Systematic Analysis of Helical Protein Interfaces Reveals Targets for Synthetic Inhibitors

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Supporting 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 wrote computer code in Perl, C and C++ programming language to identify and analyze HIPP interactions. The key steps to identifying HIPP interactions are listed below and shown in Figure S1.

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

2) Sequence alignment of all complexes was performed using the CD-HIT clustering algorithm. CD-HIT clusters similar chains according to a similarity threshold. Although this method allows for all unique chains to be clustered it does not allow for all unique protein complexes to be clustered. To overcome this problem we removed chain identifiers in the FASTA files. The popular BLAST(*36*) method was not used because the computing of "all versus all" similarities would likely not be able to identify unique complexes properly since the chain identifiers in the FASTA files were removed. Since CD-HIT uses a "short word filter" method it can cluster properly even with these FASTA file modifications.

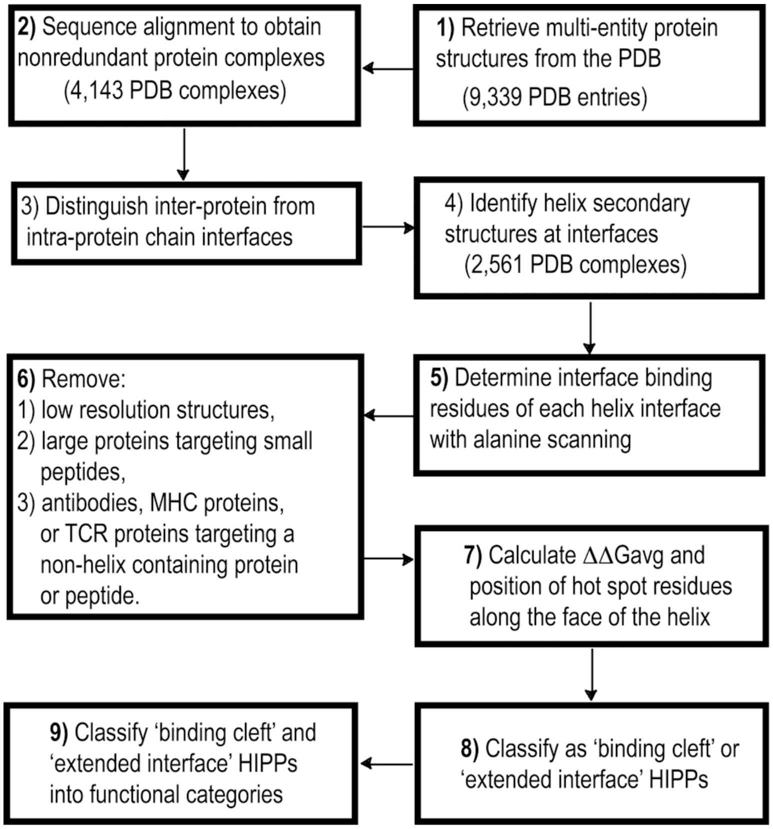

Figure S1. Protocol for the evaluation of structures from the Protein Data Bank to identify and assess helical interfaces in protein–protein (HIPP) interactions.

3) **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 (*ei*. NMR structure), only the first structure is considered.

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 contains programs that identify interface residues and assigns

secondary structure to a protein backbone using ϕ and φ dihedral angle analysis. We then link the interface and secondary structure assignment subroutines 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 (ϕ = -47° ± 25°, φ = -57° ± 25°).

The Dictionary of Secondary Structure of Proteins (DSSP)(*37*) and STRIDE(*38*) are common methods for obtaining information on protein secondary structure of proteins in the PDB. DSSP relies on hydrogen-bonding patterns in proteins to determine secondary structure and STRIDE uses a knowledge-based structure assignment. Although these methods are reliable for determining secondary structure, similar results are also obtained with ϕ and φ analysis as in Rosetta.(*38*) We performed random checks on secondary structures as calculated by Rosetta and defined by DSSP and STRIDE and found the that the three methods are comparable. We used Rosetta for secondary structure analysis to retain consistency across our computer codes.

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.(*39*) 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.(*40*) Therefore, we use a distance threshold between residues of different chains. When parsing PDB files, it is difficult to determine when contacting chains reflect crystal packing or a genuine biological assembly. The problem is amplified when hundreds of PDB files are automatically parsed. Two approaches are suggested for remedying this problem. One calculates the reduction of solvent accessibility due to oligomerisation(*41*) and while the other is based on measuring the conservation of contacting residues.(*42*) Instead of relying of these prediction algorithms, we visually inspected each candidate target in categories 1-3 for crystal packing multimers and eliminated those few interactions that were artifacts of crystal packing.

5) Hot spot residues were predicted by a computational alanine scan on each of the complexes in the dataset using the Rosetta 2.0 software. There are additional methods, besides Rosetta alanine scanning, for predicting hot spot residues. These methods are either based on determining hot spot residues based on amino acid sequence or a scoring function.(*43-46*) Glycine and proline residues were exempted from mutation to alanine as any such event may result in a conformational change in the protein backbone. In cases of multiple side chain orientations for the same residue in a PDB file, we eliminated the residue from consideration as a hot spot residue.

6) The HIPP dataset of 2,561 complexes was further analyzed to screen for potential receptors with binding clefts and extended interfaces that may be targeted by small molecules and helix mimetics, respectively. Any such undertaking inevitably involves a number of subjective decisions.(*47*) Our procedure involved (1) removal of all entries with resolution >4.00 Å and all structures determined by methods other than X-ray crystallography or NMR spectroscopy. We note that hot spot analysis becomes increasingly unreliable with lower resolution structures. (2) Visually inspection of structures to eliminate complexes that we considered too large or complex to target with a small molecule or oligomer; examples include structures of nucleosomes, ribosomes, proteasomes, rubisco, and viral capsids. We also eliminated structures where proteins containing a helix are complexed with a non-helical peptide such as T-cell receptor proteins, MHC proteins, and antibodies. Duplicate sequences and instances where a protein was identified to target a single helix or a protein with a helix targeting a non-helical peptide of length less than 12 residues were removed by automated procedures and verified by visual inspection.

7) We identified HIPP interactions with a $\Delta\Delta G_{avg} \geq 2$ kcal/mol and calculated the end-to-end separation of the hot spot residues in the identified helix using a C++ program.

8) HIPPs with a $\Delta\Delta G_{avg} \geq 2$ kcal/mol from step 7) were classified as 'binding cleft' or 'extended interface'. A binding cleft was defined as having an end-to-end separation of five or less residues while an extended interface was defined as having an end-to-end separation of greater than five but less than twenty-one residues. Twenty residues represent roughly five helical turns or 30 Å. Entries that contain longer sequences are included in Table S3.

9) The 'binding cleft' and 'extended interface' HIPP interactions were classified according to molecular function. The categories were derived from those listed in the header of the PDB file.

Supplemental References

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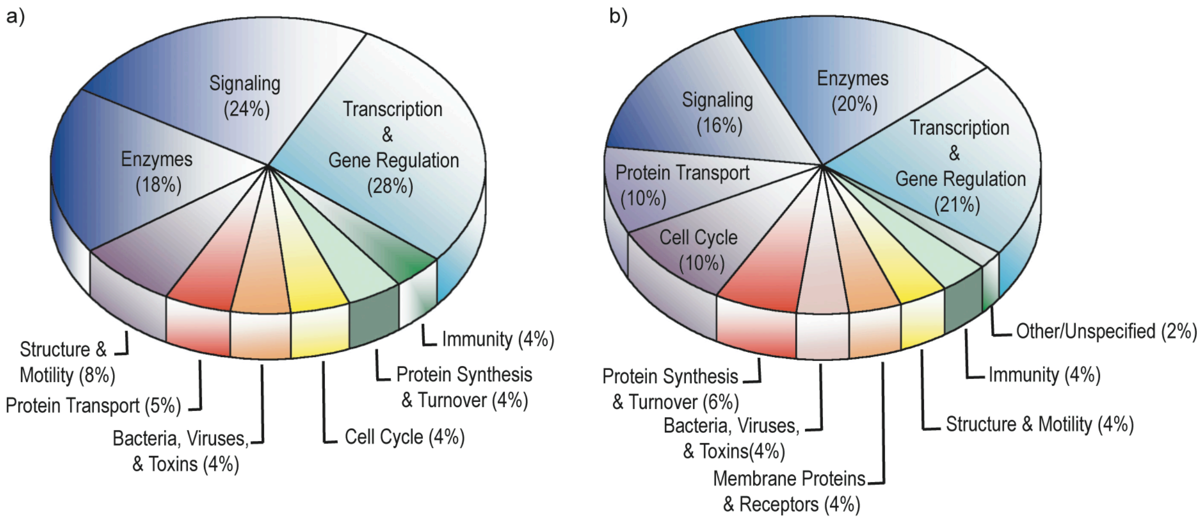
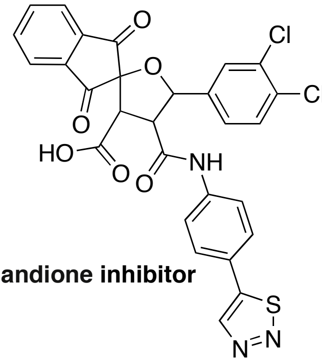


Figure S2. Classification of (a) helical interfaces with binding clefts and (b) extended helical interfaces by function.

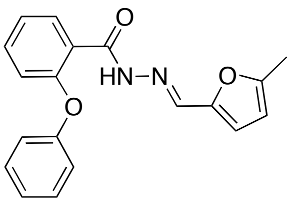
Table S1. Known Small molecule inhibitors of binding cleft protein targets (HIPP, Category 1).

Protein target (PDB code) Protein partner Small molecule[a]	$\Delta\Delta G_{avg/helix}$ (kcal/mol)[b]	Hot spot residue helix position[c]
Bcl-xL (1bxl) Bak peptide ABT-737	2.4	*i*, *i*+3
HDM2 (1ycr) p53 peptide nutlin	3.7	*i*, *i*+3, *i*+4
HPV E2 (1tue) E1 Regulator Indandione inhibitor	2.7	*i*, *i*+3, *i*+4
β-catenin (1jpw) Tcf4 PNU-74654	2.9	*i*, *i*+3, *i*+4

[a] Chains in the complex featuring a helix at the interface; candidate helix to be mimicked is part of the indicated chain. [b] $\Delta\Delta G_{avg/helix}$ is derived from Rosetta computational alanine mutagenesis studies and indicates the average free energy penalty for mutating two or more key residues at the interface to alanine. [c] Relative positioning of the hot spot residues on a helix.



indandione inhibitor



PNU-74654

Indandione inhibitor: Wang, Y., Coulombe, R., Cameron, D. R., Thauvette, L., Massariol, M. J., Amon, L. M., Fink, D., Titolo, S., Welchner, E., Yoakim, C., Archambault, J., and White, P. W. (2004) Crystal structure of the E2 transactivation domain of human papillomavirus type 11 bound to a protein interaction inhibitor, *J Biol Chem 279*, 6976-6985.

PNU-74654: Trosset, J. Y., Dalvit, C., Knapp, S., Fasolini, M., Veronesi, M., Mantegani, S., Gianellini, L. M., Catana, C., Sundstrom, M., Stouten, P. F., and Moll, J. K. (2006) Inhibition of protein-protein interactions: the discovery of druglike beta-catenin inhibitors by combining virtual and biophysical screening, *Proteins 64*, 60-67.

Table S2. Dataset of HIPP interactions with Binding Clefts

Description of Entries:

A. PDB code of predicted target.
B. Chains in the complex featuring a helix at the interface.
C. Candidate helix to be mimicked is part of the indicated chain.
D. Title of PDB entry.
E. Function of protein complex.
F. $\Delta\Delta G_{avg}$/helix is derived from Rosetta computational alanine mutagenesis studies and indicates the average free energy penalty for mutating two or more key residues in the helix at the interface to alanine.
G. $\Delta\Delta G_{sum}$/helix is derived from Rosetta computational alanine mutagenesis studies and indicates the average free energy penalty for mutating two or more key residues at the interface to alanine.
H. $\Delta\Delta G_{sum}$/chain is derived from Rosetta computational alanine mutagenesis studies and indicates the sum free energy penalty for mutating two or more key residues in the helix at the interface to alanine.
I. Helix contribution refers to the proportion of key contact residues positioned on the candidate helix as compared to the chain (see text for a detailed explanation).
J. Number of hot spot residues in helix.
K. Relative positioning of the hot spot residues on a helix.
L. Hot spot residues derived from Rosetta computational alanine scanning mutagenesis.
M. Number of residues separating end hot spot residues (see Methods for more details).
N. Length of candidate helix to be mimicked.
O. First residue of the candidate helix segment.
P. Last residue of the candidate helix segment.
Q. Sequence of candidate helix to be mimicked.
R. Resolution of PDB structure (NOT APP indicates NMR structure).

TABLE S2

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1A0O	A B	A	CHEY-BINDING DOMAIN OF CHEA IN COMPLEX WITH CHEY
1A0O	C D	D	CHEY-BINDING DOMAIN OF CHEA IN COMPLEX WITH CHEY
1A4Y	D E	E	RIBONUCLEASE INHIBITOR-ANGIOGENIN COMPLEX
1A9N	A B	B	CRYSTAL STRUCTURE OF THE SPLICEOSOMAL U2B"-U2A' PROTEIN COMPLEX BOUND TO A FRAGMENT OF
1AY7	A B	B	RIBONUCLEASE SA COMPLEX WITH BARSTAR
1B0N	A B	B	SINR PROTEIN/SINI PROTEIN COMPLEX
1B27	B E	E	STRUCTURAL RESPONSE TO MUTATION AT A PROTEIN-PROTEIN INTERFACE
1B9X	A B	B	STRUCTURAL ANALYSIS OF PHOSDUCIN AND ITS PHOSPHORYLATION- REGULATED INTERACTION WITH T
1BDJ	A B	B	COMPLEX STRUCTURE OF HPT DOMAIN AND CHEY
1BXL	A B	B	STRUCTURE OF BCL-XL/BAK PEPTIDE COMPLEX, NMR, MINIMIZED AVERAGE STRUCTURE
1D2Z	C B	C	THREE-DIMENSIONAL STRUCTURE OF A COMPLEX BETWEEN THE DEATH DOMAINS OF PELLE AND TUBE
1DE4	G I	G	HEMOCHROMATOSIS PROTEIN HFE COMPLEXED WITH TRANSFERRIN RECEPTOR
1DML	C D	D	CRYSTAL STRUCTURE OF HERPES SIMPLEX UL42 BOUND TO THE C- TERMINUS OF HSV POL
1DOA	A B	A	STRUCTURE OF THE RHO FAMILY GTP-BINDING PROTEIN CDC42 IN COMPLEX WITH THE MULTIFUNCTION
1DOA	A B	B	STRUCTURE OF THE RHO FAMILY GTP-BINDING PROTEIN CDC42 IN COMPLEX WITH THE MULTIFUNCTION
1DS6	A B	A	CRYSTAL STRUCTURE OF A RAC-RHOGDI COMPLEX
1E44	B A	B	RIBONUCLEASE DOMAIN OF COLICIN E3 IN COMPLEX WITH ITS IMMUNITY PROTEIN
1EM8	A B	B	CRYSTAL STRUCTURE OF CHI AND PSI SUBUNIT HETERODIMER FROM DNA POL III
1ES7	A D	D	COMPLEX BETWEEN BMP-2 AND TWO BMP RECEPTOR IA ECTODOMAINS
1ES7	C B	B	COMPLEX BETWEEN BMP-2 AND TWO BMP RECEPTOR IA ECTODOMAINS
1EUV	A B	A	X-RAY STRUCTURE OF THE C-TERMINAL ULP1 PROTEASE DOMAIN IN COMPLEX WITH SMT3, THE YEAST O
1EUV	A B	A	X-RAY STRUCTURE OF THE C-TERMINAL ULP1 PROTEASE DOMAIN IN COMPLEX WITH SMT3, THE YEAST O
1F47	B A	A	THE BACTERIAL CELL-DIVISION PROTEIN ZIPA AND ITS INTERACTION WITH AN FTSZ FRAGMENT REVEAL
1FM6	U X	U	THE 2.1 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HETERODIMER OF THE HUMAN RXRALPH
1FOE	C D	C	CRYSTAL STRUCTURE OF RAC1 IN COMPLEX WITH THE GUANINE NUCLEOTIDE EXCHANGE REGION OF TI
1FOE	C D	C	CRYSTAL STRUCTURE OF RAC1 IN COMPLEX WITH THE GUANINE NUCLEOTIDE EXCHANGE REGION OF TI
1FOE	C D	C	CRYSTAL STRUCTURE OF RAC1 IN COMPLEX WITH THE GUANINE NUCLEOTIDE EXCHANGE REGION OF TI
1FOE	C D	D	CRYSTAL STRUCTURE OF RAC1 IN COMPLEX WITH THE GUANINE NUCLEOTIDE EXCHANGE REGION OF TI
1FQV	A B	A	INSIGHTS INTO SCF UBIQUITIN LIGASES FROM THE STRUCTURE OF THE SKP1-SKP2 COMPLEX
1FQV	E F	E	INSIGHTS INTO SCF UBIQUITIN LIGASES FROM THE STRUCTURE OF THE SKP1-SKP2 COMPLEX
1H2M	A S	S	FACTOR INHIBITING HIF-1 ALPHA IN COMPLEX WITH HIF-1 ALPHA FRAGMENT PEPTIDE
1H3O	A B	B	CRYSTAL STRUCTURE OF THE HUMAN TAF4-TAF12 (TAFII135-TAFII20) COMPLEX
1H4L	A D	D	STRUCTURE AND REGULATION OF THE CDK5-P25(NCK5A) COMPLEX
1H59	A B	B	COMPLEX OF IGFBP-5 WITH IGF-I
1H6K	A X	X	NUCLEAR CAP BINDING COMPLEX
1HE1	A C	A	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE GAP DOMAIN OF THE PSEUDOMONAS AERUGINOS
1HH4	A D	A	RAC1-RHOGDI COMPLEX INVOLVED IN NADPH OXIDASE ACTIVATION
1HH4	B E	B	RAC1-RHOGDI COMPLEX INVOLVED IN NADPH OXIDASE ACTIVATION
1HH4	B E	E	RAC1-RHOGDI COMPLEX INVOLVED IN NADPH OXIDASE ACTIVATION
1HV2	A B	B	SOLUTION STRUCTURE OF YEAST ELONGIN C IN COMPLEX WITH A VON HIPPEL-LINDAU PEPTIDE
1HWM	A B	A	EBULIN,ORTHORHOMBIC CRYSTAL FORM MODEL
1I7W	C D	D	BETA-CATENIN/PHOSPHORYLATED E-CADHERIN COMPLEX
1IWQ	A B	A	CRYSTAL STRUCTURE OF MARCKS CALMODULIN BINDING DOMAIN PEPTIDE COMPLEXED WITH CA2+/CA
1J1D	B C	C	CRYSTAL STRUCTURE OF THE 46KDA DOMAIN OF HUMAN CARDIAC TROPONIN IN THE CA2+ SATURATED
1J2J	A B	A	CRYSTAL STRUCTURE OF GGA1 GAT N-TERMINAL REGION IN COMPLEX WITH ARF1 GTP FORM
1JPW	B E	E	CRYSTAL STRUCTURE OF A HUMAN TCF-4 / BETA-CATENIN COMPLEX
1KBH	A B	A	MUTUAL SYNERGISTIC FOLDING IN THE INTERACTION BETWEEN NUCLEAR RECEPTOR COACTIVATORS C
1KI1	A B	A	GUANINE NUCLEOTIDE EXCHANGE REGION OF INTERSECTIN IN COMPLEX WITH CDC42
1L2W	A I	I	CRYSTAL STRUCTURE OF THE YERSINIA VIRULENCE EFFECTOR YOPE CHAPERONE-BINDING DOMAIN IN C
1L8C	A B	B	STRUCTURAL BASIS FOR HIF-1ALPHA/CBP RECOGNITION IN THE CELLULAR HYPOXIC RESPONSE
1LB1	C D	D	CRYSTAL STRUCTURE OF THE DBL AND PLECKSTRIN HOMOLOGY DOMAINS OF DBS IN COMPLEX WITH R
1LB1	E F	F	CRYSTAL STRUCTURE OF THE DBL AND PLECKSTRIN HOMOLOGY DOMAINS OF DBS IN COMPLEX WITH R
1LQB	B C	B	CRYSTAL STRUCTURE OF A HYDROXYLATED HIF-1 ALPHA PEPTIDE BOUND TO THE PVHL/ELONGIN-C/ELO
1LQB	B C	C	CRYSTAL STRUCTURE OF A HYDROXYLATED HIF-1 ALPHA PEPTIDE BOUND TO THE PVHL/ELONGIN-C/ELO
1LTX	A R	A	STRUCTURE OF RAB ESCORT PROTEIN-1 IN COMPLEX WITH RAB GERANYLGERANYL TRANSFERASE AND
1LTX	A R	R	STRUCTURE OF RAB ESCORT PROTEIN-1 IN COMPLEX WITH RAB GERANYLGERANYL TRANSFERASE AND
1MDU	A B	A	CRYSTAL STRUCTURE OF THE CHICKEN ACTIN TRIMER COMPLEXED WITH HUMAN GELSOLIN SEGMENT 1

TABLE S2

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. $\Delta\Delta G_{SUM, CHAIN}$ (KCAL/MOL)	I. HELIX CONTRIBUTION
1A0O	CHEMOTAXIS	2.0	4.1	4.1	100%
1A0O	CHEMOTAXIS	2.2	4.4	4.4	100%
1A4Y	COMPLEX (INHIBITOR/NUCLEASE)	2.0	3.9	5.1	76%
1A9N	RNA BINDING PROTEIN/RNA	2.0	3.9	3.9	100%
1AY7	COMPLEX (ENZYME/INHIBITOR)	2.2	4.4	7.7	57%
1B0N	TRANSCRIPTION REGULATOR	2.0	5.9	27.4	22%
1B27	HYDROLASE/HYDROLASE INHIBITOR	3.2	6.3	11.2	56%
1B9X	SIGNALING PROTEIN	2.4	7.2	18.4	39%
1BDJ	COMPLEX (CHEMOTAXIS/TRANSFERASE)	2.1	4.1	8.0	51%
1BXL	COMPLEX (APOPTOSIS/PEPTIDE)	2.4	4.8	7.1	68%
1D2Z	APOPTOSIS	2.0	4.0	5.7	70%
1DE4	METAL TRANSPORT INHIBITOR/RECEPTOR	2.0	3.9	14.5	27%
1DML	DNA BINDING PROTEIN/TRANSFERASE	3.8	7.6	14.4	53%
1DOA	CELL CYCLE	2.0	6.0	8.4	71%
1DOA	CELL CYCLE	2.3	4.5	10.4	43%
1DS6	SIGNALING PROTEIN	2.5	4.9	13.4	37%
1E44	RIBONUCLEASE	4.0	8.0	11.4	70%
1EM8	GENE REGULATION	3.5	7.0	11.5	61%
1ES7	CYTOKINE	2.5	4.9	4.9	100%
1ES7	CYTOKINE	2.1	4.2	4.2	100%
1EUV	HYDROLASE	3.5	6.9	23.4	29%
1EUV	HYDROLASE	2.6	5.1	23.4	22%
1F47	CELL CYCLE	2.3	4.5	7.4	61%
1FM6	TRANSCRIPTION	2.1	4.2	5.6	75%
1FOE	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	3.5	10.6	24.2	44%
1FOE	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	2.9	8.6	24.2	36%
1FOE	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	4.0	7.8	24.2	32%
1FOE	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALING	2.0	4.0	32.8	12%
1FQV	LIGASE	2.0	8.1	11.7	69%
1FQV	LIGASE	3.3	6.6	12.5	53%
1H2M	TRANSCRIPTION ACTIVATOR/INHIBITOR	2.3	4.5	5.5	82%
1H3O	TRANSCRIPTION/TBP-ASSOCIATED FACTORS	2.1	4.1	14.3	29%
1H4L	KINASE/KINASE ACTIVATOR	2.8	5.6	11.7	48%
1H59	INSULIN	2.2	4.4	6.1	72%
1H6K	NUCLEAR PROTEIN	2.2	4.3	9.4	46%
1HE1	SIGNALING PROTEIN	2.4	4.7	9.5	49%
1HH4	SIGNALING PROTEIN/INHIBITOR	2.6	5.1	9.1	56%
1HH4	SIGNALING PROTEIN/INHIBITOR	2.2	4.3	13.6	32%
1HH4	SIGNALING PROTEIN/INHIBITOR	2.2	4.3	7.1	61%
1HV2	SIGNALING PROTEIN	2.2	4.3	4.3	100%
1HWM	HYDROLASE	2.1	4.1	9.2	45%
1I7W	CELL ADHESION	2.1	4.1	22.7	18%
1IWQ	METAL BINDING PROTEIN/PROTEIN BINDING	2.5	4.9	22.1	22%
1J1D	CONTRACTILE PROTEIN	2.0	4.0	19.6	20%
1J2J	PROTEIN TRANSPORT	2.4	4.7	8.3	57%
1JPW	CELL ADHESION	2.1	4.1	14.0	29%
1KBH	TRANSCRIPTION	2.2	4.3	7.8	55%
1KI1	SIGNALING PROTEIN	2.7	5.3	7.3	73%
1L2W	CHAPERONE	2.1	4.1	8.3	49%
1L8C	GENE REGULATION	2.3	4.6	16.8	27%
1LB1	SIGNALING PROTEIN	2.1	4.1	16.3	25%
1LB1	SIGNALING PROTEIN	2.0	3.9	10.6	37%
1LQB	GENE REGULATION	2.3	4.5	13.8	33%
1LQB	GENE REGULATION	2.5	7.6	10.6	72%
1LTX	TRANSFERASE/PROTEIN BINDING	2.4	4.7	6.6	71%
1LTX	TRANSFERASE/PROTEIN BINDING	3.2	6.3	9.7	65%
1MDU	STRUCTURAL PROTEIN	2.2	6.5	11.0	59%

