THE THERMOALKALIPHILIC BACTERIUM BACILLUS SP. TA2.A1	
		IMMUNE SYSTEM
2QEJ	CRYSTAL STRUCTURE OF A STAPHYLOCOCCUS AUREUS PROTEIN (SSL7) IN COMPLEX WITH FC OF HUMAN IGA1	
		RIBOSOME
2QEX	NEGAMYCIN BINDS TO THE WALL OF THE NASCENT CHAIN EXIT TUNNEL OF THE 50S RIBOSOMAL SUBUNIT	
		CELL CYCLE/CELL CYCLE/CELL CYCLE
2QFA	CRYSTAL STRUCTURE OF A SURVIVIN-BOREALIN-INCENP CORE COMPLEX	
		TRANSCRIPTION REGULATION
2QFC	CRYSTAL STRUCTURE OF BACILLUS THURINGIENSIS PLCR COMPLEXED WITH PAPR	
		TRANSFERASE/TRANSFERASE REGULATOR
2QG9	STRUCTURE OF A REGULATORY SUBUNIT MUTANT D19A OF ATCASE FROM E. COLI	
		TRANSFERASE/TRANSFERASE REGULATOR
2QGF	STRUCTURE OF REGULATORY CHAIN MUTANT H20A OF ASPARATE TRANSCARBAMOYLASE FROM E. COLI	
		TRANSCRIPTION
2QGT	CRYSTAL STRUCTURE OF THE ESTROGEN RECEPTOR ALPHA LIGAND BINDING DOMAIN COMPLEXED TO AN ETHER ESTRADIOL COMPOUND	
		TRANSCRIPTION
2QGW	CRYSTAL STRUCTURE OF THE ESTROGEN RECEPTOR ALPHA LIGAND BINDING DOMAIN COMPLEXED WITH A CHLORO-INDAZOLE COMPOUND	
		TRANSCRIPTION
2QH6	CRYSTAL STRUCTURE OF THE ESTROGEN RECEPTOR ALPHA LIGAND BINDING DOMAIN COMPLEXED WITH AN OXABICYCLIC DIARYLETHYLENE COMPOUND	
		PROTEIN BINDING/LIGASE
2QHO	CRYSTAL STRUCTURE OF THE UBA DOMAIN FROM EDD UBIQUITIN LIGASE IN COMPLEX WITH UBIQUITIN	
		IMMUNE SYSTEM/VIRAL PROTEIN
2QHR	CRYSTAL STRUCTURE OF THE 13F6-1-2 FAB FRAGMENT BOUND TO ITS EBOLA VIRUS GLYCOPROTEIN PEPTIDE EPITOPE.	
		MEMBRANE PROTEIN
2QI9	ABC-TRANSPORTER BTUCD IN COMPLEX WITH ITS PERIPLASMIC BINDING PROTEIN BTUF	
		TRANSFERASE
2QIE	STAPHYLOCOCCUS AUREUS MOLYBDOPTERIN SYNTHASE IN COMPLEX WITH PRECURSOR Z	
		HORMONE
2QIU	STRUCTURE OF HUMAN ARG-INSULIN	
		SIGNALING PROTEIN/HYDROLASE
2QIY	YEAST DEUBIQUITINASE UBP3 AND BRE5 COFACTOR COMPLEX	
		CYTOKINE/RECEPTOR
2QJ9	CRYSTAL STRUCTURE ANALYSIS OF BMP-2 IN COMPLEX WITH BMPR-IA VARIANT B1	
		CYTOKINE/RECEPTOR

2QJA	CRYSTAL STRUCTURE ANALYSIS OF BMP-2 IN COMPLEX WITH BMPR-IA VARIANT B12	
2QJB	CRYSTAL STRUCTURE ANALYSIS OF BMP-2 IN COMPLEX WITH BMPR-IA VARIANT IA/IB	CYTOKINE/RECEPTOR
2QJK	CRYSTAL STRUCTURE ANALYSIS OF MUTANT RHODOBACTER SPHAEROIDES BC1 WITH STIGMATELLIN AND ANTIMYCIN	ELECTRON TRANSPORT
2QJP	RYSTAL STRUCTURE OF WILD TYPE RHODOBACTER SPHAEROIDES WITH STIGMATELLIN AND ANTIMYCIN INHIBITED	ELECTRON TRANSPORT
2QJY	RYSTAL STRUCTURE OF RHODOBACTER SPHAEROIDES DOUBLE MUTANT WITH STIGMATELLIN AND UQ2	OXIDOREDUCTASE
2QK7	COVALENT S-F HETERODIMER OF STAPHYLOCOCCAL GAMMA-HEMOLYSIN	TOXIN
2QKH	CRYSTAL STRUCTURE OF THE EXTRACELLULAR DOMAIN OF HUMAN GIP RECEPTOR IN COMPLEX WITH THE HORMONE GIP	SIGNALING PROTEIN/HORMONE
2QKI	HUMAN C3C IN COMPLEX WITH THE INHIBITOR COMPSTATIN	IMMUNE SYSTEM
2QKL	THE CRYSTAL STRUCTURE OF FISSION YEAST MRNA DECAPPING ENZYME DCP1-DCP2 COMPLEX	HYDROLASE
2QKM	THE CRYSTAL STRUCTURE OF FISSION YEAST MRNA DECAPPING ENZYME DCP1-DCP2 COMPLEX	HYDROLASE
2QKW	STRUCTURAL BASIS FOR ACTIVATION OF PLANT IMMUNITY BY BACTERIAL EFFECTOR PROTEIN AVRPTO	TRANSFERASE
2QL2	CRYSTAL STRUCTURE OF THE BASIC-HELIX-LOOP-HELIX DOMAINS OF THE HETERODIMER E47/NEUROD1 BOUND TO DNA	TRANSCRIPTION/DNA
2QL5	CRYSTAL STRUCTURE OF CASPASE-7 WITH INHIBITOR AC-DMQD-CHO	HYDROLASE
2QL7	CRYSTAL STRUCTURE OF CASPASE-7 WITH INHIBITOR AC-IEPD-CHO	HYDROLASE
2QL9	CRYSTAL STRUCTURE OF CASPASE-7 WITH INHIBITOR AC-DQMD-CHO	HYDROLASE
2QLB	CRYSTAL STRUCTURE OF CASPASE-7 WITH INHIBITOR AC-ESMD-CHO	HYDROLASE
2QLF	CRYSTAL STRUCTURE OF CASPASE-7 WITH INHIBITOR AC-DNLD-CHO	HYDROLASE
2QLJ	CRYSTAL STRUCTURE OF CASPASE-7 WITH INHIBITOR AC-WEHD-CHO	HYDROLASE
2QLL	HUMAN LIVER GLYCOGEN PHOSPHORYLASE- GL COMPLEX	TRANSFERASE
2QLS	CRYSTAL STRUCTURE OF HEMOGLOBIN FROM DOG (CANIS FAMILIARIS) AT 3.5 ANGSTROM RESOLUTION	TRANSPORT PROTEIN
2QLV	CRYSTAL STRUCTURE OF THE HETEROTRIMER CORE OF THE S. CEREVISIAE AMPK HOMOLOG SNF1	TRANSFERASE/PROTEIN BINDING
2QM6	CRYSTAL STRUCTURE OF HELICOBACTER PYLORI GAMMA-	TRANSFERASE

	GLUTAMYLTRANSPEPTIDASE IN COMPLEX WITH GLUTAMATE	
2QMB	STRUCTURE DETERMINATION OF HAEMOGLOBIN FROM TURKEY(MELEAGRIS GALLOPAVO) AT 2.8 ANGSTROM RESOLUTION	TRANSPORT PROTEIN
2QMC	CRYSTAL STRUCTURE OF HELICOBACTER PYLORI GAMMA-GLUTAMYLTRANSPEPTIDASE T380A MUTANT	TRANSFERASE
2QME	CRYSTAL STRUCTURE OF HUMAN RAC3 IN COMPLEX WITH CRIB DOMAIN OF HUMAN P21-ACTIVATED KINASE 1 (PAK1)	SIGNALING PROTEIN/TRANSFERASE
2QMU	STRUCTURE OF AN ARCHAEAL HETEROTRIMERIC INITIATION FACTOR 2 REVEALS A NUCLEOTIDE STATE BETWEEN THE GTP AND THE GDP STATES	TRANSLATION
2QN6	STRUCTURE OF AN ARCHAEAL HETEROTRIMERIC INITIATION FACTOR 2 REVEALS A NUCLEOTIDE STATE BETWEEN THE GTP AND THE GDP STATES	TRANSLATION
2QNA	CRYSTAL STRUCTURE OF HUMAN IMPORTIN-BETA (127-876) IN COMPLEX WITH THE IBB-DOMAIN OF SNURPORTIN1 (1-65)	TRANSPORT PROTEIN
2QNS	CRYSTAL STRUCTURE OF THE G-PROTEIN BETAGAMMA SUBUNIT BOUND TO A C-TERMINAL REGION OF THE PTH1 PARATHYROID HORMONE RECEPTOR	SIGNALING PROTEIN
2QOG	CROTOXIN B, THE BASIC PLA2 FROM CROTALUS DURISSUS TERRIFICUS.	HYDROLASE
2QOS	CRYSTAL STRUCTURE OF COMPLEMENT PROTEIN C8 IN COMPLEX WITH A PEPTIDE CONTAINING THE C8 BINDING SITE ON C8	IMMUNE SYSTEM
2QOU	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH SPECTINOMYCIN. THIS FILE CONTAINS THE 30S SUBUNIT OF THE FIRST 70S RIBOSOME, WITH SPECTINOMYCIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES.	RIBOSOME
2QOV	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH SPECTINOMYCIN. THIS FILE CONTAINS THE 50S SUBUNIT OF THE FIRST 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES.	RIBOSOME
2QOW	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH SPECTINOMYCIN. THIS FILE CONTAINS THE 30S SUBUNIT OF THE SECOND 70S RIBOSOME, WITH SPECTINOMYCIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES.	RIBOSOME
2QOX	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH SPECTINOMYCIN. THIS FILE CONTAINS THE 50S SUBUNIT OF THE SECOND 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES.	RIBOSOME
2QOY	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM	RIBOSOME

	ESCHERICHIA COLI IN COMPLEX WITH SPECTINOMYCIN AND NEOMYCIN. THIS FILE CONTAINS THE 30S SUBUNIT OF THE FIRST 70S RIBOSOME, WITH SPECTINOMYCIN AND NEOMYCIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES.	
2QOZ	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH SPECTINOMYCIN AND NEOMYCIN. THIS FILE CONTAINS THE 50S SUBUNIT OF THE FIRST 70S RIBOSOME, WITH NEOMYCIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES.	RIBOSOME
2QOG	CROTOXIN B, THE BASIC PLA2 FROM CROTALUS DURISSUS TERRIFICUS.	HYDROLASE
2QOS	CRYSTAL STRUCTURE OF COMPLEMENT PROTEIN C8 IN COMPLEX WITH A PEPTIDE CONTAINING THE C8 BINDING SITE ON C8	IMMUNE SYSTEM
2QOU	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH SPECTINOMYCIN. THIS FILE CONTAINS THE 30S SUBUNIT OF THE FIRST 70S RIBOSOME, WITH SPECTINOMYCIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES.	RIBOSOME
2QOV	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH SPECTINOMYCIN. THIS FILE CONTAINS THE 50S SUBUNIT OF THE FIRST 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES.	RIBOSOME
2QOW	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH SPECTINOMYCIN. THIS FILE CONTAINS THE 30S SUBUNIT OF THE SECOND 70S RIBOSOME, WITH SPECTINOMYCIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES.	RIBOSOME
2QOX	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH SPECTINOMYCIN. THIS FILE CONTAINS THE 50S SUBUNIT OF THE SECOND 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES.	RIBOSOME
2QOY	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH SPECTINOMYCIN AND NEOMYCIN. THIS FILE CONTAINS THE 30S SUBUNIT OF THE FIRST 70S RIBOSOME, WITH SPECTINOMYCIN AND NEOMYCIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES.	RIBOSOME
2QOZ	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH SPECTINOMYCIN AND NEOMYCIN. THIS FILE CONTAINS THE 50S SUBUNIT OF THE FIRST 70S RIBOSOME, WITH NEOMYCIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES.	RIBOSOME
2QP0	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH SPECTINOMYCIN AND NEOMYCIN. THIS FILE CONTAINS THE 30S SUBUNIT OF THE SECOND 70S RIBOSOME, WITH SPECTINOMYCIN AND NEOMYCIN BOUND. THE	RIBOSOME

	ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES.	
2QP1	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH SPECTINOMYCIN AND NEOMYCIN. THIS FILE CONTAINS THE 50S SUBUNIT OF THE SECOND 70S RIBOSOME, WITH NEOMYCIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES.	RIBOSOME
2QPD	AN UNEXPECTED OUTCOME OF SURFACE-ENGINEERING AN INTEGRAL MEMBRANE PROTEIN: IMPROVED CRYSTALLIZATION OF CYTOCHROME BA3 OXIDASE FROM THERMUS THERMOPHILUS	OXIDOREDUCTASE
2QPE	AN UNEXPECTED OUTCOME OF SURFACE-ENGINEERING AN INTEGRAL MEMBRANE PROTEIN: IMPROVED CRYSTALLIZATION OF CYTOCHROME BA3 OXIDASE FROM THERMUS THERMOPHILUS	OXIDOREDUCTASE
2QPY	AR LBD WITH SMALL MOLECULE	DNA BINDING PROTEIN
2QQC	E109Q MUTANT OF PYRUVOYL-DEPENDENT ARGININE DECARBOXYLASE FROM METHANOCOCCUS JANNASHII	LYASE
2QQD	N47A MUTANT OF PYRUVOYL-DEPENDENT ARGININE DECARBOXYLASE FROM METHANOCOCCUS JANNASHII	LYASE
2QQF	HST2 BOUND TO ADP-HPD AND ACETYLATED HISTONE H4	HYDROLASE
2QQG	HST2 BOUND TO ADP-HPD, ACETYLLATED HISTONE H4 AND NICOTINAMIDE	HYDROLASE
2QQK	NEUROPILIN-2 A1A2B1B2 DOMAINS IN COMPLEX WITH A SEMAPHORIN-BLOCKING FAB	SIGNALING PROTEIN
2QQL	NEUROPILIN-2 A1A2B1B2 DOMAINS IN COMPLEX WITH A SEMAPHORIN-BLOCKING FAB	SIGNALING PROTEIN
2QQN	NEUROPILIN-1 B1 DOMAIN IN COMPLEX WITH A VEGF-BLOCKING FAB	SIGNALING PROTEIN
2QR0	STRUCTURE OF VEGF COMPLEXED TO A FAB CONTAINING TYR AND SER IN THE CDRS	IMMUNE SYSTEM
2QR1	CRYSTAL STRUCTURE OF THE ADENYLATE SENSOR FROM AMP-ACTIVATED PROTEIN KINASE IN COMPLEX WITH ADP	TRANSFERASE
2QR9	CRYSTAL STRUCTURE OF THE ESTROGEN RECEPTOR ALPHA LIGAND BINDING DOMAIN COMPLEXED WITH AN OXABICYCLIC DERIVATIVE COMPOUND	TRANSCRIPTION
2QRC	CRYSTAL STRUCTURE OF THE ADENYLATE SENSOR FROM AMP-ACTIVATED PROTEIN KINASE IN COMPLEX WITH ADP AND AMP	TRANSFERASE
2QRD	CRYSTAL STRUCTURE OF THE ADENYLATE SENSOR FROM AMP-ACTIVATED PROTEIN KINASE IN COMPLEX WITH ADP AND ATP	TRANSFERASE
2QRE	CRYSTAL STRUCTURE OF THE ADENYLATE SENSOR FROM AMP-ACTIVATED PROTEIN KINASE IN COMPLEX WITH 5-AMINOIMIDAZOLE-	TRANSFERASE

	4-CARBOXAMIDE 1-BETA-D-RIBOFURANOTIDE (ZMP)	
2QRV	STRUCTURE OF DNMT3A-DNMT3L C-TERMINAL DOMAIN COMPLEX	TRANSFERASE/TRANSFERASE REGULATOR
2QSC	CRYSTAL STRUCTURE ANALYSIS OF ANTI-HIV-1 V3-FAB F425-B4E8 IN COMPLEX WITH A V3-PEPTIDE	IMMUNE SYSTEM
2QSE	CRYSTAL STRUCTURE OF THE ESTROGEN RECEPTOR ALPHA LIGAND BINDING DOMAIN COMPLEXED WITH BURNED MEAT COMPOUND 4-OH-PHIP	TRANSCRIPTION
2QSF	CRYSTAL STRUCTURE OF THE RAD4-RAD23 COMPLEX	DNA BINDING PROTEIN
2QSG	CRYSTAL STRUCTURE OF RAD4-RAD23 BOUND TO A UV-DAMAGED DNA	DNA BINDING PROTEIN/DNA
2QSH	CRYSTAL STRUCTURE OF RAD4-RAD23 BOUND TO A MISMATCH DNA	DNA BINDING PROTEIN/DNA
2QSP	BOVINE HEMOGLOBIN AT PH 5.7	TRANSPORT PROTEIN
2QSS	BOVINE HEMOGLOBIN AT PH 6.3	OXYGEN BINDING
2QT5	CRYSTAL STRUCTURE OF GRIP1 PDZ12 IN COMPLEX WITH THE FRAS1 PEPTIDE	PEPTIDE BINDING PROTEIN
2QTV	STRUCTURE OF SEC23-SAR1 COMPLEXED WITH THE ACTIVE FRAGMENT OF SEC31	PROTEIN TRANSPORT
2QTW	THE CRYSTAL STRUCTURE OF PCSK9 AT 1.9 ANGSTROMS RESOLUTION REVEALS STRUCTURAL HOMOLOGY TO RESISTIN WITHIN THE C-TERMINAL DOMAIN	HYDROLASE
2QU0	CRYSTAL STRUCTURE DETERMINATION OF SHEEP METHEMOGLOBIN AT 2.7 ANGSTROM RESOLUTION	OXYGEN STORAGE, OXYGEN TRANSPORT
2QUR	CRYSTAL STRUCTURE OF F327A/K285P MUTANT OF CAMP-DEPENDENT PROTEIN KINASE	SIGNALING PROTEIN, TRANSFERASE
2QV1	CRYSTAL STRUCTURE OF HCV NS3-4A V36M MUTANT	HYDROLASE
2QVS	CRYSTAL STRUCTURE OF TYPE IIA HOLOENZYME OF CAMP-DEPENDENT PROTEIN KINASE	TRANSFERASE/TRANSFERASE REGULATOR
2QWN	CRYSTAL STRUCTURE OF DISULFIDE-BOND-CROSSLINKED COMPLEX OF BOVINE HSC70 (1-386AA)R171C AND BOVINE AUXILIN (810-910AA) D876C IN THE ADP*PI STATE	CHAPERONE
2QWO	CRYSTAL STRUCTURE OF DISULFIDE-BOND-CROSSLINKED COMPLEX OF BOVINE HSC70 (1-394AA)R171C AND BOVINE AUXILIN (810-910AA) D876C IN THE ADP*PI FORM #1	CHAPERONE
2QWP	CRYSTAL STRUCTURE OF DISULFIDE-BOND-CROSSLINKED COMPLEX OF BOVINE HSC70 (1-394AA)R171C AND BOVINE AUXILIN (810-910AA) D876C IN THE ADP*PI FORM #2	CHAPERONE
2QWQ	CRYSTAL STRUCTURE OF DISULFIDE-BOND-CROSSLINKED COMPLEX OF	CHAPERONE

	BOVINE HSC70 (1-394AA)R171C AND BOVINE AUXILIN (810-910AA) D876C IN THE AMPPNP HYDROLYZED FORM	
2QWR	CRYSTAL STRUCTURE OF DISULFIDE-BOND-CROSSLINKED COMPLEX OF BOVINE HSC70 (1-394AA)R171C AND BOVINE AUXILIN (810-910AA) D876C IN THE AMPPNP INTACT FORM	CHAPERONE
2QXM	CRYSTAL STRUCTURE OF THE ESTROGEN RECEPTOR ALPHA LIGAND BINDING DOMAIN COMPLEXED TO BURNED MEAT COMPOUND PHIP	TRANSCRIPTION
2QXV	STRUCTURAL BASIS OF EZH2 RECOGNITION BY EED	GENE REGULATION
2QY0	ACTIVE DIMERIC STRUCTURE OF THE CATALYTIC DOMAIN OF C1R REVEALS ENZYME-PRODUCT LIKE CONTACTS	HYDROLASE
2QYF	CRYSTAL STRUCTURE OF THE MAD2/P31(COMET)/MAD2-BINDING PEPTIDE TERNARY COMPLEX	CELL CYCLE
2QYI	CRYSTAL STRUCTURE OF A BINARY COMPLEX BETWEEN AN ENGINEERED TRYPSIN INHIBITOR AND BOVINE TRYPSIN	HYDROLASE/HYDROLASE INHIBITOR
2QZO	CRYSTAL STRUCTURE OF THE ESTROGEN RECEPTOR ALPHA LIGAND BINDING DOMAIN COMPLEXED WITH WAY-169916	TRANSCRIPTION
2R00	RYSTAL STRUCTURE OF ASPARTATE SEMIALDEHYDE DEHYDROGENASE II COMPLEXED WITH ASA FROM VIBRIO CHOLERAE	OXIDOREDUCTASE
2R02	CRYSTAL STRUCTURE OF ALIX/AIP1 IN COMPLEX WITH THE HIV-1 YPLTSL LATE DOMAIN	APOPTOSIS
2R03	CRYSTAL STRUCTURE OF ALIX/AIP1 IN COMPLEX WITH THE YPDL LATE DOMAIN	APOPTOSIS
2R05	CRYSTAL STRUCTURE OF ALIX/AIP1 IN COMPLEX WITH THE HIV-1 YPLASL LATE DOMAIN	APOPTOSIS
2R0K	PROTEASE DOMAIN OF HGFA WITH INHIBITOR FAB58	HYDROLASE, IMMUNE SYSTEM
2R0L	SHORT FORM HGFA WITH INHIBITORY FAB75	HYDROLASE, IMMUNE SYSTEM
2R0W	PFA2 FAB COMPLEXED WITH ABETA1-8	IMMUNE SYSTEM
2R0Z	PFA1 FAB COMPLEXED WITH GRIPI PEPTIDE FRAGMENT	IMMUNE SYSTEM
2R17	FUNCTIONAL ARCHITECTURE OF THE RETROMER CARGO-RECOGNITION COMPLEX	PROTEIN TRANSPORT
2R1H	MET-TROUT IV HEMOGLOBIN AT PH 6.3	OXYGEN BINDING
2R1R	RIBONUCLEOTIDE REDUCTASE R1 PROTEIN WITH DTTP OCCUPYING THE SPECIFICITY SITE FROM ESCHERICHIA COLI	COMPLEX (OXIDOREDUCTASE/PEPTIDE)
2R1T	DOPAMINE QUINONE CONJUGATION TO DJ-1	PROTEIN BINDING
2R1V	NOREPINEPHRINE QUINONE CONJUGATION TO DJ-1	PROTEIN BINDING

2R25	COMPLEX OF YPD1 AND SLN1-R1 WITH BOUND MG2+ AND BEF3-	SIGNALING PROTEIN/TRANSFERASE
2R28	THE COMPLEX STRUCTURE OF CALMODULIN BOUND TO A CALCINEURIN PEPTIDE	METAL BINDING PROTEIN/HYDROLASE
2R2L	STRUCTURE OF FARNESYL PROTEIN TRANSFERASE BOUND TO PB-93	TRANSFERASE
2R2M	2-(2-CHLORO-6-FLUOROPHENYL)ACETAMIDES AS POTENT THROMBIN INHIBITORS	HYDROLASE
2R34	CRYSTAL STRUCTURE OF MN HUMAN ARG-INSULIN	HORMONE
2R35	CRYSTAL STRUCTURE OF RB HUMAN ARG-INSULIN	HORMONE
2R36	CRYSTAL STRUCTURE OF NI HUMAN ARG-INSULIN	HORMONE
2R3C	STRUCTURE OF THE GP41 N-PEPTIDE IN COMPLEX WITH THE HIV ENTRY INHIBITOR PIE1	VIRAL PROTEIN
2R3Y	CRYSTAL STRUCTURE OF THE DEGS PROTEASE IN COMPLEX WITH THE YWF ACTIVATING PEPTIDE	HYDROLASE/HYDROLASE ACTIVATOR
2R40	CRYSTAL STRUCTURE OF 20E BOUND ECR/USP	GENE REGULATION
2R4R	CRYSTAL STRUCTURE OF THE HUMAN BETA2 ADRENOCEPTOR	SIGNALING PROTEIN
2R4S	CRYSTAL STRUCTURE OF THE HUMAN BETA2 ADRENOCEPTOR	SIGNALING PROTEIN
2R56	CRYSTAL STRUCTURE OF A RECOMBINANT IGE FAB FRAGMENT IN COMPLEX WITH BOVINE BETA-LACTOGLOBULIN ALLERGEN	IMMUNE SYSTEM
2R5B	STRUCTURE OF THE GP41 N-TRIMER IN COMPLEX WITH THE HIV ENTRY INHIBITOR PIE7	VIRAL PROTEIN
2R5C	AEDES KYNURENINE AMINOTRANSFERASE IN COMPLEX WITH CYSTEINE	TRANSFERASE
2R5D	STRUCTURE OF THE GP41 N-TRIMER IN COMPLEX WITH THE HIV ENTRY INHIBITOR PIE7	VIRAL PROTEIN
2R5Y	STRUCTURE OF SCR/EXD COMPLEX BOUND TO A CONSENSUS HOX-EXD SITE	TRANSCRIPTION/DNA
2R5Z	STRUCTURE OF SCR/EXD COMPLEX BOUND TO A DNA SEQUENCE DERIVED FROM THE FKH GENE	TRANSCRIPTION/DNA
2R6A	CRYSTAL FORM BH1	REPLICATION
2R6C	CRYSTAL FORM BH2	REPLICATION
2R6G	THE CRYSTAL STRUCTURE OF THE E. COLI MALTOSE TRANSPORTER	HYDROLASE/TRANSPORT PROTEIN
2R7G	STRUCTURE OF THE RETINOBLASTOMA PROTEIN POCKET DOMAIN IN COMPLEX WITH ADENOVIRUS E1A CR1 DOMAIN	TRANSCRIPTION REPRESSOR, CELL CYCLE
		TRANSCRIPTION, TRANSFERASE/DNA/RNA

2R7Z	CISPLATIN LESION CONTAINING RNA POLYMERASE II ELONGATION COMPLEX	
2R80	PIGEON HEMOGLOBIN (OXY FORM)	OXYGEN BINDING
2R8S	HIGH RESOLUTION STRUCTURE OF A SPECIFIC SYNTHETIC FAB BOUND TO P4-P6 RNA RIBOZYME DOMAIN	IMMUNE SYSTEM/RNA
2R92	ELONGATION COMPLEX OF RNA POLYMERASE II WITH ARTIFICIAL RDRP SCAFFOLD	TRANSFERASE/RNA
2R93	ELONGATION COMPLEX OF RNA POLYMERASE II WITH A HEPATITIS DELTA VIRUS-DERIVED RNA STEM LOOP	TRANSFERASE/RNA
2R9B	STRUCTURAL ANALYSIS OF PLASMEPSIN 2 FROM PLASMODIUM FALCIPARUM COMPLEXED WITH A PEPTIDE-BASED INHIBITOR	HYDROLASE
2R9H	CRYSTAL STRUCTURE OF Q207C MUTANT OF CLC-EC1 IN COMPLEX WITH FAB	MEMBRANE PROTEIN
2R9K	CRYSTAL STRUCTURE OF MISTELTOE LECTIN I IN COMPLEX WITH PHLORETAMIDE	HYDROLASE
2R9P	HUMAN MESOTRYPSIN COMPLEXED WITH BOVINE PANCREATIC TRYPSIN INHIBITOR(BPTI)	HYDROLASE/HYDROLASE INHIBITOR
2R9Q	CRYSTAL STRUCTURE OF 2'-DEOXYCYTIDINE 5'-TRIPHOSPHATE DEAMINASE FROM AGROBACTERIUM TUMEFACIENS	HYDROLASE
2R9R	SHAKER FAMILY VOLTAGE DEPENDENT POTASSIUM CHANNEL (KV1.2-KV2.1 PADDLE CHIMERA CHANNEL) IN ASSOCIATION WITH BETA SUBUNIT	MEMBRANE PROTEIN, TRANSPORT PROTEIN
2RA0	X-RAY STRUCTURE OF FXA IN COMPLEX WITH 7-FLUOROINDAZOLE	HYDROLASE
2RAO	X RAY CRYSTAL STRUCTURE OF RABBIT HEMOGLOBIN (OXY FORM) AT 2.0 ANGSTROM RESOLUTION	OXYGEN BINDING
2RAW	CRYSTAL STRUCTURE OF THE BOREALIN-SURVIVIN COMPLEX	CELL CYCLE
2RAX	CRYSTAL STRUCTURE OF BOREALIN (20-78) BOUND TO SURVIVIN (1-120)	CELL CYCLE
2RCR	STRUCTURE OF THE MEMBRANE-BOUND PROTEIN PHOTOSYNTHETIC REACTION CENTER FROM RHODOBACTER SPHAEROIDES	PHOTOSYNTHETIC REACTION CENTER
2RCS	IMMUNOGLOBULIN 48G7 GERMLINE FAB-AFFINITY MATURATION OF AN ESTEROLYTIC ANTIBODY	GERMLINE ANTIBODY
2RD0	STRUCTURE OF A HUMAN P110ALPHA/P85ALPHA COMPLEX	TRANSFERASE/ONCOPROTEIN
2RD4	DESIGN OF SPECIFIC INHIBITORS OF PHOSPHOLIPASE A2: CRYSTAL STRUCTURE OF THE COMPLEX OF PHOSPHOLIPASE A2 WITH PENTAPEPTIDE LEU-VAL-PHE-PHE-ALA AT 2.9 A RESOLUTION	HYDROLASE
		PROTEIN BINDING

2RD5	STRUCTURAL BASIS FOR THE REGULATION OF N-ACETYLGLUTAMATE KINASE BY PII IN ARABIDOPSIS THALIANA	
2RD7	UMAN COMPLEMENT MEMBRANE ATTACK PROTEINS SHARE A COMMON FOLD WITH BACTERIAL CYTOLYSINS	IMMUNE SYSTEM
2RD8	HUMAN THYMIDYLATE SYNTHASE STABILIZED IN ACTIVE CONFORMATION BY R163K MUTATION: ASYMMETRY AND REACTIVITY OF CYS195	TRANSFERASE
2RDB	-RAY CRYSTAL STRUCTURE OF TOLUENE/O-XYLENE MONOOXYGENASE HYDROXYLASE I100W MUTANT	OXIDOREDUCTASE
2RDD	X-RAY CRYSTAL STRUCTURE OF ACRB IN COMPLEX WITH A NOVEL TRANSMEMBRANE HELIX.	MEMBRANE PROTEIN/TRANSPORT PROTEIN
2REM	CRYSTAL STRUCTURE OF OXIDOREDUCTASE DSBA FROM XYLELLA FASTIDIOSA	OXIDOREDUCTASE
2REQ	METHYLMALONYL-COA MUTASE, NON-PRODUCTIVE COA COMPLEX, IN OPEN CONFORMATION REPRESENTING SUBSTRATE-FREE STATE	ISOMERASE
2RET	THE CRYSTAL STRUCTURE OF A BINARY COMPLEX OF TWO PSEUDOPILINS: EPSI AND EPSJ FROM THE TYPE 2 SECRETION SYSTEM OF VIBRIO VULNIFICUS	PROTEIN TRANSPORT
2REX	CRYSTAL STRUCTURE OF THE EFFECTOR DOMAIN OF PLXNB1 BOUND WITH RND1 GTPASE	SIGNALING PROTEIN/LIPOPROTEIN
2RF2	HIV REVERSE TRANSCRIPTASE IN COMPLEX WITH INHIBITOR 7E (NNRTI)	TRANSFERASE
2RF4	CRYSTAL STRUCTURE OF THE RNA POLYMERASE I SUBCOMPLEX A14/43	TRANSFERASE
2RF9	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE EGFR KINASE DOMAIN AND A MIG6 PEPTIDE	TRANSFERASE
2RFD	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE EGFR KINASE DOMAIN AND A MIG6 PEPTIDE	TRANSFERASE
2RFE	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE EGFR KINASE DOMAIN AND A MIG6 PEPTIDE	TRANSFERASE
2RFI	RYSTAL STRUCTURE OF CATALYTIC DOMAIN OF HUMAN EUCHROMATIC HISTONE METHYLTRANSFERASE 1 IN COMPLEX WITH SAH AND DIMETHYLATED H3K9 PEPTIDE	TRANSFERASE
2RFK	SUBSTRATE RNA POSITIONING IN THE ARCHAEAL H/ACA RIBONUCLEOPROTEIN COMPLEX	ISOMERASE/RNA
2RFT	CRYSTAL STRUCTURE OF INFLUENZA B VIRUS HEMAGGLUTININ IN COMPLEX WITH LSTA RECEPTOR ANALOG	VIRAL PROTEIN
2RFU	CRYSTAL STRUCTURE OF INFLUENZA B VIRUS HEMAGGLUTININ IN COMPLEX WITH LSTC RECEPTOR ANALOG	VIRAL PROTEIN

2RFX	CRYSTAL STRUCTURE OF HLA-B*5701, PRESENTING THE SELF PEPTIDE, LSSPVTKSF	IMMUNE SYSTEM
2RG9	CRYSTAL STRUCTURE OF VISCUM ALBUM MISTLETOE LECTIN I IN NATIVE STATE AT 1.95 A RESOLUTION, COMPARISON OF STRUCTURE ACTIVE SITE CONFORMATION IN RICIN AND IN VISCUMIN	HYDROLASE, TOXIN
2RGN	CRYSTAL STRUCTURE OF P63RHOGEF COMPLEX WITH GALPHA-Q AND RHOA	SIGNALING PROTEIN COMPLEX
2RH9	TRYPTOPHAN SYNTHASE COMPLEXED WITH IGP, INTERNAL ALDIMINE, PH 9.0	LYASE
2RHG	TRYPTOPHAN SYNTHASE COMPLEXED WITH IGP, PH 7.0, INTERNAL ALDIMINE	LYASE
2RHK	CRYSTAL STRUCTURE OF INFLUENZA A NS1A PROTEIN IN COMPLEX WITH F2F3 FRAGMENT OF HUMAN CELLULAR FACTOR CPSF30	VIRAL PROTEIN/NUCLEAR PROTEIN
2RHQ	PHERS FROM STAPHYLOCOCCUS HAEMOLYTICUS- RATIONAL PROTEIN ENGINEERING AND INHIBITOR STUDIES	LIGASE
2RHS	PHERS FROM STAPHYLOCOCCUS HAEMOLYTICUS- RATIONAL PROTEIN ENGINEERING AND INHIBITOR STUDIES	LIGASE
2RI4	CRYSTAL STRUCTURE DETERMINATION OF GOAT METHEMOGLOBIN AT 2.7 ANGSTROM	OXYGEN STORAGE, OXYGEN TRANSPORT
2RI7	CRYSTAL STRUCTURE OF PHD FINGER-LINKER-BROMODOMAIN Y17E MUTANT FROM HUMAN BPTF IN THE H3(1-9)K4ME2 BOUND STATE	TRANSCRIPTION/NUCLEAR PROTEIN
2RII	CRYSTAL STRUCTURE OF HUMAN PEROXIREDOXIN I IN COMPLEX WITH SULFIREDOXIN	OXIDOREDUCTASE COMPLEX
2RIV	CRYSTAL STRUCTURE OF THE REACTIVE LOOP CLEAVED HUMAN THYROXINE BINDING GLOBULIN	SIGNALING PROTEIN
2RIW	THE REACTIVE LOOP CLEAVED HUMAN THYROXINE BINDING GLOBULIN COMPLEXED WITH THYROXINE	SIGNALING PROTEIN
2RJE	CRYSTAL STRUCTURE OF L3MBTL1 IN COMPLEX WITH H4K20ME2 (RESIDUES 17-25), ORTHORHOMBIC FORM II	TRANSCRIPTION
2RJF	CRYSTAL STRUCTURE OF L3MBTL1 IN COMPLEX WITH H4K20ME2 (RESIDUES 12-30), ORTHORHOMBIC FORM I	TRANSCRIPTION
2RKI	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE (RT) IN COMPLEX WITH A TRIAZOLE DERIVED NNRTI	TRANSFERASE
2RKM	STRUCTURE OF OPPA COMPLEXED WITH LYS-LYS	COMPLEX (BINDING PROTEIN/DIPEPTIDE)
2RLN	THERMODYNAMIC AND STRUCTURAL CONSEQUENCES OF CHANGING A SULPHUR ATOM TO A METHYLENE GROUP IN THE M13NLE MUTATION IN RIBONUCLEASE S	HYDROLASE(PHOSPHORIC DIESTER,RNA)

2RMA	CRYSTAL STRUCTURES OF CYCLOPHILIN A COMPLEXED WITH CYCLOSPORIN A AND N-METHYL-4-[(E)-2-BUTENYL]-4,4-DIMETHYLTHREONINE CYCLOSPORIN A	COMPLEX (ISOMERASE/IMMUNOSUPPRESSANT)
2RMB	CRYSTAL STRUCTURES OF CYCLOPHILIN A COMPLEXED WITH CYCLOSPORIN A AND N-METHYL-4-[(E)-2-BUTENYL]-4,4-DIMETHYLTHREONINE CYCLOSPORIN A	COMPLEX (ISOMERASE/IMMUNOSUPPRESSANT)
2RMC	CRYSTAL STRUCTURE OF MURINE CYCLOPHILIN C COMPLEXED WITH IMMUNOSUPPRESSIVE DRUG CYCLOSPORIN A	COMPLEX (ISOMERASE/IMMUNOSUPPRESSANT)
2ROD	SOLUTION STRUCTURE OF MCL-1 COMPLEXED WITH NOXAA	APOPTOSIS
2SCU	A DETAILED DESCRIPTION OF THE STRUCTURE OF SUCCINYL-COA SYNTHETASE FROM ESCHERICHIA COLI	LIGASE
2SEB	X-RAY CRYSTAL STRUCTURE OF HLA-DR4 COMPLEXED WITH A PEPTIDE FROM HUMAN COLLAGEN II	COMPLEX (MHC CLASS II/SUPERANTIGEN)
2SEC	STRUCTURAL COMPARISON OF TWO SERINE PROTEINASE-PROTEIN INHIBITOR COMPLEXES. EGLIN-C-SUBTILISIN CARLSBERG AND CI-2-SUBTILISIN NOVO	COMPLEX(SERINE PROTEINASE-INHIBITOR)
2SGD	ASP 18 VARIANT OF TURKEY OVOMUCOID INHIBITOR THIRD DOMAIN COMPLEXED WITH STREPTOMYCES GRISEUS PROTEINASE B AT PH 10.7	HYDROLASE/HYDROLASE INHIBITOR
2SGE	GLU 18 VARIANT OF TURKEY OVOMUCOID INHIBITOR THIRD DOMAIN COMPLEXED WITH STREPTOMYCES GRISEUS PROTEINASE B AT PH 10.7	HYDROLASE/HYDROLASE INHIBITOR
2SGF	PHE 18 VARIANT OF TURKEY OVOMUCOID INHIBITOR THIRD DOMAIN COMPLEXED WITH STREPTOMYCES GRISEUS PROTEINASE B	HYDROLASE/HYDROLASE INHIBITOR
2SGP	PRO 18 VARIANT OF TURKEY OVOMUCOID INHIBITOR THIRD DOMAIN COMPLEXED WITH STREPTOMYCES GRISEUS PROTEINASE B AT PH 6.5	HYDROLASE/INHIBITOR
2SGQ	GLN 18 VARIANT OF TURKEY OVOMUCOID INHIBITOR THIRD DOMAIN COMPLEXED WITH STREPTOMYCES GRISEUS PROTEINASE B AT PH 6.5	HYDROLASE/HYDROLASE INHIBITOR
2SIC	REFINED CRYSTAL STRUCTURE OF THE COMPLEX OF SUBTILISIN BPN' AND STREPTOMYCES SUBTILISIN INHIBITOR AT 1.8 ANGSTROMS RESOLUTION	COMPLEX (PROTEINASE/INHIBITOR)
2SIV	SIV GP41 CORE STRUCTURE	ENVELOPE GLYCOPROTEIN
2SNI	STRUCTURAL COMPARISON OF TWO SERINE PROTEINASE-PROTEIN INHIBITOR COMPLEXES. EGLIN-C-SUBTILISIN CARLSBERG AND CI-2-SUBTILISIN NOVO	COMPLEX (PROTEINASE/INHIBITOR)
2STA	ANIONIC SALMON TRYPSIN IN COMPLEX WITH SQUASH SEED INHIBITOR (CUCURBITA MAXIMA TRYPSIN INHIBITOR I)	HYDROLASE/HYDROLASE INHIBITOR
2TCI	X-RAY CRYSTALLOGRAPHIC STUDIES ON HEXAMERIC INSULINS IN THE PRESENCE OF HELIX-STABILIZING AGENTS, THIOCYANATE, METHYLPARABEN AND PHENOL	HORMONE

2TEC	MOLECULAR DYNAMICS REFINEMENT OF A THERMITASE-EGLIN-C COMPLEX AT 1.98 ANGSTROMS RESOLUTION AND COMPARISON OF TWO CRYSTAL FORMS THAT DIFFER IN CALCIUM CONTENT	COMPLEX(SERINE PROTEINASE-INHIBITOR)
2THF	STRUCTURE OF HUMAN ALPHA-THROMBIN Y225F MUTANT BOUND TO D-PHE-PRO-ARG-CHLOROMETHYLKETONE	SERINE PROTEASE
2TLX	THERMOLYSIN (NATIVE)	HYDROLASE
2TRC	PHOSDUCIN/TRANSDUCIN BETA-GAMMA COMPLEX	COMPLEX (TRANSDUCER/TRANSDUCTION)
2TRS	CRYSTAL STRUCTURES OF MUTANT (BETAK87T) TRYPTOPHAN SYNTHASE ALPHA2 BETA2 COMPLEX WITH LIGANDS BOUND TO THE ACTIVE SITES OF THE ALPHA AND BETA SUBUNITS REVEAL LIGAND-INDUCED CONFORMATIONAL CHANGES	LYASE
2TSY	CRYSTAL STRUCTURES OF MUTANT (BETAK87T) TRYPTOPHAN SYNTHASE ALPHA2 BETA2 COMPLEX WITH LIGANDS BOUND TO THE ACTIVE SITES OF THE ALPHA AND BETA SUBUNITS REVEAL LIGAND-INDUCED CONFORMATIONAL CHANGES	LYASE
2TYS	CRYSTAL STRUCTURES OF MUTANT (BETAK87T) TRYPTOPHAN SYNTHASE ALPHA2 BETA2 COMPLEX WITH LIGANDS BOUND TO THE ACTIVE SITES OF THE ALPHA AND BETA SUBUNITS REVEAL LIGAND-INDUCED CONFORMATIONAL CHANGES	LYASE
2UBP	STRUCTURE OF NATIVE UREASE FROM BACILLUS PASTEURII	HYDROLASE
2UU9	STRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT COMPLEXED WITH A VALINE-ASL WITH CMO5U IN POSITION 34 BOUND TO AN MRNA WITH A GUG-CODON IN THE A-SITE AND PAROMOMYCIN.	RIBOSOME
2UUA	STRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT COMPLEXED WITH A VALINE-ASL WITH CMO5U IN POSITION 34 BOUND TO AN MRNA WITH A GUC-CODON IN THE A-SITE AND PAROMOMYCIN.	RIBOSOME
2UUB	STRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT COMPLEXED WITH A VALINE-ASL WITH CMO5U IN POSITION 34 BOUND TO AN MRNA WITH A GUU-CODON IN THE A-SITE AND PAROMOMYCIN.	RIBOSOME
2UUC	STRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT COMPLEXED WITH A VALINE-ASL WITH CMO5U IN POSITION 34 BOUND TO AN MRNA WITH A GUA-CODON IN THE A-SITE AND PAROMOMYCIN.	RIBOSOME
2UUE	REPLACE: A STRATEGY FOR ITERATIVE DESIGN OF CYCLIN BINDING GROOVE INHIBITORS	TRANSFERASE
2UUF	THROMBIN-HIRUGEN BINARY COMPLEX AT 1.26A RESOLUTION	BLOOD CLOTTING
2UUG	ESCHERICHIA COLI URACIL-DNA GLYCOSYLASE:INHIBITOR COMPLEX	REPLICATION, HYDROLASE

	WITH H187D MUTANT UDG AND WILD-TYPE UGI	
2UUJ	THROMBIN-HIRUGEN-GW473178 TERNARY COMPLEX AT 1.32A RESOLUTION	BLOOD CLOTTING
2UUK	THROMBIN-HIRUGEN-GW420128 TERNARY COMPLEX AT 1.39A RESOLUTION	BLOOD CLOTTING
2UUM	CRYSTAL STRUCTURE OF C-PHYCOCYANIN FROM PHORMIDIUM, LYNGBYA SPP. (MARINE) AND SPIRULINA SP. (FRESH WATER) SHOWS TWO DIFFERENT WAYS OF ENERGY TRANSFER BETWEEN TWO HEXAMERS.	ELECTRON TRANSPORT
2UUN	CRYSTAL STRUCTURE OF C-PHYCOCYANIN FROM PHORMIDIUM, LYNGBYA SPP. (MARINE) AND SPIRULINA SP. (FRESH WATER) SHOWS TWO DIFFERENT WAYS OF ENERGY TRANSFER BETWEEN TWO HEXAMERS.	ELECTRON TRANSPORT
2UVP	CRYSTAL STRUCTURE OF HOBA (HP1230)FROM HELICOBACTER PYLORI	UNKNOWN FUNCTION
2UVX	STRUCTURE OF PKA-PKB CHIMERA COMPLEXED WITH 7-AZAINDOLE	TRANSFERASE/INHIBITOR COMPLEX
2UVY	STRUCTURE OF PKA-PKB CHIMERA COMPLEXED WITH METHYL-(4-(9H-PURIN-6-YL)-BENZYL)-AMINE	TRANSFERASE/INHIBITOR COMPLEX
2UVZ	STRUCTURE OF PKA-PKB CHIMERA COMPLEXED WITH C-PHENYL-C-(4-(9H-PURIN-6-YL)-PHENYL)-METHYLAMINE	TRANSFERASE/INHIBITOR COMPLEX
2UW0	STRUCTURE OF PKA-PKB CHIMERA COMPLEXED WITH 6-(4-(4-(4-CHLORO-PHENYL)-PIPERIDIN-4-YL)-PHENYL)-9H-PURINE	TRANSFERASE/INHIBITOR COMPLEX
2UW1	IVY DESATURASE STRUCTURE	OXIDOREDUCTASE
2UW3	STRUCTURE OF PKA-PKB CHIMERA COMPLEXED WITH 5-METHYL-4-PHENYL-1H-PYRAZOLE	TRANSFERASE/INHIBITOR COMPLEX
2UW4	STRUCTURE OF PKA-PKB CHIMERA COMPLEXED WITH 2-(4-(5-METHYL-1H-PYRAZOL-4-YL)-PHENYL)-ETHYLAMINE	TRANSFERASE
2UW5	STRUCTURE OF PKA-PKB CHIMERA COMPLEXED WITH (R)-2-(4-CHLORO-PHENYL)-2-(4-1H-PYRAZOL-4-YL)-PHENYL)-ETHYLAMINE	TRANSFERASE/INHIBITOR COMPLEX
2UW6	STRUCTURE OF PKA-PKB CHIMERA COMPLEXED WITH (S)-2-(4-CHLORO-PHENYL)-2-(4-1H-PYRAZOL-4-YL)-PHENYL)-ETHYLAMINE	TRANSFERASE/INHIBITOR COMPLEX
2UW7	STRUCTURE OF PKA-PKB CHIMERA COMPLEXED WITH 4-(4-CHLORO-PHENYL)-4-(4-(1H-PYRAZOL-4-YL)-PHENYL)-PIPERIDINE	TRANSFERASE/INHIBITOR COMPLEX
2UW8	STRUCTURE OF PKA-PKB CHIMERA COMPLEXED WITH 2-(4-CHLORO-PHENYL)-2-PHENYL-ETHYLAMINE	TRANSFERASE/INHIBITOR COMPLEX
2UW9	STRUCTURE OF PKB-BETA (AKT2) COMPLEXED WITH 4-(4-CHLORO-PHENYL)-4-(4-(1H-PYRAZOL-4-YL)-PHENYL)-PIPERIDINE	TRANSFERASE/INHIBITOR COMPLEX
2UWE	LARGE CDR3A LOOP ALTERATION AS A FUNCTION OF MHC MUTATION	IMMUNE SYSTEM
2UWJ	STRUCTURE OF THE HETEROTRIMERIC COMPLEX WHICH REGULATES	CHAPERONE

	TYPE III SECRETION NEEDLE FORMATION	
2UWL	SELECTIVE AND DUAL ACTION ORALLY ACTIVE INHIBITORS OF THROMBIN AND FACTOR XA	HYDROLASE
2UWO	SELECTIVE AND DUAL ACTION ORALLY ACTIVE INHIBITORS OF THROMBIN AND FACTOR XA	HYDROLASE
2UWP	FACTOR XA INHIBITOR COMPLEX	HYDROLASE
2UWS	X-RAY HIGH RESOLUTION STRUCTURE OF THE PHOTOSYNTHETIC REACTION CENTER FROM RB. SPHAEROIDES AT PH 6.5 IN THE CHARGE-SEPARATED STATE	PHOTOSYNTHESIS
2UWT	X-RAY HIGH RESOLUTION STRUCTURE OF THE PHOTOSYNTHETIC REACTION CENTER FROM RB. SPHAEROIDES AT PH 6.5 IN THE CHARGE-SEPARATED STATE 2ND DATASET	PHOTOSYNTHESIS
2UWU	X-RAY HIGH RESOLUTION STRUCTURE OF THE PHOTOSYNTHETIC REACTION CENTER FROM RB. SPHAEROIDES AT PH 6.5 IN THE NEUTRAL STATE, 2ND DATASET	PHOTOSYNTHESIS
2UWV	X-RAY HIGH RESOLUTION STRUCTURE OF THE PHOTOSYNTHETIC REACTION CENTER FROM RB. SPHAEROIDES AT PH 6.5 IN THE CHARGE-SEPARATED STATE, 3RD DATASET	PHOTOSYNTHESIS
2UWW	X-RAY HIGH RESOLUTION STRUCTURE OF THE PHOTOSYNTHETIC REACTION CENTER FROM RB. SPHAEROIDES AT PH 6.5 IN THE NEUTRAL STATE	PHOTOSYNTHESIS
2UX3	X-RAY HIGH RESOLUTION STRUCTURE OF THE PHOTOSYNTHETIC REACTION CENTER FROM RB. SPHAEROIDES AT PH 9 IN THE NEUTRAL STATE	PHOTOSYNTHESIS
2UX4	X-RAY HIGH RESOLUTION STRUCTURE OF THE PHOTOSYNTHETIC REACTION CENTER FROM RB. SPHAEROIDES AT PH 9 IN THE CHARGE-SEPARATED STATE, 2ND DATASET	PHOTOSYNTHESIS
2UX5	X-RAY HIGH RESOLUTION STRUCTURE OF THE PHOTOSYNTHETIC REACTION CENTER FROM RB. SPHAEROIDES AT PH 9 IN THE CHARGE-SEPARATED STATE	PHOTOSYNTHESIS
2UXB	CRYSTAL STRUCTURE OF AN EXTENDED TRNA ANTICODON STEM LOOP IN COMPLEX WITH ITS COGNATE MRNA GGGU IN THE CONTEXT OF THE THERMUS THERMOPHILUS 30S SUBUNIT.	RIBOSOME
2UXC	CRYSTAL STRUCTURE OF AN EXTENDED TRNA ANTICODON STEM LOOP IN COMPLEX WITH ITS COGNATE MRNA UCGU IN THE CONTEXT OF THE THERMUS THERMOPHILUS 30S SUBUNIT.	RIBOSOME
2UXD	CRYSTAL STRUCTURE OF AN EXTENDED TRNA ANTICODON STEM LOOP IN COMPLEX WITH ITS COGNATE MRNA CGGG IN THE CONTEXT OF THE THERMUS THERMOPHILUS 30S SUBUNIT.	RIBOSOME
2UXJ	X-RAY HIGH RESOLUTION STRUCTURE OF THE PHOTOSYNTHETIC	PHOTOSYNTHESIS

REACTION CENTER FROM RB. SPHAEROIDES AT PH 10 IN THE NEUTRAL STATE

PHOTOSYNTHESIS

2UXK X-RAY HIGH RESOLUTION STRUCTURE OF THE PHOTOSYNTHETIC REACTION CENTER FROM RB. SPHAEROIDES AT PH 10 IN THE CHARGE-SEPARATED STATE

PHOTOSYNTHESIS

2UXL X-RAY HIGH RESOLUTION STRUCTURE OF THE PHOTOSYNTHETIC REACTION CENTER FROM RB. SPHAEROIDES AT PH 10 IN THE NEUTRAL STATE, 2ND DATASET

PHOTOSYNTHESIS

2UXM X-RAY HIGH RESOLUTION STRUCTURE OF THE PHOTOSYNTHETIC REACTION CENTER FROM RB. SPHAEROIDES AT PH 10 IN THE CHARGE-SEPARATED STATE, 2ND DATASET

OXIDOREDUCTASE/REPRESSOR COMPLEX

2UXN STRUCTURAL BASIS OF HISTONE DEMETHYLATION BY LSD1 REVEALED BY SUICIDE INACTIVATION

OXIDOREDUCTASE/REPRESSOR

2UXX HUMAN LSD1 HISTONE DEMETHYLASE-COREST IN COMPLEX WITH AN FAD-TRANYLCYPROMINE ADDUCT

RNA-BINDING PROTEIN

2UY1 CRYSTAL STRUCTURE OF CSTF-77

CHAPERONE

2UY6 CRYSTAL STRUCTURE OF THE P PILUS ROD SUBUNIT PAPA

CHAPERONE

2UY7 CRYSTAL STRUCTURE OF THE P PILUS ROD SUBUNIT PAPA

IMMUNE SYSTEM

2UYL RYSTAL STRUCTURE OF A MONOCLONAL ANTIBODY DIRECTED AGAINST AN ANTIGENIC DETERMINANT COMMON TO OGAWA AND INABA SEROTYPES OF VIBRIO CHOLERAE O1

UNKNOWN FUNCTION

2UYN CRYSTAL STRUCTURE OF E. COLI TDCF WITH BOUND 2-KETOBUTYRATE

LIGASE

2UYZ NON-COVALENT COMPLEX BETWEEN UBC9 AND SUMO1

LYASE

2UZ1 1.65 ANGSTROM STRUCTURE OF BENZALDEHYDE LYASE COMPLEXED WITH 2-METHYL-2,4-PENTANEDIOL

RECEPTOR

2UZ6 ACHBP-TARGETED A-CONOTOXIN CORRELATES DISTINCT BINDING ORIENTATIONS WITH NACHR SUBTYPE SELECTIVITY.

TRANSFERASE

2UZB CRYSTAL STRUCTURE OF HUMAN CDK2 COMPLEXED WITH A THIAZOLIDINONE INHIBITOR

TRANSFERASE

2UZD CRYSTAL STRUCTURE OF HUMAN CDK2 COMPLEXED WITH A THIAZOLIDINONE INHIBITOR

TRANSFERASE

2UZE CRYSTAL STRUCTURE OF HUMAN CDK2 COMPLEXED WITH A THIAZOLIDINONE INHIBITOR

SIGNALING PROTEIN/IMMUNE SYSTEM

2UZI CRYSTAL STRUCTURE OF HRAS(G12V)- ANTI-RAS FV COMPLEX

TRANSFERASE

2UZL CRYSTAL STRUCTURE OF HUMAN CDK2 COMPLEXED WITH A THIAZOLIDINONE INHIBITOR

TRANSFERASE

2UZT	PKA STRUCTURES OF AKT, INDAZOLE-PYRIDINE INHIBITORS	
2UZU	PKA STRUCTURES OF INDAZOLE-PYRIDINE SERIES OF AKT INHIBITORS	TRANSFERASE
2UZW	PKA STRUCTURES OF INDAZOLE-PYRIDINE SERIES OF AKT INHIBITORS	TRANSFERASE
2UZX	STRUCTURE OF THE HUMAN RECEPTOR TYROSINE KINASE MET IN COMPLEX WITH THE LISTERIA MONOCYTOGENES INVASION PROTEIN INLB: CRYSTAL FORM I	SIGNALING PROTEIN/RECEPTOR COMPLEX
2UZY	STRUCTURE OF THE HUMAN RECEPTOR TYROSINE KINASE MET IN COMPLEX WITH THE LISTERIA MONOCYTOGENES INVASION PROTEIN INLB: LOW RESOLUTION, CRYSTAL FORM II	SIGNALING PROTEIN/RECEPTOR COMPLEX
2V17	STRUCTURE OF THE COMPLEX OF ANTIBODY MN423 WITH A FRAGMENT OF TAU PROTEIN	IMMUNE SYSTEM
2V1C	CRYSTAL STRUCTURE AND MUTATIONAL STUDY OF RECOR PROVIDE INSIGHT INTO ITS ROLE IN DNA REPAIR	RECOMBINATION
2V1D	STRUCTURAL BASIS OF LSD1-COREST SELECTIVITY IN HISTONE H3 RECOGNITION	OXIDOREDUCTASE/REPRESSOR
2V1S	CRYSTAL STRUCTURE OF RAT TOM20-ALDH PRESEQUENCE COMPLEX	OXIDOREDUCTASE
2V1T	CRYSTAL STRUCTURE OF RAT TOM20-ALDH PRESEQUENCE COMPLEX	OXIDOREDUCTASE
2V1Y	STRUCTURE OF A PHOSPHOINOSITIDE 3-KINASE ALPHA ADAPTOR-BINDING DOMAIN (ABD) IN A COMPLEX WITH THE ISH2 DOMAIN FROM P85 ALPHA	TRANSFERASE
2V22	REPLACE: A STRATEGY FOR ITERATIVE DESIGN OF CYCLIN BINDING GROOVE INHIBITORS	TRANSFERASE
2V2W	T CELL CROSS-REACTIVITY AND CONFORMATIONAL CHANGES DURING TCR ENGAGEMENT	IMMUNE SYSTEM
2V2X	T CELL CROSS-REACTIVITY AND CONFORMATIONAL CHANGES DURING TCR ENGAGEMENT.	IMMUNE SYSTEM
2V36	CRYSTAL STRUCTURE OF GAMMA-GLUTAMYL TRANSFERASE FROM BACILLUS SUBTILIS	TRANSFERASE
2V3B	CRYSTAL STRUCTURE OF THE ELECTRON TRANSFER COMPLEX RUBREDOXIN - RUBREDOXIN REDUCTASE FROM PSEUDOMONAS AERUGINOSA.	OXIDOREDUCTASE
2V3H	THROMBIN WITH 3-CYCLE NO F	BLOOD CLOTTING
2V3O	THROMBIN WITH 3-CYCLE WITH F	BLOOD CLOTTING
2V3S	STRUCTURAL INSIGHTS INTO THE RECOGNITION OF SUBSTRATES AND ACTIVATORS BY THE OSR1 KINASE	TRANSFERASE
2V46	STRUCTURE OF THE RIBOSOME RECYCLING FACTOR BOUND TO THE	RIBOSOME

	THERMUS THERMOPHILUS 70S RIBOSOME WITH MRNA, ASL-PHE AND TRNA-FMET (PART 1 OF 4). THIS FILE CONTAINS THE 30S SUBUNIT, MRNA, P-SITE ASL, E-SITE TRNA AND RRF FOR MOLECULE 1.	
2V47	STRUCTURE OF THE RIBOSOME RECYCLING FACTOR BOUND TO THE THERMUS THERMOPHILUS 70S RIBOSOME WITH MRNA, ASL-PHE AND TRNA-FMET (PART 2 OF 4). THIS FILE CONTAINS THE 50S SUBUNIT FOR MOLECULE 1.	RIBOSOME
2V48	STRUCTURE OF THE RIBOSOME RECYCLING FACTOR BOUND TO THE THERMUS THERMOPHILUS 70S RIBOSOME WITH MRNA, ASL-PHE AND TRNA-FMET (PART 3 OF 4). THIS FILE CONTAINS THE 30S SUBUNIT, MRNA, P-SITE ASL, E-SITE TRNA AND RRF FOR MOLECULE 2.	RIBOSOME
2V49	STRUCTURE OF THE RIBOSOME RECYCLING FACTOR BOUND TO THE THERMUS THERMOPHILUS 70S RIBOSOME WITH MRNA, ASL-PHE AND TRNA-FMET (PART 4 OF 4). THIS FILE CONTAINS THE 50S SUBUNIT OF MOLECULE 2.	RIBOSOME
2V4I	STRUCTURE OF A NOVEL N-ACYL-ENZYME INTERMEDIATE OF AN N-TERMINAL NUCLEOPHILE (NTN) HYDROLASE, OAT2	TRANSFERASE
2V4J	THE CRYSTAL STRUCTURE OF DESULFOVIBRIO VULGARIS DISSIMILATORY SULFITE REDUCTASE BOUND TO DSRC PROVIDES NOVEL INSIGHTS INTO THE MECHANISM OF SULFATE RESPIRATION	OXIDOREDUCTASE
2V4Z	THE CRYSTAL STRUCTURE OF THE HUMAN G-PROTEIN SUBUNIT ALPHA (GNAI3) IN COMPLEX WITH AN ENGINEERED REGULATOR OF G-PROTEIN SIGNALING TYPE 2 DOMAIN (RGS2)	CELL CYCLE
2V51	STRUCTURE OF MAL-RPEL1 COMPLEXED TO ACTIN	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN
2V52	STRUCTURE OF MAL-RPEL2 COMPLEXED TO G-ACTIN	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN
2V53	CRYSTAL STRUCTURE OF A SPARC-COLLAGEN COMPLEX	CELL ADHESION
2V55	MECHANISM OF MULTI-SITE PHOSPHORYLATION FROM A ROCK-I:RHOE COMPLEX STRUCTURE	TRANSFERASE
2V5E	THE STRUCTURE OF THE GDNF\:CORECEPTOR COMPLEX\: INSIGHTS INTO RET SIGNALLING AND HEPARIN BINDING.	RECEPTOR/GLYCOPROTEIN COMPLEX
2V5H	CONTROLLING THE STORAGE OF NITROGEN AS ARGININE: THE COMPLEX OF PII AND ACETYLGLUTAMATE KINASE FROM SYNECHOCOCCUS ELONGATUS PCC 7942	TRANSCRIPTION
2V5P	COMPLEX STRUCTURE OF HUMAN IGF2R DOMAINS 11-13 BOUND TO IGF-II	RECEPTOR/GLYCOPROTEIN COMPLEX
2V5Q	CRYSTAL STRUCTURE OF WILD-TYPE PLK-1 KINASE DOMAIN IN COMPLEX WITH A SELECTIVE DARPIN	TRANSFERASE COMPLEX
2V5W	CRYSTAL STRUCTURE OF HDAC8-SUBSTRATE COMPLEX	HYDROLASE