TABLE S2

A. PDB CODE	J. # HOTSPOT RESIDUES	K. HOTSPOT RESIDUES, RESIDUE #, $\Delta\Delta G_{(KCAL/MOL)}$	L. HOTSPOT RESIDUE HELIX POSITIONS	M. HOTSPOT RESIDUE END TO END LENGTH
1A0O	2	K122, 2.0; E125, 2.0;	i; i+3;	4
1A0O	2	V211, 1.1; F214, 3.3;	i; i+3;	4
1A4Y	2	R5, 1.9; H8, 2.0;	i; i+3;	4
1A9N	2	R28, 1.8; Y31, 2.1;	i; i+3;	4
1AY7	2	D35, 1.5; D39, 2.9;	i; i+4;	5
1B0N	3	I32, 1.1; Y35, 2.6; L36, 2.2;	i; i+3; i+4;	5
1B27	2	D36, 1.5; D40, 4.8;	i; i+4;	5
1B9X	3	F540, 3.8; Y543, 2.4; V544, 1.0;	i; i+3; i+4;	5
1BDJ	2	E750, 1.3; E754, 2.8;	i; i+4;	5
1BXL	2	L578, 2.7; I581, 2.1;	i; i+3;	4
1D2Z	2	N112, 1.6; R115, 2.4;	i; i+3;	4
1DE4	2	E146, 1.6; H150, 2.3;	i; i+4;	5
1DML	2	F1231, 5.2; L1234, 2.4;	i; i+3;	4
1DOA	3	R66, 2.8; L67, 2.2; R68, 1.0;	i; i+1; i+2;	3
1DOA	2	Y51, 2.8; L55, 1.7;	i; i+4;	5
1DS6	2	R66, 1.6; L67, 3.3;	i; i+1;	2
1E44	2	F2, 5.4; Y5, 2.6;	i; i+3;	4
1EM8	2	R118, 1.6; W122, 5.4;	i; i+4;	5
1ES7	2	F785, 3.3; K788, 1.6;	i; i+3;	4
1ES7	2	F285, 2.6; K288, 1.6;	i; i+3;	4
1EUV	2	D451, 4.6; E455, 2.3;	i; i+4;	5
1EUV	2	F474, 3.3; T477, 1.8;	i; i+3;	4
1F47	2	F11, 2.1; I8, 2.4;	i; i+3;	4
1FM6	2	E394, 1.2; Y397, 3.0;	i; i+3;	4
1FOE	3	K1195, 4.4; L1198, 5.0; L1199, 1.2;	i; i+3; i+4;	5
1FOE	3	I1187, 1.2; I1190, 3.6; Q1191, 3.8;	i; i+3; i+4;	5
1FOE	2	I1231, 3.7; N1232, 4.1;	i; i+1;	2
1FOE	2	R66, 2.1; L67, 1.9;	i; i+1;	2
1FQV	4	K137, 1.9; R138, 1.2; W139, 2.5; Y140, 2.5;	i; i+1; i+2; i+3;	4
1FQV	2	K131, 2.8; S133, 3.8;	i; i+2;	3
1H2M	2	L818, 2.1; L819, 2.4;	i; i+1;	2
1H3O	2	L66, 2.6; V70, 1.5;	i; i+4;	5
1H4L	2	W258, 3.2; L262, 2.4;	i; i+4;	5
1H59	2	L70, 3.1; L74, 1.3;	i; i+4;	5
1H6K	2	Y100, 2.6; R99, 1.7;	i; i+1;	2
1HE1	2	Q182, 2.0; Q183, 2.7;	i; i+1;	2
1HH4	2	H103, 3.1; H104, 2.0;	i; i+1;	2
1HH4	2	R66, 2.4; L67, 1.9;	i; i+1;	2
1HH4	2	Y351, 2.5; L355, 1.8;	i; i+4;	5
1HV2	2	L158, 3.2; R161, 1.1;	i; i+3;	4
1HWM	2	E235, 2.8; I239, 1.3;	i; i+4;	5
1I7W	2	K717, 1.1; L718, 3.0;	i; i+1;	2
1IWQ	2	L105, 1.2; M109, 3.7;	i; i+4;	5
1J1D	2	K72, 2.9; L76, 1.1;	i; i+4;	5
1J2J	2	L77, 2.7; H80, 2.0;	i; i+3;	4
1JPW	2	V44, 2.0; K45, 2.1;	i; i+1;	2
1KBH	2	I34, 3.0; V38, 1.3;	i; i+4;	5
1KI1	2	L67, 3.0; L70, 2.3;	i; i+3;	4
1L2W	2	Y39, 1.9; L43, 2.2;	i; i+4;	5
1L8C	2	L141, 2.4; L145, 2.2;	i; i+4;	5
1LB1	2	L69, 1.9; L72, 2.2;	i; i+3;	4
1LB1	2	H105, 2.0; F106, 1.9;	i; i+1;	2
1LQB	2	L101, 1.4; L104, 3.1;	i; i+3;	4
1LQB	3	L158, 3.5; K159, 1.2; R161, 2.9;	i; i+1; i+3;	4
1LTX	2	Q216, 2.4; F220, 2.3;	i; i+4;	5
1LTX	2	R275, 3.5; F279, 2.8;	i; i+4;	5
1MDU	3	I79, 2.3; F80, 3.2; V82, 1.0;	i; i+1; i+3;	4

A. PDB CODE	N. HELIX LENGTH	O. HELIX START RESIDUE #	P. HELIX END RESIDUE #	Q. HELIX SEQUENCE	R. RESOLUTION
1A0O	14	113	126	AATLEEKLNKIFEK	2.95
1A0O	12	205	216	EDDITAVLCFVI	2.95
1A4Y	9	5	13	RYTHFLTQH	2.00
1A9N	12	23	34	KEELKRSLYALF	2.38
1AY7	9	34	42	LDALWDCLT	1.70
1B0N	11	29	39	PEEIRKYLLLN	1.90
1B27	9	35	43	LDALWDALT	2.10
1B9X	14	533	546	VSKCCEEFRDYVEE	3.00
1BDJ	15	744	758	WEDNVGEWIEEMKEE	2.68
1BXL	9	576	584	RQLAIIGDD	NOT APP
1D2Z	7	111	117	HNAMRLI	2.00
1DE4	12	140	151	AWPTKLEWERHK	2.80
1DML	16	1220	1235	AEETRRMLHRAFDTLA	2.70
1DOA	5	65	69	DRLRP	2.60
1DOA	12	46	57	ESLRKYKEALLG	2.60
1DS6	5	65	69	DRLRP	2.35
1E44	6	2	7	FKDYGH	2.40
1EM8	14	115	128	PTARAALWQQICTY	2.10
1ES7	7	783	789	SDFQCKD	2.90
1ES7	7	283	289	SDFQCKD	2.90
1EUV	14	451	464	DTIIEFFMKYIEKS	1.60
1EUV	10	473	482	SFFYTNLSER	1.60
1F47	9	8	16	IPAFLRKQA	1.95
1FM6	23	386	408	PAEVEALREKVYASLEAYCKHKY	2.10
1FOE	12	1195	1206	KYPLLLRELFAL	2.80
1FOE	8	1187	1194	IKPIQRVL	2.80
1FOE	8	1226	1233	KVASHINE	2.80
1FOE	5	65	69	DRLRP	2.80
1FQV	8	137	144	KRWYRLAS	2.80
1FQV	9	126	134	LPELLKVSG	2.80
1H2M	7	816	822	EELLRAL	2.50
1H3O	12	60	71	KKKLQDLVREVD	2.30
1H4L	15	254	268	KEAFWDRCLSVINLM	2.65
1H59	7	69	75	PLHALLH	2.10
1H6K	12	91	102	RADAENAMRYIN	2.00
1HE1	5	181	185	LQQWG	2.00
1HH4	13	93	105	VRAKWYPEVRHHC	2.70
1HH4	5	65	69	DRLRP	2.70
1HH4	12	346	357	ESLRKYKEALLG	2.70
1HV2	14	158	171	LKERCLQVVRSLVK	NOT APP
1HWM	9	233	241	FEELYKITG	2.80
1I7W	7	716	722	KKLADMY	2.00
1IWQ	11	102	112	AAELRHVMTNL	2.00
1J1D	18	63	80	REAEERRGEKGRALSTRA	2.61
1J2J	7	75	81	RPLWRHY	1.60
1JPW	6	42	47	ADVKSS	2.50
1KBH	8	34	41	IPELVNQG	NOT APP
1KI1	7	67	73	LRPLSYP	2.30
1L2W	8	38	45	QYANNLAG	2.00
1L8C	11	139	149	EELLRALDQVN	NOT APP
1LB1	7	69	75	LRPLSYP	2.81
1LB1	19	89	107	PDSLENIPEKWTPEVKHFC	2.81
1LQB	11	100	110	ALELLMAANFL	2.00
1LQB	11	158	168	LKERCLQVVRS	2.00
1LTX	18	205	222	ENVLLKELELVQNAFFTD	2.70
1LTX	7	275	281	RADVFNS	2.70
1MDU	18	71	88	QDESGAAAIFTVQLDDYL	2.20

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1MF8	A B	A	CRYSTAL STRUCTURE OF HUMAN CALCINEURIN COMPLEXED WITH CYCLOSPORIN A AND HUMAN CYCLO
1MZN	C D	D	CRYSTAL STRUCTURE AT 1.9 ANGSTROEMS RESOLUTION OF THE HOMODIMER OF HUMAN RXR ALPHA LIG
1N1J	A B	B	CRYSTAL STRUCTURE OF THE NF-YB/NF-YC HISTONE PAIR
1NRL	B D	D	CRYSTAL STRUCTURE OF THE HUMAN PXR-LBD IN COMPLEX WITH AN SRC-1 COACTIVATOR PEPTIDE AND
1NU7	E F	E	STAPHYLOCOAGULASE-THROMBIN COMPLEX
1OL5	A B	B	STRUCTURE OF AURORA-A 122-403, PHOSPHORYLATED ON THR287, THR288 AND BOUND TO TPX2 1-43
1OOK	A B	A	CRYSTAL STRUCTURE OF THE COMPLEX OF PLATELET RECEPTOR GPIB- ALPHA AND HUMAN ALPHA-THRO
1OR7	A C	A	CRYSTAL STRUCTURE OF ESCHERICHIA COLI SIGMAE WITH THE CYTOPLASMIC DOMAIN OF ITS ANTI-SIG
1OR7	A C	A	CRYSTAL STRUCTURE OF ESCHERICHIA COLI SIGMAE WITH THE CYTOPLASMIC DOMAIN OF ITS ANTI-SIG
1OSV	B D	D	STRUCTURAL BASIS FOR BILE ACID BINDING AND ACTIVATION OF THE NUCLEAR RECEPTOR FXR
1QLS	A D	D	S100C (S100A11),OR CALGIZZARIN, IN COMPLEX WITH ANNEXIN I N-TERMINUS
1R4A	A E	E	CRYSTAL STRUCTURE OF GTP-BOUND ADP-RIBOSYLATION FACTOR LIKE PROTEIN 1 (ARL1) AND GRIP DO
1R8Q	A E	A	FULL-LENGTH ARF1-GDP-MG IN COMPLEX WITH BREFELDIN A AND A SEC7 DOMAIN
1RP3	A B	B	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1T0F	B D	D	CRYSTAL STRUCTURE OF THE TNSA/TNSC(504-555) COMPLEX
1TTW	A B	B	CRYSTAL STRUCTURE OF THE YERSINIA PESTIS TYPE III SECRETION CHAPERONE SYCH IN COMPLEX WIT
1TUE	A B	B	THE X-RAY STRUCTURE OF THE PAPILLOMAVIRUS HELICASE IN COMPLEX WITH ITS MOLECULAR MATCH
1TUE	H J	H	THE X-RAY STRUCTURE OF THE PAPILLOMAVIRUS HELICASE IN COMPLEX WITH ITS MOLECULAR MATCH
1TY4	A C	C	CRYSTAL STRUCTURE OF A CED-9/EGL-1 COMPLEX
1U0S	Y A	A	CHEMOTAXIS KINASE CHEA P2 DOMAIN IN COMPLEX WITH RESPONSE REGULATOR CHEY FROM THE THE
1U0S	Y A	Y	CHEMOTAXIS KINASE CHEA P2 DOMAIN IN COMPLEX WITH RESPONSE REGULATOR CHEY FROM THE THE
1U7B	A B	B	CRYSTAL STRUCTURE OF HPCNA BOUND TO RESIDUES 331-350 OF THE FLAP ENDONUCLEASE-1 (FEN1)
1U8T	B F	F	CRYSTAL STRUCTURE OF CHEY D13K Y106W ALONE AND IN COMPLEX WITH A FLIM PEPTIDE
1VCB	B C	B	THE VHL-ELONGINC-ELONGINB STRUCTURE
1X86	G H	H	CRYSTAL STRUCTURE OF THE DH/PH DOMAINS OF LEUKEMIA- ASSOCIATED RHOGEF IN COMPLEX WITH R
1XCG	A B	B	CRYSTAL STRUCTURE OF HUMAN RHOA IN COMPLEX WITH DH/PH FRAGMENT OF PDZRHOGEF
1XIU	A E	E	CRYSTAL STRUCTURE OF THE AGONIST-BOUND LIGAND-BINDING DOMAIN OF BIOMPHALARIA GLABRAT
1XL3	A C	A	COMPLEX STRUCTURE OF Y.PESTIS VIRULENCE FACTORS YOPN AND TYEA
1XLS	A E	A	CRYSTAL STRUCTURE OF THE MOUSE CAR/RXR LBD HETERODIMER BOUND TO TCPOBOP AND 9CRA AND
1XV9	C G	G	CRYSTAL STRUCTURE OF CAR/RXR HETERODIMER BOUND WITH SRC1 PEPTIDE, FATTY ACID, AND 5B-PRE
1Y3A	A E	E	STRUCTURE OF G-ALPHA-I1 BOUND TO A GDP-SELECTIVE PEPTIDE PROVIDES INSIGHT INTO GUANINE NU
1YCR	A B	B	MDM2 BOUND TO THE TRANSACTIVATION DOMAIN OF P53
1YOK	A B	B	CRYSTAL STRUCTURE OF HUMAN LRH-1 BOUND WITH TIF-2 PEPTIDE AND PHOSPHATIDYLGLYCEROL
1Z2C	A B	A	CRYSTAL STRUCTURE OF MDIA1 GBD-FH3 IN COMPLEX WITH RHOC- GMPPNP
1Z56	A C	A	CO-CRYSTAL STRUCTURE OF LIF1P-LIG4P
1ZNV	C D	C	HOW A HIS-METAL FINGER ENDONUCLEASE COLE7 BINDS AND CLEAVES DNA WITH A TRANSITION METAL
1ZOQ	A C	C	IRF3-CBP COMPLEX
1ZOQ	B D	D	IRF3-CBP COMPLEX
1ZVV	B P	P	CRYSTAL STRUCTURE OF A CCPA-CRH-DNA COMPLEX
2A19	A B	B	PKR KINASE DOMAIN- EIF2ALPHA- AMP-PNP COMPLEX.
2A45	A B	A	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THROMBIN AND THE CENTRAL "E" REGION OF FIBRIN
2A4J	A B	B	SOLUTION STRUCTURE OF THE C-TERMINAL DOMAIN (T94-Y172) OF THE HUMAN CENTRIN 2 IN COMPLEX
2AGH	B C	C	STRUCTURAL BASIS FOR COOPERATIVE TRANSCRIPTION FACTOR BINDING TO THE CBP COACTIVATOR
2B5L	A C	C	CRYSTAL STRUCTURE OF DDB1 IN COMPLEX WITH SIMIAN VIRUS 5 V PROTEIN
2C9W	A C	C	CRYSTAL STRUCTURE OF SOCS-2 IN COMPLEX WITH ELONGIN-B AND ELONGIN-C AT 1.9A RESOLUTION
2CCL	C D	D	THE S45A, T46A MUTANT OF THE TYPE I COHESIN-DOCKERIN COMPLEX FROM THE CELLULOSOME OF CL
2DWZ	A B	B	STRUCTURE OF THE ONCOPROTEIN GANKYRIN IN COMPLEX WITH S6 ATPASE OF THE 26S PROTEASOME
2EHB	A D	D	THE STRUCTURE OF THE C-TERMINAL DOMAIN OF THE PROTEIN KINASE ATSOS2 BOUND TO THE CALCIU
2EKV	A B	A	THE CRYSTAL STRUCTURE OF RIGOR LIKE SQUID MYOSIN S1 IN THE ABSENCE OF NUCLEOTIDE
2EKV	A B	A	THE CRYSTAL STRUCTURE OF RIGOR LIKE SQUID MYOSIN S1 IN THE ABSENCE OF NUCLEOTIDE
2ERJ	F H	H	CRYSTAL STRUCTURE OF THE HETEROTRIMERIC INTERLEUKIN-2 RECEPTOR IN COMPLEX WITH INTERLE
2F93	A B	B	K INTERMEDIATE STRUCTURE OF SENSORY RHODOPSIN II/TRANSDUCER COMPLEX IN COMBINATION WIT
2FM8	B C	C	CRYSTAL STRUCTURE OF THE SALMONELLA SECRETION CHAPERONE INVB IN COMPLEX WITH SIPA
2FNJ	A C	A	CRYSTAL STRUCTURE OF A B30.2/SPRY DOMAIN-CONTAINING PROTEIN GUSTAVUS IN COMPLEX WITH ELO
2FO1	D E	D	CRYSTAL STRUCTURE OF THE CSL-NOTCH-MASTERMIND TERNARY COMPLEX BOUND TO DNA
2FOI	B D	D	SYNTHESIS, BIOLOGICAL ACTIVITY, AND X-RAY CRYSTAL STRUCTURAL ANALYSIS OF DIARYL ETHER INH
2G30	A P	P	BETA APPENDAGE OF AP2 COMPLEXED WITH ARH PEPTIDE

TABLE S2

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. $\Delta\Delta G_{SUM, CHAIN}$ (KCAL/MOL)	I. HELIX CONTRIBUTION
1MF8	HYDROLASE, LIGASE	2.9	8.6	33.6	26%
1MZN	TRANSCRIPTION	2.1	6.2	7.8	79%
1N1J	DNA BINDING PROTEIN	2.6	5.1	43.7	12%
1NRL	TRANSCRIPTION	2.0	6.0	6.0	100%
1NU7	HYDROLASE/PROTEIN BINDING	2.2	4.3	5.3	81%
1OL5	TRANSFERASE/CELL CYCLE	3.0	6.0	18.6	32%
1OOK	HYDROLASE	2.1	6.2	15.3	41%
1OR7	TRANSCRIPTION	2.2	4.4	31.9	14%
1OR7	TRANSCRIPTION	2.0	4.0	31.9	13%
1OSV	DNA BINDING PROTEIN	2.3	4.6	4.6	100%
1QLS	METAL-BINDING PROTEIN/INHIBITOR	7.8	15.5	15.5	100%
1R4A	PROTEIN TRANSPORT	2.1	4.2	10.5	40%
1R8Q	PROTEIN TRANSPORT/EXCHANGE FACTOR	2.5	4.9	14.3	34%
1RP3	TRANSCRIPTION	2.2	4.4	31.0	14%
1T0F	DNA BINDING PROTEIN	2.2	4.4	18.9	23%
1TTW	CHAPERONE	2.2	4.3	11.4	38%
1TUE	REPLICATION	2.7	8.1	13.8	59%
1TUE	REPLICATION	2.5	5.0	16.6	30%
1TY4	APOPTOSIS	2.0	6.0	13.8	43%
1U0S	SIGNALING PROTEIN	2.5	7.4	7.4	100%
1U0S	SIGNALING PROTEIN	2.1	4.1	13.7	30%
1U7B	REPLICATION	3.0	6.0	6.0	100%
1U8T	SIGNALING PROTEIN	2.0	5.9	7.6	78%
1VCB	TRANSCRIPTION	2.1	4.1	10.1	41%
1X86	SIGNALING PROTEIN/MEMBRANE PROTEIN	3.1	6.1	14.8	41%
1XCG	SIGNALING PROTEIN ACTIVATOR/SIGNALING PR	2.9	5.8	18.5	31%
1XIU	TRANSCRIPTION/TRANSFERASE	2.2	8.8	8.8	100%
1XL3	CELL INVASION	4.0	12.0	16.6	72%
1XLS	TRANSCRIPTION	3.3	6.6	9.5	69%
1XV9	DNA BINDING PROTEIN	2.7	5.4	6.4	84%
1Y3A	SIGNALING PROTEIN	3.1	9.3	9.3	100%
1YCR	COMPLEX (ONCOGENE PROTEIN/PEPTIDE)	3.7	11.1	12.9	86%
1YOK	TRANSCRIPTION	2.8	8.3	8.3	100%
1Z2C	SIGNALING PROTEIN	2.6	5.1	15.1	34%
1Z56	LIGASE	4.3	12.9	12.9	100%
1ZNV	HYDROLASE/PROTEIN BINDING	2.5	4.9	9.5	52%
1ZOQ	TRANSCRIPTION/TRANSFERASE	2.1	4.2	7.6	55%
1ZOQ	TRANSCRIPTION/TRANSFERASE	2.0	4.0	8.2	49%
1ZVV	TRANSCRIPTION/DNA	2.2	4.4	4.4	100%
2A19	PROTEIN SYNTHESIS/TRANSFERASE	3.4	6.7	6.7	100%
2A45	BLOOD CLOTTING	2.1	4.1	4.1	100%
2A4J	STRUCTURAL PROTEIN	3.1	6.2	14.7	42%
2AGH	TRANSCRIPTION	2.3	6.9	8.2	84%
2B5L	PROTEIN BINDING/VIRAL PROTEIN	2.4	4.7	8.4	56%
2C9W	TRANSCRIPTION REGULATION	2.1	6.3	9.1	69%
2CCL	CELL ADHESION	2.8	5.6	8.3	67%
2DWZ	ONCOPROTEIN	2.4	7.2	12.5	58%
2EHB	SIGNALLING PROTEIN/TRANSFERASE	3.0	8.9	17.9	50%
2EKV	CONTRACTILE PROTEIN	2.9	8.6	16.3	53%
2EKV	CONTRACTILE PROTEIN	3.0	5.9	16.3	36%
2ERJ	IMMUNE SYSTEM/CYTOKINE	2.0	3.9	9.7	40%
2F93	MEMBRANE PROTEIN	2.2	4.3	7.2	60%
2FM8	CHAPERONE/CELL INVASION	2.2	4.3	4.3	100%
2FNJ	PROTEIN TRANSPORT/SIGNALING PROTEIN	3.1	6.1	6.1	100%
2FO1	GENE REGULATION/SIGNALLING PROTEIN/DNA	2.2	4.3	5.3	81%
2FOI	OXIDOREDUCTASE	2.9	5.7	8.9	64%
2G30	ENDOCYTOSIS/EXOCYTOSIS	3.3	6.6	11.1	59%

TABLE S2

A. PDB CODE	J. # HOTSPOT RESIDUES	K. HOTSPOT RESIDUES, RESIDUE #, $\Delta\Delta G_{(KCAL/MOL)}$	L. HOTSPOT RESIDUE HELIX POSITIONS	M. HOTSPOT RESIDUE END TO END LENGTH
1MF8	3	F350, 4.8; W352, 1.4; L354, 2.4;	i; i+2; i+4;	5
1MZN	3	L1475, 2.2; L1478, 1.4; L1479, 2.6;	i; i+3; i+4;	5
1N1J	2	R47, 1.5; I51, 3.6;	i; i+4;	5
1NRL	3	L690, 2.6; H691, 1.0; L694, 2.4;	i; i+1; i+4;	5
1NU7	2	E14, 2.6; L14, 1.7;	i; i+1;	2
1OL5	2	W34, 2.8; F35, 3.2;	i; i+1;	2
1OOK	3	E14, 1.9; E14, 2.3; L14, 2.0;	i; 1; 1;	4
1OR7	2	R171, 1.3; F175, 3.1;	i; i+4;	5
1OR7	2	F22, 1.3; L24, 2.7;	i; i+2;	3
1OSV	2	L5, 3.3; R6, 1.3;	i; i+1;	2
1QLS	2	F6, 1.0; L7, 14.5;	i; i+1;	2
1R4A	2	E2174, 1.3; Y2177, 2.9;	i; i+3;	4
1R8Q	2	L77, 3.0; Y81, 1.9;	i; i+4;	5
1RP3	2	V60, 1.6; K64, 2.8;	i; i+4;	5
1T0F	2	L521, 1.5; R522, 2.9;	i; i+1;	2
1TTW	2	F45, 1.9; V49, 2.4;	i; i+4;	5
1TUE	3	I20, 1.7; Y23, 4.9; E24, 1.5;	i; i+3; i+4;	5
1TUE	2	F460, 2.8; I461, 2.2;	i; i+1;	2
1TY4	3	D63, 2.5; F65, 2.5; D66, 1.0;	i; i+2; i+3;	4
1U0S	3	R195, 2.5; Y197, 2.9; L198, 2.0;	i; i+2; i+3;	4
1U0S	2	I91, 2.2; I94, 1.9;	i; i+3;	4
1U7B	2	L340, 2.8; F343, 3.2;	i; i+3;	4
1U8T	3	I11, 2.0; D12, 1.5; Q8, 2.4;	i; i+3; i+4;	5
1VCB	2	L101, 1.5; L104, 2.6;	i; i+3;	4
1X86	2	D67, 3.5; L69, 2.6;	i; i+2;	3
1XCG	2	L69, 3.7; L72, 2.1;	i; i+3;	4
1XIU	4	L690, 1.8; H691, 2.2; L693, 1.9; L694, 2.9;	i; i+1; i+3; i+4;	5
1XL3	3	F278, 4.7; W279, 4.4; F282, 2.9;	i; i+1; i+4;	5
1XLS	2	R426, 2.0; S427, 4.6;	i; i+1;	2
1XV9	2	I632, 4.3; L633, 1.1;	i; i+1;	2
1Y3A	3	W5, 4.2; F8, 3.3; L9, 1.8;	i; i+3; i+4;	5
1YCR	3	F19, 2.5; L22, 2.5; W23, 6.1;	i; i+3; i+4;	5
1YOK	3	L745, 2.9; L748, 2.7; L749, 2.7;	i; i+3; i+4;	5
1Z2C	2	R68, 4.0; L69, 1.1;	i; i+1;	2
1Z56	3	R209, 1.4; M211, 1.3; M212, 10.2;	i; i+2; i+3;	3
1ZNV	2	D52, 1.3; Y55, 3.6;	i; i+3;	4
1ZOQ	2	Q2085, 2.2; I2089, 2.0;	i; i+4;	5
1ZOQ	2	L2096, 1.6; F2100, 2.4;	i; i+4;	5
1ZVV	2	I47, 2.4; M51, 2.0;	i; i+4;	5
2A19	2	F489, 5.3; E490, 1.4;	i; i+1;	2
2A45	2	E14, 1.6; L14, 2.5;	i; 1;	2
2A4J	2	2, 4.2; 5, 2.0;	i; i+3;	4
2AGH	3	I849, 2.0; F852, 3.8; V853, 1.1;	i; i+3; i+4;	5
2B5L	2	V24, 2.1; F27, 2.6;	i; i+3;	4
2C9W	3	L101, 2.2; L103, 1.0; L104, 3.1;	i; i+2; i+3;	4
2CCL	2	K18, 1.9; R19, 3.7;	i; i+1;	2
2DWZ	3	R338, 2.1; R339, 1.4; R342, 3.7;	i; i+1; i+4;	5
2EHB	3	F313, 5.6; M315, 1.3; I316, 2.0;	i; i+2; i+3;	4
2EKV	3	W828, 6.2; W829, 1.1; L831, 1.3;	i; i+1; i+3;	4
2EKV	2	K819, 2.5; L821, 3.4;	i; i+3;	3
2ERJ	2	H16, 2.9; L19, 1.0;	i; i+3;	4
2F93	2	I69, 2.1; I73, 2.2;	i; i+4;	5
2FM8	2	F54, 3.0; I58, 1.3;	i; i+4;	5
2FNJ	2	L241, 4.7; C245, 1.4;	i; i+4;	5
2FO1	2	L69, 3.1; H70, 1.2;	i; i+1;	2
2FOI	2	F368, 3.9; I369, 1.8;	i; i+1;	2
2G30	2	L11, 1.5; F8, 5.1;	i; i+3;	4

A. PDB CODE	N. HELIX LENGTH	O. HELIX START RESIDUE #	P. HELIX END RESIDUE #	Q. HELIX SEQUENCE	R. RESOLUTION
1MF8	10	349	358	VFTWSLPFVG	3.10
1MZN	9	1473	1481	KILHRLLQD	1.90
1N1J	9	45	53	LARIKKIMK	1.67
1NRL	9	688	696	KILHRLLQE	2.00
1NU7	8	14	14	ERELLESY	2.20
1OL5	9	33	41	SWFEEKANL	2.50
1OOK	7	14	14	ERELLES	2.30
1OR7	20	167	186	VGTVRSRIFRAREAIDNKVQ	2.00
1OR7	11	19	29	QKAFNLLVVRY	2.00
1OSV	8	3	10	ALLRYLLD	2.50
1QLS	9	2	10	MVSAFLKQA	2.30
1R4A	15	2173	2187	TEFEYLRKVLFEYMM	2.30
1R8Q	8	75	82	RPLWRHYF	1.86
1RP3	14	56	69	LEKKVKELKEKIEK	2.30
1T0F	7	521	527	LRYIYSQ	1.85
1TTW	7	44	50	RFAYAVL	2.38
1TUE	23	4	26	PKETLSERLSALQDKIIDHYEND	2.10
1TUE	14	460	473	FITFLGALKSFLKG	2.10
1TY4	6	63	68	DDFDAQ	2.20
1U0S	15	192	206	KSARIYLVFHKLEEL	1.90
1U0S	10	87	96	QAMVIEAIKA	1.90
1U7B	5	340	344	LDDFF	1.88
1U8T	7	8	14	QAEIDAL	1.50
1VCB	15	97	111	PEIALELLMAANFLD	2.70
1X86	5	67	71	DRLRP	3.22
1XCG	7	69	75	LRPLSYP	2.50
1XIU	10	688	697	KILHRLLQEG	2.50
1XL3	6	278	283	FWQFFS	2.20
1XLS	29	414	442	RFAKLLLRLPALRSIGLKCLEHLFFFKLI	2.96
1XV9	7	631	637	KILHRLL	2.70
1Y3A	6	5	10	WYDFLM	2.50
1YCR	6	19	24	FSDLWK	2.60
1YOK	9	743	751	ALLRYLLDK	2.50
1Z2C	5	67	71	DRLRP	3.00
1Z56	6	209	214	RAMMVT	3.92
1ZNV	6	51	56	TDLIYY	2.00
1ZOQ	13	2080	2092	PQQQQQVLNILKS	2.37
1ZOQ	12	2094	2105	PQLMAAFIKQRT	2.37
1ZVV	8	47	54	IMGLMSLA	2.98
2A19	12	488	499	AFETSKFFTDLR	2.50
2A45	8	14	14	ERELLESY	3.65
2A4J	8	2	9	WKLLAKGL	NOT APP
2AGH	12	847	858	SDIMDFVLKNTP	NOT APP
2B5L	11	23	33	TVEYFTSQQVT	2.85
2C9W	11	100	110	ALELLMAANFL	1.90
2CCL	12	11	22	STDLTMLKRSVL	2.03
2DWZ	14	338	351	RRQKRLIFSTITSK	2.40
2EHB	6	312	317	AFEMIT	2.10
2EKV	5	828	832	WWRLF	3.40
2EKV	11	815	825	RNVRKWLVLRN	3.40
2ERJ	26	4	29	SSSTKKTQLQLEHLLLDLQMILNGIN	3.00
2F93	27	53	79	AAAVQEAAVSAILGLIILLGINLGLVA	2.00
2FM8	17	54	70	FPALIKQASLDALFKCG	2.20
2FNJ	10	241	250	LMDLCRRTIR	1.80
2FO1	17	68	84	ELHRQRSELARANYEKA	3.12
2FOI	12	368	379	FIDYAIEYSEKY	2.50
2G30	11	5	15	DEAFSRLAQSR	1.60