2V63	RYSTAL STRUCTURE OF RUBISCO FROM CHLAMYDOMONAS REINHARDTII WITH A LARGE-SUBUNIT V331A MUTATION	OXIDOREDUCTASE
2V64	CRYSTALLOGRAPHIC STRUCTURE OF THE CONFORMATIONAL DIMER OF THE SPINDLE ASSEMBLY CHECKPOINT PROTEIN MAD2.	CELL CYCLE
2V67	RYSTAL STRUCTURE OF CHLAMYDOMONAS REINHARDTII RUBISCO WITH A LARGE-SUBUNIT SUPRESSOR MUTATION T342I	OXIDOREDUCTASE
2V68	RYSTAL STRUCTURE OF CHLAMYDOMONAS REINHARDTII RUBISCO WITH LARGE-SUBUNIT MUTATIONS V331A, T342I	OXIDOREDUCTASE
2V69	RYSTAL STRUCTURE OF CHLAMYDOMONAS REINHARDTII RUBISCO WITH A LARGE-SUBUNIT MUTATION D473E	OXIDOREDUCTASE
2V6A	RYSTAL STRUCTURE OF CHLAMYDOMONAS REINHARDTII RUBISCO WITH LARGE-SUBUNIT MUTATIONS V331A, G344S	OXIDOREDUCTASE
2V6Q	CRYSTAL STRUCTURE OF A BHRF-1 : BIM BH3 COMPLEX	APOPTOSIS
2V6X	STRACTURAL INSIGHT INTO THE INTERACTION BETWEEN ESCRT-III AND VPS4	PROTEIN TRANSPORT
2V7D	14-3-3 PROTEIN ZETA IN COMPLEX WITH THR758 PHOSPHORYLATED INTEGRIN BETA2 PEPTIDE	SIGNALING PROTEIN
2V7H	CRYSTAL STRUCTURE OF AN IMMUNOGEN SPECIFIC ANTI-MANNOPYRANOSIDE MONOCLONAL ANTIBODY FAB FRAGMENT	IMMUNE SYSTEM
2V7N	UNUSUAL TWINNING IN CRYSTALS OF THE CITS BINDING ANTIBODY FAB FRAGMENT F3P4	IMMUNE SYSTEM
2V7Q	THE STRUCTURE OF F1-ATPASE INHIBITED BY I1-60HIS, A MONOMERIC FORM OF THE INHIBITOR PROTEIN, IF1.	HYDROLASE
2V83	CRYSTAL STRUCTURE OF RAG2-PHD FINGER IN COMPLEX WITH H3K4ME3 PEPTIDE	PROTEIN BINDING
2V85	CRYSTAL STRUCTURE OF RAG2-PHD FINGER IN COMPLEX WITH H3R2ME1K4ME3 PEPTIDE	PROTEIN BINDING
2V86	CRYSTAL STRUCTURE OF RAG2-PHD FINGER IN COMPLEX WITH H3R2ME2AK4ME3 PEPTIDE	PROTEIN BINDING
2V87	CRYSTAL STRUCTURE OF RAG2-PHD FINGER IN COMPLEX WITH H3R2ME2SK4ME3 PEPTIDE	PROTEIN BINDING
2V88	CRYSTAL STRUCTURE OF RAG2-PHD FINGER IN COMPLEX WITH H3R2ME2SK4ME2 PEPTIDE	PROTEIN BINDING
2V89	CRYSTAL STRUCTURE OF RAG2-PHD FINGER IN COMPLEX WITH H3K4ME3 PEPTIDE AT 1.1A RESOLUTION	PROTEIN BINDING
2V8A	THE STRUCTURE OF THERMOSYNECHOCOCCUS ELONGATUS	ELECTRON TRANSPORT

	ALLOPHYCOCYANIN AT 3.5 ANGSTROEMS.	
2V8C	MOUSE PROFILIN IIA IN COMPLEX WITH THE PROLINE-RICH DOMAIN OF VASP	PROTEIN-BINDING
2V8F	MOUSE PROFILIN IIA IN COMPLEX WITH A DOUBLE REPEAT FROM THE FH1 DOMAIN OF MDIA1	PROTEIN-BINDING
2V8Q	RYSTAL STRUCTURE OF THE REGULATORY FRAGMENT OF MAMMALIAN AMPK IN COMPLEXES WITH AMP	TRANSFERASE
2V8S	VTI1B HABC DOMAIN - EPSINR ENTH DOMAIN COMPLEX	PROTEIN TRANSPORT
2V8W	RYSTALLOGRAPHIC AND MASS SPECTROMETRIC CHARACTERISATION OF EIF4E WITH N7-CAP DERIVATIVES	TRANSLATION
2V8X	RYSTALLOGRAPHIC AND MASS SPECTROMETRIC CHARACTERISATION OF EIF4E WITH N7-CAP DERIVATIVES	TRANSLATION
2V8Y	RYSTALLOGRAPHIC AND MASS SPECTROMETRIC CHARACTERISATION OF EIF4E WITH N7-CAP DERIVATIVES	TRANSLATION
2V92	RYSTAL STRUCTURE OF THE REGULATORY FRAGMENT OF MAMMALIAN AMPK IN COMPLEXES WITH ATP-AMP	TRANSFERASE
2V9J	RYSTAL STRUCTURE OF THE REGULATORY FRAGMENT OF MAMMALIAN AMPK IN COMPLEXES WITH MG.ATP-AMP	TRANSFERASE
2VAA	MHC CLASS I H-2KB HEAVY CHAIN COMPLEXED WITH BETA-2 MICROGLOBULIN AND VESICULAR STOMATITIS VIRUS NUCLEOPROTEIN	COMPLEX (MHC I/PEPTIDE)
2VAB	MHC CLASS I H-2KB HEAVY CHAIN COMPLEXED WITH BETA-2 MICROGLOBULIN AND SENDAI VIRUS NUCLEOPROTEIN	COMPLEX (MHC I/PEPTIDE)
2VAS	MYOSIN VI (MD-INSERT2-CAM, DELTA-INSERT1) POST-RIGOR STATE	MOTOR PROTEIN
2VAY	CALMODULIN COMPLEXED WITH CAV1.1 IQ PEPTIDE	METAL TRANSPORT
2VB6	MYOSIN VI (MD-INSERT2-CAM, DELTA INSERT1) POST-RIGOR STATE (CRYSTAL FORM 2)	MOTOR PROTEIN
2VB7	BETA-KETOACYL-ACP SYNTHASE I (KAS) FROM E. COLI, APO STRUCTURE AFTER SOAK IN PEG SOLUTION	TRANSFERASE
2VBC	RYSTAL STRUCTURE OF THE NS3 PROTEASE-HELICASE FROM DENGUE VIRUS	HYDROLASE
2VBJ	OLECULAR BASIS OF HUMAN XPC GENE RECOGNITION AND CLEAVAGE BY ENGINEERED HOMING ENDONUCLEASE HETERODIMERS	HYDROLASE
2VBL	OLECULAR BASIS OF HUMAN XPC GENE RECOGNITION AND CLEAVAGE BY ENGINEERED HOMING ENDONUCLEASE HETERODIMERS	HYDROLASE
2VBN	OLECULAR BASIS OF HUMAN XPC GENE RECOGNITION AND CLEAVAGE BY ENGINEERED HOMING ENDONUCLEASE HETERODIMERS	HYDROLASE

2VBO	MOLECULAR BASIS OF HUMAN XPC GENE RECOGNITION AND CLEAVAGE BY ENGINEERED HOMING ENDONUCLEASE HETERODIMERS	HYDROLASE
2VC2	RE-REFINEMENT OF INTEGRIN ALPHAIIBBETA3 HEADPIECE BOUND TO ANTAGONIST L-739758	CELL ADHESION/IMMUNE SYSTEM COMPLEX
2VCP	CRYSTAL STRUCTURE OF N-WASP VC DOMAIN IN COMPLEX WITH SKELETAL ACTIN	STRUCTURAL PROTEIN
2VDB	STRUCTURE OF HUMAN SERUM ALBUMIN WITH S-NAPROXEN AND THE GA MODULE	PROTEIN BINDING
2VDC	THE 9.5 A RESOLUTION STRUCTURE OF GLUTAMATE SYNTHASE FROM CRYO-ELECTRON MICROSCOPY AND ITS OLIGOMERIZATION BEHAVIOR IN SOLUTION: FUNCTIONAL IMPLICATIONS.	OXIDOREDUCTASE
2VDH	RYSTAL STRUCTURE OF CHLAMYDOMONAS REINHARDTII RUBISCO WITH A LARGE-SUBUNIT C172S MUTATION	LYASE
2VDI	RYSTAL STRUCTURE OF CHLAMYDOMONAS REINHARDTII RUBISCO WITH A LARGE-SUBUNIT C192S MUTATION	LYASE
2VDK	RE-REFINEMENT OF INTEGRIN ALPHAIIBBETA3 HEADPIECE	CELL ADHESION/IMMUNE SYSTEM COMPLEX
2VDL	RE-REFINEMENT OF INTEGRIN ALPHAIIBBETA3 HEADPIECE	CELL ADHESION/IMMUNE SYSTEM COMPLEX
2VDM	RE-REFINEMENT OF INTEGRIN ALPHAIIBBETA3 HEADPIECE BOUND TO ANTAGONIST TIROFIBAN	CELL ADHESION/IMMUNE SYSTEM COMPLEX
2VDN	RE-REFINEMENT OF INTEGRIN ALPHAIIBBETA3 HEADPIECE BOUND TO ANTAGONIST EPTIFIBATIDE	CELL ADHESION/IMMUNE SYSTEM COMPLEX
2VDO	INTEGRIN ALPHAIIBBETA3 HEADPIECE BOUND TO FIBRINOGEN GAMMA CHAIN PEPTIDE, HHLGGAKQAGDV	CELL ADHESION/IMMUNE SYSTEM COMPLEX
2VDP	INTEGRIN ALPHAIIBBETA3 HEADPIECE BOUND TO FIBRINOGEN GAMMA CHAIN PEPTIDE,LGGAKQAGDV	CELL ADHESION/IMMUNE SYSTEM COMPLEX
2VDQ	INTEGRIN ALPHAIIBBETA3 HEADPIECE BOUND TO A CHIMERIC FIBRINOGEN GAMMA CHAIN PEPTIDE, HHLGGAKQRGDV	CELL ADHESION/IMMUNE SYSTEM COMPLEX
2VDR	INTEGRIN ALPHAIIBBETA3 HEADPIECE BOUND TO A CHIMERIC FIBRINOGEN GAMMA CHAIN PEPTIDE, LGGAKQRGDV	CELL ADHESION/IMMUNE SYSTEM COMPLEX
2VDU	STRUCTURE OF TRM8-TRM82, THE YEAST TRNA M7G METHYLATION COMPLEX	TRANSFERASE
2VDW	GUANOSINE N7 METHYL-TRANSFERASE SUB-COMPLEX (D1-D12) OF THE VACCINIA VIRUS MRNA CAPPING ENZYME	TRANSFERASE
2VE5	CRYSTALLOGRAPHIC STRUCTURE OF BETAINE ALDEHYDE DEHYDROGENASE FROM PSEUDOMONAS AERUGINOSA	OXIDOREDUCTASE
2VE6	CRYSTAL STRUCTURE OF A MURINE MHC CLASS I H2-DB MOLECULE IN	IMMUNE SYSTEM

	COMPLEX WITH A PHOTOCLEAVABLE PEPTIDE	
2VE7	CRYSTAL STRUCTURE OF A BONSAI VERSION OF THE HUMAN NDC80 COMPLEX	CELL CYCLE
2VG5	CRYSTAL STRUCTURES OF HIV-1 REVERSE TRANSCRIPTASE COMPLEXES WITH THIOCARBAMATE NON-NUCLEOSIDE INHIBITORS	TRANSFERASE
2VG6	CRYSTAL STRUCTURES OF HIV-1 REVERSE TRANSCRIPTASE COMPLEXES WITH THIOCARBAMATE NON-NUCLEOSIDE INHIBITORS	TRANSFERASE
2VG7	CRYSTAL STRUCTURES OF HIV-1 REVERSE TRANSCRIPTASE COMPLEXES WITH THIOCARBAMATE NON-NUCLEOSIDE INHIBITORS	TRANSFERASE
2VGC	GAMMA-CHYMOTRYPSIN D-PARA-CHLORO-1-ACETAMIDO BORONIC ACID INHIBITOR COMPLEX	SERINE PROTEASE
2VGL	AP2 CLATHRIN ADAPTOR CORE	PROTEIN TRANSPORT
2VGO	CRYSTAL STRUCTURE OF AURORA B KINASE IN COMPLEX WITH REVERSINE INHIBITOR	TRANSFERASE
2VGP	CRYSTAL STRUCTURE OF AURORA B KINASE IN COMPLEX WITH A AMINOTHIAZOLE INHIBITOR	TRANSFERASE
2VGX	STRUCTURE OF THE YERSINIA ENTEROCOLITICA TYPE III SECRETION TRANSLOCATOR CHAPERONE SYCD	CHAPERONE
2VH0	STRUCTURE AND PROPERTY BASED DESIGN OF FACTOR XA INHIBITORS: BIARYL PYRROLIDIN-2-ONES INCORPORATING BASIC HETEROCYCLIC MOTIFS	HYDROLASE
2VH3	RANASMURFIN	UNKNOWN FUNCTION
2VH5	CRYSTAL STRUCTURE OF HRAS(G12V) - ANTI-RAS FV (DISULFIDE FREE MUTANT) COMPLEX	IMMUNE SYSTEM
2VH8	CRYSTAL STRUCTURE OF SYNAPTIC PROTEIN NEUROLIGIN 4 IN COMPLEX WITH NEUREXIN BETA 1.	CELL ADHESION
2VHM	STRUCTURE OF PDF BINDING HELIX IN COMPLEX WITH THE RIBOSOME (PART 1 OF 4)	RIBOSOME
2VHN	STRUCTURE OF PDF BINDING HELIX IN COMPLEX WITH THE RIBOSOME. (PART 2 OF 4)	RIBOSOME
2VH0	STRUCTURE AND PROPERTY BASED DESIGN OF FACTOR XA INHIBITORS: BIARYL PYRROLIDIN-2-ONES INCORPORATING BASIC HETEROCYCLIC MOTIFS	HYDROLASE
2VHO	STRUCTURE OF PDF BINDING HELIX IN COMPLEX WITH THE RIBOSOME (PART 3 OF 4)	RIBOSOME
2VHP	STRUCTURE OF PDF BINDING HELIX IN COMPLEX WITH THE RIBOSOME (PART 4 OF 4)	RIBOSOME

2VIF	CRYSTAL STRUCTURE OF SOCS6 SH2 DOMAIN IN COMPLEX WITH A C-KIT PHOSPHOPEPTIDE	SIGNALING PROTEIN
2VIR	INFLUENZA VIRUS HEMAGGLUTININ COMPLEXED WITH A NEUTRALIZING ANTIBODY	COMPLEX (HEMAGGLUTININ/IMMMUNOGLOBULIN)
2VIS	INFLUENZA VIRUS HEMAGGLUTININ, (ESCAPE) MUTANT WITH THR 131 REPLACED BY ILE, COMPLEXED WITH A NEUTRALIZING ANTIBODY	COMPLEX (HEMAGGLUTININ/IMMMUNOGLOBULIN)
2VIT	INFLUENZA VIRUS HEMAGGLUTININ, MUTANT WITH THR 155 REPLACED BY ILE, COMPLEXED WITH A NEUTRALIZING ANTIBODY	COMPLEX (HEMAGGLUTININ/IMMMUNOGLOBULIN)
2VIU	INFLUENZA VIRUS HEMAGGLUTININ	HEMAGGLUTININ
2VJ0	CRYSTAL STRUCTURE OF THE ALPHA-ADAPTIN APPENDAGE DOMAIN, FROM THE AP2 ADAPTOR COMPLEX, IN COMPLEX WITH AN FXDNF PEPTIDE FROM AMPHIPHYSIN1 AND A WVXF PEPTIDE FROM SYNAPTOJANIN P170	PROTEIN TRANSPORT
2VJE	RYSTAL STRUCTURE OF THE MDM2-MDMX RING DOMAIN HETERODIMER	LIGASE
2VJF	RYSTAL STRUCTURE OF THE MDM2-MDMX RING DOMAIN HETERODIMER	LIGASE
2VJH	HE STRUCTURE OF PHYCOERYTHRIN FROM GLOEOBACTER VIOLACEUS	PHOTOSYNTHESIS
2VJM	FORMYL-COA TRANSFERASE WITH ASPARTYL-FORMYL ANHYDIDE INTERMEDIATE	TRANSFERASE
2VJR	THE STRUCTURE OF PHYCOCYANIN FROM GLOEOBACTER VIOLACEUS	PHOTOSYNTHESIS
2VJT	HE STRUCTURE OF ALLOPHYCOCYANIN FROM GLOEOBACTER VIOLACEUS	PHOTOSYNTHESIS
2VJZ	CRYSTAL STRUCTURE FORM ULTALENTE INSULIN MICROCRYSTALS	HORMONE
2VK0	CRYSTAL STRUCTURE FORM ULTALENTE INSULIN MICROCRYSTALS	HORMONE
2VL2	OXIDIZED AND REDUCED FORMS OF HUMAN PEROXIREDOXIN 5	OXIDOREDUCTASE
2VL5	STRUCTURE OF ANTI-COLLAGEN TYPE II FAB CIIC1	IMMUNE SYSTEM
2VLH	QUINONOID INTERMEDIATE OF CITROBACTER FREUNDII TYROSINE PHENOL-LYASE FORMED WITH METHIONINE	LYASE
2VLJ	HE STRUCTURAL DYNAMICS AND ENERGETICS OF AN IMMUNODOMINANT T-CELL RECEPTOR ARE PROGRAMMED BY ITS VBETA DOMAIN	IMMUNE SYSTEM
2VLK	HE STRUCTURAL DYNAMICS AND ENERGETICS OF AN IMMUNODOMINANT T-CELL RECEPTOR ARE PROGRAMMED BY ITS VBETA DOMAIN	IMMUNE SYSTEM
2VLL	HE STRUCTURAL DYNAMICS AND ENERGETICS OF AN IMMUNODOMINANT T-CELL RECEPTOR ARE PROGRAMMED BY ITS VBETA DOMAIN	IMMUNE SYSTEM
2VLM	HE STRUCTURAL DYNAMICS AND ENERGETICS OF AN IMMUNODOMINANT T-CELL RECEPTOR ARE PROGRAMMED BY ITS VBETA DOMAIN	IMMUNE SYSTEM

2VLN	N75A MUTANT OF E9 DNASE DOMAIN IN COMPLEX WITH IM9	PROTEIN-BINDING
2VLO	K97A MUTANT OF E9 DNASE DOMAIN IN COMPLEX WITH IM9	PROTEIN-BINDING
2VLP	R54A MUTANT OF E9 DNASE DOMAIN IN COMPLEX WITH IM9	PROTEIN-BINDING
2VLQ	F86A MUTANT OF E9 DNASE DOMAIN IN COMPLEX WITH IM9	PROTEIN-BINDING
2VLR	HE STRUCTURAL DYNAMICS AND ENERGETICS OF AN IMMUNODOMINANT T-CELL RECEPTOR ARE PROGRAMMED BY ITS VBETA DOMAIN	IMMUNE SYSTEM
2VM6	HUMAN BCL2-A1 IN COMPLEX WITH BIM-BH3 PEPTIDE	IMMUNE SYSTEM
2VML	HE MONOCLINIC STRUCTURE OF PHYCOCYANIN FROM GLOEOBACTER VIOLACEUS	PHOTOSYNTHESIS
2VN5	THE CLOSTRIDIUM CELLULOLYTICUM DOCKERIN DISPLAYS A DUAL BINDING MODE FOR ITS COHESIN PARTNER	CELL ADHESION
2VN6	THE CLOSTRIDIUM CELLULOLYTICUM DOCKERIN DISPLAYS A DUAL BINDING MODE FOR ITS COHESIN PARTNER	CELL ADHESION
2VNW	STRUCTURE OF PKA-PKB CHIMERA COMPLEXED WITH (1-(9H-PURIN-6-YL)PIPERIDIN-4-YL)METHANAMINE	TRANSFERASE
2VNY	STRUCTURE OF PKA-PKB CHIMERA COMPLEXED WITH (1-(9H-PURIN-6-YL)PIPERIDIN-4-YL)AMINE	TRANSFERASE
2VO0	STRUCTURE OF PKA-PKB CHIMERA COMPLEXED WITH C-(4-(4-CHLOROPHENYL)-1-(7H-PYRROLO(2,3-D)PYRIMIDIN-4-YL)PIPERIDIN-4-YL)METHYLAMINE	TRANSFERASE
2VO3	STRUCTURE OF PKA-PKB CHIMERA COMPLEXED WITH C-(4-(4-CHLOROPHENYL)-1-(7H-PYRROLO(2,3-D)PYRIMIDIN-4-YL)PIPERIDIN-4-YL)METHYLAMINE	TRANSFERASE
2VO6	STRUCTURE OF PKA-PKB CHIMERA COMPLEXED WITH 4-(4-CHLOROBENZYL)-1-(7H-PYRROLO(2,3-D)PYRIMIDIN-4-YL)PIPERIDIN-4-YLAMINE	TRANSFERASE
2VO7	STRUCTURE OF PKA COMPLEXED WITH 4-(4-CHLOROBENZYL)-1-(7H-PYRROLO(2,3-D)PYRIMIDIN-4-YL)PIPERIDIN-4-YLAMINE	TRANSFERASE
2VOF	STRUCTURE OF MOUSE A1 BOUND TO THE PUMA BH3-DOMAIN	APOPTOSIS
2VOG	STRUCTURE OF MOUSE A1 BOUND TO THE BMF BH3-DOMAIN	APOPTOSIS
2VOH	STRUCTURE OF MOUSE A1 BOUND TO THE BAK BH3-DOMAIN	APOPTOSIS
2VOI	STRUCTURE OF MOUSE A1 BOUND TO THE BID BH3-DOMAIN	APOPTOSIS
2VOL	MURINE TRIM21 IN COMPLEX WITH MURINE IGG FC	IMMUNE SYSTEM
2VP7	DECODING OF METHYLATED HISTONE H3 TAIL BY THE PYGO-BCL9 WNT	GENE REGULATION

	SIGNALING COMPLEX	
2VPB	DECODING OF METHYLATED HISTONE H3 TAIL BY THE PYGO-BCL9 WNT SIGNALING COMPLEX	GENE REGULATION
2VPD	DECODING OF METHYLATED HISTONE H3 TAIL BY THE PYGO-BCL9 WNT SIGNALING COMPLEX	GENE REGULATION
2VPE	DECODING OF METHYLATED HISTONE H3 TAIL BY THE PYGO-BCL9 WNT SIGNALING COMPLEX	GENE REGULATION
2VPG	DECODING OF METHYLATED HISTONE H3 TAIL BY THE PYGO-BCL9 WNT SIGNALING COMPLEX	GENE REGULATION
2VQ6	TORPEDO CALIFORNICA ACETYLCHOLINESTERASE COMPLEXED WITH 2-PAM	HYDROLASE
2VQE	MODIFIED URIDINES WITH C5-METHYLENE SUBSTITUENTS AT THE FIRST POSITION OF THE TRNA ANTICODON STABILIZE U-G WOBBLE PAIRING DURING DECODING	RIBOSOME
2VQF	MODIFIED URIDINES WITH C5-METHYLENE SUBSTITUENTS AT THE FIRST POSITION OF THE TRNA ANTICODON STABILIZE U-G WOBBLE PAIRING DURING DECODING	RIBOSOME
2VR0	CRYSTAL STRUCTURE OF CYTOCHROME C NITRITE REDUCTASE NRFHA COMPLEX BOUND TO THE HQNO INHIBITOR	OXIDOREDUCTASE
2VRC	CRYSTAL STRUCTURE OF THE CITROBACTER SP. TRIPHENYLMETHANE REDUCTASE COMPLEXED WITH NADP(H)	OXIDOREDUCTASE
2VRP	STRUCTURE OF RHODOCYTIN	SUGAR-BINDING PROTEIN
2VRR	STRUCTURE OF SUMO MODIFIED UBC9	CELL CYCLE/LIGASE
2VRW	CRITICAL STRUCTURAL ROLE FOR THE PH AND C1 DOMAINS OF THE VAV1 EXCHANGE FACTOR	SIGNALING PROTEIN
2VRX	STRUCTURE OF AURORA B KINASE IN COMPLEX WITH ZM447439	CELL CYCLE/TRANSFERASE
2VSK	HENDRA VIRUS ATTACHMENT GLYCOPROTEIN IN COMPLEX WITH HUMAN CELL SURFACE RECEPTOR EPHRINB2	HYDROLASE
2VSL	CRYSTAL STRUCTURE OF XIAP BIR3 WITH A BIVALENT SMAC MIMETIC	LIGASE
2VSO	CRYSTAL STRUCTURE OF A TRANSLATION INITIATION COMPLEX	HYDROLASE/TRANSLATION
2VSS	WILD-TYPE HYDROXYCINNAMOYL-COA HYDRATASE LYASE IN COMPLEX WITH ACETYL-COA AND VANILLIN	LYASE
2VSU	A TERNARY COMPLEX OF HYDROXYCINNAMOYL-COA HYDRATASE-LYASE (HCHL) WITH ACETYL-COENZYME A AND VANILLIN GIVES INSIGHTS INTO SUBSTRATE SPECIFICITY AND MECHANISM.	LYASE
2VSX	CRYSTAL STRUCTURE OF A TRANSLATION INITIATION COMPLEX	TRANSLATION/HYDROLASE

2VT1	CRYSTAL STRUCTURE OF THE CYTOPLASMIC DOMAIN OF SPA40, THE SPECIFICITY SWITCH FOR THE SHIGELLA FLEXNERI TYPE III SECRETION SYSTEM	MEMBRANE PROTEIN
2VUM	ALPHA-AMANITIN INHIBITED COMPLETE RNA POLYMERASE II ELONGATION COMPLEX	TRANSFERASE
2VUS	CRYSTAL STRUCTURE OF UNLIGANDED NMRA-AREA ZINC FINGER COMPLEX	TRANSCRIPTION
2VUT	CRYSTAL STRUCTURE OF NAD-BOUND NMRA-AREA ZINC FINGER COMPLEX	TRANSCRIPTION
2VUU	CRYSTAL STRUCTURE OF NADP-BOUND NMRA-AREA ZINC FINGER COMPLEX	TRANSCRIPTION
2VV1	HPPARGAMMA LIGAND BINDING DOMAIN IN COMPLEX WITH 4-HDHA	RECEPTOR
2VV4	HPPARGAMMA LIGAND BINDING DOMAIN IN COMPLEX WITH 6-OXOOTE	RECEPTOR
2VVL	THE STRUCTURE OF MAO-N-D3, A VARIANT OF MONOAMINE OXIDASE FROM ASPERGILLUS NIGER.	OXIDOREDUCTASE
2VWE	CRYSTAL STRUCTURE OF VASCULAR ENDOTHELIAL GROWTH FACTOR-B IN COMPLEX WITH A NEUTRALIZING ANTIBODY FAB FRAGMENT	IMMUNE SYSTEM
2VXC	STRUCTURE OF THE CRB2-BRCT2 DOMAIN COMPLEX WITH PHOSPHOPEPTIDE.	CELL CYCLE
2VYN	STRUCTURE OF E.COLI GAPDH RAT SPERM GAPDH HETEROTETRAMER	OXIDOREDUCTASE
2VYR	STRUCTURE OF HUMAN MDM4 N-TERMINAL DOMAIN BOUND TO A SINGLE DOMAIN ANTIBODY	IMMUNE SYSTEM
2VYV	STRUCTURE OF E.COLI GAPDH RAT SPERM GAPDH HETEROTETRAMER	OXIDOREDUCTASE
2VZD	CRYSTAL STRUCTURE OF THE C-TERMINAL CALPONIN HOMOLOGY DOMAIN OF ALPHA PARVIN IN COMPLEX WITH PAXILLIN LD1 MOTIF	CELL ADHESION
2VZG	CRYSTAL STRUCTURE OF THE C-TERMINAL CALPONIN HOMOLOGY DOMAIN OF ALPHA-PARVIN IN COMPLEX WITH PAXILLIN LD2 MOTIF	CELL ADHESION
2VZI	CRYSTAL STRUCTURE OF THE C-TERMINAL CALPONIN HOMOLOGY DOMAIN OF ALPHA-PARVIN IN COMPLEX WITH PAXILLIN LD4 MOTIF	CELL ADHESION
2VZK	STRUCTURE OF THE ACYL-ENZYME COMPLEX OF AN N-TERMINAL NUCLEOPHILE (NTN) HYDROLASE, OAT2	TRANSFERASE
2YRS	HUMAN HEMOGLOBIN D LOS ANGELES: CRYSTAL STRUCTURE	TRANSPORT PROTEIN, OXYGEN BINDING
2YSS	CRYSTAL STRUCTURE OF HUMANIZED HYHEL-10 FV MUTANT(HQ39KW47Y)-HEN LYSOZYME COMPLEX	IMMUNE SYSTEM/HYDROLASE
2YSU	STRUCTURE OF THE COMPLEX BETWEEN BTUB AND COLICIN E2	TRANSPORT PROTEIN/HYDROLASE

	RECEPTOR BINDING DOMAIN	
2YU9	RNA POLYMERASE II ELONGATION COMPLEX IN 150 MM MG+2 WITH UTP	TRANSCRIPTION/DNA/RNA
2YVC	CRYSTAL STRUCTURE OF THE RADIXIN FERM DOMAIN COMPLEXED WITH THE NEP CYTOPLASMIC TAIL	CELL ADHESION
2YVJ	CRYSTAL STRUCTURE OF THE FERREDOXIN-FERREDOXIN REDUCTASE (BPHA3-BPHA4)COMPLEX	OXIDOREDUCTASE/ELECTRON TRANSPORT
2YXQ	THE PLUG DOMAIN OF THE SECY PROTEIN STABLIZES THE CLOSED STATE OF THE TRANSLOCATION CHANNEL AND MAINTAINS A MEMBRANE SEAL	PROTEIN TRANSPORT
2YXR	THE PLUG DOMAIN OF THE SECY PROTEIN STABLIZES THE CLOSED STATE OF THE TRANSLOCATION CHANNEL AND MAINTAINS A MEMBRANE SEAL	PROTEIN TRANSPORT
2YYR	STRUCTURAL ANALYSIS OF PHD DOMAIN OF PYGOPUS COMPLEXED WITH TRIMETHYLATED HISTONE H3 PEPTIDE	METAL BINDING PROTEIN
2Z0D	THE CRYSTAL STRUCTURE OF HUMAN ATG4B- LC3(1-120) COMPLEX	HYDROLASE/STRUCTURAL PROTEIN
2Z0E	THE CRYSTAL STRUCTURE OF HUMAN ATG4B- LC3(1-124) COMPLEX	HYDROLASE/STRUCTURAL PROTEIN
2Z23	CRYSTAL STRUCTURE OF Y.PESTIS OLIGO PEPTIDE BINDING PROTEIN OPPA WITH TRI-LYSINE LIGAND	PEPTIDE BINDING PROTEIN
2Z2L	PENICILLIN-BINDING PROTEIN 2X (PBP2X) FROM STREPTOCOCCUS PNEUMONIAE	BIOSYNTHETIC PROTEIN
2Z2M	CEFDITOREN-ACYLATED PENICILLIN-BINDING PROTEIN 2X (PBP2X) FROM STREPTOCOCCUS PNEUMONIAE	BIOSYNTHETIC PROTEIN
2Z2Q	CRYSTAL STRUCTURE OF FLOCK HOUSE VIRUS	VIRUS/RNA
2Z2S	CRYSTAL STRUCTURE OF RHODOBACTER SPHAEROIDES SIGE IN COMPLEX WITH THE ANTI-SIGMA CHRR	TRANSCRIPTION
2Z2T	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN GP41 FRAGMENT N36 AND FUSION INHIBITOR SC34EK	VIRAL PROTEIN/INHIBITOR
2Z2Y	CRYSTAL STRUCTURE OF AUTOPROCESSED FORM OF TK-SUBTILISIN	HYDROLASE
2Z30	CRYSTAL STRUCTURE OF COMPLEX FORM BETWEEN MAT-TK-SUBTILISIN AND TK-PROPEPTIDE	HYDROLASE
2Z31	CRYSTAL STRUCTURE OF IMMUNE RECEPTOR COMPLEX	IMMUNE SYSTEM
2Z3C	A MECHANISTIC VIEW OF ENZYME INHIBITION AND PEPTIDE HYDROLYSIS IN THE ACTIVE SITE OF THE SARS-COV 3C-LIKE PEPTIDASE	HYDROLASE
2Z3D	A MECHANISTIC VIEW OF ENZYME INHIBITION AND PEPTIDE HYDROLYSIS IN THE ACTIVE SITE OF THE SARS-COV 3C-LIKE	HYDROLASE