TABLE S2

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
2G4D	A B	A	CRYSTAL STRUCTURE OF HUMAN SENP1 MUTANT (C603S) IN COMPLEX WITH SUMO-1
2GPV	A G	G	ESTROGEN RELATED RECEPTOR-GAMMA LIGAND BINDING DOMAIN COMPLEXED WITH 4-HYDROXY-TAM
2HRK	A B	B	STRUCTURAL BASIS OF YEAST AMINOACYL-TRNA SYNTHETASE COMPLEX FORMATION REVEALED BY CR
2HUE	A B	B	STRUCTURE OF THE H3-H4 CHAPERONE ASF1 BOUND TO HISTONES H3 AND H4
2HUE	B C	C	STRUCTURE OF THE H3-H4 CHAPERONE ASF1 BOUND TO HISTONES H3 AND H4
2HWN	A E	E	CRYSTAL STRUCTURE OF RII ALPHA DIMERIZATION/DOCKING DOMAIN OF PKA BOUND TO THE D-AKAP2 P
2I2R	A E	E	CRYSTAL STRUCTURE OF THE KCHIP1/KV4.3 T1 COMPLEX
2I2R	B F	B	CRYSTAL STRUCTURE OF THE KCHIP1/KV4.3 T1 COMPLEX
2I3S	C D	D	BUB3 COMPLEX WITH BUB1 GLEBS MOTIF
2I3T	C D	D	BUB3 COMPLEX WITH MAD3 (BUBR1) GLEBS MOTIF
2IV8	A P	P	BETA APPENDAGE IN COMPLEX WITH B-ARRESTIN PEPTIDE
2J59	A M	M	CRYSTAL STRUCTURE OF THE ARF1:ARHGAP21-ARFBD COMPLEX
2JTT	A C	C	SOLUTION STRUCTURE OF CALCIUM LOADED S100A6 BOUND TO C- TERMINAL SIAH-1 INTERACTING PROT
2K8B	A B	B	SOLUTION STRUCTURE OF PLAA FAMILY UBIQUITIN BINDING DOMAIN (PFUC) CIS ISOMER IN COMPLEX W
2KA6	A B	B	NMR STRUCTURE OF THE CBP-TAZ2/STAT1-TAD COMPLEX
2OCF	A D	D	HUMAN ESTROGEN RECEPTOR ALPHA LIGAND-BINDING DOMAIN IN COMPLEX WITH ESTRADIOL AND TH
2OF5	C J	J	OLIGOMERIC DEATH DOMAIN COMPLEX
2OZN	A B	B	THE COHESIN-DOCKERIN COMPLEX OF NAGJ AND NAGH FROM CLOSTRIDIUM PERFRINGENS
2P5T	E F	E	MOLECULAR AND STRUCTURAL CHARACTERIZATION OF THE PEZAT CHROMOSOMAL TOXIN-ANTITOXIN
2PHE	A C	C	MODEL FOR VP16 BINDING TO PC4
2PMS	A C	C	CRYSTAL STRUCTURE OF THE COMPLEX OF HUMAN LACTOFERRIN N- LOBE AND LACTOFERRIN-BINDING
2POP	C D	C	THE CRYSTAL STRUCTURE OF TAB1 AND BIR1 COMPLEX
2PQR	B D	D	CRYSTAL STRUCTURE OF YEAST FIS1 COMPLEXED WITH A FRAGMENT OF YEAST CAF4
2PV2	A E	E	CRYSTALLOGRAPHIC STRUCTURE OF SURA FIRST PEPTIDYL-PROLYL ISOMERASE DOMAIN COMPLEXED W
2PV9	A B	A	CRYSTAL STRUCTURE OF MURINE THROMBIN IN COMPLEX WITH THE EXTRACELLULAR FRAGMENT OF M
2QB0	A D	D	STRUCTURE OF THE 2TEL CRYSTALLIZATION MODULE FUSED TO T4 LYSOZYME WITH AN ALA-GLY-PRO LI
2RHK	A C	C	CRYSTAL STRUCTURE OF INFLUENZA A NS1A PROTEIN IN COMPLEX WITH F2F3 FRAGMENT OF HUMAN CE
2UZ6	E O	O	ACHBP-TARGETED A-CONOTOXIN CORRELATES DISTINCT BINDING ORIENTATIONS WITH NACHR SUBTYP
2V1S	E L	L	CRYSTAL STRUCTURE OF RAT TOM20-ALDH PRESEQUENCE COMPLEX
2V1Y	A B	B	STRUCTURE OF A PHOSPHOINOSITIDE 3-KINASE ALPHA ADAPTOR- BINDING DOMAIN (ABD) IN A COMPLEX
2V52	B M	M	STRUCTURE OF MAL-RPEL2 COMPLEXED TO G-ACTIN
2VGO	A D	D	CRYSTAL STRUCTURE OF AURORA B KINASE IN COMPLEX WITH REVERSINE INHIBITOR
2VZD	B D	D	CRYSTAL STRUCTURE OF THE C-TERMINAL CALPONIN HOMOLOGY DOMAIN OF ALPHA PARVIN IN COMPL
2W2X	B C	B	COMPLEX OF RAC2 AND PLCG2 SPPH DOMAIN
2W2X	B C	C	COMPLEX OF RAC2 AND PLCG2 SPPH DOMAIN
2W84	A B	B	STRUCTURE OF PEX14 IN COMPEX WITH PEX5
2WAX	A B	B	STRUCTURE OF THE HUMAN DDX6 C-TERMINAL DOMAIN IN COMPLEX WITH AN EDC3-FDF PEPTIDE
2Z2S	G H	H	CRYSTAL STRUCTURE OF RHODOBACTER SPHAEROIDES SIGE IN COMPLEX WITH THE ANTI-SIGMA CHRR
2ZFD	A B	B	THE CRYSTAL STRUCTURE OF PLANT SPECIFIC CALCIUM BINDING PROTEIN ATCBL2 IN COMPLEX WITH TH
2ZNV	A B	A	CRYSTAL STRUCTURE OF HUMAN AMSH-LP DUB DOMAIN IN COMPLEX WITH LYS63-LINKED UBIQUITIN DI
2ZSH	A B	B	STRUCTURAL BASIS OF GIBBERELLIN(GA3)-INDUCED DELLA RECOGNITION BY THE GIBBERELLIN RECEPT
3A1G	A B	B	HIGH-RESOLUTION CRYSTAL STRUCTURE OF RNA POLYMERASE PB1-PB2 SUBUNITS FROM INFLUENZA A V
3BLH	A B	B	CRYSTAL STRUCTURE OF HUMAN CDK9/CYCLINT1
3BS5	A B	A	CRYSTAL STRUCTURE OF HCNK2-SAM/DHYP-SAM COMPLEX
3CJT	A B	A	RIBOSOMAL PROTEIN L11 METHYLTRANSFERASE (PRMA) IN COMPLEX WITH DIMETHYLATED RIBOSOMA
3CPH	G A	G	CRYSTAL STRUCTURE OF SEC4 IN COMPLEX WITH RAB-GDI
3CQX	B C	C	CHAPERONE COMPLEX
3D24	A B	B	CRYSTAL STRUCTURE OF LIGAND-BINDING DOMAIN OF ESTROGEN- RELATED RECEPTOR ALPHA (ERRALP
3D48	P R	P	CRYSTAL STRUCTURE OF A PROLACTIN RECEPTOR ANTAGONIST BOUND TO THE EXTRACELLULAR DOMA
3DA7	A D	D	A CONFORMATIONALLY STRAINED, CIRCULAR PERMUTANT OF BARNASE
3DAB	A B	B	STRUCTURE OF THE HUMAN MDMX PROTEIN BOUND TO THE P53 TUMOR SUPPRESSOR TRANSACTIVATIO
3DAB	E F	F	STRUCTURE OF THE HUMAN MDMX PROTEIN BOUND TO THE P53 TUMOR SUPPRESSOR TRANSACTIVATIO
3DAW	A B	B	STRUCTURE OF THE ACTIN-DEPOLYMERIZING FACTOR HOMOLOGY DOMAIN IN COMPLEX WITH ACTIN
3DD7	A B	B	STRUCTURE OF DOCH66Y IN COMPLEX WITH THE C-TERMINAL DOMAIN OF PHD
3EBA	A B	B	CABHUL6 FGLW MUTANT (HUMANIZED) IN COMPLEX WITH HUMAN LYSOZYME
3ECH	A C	C	THE MARR-FAMILY REPRESSOR MEXR IN COMPLEX WITH ITS ANTIREPRESSOR ARMR
3EG5	A B	A	CRYSTAL STRUCTURE OF MDIA1-TSH GBD-FH3 IN COMPLEX WITH CDC42-GMPPNP

TABLE S2

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. $\Delta\Delta G_{SUM, CHAIN}$ (KCAL/MOL)	I. HELIX CONTRIBUTION
2G4D	HYDROLASE/PROTEIN BINDING	3.6	10.8	17.9	60%
2GPV	TRANSCRIPTION	2.1	4.2	4.2	100%
2HRK	LIGASE/RNA BINDING PROTEIN	2.7	5.3	8.9	60%
2HUE	DNA BINDING PROTEIN	2.1	4.2	7.2	58%
2HUE	DNA BINDING PROTEIN	2.3	4.5	22.5	20%
2HWN	TRANSFERASE	2.1	4.1	4.1	100%
2I2R	TRANSPORT PROTEIN	2.0	3.9	8.3	47%
2I2R	TRANSPORT PROTEIN	3.4	6.7	19.2	35%
2I3S	CELL CYCLE	2.8	8.4	15.4	55%
2I3T	CELL CYCLE	2.8	5.5	17.7	31%
2IV8	ENDOCYTOSIS/REGULATOR	2.7	5.4	9.1	59%
2J59	HYDROLASE	2.1	4.2	4.2	100%
2JTT	CALCIUM BINDING PROTEIN/ANTITUMOR PROTEI	2.5	5.0	5.0	100%
2K8B	PROTEIN BINDING	2.1	6.4	6.4	100%
2KA6	TRANSCRIPTION REGULATOR	2.6	10.5	19.6	54%
2OCF	HORMONE/GROWTH FACTOR	2.2	4.4	4.4	100%
2OF5	APOPTOSIS	3.5	7.0	7.0	100%
2OZN	TOXIN	2.3	4.5	7.0	64%
2P5T	TRANSCRIPTION REGULATOR	2.1	4.2	17.9	23%
2PHE	TRANSCRIPTION	2.5	7.6	7.6	100%
2PMS	METAL TRANSPORT, HYDROLASE	2.0	4.0	8.1	49%
2POP	SIGNALING PROTEIN/APOPTOSIS	2.3	7.0	7.0	100%
2PQR	APOPTOSIS	2.9	5.7	22.6	25%
2PV2	ISOMERASE	2.8	5.6	11.4	49%
2PV9	HYDROLASE	2.2	4.4	8.5	52%
2QB0	HYDROLASE REGULATOR	2.1	4.2	10.6	40%
2RHK	VIRAL PROTEIN/NUCLEAR PROTEIN	2.0	4.0	13.8	29%
2UZ6	RECEPTOR	4.2	8.4	10.6	79%
2V1S	OXIDOREDUCTASE	2.8	5.5	5.5	100%
2V1Y	TRANSFERASE	2.7	5.3	7.8	68%
2V52	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN	2.0	6.0	13.8	43%
2VGO	TRANSFERASE	2.0	3.9	20.1	19%
2VZD	CELL ADHESION	2.6	5.1	7.6	67%
2W2X	SIGNALING PROTEIN/HYDROLASE	2.1	4.1	4.1	100%
2W2X	SIGNALING PROTEIN/HYDROLASE	2.9	5.8	5.8	100%
2W84	PROTEIN TRANSPORT	4.1	8.1	8.1	100%
2WAX	HYDROLASE	2.0	3.9	18.7	21%
2Z2S	TRANSCRIPTION	2.0	3.9	9.5	41%
2ZFD	SIGNALING PROTEIN/TRANSFERASE	2.8	11.1	23.2	48%
2ZNV	HYDROLASE/SIGNALING PROTEIN	2.2	4.4	9.0	49%
2ZSH	HORMONE RECEPTOR	2.4	4.8	12.3	39%
3A1G	TRANSFERASE	2.1	6.4	9.1	70%
3BLH	TRANSCRIPTION	2.7	5.3	11.8	45%
3BS5	SIGNALING PROTEIN/MEMBRANE PROTEIN	2.2	4.4	8.3	53%
3CJT	TRANSFERASE/RIBOSOMAL PROTEIN	4.0	8.0	24.6	33%
3CPH	PROTEIN TRANSPORT	2.4	4.8	8.8	55%
3CQX	CHAPERONE	2.2	4.4	7.4	59%
3D24	TRANSCRIPTION	2.1	6.4	7.5	85%
3D48	HORMONE/HORMONE RECEPTOR	2.4	7.2	16.3	44%
3DA7	PROTEIN BINDING	3.6	7.1	14.6	49%
3DAB	CELL CYCLE	3.5	7.0	8.9	79%
3DAB	CELL CYCLE	3.5	6.9	8.2	84%
3DAW	STRUCTURAL PROTEIN/STRUCTURAL PROTEIN RE	2.4	7.3	8.3	88%
3DD7	RIBOSOME INHIBITOR	3.6	7.1	12.2	58%
3EBA	IMMUNE SYSTEM/HYDROLASE	3.6	7.2	11.4	63%
3ECH	TRANSCRIPTION, TRANSCRIPTION REGULATION	5.7	11.3	12.4	91%
3EG5	SIGNALING PROTEIN	2.6	7.8	17.2	45%

A. PDB CODE	J. # HOTSPOT RESIDUES	K. HOTSPOT RESIDUES, RESIDUE #, ΔΔG $_{\text{(KCAL/MOL)}}$	L. HOTSPOT RESIDUE HELIX POSITIONS	M. HOTSPOT RESIDUE END TO END LENGTH
2G4D	3	D468, 3.2; E469, 1.2; N472, 6.4;	i; i+1; i+4;	5
2GPV	2	I1324, 2.0; L1328, 2.2;	i; i+4;	5
2HRK	2	R102, 2.2; Y106, 3.1;	i; i+4;	5
2HUE	2	L126, 2.5; I130, 1.7;	i; i+4;	5
2HUE	2	R36, 1.8; L37, 2.7;	i; i+1;	2
2HWN	2	V13, 2.8; M17, 1.3;	i; i+4;	5
2I2R	2	I77, 1.5; Y78, 2.4;	i; i+1;	2
2I2R	2	F11, 1.7; W8, 5.0;	i; i+3;	4
2I3S	3	E337, 3.5; E338, 1.9; L340, 3.0;	i; i+1; i+3;	4
2I3T	2	E383, 2.3; L385, 3.2;	i; i+2;	3
2IV8	2	D3, 1.5; F6, 3.9;	i; i+3;	4
2J59	2	I1053, 2.0; I1057, 2.2;	i; i+4;	5
2JTT	2	I211, 1.8; W215, 3.2;	i; i+4;	5
2K8B	3	M105, 1.4; F106, 2.3; Q109, 2.7;	i; i+1; i+4;	5
2KA6	4	E730, 1.8; F731, 4.5; E733, 3.0; V734, 1.2;	i; i+1; i+3; i+4;	5
2OCF	2	L78, 2.3; L82, 2.1;	i; i+4;	5
2OF5	2	D864, 5.2; E867, 1.8;	i; i+3;	4
2OZN	2	I1588, 3.1; L1591, 1.4;	i; i+3;	4
2P5T	2	H123, 2.1; Y127, 2.1;	i; i+4;	5
2PHE	3	F475, 3.0; E476, 1.1; F479, 3.5;	i; i+1; i+4;	5
2PMS	2	E182, 2.8; N183, 1.2;	i; i+1;	2
2POP	3	E2212, 2.4; D2213, 1.4; F2216, 3.2;	i; i+1; i+4;	5
2PQR	2	F101, 3.8; R102, 1.9;	i; i+1;	2
2PV2	2	F6, 4.6; I9, 1.0;	i; i+3;	4
2PV9	2	E14(E), 2.5; L14(F), 1.9;	i; i+1;	2
2QB0	2	D79, 2.4; V80, 1.8;	i; i+1;	2
2RHK	2	Y97, 1.7; F98, 2.3;	i; i+1;	2
2UZ6	2	C8, 7.0; N11, 1.4;	i; i+3;	4
2V1S	2	R17, 2.0; Y21, 3.5;	i; i+4;	5
2V1Y	2	F494, 4.3; E496, 1.0;	i; i+2;	3
2V52	3	L118, 2.7; K119, 1.6; I122, 1.7;	i; i+1; i+4;	5
2VGO	2	L833, 1.4; L836, 2.5;	i; i+3;	4
2VZD	2	L7, 3.1; L8, 2.0;	i; i+1;	2
2W2X	2	L67, 2.5; L70, 1.6;	i; i+3;	4
2W2X	2	F102, 3.5; V98, 2.3;	i; i+4;	5
2W84	2	W103, 4.9; F107, 3.2;	i; i+4;	5
2WAX	2	F206, 2.3; L210, 1.6;	i; i+4;	5
2Z2S	2	S65, 1.0; L66, 2.9;	i; i+1;	2
2ZFD	4	F313, 5.1; D314, 1.0; I315, 2.1; I316, 2.9;	i; i+1; i+2; i+3;	4
2ZNV	2	E329, 1.4; F332, 3.0;	i; i+3;	4
2ZSH	2	L50, 2.1; E51, 2.7;	i; i+1;	2
3A1G	3	R3, 2.8; I4, 2.2; L7, 1.4;	i; i+1; i+4;	5
3BLH	2	F89, 2.2; K93, 3.1;	i; i+4;	5
3BS5	2	R57, 2.4; R61, 2.0;	i; i+4;	5
3CJT	2	W59, 4.5; W63, 3.5;	i; i+4;	5
3CPH	2	R248, 3.5; I252, 1.3;	i; i+4;	5
3CQX	2	Q156, 1.6; I160, 2.8;	i; i+4;	5
3D24	3	L210, 2.6; Y213, 2.1; L214, 1.7;	i; i+3; i+4;	5
3D48	3	R177, 4.6; H180, 1.1; K181, 1.5;	i; i+3; i+4;	5
3DA7	2	D36, 1.3; D40, 5.8;	i; i+4;	5
3DAB	2	F19, 2.8; W23, 4.2;	i; i+4;	5
3DAB	2	F19, 3.3; W23, 3.6;	i; i+4;	5
3DAW	3	R267, 1.2; R269, 4.7; M270, 1.4;	i; i+2; i+3;	4
3DD7	2	F56, 2.8; F60, 4.3;	i; i+4;	5
3EBA	2	D91, 2.0; C95, 5.2;	i; i+4;	5
3ECH	2	W45, 7.0; Y48, 4.3;	i; i+3;	4
3EG5	3	R66, 4.7; L67, 1.3; L70, 1.8;	i; i+1; i+4;	5

TABLE S2

A. PDB CODE	N. HELIX LENGTH	O. HELIX START RESIDUE #	P. HELIX END RESIDUE #	Q. HELIX SEQUENCE	R. RESOLUTION
2G4D	17	468	484	DEIINFYMNMLMERSKE	2.80
2GPV	10	1321	1330	EAIIRKALMG	2.85
2HRK	14	98	111	RHILRWIDYMQNLL	2.05
2HUE	11	121	131	PKDIQLARRIR	1.70
2HUE	11	31	41	KPAIRRLARRG	1.70
2HWN	17	4	20	LAWKIAKMIVSDVMQQC	1.60
2I2R	12	71	82	EDTFKQIYAQFF	3.35
2I2R	8	8	15	WLPFARAA	3.35
2I3S	9	336	344	TEEILAMIK	1.90
2I3T	9	381	389	LEEVLAISR	2.80
2IV8	12	2	13	DDIVFEDFARQR	2.80
2J59	22	1042	1063	EEDTGVTNRDLISRRIKEYNNL	2.10
2JTT	14	205	218	DDMKRTINKAWVES	NOT APP
2K8B	17	104	120	PMFLDQVAKFIIDNTKG	NOT APP
2KA6	12	728	739	PEEFDEVSRIVG	NOT APP
2OCF	7	78	84	LRLMLAG	2.95
2OF5	12	863	874	QDVAEEVRAVLE	3.20
2OZN	10	1588	1597	IGDLAMVSKN	1.60
2P5T	19	110	128	PWILMSDDLSDLIHTNIYL	3.20
2PHE	6	475	480	FEQMFT	NOT APP
2PMS	19	174	192	PQAKIAELENQVHRLEQEL	2.91
2POP	11	2212	2222	EDELFRLSQLG	3.10
2PQR	9	97	105	SATTFRILA	1.88
2PV2	8	3	10	TLKFWDIF	1.30
2PV9	6	14E	14F	EKELLD	3.50
2QB0	14	78	91	GDVLYELLQHILKQ	2.56
2RHK	6	97	102	YFYSKF	1.95
2UZ6	7	6	12	PPCILNN	2.40
2V1S	9	15	23	LSRLLSYAG	2.05
2V1Y	25	481	505	RTAIEAFNETIKIFEEQCQTQERYS	2.40
2V52	9	116	124	DYLKRKIRS	1.45
2VGO	5	833	837	LEELF	1.70
2VZD	10	2	11	DDLDALLADL	2.10
2W2X	9	65	73	DRLRPLSYP	2.30
2W2X	16	98	113	VEELFEWFQSIREITW	2.30
2W84	17	94	110	VADLALSENWAQEFLAA	NOT APP
2WAX	7	206	212	FEGNLAL	2.30
2Z2S	5	65	69	SLASV	2.70
2ZFD	7	312	318	AFDIISG	1.20
2ZNV	10	329	338	EELFNVQDQH	1.60
2ZSH	16	43	58	MADVAQKLEQLEVMMS	1.80
3A1G	8	3	10	RIKELRNL	1.70
3BLH	16	80	95	GNSVAPAALFLAAKVE	2.48
3BS5	7	56	62	GRALLRI	2.00
3CJT	8	59	66	WLEAWRRD	2.30
3CPH	15	239	253	LGELPQGFARLSAIY	2.90
3CQX	10	153	162	QKFQSIVIGC	2.30
3D24	8	208	215	SELLKYLT	2.11
3D48	34	161	194	EESRLSAYYNLLHCLRRDSHKIDNYLKLLKCRII	2.50
3DA7	9	35	43	LDALWDCLT	2.25
3DAB	8	19	26	FSDLWKLL	1.90
3DAB	8	19	26	FSDLWKLL	1.90
3DAW	10	266	275	IRERMLYSSC	2.55
3DD7	9	55	63	EFASLFDTL	1.70
3EBA	11	90	100	ADAVACAKRVV	1.85
3ECH	7	44	50	AWDLYGE	1.80
3EG5	9	65	73	DRLRPLSYP	2.70

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
3EJB	G H	G	CRYSTAL STRUCTURE OF P450BIOI IN COMPLEX WITH TETRADECANOIC ACID LIGATED ACYL CARRIER PR
3EZQ	C D	C	CRYSTAL STRUCTURE OF THE FAS/FADD DEATH DOMAIN COMPLEX
3F75	A P	P	ACTIVATED TOXOPLASMA GONDII CATHEPSIN L (TGCPL) IN COMPLEX WITH ITS PROPEPTIDE
3F9K	B C	B	TWO DOMAIN FRAGMENT OF HIV-2 INTEGRASE IN COMPLEX WITH LEDGF IBD
3FMP	A B	B	CRYSTAL STRUCTURE OF THE NUCLEOPORIN NUP214 IN COMPLEX WITH THE DEAD-BOX HELICASE DDX1
3FUB	C D	C	CRYSTAL STRUCTURE OF GDNF-GFRALPHA1 COMPLEX
3G9V	A B	A	CRYSTAL STRUCTURE OF A SOLUBLE DECOY RECEPTOR IL-22BP BOUND TO INTERLEUKIN-22
3GCG	A B	B	CRYSTAL STRUCTURE OF MAP AND CDC42 COMPLEX
3H2U	A B	A	HUMAN RAVER1 RRM1, RRM2, AND RRM3 DOMAINS IN COMPLEX WITH HUMAN VINCULIN TAIL DOMAIN
3H9R	A B	A	CRYSTAL STRUCTURE OF THE KINASE DOMAIN OF TYPE I ACTIVIN RECEPTOR (ACVR1) IN COMPLEX WITH

TABLE S2

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. $\Delta\Delta G_{SUM, CHAIN}$ (KCAL/MOL)	I. HELIX CONTRIBUTION
3EJB	OXIDOREDUCTASE/LIPID TRANSPORT	2.3	9.3	13.5	69%
3EZQ	APOPTOSIS	2.0	4.0	7.0	57%
3F75	HYDROLASE	2.6	5.1	19.6	26%
3F9K	VIRAL PROTEIN, RECOMBINATION	2.0	3.9	5.4	72%
3FMP	ONCOPROTEIN/HYDROLASE	2.1	6.2	8.7	71%
3FUB	HORMONE	2.1	4.2	5.3	79%
3G9V	CYTOKINE/CYTOKINE RECEPTOR	2.7	5.4	12.8	42%
3GCG	SIGNALING PROTEIN/TRANSCRIPTION	2.2	4.4	13.7	32%
3H2U	CELL ADHESION	2.6	5.1	7.2	71%
3H9R	ISOMERASE/PROTEIN KINASE	2.0	3.9	6.6	59%

TABLE S2

A. PDB CODE	J. # HOTSPOT RESIDUES	K. HOTSPOT RESIDUES, RESIDUE #, $\Delta\Delta G_{(KCAL/MOL)}$	L. HOTSPOT RESIDUE HELIX POSITIONS	M. HOTSPOT RESIDUE END TO END LENGTH
3EJB	4	L57, 3.4; D58, 1.9; V60, 1.3; E61, 2.7;	i; i+1; i+3; i+4;	5
3EZQ	2	Y291, 1.9; I295, 2.1;	i; i+4;	5
3F75	2	R170, 2.6; F173, 2.5;	i; i+3;	4
3F9K	2	M128, 1.3; W131, 2.6;	i; i+3;	4
3FMP	3	D255, 1.7; Q256, 1.2; R259, 3.3;	i; i+1; i+4;	5
3FUB	2	R171, 2.5; I175, 1.7;	i; i+4;	5
3G9V	2	W123, 1.3; E125, 4.1;	i; i+2;	3
3GCG	2	I156, 1.3; F159, 3.1;	i; i+3;	4
3H2U	2	L928, 1.2; E932, 3.9;	i; i+4;	5
3H9R	2	W245, 2.1; F246, 1.8;	i; i+1;	2

TABLE S2

A. PDB CODE	N. HELIX LENGTH	O. HELIX START RESIDUE #	P. HELIX END RESIDUE #	Q. HELIX SEQUENCE	R. RESOLUTION
3EJB	14	57	70	LDTVELVMALEEEF	2.00
3EZQ	33	287	319	KKEAYDTLIKDLKKANLCTLAEKIQTIILKDIT	2.73
3F75	8	170	177	RDEFRRKY	1.99
3F9K	11	124	134	QEVKMVAWWIG	3.20
3FMP	11	253	263	HQDQSIRIQRM	3.19
3FUB	15	165	179	DTCKKYRSAYITPCT	2.35
3G9V	5	122	126	PWWET	2.76
3GCG	24	155	178	PITRFNTQTKMIEQVSQEIFERNF	2.30
3H2U	21	918	938	DIIAAAKRMALLMAEMSRLVR	2.75
3H9R	14	242	255	EKSWFRETELYNTV	2.35

Table S3. Dataset of HIPP interactions with Extended Interfaces

Description of Entries:

A. PDB code of predicted target.
B. Chains in the complex featuring a helix at the interface.
C. Candidate helix to be mimicked is part of the indicated chain.
D. Title of PDB entry.
E. Function of protein complex.
F. $\Delta\Delta G_{avg}$/helix is derived from Rosetta computational alanine mutagenesis studies and indicates the average free energy penalty for mutating two or more key residues in the helix at the interface to alanine.
G. $\Delta\Delta G_{sum}$/helix is derived from Rosetta computational alanine mutagenesis studies and indicates the average free energy penalty for mutating two or more key residues at the interface to alanine.
H. $\Delta\Delta G_{sum}$/chain is derived from Rosetta computational alanine mutagenesis studies and indicates the sum free energy penalty for mutating two or more key residues in the helix at the interface to alanine.
I. Helix contribution refers to the proportion of key contact residues positioned on the candidate helix as compared to the chain (see text for a detailed explanation).
J. Number of hot spot residues in helix.
K. Relative positioning of the hot spot residues on a helix.
L. Hot spot residues derived from Rosetta computational alanine scanning mutagenesis.
M. Number of residues separating end hot spot residues (see Methods for more details).
N. Length of candidate helix to be mimicked.
O. First residue of the candidate helix segment.
P. Last residue of the candidate helix segment.
Q. Sequence of candidate helix to be mimicked.
R. Resolution of PDB structure (NOT APP indicates NMR structure).

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1A93	A B	B	NMR SOLUTION STRUCTURE OF THE C-MYC-MAX HETERODIMERIC LEUCINE ZIPPER, NMR, MINIMIZED
1AVO	C D	D	PROTEASOME ACTIVATOR REG(ALPHA)
1AVO	E F	E	PROTEASOME ACTIVATOR REG(ALPHA)
1BCC	D H	H	CYTOCHROME BC1 COMPLEX FROM CHICKEN
1BH8	A B	B	HTAFII18/HTAFII28 HETERODIMER CRYSTAL STRUCTURE
1BIQ	A B	A	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 1 BETA CHAIN MUTANT E238A
1BIQ	A B	B	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 1 BETA CHAIN MUTANT E238A
1BP3	A B	A	THE XRAY STRUCTURE OF A GROWTH HORMONE-PROLACTIN RECEPTOR COMPLEX
1BPL	A B	B	GLYCOSYLTRANSFERASE
1CDL	A E	E	TARGET ENZYME RECOGNITION BY CALMODULIN: 2.4 ANGSTROMS STRUCTURE OF A CALMODULIN-PE
1CKK	A B	B	CALMODULIN/RAT CA2+/CALMODULIN DEPENDENT PROTEIN KINASE FRAGMENT
1CP9	A B	A	CRYSTAL STRUCTURE OF PENICILLIN G ACYLASE FROM THE BRO1 MUTANT STRAIN OF PROVIDENCIA R
1CUL	A B	A	COMPLEX OF GS-ALPHA WITH THE CATALYTIC DOMAINS OF MAMMALIAN ADENYLYL CYCLASE: COMP
1D8D	A B	A	CO-CRYSTAL STRUCTURE OF RAT PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH A K-RAS4B PEP
1DE4	G I	G	HEMOCHROMATOSIS PROTEIN HFE COMPLEXED WITH TRANSFERRIN RECEPTOR
1DKF	A B	A	CRYSTAL STRUCTURE OF A HETERODIMERIC COMPLEX OF RAR AND RXR LIGAND-BINDING DOMAINS
1DML	A B	B	CRYSTAL STRUCTURE OF HERPES SIMPLEX UL42 BOUND TO THE C- TERMINUS OF HSV POL
1DP5	A B	B	THE STRUCTURE OF PROTEINASE A COMPLEXED WITH A IA3 MUTANT INHIBITOR
1DX5	A M	A	CRYSTAL STRUCTURE OF THE THROMBIN-THROMBOMODULIN COMPLEX
1E0F	A D	A	CRYSTAL STRUCTURE OF THE HUMAN ALPHA-THROMBIN-HAEMADIN COMPLEX: AN EXOSITE II-BINDIN
1E3A	A B	A	A SLOW PROCESSING PRECURSOR PENICILLIN ACYLASE FROM ESCHERICHIA COLI
1E3A	A B	A	A SLOW PROCESSING PRECURSOR PENICILLIN ACYLASE FROM ESCHERICHIA COLI
1E7P	E F	E	QUINOL:FUMARATE REDUCTASE FROM WOLINELLA SUCCINOGENES
1EER	A C	A	CRYSTAL STRUCTURE OF HUMAN ERYTHROPOIETIN COMPLEXED TO ITS RECEPTOR AT 1.9 ANGSTROMS
1EFU	C D	D	ELONGATION FACTOR COMPLEX EF-TU/EF-TS FROM ESCHERICHIA COLI
1F51	D H	D	A TRANSIENT INTERACTION BETWEEN TWO PHOSPHORELAY PROTEINS TRAPPED IN A CRYSTAL LATTIC
1F6F	A B	A	CRYSTAL STRUCTURE OF THE TERNARY COMPLEX BETWEEN OVINE PLACENTAL LACTOGEN AND THE E
1F80	A E	A	HOLO-(ACYL CARRIER PROTEIN) SYNTHASE IN COMPLEX WITH HOLO- (ACYL CARRIER PROTEIN)
1FM6	A D	A	THE 2.1 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HETERODIMER OF THE HUMAN RXRAL
1FM6	U V	V	THE 2.1 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HETERODIMER OF THE HUMAN RXRAL
1FQJ	A B	A	CRYSTAL STRUCTURE OF THE HETEROTRIMERIC COMPLEX OF THE RGS DOMAIN OF RGS9, THE GAMMA
1G5J	A B	B	COMPLEX OF BCL-XL WITH PEPTIDE FROM BAD
1G73	A C	A	CRYSTAL STRUCTURE OF SMAC BOUND TO XIAP-BIR3 DOMAIN
1GX7	A D	A	BEST MODEL OF THE ELECTRON TRANSFER COMPLEX BETWEEN CYTOCHROME C3 AND [FE]-HYDROGE
1GX7	A D	D	BEST MODEL OF THE ELECTRON TRANSFER COMPLEX BETWEEN CYTOCHROME C3 AND [FE]-HYDROGE
1GZL	A C	A	CRYSTAL STRUCTURE OF C14LINKMID/IQN17: A CROSS-LINKED INHIBITOR OF HIV-1 ENTRY BOUND TO
1H2S	A B	A	MOLECULAR BASIS OF TRANSMENBRANE SIGNALLING BY SENSORY RHODOPSIN II-TRANSDUCER COM
1H3O	A B	B	CRYSTAL STRUCTURE OF THE HUMAN TAF4-TAF12 (TAFII135-TAFII20) COMPLEX
1H4L	B E	E	STRUCTURE AND REGULATION OF THE CDK5-P25(NCK5A) COMPLEX
1HIA	A B	B	KALLIKREIN COMPLEXED WITH HIRUSTASIN
1HL6	A B	B	A NOVEL MODE OF RBD-PROTEIN RECOGNITION IN THE Y14-MAGO COMPLEX
1HX1	A B	B	CRYSTAL STRUCTURE OF A BAG DOMAIN IN COMPLEX WITH THE HSC70 ATPASE DOMAIN
1I1R	A B	B	CRYSTAL STRUCTURE OF A CYTOKINE/RECEPTOR COMPLEX
1I2M	C D	C	RAN-RCC1-SO4 COMPLEX
1I5K	A C	C	STRUCTURE AND BINDING DETERMINANTS OF THE RECOMBINANT KRINGLE-2 DOMAIN OF HUMAN PLA
1IBR	A B	B	COMPLEX OF RAN WITH IMPORTIN BETA
1ID5	L H	L	CRYSTAL STRUCTURE OF BOVINE THROMBIN COMPLEX WITH PROTEASE INHIBITOR ECOTIN
1IHF	A B	A	INTEGRATION HOST FACTOR/DNA COMPLEX
1IHF	A B	B	INTEGRATION HOST FACTOR/DNA COMPLEX
1J7D	A B	A	CRYSTAL STRUCTURE OF HMMS2-HUBC13
1JEK	A B	B	VISNA TM CORE STRUCTURE
1JFI	A B	B	CRYSTAL STRUCTURE OF THE NC2-TBP-DNA TERNARY COMPLEX
1JFI	B C	B	CRYSTAL STRUCTURE OF THE NC2-TBP-DNA TERNARY COMPLEX
1JM7	A B	A	SOLUTION STRUCTURE OF THE BRCA1/BARD1 RING-DOMAIN HETERODIMER
1JYO	A F	A	STRUCTURE OF THE SALMONELLA VIRULENCE EFFECTOR SPTP IN COMPLEX WITH ITS SECRETION CHA
1JYO	C F	F	STRUCTURE OF THE SALMONELLA VIRULENCE EFFECTOR SPTP IN COMPLEX WITH ITS SECRETION CHA
1LDK	A D	A	STRUCTURE OF THE CUL1-RBX1-SKP1-F BOXSKP2 SCF UBIQUITIN LIGASE COMPLEX

TABLE S3

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. $\Delta\Delta G_{SUM, CHAIN}$ (KCAL/MOL)	I. HELIX CONTRIBUTION
1A93	LEUCINE ZIPPER	2.0	7.9	7.9	100%
1AVO	PROTEASOME ACTIVATOR	2.0	7.8	18.5	42%
1AVO	PROTEASOME ACTIVATOR	2.8	19.9	19.9	100%
1BCC	OXIDOREDUCTASE	5.5	11.0	15.5	71%
1BH8	TRANSCRIPTION REGULATION COMPLEX	2.0	9.8	16.0	61%
1BIQ	OXIDOREDUCTASE	2.4	7.2	37.3	19%
1BIQ	OXIDOREDUCTASE	2.2	6.7	33.2	20%
1BP3	HORMONE/GROWTH FACTOR	2.0	3.9	14.4	27%
1BPL	GLYCOSYLTRANSFERASE	2.9	17.1	48.5	35%
1CDL	CALCIUM-BINDING PROTEIN	2.4	21.8	23.3	94%
1CKK	CALMODULIN-PEPTIDE COMPLEX	2.6	5.1	11.6	44%
1CP9	HYDROLASE	2.9	11.5	68.9	17%
1CUL	LYASE/LYASE/SIGNALING PROTEIN	2.3	4.5	9.3	48%
1D8D	TRANSFERASE	2.1	10.7	49.1	22%
1DE4	METAL TRANSPORT INHIBITOR/RECEPTOR	2.7	10.6	14.5	73%
1DKF	HORMONE/GROWTH FACTOR RECEPTOR	2.6	5.2	8.1	64%
1DML	DNA BINDING PROTEIN/TRANSFERASE	3.1	9.2	12.1	76%
1DP5	HYDROLASE/HYDROLASE INHIBITOR	2.0	16.0	22.0	73%
1DX5	SERINE PROTEINASE	2.2	8.7	10.7	81%
1E0F	COAGULATION/CRYSTAL STRUCTURE/HEPARIN-B	2.0	3.9	6.1	64%
1E3A	ANTIBIOTIC RESISTANCE	2.4	11.9	110.8	11%
1E3A	ANTIBIOTIC RESISTANCE	2.8	19.7	110.8	18%
1E7P	OXIDOREDUCTASE	2.5	5.0	14.7	34%
1EER	COMPLEX (CYTOKINE/RECEPTOR)	2.1	4.1	4.1	100%
1EFU	COMPLEX (TWO ELONGATION FACTORS)	2.9	8.8	19.5	45%
1F51	TRANSFERASE	2.2	8.9	8.9	100%
1F6F	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR	2.3	9.0	10.7	84%
1F80	TRANSFERASE	2.3	9.2	12.3	75%
1FM6	TRANSCRIPTION	2.0	6.1	7.6	80%
1FM6	TRANSCRIPTION	2.1	6.4	6.4	100%
1FQJ	SIGNALING PROTEIN	2.0	5.9	5.9	100%
1G5J	APOPTOSIS	2.3	4.6	4.6	100%
1G73	APOPTOSIS/APOPTOSIS INHIBITOR	3.3	13.2	13.2	100%
1GX7	OXIDOREDUCTASE	2.8	8.5	40.2	21%
1GX7	OXIDOREDUCTASE	2.2	13.3	51.0	26%
1GZL	GLYCOPROTEIN	2.6	5.1	5.1	100%
1H2S	MEMBRANE PROTEIN	2.0	4.0	9.0	44%
1H3O	TRANSCRIPTION/TBP-ASSOCIATED FACTORS	2.0	5.9	14.3	41%
1H4L	KINASE/KINASE ACTIVATOR	2.3	6.9	9.1	76%
1HIA	COMPLEX (PROTEASE/INHIBITOR)	2.9	5.8	27.9	21%
1HL6	SIGNAL PROTEIN	3.0	11.9	26.6	45%
1HX1	CHAPERONE/CHAPERONE INHIBITOR	2.5	4.9	11.1	44%
1I1R	CYTOKINE	2.3	7.0	8.2	85%
1I2M	CELL CYCLE	2.1	8.2	13.3	62%
1I5K	BLOOD CLOTTING	2.7	8.0	8.0	100%
1IBR	CELL CYCLE,TRANSLATION	2.1	4.1	20.4	20%
1ID5	HYDROLASE	2.7	13.5	13.5	100%
1IHF	TRANSCRIPTION/DNA	2.0	18.3	38.1	48%
1IHF	TRANSCRIPTION/DNA	2.4	11.9	32.3	37%
1J7D	UNKNOWN FUNCTION	2.2	6.6	6.6	100%
1JEK	VIRAL PROTEIN	2.2	8.6	12.5	69%
1JFI	TRANSCRIPTION/DNA	2.3	9.0	16.5	55%
1JFI	TRANSCRIPTION/DNA	2.7	8.1	8.1	100%
1JM7	ANTITUMOR	3.0	12.0	15.8	76%
1JYO	CHAPERONE	2.5	5.0	6.5	77%
1JYO	CHAPERONE	2.3	9.3	26.1	36%
1LDK	LIGASE	2.3	6.9	6.9	100%

TABLE S3

A. PDB CODE	J. # HOTSPOT RESIDUES	K. HOTSPOT RESIDUES, RESIDUE #, ΔΔG (KCAL/MOL)
1A93	4	N10, 2.3; H13, 1.9; I17, 1.7; L20, 2.0;
1AVO	4	H202, 1.4; Y209, 2.7; V216, 1.3; R220, 2.4;
1AVO	7	L29, 1.3; Y32, 4.0; F33, 2.7; K36, 6.9; I37, 1.6; L40, 1.2; L44, 2.2;
1BCC	2	F59, 3.8; F74, 7.2;
1BH8	5	M154, 1.1; K159, 1.0; F161, 4.5; V162, 1.7; V166, 1.5;
1BIQ	3	D158, 3.2; Y166, 1.4; L169, 2.6;
1BIQ	3	L82, 1.3; I86, 1.0; R89, 4.4;
1BP3	2	H18, 1.0; F25, 2.9;
1BPL	6	E211, 1.0; I212, 1.3; W215, 3.5; W218, 5.1; Y219, 4.4; E222, 1.8;
1CDL	9	R798, 2.1; K799, 2.2; W800, 7.1; H805, 2.3; V807, 2.1; R808, 2.1; I810, 1.2; R812, 1.3; L813, 1.4;
1CKK	2	W7, 3.5; K14, 1.6;
1CP9	4	L25, 2.4; F26, 2.3; Y29, 5.0; D36, 1.8;
1CUL	2	V413, 1.9; D424, 2.6;
1D8D	5	N234, 3.2; S235, 2.9; W237, 1.9; N238, 1.6; H241, 1.1;
1DE4	4	H74, 1.9; T77, 2.8; V78, 4.2; W81, 1.7;
1DKF	2	E395, 1.7; Y402, 3.5;
1DML	3	L1227, 1.2; F1231, 5.3; L1234, 2.7;
1DP5	8	V8, 2.9; I11, 1.5; F12, 2.8; L19, 1.6; D22, 2.0; V25, 1.0; V26, 1.9; F30, 2.3;
1DX5	4	E14, 2.0; E14, 2.1; L14, 1.0; Y14, 3.6;
1E0F	2	E14, 1.0; Y14, 2.9;
1E3A	5	E152, 3.2; I153, 2.1; D154, 1.7; N155, 2.6; L158, 2.3;
1E3A	7	W25, 3.5; L27, 3.0; F28, 1.9; Y29, 1.2; Y31, 6.1; Y33, 2.3; D38, 1.7;
1E7P	2	Q225, 3.6; V236, 1.4;
1EER	2	R103, 2.9; L108, 1.2;
1EFU	3	F271, 4.4; V275, 3.4; M278, 1.0;
1F51	4	H630, 3.4; N634, 2.6; L638, 1.4; K640, 1.5;
1F6F	4	H177, 1.7; R178, 4.6; S181, 1.5; K182, 1.2;
1F80	4	R21, 1.7; R24, 2.4; F25, 1.2; R28, 3.9;
1FM6	3	E394, 1.8; Y397, 3.1; E401, 1.2;
1FM6	3	I632, 3.2; L636, 1.2; L637, 2.0;
1FQJ	3	E203, 1.1; K206, 3.5; H209, 1.3;
1G5J	2	R313, 1.0; F319, 3.6;
1G73	4	H92, 5.3; Y95, 2.8; L96, 1.3; E99, 3.8;
1GX7	3	F147, 2.5; W154, 4.1; E155, 1.9;
1GX7	6	K40, 1.3; Y42, 2.7; M43, 1.4; R46, 1.9; I47, 1.0; Y51, 5.0;
1GZL	2	L29, 1.0; W35, 4.1;
1H2S	2	T191, 1.2; L196, 2.8;
1H3O	3	F91, 2.3; I92, 1.8; V96, 1.8;
1H4L	3	W258, 3.6; L262, 1.8; I265, 1.5;
1HIA	2	W237, 2.8; I242, 3.0;
1HL6	4	Y125, 2.7; S136, 1.7; L140, 2.6; H141, 4.9;
1HX1	2	R237, 2.8; D252, 2.1;
1I1R	3	L11, 1.1; R15, 2.4; W18, 3.5;
1I2M	4	N103, 1.0; R106, 3.2; D107, 2.0; R110, 2.0;
1I5K	3	L310, 2.5; L313, 1.5; R317, 4.0;
1IBR	2	E281, 2.7; D288, 1.4;
1ID5	5	E14, 2.4; E14, 2.6; F14, 1.7; L14, 3.0; Y14, 3.8;
1IHF	9	D22, 1.4; E25, 1.4; L26, 1.4; F30, 2.9; F31, 4.0; E33, 1.0; R35, 2.7; L38, 1.8; E39, 1.7;
1IHF	5	E28, 4.2; M29, 1.9; L30, 2.3; H32, 2.3; M33, 1.2;
1J7D	3	F13, 4.6; E17, 1.0; E20, 1.0;
1JEK	4	W631, 1.7; I635, 1.3; H638, 3.1; L642, 2.5;
1JFI	4	L138, 2.0; F146, 3.4; I147, 2.6; H148, 1.0;
1JFI	3	L219, 1.1; Q222, 1.2; L225, 5.8;
1JM7	4	Q81, 1.1; E85, 2.2; L86, 7.7; D96, 1.0;
1JYO	2	E111, 2.2; E118, 2.8;
1JYO	4	F83, 4.5; H85, 1.1; E89, 1.3; K90, 2.4;
1LDK	3	M43, 1.3; Y46, 1.0; Y50, 4.6;

TABLE S3

A. PDB CODE	L. HOTSPOT RESIDUE HELIX POSITIONS	M. HOTSPOT RESIDUE END TO END LENGTH	N. HELIX LENGTH	O. HELIX START RESIDUE #	P. HELIX END RESIDUE #
1A93	i; i+3; i+7; i+10;	11	29	6	34
1AVO	i; i+7; i+14; i+18;	19	39	195	233
1AVO	i; i+3; i+4; i+7; i+8; i+11; i+15;	16	38	8	45
1BCC	i; i+15;	16	23	55	77
1BH8	i; i+5; i+7; i+8; i+12;	13	29	148	176
1BIQ	i; i+8; i+11;	12	19	153	171
1BIQ	i; i+4; i+7;	8	32	67	98
1BP3	i; i+7;	8	30	6	35
1BPL	i; i+1; i+4; i+7; i+8; i+11;	12	18	206	223
1CDL	i; i+1; i+2; i+7; i+9; i+10; i+12; i+14; i+15;	16	17	798	814
1CKK	i; i+7;	8	11	7	17
1CP9	i; i+1; i+4; i+11;	12	16	22	37
1CUL	i; i+11;	12	22	409	430
1D8D	i; i+1; i+3; i+4; i+7;	8	13	234	246
1DE4	i; i+3; i+4; i+7;	8	28	59	86
1DKF	i; i+7;	8	23	391	413
1DML	i; i+4; i+7;	8	16	1220	1235
1DP5	i; i+3; i+4; i+11; i+14; i+17; i+18; i+22 ;	23	29	3	31
1DX5	i; i+2 ; i+3 ; i+7;	8	9	14	14
1E0F	i; i+5;	6	11	14A	14J
1E3A	i; i+1; i+2; i+3; i+6;	7	15	152	166
1E3A	i; i+2; i+3; i+4; i+6; i+8; i+13;	14	16	24	39
1E7P	i; i+11;	12	14	224	237
1EER	i; i+5;	6	25	89	113
1EFU	i; i+4; i+7;	8	9	271	279
1F51	i; i+4; i+8; i+10;	11	23	620	642
1F6F	i; i+1; i+4; i+5;	6	34	162	195
1F80	i; i+3; i+4; i+7;	8	10	21	30
1FM6	i; i+3; i+7;	8	23	386	408
1FM6	i; i+4; i+5;	6	9	631	639
1FQJ	i; i+3; i+6;	7	10	201	210
1G5J	i; i+6;	7	15	306	320
1G73	i; i+3; i+4; i+7;	8	48	72	119
1GX7	i; i+7; i+8;	9	20	146	165
1GX7	i; i+2; i+3; i+6; i+7; i+11;	12	18	39	56
1GZL	i; i+6;	7	43	2	44
1H2S	i; i+5;	6	34	190	223
1H3O	i; i+1; i+5;	6	22	85	106
1H4L	i; i+4; i+7;	8	15	254	268
1HIA	i; i+5;	6	11	235	245
1HL6	i; i+11; i+15; i+16;	17	27	117	143
1HX1	i; i+15;	16	27	231	257
1I1R	i; i+4; i+7;	8	27	9	35
1I2M	i; i+3; i+4; i+7;	8	13	101	113
1I5K	i; i+3; i+7;	8	22	306	327
1IBR	i; i+7;	8	26	273	298
1ID5	i; i+2 ; i+3 ; i+4 ; i+7;	8	9	14	14
1IHF	i; i+3; i+4; i+8; i+9; i+11; i+13; i+16; i+17;	18	21	20	40
1IHF	i; i+1; i+2; i+4; i+5;	6	21	19	39
1J7D	i; i+4; i+7;	8	15	11	25
1JEK	i; i+4; i+7; i+11;	12	33	629	661
1JFI	i; i+8; i+9; i+10;	11	29	133	161
1JFI	i; i+3; i+6;	7	28	215	242
1JM7	i; i+4; i+5; i+15;	16	19	80	98
1JYO	i; i+7;	8	22	103	124
1JYO	i; i+2; i+6; i+7;	8	15	77	91
1LDK	i; i+3; i+7;	8	14	40	53

TABLE S3

A. PDB CODE	Q. HELIX SEQUENCE	R. RESOLUTION
1A93	MRRKNDTHQQDIDDLKRQNALLEQQVRAL	NOT APP
1AVO	GDYRQLVHELDEAEYRDIRLMVMEIRNAYAVLYDIILKN	2.80
1AVO	PEAQAKVDVFREDLCTKTENLLGSYFPKKISELDAFLK	2.80
1BCC	TEELFDFLHARDHCVAHKLFNSL	3.16
1BH8	QNVVIAMSGISKVFVGEVVEEALDVCEKW	3.00
1BIQ	ISSYYDELIEMTSYWHLLG	2.05
1BIQ	EHEKHIFISNLKYQTLLDSIQGRSPNVALLPL	2.05
1BP3	LSRLFDNAMLRAHRLHQLAFDTYQEFEEAY	2.90
1BPL	PDVAAEIKRWGTWYANEL	2.20
1CDL	RKWQKTGHAVRAIGRLS	2.00
1CKK	WTTVILVKSML	NOT APP
1CP9	TYSLFYGYGYAVAQDR	2.50
1CUL	AQELVMTLNELFARFDKLAAEN	2.40
1D8D	NSVWNQRHFVISN	2.00
1DE4	SQMWLQLSQSLKGWDHMFTVDFWTIMEN	2.80
1DKF	PAEVEALREKVYASLEAYCKHKY	2.50
1DML	AEETRRMLHRAFDTLA	2.70
1DP5	TDQQKVSEIFQSSKEKLQGDAKVVSDAFM	2.20
1DX5	ERELLESYI	2.30
1E0F	KTERELLESYI	3.10
1E3A	EIDNLALLTALKDKY	1.80
1E3A	TWHLFYGYGYVVAQDR	1.80
1E7P	LQSKIAYLRRKMVS	3.10
1EER	EPLQLHVDKAVSGLRSLTTLLRALG	1.90
1EFU	FAAEVAAMS	2.50
1F51	ELIHLLGHSRHDWMNKLQLIKGN	3.00
1F6F	ENVRRVAFYRLFHCLHRDSSKIYTYLRILKCRLT	2.30
1F80	RQKRFAERIL	2.30
1FM6	PAEVEALREKVYASLEAYCKHKY	2.10
1FM6	KILHRLLQE	2.10
1FQJ	RSERKKWIHC	2.02
1G5J	QRYGRELRRMSDEFV	NOT APP
1G73	EEEDEVWQVIIGARAEMTSKHQEYLKLETTWMTAVGLSEMAAEAAYQT	2.00
1GX7	EFTADVTIWEEGSEFVERLT	NOT APP
1GX7	IKDYMLDRINGVYGADAK	NOT APP
1GZL	MKQIEDKIEEIESKQKKIENEIARIKKLLQLTVWGIKQLQARI	1.80
1H2S	PTVDVALIVYLDLVTKVGFGFIALDAAATLRAEH	1.93
1H3O	LQIADDFIESVVTAACQLARHR	2.30
1H4L	KEAFWDRCLSVINLM	2.65
1HIA	LDWIDDTITEN	2.40
1HL6	PEGLRCFYYLVQDLKCLVFSLIGLHFK	2.50
1HX1	KDSRLKRKGLVKKVQAFLAECDTVEQN	1.90
1I1R	KDLLIQRLNWMLWVIDECFRDLCYRTG	2.40
1I2M	VPNWHRDLVRVCE	1.76
1I5K	ADAELQRLKNERHEEAELERLK	2.70
1IBR	DEVALQGIEFWSNVCDEEMDLAIEAS	2.30
1ID5	EKELFESYI	2.50
1IHF	KRDAKELVELFFEEIRRALEN	2.20
1IHF	AKTVEDAVKEMLEHMASTLAQ	2.20
1J7D	RNFRLLEELEEGQKG	1.85
1JEK	QQWEEEIEQHEGNLSLLLREAALQVHIAQRDAR	1.50
1JFI	NDARELVVNCCTEFIHLISSEANEICNKS	2.62
1JFI	EEELLRQQQELFAKARQQQAELAQQEWL	2.62
1JM7	SQLVEELLKIICAFQLDTG	NOT APP
1JYO	TYHIISQLESFVNQQEALKNIL	1.90
1JYO	QKILQTFLHALTEKY	1.90
1LDK	SRYMELYTHVYNYC	3.10