	PEPTIDASE	
2Z3F	CRYSTAL STRUCTURE OF SPCIA1/ASF1 COMPLEXED WITH CAC2 PEPTIDE	CHAPERONE
2Z3L	COMPLEX STRUCTURE OF LF-TRANSFERASE AND PEPTIDE A	TRANSFERASE
2Z3N	COMPLEX STRUCTURE OF LF-TRANSFERASE AND PEPTIDE B	TRANSFERASE
2Z3Q	CRYSTAL STRUCTURE OF THE IL-15/IL-15RA COMPLEX	CYTOKINE/CYTOKINE RECEPTOR
2Z3R	CRYSTAL STRUCTURE OF THE IL-15/IL-15RA COMPLEX	CYTOKINE/CYTOKINE RECEPTOR
2Z4E	CRYSTAL STRUCTURE OF D-DIMER FROM HUMAN FIBRIN COMPLEXED WITH GLY-HIS-ARG-PRO-TYR-AMIDE	BLOOD CLOTTING
2Z4J	CRYSTAL STRUCTURE OF AR LBD WITH SHP PEPTIDE NR BOX 2	TRANSCRIPTION
2Z4K	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH PAROMOMYCIN AND RIBOSOME RECYCLING FACTOR (RRF). THIS FILE CONTAINS THE 30S SUBUNIT OF THE FIRST 70S RIBOSOME, WITH PAROMOMYCIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2Z4L	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH PAROMOMYCIN AND RIBOSOME RECYCLING FACTOR (RRF). THIS FILE CONTAINS THE 50S SUBUNIT OF THE FIRST 70S RIBOSOME, WITH PAROMOMYCIN AND RRF BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2Z4M	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH PAROMOMYCIN AND RIBOSOME RECYCLING FACTOR (RRF). THIS FILE CONTAINS THE 30S SUBUNIT OF THE SECOND 70S RIBOSOME, WITH PAROMOMYCIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2Z4N	CRYSTAL STRUCTURE OF THE BACTERIAL RIBOSOME FROM ESCHERICHIA COLI IN COMPLEX WITH PAROMOMYCIN AND RIBOSOME RECYCLING FACTOR (RRF). THIS FILE CONTAINS THE 50S SUBUNIT OF THE SECOND 70S RIBOSOME, WITH PAROMOMYCIN AND RRF BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
2Z4Q	CRYSTAL STRUCTURE OF A MURINE ANTIBODY FAB 528	IMMUNE SYSTEM
2Z56	CRYSTAL STRUCTURE OF G56S-PROPEPTIDE:S324A-SUBTILISIN COMPLEX	HYDROLASE
2Z57	CRYSTAL STRUCTURE OF G56E-PROPEPTIDE:S324A-SUBTILISIN COMPLEX	HYDROLASE
2Z58	CRYSTAL STRUCTURE OF G56W-PROPEPTIDE:S324A-SUBTILISIN COMPLEX	HYDROLASE

2Z5C	CRYSTAL STRUCTURE OF A NOVEL CHAPERONE COMPLEX FOR YEAST 20S PROTEASOME ASSEMBLY	CHAPERONE/HYDROLASE
2Z5H	CRYSTAL STRUCTURE OF THE HEAD-TO-TAIL JUNCTION OF TROPOMYOSIN COMPLEXED WITH A FRAGMENT OF TNT	CONTRACTILE PROTEIN
2Z5I	CRYSTAL STRUCTURE OF THE HEAD-TO-TAIL JUNCTION OF TROPOMYOSIN	CONTRACTILE PROTEIN
2Z5K	COMPLEX OF TRANSPORTIN 1 WITH TAP NLS	TRANSPORT PROTEIN/RNA BINDING PROTEIN
2Z5N	COMPLEX OF TRANSPORTIN 1 WITH HNRNP D NLS	TRANSPORT PROTEIN/RNA BINDING PROTEIN
2Z5S	MOLECULAR BASIS FOR THE INHIBITION OF P53 BY MDMX	CELL CYCLE
2Z5T	MOLECULAR BASIS FOR THE INHIBITION OF P53 BY MDMX	CELL CYCLE
2Z65	CRYSTAL STRUCTURE OF THE HUMAN TLR4 TV3 HYBRID-MD-2-ERITORAN COMPLEX	IMMUNE SYSTEM
2Z6B	CRYSTAL STRUCTURE ANALYSIS OF (GP27-GP5)3 CONJUGATED WITH FE(III) PROTOPORPHYRIN	HYDROLASE/STRUCTURAL PROTEIN
2Z6K	CRYSTAL STRUCTURE OF FULL-LENGTH HUMAN RPA14/32 HETERODIMER	REPLICATION
2Z6N	CRYSTAL STRUCTURE OF CARBONMONOXY HEMOGLOBIN D FROM THE ALDABRA GIANT TORTOISE, GEOCHELONE GIGANTEA	TRANSPORT PROTEIN
2Z6W	CRYSTAL STRUCTURE OF HUMAN CYCLOPHILIN D IN COMPLEX WITH CYCLOSPORIN A	ISOMERASE
2Z7X	CRYSTAL STRUCTURE OF THE TLR1-TLR2 HETERODIMER INDUCED BY BINDING OF A TRI-ACYLATED LIPOPEPTIDE	IMMUNE SYSTEM
2Z8C	PHOSPHORYLATED INSULIN RECEPTOR TYROSINE KINASE IN COMPLEX WITH (4-{[5-CARBAMOYL-4-(3-METHYLANILINO)PYRIMIDIN-2-YL]AMINO}PHENYL)ACETIC ACID	TRANSFERASE
2Z8I	CRYSTAL STRUCTURE OF ESCHERICHIA COLI GAMMA-GLUTAMYLTRANSPEPTIDASE IN COMPLEX WITH AZASERINE	TRANSFERASE
2Z8J	CRYSTAL STRUCTURE OF ESCHERICHIA COLI GAMMA-GLUTAMYLTRANSPEPTIDASE IN COMPLEX WITH AZASERINE PREPARED IN THE DARK	TRANSFERASE
2Z8K	CRYSTAL STRUCTURE OF ESCHERICHIA COLI GAMMA-GLUTAMYLTRANSPEPTIDASE IN COMPLEX WITH ACIVICIN	TRANSFERASE
2Z8V	STRUCTURE OF AN IGNAR-AMA1 COMPLEX	IMMUNE SYSTEM
2Z8W	STRUCTURE OF AN IGNAR-AMA1 COMPLEX	IMMUNE SYSTEM
2Z8Y	XENON-BOUND STRUCTURE OF BIFUNCTIONAL CARBON MONOXIDE DEHYDROGENASE/ACETYL-COA SYNTHASE(CODH/ACS) FROM MOORELLA	OXIDOREDUCTASE/TRANSFERASE

	THERMOACETICA	
2Z91	CRYSTAL STRUCTURE OF THE FAB FRAGMENT OF ANTI-CIGUATOXIN ANTIBODY 10C9	IMMUNE SYSTEM
2Z92	CRYSTAL STRUCTURE OF THE FAB FRAGMENT OF ANTI-CIGUATOXIN ANTIBODY 10C9 IN COMPLEX WITH CTX3C_ABCDE	IMMUNE SYSTEM
2Z93	CRYSTAL STRUCTURE OF FAB FRAGMENT OF ANTI-CIGUATOXIN ANTIBODY 10C9 IN COMPLEX WITH CTX3C-ABCD	IMMUNE SYSTEM
2Z9I	RYSTAL STRUCTURE OF RV0983 FROM MYCOBACTERIUM TUBERCULOSIS-PROTEOLYTICALLY ACTIVE FORM	HYDROLASE
2ZA4	CRYSTAL STRUCTURAL ANALYSIS OF BARNASE-BARSTAR COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
2ZAE	CRYSTAL STRUCTURE OF PROTEIN PH1601P IN COMPLEX WITH PROTEIN PH1771P OF ARCHAEAL RIBONUCLEASE P FROM PYROCOCCUS HORIKOSHII OT3	HYDROLASE
2ZAL	CRYSTAL STRUCTURE OF E. COLI ISOASPARTYL AMINOPEPTIDASE/L-ASPARAGINASE IN COMPLEX WITH L-ASPARTATE	HYDROLASE
2ZBK	CRYSTAL STRUCTURE OF AN INTACT TYPE II DNA TOPOISOMERASE: INSIGHTS INTO DNA TRANSFER MECHANISMS	ISOMERASE
2ZC3	PENICILLIN-BINDING PROTEIN 2X (PBP 2X) ACYL-ENZYME COMPLEX (BIAPENEM) FROM STREPTOCOCCUS PNEUMONIAE	BIOSYNTHETIC PROTEIN
2ZC4	PENICILLIN-BINDING PROTEIN 2X (PBP 2X) ACYL-ENZYME COMPLEX (TEBIPENEM) FROM STREPTOCOCCUS PNEUMONIAE	BIOSYNTHETIC PROTEIN
2ZC5	PENICILLIN-BINDING PROTEIN 1A (PBP 1A) ACYL-ENZYME COMPLEX (BIAPENEM) FROM STREPTOCOCCUS PNEUMONIAE	BIOSYNTHETIC PROTEIN
2ZC6	PENICILLIN-BINDING PROTEIN 1A (PBP 1A) ACYL-ENZYME COMPLEX (TEBIPENEM) FROM STREPTOCOCCUS PNEUMONIAE	BIOSYNTHETIC PROTEIN
2ZC9	THROMBIN IN COMPLEX WITH INHIBITOR	BLOOD CLOTTING/HYDROLASE INHIBITOR
2ZCF	MUTATIONAL STUDY ON ALPHA-GLN90 OF FE-TYPE NITRILE HYDRATASE FROM RHODOCOCCUS SP. N771	LYASE
2ZCH	CRYSTAL STRUCTURE OF HUMAN PROSTATE SPECIFIC ANTIGEN COMPLEXED WITH AN ACTIVATING ANTIBODY	IMMUNE SYSTEM
2ZCK	CRYSTAL STRUCTURE OF A TERNARY COMPLEX BETWEEN PSA, A SUBSTRAT-ACYL INTERMEDIATE AND AN ACTIVATING ANTIBODY	IMMUNE SYSTEM
2ZCL	CRYSTAL STRUCTURE OF HUMAN PROSTATE SPECIFIC ANTIGEN COMPLEXED WITH AN ACTIVATING ANTIBODY	IMMUNE SYSTEM
2ZCY	YEAST 20S PROTEASOME:SYRINGOLIN A-COMPLEX	HYDROLASE
2ZD1	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE (RT) IN	TRANSFERASE, HYDROLASE

	COMPLEX WITH TMC278 (RILPIVIRINE), A NON-NUCLEOSIDE RT INHIBITOR	
2ZD7	THE STRUCTURE OF VPS75 (VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN 75)	PROTEIN TRANSPORT
2ZDA	EXPLORING THROMBIN S1 POCKET	BLOOD CLOTTING/HYDROLASE INHIBITOR
2ZDI	CRYSTAL STRUCTURE OF PREFOLDIN FROM PYROCOCCUS HORIKOSHII OT3	CHAPERONE
2ZDV	EXPLORING THROMBIN S1 POCKET	BLOOD CLOTTING/HYDROLASE INHIBITOR
2ZE2	CRYSTAL STRUCTURE OF L100I/K103N MUTANT HIV-1 REVERSE TRANSCRIPTASE (RT) IN COMPLEX WITH TMC278 (RILPIVIRINE), A NON-NUCLEOSIDE RT INHIBITOR	TRANSFERASE, HYDROLASE
2ZET	CRYSTAL STRUCTURE OF THE SMALL GTPASE RAB27B COMPLEXED WITH THE SLP HOMOLOGY DOMAIN OF SLAC2-A/MELANOPHILIN	SIGNALING PROTEIN
2ZF0	EXPLORING THROMBIN S1 POCKET	BLOOD CLOTTING/HYDROLASE INHIBITOR
2ZFB	CRYSTAL STRUCTURE OF PARROT HEMOGLOBIN (PSITTACULA KRAMERI) AT PH 7.5	METAL BINDING PROTEIN
2ZFD	THE CRYSTAL STRUCTURE OF PLANT SPECIFIC CALCIUM BINDING PROTEIN ATCBL2 IN COMPLEX WITH THE REGULATORY DOMAIN OF ATCIPK14	SIGNALING PROTEIN/TRANSFERASE
2ZFO	STRUCTURE OF THE PARTIALLY UNLIGANDED MET STATE OF 400 KDA HEMOGLOBIN: INSIGHTS INTO LIGAND-INDUCED STRUCTURAL CHANGES OF GIANT HEMOGLOBINS	OXYGEN BINDING, TRANSPORT PROTEIN
2ZHX	CRYSTAL STRUCTURE OF URACIL-DNA GLYCOSYLASE FROM MYCOBACTERIUM TUBERCULOSIS IN COMPLEX WITH A PROTEINACEOUS INHIBITOR	HYDROLASE/HYDROLASE INHIBITOR
2ZIT	STRUCTURE OF THE EEF2-EXOA-NAD+ COMPLEX	BIOSYNTHETIC PROTEIN/TRANSFERASE
2ZIU	CRYSTAL STRUCTURE OF THE MUS81-EME1 COMPLEX	HYDROLASE
2ZIV	CRYSTAL STRUCTURE OF THE MUS81-EME1 COMPLEX	HYDROLASE
2ZIW	CRYSTAL STRUCTURE OF THE MUS81-EME1 COMPLEX	HYDROLASE
2ZIX	CRYSTAL STRUCTURE OF THE MUS81-EME1 COMPLEX	HYDROLASE
2ZJD	CRYSTAL STRUCTURE OF LC3-P62 COMPLEX	APOPTOSIS INHIBITOR/APOPTOSIS
2ZJP	THIOPEPTIDE ANTIBIOTIC NOSIHEPTIDE BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF DEINOCOCCUS RADIODURANS	RIBOSOME
2ZJQ	INTERACTION OF L7 WITH L11 INDUCED BY MICROCCOCIN BINDING TO THE DEINOCOCCUS RADIODURANS 50S SUBUNIT	RIBOSOME
		RIBOSOME

2ZJR	REFINED NATIVE STRUCTURE OF THE LARGE RIBOSOMAL SUBUNIT (50S) FROM DEINOCOCCUS RADIODURANS	
2ZJS	CRYSTAL STRUCTURE OF SECYE TRANSLOCON FROM THERMUS THERMOPHILUS WITH A FAB FRAGMENT	PROTEIN TRANSPORT/IMMUNE SYSTEM
2ZL1	MP1-P14 SCAFFOLDING COMPLEX	PROTEIN BINDING
2ZL2	CRYSTAL STRUCTURE OF H.PYLORI CLPP IN COMPLEX WITH THE PEPTIDE NVLGFTQ	HYDROLASE
2ZL4	CRYSTAL STRUCTURE OF H.PYLORI CLPP S99A IN COMPLEX WITH THE PEPTIDE AAAA	HYDROLASE
2ZL9	2-SUBSTITUTED-16-ENE-22-THIA-1ALPHA,25-DIHYDROXY-26,27-DIMETHYL-19-NORVITAMIN D3 ANALOGS: SYNTHESIS, BIOLOGICAL EVALUATION AND CRYSTAL STRUCTURE	HORMONE
2ZLA	2-SUBSTITUTED-16-ENE-22-THIA-1ALPHA,25-DIHYDROXY-26,27-DIMETHYL-19-NORVITAMIN D3 ANALOGS: SYNTHESIS, BIOLOGICAL EVALUATION AND CRYSTAL STRUCTURE	HORMONE
2ZLC	2-SUBSTITUTED-16-ENE-22-THIA-1ALPHA,25-DIHYDROXY-26,27-DIMETHYL-19-NORVITAMIN D3 ANALOGS: SYNTHESIS, BIOLOGICAL EVALUATION AND CRYSTAL STRUCTURE	HORMONE
2ZLE	CRYO-EM STRUCTURE OF DEGP12/OMP	HYDROLASE
2ZLF	THE STRUCTURAL BASIS FOR PEPTIDOMIMETIC INHIBITION OF EUKARYOTIC RIBONUCLEOTIDE REDUCTASE	OXIDOREDUCTASE
2ZLT	HORSE METHEMOGLOBIN HIGH SALT, PH 7.0	OXYGEN STORAGE, OXYGEN TRANSPORT
2ZLU	HORSE METHEMOGLOBIN HIGH SALT, PH 7.0 (88% RELATIVE HUMIDITY)	OXYGEN STORAGE, OXYGEN TRANSPORT
2ZLV	HORSE METHEMOGLOBIN HIGH SALT, PH 7.0 (79% RELATIVE HUMIDITY)	OXYGEN STORAGE, OXYGEN TRANSPORT
2ZLW	HORSE METHEMOGLOBIN HIGH SALT, PH 7.0 (75% RELATIVE HUMIDITY)	OXYGEN STORAGE, OXYGEN TRANSPORT
2ZLX	HORSE METHEMOGLOBIN HIGH SALT, PH 7.0 (66% RELATIVE HUMIDITY)	OXYGEN STORAGE, OXYGEN TRANSPORT
2ZME	INTEGRATED STRUCTURAL AND FUNCTIONAL MODEL OF THE HUMAN ESCRT-II COMPLEX	PROTEIN TRANSPORT
2ZMH	CRYSTAL STRUCTURE OF RAT VITAMIN D RECEPTOR BOUND TO ADAMANTYL VITAMIN D ANALOGS: STRUCTURAL BASIS FOR VITAMIN D RECEPTOR ANTAGONISM AND/OR PARTIAL AGONISM	TRANSCRIPTION
2ZMI	CRYSTAL STRUCTURE OF RAT VITAMIN D RECEPTOR BOUND TO ADAMANTYL VITAMIN D ANALOGS: STRUCTURAL BASIS FOR VITAMIN D RECEPTOR ANTAGONISM AND/OR PARTIAL AGONISM	TRANSCRIPTION

2ZMJ	CRYSTAL STRUCTURE OF RAT VITAMIN D RECEPTOR BOUND TO ADAMANTYL VITAMIN D ANALOGS: STRUCTURAL BASIS FOR VITAMIN D RECEPTOR ANTAGONISM AND/OR PARTIAL AGONISM	TRANSCRIPTION
2ZNE	CRYSTAL STRUCTURE OF ZN2+-BOUND FORM OF DES3-23ALG-2 COMPLEXED WITH ALIX ABS PEPTIDE	APOPTOSIS
2ZNL	CRYSTAL STRUCTURE OF PA-PB1 COMPLEX FORM INFLUENZA VIRUS RNA POLYMERASE	TRANSCRIPTION
2ZNV	CRYSTAL STRUCTURE OF HUMAN AMSH-LP DUB DOMAIN IN COMPLEX WITH LYS63-LINKED UBIQUITIN DIMER	HYDROLASE/SIGNALING PROTEIN
2ZOE	A3 SUBCOMPONENT OF CLOSTRIDIUM BOTULINUM TYPE C PROGENITOR TOXIN, COMPLEX WITH N-ACETYLNEURAMIC ACID	TOXIN
2ZOK	CRYSTAL STRUCTURE OF H-2DB IN COMPLEX WITH JHMV EPITOPE S510	IMMUNE SYSTEM
2ZOL	CRYSTAL STRUCTURE OF H-2DB IN COMPLEX WITH THE W513S VARIANT OF JHMV EPITOPE S510	IMMUNE SYSTEM
2ZP0	HUMAN FACTOR VIIA-TISSUE FACTOR COMPLEXED WITH BENZYLSULFONAMIDE-D-ILE-GLN-P-AMINOBENZAMIDINE	HYDROLASE/BLOOD CLOTTING
2ZP6	CRYSTAL STRUCTURE OF BOVINE INSULIN (HEXAMERIC FORM)	HORMONE
2ZPB	NITROSYLATED FE-TYPE NITRILE HYDRATASE	LYASE
2ZPE	NITROSYLATED FE-TYPE NITRILE HYDRATASE WITH TERT-BUTYLISONITRILE	LYASE
2ZPF	COMPLEX OF FE-TYPE NITRILE HYDRATASE WITH TERT-BUTYLISONITRILE, PHOTO-ACTIVATED FOR 18MIN AT 293K	LYASE
2ZPG	COMPLEX OF FE-TYPE NITRILE HYDRATASE WITH TERT-BUTYLISONITRILE, PHOTO-ACTIVATED FOR 120MIN AT 293K	LYASE
2ZPH	COMPLEX OF FE-TYPE NITRILE HYDRATASE WITH TERT-BUTYLISONITRILE, PHOTO-ACTIVATED FOR 340MIN AT 293K	LYASE
2ZPI	COMPLEX OF FE-TYPE NITRILE HYDRATASE WITH TERT-BUTYLISONITRILE, PHOTO-ACTIVATED FOR 440MIN AT 293K	LYASE
2ZPP	NEUTRON CRYSTAL STRUCTURE OF CUBIC INSULIN AT PD9	HORMONE
2ZPY	RYSTAL STRUCTURE OF THE MOUSE RADXIN FERM DOMAIN COMPLEXED WITH THE MOUSE CD44 CYTOPLASMIC PEPTIDE	CELL ADHESION
2ZS6	HA3 SUBCOMPONENT OF BOTULINUM TYPE C PROGENITOR TOXIN	TOXIN
2ZSH	STRUCTURAL BASIS OF GIBBERELLIN(GA3)-INDUCED DELLA RECOGNITION BY THE GIBBERELLIN RECEPTOR	HORMONE RECEPTOR
2ZSI	STRUCTURAL BASIS OF GIBBERELLIN(GA4)-INDUCED DELLA	HORMONE RECEPTOR

	RECOGNITION BY THE GIBBERELLIN RECEPTOR	
2ZSV	CRYSTAL STRUCTURE OF H-2KB IN COMPLEX WITH JHMV EPITOPE S598	IMMUNE SYSTEM
2ZSW	CRYSTAL STRUCTURE OF H-2KB IN COMPLEX WITH THE Q600Y VARIANT OF JHMV EPITOPE S598	IMMUNE SYSTEM
32C2	STRUCTURE OF AN ACTIVITY SUPPRESSING FAB FRAGMENT TO CYTOCHROME P450 AROMATASE	IMMUNE SYSTEM
35C8	CATALYTIC ANTIBODY 5C8, FAB-INHIBITOR COMPLEX	CATALYTIC ANTIBODY
3AIY	R6 HUMAN INSULIN HEXAMER (SYMMETRIC), NMR, REFINED AVERAGE STRUCTURE	HORMONE/GROWTH FACTOR
3AT1	CRYSTAL STRUCTURES OF PHOSPHONOACETAMIDE LIGATED T AND PHOSPHONOACETAMIDE AND MALONATE LIGATED R STATES OF ASPARTATE CARBAMOYLTRANSFERASE AT 2.8-ANGSTROMS RESOLUTION AND NEUTRAL PH	TRANSFERASE (CARBAMOYL-P,ASPARTATE)
3B2U	CRYSTAL STRUCTURE OF ISOLATED DOMAIN III OF THE EXTRACELLULAR REGION OF THE EPIDERMAL GROWTH FACTOR RECEPTOR IN COMPLEX WITH THE FAB FRAGMENT OF IMC-11F8	IMMUNE SYSTEM/TRANSFERASE
3B2V	CRYSTAL STRUCTURE OF THE EXTRACELLULAR REGION OF THE EPIDERMAL GROWTH FACTOR RECEPTOR IN COMPLEX WITH THE FAB FRAGMENT OF IMC-11F8	IMMUNE SYSTEM/TRANSFERASE
3B3I	CITRULLINATION-DEPENDENT DIFFERENTIAL PRESENTATION OF A SELF-PEPTIDE BY HLA-B27 SUBTYPES	IMMUNE SYSTEM
3B3Q	CRYSTAL STRUCTURE OF A SYNAPTIC ADHESION COMPLEX	CELL ADHESION
3B4V	X-RAY STRUCTURE OF ACTIVIN IN COMPLEX WITH FSTL3	HORMONE REGULATOR COMPLEX
3B5N	STRUCTURE OF THE YEAST PLASMA MEMBRANE SNARE COMPLEX	MEMBRANE PROTEIN
3B6F	NUCLEOSOME CORE PARTICLE TREATED WITH CISPLATIN	STRUCTURAL PROTEIN/DNA
3B6G	NUCLEOSOME CORE PARTICLE TREATED WITH OXALIPLATIN	STRUCTURAL PROTEIN/DNA
3B6S	CRYSTAL STRUCTURE OF HLA-B*2705 COMPLEXED WITH THE CITRULLINATED VASOACTIVE INTESTINAL PEPTIDE TYPE 1 RECEPTOR (VIPR) PEPTIDE (RESIDUES 400-408)	IMMUNE SYSTEM
3B71	CD4 ENDOCYTOSIS MOTIF BOUND TO THE FOCAL ADHESION TARGETING (FAT) DOMAIN OF THE FOCAL ADHESION KINASE	PROTEIN BINDING
3B75	CRYSTAL STRUCTURE OF GLYCATED HUMAN HAEMOGLOBIN	TRANSPORT PROTEIN, OXYGEN BINDING
3B78	STRUCTURE OF THE EEF2-EXOA(R551H)-NAD+ COMPLEX	BIOSYNTHETIC PROTEIN/TRANSFERASE
3B7S	[E296Q]LTA4H IN COMPLEX WITH RSR SUBSTRATE	HYDROLASE
3B7T	[E296Q]LTA4H IN COMPLEX WITH ARG-ALA-ARG SUBSTRATE	HYDROLASE

3B7V	HIV-1 PROTEASE COMPLEXED WITH GEM-DIOL-AMINE TETRAHEDRAL INTERMEDIATE NLLTQI	HYDROLASE
3B80	HIV-1 PROTEASE MUTANT I54V COMPLEXED WITH GEM-DIOL-AMINE INTERMEDIATE NLLTQI	HYDROLASE
3B82	STRUCTURE OF THE EEF2-EXOA(E546H)-NAD+ COMPLEX	BIOSYNTHETIC PROTEIN/TRANSFERASE
3B8E	CRYSTAL STRUCTURE OF THE SODIUM-POTASSIUM PUMP	HYDROLASE/TRANSPORT PROTEIN
3B8H	STRUCTURE OF THE EEF2-EXOA(E546A)-NAD+ COMPLEX	BIOSYNTHETIC PROTEIN/TRANSFERASE
3B95	EUHMT1 (GLP) ANKYRIN REPEAT DOMAIN (STRUCTURE 2)	TRANSFERASE/STRUCTUAL PROTEIN
3B9F	1.6 A STRUCTURE OF THE PCI-THROMBIN-HEPARIN COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
3B9J	STRUCTURE OF XANTHINE OXIDASE WITH 2-HYDROXY-6-METHYLPURINE	OXIDOREDUCTASE
3B9K	CRYSTAL STRUCTURE OF CD8ALPHA-BETA IN COMPLEX WITH YTS 156.7 FAB	IMMUNE SYSTEM
3BAE	CRYSTAL STRUCTURE OF FAB WO2 BOUND TO THE N TERMINAL DOMAIN OF AMYLOID BETA PEPTIDE (1-28)	IMMUNE SYSTEM
3BBN	HOMOLOGY MODEL FOR THE SPINACH CHLOROPLAST 30S SUBUNIT FITTED TO 9.4A CRYO-EM MAP OF THE 70S CHLORORIBOSOME.	RIBOSOME
3BBO	HOMOLOGY MODEL FOR THE SPINACH CHLOROPLAST 50S SUBUNIT FITTED TO 9.4A CRYO-EM MAP OF THE 70S CHLORORIBOSOME	RIBOSOME
3BBP	RAB6-GTP:GCC185 RAB BINDING DOMAIN COMPLEX	PROTEIN TRANSPORT/SPLICING
3BC1	CRYSTAL STRUCTURE OF THE COMPLEX RAB27A-SLP2A	SIGNALING PROTEIN/TRANSPORT PROTEIN
3BCC	STIGMATELLIN AND ANTIMYCIN BOUND CYTOCHROME BC1 COMPLEX FROM CHICKEN	OXIDOREDUCTASE
3BCQ	CRYSTAL STRUCTURE OF OXY-HEMOGLOBIN FROM BRYCON CEPHALUS	TRANSPORT PROTEIN/OXYGEN BINDING
3BDG	CRYSTAL STRUCTURE OF WILD-TYPE/T155V MIXED DIMER OF E. COLI ALKALINE PHOSPHATASE	HYDROLASE
3BDM	YEAST 20S PROTEASOME:GLIDOBACTIN A-COMPLEX	HYDROLASE
3BDW	HUMAN CD94/NKG2A	IMMUNE SYSTEM RECEPTOR
3BDY	FAB COMPLEX STRUCTURE	HORMONE
3BE1	FAB/RECEPTOR COMPLEX	TRANSFERASE
3BEF	CRYSTAL STRUCTURE OF THROMBIN BOUND TO THE EXTRACELLULAR FRAGMENT OF PAR1	HYDROLASE
3BEG	CRYSTAL STRUCTURE OF SR PROTEIN KINASE 1 COMPLEXED TO ITS	TRANSFERASE/SPLICING

	SUBSTRATE ASF/SF2	
3BEI	CRYSTAL STRUCTURE OF THE SLOW FORM OF THROMBIN IN A SELF_INHIBITED CONFORMATION	HYDROLASE
3BEJ	STRUCTURE OF HUMAN FXR IN COMPLEX WITH MFA-1 AND CO-ACTIVATOR PEPTIDE	TRANSCRIPTION REGULATOR
3BES	STRUCTURE OF A POXVIRUS IFNGBP/IFNG COMPLEX	IMMUNE SYSTEM
3BEV	11MER STRUCTURE OF AN MHC CLASS I MOLECULE FROM B21 CHICKENS ILLUSTRATE PROMISCUOUS PEPTIDE BINDING	IMMUNE SYSTEM
3BEW	10MER CRYSTAL STRUCTURE OF CHICKEN MHC CLASS I HAPLOTYPE B21	IMMUNE SYSTEM
3BF6	THROMBIN:SURAMIN COMPLEX	HYDROLASE
3BG0	ARCHITECTURE OF A COAT FOR THE NUCLEAR PORE MEMBRANE	PROTEIN TRANSPORT, HYDROLASE
3BG1	ARCHITECTURE OF A COAT FOR THE NUCLEAR PORE MEMBRANE	PROTEIN TRANSPORT, HYDROLASE
3BG4	THE CRYSTAL STRUCTURE OF GUAMERIN IN COMPLEX WITH CHYMOTRYPSIN AND THE DEVELOPMENT OF AN ELASTASE-SPECIFIC INHIBITOR	HYDROLASE/HYDROLASE INHIBITOR
3BGF	X-RAY CRYSTAL STRUCTURE OF THE SARS CORONAVIRUS SPIKE RECEPTOR BINDING DOMAIN IN COMPLEX WITH F26G19 FAB	VIRAL PROTEIN/IMMUNE SYSTEM
3BGM	CRYSTAL STRUCTURE OF PKD2 PHOSPHOPEPTIDE BOUND TO HUMAN CLASS I MHC HLA-A2	IMMUNE SYSTEM
3BGO	AZIDE COMPLEX OF ENGINEERED SUBTILISIN SUBT_BACAM	HYDROLASE
3BGR	CRYSTAL STRUCTURE OF K103N/Y181C MUTANT HIV-1 REVERSE TRANSCRIPTASE (RT) IN COMPLEX WITH TMC278 (RILPIVIRINE), A NON-NUCLEOSIDE RT INHIBITOR	TRANSFERASE, HYDROLASE
3BH6	CRYSTAL STRUCTURE OF THE RP2-ARL3 COMPLEX BOUND TO GPPNHP	SIGNALING PROTEIN
3BH7	CRYSTAL STRUCTURE OF THE RP2-ARL3 COMPLEX BOUND TO GDP-ALF4	SIGNALING PROTEIN
3BH8	CRYSTAL STRUCTURE OF RQA_M PHOSPHOPEPTIDE BOUND TO HUMAN CLASS I MHC HLA-A2	IMMUNE SYSTEM
3BH9	CRYSTAL STRUCTURE OF RTY PHOSPHOPEPTIDE BOUND TO HUMAN CLASS I MHC HLA-A2	IMMUNE SYSTEM
3BHB	CRYSTAL STRUCTURE OF KMD PHOSPHOPEPTIDE BOUND TO HUMAN CLASS I MHC HLA-A2	IMMUNE SYSTEM
3BHT	STRUCTURE OF PHOSPHORYLATED THR160 CDK2/CYCLIN A IN COMPLEX WITH THE INHIBITOR MERIOLIN 3	TRANSFERASE
3BHU	STRUCTURE OF PHOSPHORYLATED THR160 CDK2/CYCLIN A IN COMPLEX WITH THE INHIBITOR MERIOLIN 5	TRANSFERASE