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1LQB	A B	B	CRYSTAL STRUCTURE OF A HYDROXYLATED HIF-1 ALPHA PEPTIDE BOUND TO THE PVHL/ELONGIN-C/EL
1LUJ	A B	A	CRYSTAL STRUCTURE OF THE BETA-CATENIN/ICAT COMPLEX
1M1E	A B	A	BETA-CATENIN ARMADILLO REPEAT DOMAIN BOUND TO ICAT
1M63	A B	A	CRYSTAL STRUCTURE OF CALCINEURIN-CYCLOPHILIN-CYCLOSPORIN SHOWS COMMON BUT DISTINCT
1MF8	A B	A	CRYSTAL STRUCTURE OF HUMAN CALCINEURIN COMPLEXED WITH CYCLOSPORIN A AND HUMAN CYC
1MXE	A E	E	STRUCTURE OF THE COMPLEX OF CALMODULIN WITH THE TARGET SEQUENCE OF CAMKI
1N1J	A B	A	CRYSTAL STRUCTURE OF THE NF-YB/NF-YC HISTONE PAIR
1N1J	A B	A	CRYSTAL STRUCTURE OF THE NF-YB/NF-YC HISTONE PAIR
1N1J	A B	B	CRYSTAL STRUCTURE OF THE NF-YB/NF-YC HISTONE PAIR
1N2D	A C	C	TERNARY COMPLEX OF MLC1P BOUND TO IQ2 AND IQ3 OF MYO2P, A CLASS V MYOSIN
1N4Q	E F	F	PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A KKKSKT
1NGM	E F	F	CRYSTAL STRUCTURE OF A YEAST BRF1-TBP-DNA TERNARY COMPLEX
1NH2	B D	B	CRYSTAL STRUCTURE OF A YEAST TFIIA/TBP/DNA COMPLEX
1NH2	B D	B	CRYSTAL STRUCTURE OF A YEAST TFIIA/TBP/DNA COMPLEX
1NH2	B D	D	CRYSTAL STRUCTURE OF A YEAST TFIIA/TBP/DNA COMPLEX
1NU7	B D	D	STAPHYLOCOAGULASE-THROMBIN COMPLEX
1NU9	D F	F	STAPHYLOCOAGULASE-PRETHROMBIN-2 COMPLEX
1NVM	G H	G	CRYSTAL STRUCTURE OF A BIFUNCTIONAL ALDOLASE-DEHYDROGENASE : SEQUESTERING A REACTIVE
1NX0	A C	C	STRUCTURE OF CALPAIN DOMAIN 6 IN COMPLEX WITH CALPASTATIN DIC
1OO0	A B	A	CRYSTAL STRUCTURE OF THE DROSOPHILA MAGO NASHI-Y14 COMPLEX
1OQP	A B	B	STRUCTURE OF THE CA2+/C-TERMINAL DOMAIN OF CALTRACTIN IN COMPLEX WITH THE CDC31P-BIND
1OQS	A B	A	CRYSTAL STRUCTURE OF RV4/RV7 COMPLEX
1OR0	A B	A	CRYSTAL STRUCTURES OF GLUTARYL 7-AMINOCEPHALOSPORANIC ACID ACYLASE: INSIGHT INTO AUT
1OR0	A B	A	CRYSTAL STRUCTURES OF GLUTARYL 7-AMINOCEPHALOSPORANIC ACID ACYLASE: INSIGHT INTO AUT
1OR0	C D	C	CRYSTAL STRUCTURES OF GLUTARYL 7-AMINOCEPHALOSPORANIC ACID ACYLASE: INSIGHT INTO AUT
1OR7	A C	C	CRYSTAL STRUCTURE OF ESCHERICHIA COLI SIGMAE WITH THE CYTOPLASMIC DOMAIN OF ITS ANTI-SI
1OR7	A C	C	CRYSTAL STRUCTURE OF ESCHERICHIA COLI SIGMAE WITH THE CYTOPLASMIC DOMAIN OF ITS ANTI-SI
1OXK	A B	B	COMPLEX BETWEEN YPD1 AND SLN1 RESPONSE REGULATOR DOMAIN IN SPACE GROUP P3(2)
1P27	A B	A	CRYSTAL STRUCTURE OF THE HUMAN Y14/MAGOH COMPLEX
1PGR	E F	E	2:2 COMPLEX OF G-CSF WITH ITS RECEPTOR
1PQ1	A B	B	CRYSTAL STRUCTURE OF BCL-XL/BIM
1PZL	A B	B	CRYSTAL STRUCTURE OF HNF4A LBD IN COMPLEX WITH THE LIGAND AND THE COACTIVATOR SRC-1 PE
1QZ7	A B	B	BETA-CATENIN BINDING DOMAIN OF AXIN IN COMPLEX WITH BETA- CATENIN
1R4M	A B	A	APPBP1-UBA3-NEDD8, AN E1-UBIQUITIN-LIKE PROTEIN COMPLEX
1R8U	A B	A	NMR STRUCTURE OF CBP TAZ1/CITED2 COMPLEX
1RF8	A B	B	SOLUTION STRUCTURE OF THE YEAST TRANSLATION INITIATION FACTOR EIF4E IN COMPLEX WITH M7G
1RIW	B C	C	THROMBIN IN COMPLEX WITH NATURAL PRODUCT INHIBITOR OSCILLARIN
1RK8	A B	B	STRUCTURE OF THE CYTOSOLIC PROTEIN PYM BOUND TO THE MAGO- Y14 CORE OF THE EXON JUNCTIO
1RM1	B C	B	STRUCTURE OF A YEAST TFIIA/TBP/TATA-BOX DNA COMPLEX
1RM1	B C	B	STRUCTURE OF A YEAST TFIIA/TBP/TATA-BOX DNA COMPLEX
1RP3	A B	B	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	E F	E	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1SA0	C D	C	TUBULIN-COLCHICINE: STATHMIN-LIKE DOMAIN COMPLEX
1SB0	A B	B	SOLUTION STRUCTURE OF THE KIX DOMAIN OF CBP BOUND TO THE TRANSACTIVATION DOMAIN OF C-
1SYQ	A B	B	HUMAN VINCULIN HEAD DOMAIN VH1, RESIDUES 1-258, IN COMPLEX WITH HUMANTALIN'S VINCULIN B
1TCO	A B	A	TERNARY COMPLEX OF A CALCINEURIN A FRAGMENT, CALCINEURIN B, FKBP12 AND THE IMMUNOSUPP
1TI2	A B	B	CRYSTAL STRUCTURE OF PYROGALLOL-PHLOROGLUCINOL TRANSHYDROXYLASE FROM PELOBACTER
1TN6	A B	A	PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH A RAP2A PEPTIDE SUBSTRATE AND A FPP ANALO
1TQY	A B	B	THE ACTINORHODIN KETOSYNTHASE/CHAIN LENGTH FACTOR
1TQY	C D	C	THE ACTINORHODIN KETOSYNTHASE/CHAIN LENGTH FACTOR
1TQY	E F	E	THE ACTINORHODIN KETOSYNTHASE/CHAIN LENGTH FACTOR
1TUE	H J	J	THE X-RAY STRUCTURE OF THE PAPILLOMAVIRUS HELICASE IN COMPLEX WITH ITS MOLECULAR MAT
1TY4	A C	C	CRYSTAL STRUCTURE OF A CED-9/EGL-1 COMPLEX
1UKL	A C	C	CRYSTAL STRUCTURE OF IMPORTIN-BETA AND SREBP-2 COMPLEX
1UKV	G Y	G	STRUCTURE OF RABGDP-DISSOCIATION INHIBITOR IN COMPLEX WITH PRENYLATED YPT1 GTPASE
1VCB	K L	L	THE VHL-ELONGINC-ELONGINB STRUCTURE
1VF6	A C	C	2.1 ANGSTROM CRYSTAL STRUCTURE OF THE PALS-1-L27N AND PATJ L27 HETERODIMER COMPLEX

TABLE S3

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. $\Delta\Delta G_{SUM, CHAIN}$ (KCAL/MOL)	I. HELIX CONTRIBUTION
1LQB	GENE REGULATION	2.3	9.0	12.1	74%
1LUJ	STRUCTURAL PROTEIN	2.0	7.9	10.0	79%
1M1E	STRUCTURAL PROTEIN	2.4	4.8	15.4	31%
1M63	HYDROLASE/ISOMERASE	2.0	9.9	22.4	44%
1MF8	HYDROLASE, LIGASE	2.1	10.4	33.6	31%
1MXE	METAL BINDING PROTEIN	2.4	23.8	27.5	87%
1N1J	DNA BINDING PROTEIN	4.3	17.3	23.2	75%
1N1J	DNA BINDING PROTEIN	2.0	4.0	23.2	17%
1N1J	DNA BINDING PROTEIN	2.5	17.2	43.7	39%
1N2D	CELL CYCLE	2.0	15.7	15.7	100%
1N4Q	TRANSFERASE	2.0	7.9	46.8	17%
1NGM	TRANSCRIPTION/DNA	2.6	5.2	15.8	33%
1NH2	TRANSCRIPTION/DNA	2.2	8.7	20.3	43%
1NH2	TRANSCRIPTION/DNA	2.5	10.0	20.3	49%
1NH2	TRANSCRIPTION/DNA	2.3	6.8	9.3	73%
1NU7	HYDROLASE/PROTEIN BINDING	2.0	6.1	15.2	40%
1NU9	HYDROLASE/PROTEIN BINDING	3.2	6.3	7.4	85%
1NVM	LYASE/OXIDOREDUCTASE	2.1	6.3	17.2	37%
1NX0	HYDROLASE	2.2	6.7	9.8	68%
1OO0	SIGNALING PROTEIN	2.2	13.0	20.8	63%
1OQP	PROTEIN BINDING	2.5	12.7	12.7	100%
1OQS	HYDROLASE	3.0	5.9	17.4	34%
1OR0	HYDROLASE	2.2	10.8	58.0	19%
1OR0	HYDROLASE	4.0	7.9	58.0	14%
1OR0	HYDROLASE	3.2	9.7	63.2	15%
1OR7	TRANSCRIPTION	2.0	5.9	33.3	18%
1OR7	TRANSCRIPTION	2.2	11.1	33.3	33%
1OXK	SIGNALING PROTEIN	2.7	8.2	11.7	70%
1P27	RNA BINDING PROTEIN	2.3	7.0	15.0	47%
1PGR	CYTOKINE	2.2	6.5	7.9	82%
1PQ1	APOPTOSIS	2.3	20.4	20.4	100%
1PZL	TRANSCRIPTION	2.2	8.7	8.7	100%
1QZ7	CELL ADHESION	2.0	10.1	10.1	100%
1R4M	CELL CYCLE	2.1	6.3	24.4	26%
1R8U	TRANSCRIPTION/TRANSCRIPTION ACTIVATOR	2.1	6.2	13.8	45%
1RF8	BIOSYNTHETIC PROTEIN, TRANSLATION	2.1	6.4	15.1	42%
1RIW	HYDROLASE/BLOOD CLOTTING	2.8	11.2	64.3	17%
1RK8	TRANSLATION	2.5	10.0	15.4	65%
1RM1	TRANSCRIPTION/DNA	2.1	8.5	29.3	29%
1RM1	TRANSCRIPTION/DNA	2.0	9.8	29.3	33%
1RP3	TRANSCRIPTION	2.2	17.7	31.0	57%
1RP3	TRANSCRIPTION	2.0	10.0	25.0	40%
1SA0	CELL CYCLE	2.6	7.8	22.0	35%
1SB0	TRANSCRIPTION	2.2	6.5	6.5	100%
1SYQ	CELL ADHESION	2.0	14.1	14.1	100%
1TCO	COMPLEX (HYDROLASE/ISOMERASE)	2.3	16.1	22.5	72%
1TI2	OXIDOREDUCTASE	2.1	6.3	52.3	12%
1TN6	TRANSFERASE	2.0	6.0	55.1	11%
1TQY	TRANSFERASE	2.2	8.8	30.6	29%
1TQY	TRANSFERASE	2.0	3.9	38.9	10%
1TQY	TRANSFERASE	2.0	5.9	28.4	21%
1TUE	REPLICATION	3.3	10.0	10.0	100%
1TY4	APOPTOSIS	2.1	8.4	13.8	61%
1UKL	PROTEIN TRANSPORT/DNA BINDING PROTEIN	2.0	3.9	6.8	57%
1UKV	PROTEIN TRANSPORT	2.3	9.0	18.5	49%
1VCB	TRANSCRIPTION	2.0	7.8	7.8	100%
1VF6	PROTEIN BINDING/PROTEIN TRANSPORT	2.0	3.9	21.9	18%

A. PDB CODE	J. # HOTSPOT RESIDUES	K. HOTSPOT RESIDUES, RESIDUE #, ΔΔG (KCAL/MOL)
1LQB	4	H68, 3.0; M75, 1.1; Y79, 1.4; R82, 3.5;
1LUJ	4	T653, 1.3; Y654, 1.8; F660, 2.7; R661, 2.1;
1M1E	2	T653, 1.1; F660, 3.7;
1M63	5	F350, 4.8; W352, 1.5; L354, 1.1; K360, 1.1; V361, 1.4;
1MF8	5	V361, 1.6; M364, 3.7; L365, 1.8; V368, 1.8; L369, 1.5;
1MXE	10	F298, 2.8; K302, 1.6; W303, 6.9; K304, 1.1; F307, 2.6; V312, 1.4; V313, 1.6; R314, 2.1; H315, 1.8; M316, 1.9;
1N1J	4	Y128, 2.4; L132, 1.5; Y135, 1.4; L136, 12.0;
1N1J	2	V84, 1.1; I92, 2.9;
1N1J	7	V67, 1.1; L68, 2.7; F69, 4.7; K71, 1.5; I75, 1.3; I77, 3.0; W85, 2.9;
1N2D	8	K812, 1.4; L814, 2.5; Q815, 2.8; I818, 1.7; F821, 2.4; I822, 1.4; I823, 1.1; R824, 2.4;
1N4Q	4	K243, 1.7; R250, 2.1; W251, 2.2; I253, 1.9;
1NGM	2	S480, 1.5; W487, 3.7;
1NH2	4	L38, 2.1; W42, 3.7; K45, 1.6; L46, 1.3;
1NH2	4	V9, 1.0; Y10, 5.0; I13, 2.4; V17, 1.6;
1NH2	3	I15, 3.3; L19, 2.0; L26, 1.5;
1NU7	3	L67, 3.0; Q71, 2.1; L74, 1.0;
1NU9	2	K59, 4.9; L67, 1.4;
1NVM	3	M328, 1.6; D331, 3.6; D335, 1.1;
1NX0	3	I603, 2.4; L606, 2.9; D609, 1.4;
1OO0	6	Y125, 1.9; D129, 1.8; L133, 1.2; S136, 1.7; L140, 2.5; H141, 3.9;
1OQP	5	E245, 1.4; K247, 1.0; W248, 5.7; L251, 2.4; L252, 2.2;
1OQS	2	F3, 4.4; I9, 1.5;
1OR0	5	F39, 1.7; Y40, 2.8; Y42, 2.5; Q46, 2.5;
1OR0	2	F100, 3.8; F107, 4.1;
1OR0	3	E74, 1.8; V78, 1.0; W79, 6.9;
1OR7	3	I55, 1.9; V59, 1.9; I63, 2.1;
1OR7	5	W33, 2.8; H37, 2.4; L38, 1.2; I39, 2.4; M43, 2.3;
1OXK	3	V1098, 1.7; R1105, 2.9; M1106, 3.6;
1P27	3	Y124, 2.6; S135, 2.2; H140, 2.2;
1PGR	3	K17, 1.3; E20, 3.4; R23, 1.8;
1PQ1	9	F101, 4.3; Y105, 2.8; E87, 1.7; I90, 1.5; E93, 1.0; L94, 1.9; R95, 1.6; I97, 2.0; D99, 3.6;
1PZL	4	L10, 2.3; H11, 1.1; L14, 3.5; Q15, 1.8;
1QZ7	5	E470, 1.0; L473, 2.9; D474, 2.3; H476, 2.9; V480, 1.0;
1R4M	3	T492, 1.3; F496, 1.5; Q503, 3.5;
1R8U	3	E225, 1.7; L228, 2.1; L231, 2.4;
1RF8	3	F282, 6.6; K287, 2.5; K289, 2.4;
1RIW	4	W279, 6.0; I280, 1.6; V283, 1.7; I284, 1.9;
1RK8	4	L133, 1.0; S136, 2.0; L140, 2.7; H141, 4.3;
1RM1	4	T14, 1.2; I15, 4.0; L23, 1.2; L26, 2.1;
1RM1	5	L36, 3.0; R39, 1.6; V40, 1.3; V47, 1.9; L52, 2.0;
1RP3	8	D76, 1.8; K78, 1.5; V79, 1.4; V80, 1.7; L83, 2.3; I84, 1.7; F86, 2.5; F87, 4.8;
1RP3	5	K190, 1.8; Q194, 2.1; L195, 1.2; F197, 2.4; Y198, 2.5;
1SA0	3	H406, 2.1; W407, 4.5; E411, 1.2;
1SB0	3	E105, 1.1; L95, 2.0; L99, 3.4;
1SYQ	7	L608, 2.2; L609, 1.1; K613, 1.1; L615, 3.0; L622, 3.0; L623, 2.5; R624, 1.2;
1TCO	7	V349, 1.3; F350, 5.1; L354, 1.8; F356, 3.0; K360, 1.0; M364, 1.6; L369, 2.3;
1TI2	3	N18, 1.4; D25, 1.5; E26, 3.4;
1TN6	3	Y355, 1.8; Y358, 2.6; R361, 1.6;
1TQY	4	F109, 1.0; F116, 3.8; L119, 1.7; W120, 2.3;
1TQY	2	P149, 1.1; W154, 2.8;
1TQY	3	L114, 1.1; Y118, 3.8; L119, 1.0;
1TUE	3	I19, 2.4; Y23, 5.5; E24, 2.1;
1TY4	4	I50, 1.5; I54, 3.3; K57, 1.1; L58, 2.5;
1UKL	2	R371, 1.7; Y376, 2.2;
1UKV	4	E241, 1.9; Q244, 2.2; R248, 3.9; I252, 1.0;
1VCB	4	L158, 3.4; R161, 2.4; V166, 1.0; L169, 1.0;
1VF6	2	F159, 1.4; H166, 2.5;

A. PDB CODE	L. HOTSPOT RESIDUE HELIX POSITIONS	M. HOTSPOT RESIDUE END TO END LENGTH	N. HELIX LENGTH	O. HELIX START RESIDUE #	P. HELIX END RESIDUE #
1LQB	i; i+7; i+11; i+14;	15	17	67	83
1LUJ	i; i+1; i+7; i+8;	9	14	649	662
1M1E	i; i+7;	8	15	649	663
1M63	i; i+2; i+4; i+10; i+11;	12	15	349	363
1MF8	i; i+3; i+4; i+7; i+8;	9	12	359	370
1MXE	i; i+4; i+5; i+6; i+9; i+14; i+15; i+16; i+17; i+18;	19	21	298	318
1N1J	i; i+4; i+7; i+8;	9	15	126	140
1N1J	i; i+8;	9	29	78	106
1N1J	i; i+1; i+2; i+4; i+8; i+10; i+18;	19	29	63	91
1N2D	i; i+2; i+3; i+6; i+9; i+10; i+11; i+12;	12	46	808	853
1N4Q	i; i+7; i+8; i+10;	11	13	242	254
1NGM	i; i+7;	8	15	477	491
1NH2	i; i+4; i+7; i+8;	9	17	32	48
1NH2	i; i+1; i+4; i+8;	9	18	4	21
1NH2	i; i+4; i+11;	12	16	14	29
1NU7	i; i+4; i+7;	8	40	56	95
1NU9	i; i+8;	9	40	56	95
1NVM	i; i+3; i+7;	8	15	326	340
1NX0	i; i+3; i+6;	7	9	602	610
1OO0	i; i+4; i+8; i+11; i+15; i+16;	17	26	117	142
1OQP	i; i+2; i+3; i+6; i+7;	8	14	240	253
1OQS	i; i+6;	7	13	2	14
1OR0	i; i+1; i+3; i+7;	8	16	35	50
1OR0	i; i+7;	8	21	98	118
1OR0	i; i+4; i+5;	6	10	74	83
1OR7	i; i+4; i+8;	9	11	55	65
1OR7	i; i+4; i+5; i+6; i+10;	11	18	27	44
1OXK	i; i+7; i+8;	9	14	1097	1110
1P27	i; i+11; i+16;	17	26	116	141
1PGR	i; i+3; i+6;	7	29	12	40
1PQ1	i; i+3; i+6; i+7; i+8; i+10; i+12; i+14; i+18;	19	27	86	112
1PZL	i; i+1; i+4; i+5;	6	11	8	18
1QZ7	i; i+3; i+4; i+6; i+10;	11	12	470	481
1R4M	i; i+4; i+11;	12	21	491	511
1R8U	i; i+3; i+6;	7	12	225	236
1RF8	i; i+5; i+7;	8	12	280	291
1RIW	i; i+1; i+4; i+5;	6	10	277	286
1RK8	i; i+3; i+7; i+8;	9	26	117	142
1RM1	i; i+1; i+9; i+12;	13	16	14	29
1RM1	i; i+3; i+4; i+11; i+16;	17	22	34	55
1RP3	i; i+2; i+3; i+4; i+7; i+8; i+10; i+11;	11	13	76	88
1RP3	i; i+4; i+5; i+7; i+8;	9	13	187	199
1SA0	i; i+1; i+5;	6	8	405	412
1SB0	i; i+4; i+10;	11	21	89	109
1SYQ	i; i+1; i+5; i+7; i+14; i+15; i+16;	17	20	608	627
1TCO	i; i+1; i+5; i+7; i+11; i+15; i+20;	21	22	349	370
1TI2	i; i+7; i+8;	9	12	18	29
1TN6	i; i+3; i+6;	7	15	353	367
1TQY	i; i+7; i+10; i+11;	12	15	109	123
1TQY	i; i+5;	6	12	145	156
1TQY	i; i+4; i+5;	6	12	111	122
1TUE	i; i+4; i+5;	6	22	5	26
1TY4	i; i+4; i+7; i+8;	9	11	50	60
1UKL	i; i+5;	6	21	371	391
1UKV	i; i+3; i+7; i+11;	12	15	239	253
1VCB	i; i+3; i+8; i+11;	12	13	158	170
1VF6	i; i+7;	8	13	157	169

TABLE S3

A. PDB CODE	Q. HELIX SEQUENCE	R. RESOLUTION
1LQB	SHVLSKVCMYFTYKVRY	2.00
1LUJ	EGVATYAAAVLFRM	2.50
1M1E	EGVATYAAAVLFRMS	2.10
1M63	VFTWSLPFVGEKVTE	2.80
1MF8	EKVTEMLVNVLN	3.10
1MXE	FAKSKWKQAFNATAVVRHMRK	1.70
1N1J	DSYVEPLKLYLQKFR	1.67
1N1J	KDAKECVQECVSEFISFITSEASERCHQE	1.67
1N1J	AEAPVLFAKAAQIFITELTLRAWIHTEDN	1.67
1N2D	SQAIKYLQNNIKGFIIRQRVNDEMKVNCATLLQAAYRGHSIRANVF	2.00
1N4Q	EKELNRIKRWCIM	2.40
1NGM	EEASKLKERIWIGLN	2.95
1NH2	EQTLQDLKNIWQKKLTE	1.90
1NH2	AEASRVYEIIVESVVNEV	1.90
1NH2	TIGNSLVDALDTLISD	1.90
1NU7	KDAKDKLMTRILGEDQYLLERKKVQYEEYKKLYKKYKEEN	2.20
1NU9	KDAKDKLMTRILGEDQYLLERKKVQYEEYKKLYKKYKEEN	2.20
1NVM	EDMIVDVALDLLAAH	1.70
1NX0	AIDALSSDF	2.30
1OO0	PEGLRCFYYLVQDLKCLVFSLIGLHF	1.85
1OQP	KRELIESKWHRLLF	NOT APP
1OQS	LFQFGEMILQKTG	1.90
1OR0	APSAFYGYGWAQARSH	2.00
1OR0	PDFRANLDAFAAGINAYAQQN	2.00
1OR0	EQTTVWLLTN	2.00
1OR7	ISSRVMAAIEE	2.00
1OR7	PEMQKTWESYHLIRDSMR	2.00
1OXK	HVNQEVIKRMLNLE	2.10
1P27	PEGLRVFYYLVQDLKCLVFSLIGLHF	2.00
1PGR	QSFLLKCLEQVRKIQGDGAALQEKLCATY	3.50
1PQ1	PEIRIAQELRRIGDEFNETYTRRVFAN	1.65
1PZL	KILHRLLQEGS	2.10
1QZ7	ESILDEHVQRVM	2.20
1R4M	HTIAAFLGGAAAQEVIKIITK	3.00
1R8U	EEVLMSLVIEMG	NOT APP
1RF8	PTFLLQFKDKLN	NOT APP
1RIW	KKWIQKVIDQ	2.04
1RK8	PEGLRCFYYLVQDLKCLVFSLIGLHF	1.90
1RM1	TIGNSLVDALDTLISD	2.50
1RM1	ASLAMRVLETFDKVVAETLKDN	2.50
1RP3	DEKVVKGLIEFFT	2.30
1RP3	EREKLVIQLIFYE	2.30
1SA0	VHWYVGEG	3.58
1SB0	EKRIKELELLLMSTENELKGQ	NOT APP
1SYQ	LLQAAKGLAGAVSELLRSAQ	2.42
1TCO	VFTWSLPFVGEKVTEMLVNVLN	2.50
1TI2	NCFMGCMDEHEL	2.35
1TN6	KEYWRYIGRSLQSKH	1.80
1TQY	FDFTHREFRKLWSEG	2.00
1TQY	PSVMPAEVAWAV	2.00
1TQY	ATSLEREYLLLS	2.00
1TUE	KETLSERLSALQDKIIDHYEND	2.10
1TY4	IGYEIGSKLAA	2.20
1UKL	RKAIDYIKYLQQVNHKLRQEN	3.00
1UKV	LGELPQGFARLSAIY	1.50
1VCB	LKERCLQVVRSLV	2.70
1VF6	RDFQNAFKIHNAV	2.10

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1VG9	G H	G	THE CRYSTAL STRUCTURES OF THE REP-1 PROTEIN IN COMPLEX WITH C-TERMINALLY TRUNCATED RA
1VYT	A E	E	BETA3 SUBUNIT COMPLEXED WITH AID
1WA8	A B	A	SOLUTION STRUCTURE OF THE CFP-10.ESAT-6 COMPLEX. MAJOR VIRULENCE DETERMINANTS OF PATHO
1WA8	A B	B	SOLUTION STRUCTURE OF THE CFP-10.ESAT-6 COMPLEX. MAJOR VIRULENCE DETERMINANTS OF PATHO
1WPX	A B	A	CRYSTAL STRUCTURE OF CARBOXYPEPTIDASE Y INHIBITOR COMPLEXED WITH THE COGNATE PROTEIN
1WPX	A B	B	CRYSTAL STRUCTURE OF CARBOXYPEPTIDASE Y INHIBITOR COMPLEXED WITH THE COGNATE PROTEIN
1XB2	A B	A	CRYSTAL STRUCTURE OF BOS TAURUS MITOCHONDRIAL ELONGATION FACTOR TU/TS COMPLEX
1XB2	A B	B	CRYSTAL STRUCTURE OF BOS TAURUS MITOCHONDRIAL ELONGATION FACTOR TU/TS COMPLEX
1XKP	B C	C	CRYSTAL STRUCTURE OF THE VIRULENCE FACTOR YOPN IN COMPLEX WITH ITS HETERODIMERIC CHAP
1XLS	E M	M	CRYSTAL STRUCTURE OF THE MOUSE CAR/RXR LBD HETERODIMER BOUND TO TCPOBOP AND 9CRA AN
1Y74	A D	A	SOLUTION STRUCTURE OF MLIN-2/MLIN-7 L27 DOMAIN COMPLEX
1Y76	C B	C	SOLUTION STRUCTURE OF PATJ/PALS1 L27 DOMAIN COMPLEX
1YDI	A B	B	HUMAN VINCULIN HEAD DOMAIN (VH1, 1-258) IN COMPLEX WITH HUMAN ALPHA-ACTININ'S VINCULIN-
1YFN	D H	H	VERSATILE MODES OF PEPTIDE RECOGNITION BY THE AAA+ ADAPTOR PROTEIN SSPB- THE CRYSTAL ST
1YKE	C D	D	STRUCTURE OF THE MEDIATOR MED7/MED21 SUBCOMPLEX
1YOV	A B	A	INSIGHTS INTO THE UBIQUITIN TRANSFER CASCADE FROM THE REFINED STRUCTURE OF THE ACTIVAT
1Z8U	C D	C	CRYSTAL STRUCTURE OF OXIDIZED ALPHA HEMOGLOBIN BOUND TO AHSP
1ZDT	A P	P	THE CRYSTAL STRUCTURE OF HUMAN STEROIDOGENIC FACTOR-1
1ZL8	A B	A	NMR STRUCTURE OF L27 HETERODIMER FROM C. ELEGANS LIN-7 AND H. SAPIENS LIN-2 SCAFFOLD PRO
1ZUN	A B	A	CRYSTAL STRUCTURE OF A GTP-REGULATED ATP SULFURYLASE HETERODIMER FROM PSEUDOMONAS
1ZUZ	A B	B	CALMODULIN IN COMPLEX WITH A MUTANT PEPTIDE FROM HUMAN DRP- 1 KINASE
1ZW3	A B	B	VINCULIN HEAD (0-258) IN COMPLEX WITH THE TALIN ROD RESIDUES 1630-1652
2A6Q	A E	A	CRYSTAL STRUCTURE OF YEFM-YOEB COMPLEX
2A6Q	A E	A	CRYSTAL STRUCTURE OF YEFM-YOEB COMPLEX
2A6Q	C F	F	CRYSTAL STRUCTURE OF YEFM-YOEB COMPLEX
2AFF	A B	B	THE SOLUTION STRUCTURE OF THE KI67FHA/HNIFK(226-269)3P COMPLEX
2AST	B C	C	CRYSTAL STRUCTURE OF SKP1-SKP2-CKS1 IN COMPLEX WITH A P27 PEPTIDE
2AVU	B E	E	STRUCTURE OF THE ESCHERICHIA COLI FLHDC COMPLEX, A PROKARYOTIC HETEROMERIC REGULATOR
2B87	A B	A	STRUCTURAL BASIS FOR MOLECULAR RECOGNITION IN AN AFFIBODY:AFFIBODY COMPLEX
2B9S	A B	B	CRYSTAL STRUCTURE OF HETERODIMERIC L. DONOVANI TOPOISOMERASE I-VANADATE-DNA COMPLEX
2BCX	A B	B	CRYSTAL STRUCTURE OF CALMODULIN IN COMPLEX WITH A RYANODINE RECEPTOR PEPTIDE
2BE6	B E	E	2.0 A CRYSTAL STRUCTURE OF THE CAV1.2 IQ DOMAIN-CA/CAM COMPLEX
2BGN	B E	E	HIV-1 TAT PROTEIN DERIVED N-TERMINAL NONAPEPTIDE TRP2-TAT (1-9) BOUND TO THE ACTIVE SITE OF
2BNQ	A E	A	STRUCTURAL AND KINETIC BASIS FOR HEIGHTENED IMMUNOGENICITY OF T CELL VACCINES
2BYK	D C	D	HISTONE FOLD HETERODIMER OF THE CHROMATIN ACCESSIBILITY COMPLEX
2BYK	D C	D	HISTONE FOLD HETERODIMER OF THE CHROMATIN ACCESSIBILITY COMPLEX
2BZW	A B	B	THE CRYSTAL STRUCTURE OF BCL-XL IN COMPLEX WITH FULL-LENGTH BAD
2C2V	B C	C	CRYSTAL STRUCTURE OF THE CHIP-UBC13-UEV1A COMPLEX
2C5I	T P	P	N-TERMINAL DOMAIN OF TLG1 COMPLEXED WITH N-TERMINUS OF VPS51 IN DISTORTED CONFORMATI
2C9W	B C	C	CRYSTAL STRUCTURE OF SOCS-2 IN COMPLEX WITH ELONGIN-B AND ELONGIN-C AT 1.9A RESOLUTION
2CJS	A C	A	STRUCTURAL BASIS FOR A MUNC13-1 DIMERIC - MUNC13-1 - RIM HETERODIMER SWITCH: C2-DOMAINS
2D10	A E	E	CRYSTAL STRUCTURE OF THE RADIXIN FERM DOMAIN COMPLEXED WITH THE NHERF-1 C-TERMINAL T
2D1P	G I	I	CRYSTAL STRUCTURE OF HETEROHEXAMERIC TUSBCD PROTEINS, WHICH ARE CRUCIAL FOR THE TRNA
2D7D	A B	A	STRUCTURAL INSIGHTS INTO THE CRYPTIC DNA DEPENDENT ATP-ASE ACTIVITY OF UVRB
2D7D	A B	B	STRUCTURAL INSIGHTS INTO THE CRYPTIC DNA DEPENDENT ATP-ASE ACTIVITY OF UVRB
2DOI	X C	C	THE X-RAY CRYSTALLOGRAPHIC STRUCTURE OF THE ANGIOGENESIS INHIBITOR, ANGIOSTATIN, BOUND
2DOQ	A D	D	CRYSTAL STRUCTURE OF SFI1P/CDC31P COMPLEX
2DOQ	B D	D	CRYSTAL STRUCTURE OF SFI1P/CDC31P COMPLEX
2DSR	B I	I	STRUCTURAL BASIS FOR THE INHIBITION OF INSULIN-LIKE GROWTH FACTORS BY IGF BINDING PROTEI
2DYM	E F	F	THE CRYSTAL STRUCTURE OF SACCHAROMYCES CEREVISIAE ATG5- ATG16(1-46) COMPLEX
2E30	A B	B	SOLUTION STRUCTURE OF THE CYTOPLASMIC REGION OF NA+/H+ EXCHANGER 1 COMPLEXED WITH ES
2E9X	A C	A	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	A D	A	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	A D	D	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	A D	D	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	B C	B	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	B C	C	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. $\Delta\Delta G_{SUM, CHAIN}$ (KCAL/MOL)	I. HELIX CONTRIBUTION
1VG9	PROTEIN BINDING/PROTEIN TRANSPORT	2.2	6.6	10.1	65%
1VYT	TRANSPORT PROTEIN	2.9	14.5	14.5	100%
1WA8	TUBERCULOSIS	4.2	12.6	29.6	43%
1WA8	TUBERCULOSIS	4.4	8.7	13.6	64%
1WPX	HYDROLASE	2.4	4.7	16.8	28%
1WPX	HYDROLASE	2.6	5.2	20.3	26%
1XB2	TRANSLATION	2.2	6.7	10.7	63%
1XB2	TRANSLATION	2.5	5.0	23.0	22%
1XKP	MEMBRANE PROTEIN/CHAPERON	2.1	8.5	12.2	70%
1XLS	TRANSCRIPTION	2.1	6.2	9.1	68%
1Y74	TRANSPORT PROTEIN	4.7	14.2	18.8	76%
1Y76	TRANSPORT PROTEIN	5.9	17.7	24.0	74%
1YDI	CELL ADHESION, STRUCTURAL PROTEIN	2.4	16.6	16.6	100%
1YFN	PROTEIN BINDING	2.4	4.7	11.7	40%
1YKE	GENE REGULATION	2.9	8.7	11.9	73%
1YOV	SIGNALING PROTEIN	2.0	6.1	32.9	19%
1Z8U	ELECTRON TRANSPORT	2.0	8.0	8.0	100%
1ZDT	TRANSCRIPTION	2.0	8.1	8.1	100%
1ZL8	PROTEIN BINDING	2.2	4.3	25.2	17%
1ZUN	TRANSFERASE	2.0	6.0	14.8	41%
1ZUZ	METAL BINDING PROTEIN/TRANSFERASE	2.6	21.1	22.7	93%
1ZW3	PROTEIN BINDING	2.2	8.6	10.0	86%
2A6Q	TOXIN INHIBITOR/TOXIN	2.1	8.5	15.0	57%
2A6Q	TOXIN INHIBITOR/TOXIN	2.4	9.5	15.0	63%
2A6Q	TOXIN INHIBITOR/TOXIN	2.2	6.7	22.9	29%
2AFF	CELL CYCLE	3.0	11.9	11.9	100%
2AST	CELL CYCLE/LIGASE/PROTEIN TURNOVER	2.6	12.9	18.6	69%
2AVU	TRANSCRIPTION ACTIVATOR	2.8	5.5	8.4	65%
2B87	PROTEIN BINDING	2.3	7.0	11.1	63%
2B9S	ISOMERASE/DNA	2.0	8.1	28.1	29%
2BCX	CALCIUM BINDING PROTEIN	2.2	15.1	15.1	100%
2BE6	MEMBRANE PROTEIN	2.1	14.9	14.9	100%
2BGN	HYDROLASE	2.3	6.8	15.1	45%
2BNQ	IMMUNE SYSTEM/RECEPTOR	2.2	6.6	6.6	100%
2BYK	DNA-BINDING PROTEIN	2.5	10.1	26.1	39%
2BYK	DNA-BINDING PROTEIN	2.7	5.4	26.1	21%
2BZW	TRANSCRIPTION	2.4	12.2	18.3	67%
2C2V	CHAPERONE	5.5	16.4	16.4	100%
2C5I	PROTEIN TRANSPORT	2.1	6.4	9.4	68%
2C9W	TRANSCRIPTION REGULATION	2.4	4.7	12.0	39%
2CJS	EXOCYTOSIS	2.1	6.2	11.6	53%
2D10	CELL ADHESION	2.9	8.6	9.9	87%
2D1P	TRANSLATION	2.6	15.5	15.5	100%
2D7D	HYDROLASE/DNA	2.5	7.6	12.7	60%
2D7D	HYDROLASE/DNA	3.1	9.3	10.5	89%
2DOI	HYDROLASE	2.0	6.1	6.1	100%
2DOQ	CELL CYCLE	2.5	7.6	7.6	100%
2DOQ	CELL CYCLE	3.4	13.7	13.7	100%
2DSR	PROTEIN BINDING/HORMONE/GROWTH FACTOR	2.4	4.7	8.0	59%
2DYM	PROTEIN TURNOVER/PROTEIN TURNOVER	2.2	13.0	25.8	50%
2E30	METAL BINDING PROTEIN/TRANSPORT PROTEIN	2.6	7.7	9.2	84%
2E9X	REPLICATION	2.0	8.0	13.1	61%
2E9X	REPLICATION	2.2	4.3	15.1	28%
2E9X	REPLICATION	2.6	10.4	21.8	48%
2E9X	REPLICATION	2.5	7.4	21.8	34%
2E9X	REPLICATION	2.1	4.1	27.3	15%
2E9X	REPLICATION	2.4	14.2	32.0	44%

A. PDB CODE	J. # HOTSPOT RESIDUES	K. HOTSPOT RESIDUES, RESIDUE #, ΔΔG (KCAL/MOL)
1VG9	3	Q382, 1.0; R386, 3.0; V390, 2.6;
1VYT	5	L430, 1.0; L434, 1.1; Y437, 4.8; W440, 5.9; I441, 1.7;
1WA8	3	F17, 1.9; D23, 1.0; L24, 9.7;
1WA8	2	I625, 7.5; L636, 1.2;
1WPX	2	W231, 3.5; Y239, 1.2;
1WPX	2	F507, 4.0; S514, 1.2;
1XB2	3	E193, 2.6; L194, 1.7; E198, 2.4;
1XB2	2	K60, 1.4; R67, 3.6;
1XKP	4	R66, 1.6; M69, 2.9; Q70, 1.3; L73, 2.7;
1XLS	3	L744, 1.4; L745, 2.9; L749, 1.9;
1Y74	3	L19, 1.8; D22, 5.2; L33, 7.2;
1Y76	3	L35, 3.7; F38, 11.8; L42, 2.2;
1YDI	7	W743, 5.8; L746, 1.5; L747, 2.6; I750, 1.8; I754, 1.7; E758, 1.2; I761, 2.0;
1YFN	2	P6, 1.1; K11, 3.6;
1YKE	3	M15, 2.6; F19, 4.4; L23, 1.7;
1YOV	3	Y478, 1.2; E481, 1.3; R484, 3.6;
1Z8U	4	D43, 1.7; F47, 2.8; Y48, 1.0; Y51, 2.5;
1ZDT	4	L744, 1.9; L745, 2.8; L748, 1.2; L749, 2.2;
1ZL8	2	L5, 1.6; L15, 2.7;
1ZUN	3	L11, 2.9; R20, 1.6; H7, 1.5;
1ZUZ	8	R304, 1.9; W305, 6.6; L307, 1.6; F309, 3.2; V312, 2.2; L314, 1.6; H317, 2.3; L318, 1.7;
1ZW3	4	L1633, 1.6; V1640, 1.6; L1647, 3.2; I1648, 2.2;
2A6Q	4	E53, 1.0; E59, 2.9; Y62, 2.6; L63, 2.0;
2A6Q	4	N69, 1.4; R72, 2.9; L73, 1.8; L80, 3.4;
2A6Q	3	W10, 2.5; Y13, 2.2; E8, 2.0;
2AFF	4	F241, 1.8; L242, 3.9; R245, 2.8; V249, 3.4;
2AST	5	E3040, 2.1; S3041, 1.4; E3042, 6.5; R3044, 1.7; N3045, 1.2;
2AVU	2	V71, 2.1; F82, 3.4;
2B87	3	W11, 1.2; W14, 3.5; F17, 2.3;
2B9S	4	R226, 2.1; I227, 1.6; I228, 1.0; W231, 3.4;
2BCX	7	L3623, 2.3; K3626, 1.0; R3628, 2.7; R3629, 1.6; V3632, 1.5; V3633, 1.8; F3636, 4.2;
2BE6	7	T1614, 1.3; K1617, 1.5; F1618, 4.5; Y1619, 1.6; F1622, 2.6; L1623, 1.0; I1624, 2.4;
2BGN	3	L132, 2.1; Q135, 2.4; E139, 2.3;
2BNQ	3	R65, 1.7; Q72, 3.3; T73, 1.6;
2BYK	4	F81, 3.6; L85, 2.1; L89, 1.1; Y92, 3.3;
2BYK	2	I37, 1.9; F44, 3.5;
2BZW	5	Y105, 2.8; L109, 2.5; D114, 2.0; F116, 3.7; E117, 1.2;
2C2V	3	F42, 1.8; L45, 13.1; L48, 1.5;
2C5I	3	R20, 2.3; L23, 2.5; F27, 1.6;
2C9W	2	H68, 3.6; R82, 1.1;
2CJS	3	E137, 2.1; W141, 2.4; L145, 1.7;
2D10	3	W348, 2.8; K351, 1.7; F355, 4.1;
2D1P	6	Y79, 3.5; T80, 1.4; F82, 3.7; V83, 3.3; R84, 1.3; V87, 2.3;
2D7D	3	F644, 3.7; E645, 1.6; R651, 2.3;
2D7D	3	F644, 4.0; E645, 1.5; R651, 3.8;
2DOI	3	L310, 3.1; K314, 1.9; H318, 1.1;
2DOQ	3	F237, 2.3; W240, 3.8; L245, 1.5;
2DOQ	4	F258, 3.2; L264, 2.6; F268, 2.2; W271, 5.7;
2DSR	2	E9, 1.4; F16, 3.3;
2DYM	6	L28, 1.8; I29, 1.5; R31, 1.8; L32, 2.6; R35, 3.9; E39, 1.4;
2E30	3	I522, 5.5; H523, 1.0; E535, 1.2;
2E9X	4	R71, 3.3; R74, 1.9; Y81, 1.3; R86, 1.5;
2E9X	2	W113, 2.2; Y124, 2.1;
2E9X	4	F129, 3.3; F133, 2.8; Y140, 3.1; L141, 1.2;
2E9X	3	Y87, 3.4; R94, 2.5; L97, 1.5;
2E9X	2	W121, 1.9; R129, 2.2;
2E9X	6	M1171, 1.3; L1175, 3.6; K1181, 1.2; D1185, 1.3; F1186, 2.8; W1189, 4.0;

TABLE S3

A. PDB CODE	L. HOTSPOT RESIDUE HELIX POSITIONS	M. HOTSPOT RESIDUE END TO END LENGTH	N. HELIX LENGTH	O. HELIX START RESIDUE #	P. HELIX END RESIDUE #
1VG9	i; i+4; i+8;	9	15	377	391
1VYT	i; i+4; i+7; i+10; i+11;	12	22	424	445
1WA8	i; i+6; i+7;	8	34	7	40
1WA8	i; i+11;	12	34	610	643
1WPX	i; i+8;	9	22	230	251
1WPX	i; i+7;	8	12	507	518
1XB2	i; i+1; i+5;	6	14	193	206
1XB2	i; i+7;	8	15	57	71
1XKP	i; i+3; i+4; i+7;	8	14	62	75
1XLS	i; i+1; i+5;	6	9	743	751
1Y74	i; i+3; i+14;	15	19	19	37
1Y76	i; i+3; i+7;	8	15	30	44
1YDI	i; i+3; i+4; i+7; i+11; i+15; i+18;	19	22	743	764
1YFN	i; i+5;	6	6	6	11
1YKE	i; i+4; i+8;	9	22	4	25
1YOV	i; i+3; i+6;	7	11	476	486
1Z8U	i; i+4; i+5; i+8;	9	21	34	54
1ZDT	i; i+1; i+4; i+5;	6	9	743	751
1ZL8	i; i+10;	11	17	4	20
1ZUN	i; i+4; i+13;	14	20	7	26
1ZUZ	i; i+1; i+3; i+5; i+8; i+10; i+13; i+14;	14	16	304	319
1ZW3	i; i+7; 15; 16;	16	19	1631	1649
2A6Q	i; i+6; i+9; i+10;	11	16	51	66
2A6Q	i; i+3; i+4; i+11;	12	16	67	82
2A6Q	i; i+2; i+5;	6	12	7	18
2AFF	i; i+1; i+4; i+8;	9	14	239	252
2AST	i; i+1; i+2; i+4; i+5;	7	8	3040	3047
2AVU	i; i+11;	12	20	67	86
2B87	i; i+3; i+6;	7	15	4	18
2B9S	i; i+1; i+2; i+5;	6	10	225	234
2BCX	i; i+3; i+5; i+6; 10; 11; 14;	14	23	3617	3639
2BE6	i; i+3; i+4; i+5; i+8; 10; 11;	11	13	1613	1625
2BGN	i; i+3; i+7;	8	19	126	144
2BNQ	i; i+7; i+8;	9	29	57	85
2BYK	i; i+4; i+8; i+11;	12	19	79	97
2BYK	i; i+7;	8	29	31	59
2BZW	i; i+4; i+9; i+11; i+12;	13	20	100	119
2C2V	i; i+3; i+6;	7	14	40	53
2C5I	i; i+3; i+7;	8	14	16	29
2C9W	i; i+14;	15	17	67	83
2CJS	i; i+4; i+8;	9	20	135	154
2D10	i; i+3; i+7;	8	10	348	357
2D1P	i; i+1; i+3; i+4; i+5; i+8;	9	11	79	89
2D7D	i; i+1; i+7;	8	11	644	654
2D7D	i; i+1; i+7;	8	16	644	659
2DOI	i; i+4; i+8;	9	20	307	326
2DOQ	i; i+3; i+8;	9	26	224	249
2DOQ	i; i+6; i+10; i+13;	14	41	252	292
2DSR	i; i+7;	8	12	8	19
2DYM	i; i+1; i+3; i+4; i+7; i+11;	12	18	24	41
2E30	i; i+1; i+13;	14	21	518	538
2E9X	i; i+3; i+10; i+15;	16	37	58	94
2E9X	i; i+11;	12	22	108	129
2E9X	i; i+4; i+11; i+12;	13	24	124	147
2E9X	i; i+7; i+10;	11	32	72	103
2E9X	i; i+8;	9	29	110	138
2E9X	i; i+4; 11; 15; 16; 19;	19	22	1170	1191

TABLE S3

A. PDB CODE	Q. HELIX SEQUENCE	R. RESOLUTION
1VG9	QGELPQCFCRMCAVF	2.50
1VYT	LREKQQLEEDLKGYLDWITQAE	2.60
1WA8	AATLAQEAGNFERISGDLKTQIDQVESTAGSLQG	NOT APP
1WA8	GIEAAASAIQGNVTSIHSLLDEGKQSLTKLAAAW	NOT APP
1WPX	VWSCVPATIYCNNAQLAPYQRT	2.70
1WPX	FAQASIDSYKKH	2.70
1XB2	ELVELEIRELLTEF	2.20
1XB2	ASSKELLMKLRRKTG	2.20
1XKP	VTLLRSLMQQALAW	1.70
1XLS	ALLRYLLDK	2.96
1Y74	LERDVSRAVELLERLQRSG	NOT APP
1Y76	TQNEKLSAFYETLKS	NOT APP
1YDI	WEQLLTTIARTINEVENQILTR	1.80
1YFN	PHQWQK	1.80
1YKE	RLTQLQICLDQMTEQFCATLNY	3.30
1YOV	DDYVHEFCRYG	2.60
1Z8U	EEDMVTVVEDWMNFYINYYRQ	2.40
1ZDT	ALLRYLLDK	2.10
1ZL8	NLERDVQRILELMEHVQ	NOT APP
1ZUN	HLKQLEAESIHIIREVAAEF	2.70
1ZUZ	RWKLDFSIVSLCNHLT	1.91
1ZW3	SVLAGHSRTVSDSIKKLIT	3.30
2A6Q	LEEYNSLEETAYLLRS	2.05
2A6Q	PANARRLMDSIDSLKS	2.05
2A6Q	EESWDDYLYWQE	2.05
2AFF	PTFLERRKSQVAEL	NOT APP
2AST	ESEWRNLG	2.30
2AVU	WEQNVHASMFCNAWQFLLKT	3.00
2B87	KFNKELGWATWEIFN	NOT APP
2B9S	PRIICSWAKA	2.27
2BCX	KAVWHKLLSKQRRRAVVACFRMT	2.00
2BE6	VTVGKFYATFLIQ	2.00
2BGN	PDEVVSLVNQGLQEGERDF	3.15
2BNQ	PEYWDGETRKVKAHSQTHRVDLGTLRGYY	1.70
2BYK	ESFVPSLTQDLEVYRKVVK	2.40
2BYK	KEARAAIARAASVFAIFVTSSSTALAHKQ	2.40
2BZW	WAAQRYGRELRRMSDEFEGS	2.30
2C2V	RNFRLLEELEEGQK	2.90
2C5I	LNKDRRLLLREFYN	2.30
2C9W	SHVLSKVCMYFTYKVRY	1.90
2CJS	EEEARYWAKKLEQLNAKLNS	1.78
2D10	WSKKNELFSN	2.50
2D1P	YTDFVRLTVKH	2.15
2D7D	FERAAELRDLL	2.10
2D7D	FERAAELRDLLLELKA	2.10
2DOI	DAELQRLKNERHEEAELERL	3.10
2DOQ	FANQAKLRVQEAVFYIWSDKTLKYSQ	3.00
2DOQ	NDEAESFRNTWLLFRSFQQWITLTQTFKEQSRLADQAFLNK	3.00
2DSR	AELVDALQFVCG	2.10
2DYM	MDDLLIRRLTDRNDKEAH	2.20
2E30	INEEIHTQFLDHLLTGIEDIC	NOT APP
2E9X	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRWEY	2.30
2E9X	AEEMEWFNNYKRSLATYMRSLG	2.30
2E9X	PEELAFAREFMANTESYLKNVALK	2.30
2E9X	DLKVSIHQMEMERIRYVLSSYLRCRLMKIEKF	2.30
2E9X	ADEIRTLVKDMWDTRIAKLRVSADSFVRQ	2.30
2E9X	EMERGLFQTGQKGLNDFQCWEK	2.30

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
2E9X	F G	G	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	F G	G	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2EFC	A B	A	ARA7-GDP/ATVPS9A
2EHB	A D	A	THE STRUCTURE OF THE C-TERMINAL DOMAIN OF THE PROTEIN KINASE ATSOS2 BOUND TO THE CALCIU
2EHO	B D	B	CRYSTAL STRUCTURE OF HUMAN GINS COMPLEX
2EHO	E F	E	CRYSTAL STRUCTURE OF HUMAN GINS COMPLEX
2EHO	J L	L	CRYSTAL STRUCTURE OF HUMAN GINS COMPLEX
2EQB	A B	B	CRYSTAL STRUCTURE OF THE RAB GTPASE SEC4P, THE SEC2P GEF DOMAIN, AND PHOSPHATE COMPLEX
2ES4	A D	D	CRYSTAL STRUCTURE OF THE BURKHOLDERIA GLUMAE LIPASE- SPECIFIC FOLDASE IN COMPLEX WITH
2EY4	A E	E	CRYSTAL STRUCTURE OF A CBF5-NOP10-GAR1 COMPLEX
2F66	A B	A	STRUCTURE OF THE ESCRT-I ENDOSOMAL TRAFFICKING COMPLEX
2F66	A C	A	STRUCTURE OF THE ESCRT-I ENDOSOMAL TRAFFICKING COMPLEX
2F66	A C	C	STRUCTURE OF THE ESCRT-I ENDOSOMAL TRAFFICKING COMPLEX
2FK0	Q R	R	CRYSTAL STRUCTURE OF A H5N1 INFLUENZA VIRUS HEMAGGLUTININ.
2FO1	A D	D	CRYSTAL STRUCTURE OF THE CSL-NOTCH-MASTERMIND TERNARY COMPLEX BOUND TO DNA
2FOT	A C	C	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN CALMODULIN AND ALPHAII-SPECTRIN
2FUG	A C	C	CRYSTAL STRUCTURE OF THE HYDROPHILIC DOMAIN OF RESPIRATORY COMPLEX I FROM THERMUS TH
2G38	A B	B	A PE/PPE PROTEIN COMPLEX FROM MYCOBACTERIUM TUBERCULOSIS
2G38	A B	B	A PE/PPE PROTEIN COMPLEX FROM MYCOBACTERIUM TUBERCULOSIS
2GGM	A C	C	HUMAN CENTRIN 2 XERODERMA PIGMENTOSUM GROUP C PROTEIN COMPLEX
2GL7	D E	E	CRYSTAL STRUCTURE OF A BETA-CATENIN/BCL9/TCF4 COMPLEX
2GMI	A B	B	MMS2/UBC13~UBIQUITIN
2GOX	C D	D	CRYSTAL STRUCTURE OF EFB-C / C3D COMPLEX
2HQW	A B	B	CRYSTAL STRUCTURE OF CA2+/CALMODULIN BOUND TO NMDA RECEPTOR NR1C1 PEPTIDE
2HUE	B C	B	STRUCTURE OF THE H3-H4 CHAPERONE ASF1 BOUND TO HISTONES H3 AND H4
2HUE	B C	B	STRUCTURE OF THE H3-H4 CHAPERONE ASF1 BOUND TO HISTONES H3 AND H4
2HUE	B C	C	STRUCTURE OF THE H3-H4 CHAPERONE ASF1 BOUND TO HISTONES H3 AND H4
2HV8	A D	D	CRYSTAL STRUCTURE OF GTP-BOUND RAB11 IN COMPLEX WITH FIP3
2I2R	B F	F	CRYSTAL STRUCTURE OF THE KCHIP1/KV4.3 T1 COMPLEX
2IBF	A B	B	HUMAN VINCULIN'S HEAD DOMAIN (VH1, RESIDUES 1-258) IN COMPLEX WITH TWO VINCULIN BINDING
2IO5	B C	B	CRYSTAL STRUCTURE OF THE CIA- HISTONE H3-H4 COMPLEX
2IZV	B C	C	CRYSTAL STRUCTURE OF SOCS-4 IN COMPLEX WITH ELONGIN-B AND ELONGIN-C AT 2.55A RESOLUTION
2J9U	C D	C	2 ANGSTROM X-RAY STRUCTURE OF THE YEAST ESCRT-I VPS28 C- TERMINUS IN COMPLEX WITH THE NZ
2JF9	B Q	Q	ESTROGEN RECEPTOR ALPHA LBD IN COMPLEX WITH A TAMOXIFEN- SPECIFIC PEPTIDE ANTAGONIST
2JFA	A P	P	ESTROGEN RECEPTOR ALPHA LBD IN COMPLEX WITH AN AFFINITY- SELECTED COREPRESSOR PEPTIDE
2JRI	A C	A	SOLUTION STRUCTURE OF THE JOSEPHIN DOMAIN OF ATAXIN-3 IN COMPLEX WITH UBIQUITIN MOLECU
2K2I	A B	B	NMR SOLUTION STRUCTURE OF THE C-TERMINAL DOMAIN (T94-Y172) OF THE HUMAN CENTRIN 2 IN CO
2NLA	A B	B	CRYSTAL STRUCTURE OF THE MCL-1:MNOXAB BH3 COMPLEX
2NNU	A B	B	CRYSTAL STRUCTURE OF THE PAPILLOMAVIRUS DNA TETHERING COMPLEX E2:BRD4
2NOJ	A B	B	CRYSTAL STRUCTURE OF EHP / C3D COMPLEX
2NUP	B C	C	CRYSTAL STRUCTURE OF THE HUMAN SEC23A/24A HETERODIMER, COMPLEXED WITH THE SNARE PROT
2O60	A B	B	CALMODULIN BOUND TO PEPTIDE FROM NEURONAL NITRIC OXIDE SYNTHASE
2O8A	B J	J	RAT PP1CGAMMA COMPLEXED WITH MOUSE INHIBITOR-2
2O8F	A B	B	HUMAN MUTSALPHA (MSH2/MSH6) BOUND TO DNA WITH A SINGLE BASE T INSERT
2OBH	A C	C	CENTRIN-XPC PEPTIDE
2ODE	A B	A	CRYSTAL STRUCTURE OF THE HETERODIMERIC COMPLEX OF HUMAN RGS8 AND ACTIVATED GI ALPHA 3
2OF5	E K	E	OLIGOMERIC DEATH DOMAIN COMPLEX
2ONL	B D	B	CRYSTAL STRUCTURE OF THE P38A-MAPKAP KINASE 2 HETERODIMER
2OT3	A B	A	CRYSTAL STRUCTURE OF RABEX-5 VPS9 DOMAIN IN COMPLEX WITH NUCLEOTIDE FREE RAB21
2OZA	A B	B	STRUCTURE OF P38ALPHA COMPLEX
2P1L	A B	B	STRUCTURE OF THE BCL-XL:BECLIN 1 COMPLEX
2P1N	D E	D	MECHANISM OF AUXIN PERCEPTION BY THE TIR1 UBIQUTIN LIGASE
2P22	A C	A	STRUCTURE OF THE YEAST ESCRT-I HETEROTETRAMER CORE
2P22	A C	C	STRUCTURE OF THE YEAST ESCRT-I HETEROTETRAMER CORE
2PBI	A B	A	THE MULTIFUNCTIONAL NATURE OF GBETA5/RGS9 REVEALED FROM ITS CRYSTAL STRUCTURE
2PBI	A B	A	THE MULTIFUNCTIONAL NATURE OF GBETA5/RGS9 REVEALED FROM ITS CRYSTAL STRUCTURE
2PBI	A B	A	THE MULTIFUNCTIONAL NATURE OF GBETA5/RGS9 REVEALED FROM ITS CRYSTAL STRUCTURE