3BHV	STRUCTURE OF PHOSPHORYLATED THR160 CDK2/CYCLIN A IN COMPLEX WITH THE INHIBITOR VARIOLIN B	TRANSFERASE
3BII	CRYSTAL STRUCTURE OF ACTIVATED MPT SYNTHASE	TRANSFERASE
3BIM	CRYSTAL STRUCTURE OF THE BCL6 BTB DOMAIN DIMER IN COMPLEX WITH THE BCOR BBD COREPRESSOR PEPTIDE	TRANSCRIPTION REPRESSOR
3BIN	STRUCTURE OF THE DAL-1 AND TSLC1 (372-383) COMPLEX	CELL ADHESION
3BIU	HUMAN THROMBIN-IN COMPLEX WITH UB-THR10	HYDROLASE/HYDROLASE INHIBITOR
3BIV	HUMAN THROMBIN-IN COMPLEX WITH UB-THR11	HYDROLASE/HYDROLASE INHIBITOR
3BIW	CRYSTAL STRUCTURE OF THE NEUROLIGIN-1/NEUREXIN-1BETA SYNAPTIC ADHESION COMPLEX	CELL ADHESION/CELL ADHESION
3BJ1	MET-PERCH HEMOGLOBIN AT PH 5.7	OXYGEN BINDING
3BJ2	MET-PERCH HEMOGLOBIN AT PH 6.3	OXYGEN BINDING
3BJ3	MET-PERCH HEMOGLOBIN AT PH 8.0	OXYGEN BINDING
3BJI	TRUCTURAL BASIS OF PROMISCUOUS GUANINE NUCLEOTIDE EXCHANGE BY THE T-CELL ESSENTIAL VAV1	SIGNALING PROTEIN
3BK3	CRYSTAL STRUCTURE OF THE COMPLEX OF BMP-2 AND THE FIRST VON WILLEBRAND DOMAIN TYPE C OF CROSSVEINLESS-2	HORMONE/GROWTH FACTOR
3BKC	CRYSTAL STRUCTURE OF ANTI-AMYLOID BETA FAB WO2 (P21, FORMB)	IMMUNE SYSTEM
3BKJ	CRYSTAL STRUCTURE OF FAB WO2 BOUND TO THE N TERMINAL DOMAIN OF AMYLOID BETA PEPTIDE (1-16)	IMMUNE SYSTEM
3BKM	STRUCTURE OF ANTI-AMYLOID-BETA FAB WO2 (FORM A, P212121)	IMMUNE SYSTEM
3BKY	CRYSTAL STRUCTURE OF CHIMERIC ANTIBODY C2H7 FAB IN COMPLEX WITH A CD20 PEPTIDE	IMMUNE SYSTEM
3BL2	CRYSTAL STRUCTURE OF M11, THE BCL-2 HOMOLOG OF MURINE GAMMA-HERPESVIRUS 68, COMPLEXED WITH MOUSE BECLIN1 (RESIDUES 106-124)	VIRAL PROTEIN/APOPTOSIS
3BLH	CRYSTAL STRUCTURE OF HUMAN CDK9/CYCLINT1	TRANSCRIPTION
3BLQ	CRYSTAL STRUCTURE OF HUMAN CDK9/CYCLINT1 IN COMPLEX WITH ATP	TRANSCRIPTION
3BLR	CRYSTAL STRUCTURE OF HUMAN CDK9/CYCLINT1 IN COMPLEX WITH FLAVOPIRIDOL	TRANSCRIPTION
3BLV	YEAST ISOCITRATE DEHYDROGENASE WITH CITRATE BOUND IN THE REGULATORY SUBUNITS	OXIDOREDUCTASE
3BLW	YEAST ISOCITRATE DEHYDROGENASE WITH CITRATE AND AMP BOUND	OXIDOREDUCTASE

	IN THE REGULATORY SUBUNITS	
3BLX	YEAST ISOCITRATE DEHYDROGENASE (APO FORM)	OXIDOREDUCTASE
3BMC	STRUCTURE OF PTERIDINE REDUCTASE 1 (PTR1) FROM TRYPANOSOMA BRUCEI IN TERNARY COMPLEX WITH COFACTOR (NADP+) AND SUBSTRATE (FOLATE)	OXIDOREDUCTASE
3BME	STRUCTURE OF PTERIDINE REDUCTASE 1 (PTR1) FROM TRYPANOSOMA BRUCEI IN TERNARY COMPLEX WITH COFACTOR (NADP+) AND INHIBITOR (COMPOUND DX2)	OXIDOREDUCTASE
3BMF	STRUCTURE OF PTERIDINE REDUCTASE 1 (PTR1) FROM TRYPANOSOMA BRUCEI IN TERNARY COMPLEX WITH COFACTOR (NADP+) AND INHIBITOR DX3	OXIDOREDUCTASE
3BMG	STRUCTURE OF PTERIDINE REDUCTASE 1 (PTR1) FROM TRYPANOSOMA BRUCEI IN TERNARY COMPLEX WITH COFACTOR (NADP+) AND INHIBITOR (COMPOUND DX4)	OXIDOREDUCTASE
3BMH	STRUCTURE OF PTERIDINE REDUCTASE 1 (PTR1) FROM TRYPANOSOMA BRUCEI IN TERNARY COMPLEX WITH COFACTOR (NADP+) AND INHIBITOR (COMPOUND DX6)	OXIDOREDUCTASE
3BML	STRUCTURE OF PTERIDINE REDUCTASE 1 (PTR1) FROM TRYPANOSOMA BRUCEI IN TERNARY COMPLEX WITH COFACTOR (NADP+) AND INHIBITOR (COMPOUND AX1)	OXIDOREDUCTASE
3BMM	STRUCTURE OF PTERIDINE REDUCTASE 1 (PTR1) FROM TRYPANOSOMA BRUCEI IN TERNARY COMPLEX WITH COFACTOR (NADP+) AND INHIBITOR (COMPOUND AX2)	OXIDOREDUCTASE
3BMN	STRUCTURE OF PTERIDINE REDUCTASE 1 (PTR1) FROM TRYPANOSOMA BRUCEI IN TERNARY COMPLEX WITH COFACTOR (NADP+) AND INHIBITOR (COMPOUND AX3)	OXIDOREDUCTASE
3BMO	STRUCTURE OF PTERIDINE REDUCTASE 1 (PTR1) FROM TRYPANOSOMA BRUCEI IN TERNARY COMPLEX WITH COFACTOR (NADP+) AND INHIBITOR (COMPOUND AX4)	OXIDOREDUCTASE
3BMQ	STRUCTURE OF PTERIDINE REDUCTASE 1 (PTR1) FROM TRYPANOSOMA BRUCEI IN TERNARY COMPLEX WITH COFACTOR (NADP+) AND INHIBITOR (COMPOUND AX5)	OXIDOREDUCTASE
3BMR	STRUCTURE OF PTERIDINE REDUCTASE 1 (PTR1) FROM TRYPANOSOMA BRUCEI IN TERNARY COMPLEX WITH COFACTOR (NADP+) AND INHIBITOR (COMPOUND AX6)	OXIDOREDUCTASE
3BN3	CRYSTAL STRUCTURE OF ICAM-5 IN COMPLEX WITH AL I DOMAIN	CELL ADHESION, IMMUNE SYSTEM
3BN9	CRYSTAL STRUCTURE OF MT-SP1 IN COMPLEX WITH FAB INHIBITOR E2	HYDROLASE
3BO0	RIBOSOME-SECY COMPLEX	RIBOSOME
3BO1	RIBOSOME-SECY COMPLEX	RIBOSOME

3BO8	THE HIGH RESOLUTION CRYSTAL STRUCTURE OF HLA-A1 COMPLEXED WITH THE MAGE-A1 PEPTIDE	IMMUNE SYSTEM
3BOM	CRYSTAL STRUCTURE OF TROUT HEMOGLOBIN AT 1.35 ANGSTROM RESOLUTION	OXYGEN STORAGE/TRANSPORT
3BOO	STRUCTURE OF THE C. BOTULINUM NEUROTOXIN SEROTYPE A WITH AN INHIBITORY PEPTIDE BOUND	TOXIN/TOXIN INHIBITOR
3BOW	STRUCTURE OF M-CALPAIN IN COMPLEX WITH CALPASTATIN	HYDROLASE/HYDROLASE INHIBITOR
3BP4	THE HIGH RESOLUTION CRYSTAL STRUCTURE OF HLA-B*2705 IN COMPLEX WITH A CATHEPSIN A SIGNAL SEQUENCE PEPTIDE PCATA	IMMUNE SYSTEM
3BP7	THE HIGH RESOLUTION CRYSTAL STRUCTURE OF HLA-B*2709 IN COMPLEX WITH A CATHEPSIN A SIGNAL SEQUENCE PEPTIDE, PCATA	IMMUNE SYSTEM
3BP8	CRYSTAL STRUCTURE OF MLC/EIIB COMPLEX	TRANSCRIPTION
3BPL	CRYSTAL STRUCTURE OF THE IL4-IL4R-COMMON GAMMA TERNARY COMPLEX	CYTOKINE/CYTOKINE RECEPTOR
3BPN	CRYSTAL STRUCTURE OF THE IL4-IL4R-IL13RA TERNARY COMPLEX	CYTOKINE/CYTOKINE RECEPTOR
3BPO	CRYSTAL STRUCTURE OF THE IL13-IL4R-IL13RA TERNARY COMPLEX	CYTOKINE/CYTOKINE RECEPTOR
3BPQ	CRYSTAL STRUCTURE OF RELB-RELE ANTITOXIN-TOXIN COMPLEX FROM METHANOCOCCUS JANNASCHII	TOXIN
3BPS	PCSK9:EGF-A COMPLEX	HYDROLASE/LIPID TRANSPORT
3BQD	DOUBLING THE SIZE OF THE GLUCOCORTICOID RECEPTOR LIGAND BINDING POCKET BY DEACYLCORTIVAZOL	PROTEIN BINDING
3BQO	CRYSTAL STRUCTURE OF TRF1 TRFH DOMAIN AND TIN2 PEPTIDE COMPLEX	DNA BINDING PROTEIN
3BQU	CRYSTAL STRUCTURE OF THE 2F5 FAB'-3H6 FAB COMPLEX	IMMUNE SYSTEM
3BRR	CRYSTAL STRUCTURE OF INSULIN IN COMPLEX WITH SULFATIDE	HORMONE
3BRT	NEMO/IKK ASSOCIATION DOMAIN STRUCTURE	TRANSFERASE/TRANSCRIPTION
3BRV	NEMO/IKKB ASSOCIATION DOMAIN STRUCTURE	TRANSFERASE/TRANSCRIPTION
3BRW	STRUCTURE OF THE RAP-RAPGAP COMPLEX	GTP BINDING PROTEIN
3BS4	CRYSTAL STRUCTURE OF UNCHARACTERIZED PROTEIN PH0321 FROM PYROCOCCUS HORIKOSHII IN COMPLEX WITH AN UNKNOWN PEPTIDE	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
3BS5	CRYSTAL STRUCTURE OF HCNK2-SAM/DHYP-SAM COMPLEX	SIGNALING PROTEIN/MEMBRANE PROTEIN
3BSZ	CRYSTAL STRUCTURE OF THE TRANSTHYRETIN-RETINOL BINDING PROTEIN-FAB COMPLEX	TRANSPORT PROTEIN/IMMUNE SYSTEM

3BT1	STRUCTURE OF UROKINASE RECEPTOR, UROKINASE AND VITRONECTIN COMPLEX	IMMUNE SYSTEM
3BT2	STRUCTURE OF UROKINASE RECEPTOR, UROKINASE AND VITRONECTIN COMPLEX	IMMUNE SYSTEM
3BT6	CRYSTAL STRUCTURE OF INFLUENZA B VIRUS HEMAGGLUTININ	VIRAL PROTEIN
3BTP	CRYSTAL STRUCTURE OF AGROBACTERIUM TUMEFACIENS VIRE2 IN COMPLEX WITH ITS CHAPERONE VIRE1: A NOVEL FOLD AND IMPLICATIONS FOR DNA BINDING	DNA BINDING PROTEIN, CHAPERONE
3BTS	CRYSTAL STRUCTURE OF A TERNARY COMPLEX OF THE TRANSCRIPTIONAL REPRESSOR GAL80P (GAL80S0 [G301R]) AND THE ACIDIC ACTIVATION DOMAIN OF GAL4P (AA 854-874) FROM SACCHAROMYCES CEREVISIAE WITH NAD	TRANSCRIPTION
3BU3	CRYSTAL STRUCTURE OF THE INSULIN RECEPTOR KINASE IN COMPLEX WITH IRS2 KRLB PEPTIDE	TRANSFERASE
3BU5	CRYSTAL STRUCTURE OF THE INSULIN RECEPTOR KINASE IN COMPLEX WITH IRS2 KRLB PEPTIDE AND ATP	TRANSFERASE
3BU6	CRYSTAL STRUCTURE OF THE INSULIN RECEPTOR KINASE IN COMPLEX WITH IRS2 KRLB PHOSPHOPEPTIDE	TRANSFERASE
3BU8	CRYSTAL STRUCTURE OF TRF2 TRFH DOMAIN AND TIN2 PEPTIDE COMPLEX	DNA BINDING PROTEIN
3BUA	CRYSTAL STRUCTURE OF TRF2 TRFH DOMAIN AND APOLLO PEPTIDE COMPLEX	DNA BINDING PROTEIN
3BUM	CRYSTAL STRUCTURE OF C-CBL-TKB DOMAIN COMPLEXED WITH ITS BINDING MOTIF IN SPROUTY2	LIGASE
3BUN	CRYSTAL STRUCTURE OF C-CBL-TKB DOMAIN COMPLEXED WITH ITS BINDING MOTIF IN SPROUTY4	LIGASE/SIGNALING PROTEIN
3BUO	CRYSTAL STRUCTURE OF C-CBL-TKB DOMAIN COMPLEXED WITH ITS BINDING MOTIF IN EGF RECEPTOR'	LIGASE/SIGNALING PROTEIN
3BUW	CRYSTAL STRUCTURE OF C-CBL-TKB DOMAIN COMPLEXED WITH ITS BINDING MOTIF IN SYK	LIGASE/SIGNALING PROTEIN
3BUX	CRYSTAL STRUCTURE OF C-CBL-TKB DOMAIN COMPLEXED WITH ITS BINDING MOTIF IN C-MET	LIGASE/SIGNALING PROTEIN
3BUY	MHC-I IN COMPLEX WITH PEPTIDE	IMMUNE SYSTEM
3BUZ	CRYSTAL STRUCTURE OF IA-BTAD-ACTIN COMPLEX	TOXIN/STRUCTURAL PROTEIN
3BV9	STRUCTURE OF THROMBIN BOUND TO THE INHIBITOR FM19	HYDROLASE
3BVD	TRUCTURE OF SURFACE-ENGINEERED CYTOCHROME BA3 OXIDASE FROM	OXIDOREDUCTASE

	THERMUS THERMOPHILUS UNDER XENON PRESSURE, 100PSI 5MIN	
3BVH	CRYSTAL STRUCTURE OF RECOMBINANT GAMMAD364A FIBRINOGEN FRAGMENT D WITH THE PEPTIDE LIGAND GLY-PRO-ARG-PRO-AMIDE	BLOOD CLOTTING
3BW9	CRYSTAL STRUCTURE OF HLA B*3508 IN COMPLEX WITH A HCMV 12-MER PEPTIDE FROM THE PP65 PROTEIN	IMMUNE SYSTEM
3BWA	CRYSTAL STRUCTURE OF HLA B*3508 IN COMPLEX WITH A HCMV 8-MER PEPTIDE FROM THE PP65 PROTEIN	IMMUNE SYSTEM
3BWN	L-TRYPTOPHAN AMINOTRANSFERASE	TRANSFERASE
3BWU	CRYSTAL STRUCTURE OF THE TERNARY COMPLEX OF FIMD (N-TERMINAL DOMAIN, FIMDN) WITH FIMC AND THE N-TERMINALLY TRUNCATED PILUS SUBUNIT FIMF (FIMFT)	CHAPERONE, STRUCTURAL, MEMBRANE PROTEIN
3BX1	COMPLEX BETWEEN THE BARLEY ALPHA-AMYLASE/SUBTILISIN INHIBITOR AND THE SUBTILISIN SAVINASE	HYDROLASE/HYDROLASE INHIBITOR
3BX4	CRYSTAL STRUCTURE OF THE SNAKE VENOM TOXIN AGGRETIN	TOXIN
3BXK	CRYSTAL STRUCTURE OF THE P/Q-TYPE CALCIUM CHANNEL (CAV2.1) IQ DOMAIN AND CA2+CALMODULIN COMPLEX	MEMBRANE PROTEIN, SIGNALING PROTEIN
3BXL	CRYSTAL STRUCTURE OF THE R-TYPE CALCIUM CHANNEL (CAV2.3) IQ DOMAIN AND CA2+CALMODULIN COMPLEX	MEMBRANE PROTEIN, SIGNALING PROTEIN
3BXQ	THE STRUCTURE OF A MUTANT INSULIN UNCOUPLES RECEPTOR BINDING FROM PROTEIN ALLOSTERY. AN ELECTROSTATIC BLOCK TO THE TR TRANSITION	HORMONE
3BY4	STRUCTURE OF OVARIAN TUMOR (OTU) DOMAIN IN COMPLEX WITH UBIQUITIN	CELL CYCLE, HYDROLASE
3BYH	MODEL OF ACTIN-FIMBRIN ABD2 COMPLEX	STRUCTURAL PROTEIN
3BZ4	CRYSTAL STRUCTURE OF FAB F22-4 IN COMPLEX WITH A SHIGELLA FLEXNERI 2A O-AG DECASACCHARIDE	IMMUNE SYSTEM
3BZE	THE HUMAN NON-CLASSICAL MAJOR HISTOCOMPATIBILITY COMPLEX MOLECULE HLA-E	IMMUNE SYSTEM
3BZF	THE HUMAN NON-CLASSICAL MAJOR HISTOCOMPATIBILITY COMPLEX MOLECULE HLA-E	IMMUNE SYSTEM
3BZI	MOLECULAR AND STRUCTURAL BASIS OF POLO-LIKE KINASE 1 SUBSTRATE RECOGNITION: IMPLICATIONS IN CENTROSOMAL LOCALIZATION	TRANSFERASE
3BZL	CRYSTAL STRUCTURAL OF NATIVE ESCU C-TERMINAL DOMAIN	MEMBRANE PROTEIN, PROTEIN TRANSPORT
3BZO	CRYSTAL STRUCTURAL OF NATIVE ESCU C-TERMINAL DOMAIN	MEMBRANE PROTEIN, PROTEIN TRANSPORT
3BZV	CRYSTAL STRUCTURAL OF THE MUTATED T264A ESCU C-TERMINAL	MEMBRANE PROTEIN, PROTEIN TRANSPORT

	DOMAIN	
3BZX	CRYSTAL STRUCTURE OF THE MUTATED H265A ESCU C-TERMINAL DOMAIN	MEMBRANE PROTEIN, PROTEIN TRANSPORT
3BZY	CRYSTAL STRUCTURE OF THE MUTATED Y316D ESCU C-TERMINAL DOMAIN	MEMBRANE PROTEIN, PROTEIN TRANSPORT
3BZZ	CRYSTAL STRUCTURAL OF THE MUTATED R313T ESCU/SPAS C-TERMINAL DOMAIN	MEMBRANE PROTEIN, PROTEIN TRANSPORT
3C00	CRYSTAL STRUCTURAL OF THE MUTATED G247T ESCU/SPAS C-TERMINAL DOMAIN	MEMBRANE PROTEIN, PROTEIN TRANSPORT
3C01	CRYSTAL STRUCTURAL OF NATIVE SPAS C-TERMINAL DOMAIN	MEMBRANE PROTEIN, PROTEIN TRANSPORT
3C03	CRYSTAL STRUCTURE OF THE ESCU C-TERMINAL DOMAIN WITH P263A MUTATION,SPACE GROUP P 1 21 1	MEMBRANE PROTEIN, PROTEIN TRANSPORT
3C08	CRYSTAL STRUCTURE THE FAB FRAGMENT OF MATUZUMAB/EMD72000 (FAB72000)	IMMUNE SYSTEM
3C09	CRYSTAL STRUCTURE THE FAB FRAGMENT OF MATUZUMAB (FAB72000) IN COMPLEX WITH DOMAIN III OF THE EXTRACELLULAR REGION OF EGFR	IMMUNE SYSTEM/TRANSFERASE
3C0R	STRUCTURE OF OVARIAN TUMOR (OTU) DOMAIN IN COMPLEX WITH UBIQUITIN	CELL CYCLE, HYDROLASE
3C0T	STRUCTURE OF THE SCHIZOSACCHAROMYCES POMBE MEDIATOR SUBCOMPLEX MED8C/18	TRANSCRIPTION
3C1B	THE EFFECT OF H3 K79 DIMETHYLATION AND H4 K20 TRIMETHYLATION ON NUCLEOSOME AND CHROMATIN STRUCTURE	STRUCTURAL PROTEIN/DNA
3C1C	THE EFFECT OF H3 K79 DIMETHYLATION AND H4 K20 TRIMETHYLATION ON NUCLEOSOME AND CHROMATIN STRUCTURE	STRUCTURAL PROTEIN/DNA
3C2A	ANTIBODY FAB FRAGMENT 447-52D IN COMPLEX WITH UG1033 PEPTIDE	IMMUNE SYSTEM
3C2G	CRYSTAL COMPLEX OF SYS-1/POP-1 AT 2.5A RESOLUTION	CELL ADHESION/TRANSCRIPTION
3C3O	ALIX BRO1-DOMAIN:CHMIP4A CO-CRYSTAL STRUCTURE	TRANSPORT PROTEIN
3C3Q	ALIX BRO1-DOMAIN:CHMIP4B CO-CRYSTAL STRUCTURE	TRANSPORT PROTEIN
3C3R	ALIX BRO1 CHMP4C COMPLEX	TRANSPORT PROTEIN
3C4M	TRUCTURE OF HUMAN PARATHYROID HORMONE IN COMPLEX WITH THE EXTRACELLULAR DOMAIN OF ITS G-PROTEIN-COUPLED RECEPTOR (PTH1R)	MEMBRANE PROTEIN
3C4O	CRYSTAL STRUCTURE OF THE SHV-1 BETA-LACTAMASE/BETA-LACTAMASE INHIBITOR PROTEIN (BLIP) E73M/S130K/S146M COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
		HYDROLASE/HYDROLASE INHIBITOR

3C4P	CRYSTAL STRUCTURE OF THE SHV-1 BETA-LACTAMASE/BETA-LACTAMASE INHIBITOR PROTEIN (BLIP) E73M COMPLEX	
3C59	CRYSTAL STRUCTURE OF THE LIGAND-BOUND GLUCAGON-LIKE PEPTIDE-1 RECEPTOR EXTRACELLULAR DOMAIN	SIGNALING PROTEIN/SIGNALING PROTEIN
3C5I	CRYSTAL STRUCTURE OF PLASMODIUM KNOWLESI CHOLINE KINASE, PKH_134520	TRANSFERASE
3C5J	CRYSTAL STRUCTURE OF HLA DR52C	MEMBRANE PROTEIN
3C5S	CRYSTAL STRUCTURE OF MONOCLONAL FAB F22-4 SPECIFIC FOR SHIGELLA FLEXNERI 2A O-AG	IMMUNE SYSTEM
3C5T	CRYSTAL STRUCTURE OF THE LIGAND-BOUND GLUCAGON-LIKE PEPTIDE-1 RECEPTOR EXTRACELLULAR DOMAIN	SIGNALING PROTEIN/SIGNALING PROTEIN
3C5W	COMPLEX BETWEEN PP2A-SPECIFIC METHYLESTERASE PME-1 AND PP2A CORE ENZYME	HYDROLASE
3C5X	CRYSTAL STRUCTURE OF THE PRECURSOR MEMBRANE PROTEIN-ENVELOPE PROTEIN HETERODIMER FROM THE DENGUE 2 VIRUS AT LOW PH	VIRAL PROTEIN
3C5Z	CRYSTAL STRUCTURE OF MOUSE MHC CLASS II I-AB/3K PEPTIDE COMPLEXED WITH MOUSE TCR B3K506	SUGAR BINDING PROTEIN/IMMUNE SYSTEM
3C60	CRYSTAL STRUCTURE OF MOUSE MHC CLASS II I-AB/3K PEPTIDE COMPLEXED WITH MOUSE TCR YAE62	SUGAR BINDING PROTEIN/IMMUNE SYSTEM
3C66	YEAST POLY(A) POLYMERASE IN COMPLEX WITH FIP1 RESIDUES 80-105	TRANSFERASE
3C6L	CRYSTAL STRUCTURE OF MOUSE MHC CLASS II I-AB/3K PEPTIDE COMPLEXED WITH MOUSE TCR 2W20	SUGAR BINDING PROTEIN/IMMUNE SYSTEM
3C6N	SMALL MOLECULE AGONISTS AND ANTAGONISTS OF F-BOX PROTEIN-SUBSTRATE INTERACTIONS IN AUXIN PERCEPTION AND SIGNALING	SIGNALING PROTEIN
3C6O	SMALL MOLECULE AGONISTS AND ANTAGONISTS OF F-BOX PROTEIN-SUBSTRATE INTERACTIONS IN AUXIN PERCEPTION AND SIGNALING	SIGNALING PROTEIN
3C6P	SMALL MOLECULE AGONISTS AND ANTAGONISTS OF F-BOX PROTEIN-SUBSTRATE INTERACTIONS IN AUXIN PERCEPTION AND SIGNALING	SIGNALING PROTEIN
3C6S	CRYSTAL STRUCTURE OF FAB F22-4 IN COMPLEX WITH A SHIGELLA FLEXNERI 2A O-AG PENTADECASACCHARIDE	IMMUNE SYSTEM
3C6T	CRYSTAL STRUCTURE OF HIV REVERSE TRANSCRIPTASE IN COMPLEX WITH INHIBITOR 14	TRANSFERASE
3C6U	CRYSTAL STRUCTURE OF HIV REVERSE TRANSCRIPTASE IN COMPLEX WITH INHIBITOR 22	TRANSFERASE
3C72	ENGINEERED RABGGTASE IN COMPLEX WITH A PEPTIDOMIMETIC	TRANSFERASE

	INHIBITOR	
3C7B	STRUCTURE OF THE DISSIMILATORY SULFITE REDUCTASE FROM ARCHAEOGLOBUS FULGIDUS	OXIDOREDUCTASE
3C7K	MOLECULAR ARCHITECTURE OF GALPHAO AND THE STRUCTURAL BASIS FOR RGS16-MEDIATED DEACTIVATION	SIGNALING PROTEIN
3C7N	STRUCTURE OF THE HSP110:HSC70 NUCLEOTIDE EXCHANGE COMPLEX	CHAPERONE/CHAPERONE
3C7U	STRUCTURAL INSIGHT INTO THE KINETICS AND CP OF INTERACTIONS BETWEEN TEM-1-LACTAMASE AND BLIP	HYDROLASE/HYDROLASE INHIBITOR
3C7V	STRUCTURAL INSIGHT INTO THE KINETICS AND DELTA-CP OF INTERACTIONS BETWEEN TEM-1 BETA-LACTAMASE AND BLIP	HYDROLASE/HYDROLASE INHIBITOR
3C88	CRYSTAL STRUCTURE OF THE CATALYTIC DOMAIN OF BOTULINUM NEUROTOXIN SEROTYPE A WITH INHIBITORY PEPTIDE RRGC	HYDROLASE
3C89	CRYSTAL STRUCTURE OF THE CATALYTIC DOMAIN OF BOTULINUM NEUROTOXIN SEROTYPE A WITH INHIBITORY PEPTIDE RRGM	HYDROLASE
3C8A	CRYSTAL STRUCTURE OF THE CATALYTIC DOMAIN OF BOTULINUM NEUROTOXIN SEROTYPE A WITH INHIBITORY PEPTIDE RRGL	HYDROLASE
3C8B	CRYSTAL STRUCTURE OF THE CATALYTIC DOMAIN OF BOTULINUM NEUROTOXIN SEROTYPE A WITH INHIBITORY PEPTIDE RRGI	HYDROLASE
3C8G	CRYSTAL STRUCTURE OF A POSSIBLE TRANSCIPTIONAL REGULATOR YGGD FROM SHIGELLA FLEXNERI 2A STR. 2457T	TRANSCRIPTION REGULATOR
3C8K	THE CRYSTAL STRUCTURE OF LY49C BOUND TO H-2KB	IMMUNE SYSTEM
3C91	THERMOPLASMA ACIDOPHILUM 20S PROTEASOME WITH AN OPEN GATE	HYDROLASE
3C92	THERMOPLASMA ACIDOPHILUM 20S PROTEASOME WITH A CLOSED GATE	HYDROLASE
3C94	EXOI/SSB-CT COMPLEX	HYDROLASE
3C98	REVISED STRUCTURE OF THE MUNC18A-SYNTAXIN1 COMPLEX	ENDOCYTOSIS/EXOCYTOSIS
3C9A	HIGH RESOLUTION CRYSTAL STRUCTURE OF ARGOS BOUND TO THE EGF DOMAIN OF SPITZ	HORMONE/SIGNALING PROTEIN
3C9C	STRUCTURAL BASIS OF HISTONE H4 RECOGNITION BY P55	TRANSCRIPTION REPRESSOR
3C9N	CRYSTAL STRUCTURE OF A SARS CORONA VIRUS DERIVED PEPTIDE BOUND TO THE HUMAN MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I MOLECULE HLA-B*1501	IMMUNE SYSTEM
3C9Q	CRYSTAL STRUCTURE OF THE UNCHARACTERIZED HUMAN PROTEIN C8ORF32 WITH BOUND PEPTIDE	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
3CAA	CLEAVED ANTICHYMOTRYPSIN A347R	SERPIN
		OXIDOREDUCTASE

3CB8	4FE-4S-PYRUVATE FORMATE-LYASE ACTIVATING ENZYME IN COMPLEX WITH ADOMET AND A PEPTIDE SUBSTRATE	
3CBJ	CHAGASIN-CATHEPSIN B COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
3CBK	CHAGASIN-CATHEPSIN B	HYDROLASE/HYDROLASE INHIBITOR
3CBL	CRYSTAL STRUCTURE OF HUMAN FELINE SARCOMA VIRAL ONCOGENE HOMOLOGUE (V-FES) IN COMPLEX WITH STAUROSPORINE AND A CONSENSUS PEPTIDE	TRANSFERASE
3CBM	SET7/9-ER-ADOMET COMPLEX	TRANSFERASE/TRANSFERASE RECEPTOR
3CBO	SET7/9-ER-ADOHCY COMPLEX	TRANSFERASE/TRANSFERASE RECEPTOR
3CBP	SET7/9-ER-SINEFUNGIN COMPLEX	TRANSFERASE/TRANSFERASE RECEPTOR
3CC2	HE REFINED CRYSTAL STRUCTURE OF THE HALOARCULA MARISMORTUI LARGE RIBOSOMAL SUBUNIT AT 2.4 ANGSTROM RESOLUTION WITH RRNA SEQUENCE FOR THE 23S RRNA AND GENOME-DERIVED SEQUENCES FOR R-PROTEINS	RIBOSOME
3CC4	CO-CRYSTAL STRUCTURE OF ANISOMYCIN BOUND TO THE 50S RIBOSOMAL SUBUNIT	RIBOSOME
3CC7	STRUCTURE OF ANISOMYCIN RESISTANT 50S RIBOSOMAL SUBUNIT: 23S RRNA MUTATION C2487U	RIBOSOME
3CCE	STRUCTURE OF ANISOMYCIN RESISTANT 50S RIBOSOMAL SUBUNIT: 23S RRNA MUTATION U2535A	RIBOSOME
3CCJ	STRUCTURE OF ANISOMYCIN RESISTANT 50S RIBOSOMAL SUBUNIT: 23S RRNA MUTATION C2534U	RIBOSOME
3CCL	STRUCTURE OF ANISOMYCIN RESISTANT 50S RIBOSOMAL SUBUNIT: 23S RRNA MUTATION U2535C. DENSITY FOR ANISOMYCIN IS VISIBLE BUT NOT INCLUDED IN MODEL.	RIBOSOME
3CCM	STRUCTURE OF ANISOMYCIN RESISTANT 50S RIBOSOMAL SUBUNIT: 23S RRNA MUTATION G2611U	RIBOSOME
3CCQ	STRUCTURE OF ANISOMYCIN RESISTANT 50S RIBOSOMAL SUBUNIT: 23S RRNA MUTATION A2488U	RIBOSOME
3CCR	STRUCTURE OF ANISOMYCIN RESISTANT 50S RIBOSOMAL SUBUNIT: 23S RRNA MUTATION A2488C. DENSITY FOR ANISOMYCIN IS VISIBLE BUT NOT INCLUDED IN THE MODEL.	RIBOSOME
3CCS	STRUCTURE OF ANISOMYCIN RESISTANT 50S RIBOSOMAL SUBUNIT: 23S RRNA MUTATION G2482A	RIBOSOME
3CCU	STRUCTURE OF ANISOMYCIN RESISTANT 50S RIBOSOMAL SUBUNIT: 23S RRNA MUTATION G2482C	RIBOSOME
3CCV	STRUCTURE OF ANISOMYCIN RESISTANT 50S RIBOSOMAL SUBUNIT:	RIBOSOME