TABLE S3

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. $\Delta\Delta G_{SUM, CHAIN}$ (KCAL/MOL)	I. HELIX CONTRIBUTION
2E9X	REPLICATION	3.2	9.6	16.9	57%
2E9X	REPLICATION	2.0	8.0	16.9	47%
2EFC	TRANSPORT PROTEIN	2.7	8.0	15.5	52%
2EHB	SIGNALLING PROTEIN/TRANSFERASE	2.0	5.9	17.9	33%
2EHO	REPLICATION	3.6	10.7	14.4	74%
2EHO	REPLICATION	2.4	4.7	15.7	30%
2EHO	REPLICATION	2.1	6.2	13.7	45%
2EQB	ENDOCYTOSIS/EXOCYTOSIS	2.3	6.9	6.9	100%
2ES4	HYDROLASE	2.0	4.0	9.5	42%
2EY4	ISOMERASE/BIOSYNTHETIC PROTEIN	2.0	7.8	18.6	42%
2F66	TRANSPORT PROTEIN	2.2	13.1	15.5	85%
2F66	TRANSPORT PROTEIN	3.4	10.2	11.3	90%
2F66	TRANSPORT PROTEIN	2.6	20.5	21.5	95%
2FK0	VIRAL PROTEIN	2.0	3.9	10.6	37%
2FO1	GENE REGULATION/SIGNALLING PROTEIN/DNA	2.2	4.4	5.4	81%
2FOT	METAL BINDING, STRUCTURAL PROTEIN	2.9	20.3	20.3	100%
2FUG	OXIDOREDUCTASE	3.4	6.8	7.9	86%
2G38	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	2.4	7.2	22.9	31%
2G38	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	2.5	4.9	22.9	21%
2GGM	CELL CYCLE	3.1	12.2	12.2	100%
2GL7	TRANSCRIPTION	2.1	6.3	13.6	46%
2GMI	LIGASE, HUMAN PROTEIN	2.6	7.9	9.5	83%
2GOX	CELL ADHESION/TOXIN	2.3	6.8	8.0	85%
2HQW	METAL BINDING PROTEIN	3.2	12.6	14.5	87%
2HUE	DNA BINDING PROTEIN	3.1	9.3	24.8	38%
2HUE	DNA BINDING PROTEIN	2.1	10.3	24.8	42%
2HUE	DNA BINDING PROTEIN	2.5	17.2	22.5	76%
2HV8	PROTEIN TRANSPORT	2.4	7.2	7.2	100%
2I2R	TRANSPORT PROTEIN	3.7	7.3	46.4	16%
2IBF	CELL ADHESION, STRUCTURAL PROTEIN	3.3	19.8	27.9	71%
2IO5	CHAPERONE/STRUCTURAL PROTEIN	2.0	7.8	13.3	59%
2IZV	TRANSCRIPTION	2.0	6.1	10.3	59%
2J9U	PROTEIN TRANSPORT	2.0	3.9	3.9	100%
2JF9	TRANSCRIPTION	2.2	10.9	10.9	100%
2JFA	TRANSCRIPTION	2.3	6.8	6.8	100%
2JRI	HYDROLASE/SIGNALING PROTEIN	2.0	6.0	17.9	34%
2K2I	CELL CYCLE	4.6	9.2	9.2	100%
2NLA	APOPTOSIS	2.2	8.6	8.6	100%
2NNU	TRANSCRIPTION	2.6	10.2	14.3	71%
2NOJ	IMMUNE SYSTEM	2.0	6.1	6.1	100%
2NUP	PROTEIN TRANSPORT	2.5	10.1	14.1	72%
2O60	METAL BINDING PROTEIN	2.5	25.1	25.1	100%
2O8A	HYDROLASE/INHIBITOR	2.1	6.4	25.3	25%
2O8F	DNA BINDING PROTEIN/DNA	2.1	4.2	25.5	16%
2OBH	CELL CYCLE	3.6	14.4	14.4	100%
2ODE	SIGNALING PROTEIN	2.1	6.3	8.6	73%
2OF5	APOPTOSIS	2.8	5.5	9.3	59%
2ONL	TRANSFERASE	2.6	10.5	14.1	74%
2OT3	PROTEIN TRANSPORT	2.7	5.4	11.2	48%
2OZA	SIGNALING PROTEIN/TRANSFERASE	2.2	6.6	27.8	24%
2P1L	APOPTOSIS	2.0	10.2	10.2	100%
2P1N	SIGNALING PROTEIN	2.1	4.1	12.4	33%
2P22	TRANSPORT PROTEIN	3.2	12.8	27.7	46%
2P22	TRANSPORT PROTEIN	2.0	8.0	19.9	40%
2PBI	SIGNALING PROTEIN	2.4	7.1	45.7	16%
2PBI	SIGNALING PROTEIN	2.1	8.2	45.7	18%
2PBI	SIGNALING PROTEIN	2.7	10.7	45.7	23%

TABLE S3

A. PDB CODE	J. # HOTSPOT RESIDUES	K. HOTSPOT RESIDUES, RESIDUE #, ΔΔG (KCAL/MOL)
2E9X	3	L175, 2.3; F186, 3.3; W189, 4.0;
2E9X	4	L139, 1.1; F142, 1.4; F146, 3.4; M150, 2.1;
2EFC	3	Y225, 4.7; T228, 1.0; F236, 2.3;
2EHB	3	L132, 1.6; L139, 2.0; E142, 2.3;
2EHO	3	R74, 1.0; D82, 1.1;
2EHO	2	Y87, 3.3; R94, 1.4;
2EHO	3	W71, 1.5; L72, 3.2; L76, 1.5;
2EQB	3	E102, 2.4; D103, 1.3; F109, 3.2;
2ES4	2	R268, 1.0; D276, 3.0;
2EY4	4	R45, 2.8; K49, 2.2; R50, 1.4; L53, 1.4;
2F66	6	L356, 2.7; F359, 1.0; R368, 1.1; F371, 3.0; W375, 2.3; H376, 3.0;
2F66	3	V332, 2.4; D340, 6.5; M348, 1.3;
2F66	8	F184, 1.0; I185, 1.7; Y188, 4.9; L189, 1.7; R192, 4.1; H196, 2.4; L197, 2.4; E200, 2.3;
2FK0	2	V100, 1.9; H111, 2.0;
2FO1	2	R71, 2.3; Y81, 2.1;
2FOT	7	W1192, 4.5; R1196, 2.1; L1197, 2.8; V1199, 2.3; T1204, 1.2; F1205, 4.4; K1209, 3.0;
2FUG	2	M107, 5.1; L113, 1.7;
2G38	3	W31, 3.5; E37, 2.0; F45, 1.7;
2G38	2	Y153, 3.0; L161, 1.9;
2GGM	4	W848, 5.4; L851, 2.1; L855, 2.9; L856, 1.8;
2GL7	3	V44, 1.1; L48, 3.6; V49, 1.6;
2GMI	3	L11, 1.0; E18, 1.4; F8, 5.5;
2GOX	3	H130, 2.1; R131, 1.9; N138, 2.8;
2HQW	4	T879, 1.5; F880, 5.0; L887, 4.6; S890, 1.5;
2HUE	3	F67, 4.9; I74, 1.4; F78, 3.0;
2HUE	5	L100, 2.0; V101, 1.5; F104, 1.9; L92, 2.8; Y99, 2.1;
2HUE	7	I50, 2.7; L58, 1.3; K59, 1.0; F61, 2.8; E63, 4.9; I66, 3.3; V70, 1.2;
2HV8	3	Q735, 1.0; D739, 4.0; M746, 2.2;
2I2R	2	F111, 6.2; L118, 1.1;
2IBF	6	I566, 2.4; Y567, 10.2; K571, 1.2; L577, 3.2; S578, 1.1; L581, 1.7;
2IO5	4	L100, 1.9; F104, 3.0; L92, 1.5; Y99, 1.4;
2IZV	3	S67, 1.3; H68, 3.6; R82, 1.2;
2J9U	2	H178, 1.7; R190, 2.2;
2JF9	5	L12, 2.1; R5, 1.0; W7, 2.8; F8, 4.0; K9, 1.0;
2JFA	3	L13, 2.1; L5, 1.2; I9, 3.5;
2JRI	3	V31, 1.4; S34, 1.5; H38, 3.1;
2K2I	2	L651, 2.2; W658, 7.0;
2NLA	4	L78, 2.8; I81, 1.6; D83, 2.8; V85, 1.4;
2NNU	4	I1345, 2.2; F1349, 3.3; D1352, 2.3; L1353, 2.4;
2NOJ	3	H74, 1.7; R75, 1.3; N82, 3.1;
2NUP	4	D116, 6.6; Q120, 1.2; K121, 1.2; K124, 1.1;
2O60	10	L10, 4.5; E12, 1.0; V14, 2.1; K15, 1.0; F16, 3.9; K19, 1.0; L20, 2.0; F7, 5.0; K8, 1.4; K9, 3.2;
2O8A	3	K137, 2.1; F141, 2.4; H148, 1.9;
2O8F	2	F1222, 2.8; I1227, 1.4;
2OBH	4	W848, 7.7; L851, 1.7; L855, 3.1; L856, 1.9;
2ODE	3	E207, 2.7; K210, 2.4; H213, 1.2;
2OF5	2	R118, 3.1; Q125, 2.4;
2ONL	4	H126, 2.6; F129, 4.4; L130, 2.5; R136, 1.0;
2OT3	2	Y354, 3.6; F365, 1.8;
2OZA	3	H126, 2.6; F129, 1.9; Y132, 2.1;
2P1L	5	L112, 1.6; L116, 2.2; K117, 1.3; D121, 2.0; F123, 3.1;
2P1N	2	V151, 3.0; W157, 1.1;
2P22	4	Y329, 9.2; D340, 1.4; L345, 1.0; R347, 1.2;
2P22	4	L150, 2.6; K153, 2.4; L154, 1.0; E169, 2.0;
2PBI	3	E69, 2.8; L73, 1.0; F76, 3.3;
2PBI	4	L244, 2.5; I247, 1.4; V248, 1.6; Y250, 2.7;
2PBI	4	I226, 1.8; Y228, 3.2; Y229, 2.7; L233, 3.0;

A. PDB CODE	L. HOTSPOT RESIDUE HELIX POSITIONS	M. HOTSPOT RESIDUE END TO END LENGTH	N. HELIX LENGTH	O. HELIX START RESIDUE #	P. HELIX END RESIDUE #
2E9X	i; i+11; i+14;	15	23	170	192
2E9X	i; i+3; i+7; i+11;	12	24	131	154
2EFC	i; i+3; i+11;	12	18	222	239
2EHB	i; i+7; i+10;	11	15	129	143
2EHO	i; i+8;	9	35	58	92
2EHO	i; i+7;	8	14	84	97
2EHO	i; i+1; i+5;	6	8	70	77
2EQB	i; i+1; i+7;	8	54	84	137
2ES4	i; i+8;	9	35	263	297
2EY4	i; i+4; i+5; i+8;	9	13	42	54
2F66	i; i+3; i+12; i+15; i+19; i+20;	21	26	356	381
2F66	i; i+8; i+16;	17	29	323	351
2F66	i; i+1; i+4; i+5; i+8; i+12; i+13; i+16;	14	26	178	203
2FK0	i; i+11;	12	24	94	117
2FO1	i; i+10;	11	17	68	84
2FOT	i; i+4; i+5; i+7; 13; 14; 18;	18	21	1191	1211
2FUG	i; i+6;	7	17	98	114
2G38	i; i+6; i+14;	15	29	22	50
2G38	i; i+8;	9	36	129	164
2GGM	i; i+3; i+7; i+8;	9	16	848	863
2GL7	i; i+4; i+5;	6	9	42	50
2GMI	i; i+3; i+10;	11	14	6	19
2GOX	i; i+1; i+8;	9	14	127	140
2HQW	i; i+1; i+8; i+11;	12	16	877	892
2HUE	i; i+7; i+11;	12	16	64	79
2HUE	i; i+7; i+8; i+9; i+12;	13	29	86	114
2HUE	i; i+8; i+9; i+11; i+13; i+16; i+20;	21	27	50	76
2HV8	i; i+4; i+11;	12	31	717	747
2I2R	i; i+7;	8	14	108	121
2IBF	i; i+1; i+5; i+11; i+12; i+15;	16	18	565	582
2IO5	i; i+7; i+8; i+12;	13	29	86	114
2IZV	i; i+1; i+15;	16	17	67	83
2J9U	i; i+12;	13	19	174	192
2JF9	i; i+2; i+3; i+4; i+7;	8	9	5	13
2JFA	i; i+4; i+8;	9	13	2	14
2JRI	i; i+3; i+7;	8	22	30	51
2K2I	i; i+7;	8	10	651	660
2NLA	i; i+3; i+5; i+7;	8	15	77	91
2NNU	i; i+4; i+7; i+8;	9	11	1345	1355
2NOJ	i; i+1; i+8;	9	14	71	84
2NUP	i; i+4; i+5; i+8;	9	10	116	125
2O60	i; i+1; i+2; i+3; i+5; i+7; i+8; i+9; i+12; i+13;	14	15	7	21
2O8A	i; i+4; i+11;	12	18	132	149
2O8F	i; i+5;	6	20	1221	1240
2OBH	i; i+3; i+7; i+8;	9	15	848	862
2ODE	i; i+3; i+6;	7	10	205	214
2OF5	i; i+7;	8	11	117	127
2ONL	i; i+3; i+4; i+10;	11	21	124	144
2OT3	i; i+11;	12	18	351	368
2OZA	i; i+3; i+6;	7	21	124	144
2P1L	i; i+4; i+5; i+9; i+11;	12	21	106	126
2P1N	i; i+6;	7	14	146	159
2P22	i; i+11; i+16; i+18;	19	30	323	352
2P22	i; i+3; i+4; i+19;	20	25	147	171
2PBI	i; i+4; i+7;	8	14	67	80
2PBI	i; i+3; i+4; i+6;	7	15	240	254
2PBI	i; i+2; i+3; i+7;	8	17	219	235

A. PDB CODE	Q. HELIX SEQUENCE	R. RESOLUTION
2E9X	EMERGLFQTGQKGLNDFQCWEKG	2.30
2E9X	NADISQSLLQTFIGRFRRIMDSSQ	2.30
2EFC	EAAYFFTNILSAESFISN	2.09
2EHB	REELKEMVVALLHES	2.10
2EHO	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRW	3.00
2EHO	RIRYVLSSYLRCRL	3.00
2EHO	LWLAKGLF	3.00
2EQB	NELRTKAEEEADKLNKEVEDLTASLFDEANNMVADARKEKYAIEILNKRLTEQL	2.70
2ES4	PEAAARAAQMQQDDEAWQTRYQAYAAERDRIAAQG	1.85
2EY4	GEYRRRWKREVLG	2.11
2F66	LDTFVKQGRELARQQFLVRWHIQRIT	2.80
2F66	DGLNQLYNLVAQDYALTDTIEALSRMLHR	2.80
2F66	ADDLDQFIKNYLDIRTQYHLRREKLA	2.80
2FK0	YNAELLVLMENERTLDFHDSNVKN	2.95
2FO1	ELHRQRSELARANYEKA	3.12
2FOT	PWKSARLMVHTVATFNSIKER	2.45
2FUG	DVVREAQAGMVEFTLLN	3.30
2G38	DSMLAAARAWRSLDVEMTAVQRSFNRTLL	2.20
2G38	TAQIADLDQEYDDFWDEDGEVMRDYRLRVSDALSKL	2.20
2GGM	WKLLAKGLLIRERLKR	2.35
2GL7	ADVKSSLVN	2.60
2GMI	RNFRLLEELEKGEK	2.50
2GOX	VSAHRKAQKAVNLV	2.20
2HQW	KATFRAITSTLASSFK	1.90
2HUE	KLPFQRLVREIAQDFK	1.70
2HUE	SSAVMALQEASEAYLVALFEDTNLCAIHA	1.70
2HUE	IYEETRGVLKVFLENVIRDAVTYTEHA	1.70
2HV8	RDELMEAIQKQEEINFRLQDYIDRIIVAIME	1.86
2I2R	FEDFVTALSILLRG	3.35
2IBF	AIYEKAKEVSSALSKVLS	3.20
2IO5	SSAVMALQEASEAYLVGLFEDTNLCAIHA	2.70
2IZV	SHVLSKVCMYFTYKVRY	2.55
2J9U	KDQLHPLLAELLISINRVT	2.00
2JF9	REWFKDMLS	2.10
2JFA	AFQLRQLILRGLQ	2.55
2JRI	PVELSSIAHQLDEEERMRMAEG	NOT APP
2K2I	LHRALQAWVT	NOT APP
2NLA	QLRRIGDKVNLRQKL	2.80
2NNU	IDMNFQSDLLS	1.59
2NOJ	VATHRKAQRAVNLI	2.70
2NUP	DTFIQKTKKL	2.80
2O60	FKKLAEAVKFSAKLM	1.55
2O8A	PEEREKKRQFEMKRKLHY	2.61
2O8F	TFDGTAIANAVVKELAETIK	3.25
2OBH	WKLLAKGLLIRERLK	1.80
2ODE	RSERKKWIHC	1.90
2OF5	DRQINQLAQRL	3.20
2ONL	DDHVQFLIYQILRGLKYIHSA	4.00
2OT3	EDGYYFTNLCCAVAFIEK	2.10
2OZA	DDHVQFLIYQILRGLKYIHSA	2.70
2P1L	SGTMENLSRRLKVTGDLFDIM	2.50
2P1N	EEEEEVRRENQWAF	2.50
2P22	DGLNQLYNLVAQDYALTDTIECLSRMLHRG	2.70
2P22	DIALKKKLEQNTKKLDEESSQLETT	2.70
2PBI	NLEAQNLGNFIVKY	1.95
2PBI	SSVSLGGIVKYSEQF	1.95
2PBI	VTAVRKEIMYYQQALMR	1.95

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
2PJW	H V	H	THE VPS27/HSE1 COMPLEX IS A GAT DOMAIN-BASED SCAFFOLD FOR UBIQUITIN-DEPENDENT SORTING
2PQK	A B	B	X-RAY CRYSTAL STRUCTURE OF HUMAN MCL-1 IN COMPLEX WITH BIM BH3
2PQN	A B	B	CRYSTAL STRUCTURE OF YEAST FIS1 COMPLEXED WITH A FRAGMENT OF YEAST MDV1
2PQR	A C	C	CRYSTAL STRUCTURE OF YEAST FIS1 COMPLEXED WITH A FRAGMENT OF YEAST CAF4
2PRG	A C	C	LIGAND-BINDING DOMAIN OF THE HUMAN PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR GAMM
2PSM	B C	B	CRYSTAL STRUCTURE OF INTERLEUKIN 15 IN COMPLEX WITH INTERLEUKIN 15 RECEPTOR ALPHA
2PV2	D F	F	CRYSTALLOGRAPHIC STRUCTURE OF SURA FIRST PEPTIDYL-PROLYL ISOMERASE DOMAIN COMPLEXED
2Q0O	A C	C	CRYSTAL STRUCTURE OF AN ANTI-ACTIVATION COMPLEX IN BACTERIAL QUORUM SENSING
2QAC	A T	T	THE CLOSED MTIP-MYOSINA-TAIL COMPLEX FROM THE MALARIA PARASITE INVASION MACHINERY
2QB0	A D	A	STRUCTURE OF THE 2TEL CRYSTALLIZATION MODULE FUSED TO T4 LYSOZYME WITH AN ALA-GLY-PRO
2QIY	A C	C	YEAST DEUBIQUITINASE UBP3 AND BRE5 COFACTOR COMPLEX
2QL2	A B	B	CRYSTAL STRUCTURE OF THE BASIC-HELIX-LOOP-HELIX DOMAINS OF THE HETERODIMER E47/NEUROD
2QLV	A B	A	CRYSTAL STRUCTURE OF THE HETEROTRIMER CORE OF THE S. CEREVISIAE AMPK HOMOLOG SNF1
2QXV	A B	B	STRUCTURAL BASIS OF EZH2 RECOGNITION BY EED
2R17	A C	C	FUNCTIONAL ARCHITECTURE OF THE RETROMER CARGO-RECOGNITION COMPLEX
2RGN	D E	E	CRYSTAL STRUCTURE OF P63RHOGEF COMPLEX WITH GALPHA-Q AND RHOA
2ROC	A B	B	SOLUTION STRUCTURE OF MCL-1 COMPLEXED WITH PUMA
2ROD	A B	B	SOLUTION STRUCTURE OF MCL-1 COMPLEXED WITH NOXAA
2SIV	C D	C	SIV GP41 CORE STRUCTURE
2SIV	C D	D	SIV GP41 CORE STRUCTURE
2UXN	A B	A	STRUCTURAL BASIS OF HISTONE DEMETHYLATION BY LSD1 REVEALED BY SUICIDE INACTIVATION
2V1D	A B	A	STRUCTURAL BASIS OF LSD1-COREST SELECTIVITY IN HISTONE H3 RECOGNITION
2V6Q	A B	B	CRYSTAL STRUCTURE OF A BHRF-1 : BIM BH3 COMPLEX
2V6X	A B	A	STRACTURAL INSIGHT INTO THE INTERACTION BETWEEN ESCRT-III AND VPS4
2VE7	A C	A	CRYSTAL STRUCTURE OF A BONSAI VERSION OF THE HUMAN NDC80 COMPLEX
2VE7	A C	A	CRYSTAL STRUCTURE OF A BONSAI VERSION OF THE HUMAN NDC80 COMPLEX
2VE7	A C	C	CRYSTAL STRUCTURE OF A BONSAI VERSION OF THE HUMAN NDC80 COMPLEX
2VE7	A C	C	CRYSTAL STRUCTURE OF A BONSAI VERSION OF THE HUMAN NDC80 COMPLEX
2VGO	A D	D	CRYSTAL STRUCTURE OF AURORA B KINASE IN COMPLEX WITH REVERSINE INHIBITOR
2VOF	C D	D	STRUCTURE OF MOUSE A1 BOUND TO THE PUMA BH3-DOMAIN
2VOI	A B	B	STRUCTURE OF MOUSE A1 BOUND TO THE BID BH3-DOMAIN
2W85	A B	B	STRUCTURE OF PEX14 IN COMPEX WITH PEX19
2WAX	A B	B	STRUCTURE OF THE HUMAN DDX6 C-TERMINAL DOMAIN IN COMPLEX WITH AN EDC3-FDF PEPTIDE
2WIN	H N	N	C3 CONVERTASE (C3BBB) STABILIZED BY SCIN
2WME	D C	D	CRYSTALLOGRAPHIC STRUCTURE OF BETAINE ALDEHYDE DEHYDROGENASE FROM PSEUDOMONAS AE
2Z2S	A B	A	CRYSTAL STRUCTURE OF RHODOBACTER SPHAEROIDES SIGE IN COMPLEX WITH THE ANTI-SIGMA CHR
2Z2T	A D	A	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN GP41 FRAGMENT N36 AND FUSION INHIBITOR SC34E
2Z2T	B E	B	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN GP41 FRAGMENT N36 AND FUSION INHIBITOR SC34E
2Z2T	C F	C	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN GP41 FRAGMENT N36 AND FUSION INHIBITOR SC34E
2Z3R	C D	C	CRYSTAL STRUCTURE OF THE IL-15/IL-15RA COMPLEX
2ZL1	A B	B	MP1-P14 SCAFFOLDING COMPLEX
3B9F	L H	L	1.6 A STRUCTURE OF THE PCI-THROMBIN-HEPARIN COMPLEX
3BC1	A B	B	CRYSTAL STRUCTURE OF THE COMPLEX RAB27A-SLP2A
3BEG	A B	A	CRYSTAL STRUCTURE OF SR PROTEIN KINASE 1 COMPLEXED TO ITS SUBSTRATE ASF/SF2
3BL2	A C	C	CRYSTAL STRUCTURE OF M11, THE BCL-2 HOMOLOG OF MURINE GAMMA- HERPESVIRUS 68, COMPLEXE
3BOW	B C	B	STRUCTURE OF M-CALPAIN IN COMPLEX WITH CALPASTATIN
3BOW	B C	C	STRUCTURE OF M-CALPAIN IN COMPLEX WITH CALPASTATIN
3BPL	A B	A	CRYSTAL STRUCTURE OF THE IL4-IL4R-COMMON GAMMA TERNARY COMPLEX
3BPQ	A B	A	CRYSTAL STRUCTURE OF RELB-RELE ANTITOXIN-TOXIN COMPLEX FROM METHANOCOCCUS JANNASC
3BRT	A B	B	NEMO/IKK ASSOCIATION DOMAIN STRUCTURE
3BRV	A B	B	NEMO/IKKB ASSOCIATION DOMAIN STRUCTURE
3BS5	A B	B	CRYSTAL STRUCTURE OF HCNK2-SAM/DHYP-SAM COMPLEX
3BXK	A B	B	CRYSTAL STRUCTURE OF THE P/Q-TYPE CALCIUM CHANNEL (CAV2.1) IQ DOMAIN AND CA2+CALMODUL
3C4M	A C	C	STRUCTURE OF HUMAN PARATHYROID HORMONE IN COMPLEX WITH THE EXTRACELLULAR DOMAIN O
3C59	A B	A	CRYSTAL STRUCTURE OF THE LIGAND-BOUND GLUCAGON-LIKE PEPTIDE- 1 RECEPTOR EXTRACELLULA
3D7V	A B	B	CRYSTAL STRUCTURE OF MCL-1 IN COMPLEX WITH AN MCL-1 SELECTIVE BH3 LIGAND
3DA7	G H	H	A CONFORMATIONALLY STRAINED, CIRCULAR PERMUTANT OF BARNASE