	23S RRNA MUTATION G2616A	
3CD3	CRYSTAL STRUCTURE OF PHOSPHORYLATED HUMAN FELINE SARCOMA VIRAL ONCOGENE HOMOLOGUE (V-FES) IN COMPLEX WITH STAUROSPORINE AND A CONSENSUS PEPTIDE	TRANSFERASE
3CD6	CO-CYSTAL OF LARGE RIBOSOMAL SUBUNIT MUTANT G2616A WITH CC-PUROMYCIN	RIBOSOME
3CDG	HUMAN CD94/NKG2A IN COMPLEX WITH HLA-E	IMMUNE SYSTEM
3CDK	CRYSTAL STRUCTURE OF THE CO-EXPRESSED SUCCINYL-COA TRANSFERASE A AND B COMPLEX FROM BACILLUS SUBTILIS	TRANSFERASE
3CDW	CRYSTAL STRUCTURE OF COXSACKIEVIRUS B3 RNA-DEPENDENT RNA POLYMERASE (3DPOL) IN COMPLEX WITH PROTEIN PRIMER VPG AND A PYROPHOSPHATE	TRANSFERASE/VIRAL PROTEIN
3CDZ	CRYSTAL STRUCTURE OF HUMAN FACTOR VIII	BLOOD CLOTTING
3CEN	FACTOR XA IN COMPLEX WITH THE INHIBITOR N-(2-(((5-CHLORO-2-PYRIDINYL) AMINO)SULFONYL)PHENYL)-4-(2-OXO-1(2H)-PYRIDINYL)BENZAMIDE	HYDROLASE
3CEP	STRUCTURE OF A TRYPTOPHAN SYNTHASE QUINONOID INTERMEDIATE	LYASE
3CF4	STRUCTURE OF THE CODH COMPONENT OF THE M. BARKERI ACDS COMPLEX	OXIDOREDUCTASE
3CF5	THIOPEPTIDE ANTIBIOTIC THIOSTREPTON BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF DEINOCOCCUS RADIODURANS	RIBOSOME
3CF6	STRUCTURE OF EPAC2 IN COMPLEX WITH CYCLIC-AMP AND RAP	SIGNALING PROTEIN/GTP-BINDING PROTEIN
3CFB	HIGH-RESOLUTION STRUCTURE OF BLUE FLUORESCENT ANTIBODY EP2-19G2 IN COMPLEX WITH STILBENE HAPTEN AT 100K	IMMUNE SYSTEM
3CFC	HIGH-RESOLUTION STRUCTURE OF BLUE FLUORESCENT ANTIBODY EP2-19G2	IMMUNE SYSTEM
3CFD	PURPLE-FLUORESCENT ANTIBODY EP2-25C10 IN COMPLEX WITH ITS STILBENE HAPTEN	IMMUNE SYSTEM
3CFE	CRYSTAL STRUCTURE OF PURPLE-FLUORESCENT ANTIBODY EP2-25C10	IMMUNE SYSTEM
3CFJ	CRYSTAL STRUCTURE OF CATALYTIC ELIMINATION ANTIBODY 34E4, ORTHORHOMBIC CRYSTAL FORM	IMMUNE SYSTEM
3CFK	CRYSTAL STRUCTURE OF CATALYTIC ELIMINATION ANTIBODY 34E4, TRICLINIC CRYSTAL FORM	IMMUNE SYSTEM
3CFS	STRUCTURAL BASIS OF THE INTERACTION OF RBAP46/RBAP48 WITH HISTONE H4	HISTONE/CHAPERONE
3CFV	STRUCTURAL BASIS OF THE INTERACTION OF RBAP46/RBAP48 WITH	HISTONE/CHAPERONE

	HISTONE H4	
3CH5	THE CRYSTAL STRUCTURE OF THE RANGDP-NUP153ZNF2 COMPLEX	TRANSPORT PROTEIN
3CHW	COMPLEX OF DICTYOSTELIUM DISCOIDEUM ACTIN WITH PROFILIN AND THE LAST POLY-PRO OF HUMAN VASP	STRUCTURAL PROTEIN
3CHX	CRYSTAL STRUCTURE OF METHYLOSINUS TRICHOSPORIUM OB3B PARTICULATE METHANE MONOOXYGENASE (PMMO)	MEMBRANE PROTEIN
3CI0	THE CRYSTAL STRUCTURE OF THE GSPK-GSPI-GSPJ COMPLEX FROM ENTEROTOXIGENIC ESCHERICHIA COLI TYPE 2 SECRETION SYSTEM	PROTEIN TRANSPORT
3CI5	COMPLEX OF PHOSPHORYLATED DICTYOSTELIUM DISCOIDEUM ACTIN WITH GELSOLIN	STRUCTURAL PROTEIN
3CII	STRUCTURE OF NKG2A/CD94 BOUND TO HLA-E	IMMUNE SYSTEM
3CIP	COMPLEX OF DICTYOSTELIUM DISCOIDEUM ACTIN WITH GELSOLIN	STRUCTURAL PROTEIN
3CIR	E. COLI QUINOL FUMARATE REDUCTASE FRDA T234A MUTATION	OXIDOREDUCTASE
3CIU	SITE-SELECTIVE GLYCOSYLATION OF CYSTEINE-93 BETA ON THE SURFACE OF BOVINE HEMOGLOBIN AND ITS APPLICATION AS A NOVEL OXYGEN THERAPEUTIC	OXYGEN BINDING
3CJB	ACTIN DIMER CROSS-LINKED BY V. CHOLERAE MARTX TOXIN AND COMPLEXED WITH GELSOLIN-SEGMENT 1	STRUCTURAL PROTEIN
3CJC	ACTIN DIMER CROSS-LINKED BY V. CHOLERAE MARTX TOXIN AND COMPLEXED WITH DNASE I AND GELSOLIN-SEGMENT 1	STRUCTURAL PROTEIN/HYDROLASE
3CJH	TIM8-TIM13 COMPLEX	PROTEIN TRANSPORT
3CJI	STRUCTURE OF SENECA VALLEY VIRUS-001	VIRUS
3CJQ	RIBOSOMAL PROTEIN L11 METHYLTRANSFERASE (PRMA) IN COMPLEX WITH DIMETHYLATED RIBOSOMAL PROTEIN L11 IN SPACE GROUP P212121	TRANSFERASE/RIBOSOMAL PROTEIN
3CJR	RIBOSOMAL PROTEIN L11 METHYLTRANSFERASE (PRMA) IN COMPLEX WITH RIBOSOMAL PROTEIN L11 (K39A) AND INHIBITOR SINEFUNGIN.	TRANSFERASE/RIBOSOMAL PROTEIN
3CJS	MINIMAL RECOGNITION COMPLEX BETWEEN PRMA AND RIBOSOMAL PROTEIN L11	TRANSFERASE/RIBOSOMAL PROTEIN
3CJT	RIBOSOMAL PROTEIN L11 METHYLTRANSFERASE (PRMA) IN COMPLEX WITH DIMETHYLATED RIBOSOMAL PROTEIN L11	TRANSFERASE/RIBOSOMAL PROTEIN
3CK0	ANTI-ANTI-IDIOTYPIC ANTIBODY AGAINST HUMAN ANGIOTENSIN II, COMPLEX WITH HUMAN ANGIOTENSIN II	IMMUNE SYSTEM
3CK4	A HETEROSPECIFIC LEUCINE ZIPPER TETRAMER	PROTEIN BINDING
3CKI	CRYSTAL STRUCTURE OF THE TACE-N-TIMP-3 COMPLEX	HYDROLASE, HYDROLASE INHIBITOR

3CL3	CRYSTAL STRUCTURE OF A VFLIP-IKKGAMMA COMPLEX: INSIGHTS INTO VIRAL ACTIVATION OF THE IKK SIGNALOSOME	VIRAL PROTEIN/SIGNALING PROTEIN
3CLD	LIGAND BINDING DOMAIN OF THE GLUCOCORTICOID RECEPTOR COMPLEXED WITH FLUTICAZONE FUROATE	TRANSCRIPTION
3CLE	HIV NEUTRALIZING MONOCLONAL ANTIBODY YZ23	IMMUNE SYSTEM
3CLF	HIV NEUTRALIZING MONOCLONAL ANTIBODY YZ23	IMMUNE SYSTEM
3CLR	CRYSTAL STRUCTURE OF THE R236A ETF MUTANT FROM M. METHYLOTROPHUS	ELECTRON TRANSPORT
3CLS	CRYSTAL STRUCTURE OF THE R236C MUTANT OF ETF FROM METHYLOPHILUS METHYLOTROPHUS	ELECTRON TRANSPORT
3CLT	CRYSTAL STRUCTURE OF THE R236E MUTANT OF METHYLOPHILUS METHYLOTROPHUS ETF	ELECTRON TRANSPORT
3CLU	CRYSTAL STRUCTURE OF THE R236K MUTANT FROM METHYLOPHILUS METHYLOTROPHUS ETF	ELECTRON TRANSPORT
3CM8	A RNA POLYMERASE SUBUNIT STRUCTURE FROM VIRUS	RNA BINDING PROTEIN/TRANSFERASE
3CMA	THE STRUCTURE OF CCA AND CCA-PHE-CAP-BIO BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
3CME	THE STRUCTURE OF CA AND CCA-PHE-CAP-BIO BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
3CMM	CRYSTAL STRUCTURE OF THE UBA1-UBIQUITIN COMPLEX	LIGASE/PROTEIN BINDING
3CMO	HIV NEUTRALIZING MONOCLONAL ANTIBODY YZ18	IMMUNE SYSTEM
3CNQ	PROSUBTILISIN SUBSTRATE COMPLEX OF SUBTILISIN SUBT_BACAM	HYDROLASE
3CO0	SUBSTRATE COMPLEX OF FLUORIDE-SENSITIVE ENGINEERED SUBTILISIN SUBT_BACAM	HYDROLASE
3COJ	CRYSTAL STRUCTURE OF THE BRCT DOMAINS OF HUMAN BRCA1 IN COMPLEX WITH A PHOSPHORYLATED PEPTIDE FROM HUMAN ACETYL-COA CARBOXYLASE 1	ANTITUMOR PROTEIN/LIGASE
3CPA	X-RAY CRYSTALLOGRAPHIC INVESTIGATION OF SUBSTRATE BINDING TO CARBOXYPEPTIDASE A AT SUBZERO TEMPERATURE	HYDROLASE (C-TERMINAL PEPTIDASE)
3CPH	CRYSTAL STRUCTURE OF SEC4 IN COMPLEX WITH RAB-GDI	PROTEIN TRANSPORT
3CPJ	CRYSTAL STRUCTURE OF YPT31 IN COMPLEX WITH YEAST RAB-GDI	PROTEIN TRANSPORT
3CPL	CRYSTAL STRUCTURE OF H-2DB IN COMPLEX WITH A VARIANT M6A OF THE NP366 PEPTIDE FROM INFLUENZA A VIRUS	IMMUNE SYSTEM
3CPT	MP1-P14 SCAFFOLDING COMPLEX	PROTEIN BINDING

3CQC	NUCLEOPORIN NUP107/NUP133 INTERACTION COMPLEX	PROTEIN TRANSPORT
3CQG	NUCLEOPORIN NUP107/NUP133 INTERACTION COMPLEX, DELTA FINGER MUTANT	PROTEIN TRANSPORT
3CQU	CRYSTAL STRUCTURE OF AKT-1 COMPLEXED WITH SUBSTRATE PEPTIDE AND INHIBITOR	TRANSFERASE
3CQW	CRYSTAL STRUCTURE OF AKT-1 COMPLEXED WITH SUBSTRATE PEPTIDE AND INHIBITOR	TRANSFERASE
3CQX	CHAPERONE COMPLEX	CHAPERONE
3CQZ	CRYSTAL STRUCTURE OF 10 SUBUNIT RNA POLYMERASE II IN COMPLEX WITH THE INHIBITOR ALPHA-AMANITIN	TRANSCRIPTION
3CR3	STRUCTURE OF A TRANSIENT COMPLEX BETWEEN DHA-KINASE SUBUNITS DHAM AND DHAL FROM LACTOCOCCUS LACTIS	TRANSFERASE
3CRK	CRYSTAL STRUCTURE OF THE PDHK2-L2 COMPLEX.	TRANSFERASE
3CRL	CRYSTAL STRUCTURE OF THE PDHK2-L2 COMPLEX.	TRANSFERASE
3CRP	A HETEROSPECIFIC LEUCINE ZIPPER TETRAMER	PROTEIN BINDING
3CS7	FACTOR XA IN COMPLEX WITH THE INHIBITOR 1-(4-METHOXYPHENYL)-6-(4-(1-(PYRROLIDIN-1-YLMETHYL)CYCLOPROPYL)PHENYL)-3-(TRIFLUOROMETHYL)-5,6-DIHYDRO-1H-PYRAZOLO[3,4-C]PYRIDIN-7(4H)-ONE	HYDROLASE
3CS8	STRUCTURAL AND BIOCHEMICAL BASIS FOR THE BINDING SELECTIVITY OF PPARG TO PGC-1A	NUCLEAR PROTEIN
3CSY	CRYSTAL STRUCTURE OF THE TRIMERIC PREFUSION EBOLA VIRUS GLYCOPROTEIN IN COMPLEX WITH A NEUTRALIZING ANTIBODY FROM A HUMAN SURVIVOR	IMMUNE SYSTEM/VIRAL PROTEIN
3CUE	CRYSTAL STRUCTURE OF A TRAPP SUBASSEMBLY ACTIVATING THE RAB YPT1P	PROTEIN TRANSPORT
3CUQ	INTEGRATED STRUCTURAL AND FUNCTIONAL MODEL OF THE HUMAN ESCRT-II COMPLEX	PROTEIN TRANSPORT
3CUR	STRUCTURE OF A DOUBLE METHIONINE MUTANT OF NI-FE HYDROGENASE	OXIDOREDUCTASE
3CUS	STRUCTURE OF A DOUBLE ILE/PHE MUTANT OF NI-FE HYDROGENASE REFINED AT 2.2 ANGSTROM RESOLUTION	OXIDOREDUCTASE
3CV0	STRUCTURE OF PEROXISOMAL TARGETING SIGNAL 1 (PTS1) BINDING DOMAIN OF TRYPANOSOMA BRUCEI PEROXIN 5 (TBPEX5)COMPLEXED TO T. BRUCEI PHOSPHOGLUCOISOMERASE (PGI) PTS1 PEPTIDE	TRANSPORT PROTEIN
3CVH	HOW TCR-LIKE ANTIBODY RECOGNIZES MHC-BOUND PEPTIDE	IMMUNE SYSTEM
		IMMUNE SYSTEM

3CVI	HOW TCR-LIKE ANTIBODY RECOGNIZES MHC-BOUND PEPTIDE	
3CVL	STRUCTURE OF PEROXISOMAL TARGETING SIGNAL 1 (PTS1) BINDING DOMAIN OF TRYPANOSOMA BRUCEI PEROXIN 5 (TBPEX5)COMPLEXED TO T. BRUCEI PHOSPHOFRUCTOKINASE (PFK) PTS1 PEPTIDE	TRANSPORT PROTEIN
3CVN	STRUCTURE OF PEROXISOMAL TARGETING SIGNAL 1 (PTS1) BINDING DOMAIN OF TRYPANOSOMA BRUCEI PEROXIN 5 (TBPEX5)COMPLEXED TO T. BRUCEI GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (GAPDH) PTS1 PEPTIDE	TRANSPORT PROTEIN
3CVP	STRUCTURE OF PEROXISOMAL TARGETING SIGNAL 1 (PTS1) BINDING DOMAIN OF TRYPANOSOMA BRUCEI PEROXIN 5 (TBPEX5)COMPLEXED TO PTS1 PEPTIDE (10-SKL)	TRANSPORT PROTEIN
3CVQ	STRUCTURE OF PEROXISOMAL TARGETING SIGNAL 1 (PTS1) BINDING DOMAIN OF TRYPANOSOMA BRUCEI PEROXIN 5 (TBPEX5)COMPLEXED TO PTS1 PEPTIDE (7-SKL)	TRANSPORT PROTEIN
3CWB	CHICKEN CYTOCHROME BC1 COMPLEX INHIBITED BY AN IODINATED ANALOGUE OF THE POLYKETIDE CROCACIN-D	OXIDOREDUCTASE
3CWD	MOLECULAR RECOGNITION OF NITRO-FATTY ACIDS BY PPAR GAMMA	TRANSCRIPTION
3CWW	CRYSTAL STRUCTURE OF IDE-BRADYKININ COMPLEX	HYDROLASE
3CWZ	STRUCURE OF RAB6(GTP)-R6IP1 COMPLEX	TRANSPORT PROTEIN
3CX5	STRUCTURE OF COMPLEX III WITH BOUND CYTOCHROME C IN REDUCED STATE AND DEFINITION OF A MINIMAL CORE INTERFACE FOR ELECTRON TRANSFER.	OXIDOREDUCTASE
3CX6	CRYSTAL STRUCTURE OF PDZRHOGEF RGRGS DOMAIN IN A COMPLEX WITH GALPHA-13 BOUND TO GDP	SIGNALING PROTEIN
3CX7	CRYSTAL STRUCTURE OF PDZRHOGEF RGRGS DOMAIN IN A COMPLEX WITH GALPHA-13 BOUND TO GDP-ALF4	SIGNALING PROTEIN
3CX8	CRYSTAL STRUCTURE OF PDZRHOGEF RGRGS DOMAIN IN A COMPLEX WITH GALPHA-13 BOUND TO GTP-GAMMA-S	SIGNALING PROTEIN
3CXB	CRYSTAL STRUCTURE OF SIFA AND SKIP	SIGNALING PROTEIN
3CXD	CRYSTAL STRUCTURE OF ANTI-OSTEOPONTIN ANTIBODY 23C3 IN COMPLEX WITH ITS EPITOPE PEPTIDE	IMMUNE SYSTEM
3CXE	STRUCTURE OF THE GM-CSF RECEPTOR COMPLEX	CYTOKINE
3CXH	STRUCTURE OF YEAST COMPLEX III WITH ISOFORM-2 CYTOCHROME C BOUND AND DEFINITION OF A MINIMAL CORE INTERFACE FOR ELECTRON TRANSFER.	OXIDOREDUCTASE
3CXW	RYSTAL STRUCTURE OF HUMAN PROTO-ONCOGENE SERINE THREONINE KINASE (PIM1) IN COMPLEX WITH A CONSENSUS PEPTIDE AND A BETA CARBOLINE LIGAND I	TRANSFERASE

		TRANSFERASE
3CY2	RYSTAL STRUCTURE OF HUMAN PROTO-ONCOGENE SERINE THREONINE KINASE (PIM1) IN COMPLEX WITH A CONSENSUS PEPTIDE AND A BETA CARBOLINE LIGAND II	
		TRANSFERASE
3CY3	RYSTAL STRUCTURE OF HUMAN PROTO-ONCOGENE SERINE THREONINE KINASE (PIM1) IN COMPLEX WITH A CONSENSUS PEPTIDE AND THE JNK INHIBITOR V	
		PEPTIDE BINDING PROTEIN
3CYY	THE CRYSTAL STRUCTURE OF ZO-1 PDZ2 IN COMPLEX WITH THE CX43 PEPTIDE	
		TRANSFERASE/SIGNALING PROTEIN
3CZU	CRYSTAL STRUCTURE OF THE HUMAN EPHRIN A2- EPHRIN A1 COMPLEX	
		HYDROLASE
3D0G	CRYSTAL STRUCTURE OF SPIKE PROTEIN RECEPTOR-BINDING DOMAIN FROM THE 2002-2003 SARS CORONAVIRUS HUMAN STRAIN COMPLEXED WITH HUMAN-CIVET CHIMERIC RECEPTOR ACE2	
		HYDROLASE
3D0H	CRYSTAL STRUCTURE OF SPIKE PROTEIN RECEPTOR-BINDING DOMAIN FROM THE 2002-2003 SARS CORONAVIRUS CIVET STRAIN COMPLEXED WITH HUMAN-CIVET CHIMERIC RECEPTOR ACE2	
		HYDROLASE
3D0I	CRYSTAL STRUCTURE OF SPIKE PROTEIN RECEPTOR-BINDING DOMAIN FROM THE 2005-2006 SARS CORONAVIRUS CIVET STRAIN COMPLEXED WITH HUMAN-CIVET CHIMERIC RECEPTOR ACE2	
		IMMUNE SYSTEM
3D0L	CRYSTAL STRUCTURE OF THE HIV-1 BROADLY NEUTRALIZING ANTIBODY 2F5 IN COMPLEX WITH THE GP41 FP-MPER HYB3K CONSTRUCT 514GIGALFLGFLGAAGS528KK-AHX-655KNEQELLELDKWASLWN671	
		IMMUNE SYSTEM
3D0V	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE LLELDKWASLW	
		OXYGEN BINDING
3D17	A TRIPLY LIGATED CRYSTAL STRUCTURE OF RELAXED STATE HUMAN HEMOGLOBIN	
		TRANSFERASE, TRANSCRIPTION
3D1E	CRYSTAL STRUCTURE OF E. COLI SLIDING CLAMP (BETA) BOUND TO A POLYMERASE II PEPTIDE	
		TRANSFERASE, TRANSCRIPTION
3D1F	CRYSTAL STRUCTURE OF E. COLI SLIDING CLAMP (BETA) BOUND TO A POLYMERASE III PEPTIDE	
		OXYGEN BINDING
3D1K	R/T INTERMEDIATE QUATERNARY STRUCTURE OF AN ANTARCTIC FISH HEMOGLOBIN IN AN ALPHA(CO)-BETA(PENTACOORDINATE) STATE	
		SIGNALING PROTEIN / CELL ADHESION
3D1M	CRYSTAL STRUCTURE OF SONIC HEDGEHOG BOUND TO THE THIRD FNIII DOMAIN OF CDO	
		TRANSCRIPTION
3D24	CRYSTAL STRUCTURE OF LIGAND-BINDING DOMAIN OF ESTROGEN-RELATED RECEPTOR ALPHA (ERRALPHA) IN COMPLEX WITH THE PEROXISOME PROLIFERATORS-ACTIVATED RECEPTOR COACTIVATOR-1ALPHA BOX3 PEPTIDE (PGC-1ALPHA)	
		HYDROLASE

3D29	PROTEASOME INHIBITION BY FELLUTAMIDE B	
3D2E	CRYSTAL STRUCTURE OF A COMPLEX OF SSE1P AND HSP70, SELENOMETHIONINE-LABELED CRYSTALS	CHAPERONE
3D2F	CRYSTAL STRUCTURE OF A COMPLEX OF SSE1P AND HSP70	CHAPERONE
3D2U	STRUCTURE OF UL18, A PEPTIDE-BINDING VIRAL MHC MIMIC, BOUND TO A HOST INHIBITORY RECEPTOR	IMMUNE SYSTEM
3D31	MODBC FROM METHANOSARCINA ACETIVORANS	TRANSPORT PROTEIN
3D32	COMPLEX OF GABA(A) RECEPTOR-ASSOCIATED PROTEIN (GABARAP) WITH A SYNTHETIC PEPTIDE	TRANSPORT PROTEIN
3D38	CRYSTAL STRUCTURE OF NEW TRIGONAL FORM OF PHOTOSYNTHETIC REACTION CENTER FROM BLASTOCHLORIS VIRIDIS. CRYSTALS GROWN IN MICROFLUIDICS BY DETERGENT CAPTURE	PHOTOSYNTHESIS
3D3T	CRYSTAL STRUCTURE OF HIV-1 CRF01_AE IN COMPLEX WITH THE SUBSTRATE P1-P6	HYDROLASE
3D3X	CRYSTAL STRUCTURE OF BOTULINUM NEUROTOXIN SEROTYPE E CATALYTIC DOMAIN IN COMPLEX WITH SNAP-25 SUBSTRATE PEPTIDE	HYDROLASE
3D48	CRYSTAL STRUCTURE OF A PROLACTIN RECEPTOR ANTAGONIST BOUND TO THE EXTRACELLULAR DOMAIN OF THE PROLACTIN RECEPTOR	HORMONE/HORMONE RECEPTOR
3D4B	CRYSTAL STRUCTURE OF SIR2TM IN COMPLEX WITH ACETYL P53 PEPTIDE AND DADME-NAD+	HYDROLASE
3D4U	BOVINE THROMBIN-ACTIVATABLE FIBRINOLYSIS INHIBITOR (TAFIA) IN COMPLEX WITH TICK-DERIVED CARBOXYPEPTIDASE INHIBITOR.	HYDROLASE/HYDROLASE INHIBITOR
3D54	STUCTURE OF PURLQS FROM THERMOTOGA MARITIMA	LIGASE
3D5A	STRUCTURAL BASIS FOR TRANSLATION TERMINATION ON THE 70S RIBOSOME. THIS FILE CONTAINS THE 30S SUBUNIT, RELEASE FACTOR 1 (RF1), TWO TRNA, AND MRNA MOLECULES OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AS DESCRIBED IN REMARK 400.	RIBOSOME
3D5B	STRUCTURAL BASIS FOR TRANSLATION TERMINATION ON THE 70S RIBOSOME. THIS FILE CONTAINS THE 50S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AS DESCRIBED IN REMARK 400.	RIBOSOME
3D5C	STRUCTURAL BASIS FOR TRANSLATION TERMINATION ON THE 70S RIBOSOME. THIS FILE CONTAINS THE 30S SUBUNIT, RELEASE FACTOR 1 (RF1), TWO TRNA, AND MRNA MOLECULES OF THE SECOND 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AS DESCRIBED IN REMARK 400.	RIBOSOME
3D5D	STRUCTURAL BASIS FOR TRANSLATION TERMINATION ON THE 70S RIBOSOME. THIS FILE CONTAINS THE 50S SUBUNIT OF THE SECOND	RIBOSOME

	70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AS DESCRIBED IN REMARK 400.	
		IMMUNE SYSTEM
3D5O	STRUCTURAL RECOGNITION AND FUNCTIONAL ACTIVATION OF FCRR BY INNATE PENTRAXINS	
		CELL ADHESION/TOXIN
3D5R	CRYSTAL STRUCTURE OF EFB-C (N138A) / C3D COMPLEX	
		CELL ADHESION/TOXIN
3D5S	CRYSTAL STRUCTURE OF EFB-C (R131A) / C3D COMPLEX	
		TRANSFERASE
3D7S	CRYSTAL STRUCTURE OF WILD-TYPE E. COLI ASPARATE TRANSCARBAMOYLASE AT PH 8.5 AT 2.80 A RESOLUTION	
		TRANSFERASE
3D7T	STRUCTURAL BASIS FOR THE RECOGNITION OF C-SRC BY ITS INACTIVATOR CSK	
		APOPTOSIS
3D7V	CRYSTAL STRUCTURE OF MCL-1 IN COMPLEX WITH AN MCL-1 SELECTIVE BH3 LIGAND	
		HYDROLASE
3D7W	MISTLETOE LECTIN I IN COMPLEX WITH ZEATIN	
		HYDROLASE
3D81	SIR2-S-ALKYLAMIDATE COMPLEX CRYSTAL STRUCTURE	
		IMMUNE SYSTEM/CYTOKINE
3D85	CRYSTAL STRUCTURE OF IL-23 IN COMPLEX WITH NEUTRALIZING FAB	
		CYTOKINE
3D87	CRYSTAL STRUCTURE OF INTERLEUKIN-23	
		DNA BINDING PROTEIN
3D8A	CO-CRYSTAL STRUCTURE OF TRAM-TRAD COMPLEX.	
		TRANSCRIPTION REGULATOR, OXIDOREDUCTASE
3D8C	FACTOR INHIBITING HIF-1 ALPHA D201G MUTANT IN COMPLEX WITH ZN(II), ALPHA-KETOGLUTARATE AND HIF-1 ALPHA 19MER	
		HYDROLASE/IMMUNE SYSTEM
3D9A	HIGH RESOLUTION CRYSTAL STRUCTURE STRUCTURE OF HYHEL10 FAB COMPLEXED TO HEN EGG LYSOZYME	
		TRANSCRIPTION
3D9K	SNAPSHOTS OF THE RNA PROCESSING FACTOR SCAF8 BOUND TO DIFFERENT PHOSPHORYLATED FORMS OF THE CARBOXY-TERMINAL DOMAIN OF RNA-POLYMERASE II	
		TRANSCRIPTION
3D9L	SNAPSHOTS OF THE RNA PROCESSING FACTOR SCAF8 BOUND TO DIFFERENT PHOSPHORYLATED FORMS OF THE CARBOXY-TERMINAL DOMAIN OF RNA-POLYMERASE II	
		TRANSCRIPTION
3D9M	SNAPSHOTS OF THE RNA PROCESSING FACTOR SCAF8 BOUND TO DIFFERENT PHOSPHORYLATED FORMS OF THE CARBOXY-TERMINAL DOMAIN OF RNA-POLYMERASE II	
		TRANSCRIPTION
3D9N	SNAPSHOTS OF THE RNA PROCESSING FACTOR SCAF8 BOUND TO DIFFERENT PHOSPHORYLATED FORMS OF THE CARBOXY-TERMINAL DOMAIN OF RNA-POLYMERASE II	
		TRANSCRIPTION
3D9O	SNAPSHOTS OF THE RNA PROCESSING FACTOR SCAF8 BOUND TO DIFFERENT PHOSPHORYLATED FORMS OF THE CARBOXY-TERMINAL DOMAIN OF RNA-POLYMERASE II	
		TRANSCRIPTION

3D9P	SNAPSHOTS OF THE RNA PROCESSING FACTOR SCAF8 BOUND TO DIFFERENT PHOSPHORYLATED FORMS OF THE CARBOXY-TERMINAL DOMAIN OF RNA-POLYMERASE II	
3D9T	CIAP1-BIR3 IN COMPLEX WITH N-TERMINAL PEPTIDE FROM CASPASE-9 (ATPFQE)	APOPTOSIS
3D9U	THE BIR3 DOMAIN OF CIAP1 IN COMPLEX WITH THE N TERMINAL PEPTIDE FROM SMAC/DIABLO (AVPIAQ).	APOPTOSIS
3DAB	STRUCTURE OF THE HUMAN MDMX PROTEIN BOUND TO THE P53 TUMOR SUPPRESSOR TRANSACTIVATION DOMAIN	CELL CYCLE
3DAC	STRUCTURE OF THE HUMAN MDMX PROTEIN BOUND TO THE P53 TUMOR SUPPRESSOR TRANSACTIVATION DOMAIN	CELL CYCLE
3DAW	STRUCTURE OF THE ACTIN-DEPOLYMERIZING FACTOR HOMOLOGY DOMAIN IN COMPLEX WITH ACTIN	STRUCTURAL PROTEIN/STRUCTURAL PROTEIN RE
3DBH	STRUCTURAL DISSECTION OF A GATING MECHANISM PREVENTING MISACTIVATION OF UBIQUITIN BY NEDD8'S E1 (APPBP1-UBA3ARG190ALA-NEDD8ALA72ARG)	CELL CYCLE
3DBJ	ALLOPHYCOCYANIN FROM THERMOSYNECHOCOCCUS VULCANUS	PHOTOSYNTHESIS
3DBL	STRUCTURAL DISSECTION OF A GATING MECHANISM PREVENTING MISACTIVATION OF UBIQUITIN BY NEDD8'S E1 (APPBP1-UBA3ARG190WT-NEDD8ALA72GLN)	CELL CYCLE
3DBO	CRYSTAL STRUCTURE OF A MEMBER OF THE VAPBC FAMILY OF TOXIN-ANTITOXIN SYSTEMS, VAPBC-5, FROM MYCOBACTERIUM TUBERCULOSIS	TOXIN/ANTITOXIN
3DBR	STRUCTURAL DISSECTION OF A GATING MECHANISM PREVENTING MISACTIVATION OF UBIQUITIN BY NEDD8'S E1 (APPBP1-UBA3ARG190GLN-NEDD8ALA72ARG)	CELL CYCLE
3DCG	CRYSTAL STRUCTURE OF THE HIV VIF BC-BOX IN COMPLEX WITH HUMAN ELONGINB AND ELONGINC	LIGASE/VIRAL PROTEIN
3DCK	X-RAY STRUCTURE OF D25N CHEMICAL ANALOGUE OF HIV-1 PROTEASE COMPLEXED WITH KETOMETHYLENE ISOSTERE INHIBITOR	HYDROLASE
3DCR	X-RAY STRUCTURE OF HIV-1 PROTEASE AND HYDRATED FORM OF KETOMETHYLENE ISOSTERE INHIBITOR	HYDROLASE
3DCT	FXR WITH SRC1 AND GW4064	TRANSCRIPTION/TRANSCRIPTION ACTIVATOR
3DCU	FXR WITH SRC1 AND GSK8062	TRANSCRIPTION/TRANSCRIPTION ACTIVATOR
3DD2	RYSTAL STRUCTURE OF AN RNA APTAMER BOUND TO HUMAN THROMBIN	HYDROLASE/RNA
3DD7	STRUCTURE OF DOCH66Y IN COMPLEX WITH THE C-TERMINAL DOMAIN OF PHD	RIBOSOME INHIBITOR
3DDA	CRYSTAL STRUCTURE OF THE CATALYTIC DOMAIN OF BOTULINUM	HYDROLASE

	NEUROTOXIN SEROTYPE A WITH A SNAP-25 PEPTIDE	
3DDB	CRYSTAL STRUCTURE OF THE CATALYTIC DOMAIN OF BOTULINUM NEUROTOXIN SEROTYPE A WITH A SUBSTRATE ANALOG PEPTIDE	HYDROLASE
3DDC	CRYSTAL STRUCTURE OF NORE1A IN COMPLEX WITH RAS	HYDROLASE/APOPTOSIS
3DDP	STRUCTURE OF PHOSPHORYLATED THR160 CDK2/CYCLIN A IN COMPLEX WITH THE INHIBITOR CR8	TRANSFERASE/CELL CYCLE
3DDQ	STRUCTURE OF PHOSPHORYLATED THR160 CDK2/CYCLIN A IN COMPLEX WITH THE INHIBITOR ROSCOVITINE	TRANSFERASE/CELL CYCLE
3DF0	CALCIUM-DEPENDENT COMPLEX BETWEEN M-CALPAIN AND CALPASTATIN	HYDROLASE
3DEG	COMPLEX OF ELONGATING ESCHERICHIA COLI 70S RIBOSOME AND EF4(LEPA)-GMPPNP	RIBOSOME
3DEP	STRUCTURAL BASIS FOR SPECIFIC SUBSTRATE RECOGNITION BY THE CHLOROPLAST SIGNAL RECOGNITION PARTICLE PROTEIN CPSRP43	PROTEIN TRANSPORT, MEMBRANE PROTEIN
3DET	STRUCTURE OF THE E418A, Y445A DOUBLY UNGATED MUTANT OF E.COLI CLC_EC1, CL-/H+ ANTIPORTER	MEMBRANE PROTEIN
3DGC	STRUCTURE OF IL-22/IL-22R1	CYTOKINE/SIGNALING PROTEIN
3DGG	CRYSTAL STRUCTURE OF FABOX108	IMMUNE SYSTEM
3DGP	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN TFB5 AND THE C-TERMINAL DOMAIN OF TFB2	TRANSCRIPTION
3DHW	CRYSTAL STRUCTURE OF METHIONINE IMPORTER METNI	MEMBRANE PROTEIN/HYDROLASE
3DI6	HIV-1 RT WITH PYRIDAZINONE NON-NUCLEOSIDE INHIBITOR	TRANSFERASE
3DIF	CRYSTAL STRUCTURE OF FABOX117	IMMUNE SYSTEM
3DIN	CRYSTAL STRUCTURE OF THE PROTEIN-TRANSLOCATION COMPLEX FORMED BY THE SECY CHANNEL AND THE SECA ATPASE	MEMBRANE PROTEIN, PROTEIN TRANSPORT
3DIW	C-TERMINAL BETA-CATENIN BOUND TIP-1 STRUCTURE	SIGNALING PROTEIN/CELL ADHESION
3DKT	CRYSTAL STRUCTURE OF THERMOTOGA MARITIMA ENCAPSULIN	STRUCTURAL PROTEIN/VIRUS LIKE PARTICLE
3DL8	STRUCTURE OF THE COMPLEX OF AQUIFEX AEOLICUS SECYEG AND BASCILLUS SUBTILIS SECA	PROTEIN TRANSPORT
3DLE	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH GF128590.	TRANSFERASE
3DLG	CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH GW564511.	TRANSFERASE
3DLK	CRYSTAL STRUCTURE OF AN ENGINEERED FORM OF THE HIV-1 REVERSE TRANSCRIPTASE, RT69A	TRANSFERASE

3DLL	THE OXAZOLIDINONE ANTIBIOTICS PERTURB THE RIBOSOMAL PEPTIDYL-TRANSFERASE CENTER AND EFFECT TRNA POSITIONING	RIBOSOME
3DLQ	CRYSTAL STRUCTURE OF THE IL-22/IL-22R1 COMPLEX	CYTOKINE/CYTOKINE RECEPTOR
3DM1	YSTAL STRUCTURE OF THE COMPLEX OF HUMAN CHROMOBOX HOMOLOG 3 (CBX3) WITH PEPTIDE	TRANSCRIPTION
3DM2	CRYSTAL STRUCTURE OF HIV-1 K103N MUTANT REVERSE TRANSCRIPTASE IN COMPLEX WITH GW564511.	TRANSFERASE
3DMJ	CRYSTAL STRUCTURE OF HIV-1 V106A AND Y181C MUTANT REVERSE TRANSCRIPTASE IN COMPLEX WITH GW564511.	TRANSFERASE
3DMT	STRUCTURE OF GLYCOSOMAL GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE FROM TRYPANOSOMA CRUZI IN COMPLEX WITH THE IRREVERSIBLE IODOACETATE INHIBITOR	OXIDOREDUCTASE
3DNJ	HE STRUCTURE OF THE CAULOBACTER CRESCENTUS CLPS PROTEASE ADAPTOR PROTEIN IN COMPLEX WITH A N-END RULE PEPTIDE	PEPTIDE BINDING PROTEIN
3DOG	STRUCTURE OF THR 160 PHOSPHORYLATED CDK2/CYCLIN A IN COMPLEX WITH THE INHIBITOR N-&-N1	TRANSFERASE, CELL CYCLE
3DOK	CRYSTAL STRUCTURE OF K103N MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH GW678248.	TRANSFERASE
3DOL	CRYSTAL STRUCTURE OF L100I MUTANT HIV-1 REVERSE TRANSCRIPTASE IN COMPLEX WITH GW695634.	TRANSFERASE
3DOM	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN TFB5 AND THE C-TERMINAL DOMAIN OF TFB2	TRANSCRIPTION
3DPL	STRUCTURAL INSIGHTS INTO NEDD8 ACTIVATION OF CULLIN-RING LIGASES: CONFORMATIONAL CONTROL OF CONJUGATION.	LIGASE
3DPY	PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH FPP AND CAGED TKCVIM SUBSTRATE	TRANSFERASE
3DQB	CRYSTAL STRUCTURE OF THE ACTIVE G-PROTEIN-COUPLED RECEPTOR OPSIN IN COMPLEX WITH A C-TERMINAL PEPTIDE DERIVED FROM THE GALPHA SUBUNIT OF TRANSDUCIN	SIGNALING PROTEIN
3DQV	STRUCTURAL INSIGHTS INTO NEDD8 ACTIVATION OF CULLIN-RING LIGASES: CONFORMATIONAL CONTROL OF CONJUGATION	LIGASE
3DRA	CANDIDA ALBICANS PROTEIN GERANYLGERANYLTRANSFERASE-I COMPLEXED WITH GGPP	TRANSFERASE
3DRP	HIV REVERSE TRANSCRIPTASE IN COMPLEX WITH INHIBITOR R8E	TRANSFERASE
3DRQ	CRYSTAL STRUCTURE OF THE HIV-1 BROADLY NEUTRALIZING ANTIBODY 2F5 IN COMPLEX WITH THE GP41 FP-MPER HYB3K CONSTRUCT 514GIGALFLGFLGAAGS528KK-AHX-	IMMUNE SYSTEM

	655KNEQELLELDKWASLWN671 SOAKED IN PEG/2-PROPANOL SOLUTION	
3DRR	HIV REVERSE TRANSCRIPTASE Y181C MUTANT IN COMPLEX WITH INHIBITOR R8E	TRANSFERASE
3DRS	HIV REVERSE TRANSCRIPTASE K103N MUTANT IN COMPLEX WITH INHIBITOR R8D	TRANSFERASE
3DS0	HIV-1 CAPSID C-TERMINAL DOMAIN MUTANT (N183A) IN COMPLEX WITH AN INHIBITOR OF PARTICLE ASSEMBLY (CAI)	VIRAL PROTEIN
3DS1	HIV-1 CAPSID C-TERMINAL DOMAIN MUTANT (E187A) IN COMPLEX WITH AN INHIBITOR OF PARTICLE ASSEMBLY (CAI)	VIRAL PROTEIN
3DS3	HIV-1 CAPSID C-TERMINAL DOMAIN MUTANT (Y169A) IN COMPLEX WITH AN INHIBITOR OF PARTICLE ASSEMBLY (CAI)	VIRAL PROTEIN
3DS4	HIV-1 CAPSID C-TERMINAL DOMAIN MUTANT (L211S) IN COMPLEX WITH AN INHIBITOR OF PARTICLE ASSEMBLY (CAI)	VIRAL PROTEIN
3DSF	CRYSTAL STRUCTURE OF ANTI-OSTEOPONTIN ANTIBODY 23C3 IN COMPLEX WITH W43A MUTATED EPITOPE PEPTIDE	IMMUNE SYSTEM
3DSS	CRYSTAL STRUCTURE OF RABGGTASE(DELTA LRR; DELTA IG)	TRANSFERASE
3DST	CRYSTAL STRUCTURE OF RABGGTASE(DELTA LRR; DELTA IG)IN COMPLEX WITH GERANYLGERANYL PYROPHOSPHATE	TRANSFERASE
3DSU	CRYSTAL STRUCTURE OF RABGGTASE(DELTA LRR; DELTA IG)IN COMPLEX WITH FARNESYL PYROPHOSPHATE	TRANSFERASE
3DSV	CRYSTAL STRUCTURE OF RABGGTASE(DELTA LRR; DELTA IG)IN COMPLEX WITH MONO-PRENYLATED PEPTIDE SER-CYS-SER-CYS(GG) DERIVATED FROM RAB7	TRANSFERASE
3DSW	CRYSTAL STRUCTURE OF RABGGTASE(DELTA LRR; DELTA IG)IN COMPLEX WITH MONO-PRENYLATED PEPTIDE SER-CYS(GG)-SER-CYS DERIVATED FROM RAB7	TRANSFERASE
3DSX	CRYSTAL STRUCTURE OF RABGGTASE(DELTA LRR; DELTA IG)IN COMPLEX WITH DI-PRENYLATED PEPTIDE SER-CYS(GG)-SER-CYS(GG) DERIVATED FROM RAB7	TRANSFERASE
3DTP	TARANTULA HEAVY MEROMYOSIN OBTAINED BY FLEXIBLE DOCKING TO TARANTULA MUSCLE THICK FILAMENT CRYO-EM 3D-MAP	CONTRACTILE PROTEIN
3DTU	CATALYTIC CORE SUBUNITS (I AND II) OF CYTOCHROME C OXIDASE FROM RHODOBACTER SPHAEROIDES COMPLEXED WITH DEOXYCHOLIC ACID	OXIDOREDUCTASE
3DU7	TUBULIN-COLCHICINE-PHOMOPSIN A: STATHMIN-LIKE DOMAIN COMPLEX	CELL CYCLE
3DUH	STRUCTURE OF INTERLEUKIN-23	IMMUNE SYSTEM/CYTOKINE
3DVE	CRYSTAL STRUCTURE OF CA2+/CAM-CAV2.2 IQ DOMAIN COMPLEX	MEMBRANE PROTEIN

3DVG	CRYSTAL STRUCTURE OF K63-SPECIFIC FAB APU.3A8 BOUND TO K63-LINKED DI-UBIQUITIN	IMMUNE SYSTEM
3DVJ	CRYSTAL STRUCTURE OF CA2+/CAM-CAV2.2 IQ DOMAIN (WITHOUT CLONING ARTIFACT, HM TO TV) COMPLEX	MEMBRANE PROTEIN
3DVK	CRYSTAL STRUCTURE OF CA2+/CAM-CAV2.3 IQ DOMAIN COMPLEX	MEMBRANE PROTEIN
3DVM	CRYSTAL STRUCTURE OF CA2+/CAM-CAV2.1 IQ DOMAIN COMPLEX	MEMBRANE PROTEIN
3DVN	CRYSTAL STRUCTURE OF K63-SPECIFIC FAB APU2.16 BOUND TO K63-LINKED DI-UBIQUITIN	IMMUNE SYSTEM
3DVU	CRYSTAL STRUCTURE OF THE COMPLEX OF MURINE GAMMA-HERPESVIRUS 68 BCL-2 HOMOLOG M11 AND THE BECLIN 1 BH3 DOMAIN	VIRAL PROTEIN/APOPTOSIS
3DW8	STRUCTURE OF A PROTEIN PHOSPHATASE 2A HOLOENZYME WITH B55 SUBUNIT	HYDROLASE
3DWG	CRYSTAL STRUCTURE OF A SULFUR CARRIER PROTEIN COMPLEX FOUND IN THE CYSTEINE BIOSYNTHETIC PATHWAY OF MYCOBACTERIUM TUBERCULOSIS	TRANSFERASE
3DWL	CRYSTAL STRUCTURE OF FISSION YEAST ARP2/3 COMPLEX LACKING THE ARP2 SUBUNIT	STRUCTURAL PROTEIN
3DXC	CRYSTAL STRUCTURE OF THE INTRACELLULAR DOMAIN OF HUMAN APP IN COMPLEX WITH FE65-PTB2	PROTEIN BINDING
3DXD	CRYSTAL STRUCTURE OF THE INTRACELLULAR DOMAIN OF HUMAN APP (T668E MUTANT) IN COMPLEX WITH FE65-PTB2	PROTEIN BINDING
3DXE	CRYSTAL STRUCTURE OF THE INTRACELLULAR DOMAIN OF HUMAN APP (T668A MUTANT) IN COMPLEX WITH FE65-PTB2	PROTEIN BINDING
3DXJ	CRYSTAL STRUCTURE OF THERMUS THERMOPHILUS RNA POLYMERASE HOLOENZYME IN COMPLEX WITH THE ANTIBIOTIC MYXOPYRONIN	TRANSCRIPTION,TRANSFERASE
3DXR	CRYSTAL STRUCTURE OF THE YEAST INTER-MEMBRANE SPACE CHAPERONE ASSEMBLY TIM9.10	PROTEIN TRANSPORT
3DY0	CRYSTAL STRUCTURE OF CLEAVED PCI BOUND TO HEPARIN	BLOOD CLOTTING, HYDROLASE INHIBITOR
3DY3	CRYSTAL STRUCTURE OF YEAST 20S PROTEASOME IN COMPLEX WITH THE EPIMER FORM OF SPIROLACTACYSTIN	HYDROLASE
3DY4	CRYSTAL STRUCTURE OF YEAST 20S PROTEASOME IN COMPLEX WITH SPIROLACTACYSTIN	HYDROLASE
3DYA	HIV-1 RT WITH NON-NUCLEOSIDE INHIBITOR ANNULATED PYRAZOLE 1	TRANSFERASE
3DZU	INTACT PPAR GAMMA - RXR ALPHA NUCLEAR RECEPTOR COMPLEX ON DNA BOUND WITH BVT.13, 9-CIS RETINOIC ACID AND NCOA2	TRANSCRIPTION/DNA

	PEPTIDE	
3DZY	INTACT PPAR GAMMA - RXR ALPHA NUCLEAR RECEPTOR COMPLEX ON DNA BOUND WITH ROSIGLITAZONE, 9-CIS RETINOIC ACID AND NCOA2 PEPTIDE	TRANSCRIPTION/DNA
3.00E+00	INTACT PPAR GAMMA - RXR ALPHA NUCLEAR RECEPTOR COMPLEX ON DNA BOUND WITH GW9662, 9-CIS RETINOIC ACID AND NCOA2 PEPTIDE	TRANSCRIPTION/DNA
3.00E+01	HIV-RT WITH NON-NUCLEOSIDE INHIBITOR ANNULATED PYRAZOLE 2	TRANSFERASE
3E0J	X-RAY STRUCTURE OF THE COMPLEX OF REGULATORY SUBUNITS OF HUMAN DNA POLYMERASE DELTA	TRANSFERASE
3E1K	CRYSTAL STRUCTURE OF KLUYVEROMYCES LACTIS GAL80P IN COMPLEX WITH THE ACIDIC ACTIVATION DOMAIN OF GAL4P	TRANSCRIPTION
3E1R	MIDBODY TARGETING OF THE ESCRT MACHINERY BY A NON-CANONICAL COILED-COIL IN CEP55	CELL CYCLE/TRANSPORT PROTEIN
3.00E+22	TUBULIN-COLCHICINE-SOBLIDOTIN: STATHMIN-LIKE DOMAIN COMPLEX	CELL CYCLE
3E2H	STRUCTURE OF THE M67 HIGH-AFFINITY MUTANT OF THE 2C TCR IN COMPLEX WITH LD/QL9	IMMUNE SYSTEM
3E3Q	STRUCTURE OF THE 3ALPHAM13 HIGH-AFFINITY MUTANT OF THE 2C TCR IN COMPLEX WITH LD/QL9	IMMUNE SYSTEM
3.00E+47	CRYSTAL STRUCTURE OF THE YEAST 20S PROTEASOME IN COMPLEX WITH HOMOBELACTOSIN C	HYDROLASE
3E5A	CRYSTAL STRUCTURE OF AURORA A IN COMPLEX WITH VX-680 AND TPX2	TRANSFERASE
3E6P	CRYSTAL STRUCTURE OF HUMAN MEIZOTHROMBIN DESF1	HYDROLASE
3E7C	GLUCOCORTICOID RECEPTOR LBD BOUND TO GSK866	TRANSCRIPTION
3E7S	STRUCTURE OF BOVINE INOS OXYGENASE DOMAIN WITH INHIBITOR AR-C95791	OXIDOREDUCTASE
3.00E+87	CRYSTAL STRUCTURES OF THE KINASE DOMAIN OF AKT2 IN COMPLEX WITH ATP-COMPETITIVE INHIBITORS	TRANSFERASE
3.00E+88	CRYSTAL STRUCTURES OF THE KINASE DOMAIN OF AKT2 IN COMPLEX WITH ATP-COMPETITIVE INHIBITORS	TRANSFERASE
3E8C	CRYSTAL STRUCTURES OF THE KINASE DOMAIN OF PKA IN COMPLEX WITH ATP-COMPETITIVE INHIBITORS	TRANSFERASE
3E8D	CRYSTAL STRUCTURES OF THE KINASE DOMAIN OF AKT2 IN COMPLEX WITH ATP-COMPETITIVE INHIBITORS	TRANSFERASE
3E8E	CRYSTAL STRUCTURES OF THE KINASE DOMAIN OF PKA IN COMPLEX	TRANSFERASE

	WITH ATP-COMPETITIVE INHIBITORS	
3.00E+95	CRYSTAL STRUCTURE OF THE PLASMODIUM FALCIPARUM UBIQUITIN CONJUGATING ENZYME COMPLEX, PFUBC13-PFUEV1A	LIGASE
3E9J	STRUCTURE OF THE CHARGE-TRANSFER INTERMEDIATE OF THE TRANSMEMBRANE REDOX CATALYST DSBB	OXIDOREDUCTASE
3EA5	KAP95P BINDING INDUCES THE SWITCH LOOPS OF RANGDP TO ADOPT THE GTP-BOUND CONFORMATION: IMPLICATIONS FOR NUCLEAR IMPORT COMPLEX ASSEMBLY DYNAMICS	TRANSPORT PROTEIN
3EAB	CRYSTAL STRUCTURE OF SPASTIN MIT IN COMPLEX WITH ESCRT III	CELL CYCLE
3EB6	STRUCTURE OF THE CIAP2 RING DOMAIN BOUND TO UBCH5B	APOPTOSIS, LIGASE
3EBA	CABHUL6 FGLW MUTANT (HUMANIZED) IN COMPLEX WITH HUMAN LYSOZYME	IMMUNE SYSTEM/HYDROLASE
3ECH	THE MARR-FAMILY REPRESSOR MEXR IN COMPLEX WITH ITS ANTIREPRESSOR ARMR	TRANSCRIPTION, TRANSCRIPTION REGULATION
3EDQ	CRYSTAL STRUCTURE OF CASPASE-3 WITH INHIBITOR AC-LDESD-CHO	HYDROLASE
3EDR	THE CRYSTAL STRUCTURE OF CASPASE-7 IN COMPLEX WITH ACETYL-LDESD-CHO	HYDROLASE
3EFO	CRYSTAL STRUCTURE OF THE MAMMALIAN COPII-COAT PROTEIN SEC23/24 BOUND TO THE TRANSPORT SIGNAL SEQUENCE OF SYNTAXIN 5	PROTEIN TRANSPORT
3EG5	CRYSTAL STRUCTURE OF MDIA1-TSH GBD-FH3 IN COMPLEX WITH CDC42-GMPPNP	SIGNALING PROTEIN
3EG9	CRYSTAL STRUCTURE OF THE MAMMALIAN COPII-COAT PROTEIN SEC23/24 BOUND TO THE TRANSPORT SIGNAL SEQUENCE OF MEMBRIN	PROTEIN TRANSPORT
3EGD	CRYSTAL STRUCTURE OF THE MAMMALIAN COPII-COAT PROTEIN SEC23A/24A COMPLEXED WITH THE SNARE PROTEIN SEC22 AND BOUND TO THE TRANSPORT SIGNAL SEQUENCE OF VESICULAR STOMATITIS VIRUS GLYCOPROTEIN	PROTEIN TRANSPORT
3EGK	KNOBLE INHIBITOR	BLOOD CLOTTING/HYDROLASE INHIBITOR
3EGV	RIBOSOMAL PROTEIN L11 METHYLTRANSFERASE (PRMA) IN COMPLEX WITH TRIMETHYLATED RIBOSOMAL PROTEIN L11	TRANSFERASE/RIBOSOMAL PROTEIN
3EGX	CRYSTAL STRUCTURE OF THE MAMMALIAN COPII-COAT PROTEIN SEC23A/24A COMPLEXED WITH THE SNARE PROTEIN SEC22B AND BOUND TO THE TRANSPORT SIGNAL SEQUENCE OF THE SNARE PROTEIN BET1	PROTEIN TRANSPORT
3EHT	CRYSTAL STRUCTURE OF THE EXTRACELLULAR DOMAIN OF HUMAN CORTICOTROPIN RELEASING FACTOR RECEPTOR TYPE 1 (CRFR1) IN COMPLEX WITH CRF	MEMBRANE PROTEIN

3EHU	CRYSTAL STRUCTURE OF THE EXTRACELLULAR DOMAIN OF HUMAN CORTICOTROPIN RELEASING FACTOR RECEPTOR TYPE 1 (CRFR1) IN COMPLEX WITH CRF	MEMBRANE PROTEIN
3EID	CDK2/CYCLINA COMPLEXED WITH A PYRAZOLOPYRIDAZINE INHIBITOR	TRANSFERASE/CELL CYCLE
3EJ1	CDK2/CYCLINA COMPLEXED WITH A PYRAZOLOPYRIDAZINE INHIBITOR	TRANSFERASE/CELL CYCLE
3EJ3	STRUCTURAL AND MECHANISTIC ANALYSIS OF TRANS-3-CHLOROACRYLIC ACID DEHALOGENASE ACTIVITY	HYDROLASE
3EJ7	STRUCTURAL AND MECHANISTIC ANALYSIS OF TRANS-3-CHLOROACRYLIC ACID DEHALOGENASE ACTIVITY	HYDROLASE
3EJ9	STRUCTURAL AND MECHANISTIC ANALYSIS OF TRANS-3-CHLOROACRYLIC ACID DEHALOGENASE ACTIVITY	HYDROLASE
3EJB	CRYSTAL STRUCTURE OF P450BIOI IN COMPLEX WITH TETRADECANOIC ACID LIGATED ACYL CARRIER PROTEIN	OXIDOREDUCTASE/LIPID TRANSPORT
3EJD	CRYSTAL STRUCTURE OF P450BIOI IN COMPLEX WITH HEXADEC-9Z-ENOIC ACID LIGATED ACYL CARRIER PROTEIN	OXIDOREDUCTASE/LIPID TRANSPORT
3EJE	CRYSTAL STRUCTURE OF P450BIOI IN COMPLEX WITH OCTADEC-9Z-ENOIC ACID LIGATED ACYL CARRIER PROTEIN	OXIDOREDUCTASE/LIPID TRANSPORT
3EJJ	STRUCTURE OF M-CSF BOUND TO THE FIRST THREE DOMAINS OF FMS	CYTOKINE/SIGNALING PROTEIN
3ELA	CRYSTAL STRUCTURE OF ACTIVE SITE INHIBITED COAGULATION FACTOR VIIA MUTANT IN COMPLEX WITH SOLUBLE TISSUE FACTOR	BLOOD CLOTTING
3ENH	CRYSTAL STRUCTURE OF CGI121/BUD32/KAE1 COMPLEX	HYDROLASE/UNKNOWN FUNCTION
3ENO	CRYSTAL STRUCTURE OF PYROCOCCUS FURIOSUS PCC1 IN COMPLEX WITH THERMOPLASMA ACIDOPHILUM KAE1	HYDROLASE/UNKNOWN FUNCTION
3EO0	STRUCTURE OF THE TRANSFORMING GROWTH FACTOR-BETA NEUTRALIZING ANTIBODY GC-1008	IMMUNE SYSTEM
3EO1	STRUCTURE OF THE FAB FRAGMENT OF GC-1008 IN COMPLEX WITH TRANSFORMING GROWTH FACTOR-BETA 3	IMMUNE SYSTEM/CYTOKINE
3EOC	CDK2/CYCLINA COMPLEXED WITH A IMIDAZO TRIAZIN-2-AMINE	TRANSFERASE/CELL CYCLE
3EOY	STRUCTURE OF REOVIRUS SIGMA1 IN COMPLEX WITH ITS RECEPTOR JUNCTIONAL ADHESION MOLECULE-A	VIRAL PROTEIN/CELL ADHESION
3EP3	HUMAN ADOMETDC D174N MUTANT WITH NO PUTRESCINE BOUND	LYASE
3EP4	HUMAN ADOMETDC E256Q MUTANT WITH NO PUTRESCINE BOUND	LYASE
3EP5	HUMAN ADOMETDC E178Q MUTANT WITH NO PUTRESCINE BOUND	LYASE
3EP6	HUMAN ADOMETDC D174N MUTANT COMPLEXED WITH S-	LYASE

	ADENOSYLMETHIONINE METHYL ESTER AND NO PUTRESCINE BOUND	
3EP7	HUMAN ADOMETDC E256Q MUTANT COMPLEXED WITH S-ADENOSYLMETHIONINE METHYL ESTER AND NO PUTRESCINE BOUND	LYASE
3EP8	HUMAN ADOMETDC E178Q MUTANT COMPLEXED WITH S-ADENOSYLMETHIONINE METHYL ESTER AND NO PUTRESCINE BOUND	LYASE
3EP9	HUMAN ADOMETDC WITH NO PUTRESCINE BOUND	LYASE
3EPA	HUMAN ADOMETDC E178Q MUTANT COMPLEXED WITH PUTRESCINE	LYASE
3EPB	HUMAN ADOMETDC E256Q MUTANT COMPLEXED WITH PUTRESCINE	LYASE
3EQL	CRYSTAL STRUCTURE OF THE T. THERMOPHILUS RNA POLYMERASE HOLOENZYME IN COMPLEX WITH ANTIBIOTIC MYXOPYRONIN	TRANSFERASE
3ER3	THE ACTIVE SITE OF ASPARTIC PROTEINASES	HYDROLASE (ACID PROTEINASE)
3ER5	THE ACTIVE SITE OF ASPARTIC PROTEINASES	HYDROLASE (ACID PROTEINASE)
3ERY	DIFFERENT THERMODYNAMIC BINDING MECHANISMS AND PEPTIDE FINE SPECIFICITIES ASSOCIATED WITH A PANEL OF STRUCTURALLY SIMILAR HIGH-AFFINITY T CELL RECEPTORS	IMMUNE SYSTEM
3ESW	COMPLEX OF YEAST PNGASE WITH GLCNAC2-IAC.	HYDROLASE
3ET6	THE CRYSTAL STRUCTURE OF THE CATALYTIC DOMAIN OF A EUKARYOTIC GUANYLATE CYCLASE	LYASE
3EWE	CRYSTAL STRUCTURE OF THE NUP85/SEH1 COMPLEX	PROTEIN TRANSPORT,STRUCTURAL PROTEIN
3EX7	THE CRYSTAL STRUCTURE OF EJC IN ITS TRANSITION STATE	HYDROLASE/RNA BINDING PROTEIN/RNA
3EXE	CRYSTAL STRUCTURE OF THE PYRUVATE DEHYDROGENASE (E1P) COMPONENT OF HUMAN PYRUVATE DEHYDROGENASE COMPLEX	OXIDOREDUCTASE
3EXF	CRYSTAL STRUCTURE OF THE PYRUVATE DEHYDROGENASE (E1P) COMPONENT OF HUMAN PYRUVATE DEHYDROGENASE COMPLEX	OXIDOREDUCTASE
3EXG	CRYSTAL STRUCTURE OF THE PYRUVATE DEHYDROGENASE (E1P) COMPONENT OF HUMAN PYRUVATE DEHYDROGENASE COMPLEX	OXIDOREDUCTASE
3EXH	CRYSTAL STRUCTURE OF THE PYRUVATE DEHYDROGENASE (E1P) COMPONENT OF HUMAN PYRUVATE DEHYDROGENASE COMPLEX	OXIDOREDUCTASE
3EXI	CRYSTAL STRUCTURE OF THE PYRUVATE DEHYDROGENASE (E1P) COMPONENT OF HUMAN PYRUVATE DEHYDROGENASE COMPLEX WITH THE SUBUNIT-BINDING DOMAIN (SBD) OF E2P, BUT SBD CANNOT BE MODELED INTO THE ELECTRON DENSITY	OXIDOREDUCTASE
3EYF	CRYSTAL STRUCTURE OF ANTI-HUMAN CYTOMEGALOVIRUS ANTIBODY 8F9 PLUS GB PEPTIDE	IMMUNE SYSTEM
3EYO	RYSTAL STRUCTURE OF ANTI-HUMAN CYTOMEGALOVIRUS ANTIBODY 8F9	IMMUNE SYSTEM

3EYQ	CRYSTAL STRUCTURE OF MJ5 FAB, A GERMLINE ANTIBODY VARIANT OF ANTI-HUMAN CYTOMEGALOVIRUS ANTIBODY 8F9	IMMUNE SYSTEM
3EZA	COMPLEX OF THE AMINO TERMINAL DOMAIN OF ENZYME I AND THE HISTIDINE-CONTAINING PHOSPHOCARRIER PROTEIN HPR FROM ESCHERICHIA COLI NMR, RESTRAINED REGULARIZED MEAN STRUCTURE	COMPLEX (TRANSFERASE/PHOSPHOCARRIER)
3EZE	COMPLEX OF THE AMINO TERMINAL DOMAIN OF ENZYME I AND THE HISTIDINE-CONTAINING PHOSPHOCARRIER PROTEIN HPR FROM ESCHERICHIA COLI NMR, RESTRAINED REGULARIZED MEAN STRUCTURE	TRANSFERASE
3EZQ	CRYSTAL STRUCTURE OF THE FAS/FADD DEATH DOMAIN COMPLEX	APOPTOSIS
3F1E	CRYSTAL STRUCTURE OF A TRANSLATION TERMINATION COMPLEX FORMED WITH RELEASE FACTOR RF2. THIS FILE CONTAINS THE 30S SUBUNIT, RF2, TWO TRNA, AND MRNA MOLECULES OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AS DESCRIBED IN REMARK 400.	RIBOSOME
3F1F	CRYSTAL STRUCTURE OF A TRANSLATION TERMINATION COMPLEX FORMED WITH RELEASE FACTOR RF2. THIS FILE CONTAINS THE 50S SUBUNIT OF ONE 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AS DESCRIBED IN REMARK 400.	RIBOSOME
3F1G	CRYSTAL STRUCTURE OF A TRANSLATION TERMINATION COMPLEX FORMED WITH RELEASE FACTOR RF2. THIS FILE CONTAINS THE 30S SUBUNIT, RF2, TWO TRNA, AND MRNA MOLECULES OF THE SECOND 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AS DESCRIBED IN REMARK 400.	RIBOSOME
3F1H	CRYSTAL STRUCTURE OF A TRANSLATION TERMINATION COMPLEX FORMED WITH RELEASE FACTOR RF2. THIS FILE CONTAINS THE 50S SUBUNIT OF THE SECOND 70S RIBOSOME. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AS DESCRIBED IN REMARK 400.	RIBOSOME
3F2K	TRUCTURE OF THE TRANSPOSASE DOMAIN OF HUMAN HISTONE-LYSINE N-METHYLTRANSFERASE SETMAR	TRANSFERASE
3F2O	RYSTAL STRUCTURE OF HUMAN SPLA/RYANODINE RECEPTOR DOMAIN AND SOCS BOX CONTAINING 1 (SPSB1) IN COMPLEX WITH A 20-RESIDUE VASA PEPTIDE	APOPTOSIS/HYDROLASE
3F58	IGG1 FAB FRAGMENT (58.2) COMPLEX WITH 12-RESIDUE CYCLIC PEPTIDE (INCLUDING RESIDUES 315-324 OF HIV-1 GP120 (MN ISOLATE); H315S MUTATION	IMMUNE SYSTEM
3F5C	STRUCTURE OF DAX-1:LRH-1 COMPLEX	TRANSCRIPTION
3F6Q	CRYSTAL STRUCTURE OF INTEGRIN-LINKED KINASE ANKYRIN REPEAT DOMAIN IN COMPLEX WITH PINCH1 LIM1 DOMAIN	SIGNALING PROTEIN/SIGNALING PROTEIN
3F6U	CRYSTAL STRUCTURE OF HUMAN ACTIVATED PROTEIN C (APC) COMPLEXED WITH PPACK	HYDROLASE

3F6Z	RYSTAL STRUCTURE OF PSEUDOMONAS AERUGINOSA MLIC IN COMPLEX WITH HEN EGG WHITE LYSOZYME	HYDROLASE
3F75	ACTIVATED TOXOPLASMA GONDII CATHEPSIN L (TGCPL) IN COMPLEX WITH ITS PROPEPTIDE	HYDROLASE
3F7D	SF-1 LBD BOUND BY PHOSPHATIDYLCHOLINE	TRANSCRIPTION
3F9W	STRUCTURAL INSIGHTS INTO LYSINE MULTIPLE METHYLATION BY SET DOMAIN METHYLTRANSFERASES, SET8-Y334F / H4-LYS20 / ADOHCY	TRANSFERASE
3F9X	STRUCTURAL INSIGHTS INTO LYSINE MULTIPLE METHYLATION BY SET DOMAIN METHYLTRANSFERASES, SET8-Y334F / H4-LYS20ME2 / ADOHCY	TRANSFERASE
3F9Y	STRUCTURAL INSIGHTS INTO LYSINE MULTIPLE METHYLATION BY SET DOMAIN METHYLTRANSFERASES, SET8-Y334F / H4-LYS20ME1 / ADOHCY	TRANSFERASE
3F9Z	STRUCTURAL INSIGHTS INTO LYSINE MULTIPLE METHYLATION BY SET DOMAIN METHYLTRANSFERASES, SET8-Y245F / H4-LYS20 / ADOHCY	TRANSFERASE
3FAP	ATOMIC STRUCTURES OF THE RAPAMYCIN ANALOGS IN COMPLEX WITH BOTH HUMAN FKBP12 AND FRB DOMAIN OF FRAP	CELL CYCLE
3FBI	STRUCTURE OF THE MEDIATOR SUBMODULE MED7N/31	TRANSCRIPTION
3FBN	STRUCTURE OF THE MEDIATOR SUBMODULE MED7N/31	TRANSCRIPTION
3FCT	MATURE METAL CHELATASE CATALYTIC ANTIBODY WITH HAPTEN	IMMUNE SYSTEM
3FDO	STRUCTURE OF HUMAN MDMX IN COMPLEX WITH HIGH AFFINITY PEPTIDE	CELL CYCLE
3FG5	CRYSTAL STRUCTURE DETERMINATION OF A TERNARY COMPLEX OF PHOSPHOLIPASE A2 WITH A PENTAPETIDE FLSYK AND AJMALINE AT 2.5 A RESOLUTION	HYDROLASE
3FIV	CRYSTAL STRUCTURE OF FELINE IMMUNODEFICIENCY VIRUS PROTEASE COMPLEXED WITH A SUBSTRATE	COMPLEX (ACID PROTEINASE/SUBSTRATE)
3FRU	NEONATAL FC RECEPTOR, PH 6.5	COMPLEX (IMMUNOGLOBULIN/BINDING PROTEIN)
3GCT	STRUCTURE OF GAMMA-*CHYMOTRYPSIN IN THE RANGE $P*H 2.0 TO $P*H 10.5 SUGGESTS THAT GAMMA-CHYMOTRYPSIN IS A COVALENT ACYL-ENZYME ADDUCT AT LOW $P*H	HYDROLASE (SERINE PROTEINASE)
3GTU	LIGAND-FREE HETERODIMERIC HUMAN GLUTATHIONE S-TRANSFERASE M2-3 (EC 2.5.1.18), MONOCLINIC CRYSTAL FORM	TRANSFERASE
3HAT	ACTIVE SITE MIMETIC INHIBITION OF THROMBIN	COMPLEX (SERINE PROTEASE/INHIBITOR)
3HFM	STRUCTURE OF AN ANTIBODY-ANTIGEN COMPLEX. CRYSTAL STRUCTURE OF THE HY/HEL-10 FAB-LYSOZYME COMPLEX	COMPLEX(ANTIBODY-ANTIGEN)

3HHB	THE CRYSTAL STRUCTURE OF HUMAN DEOXYHAEMOGLOBIN AT 1.74 ANGSTROMS RESOLUTION	OXYGEN TRANSPORT
3HHR	HUMAN GROWTH HORMONE AND EXTRACELLULAR DOMAIN OF ITS RECEPTOR: CRYSTAL STRUCTURE OF THE COMPLEX	HORMONE/RECEPTOR
3HMG	REFINEMENT OF THE INFLUENZA VIRUS HEMAGGLUTININ BY SIMULATED ANNEALING	VIRAL PROTEIN
3HVT	STRUCTURAL BASIS OF ASYMMETRY IN THE HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 REVERSE TRANSCRIPTASE HETERODIMER	NUCLEOTIDYLTRANSFERASE
3INS	STRUCTURE OF INSULIN. RESULTS OF JOINT NEUTRON AND X-RAY REFINEMENT	HORMONE
3KIN	KINESIN (DIMERIC) FROM RATTUS NORVEGICUS	MOTOR PROTEIN
3MIN	NITROGENASE MOFE PROTEIN FROM AZOTOBACTER VINELANDII, OXIDIZED STATE	NITROGEN FIXATION
3MON	CRYSTAL STRUCTURES OF TWO INTENSELY SWEET PROTEINS	SWEET-TASTING PROTEIN
3MTH	X-RAY CRYSTALLOGRAPHIC STUDIES ON HEXAMERIC INSULINS IN THE PRESENCE OF HELIX-STABILIZING AGENTS, THIOCYANATE, METHYLPARABEN AND PHENOL	HORMONE
3PCA	TRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 3,4-DIHYDROXYBENZOATE	DIOXYGENASE
3PCB	TRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 3-HYDROXYBENZOATE	DIOXYGENASE
3PCC	TRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 4-HYDROXYBENZOATE	DIOXYGENASE
3PCD	PROTOCATECHUATE 3,4-DIOXYGENASE Y447H MUTANT	DIOXYGENASE
3PCE	TRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 3-HYDROXYPHENYLACETATE	DIOXYGENASE
3PCF	TRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 3-FLURO-4-HYDROXYBENZOATE	DIOXYGENASE
3PCG	TRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH THE INHIBITOR 4-HYDROXYPHENYLACETATE	DIOXYGENASE
3PCH	TRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 3-CHLORO-4-HYDROXYBENZOATE	DIOXYGENASE
3PCI	TRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 3-IODO-4-HYDROXYBENZOATE	DIOXYGENASE
3PCJ	TRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 2-HYDROXYISONICOTINIC ACID N-OXIDE	DIOXYGENASE

3PCK	TRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 6-HYDROXYNICOTINIC ACID N-OXIDE	DIOXYGENASE
3PCL	TRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 2-HYDROXYISONICOTINIC ACID N-OXIDE AND CYANIDE	DIOXYGENASE
3PCM	TRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 6-HYDROXYNICOTINIC ACID N-OXIDE AND CYANIDE	DIOXYGENASE
3PCN	TRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 3,4-DIHYDROXYPHENYLACETATE	DIOXYGENASE
3PRC	HOTOSYNTHETIC REACTION CENTER FROM RHODOPSEUDOMONAS VIRIDIS (QB-DEPLETED)	PHOTOSYNTHETIC REACTION CENTER
3PRK	INHIBITION OF PROTEINASE K BY METHOXYSUCCINYL-ALA-ALA-PRO-ALA-CHLOROMETHYL KETONE. AN X-RAY STUDY AT 2.2-ANGSTROMS RESOLUTION	HYDROLASE(SERINE PROTEINASE)
3PRO	ALPHA-LYTIC PROTEASE COMPLEXED WITH C-TERMINAL TRUNCATED PRO REGION	PRO REGION
3R1R	IBONUCLEOTIDE REDUCTASE R1 PROTEIN WITH AMPPNP OCCUPYING THE ACTIVITY SITE FROM ESCHERICHIA COLI	COMPLEX (OXIDOREDUCTASE/PEPTIDE)
3REQ	METHYLMALONYL-COA MUTASE, SUBSTRATE-FREE STATE (POOR QUALITY STRUCTURE)	COMPLEX (ISOMERASE/DEOXYADENOSINE)
3RUB	CRYSTAL STRUCTURE OF THE UNACTIVATED FORM OF RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE(SLASH)OXYGENASE FROM TOBACCO REFINED AT 2.0-ANGSTROMS RESOLUTION	LYASE(CARBON-CARBON)
3SC2	REFINED ATOMIC MODEL OF WHEAT SERINE CARBOXYPEPTIDASE II AT 2.2-ANGSTROMS RESOLUTION	HYDROLASE(CARBOXYPEPTIDASE)
3SGA	STRUCTURES OF PRODUCT AND INHIBITOR COMPLEXES OF STREPTOMYCES GRISEUS PROTEASE A AT 1.8 ANGSTROMS RESOLUTION. A MODEL FOR SERINE PROTEASE CATALYSIS	HYDROLASE (SERINE PROTEINASE)
3SGB	TRUCTURE OF THE COMPLEX OF STREPTOMYCES GRISEUS PROTEASE B AND THE THIRD DOMAIN OF THE TURKEY OVOMUCOID INHIBITOR AT 1.8 ANGSTROMS RESOLUTION	COMPLEX(SERINE PROTEINASE-INHIBITOR)
3SGQ	GLN 18 VARIANT OF TURKEY OVOMUCOID INHIBITOR THIRD DOMAIN COMPLEXED WITH STREPTOMYCES GRISEUS PROTEINASE B AT PH 10.7	HYDROLASE/HYDROLASE INHIBITOR
3SIC	MOLECULAR RECOGNITION AT THE ACTIVE SITE OF SUBTILISIN BPN': CRYSTALLOGRAPHIC STUDIES USING GENETICALLY ENGINEERED PROTEINACEOUS INHIBITOR SSI (STREPTOMYCES SUBTILISIN INHIBITOR)	COMPLEX(PROTEINASE/INHIBITOR)
3SRN	STRUCTURAL CHANGES THAT ACCOMPANY THE REDUCED CATALYTIC EFFICIENCY OF TWO SEMISYNTHETIC RIBONUCLEASE ANALOGS	HYDROLASE(NUCLEIC ACID,RNA)
		COMPLEX(SERINE PROTEINASE-INHIBITOR)

3TEC	CALCIUM BINDING TO THERMITASE. CRYSTALLOGRAPHIC STUDIES OF THERMITASE AT 0, 5 AND 100 MM CALCIUM	
		HYDROLASE (METALLOPROTEINASE)
3TMN	THE BINDING OF L-VALYL-L-TRYPTOPHAN TO CRYSTALLINE THERMOLYSIN ILLUSTRATES THE MODE OF INTERACTION OF A PRODUCT OF PEPTIDE HYDROLYSIS	
		HYDROLASE
3UBP	DIAMIDOPHOSPHATE INHIBITED BACILLUS PASTEURII UREASE	
		SERINE PROTEASE
3VGC	GAMMA-CHYMOTRYPSIN L-NAPHTHYL-1-ACETAMIDO BORONIC ACID ACID INHIBITOR COMPLEX	
		APOPTOSIS
3YGS	APAF-1 CARD IN COMPLEX WITH PRODOMAIN OF PROCASPASE-9	
		IMMUNOGLOBULIN
43C9	CRYSTALLOGRAPHIC STRUCTURE OF THE ESTEROLYTIC AND AMIDOLYTIC 43C9 ANTIBODY	
		OXIDOREDUCTASE (PQQ(A)-CHOH(D))
4AAH	METHANOL DEHYDROGENASE FROM METHYLOPHILUS W3A1	
		HORMONE/GROWTH FACTOR
4AIY	R6 HUMAN INSULIN HEXAMER (SYMMETRIC), NMR, 'GREEN' SUBSTATE, AVERAGE STRUCTURE	
		TRANSFERASE (CARBAMOYL-P,ASPARTATE)
4AT1	STRUCTURAL CONSEQUENCES OF EFFECTOR BINDING TO THE T STATE OF ASPARTATE CARBAMOYLTRANSFERASE. CRYSTAL STRUCTURES OF THE UNLIGATED AND ATP-, AND CTP-COMPLEXED ENZYMES AT 2.6-ANGSTROMS RESOLUTION	
		IMMUNOGLOBULIN
4BJL	LOCW, A LAMBDA 1 TYPE LIGHT-CHAIN DIMER (BENCE-JONES PROTEIN) CRYSTALLIZED IN DISTILLED WATER	
		SERPIN
4CAA	CLEAVED ANTICHYMOTRYPSIN T345R	
		HYDROLASE (SERINE PROTEINASE)
4CHA	STRUCTURE OF ALPHA-*CHYMOTRYPSIN REFINED AT 1.68 ANGSTROMS RESOLUTION	
		HYDROLASE (C-TERMINAL PEPTIDASE)
4CPA	REFINED CRYSTAL STRUCTURE OF THE POTATO INHIBITOR COMPLEX OF CARBOXYPEPTIDASE A AT 2.5 ANGSTROMS RESOLUTION	
		IMMUNOGLOBULIN
4FAB	THREE-DIMENSIONAL STRUCTURE OF A FLUORESCEIN-FAB COMPLEX CRYSTALLIZED IN 2-METHYL-2,4-PENTANEDIOL	
		CELL CYCLE
4FAP	ATOMIC STRUCTURES OF THE RAPAMYCIN ANALOGS IN COMPLEX WITH BOTH HUMAN FKBP12 AND FRB DOMAIN OF FRAP	
		HYDROLASE (SERINE PROTEINASE)
4GCH	STRUCTURE AND ACTIVITY OF TWO PHOTOREVERSIBLE CINNAMATES BOUND TO CHYMOTRYPSIN	
		OXYGEN TRANSPORT
4HHB	THE CRYSTAL STRUCTURE OF HUMAN DEOXYHAEMOGLOBIN AT 1.74 ANGSTROMS RESOLUTION	
		VIRAL PROTEIN
4HMG	REFINEMENT OF THE INFLUENZA VIRUS HEMAGGLUTININ BY SIMULATED ANNEALING	
		HYDROLASE(SERINE PROTEASE)
4HTC	THE REFINED STRUCTURE OF THE HIRUDIN-THROMBIN COMPLEX	
		HYDROLASE(ACID PROTEINASE)

4HVP	STRUCTURE OF COMPLEX OF SYNTHETIC HIV-1 PROTEASE WITH A STUBTRATE-BASED INHIBITOR AT 2.3 ANGSTROMS RESOLUTION	
4INS	THE STRUCTURE OF 2ZN PIG INSULIN CRYSTALS AT 1.5 ANGSTROMS RESOLUTION	HORMONE
4MON	ORTHORHOMBIC MONELLIN	SWEET-TASTING PROTEIN
4PRO	ALPHA-LYTIC PROTEASE COMPLEXED WITH PRO REGION	SERINE PROTEASE
4R1R	RIBONUCLEOTIDE REDUCTASE R1 PROTEIN WITH SUBSTRATE, GDP AND EFFECTOR DTTP FROM ESCHERICHIA COLI	COMPLEX (OXIDOREDUCTASE/PEPTIDE)
4RCR	STRUCTURE OF THE REACTION CENTER FROM RHODOBACTER SPHAEROIDES R-26 AND 2.4.1: PROTEIN-COFACTOR (BACTERIOCHLOROPHYLL, BACTERIOPHEOPHYTIN, AND CAROTENOID) INTERACTIONS	PHOTOSYNTHETIC REACTION CENTER
4REQ	METHYLMALONYL-COA MUTASE SUBSTRATE COMPLEX	ISOMERASE
4RUB	A CRYSTAL FORM OF RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE(SLASH)OXYGENASE FROM NICOTIANA TABACUM IN THE ACTIVATED STATE	LYASE(CARBON-CARBON)
4SGA	STRUCTURES OF PRODUCT AND INHIBITOR COMPLEXES OF STREPTOMYCES GRISEUS PROTEASE A AT 1.8 ANGSTROMS RESOLUTION. A MODEL FOR SERINE PROTEASE CATALYSIS	HYDROLASE (SERINE PROTEINASE)
4SGB	TRUCTURE OF THE COMPLEX OF STREPTOMYCES GRISEUS PROTEINASE B AND POLYPEPTIDE CHYMOTRYPSIN INHIBITOR-1 FROM RUSSET BURBANK POTATO TUBERS AT 2.1 ANGSTROMS RESOLUTION	COMPLEX(SERINE PROTEINASE-INHIBITOR)
4SRN	STRUCTURAL CHANGES THAT ACCOMPANY THE REDUCED CATALYTIC EFFICIENCY OF TWO SEMISYNTHETIC RIBONUCLEASE ANALOGS	HYDROLASE(NUCLEIC ACID,RNA)
4TMN	SLOW-AND FAST-BINDING INHIBITORS OF THERMOLYSIN DISPLAY DIFFERENT MODES OF BINDING. CRYSTALLOGRAPHIC ANALYSIS OF EXTENDED PHOSPHONAMIDATE TRANSITION-STATE ANALOGUES	HYDROLASE (METALLOPROTEINASE)
4TPI	THE REFINED 2.2-ANGSTROMS (0.22-NM) X-RAY CRYSTAL STRUCTURE OF THE TERNARY COMPLEX FORMED BY BOVINE TRYPSINOGEN, VALINE-VALINE AND THE ARG15 ANALOGUE OF BOVINE PANCREATIC TRYPSIN INHIBITOR	COMPLEX (PROTEINASE/INHIBITOR)
4UBP	STRUCTURE OF BACILLUS PASTEURII UREASE INHIBITED WITH ACETOHYDROXAMIC ACID AT 1.55 A RESOLUTION	HYDROLASE
4VGC	GAMMA-CHYMOTRYPSIN D-NAPHTHYL-1-ACETAMIDO BORONIC ACID INHIBITOR COMPLEX	SERINE PROTEASE
5AIY	R6 HUMAN INSULIN HEXAMER (SYMMETRIC), NMR, 'RED' SUBSTATE, AVERAGE STRUCTURE	HORMONE/GROWTH FACTOR
5-Apr	STRUCTURES OF COMPLEXES OF RHIZOPUSPEPSIN WITH PEPSTATIN AND OTHER STATINE-CONTAINING INHIBITORS	HYDROLASE (ACID PROTEINASE)

5AT1	STRUCTURAL CONSEQUENCES OF EFFECTOR BINDING TO THE T STATE OF ASPARTATE CARBAMOYLTRANSFERASE. CRYSTAL STRUCTURES OF THE UNLIGATED AND ATP-, AND CTP-COMPLEXED ENZYMES AT 2.6-ANGSTROMS RESOLUTION	TRANSFERASE (CARBAMOYL-P,ASPARTATE)
5CHA	THE REFINEMENT AND THE STRUCTURE OF THE DIMER OF ALPHA-*CHYMOTRYPSIN AT 1.67-*ANGSTROMS RESOLUTION	HYDROLASE (SERINE PROTEINASE)
5CSC	STRUCTURE OF AN OPEN FORM OF CHICKEN HEART CITRATE SYNTHASE AT 2.8 ANGSTROMS RESOLUTION	OXO-ACID-LYASE
5ER2	HIGH-RESOLUTION X-RAY DIFFRACTION STUDY OF THE COMPLEX BETWEEN ENDOTHIAPEPSIN AND AN OLIGOPEPTIDE INHIBITOR. THE ANALYSIS OF THE INHIBITOR BINDING AND DESCRIPTION OF THE RIGID BODY SHIFT IN THE ENZYME	HYDROLASE (ACID PROTEINASE)
5GCH	CHEMISTRY OF CAGED ENZYMES /II$. PHOTOACTIVATION OF INHIBITED CHYMOTRYPSIN	HYDROLASE (SERINE PROTEINASE)
5HMG	REFINEMENT OF THE INFLUENZA VIRUS HEMAGGLUTININ BY SIMULATED ANNEALING	VIRAL PROTEIN
5HVP	CRYSTALLOGRAPHIC ANALYSIS OF A COMPLEX BETWEEN HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 PROTEASE AND ACETYL-PEPSTATIN AT 2.0-ANGSTROMS RESOLUTION	HYDROLASE(ACID PROTEINASE)
5PAD	BINDING OF CHLOROMETHYL KETONE SUBSTRATE ANALOGUES TO CRYSTALLINE PAPAIN	HYDROLASE (SULFHYDRYL PROTEINASE)
5PRC	PHOTOSYNTHETIC REACTION CENTER FROM RHODOPSEUDOMONAS VIRIDIS (ATRAZINE COMPLEX)	PHOTOSYNTHETIC REACTION CENTER
5R1R	RIBONUCLEOTIDE REDUCTASE E441A MUTANT R1 PROTEIN FROM ESCHERICHIA COLI	COMPLEX (OXIDOREDUCTASE/PEPTIDE)
5REQ	METHYLMALONYL-COA MUTASE, Y89F MUTANT, SUBSTRATE COMPLEX	ISOMERASE
5SGA	STRUCTURES OF PRODUCT AND INHIBITOR COMPLEXES OF STREPTOMYCES GRISEUS PROTEASE A AT 1.8 ANGSTROMS RESOLUTION. A MODEL FOR SERINE PROTEASE CATALYSIS	HYDROLASE (SERINE PROTEINASE)
5SIC	MOLECULAR RECOGNITION AT THE ACTIVE SITE OF SUBTILISIN BPN': CRYSTALLOGRAPHIC STUDIES USING GENETICALLY ENGINEERED PROTEINACEOUS INHIBITOR SSI (STREPTOMYCES SUBTILISIN INHIBITOR)	COMPLEX(PROTEINASE/INHIBITOR)
5TMN	SLOW-AND FAST-BINDING INHIBITORS OF THERMOLYSIN DISPLAY DIFFERENT MODES OF BINDING. CRYSTALLOGRAPHIC ANALYSIS OF EXTENDED PHOSPHONAMIDATE TRANSITION-STATE ANALOGUES	HYDROLASE (METALLOPROTEINASE)
6AT1	STRUCTURAL CONSEQUENCES OF EFFECTOR BINDING TO THE T STATE OF ASPARTATE CARBAMOYLTRANSFERASE. CRYSTAL STRUCTURES OF THE UNLIGATED AND ATP-, AND CTP-COMPLEXED ENZYMES AT 2.6-ANGSTROMS RESOLUTION	TRANSFERASE (CARBAMOYL-P,ASPARTATE)

6CHA	STRUCTURE OF A TETRAHEDRAL TRANSITION STATE COMPLEX OF ALPHA-*CHYMOTRYPSIN AT 1.8-*ANGSTROMS RESOLUTION	HYDROLASE (SERINE PROTEINASE)
6FAB	THREE-DIMENSIONAL STRUCTURE OF MURINE ANTI-P-AZOPHENYLARSONATE FAB 36-71. 1. X-RAY CRYSTALLOGRAPHY, SITE-DIRECTED MUTAGENESIS, AND MODELING OF THE COMPLEX WITH HAPTEN	IMMUNOGLOBULIN
6GCH	TRUCTURE OF CHYMOTRYPSIN-*TRIFLUOROMETHYL KETONE INHIBITOR COMPLEXES. COMPARISON OF SLOWLY AND RAPIDLY EQUILIBRATING INHIBITORS	HYDROLASE (SERINE PROTEINASE)
6HBW	RYSTAL STRUCTURE OF DEOXY-HUMAN HEMOGLOBIN BETA6 GLU->TRP	OXYGEN STORAGE/TRANSPORT
6PAD	BINDING OF CHLOROMETHYL KETONE SUBSTRATE ANALOGUES TO CRYSTALLINE PAPAIN	HYDROLASE (SULFHYDRYL PROTEINASE)
6PRC	HOTOSYNTHETIC REACTION CENTER FROM RHODOPSEUDOMONAS VIRIDIS (DG-420314 (TRIAZINE) COMPLEX)	PHOTOSYNTHETIC REACTION CENTER
6R1R	RIBONUCLEOTIDE REDUCTASE E441D MUTANT R1 PROTEIN FROM ESCHERICHIA COLI	COMPLEX (OXIDOREDUCTASE/PEPTIDE)
6REQ	METHYLMALONYL-COA MUTASE, 3-CARBOXYPROPYL-COA INHIBITOR COMPLEX	ISOMERASE
6RLX	X-RAY STRUCTURE OF HUMAN RELAXIN AT 1.5 ANGSTROMS. COMPARISON TO INSULIN AND IMPLICATIONS FOR RECEPTOR BINDING DETERMINANTS	HORMONE(MUSCLE RELAXANT)
6TMN	STRUCTURES OF TWO THERMOLYSIN-INHIBITOR COMPLEXES THAT DIFFER BY A SINGLE HYDROGEN BOND	HYDROLASE (METALLOPROTEINASE)
7API	THE S VARIANT OF HUMAN ALPHA1-ANTITRYPSIN, STRUCTURE AND IMPLICATIONS FOR FUNCTION AND METABOLISM	PROTEINASE INHIBITOR
7AT1	CRYSTAL STRUCTURES OF ASPARTATE CARBAMOYLTRANSFERASE LIGATED WITH PHOSPHONOACETAMIDE, MALONATE, AND CTP OR ATP AT 2.8-ANGSTROMS RESOLUTION AND NEUTRAL P*H	TRANSFERASE (CARBAMOYL-P,ASPARTATE)
7CEI	THE ENDONUCLEASE DOMAIN OF COLICIN E7 IN COMPLEX WITH ITS INHIBITOR IM7 PROTEIN	IMMUNE SYSTEM
7FAB	RYSTAL STRUCTURE OF HUMAN IMMUNOGLOBULIN FRAGMENT FAB NEW REFINED AT 2.0 ANGSTROMS RESOLUTION	IMMUNOGLOBULIN
7GCH	TRUCTURE OF CHYMOTRYPSIN-*TRIFLUOROMETHYL KETONE INHIBITOR COMPLEXES. COMPARISON OF SLOWLY AND RAPIDLY EQUILIBRATING INHIBITORS	HYDROLASE (SERINE PROTEINASE)
7HVP	X-RAY CRYSTALLOGRAPHIC STRUCTURE OF A COMPLEX BETWEEN A SYNTHETIC PROTEASE OF HUMAN IMMUNODEFICIENCY VIRUS 1 AND A SUBSTRATE-BASED HYDROXYETHYLAMINE INHIBITOR	HYDROLASE(ACID PROTEINASE)
		HORMONE

7INS	STRUCTURE OF PORCINE INSULIN COCRYSTALLIZED WITH CLUPEINE Z	
7KME	CRYSTAL STRUCTURE OF HUMAN ALPHA-THROMBIN INHIBITED WITH SEL2711.	HYDROLASE
7PRC	PHOTOSYNTHETIC REACTION CENTER FROM RHODOPSEUDOMONAS VIRIDIS (DG-420315 (TRIAZINE) COMPLEX)	PHOTOSYNTHETIC REACTION CENTER
7R1R	RIBONUCLEOTIDE REDUCTASE E441Q MUTANT R1 PROTEIN FROM ESCHERICHIA COLI	COMPLEX (OXIDOREDUCTASE/PEPTIDE)
7REQ	METHYLMALONYL-COA MUTASE, 2-CARBOXYPROPYL-COA INHIBITOR COMPLEX	ISOMERASE
8API	THE S VARIANT OF HUMAN ALPHA1-ANTITRYPSIN, STRUCTURE AND IMPLICATIONS FOR FUNCTION AND METABOLISM	PROTEINASE INHIBITOR
8AT1	CRYSTAL STRUCTURES OF ASPARTATE CARBAMOYLTRANSFERASE LIGATED WITH PHOSPHONOACETAMIDE, MALONATE, AND CTP OR ATP AT 2.8-ANGSTROMS RESOLUTION AND NEUTRAL P*H	TRANSFERASE (CARBAMOYL-P,ASPARTATE)
8ATC	COMPLEX OF N-PHOSPHONACETYL-L-ASPARTATE WITH ASPARTATE CARBAMOYLTRANSFERASE. X-RAY REFINEMENT, ANALYSIS OF CONFORMATIONAL CHANGES AND CATALYTIC AND ALLOSTERIC MECHANISMS	TRANSFERASE (CARBAMOYL-P,ASPARTATE)
8FAB	CRYSTAL STRUCTURE OF THE FAB FRAGMENT FROM THE HUMAN MYELOMA IMMUNOGLOBULIN IGG HIL AT 1.8 ANGSTROMS RESOLUTION	IMMUNOGLOBULIN
8GCH	GAMMA-CHYMOTRYPSIN IS A COMPLEX OF ALPHA-CHYMOTRYPSIN WITH ITS OWN AUTOLYSIS PRODUCTS	HYDROLASE (SERINE PROTEINASE)
8HVP	STRUCTURE AT 2.5-ANGSTROMS RESOLUTION OF CHEMICALLY SYNTHESIZED HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 PROTEASE COMPLEXED WITH A HYDROXYETHYLENE*-BASED INHIBITOR	HYDROLASE(ACID PROTEINASE)
8PCH	CRYSTAL STRUCTURE OF PORCINE CATHEPSIN H DETERMINED AT 2.1 ANGSTROM RESOLUTION: LOCATION OF THE MINI-CHAIN C-TERMINAL CARBOXYL GROUP DEFINES CATHEPSIN H AMINOPEPTIDASE FUNCTION	HYDROLASE
8RUC	ACTIVATED SPINACH RUBISCO COMPLEXED WITH 2-CARBOXYARABINITOL BISPHOSPHATE	LYASE (CARBON-CARBON)
8TLN	TRUCTURAL COMPARISON SUGGESTS THAT THERMOLYSIN AND RELATED NEUTRAL PROTEASES UNDERGO HINGE-BENDING MOTION DURING CATALYSIS	HYDROLASE(METALLOPROTEINASE)
9API	THE S VARIANT OF HUMAN ALPHA1-ANTITRYPSIN, STRUCTURE AND IMPLICATIONS FOR FUNCTION AND METABOLISM	PROTEINASE INHIBITOR
9ATC	ATCASE Y165F MUTANT	TRANSFERASE
9INS	MONOVALENT CATION BINDING IN CUBIC INSULIN CRYSTALS	HORMONE