TABLE S3

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM,\ HELIX}$ (KCAL/MOL)	H. $\Delta\Delta G_{SUM,\ CHAIN}$ (KCAL/MOL)	I. HELIX CONTRIBUTION
2PJW	ENDOCYTOSIS/EXOCYTOSIS	2.2	6.6	28.3	23%
2PQK	APOPTOSIS	2.2	20.0	21.1	95%
2PQN	APOPTOSIS	2.4	12.2	14.1	87%
2PQR	APOPTOSIS	3.2	12.6	12.6	100%
2PRG	COMPLEX (THIAZOLIDINEDIONE/RECEPTOR)	2.0	8.1	8.1	100%
2PSM	CYTOKINE	2.7	13.5	19.5	69%
2PV2	ISOMERASE	2.1	10.4	11.5	90%
2Q0O	TRANSCRIPTION	2.4	9.4	14.2	66%
2QAC	MEMBRANE PROTEIN	2.3	18.0	18.0	100%
2QB0	HYDROLASE REGULATOR	3.0	9.0	11.5	78%
2QIY	SIGNALING PROTEIN/HYDROLASE	2.4	7.1	14.8	48%
2QL2	TRANSCRIPTION/DNA	2.0	12.0	13.8	87%
2QLV	TRANSFERASE/PROTEIN BINDING	2.6	5.1	11.9	43%
2QXV	GENE REGULATION	2.4	14.2	14.2	100%
2R17	PROTEIN TRANSPORT	2.3	4.5	9.5	47%
2RGN	SIGNALING PROTEIN COMPLEX	2.1	6.3	13.8	46%
2ROC	APOPTOSIS	2.4	12.1	12.1	100%
2ROD	APOPTOSIS	2.5	12.4	12.4	100%
2SIV	ENVELOPE GLYCOPROTEIN	2.1	8.2	9.6	85%
2SIV	ENVELOPE GLYCOPROTEIN	2.0	3.9	9.6	41%
2UXN	OXIDOREDUCTASE/TRANSCRIPTION REGULATOR	2.4	9.7	26.6	36%
2V1D	OXIDOREDUCTASE/REPRESSOR	2.0	5.9	23.3	25%
2V6Q	APOPTOSIS	2.1	12.7	12.7	100%
2V6X	PROTEIN TRANSPORT	2.3	6.8	11.5	59%
2VE7	CELL CYCLE	2.4	7.2	30.1	24%
2VE7	CELL CYCLE	2.0	4.0	30.1	13%
2VE7	CELL CYCLE	2.6	5.1	28.9	18%
2VE7	CELL CYCLE	2.7	13.4	28.9	46%
2VGO	TRANSFERASE	2.5	4.9	20.1	24%
2VOF	APOPTOSIS	2.5	17.3	19.4	89%
2VOI	APOPTOSIS	2.1	8.2	8.2	100%
2W85	PROTEIN TRANSPORT	2.0	4.0	4.0	100%
2WAX	HYDROLASE	2.3	6.8	18.7	36%
2WIN	IMMUNE SYSTEM	2.0	6.1	10.8	56%
2WME	OXIDOREDUCTASE	2.3	4.5	18.4	24%
2Z2S	TRANSCRIPTION	2.4	7.1	27.8	26%
2Z2T	VIRAL PROTEIN/INHIBITOR	2.4	9.4	9.4	100%
2Z2T	VIRAL PROTEIN/INHIBITOR	2.0	7.8	7.8	100%
2Z2T	VIRAL PROTEIN/INHIBITOR	2.2	6.6	9.0	73%
2Z3R	CYTOKINE/CYTOKINE RECEPTOR	2.8	8.3	10.4	80%
2ZL1	PROTEIN BINDING	2.0	6.1	14.4	42%
3B9F	HYDROLASE/HYDROLASE INHIBITOR	2.3	9.0	17.6	51%
3BC1	SIGNALING PROTEIN/TRANSPORT PROTEIN	2.1	10.6	15.3	69%
3BEG	TRANSFERASE/SPLICING	3.5	7.0	12.4	56%
3BL2	VIRAL PROTEIN/APOPTOSIS	2.4	12.1	12.1	100%
3BOW	HYDROLASE/HYDROLASE INHIBITOR	2.0	5.9	13.7	43%
3BOW	HYDROLASE/HYDROLASE INHIBITOR	2.2	6.5	8.8	74%
3BPL	CYTOKINE/CYTOKINE RECEPTOR	2.0	8.1	12.6	64%
3BPQ	TOXIN	2.2	11.1	13.1	85%
3BRT	TRANSFERASE/TRANSCRIPTION	2.5	4.9	7.8	63%
3BRV	TRANSFERASE/TRANSCRIPTION	2.0	8.0	12.7	63%
3BS5	SIGNALING PROTEIN/MEMBRANE PROTEIN	2.3	11.5	11.5	100%
3BXK	MEMBRANE PROTEIN, SIGNALING PROTEIN	2.1	12.3	12.3	100%
3C4M	MEMBRANE PROTEIN	2.8	11.3	12.4	91%
3C59	SIGNALING PROTEIN/SIGNALING PROTEIN	2.2	4.3	8.6	50%
3D7V	APOPTOSIS	2.4	17.1	17.1	100%
3DA7	PROTEIN BINDING	2.7	13.7	18.3	75%

A. PDB CODE	J. # HOTSPOT RESIDUES	K. HOTSPOT RESIDUES, RESIDUE #, ΔΔG (KCAL/MOL)
2PJW	3	L359, 2.6; E363, 1.6; Y366, 2.4;
2PQK	9	L10, 2.2; R11, 3.2; I13, 2.2; D15, 2.7; F17, 2.7; Y21, 2.2; E3, 1.8; W5, 1.0; I6, 2.0;
2PQN	5	L148, 1.6; F149, 4.0; F152, 3.9; Y155, 1.5; L156, 1.2;
2PQR	4	L126, 2.3; F127, 4.6; F130, 4.0; I137, 1.7;
2PRG	4	K632, 1.1; L633, 2.3; L636, 1.5; L637, 3.2;
2PSM	5	E46, 4.6; Q48, 1.1; V49, 2.4; H52, 2.0; E53, 3.4;
2PV2	5	F10, 1.1; T3, 1.2; L4, 1.6; W7, 5.2; D8, 1.3;
2Q0O	4	R40, 1.8; Y50, 2.6; W53, 3.8; L54, 1.2;
2QAC	8	R806, 4.3; V807, 1.7; Q808, 2.2; H810, 3.4; I811, 2.3; R812, 1.1; K813, 2.0; V816, 1.0;
2QB0	3	E68, 1.3; Y72, 3.4; R73, 4.3;
2QIY	3	E216, 1.8; F217, 2.4; R224, 2.9;
2QL2	6	K139, 1.1; L143, 3.0; K147, 2.1; Y149, 1.9; I150, 1.9; L153, 2.0;
2QLV	2	L516, 2.5; Y523, 2.6;
2QXV	6	F42, 4.3; R46, 1.5; I49, 2.2; R52, 2.4; L56, 1.7; W60, 2.1;
2R17	2	F534, 3.4; F541, 1.1;
2RGN	3	E215, 1.4; W216, 1.3; Y220, 3.6;
2ROC	5	L141, 3.9; I144, 2.1; D146, 1.1; L148, 1.8; Y152, 3.2;
2ROD	5	F23, 3.6; L27, 2.4; I30, 2.7; D32, 1.1; W38, 2.6;
2SIV	4	V558, 1.0; L565, 1.8; W571, 2.3; L576, 3.1;
2SIV	2	W631, 2.6; I642, 1.3;
2UXN	4	I474, 2.4; F478, 3.7; D486, 1.5; Y494, 2.1;
2V1D	3	F478, 2.8; R485, 1.9; D486, 1.2;
2V6Q	6	W57, 2.2; I58, 1.8; E61, 3.1; L62, 2.3; R63, 1.4; F69, 1.9;
2V6X	3	F60, 2.1; L64, 1.5; R66, 3.2;
2VE7	3	L1128, 1.0; Y1138, 3.8; L1142, 2.4;
2VE7	2	W187, 2.1; I194, 1.9;
2VE7	2	F82, 3.5; I98, 1.6;
2VE7	5	F127, 1.1; F130, 4.2; R131, 1.2; Y138, 5.7; F141, 1.2;
2VGO	2	L807, 1.2; Y815, 3.7;
2VOF	7	W133, 3.2; I137, 2.2; L141, 2.1; R142, 2.7; I144, 1.1; D146, 3.9; L148, 2.1;
2VOI	4	I82, 1.5; I86, 2.3; L90, 2.0; D95, 2.4;
2W85	2	F105, 1.3; F110, 2.7;
2WAX	3	K215, 1.9; F219, 3.4; I222, 1.5;
2WIN	3	F60, 2.7; K61, 1.5; Y68, 1.9;
2WME	2	R269, 2.8; M276, 1.7;
2Z2S	3	F30, 3.6; H32, 1.1; K38, 2.4;
2Z2T	4	Q1551, 1.0; L1565, 4.2; L1568, 2.2; W1571, 2.0;
2Z2T	4	H2564, 1.0; L2565, 2.1; L2568, 2.2; W2571, 2.5;
2Z2T	3	Q3551, 1.6; L3568, 2.3; W3571, 2.7;
2Z3R	3	E46, 3.6; V49, 1.0; E53, 3.7;
2ZL1	3	I48, 1.5; I52, 1.8; Y56, 2.8;
3B9F	4	E14, 1.4; E14, 2.9; L14, 2.1; Y14, 2.6;
3BC1	5	I15, 1.3; V18, 1.7; R21, 2.6; L25, 2.0; R32, 3.0;
3BEG	2	D564, 3.6; E571, 3.4;
3BL2	5	L110, 2.9; L114, 2.5; K115, 1.3; D119, 1.3; F121, 4.1;
3BOW	3	F103, 1.4; L106, 2.7; L110, 1.8;
3BOW	3	I653, 2.7; L656, 2.7; D659, 1.1;
3BPL	4	R81, 2.1; R85, 1.0; R88, 3.4; W91, 1.6;
3BPQ	5	E21, 3.0; I23, 1.0; L24, 2.4; L28, 2.6; M32, 2.1;
3BRT	2	R75, 2.0; L93, 2.9;
3BRV	4	R75, 2.4; F82, 2.1; E89, 1.3; F92, 2.2;
3BS5	5	I165, 1.7; H167, 2.9; Q168, 1.6; L170, 3.2; E173, 2.1;
3BXK	6	I1961, 1.9; Y1962, 1.6; M1965, 1.0; I1967, 3.1; Y1971, 2.7; R1972, 2.0;
3C4M	4	R20, 5.9; W23, 1.8; L24, 2.6; L28, 1.0;
3C59	2	L32, 1.7; W39, 2.6;
3D7V	7	E55, 2.7; W57, 1.0; I58, 3.3; R63, 2.7; I65, 2.4; D67, 2.9; Y73, 2.1;
3DA7	5	L35, 1.6; D36, 1.5; D40, 6.7; C41, 1.0; W45, 2.9;

A. PDB CODE	L. HOTSPOT RESIDUE HELIX POSITIONS	M. HOTSPOT RESIDUE END TO END LENGTH	N. HELIX LENGTH	O. HELIX START RESIDUE #	P. HELIX END RESIDUE #
2PJW	i; i+4; i+7;	8	16	354	369
2PQK	i; i+2; i+3; i+7; i+8; i+10; i+12; i+14; i+18;	19	22	1	22
2PQN	i; i+1; i+4; i+7; i+8;	9	16	148	163
2PQR	i; i+1; i+4; i+11;	12	15	126	140
2PRG	i; i+1; i+4; i+5;	6	8	631	638
2PSM	i; i+2; i+3; i+6; i+7;	8	19	36	54
2PV2	i; i+1; i+4; i+5; i+7;	8	9	3	11
2Q0O	i; i+10; i+13; i+14;	15	33	25	57
2QAC	i; i+1; i+2; i+4; i+5; i+6; i+7; i+10;	8	13	805	817
2QB0	i; i+4; i+5;	6	8	67	74
2QIY	i; i+1; i+8;	9	16	214	229
2QL2	i; i+4; i+8; i+10; i+11; i+14;	15	19	139	157
2QLV	i; i+7;	8	14	516	529
2QXV	i; i+4; i+7; i+10; i+14; i+18;	19	23	41	63
2R17	i; i+7;	8	22	524	545
2RGN	i; i+1; i+5;	6	21	210	230
2ROC	i; i+3; i+5; i+7; i+11;	12	25	131	155
2ROD	i; i+4; i+7; i+9; i+15;	16	19	22	40
2SIV	i; i+7; i+13; i+18;	19	35	547	581
2SIV	i; i+11;	12	32	629	660
2UXN	i; i+4; i+12; i+20;	21	40	474	513
2V1D	i; i+7; i+8;	9	34	474	507
2V6Q	i; i+1; i+4; i+5; i+6; i+12;	13	19	53	71
2V6X	i; i+4; i+6;	7	31	50	80
2VE7	i; 11; 15;	15	20	1124	1143
2VE7	i; i+7;	8	22	177	198
2VE7	i; i+16;	17	21	79	99
2VE7	i; i+3; i+4; i+11; i+14;	15	29	114	142
2VGO	i; i+8;	9	13	805	817
2VOF	i; i+4; i+8; i+9; i+11; i+13; i+15;	16	20	133	152
2VOI	i; i+4; i+8; i+13;	14	21	79	99
2W85	i; i+5;	6	11	102	112
2WAX	i; i+4; i+7;	8	12	215	226
2WIN	i; i+1; i+8;	9	24	60	83
2WME	i; i+7;	8	11	267	277
2Z2S	i; i+2; i+8;	9	19	23	41
2Z2T	i; i+14; i+17; i+20;	21	35	1547	1581
2Z2T	i; i+1; i+4; i+7;	8	34	2547	2580
2Z2T	i; 18; 21;	21	35	3547	3581
2Z3R	i; i+3; i+7;	8	20	36	55
2ZL1	i; i+4; i+8;	9	20	42	61
3B9F	i; i+2; i+3; i+7;	8	9	14	14
3BC1	i; i+3; i+6; i+10; i+17;	18	29	7	35
3BEG	i; i+7;	8	13	561	573
3BL2	i; i+4; i+5; i+9; i+11;	12	17	107	123
3BOW	i; i+3; i+7;	8	14	99	112
3BOW	i; i+3; i+6;	7	9	652	660
3BPL	i; i+4; i+7; i+10;	11	26	70	95
3BPQ	i; i+2; i+3; i+7; i+11;	12	22	14	35
3BRT	i; i+18;	19	60	50	109
3BRV	i; i+7; i+14; i+17;	18	60	50	109
3BS5	i; i+2; i+3; i+5; i+8;	9	19	165	183
3BXK	i; i+1; i+4; i+6; 11; 12;	12	16	1961	1976
3C4M	i; i+3; i+4; i+8;	9	19	16	34
3C59	i; i+7;	8	22	32	53
3D7V	i; i+2; i+3; i+8; i+10; i+12; i+18;	19	22	54	75
3DA7	i; i+1; i+5; i+10;	11	12	35	46

TABLE S3

A. PDB CODE	Q. HELIX SEQUENCE	R. RESOLUTION
2PJW	SLRQVLANAERSYNQL	3.01
2PQK	RPEIWIAQELRRIGDEFNAYYA	2.00
2PQN	LFQGFKSYLPIAELAI	2.15
2PQR	LFEGFKATVSIIQQR	1.88
2PRG	HKLVQLLT	2.30
2PSM	KVTAMNCFLLELQVILHEY	2.19
2PV2	TLKFWDIFR	1.30
2Q0O	KSELEALAVSAIREHRRLLWADQAVYEEWLRAS	2.00
2QAC	MRVQAHIRKRMVA	1.70
2QB0	KEDFRYRS	2.56
2QIY	EAEFAAASVQRYELNM	1.69
2QL2	KIETLRLAKNYIWALSEIL	2.50
2QLV	LDVMGEIYIALKNL	2.60
2QXV	MFSSNRQKILERTETLNQEWKQR	1.82
2R17	RIRFTLPPLVFAAYQLAFRYKE	2.80
2RGN	IQQIYEWHRDYFLQELQRCLK	3.50
2ROC	EEWAREIGAQLRRIADDLNAQYERR	NOT APP
2ROD	EFAAQLRKIGDKVYCTWSA	NOT APP
2SIV	GIVQQQQQLLDVVKRQQELLRLTVWGTKNLQTRVT	2.20
2SIV	QEWERKVDFLEENITALLEEAQIQQEKNMYEL	2.20
2UXN	ITAEFLVKSKHRDLTALCKEYDELAETQGKLEEKLQELEA	2.72
2V1D	ITAEFLVKSKHRDLTALCKEYDELAETQGKLEEK	3.10
2V6Q	RPEIWIAQELRRIGDEFNA	2.70
2V6X	PKSKDLIRAKFTEYLNRAEQLKKHLESEEAN	1.98
2VE7	NAERLKRLQKSADLYKDRLG	2.88
2VE7	TWPHIVAALVWLIDCIKIHTAM	2.88
2VE7	MEGFLPFSNLVTHLDSFLPIC	2.88
2VE7	AKRTSRFLSGIINFIHFREACRETYMEFL	2.88
2VGO	NLLTQAIRQQYYK	1.70
2VOF	WAREIGAQLRRIADDLNAQY	1.80
2VOI	QEEIIHNIARHLAQIGDEMDH	2.10
2W85	QEKFFQELFDS	NOT APP
2WAX	KAAVFEEIDTYE	2.30
2WIN	FKKMSEAKYQLQKIYNEIDEALKS	3.90
2WME	LDRAADIAVMA	2.10
2Z2S	EAAFAELFQHFAPKVKGFL	2.70
2Z2T	DIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL	2.10
2Z2T	DIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARI	2.10
2Z2T	DIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL	2.10
2Z3R	KVTAMKCFLLELQVISLESG	2.00
2ZL1	ARVTAAIASNIWAAYDRNGN	2.00
3B9F	ERELLESYI	1.60
3BC1	PEFEEQEAIMKVLQRDAALKRAEEERVRH	1.80
3BEG	RDEDHIALIIELL	2.90
3BL2	MENLSRRLKVTGDLFDI	2.30
3BOW	EERQFRKLFVQLAG	2.40
3BOW	PIDALSEDL	2.40
3BPL	AQQFHRHKQLIRFLKRLDRNLWGLAG	2.93
3BPQ	RKEYEKIEEILDIGLAKAMEET	2.20
3BRT	TLQRCLEENQELRDAIRQSNQILRERCEELLHFQASQREEKEFLMCKFQEARKLVERLGL	2.25
3BRV	TLQRCLEENQELRDAIRQSNQILRERCEELLHFQASQREEKEFLMCKFQEARKLVERLGL	2.20
3BS5	IGHQELILEAVDLLCALNY	2.00
3BXK	IYAAMMIMEYYRQSKA	2.55
3C4M	NSMERVEWLRKKLQDVHNF	1.95
3C59	LWETVQKWREYRRQCQRSLTED	2.30
3D7V	PEIWIAQEARRIGDEANAYYAR	2.03
3DA7	LDALWDCLTGWV	2.25

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
3DCG	A B	B	CRYSTAL STRUCTURE OF THE HIV VIF BC-BOX IN COMPLEX WITH HUMAN ELONGINB AND ELONGINC
3DD7	C D	D	STRUCTURE OF DOCH66Y IN COMPLEX WITH THE C-TERMINAL DOMAIN OF PHD
3DI2	A B	A	CRYSTAL STRUCTURE OF THE COMPLEX OF HUMAN INTERLEUKIN-7 WITH UNGLYCOSYLATED HUMAN
3DI2	C D	C	CRYSTAL STRUCTURE OF THE COMPLEX OF HUMAN INTERLEUKIN-7 WITH UNGLYCOSYLATED HUMAN
3DVE	A B	B	CRYSTAL STRUCTURE OF CA2+/CAM-CAV2.2 IQ DOMAIN COMPLEX
3DVU	B D	D	CRYSTAL STRUCTURE OF THE COMPLEX OF MURINE GAMMA- HERPESVIRUS 68 BCL-2 HOMOLOG M11 A
3E95	B C	C	CRYSTAL STRUCTURE OF THE PLASMODIUM FALCIPARUM UBIQUITIN CONJUGATING ENZYME COMPLE
3EAB	B H	B	CRYSTAL STRUCTURE OF SPASTIN MIT IN COMPLEX WITH ESCRT III
3EAB	D J	J	CRYSTAL STRUCTURE OF SPASTIN MIT IN COMPLEX WITH ESCRT III
3EX7	A B	A	THE CRYSTAL STRUCTURE OF EJC IN ITS TRANSITION STATE
3EX7	A C	C	THE CRYSTAL STRUCTURE OF EJC IN ITS TRANSITION STATE
3EZQ	K L	K	CRYSTAL STRUCTURE OF THE FAS/FADD DEATH DOMAIN COMPLEX
3FAL	C D	D	HUMANRXR ALPHA & MOUSE LXR ALPHA COMPLEXED WITH RETENOIC ACID AND GSK2186
3FWB	A B	B	SAC3:SUS1:CDC31 COMPLEX
3G9V	C D	D	CRYSTAL STRUCTURE OF A SOLUBLE DECOY RECEPTOR IL-22BP BOUND TO INTERLEUKIN-22
3GJX	B A	A	CRYSTAL STRUCTURE OF THE NUCLEAR EXPORT COMPLEX CRM1- SNURPORTIN1-RANGTP
3GJX	B A	B	CRYSTAL STRUCTURE OF THE NUCLEAR EXPORT COMPLEX CRM1- SNURPORTIN1-RANGTP
3GJX	E D	D	CRYSTAL STRUCTURE OF THE NUCLEAR EXPORT COMPLEX CRM1- SNURPORTIN1-RANGTP
3H6P	A C	C	CRYSTAL STRUCTURE OF RV3019C-RV3020C FROM MYCOBACTERIUM TUBERCULOSIS
3HHR	A C	A	HUMAN GROWTH HORMONE AND EXTRACELLULAR DOMAIN OF ITS RECEPTOR: CRYSTAL STRUCTURE
3HJW	A B	B	STRUCTURE OF A FUNCTIONAL RIBONUCLEOPROTEIN PSEUDOURIDINE SYNTHASE BOUND TO A SUBST

TABLE S3

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. $\Delta\Delta G_{SUM, CHAIN}$ (KCAL/MOL)	I. HELIX CONTRIBUTION
3DCG	LIGASE/VIRAL PROTEIN	2.0	3.9	7.9	49%
3DD7	RIBOSOME INHIBITOR	4.9	24.4	26.6	92%
3DI2	CYTOKINE/CYTOKINE RECEPTOR	2.4	9.7	13.5	72%
3DI2	CYTOKINE/CYTOKINE RECEPTOR	2.1	6.4	9.2	70%
3DVE	MEMBRANE PROTEIN	2.6	18.1	20.0	91%
3DVU	VIRAL PROTEIN/APOPTOSIS	2.0	7.9	9.1	87%
3E95	LIGASE	2.2	11.2	11.2	100%
3EAB	CELL CYCLE	2.8	8.3	9.6	86%
3EAB	CELL CYCLE	2.1	10.6	12.1	88%
3EX7	HYDROLASE/RNA BINDING PROTEIN/RNA	2.4	12.1	14.7	82%
3EX7	HYDROLASE/RNA BINDING PROTEIN/RNA	2.7	10.6	10.6	100%
3EZQ	APOPTOSIS	2.6	7.7	9.2	84%
3FAL	SIGNALING PROTEIN	2.0	3.9	6.2	63%
3FWB	CELL CYCLE, TRANSCRIPTION	3.3	19.9	19.9	100%
3G9V	CYTOKINE/CYTOKINE RECEPTOR	2.2	4.3	8.6	50%
3GJX	PROTEIN TRANSPORT	2.7	5.3	13.1	40%
3GJX	PROTEIN TRANSPORT	2.1	8.3	14.9	56%
3GJX	PROTEIN TRANSPORT	2.0	3.9	9.7	40%
3H6P	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	2.1	6.4	7.5	85%
3HHR	HORMONE/RECEPTOR	2.1	8.3	8.3	100%
3HJW	ISOMERASE/RNA	2.1	8.3	18.7	44%

A. PDB CODE	J. # HOTSPOT RESIDUES	K. HOTSPOT RESIDUES, RESIDUE #, ΔΔG (KCAL/MOL)
3DCG	2	H68, 2.6; M75, 1.3;
3DD7	5	E55, 1.6; F56, 2.6; L59, 2.0; F60, 17.0; D61, 1.2;
3DI2	4	K10, 3.2; V15, 1.8; L16, 3.3; V18, 1.4;
3DI2	3	D74, 1.0; L77, 1.4; L80, 4.0;
3DVE	7	M1854, 1.5; K1856, 1.6; I1863, 3.1; F1864, 1.9; F1866, 3.9; Y1867, 4.3; K1868, 1.8;
3DVU	4	L112, 1.9; L116, 1.6; D121, 1.2; F123, 3.2;
3E95	5	F28, 5.1; L31, 1.3; D32, 1.6; L34, 2.2; Q38, 1.0;
3EAB	3	R117, 1.5; H120, 2.1; F124, 4.7;
3EAB	5	E184, 2.9; Q185, 3.7; D186, 1.1; L188, 1.9; R191, 1.0;
3EX7	5	Y124, 2.1; D128, 1.7; S135, 2.4; L139, 1.9; H140, 4.0;
3EX7	4	R387, 2.0; R390, 4.5; D391, 2.2; Q394, 1.9;
3EZQ	3	Y291, 2.2; I295, 4.5; T305, 1.0;
3FAL	2	L400, 1.4; R413, 2.5;
3FWB	6	K789, 1.7; L794, 1.0; K795, 3.5; F798, 1.3; F799, 4.1; W802, 8.3;
3G9V	2	P50, 1.4; F57, 2.9;
3GJX	2	F561, 2.4; K568, 2.9;
3GJX	4	M1, 1.5; E2, 1.1; L4, 2.9; L8, 2.8;
3GJX	2	V518, 1.2; L525, 2.7;
3H6P	3	Y21, 3.0; L25, 1.2; I32, 2.2;
3HHR	4	D11, 2.1; N12, 2.0; R16, 1.9; R8, 2.3;
3HJW	4	R45, 2.8; R46, 2.3; K49, 1.7; R50, 1.5;

TABLE S3

A. PDB CODE	L. HOTSPOT RESIDUE HELIX POSITIONS	M. HOTSPOT RESIDUE END TO END LENGTH	N. HELIX LENGTH	O. HELIX START RESIDUE #	P. HELIX END RESIDUE #
3DCG	i; i+7;	8	17	67	83
3DD7	i; i+1; i+4; i+5; i+6;	7	11	53	63
3DI2	i; i+5; i+6; i+8;	9	18	9	26
3DI2	i; i+3; i+6;	7	18	74	123
3DVE	i; i+2; i+9; i+10; i+12; i+13; i+14;	15	17	1854	1870
3DVU	i; i+4; i+9; i+11;	12	18	108	125
3E95	i; i+3; i+4; i+6; i+10;	11	15	26	40
3EAB	i; i+3; i+7;	8	28	110	137
3EAB	i; i+1; i+2; i+4; i+7;	8	19	174	192
3EX7	i; i+4; i+11; i+15; i+16;	17	27	116	142
3EX7	i; i+3; i+4; i+7;	8	12	385	396
3EZQ	i; i+4; i+14;	15	32	287	318
3FAL	i; i+13;	14	30	399	428
3FWB	i; i+5; i+6; i+9; i+10; i+13;	14	52	753	804
3G9V	i; i+7;	8	17	50	66
3GJX	i; i+7;	8	14	559	572
3GJX	i; i+1; i+3; i+7;	8	11	0	10
3GJX	i; i+7;	8	22	510	531
3H6P	i; i+4; i+11;	12	19	21	39
3HHR	i; i+3; i+4; i+8;	9	28	6	33
3HJW	i; i+1; i+4; i+5;	6	12	42	53

TABLE S3

A. PDB CODE	Q. HELIX SEQUENCE	R. RESOLUTION
3DCG	SHVLSKVCMYFTYKVRY	2.40
3DD7	DAEFASLFDTL	1.70
3DI2	GKQYESVLMVSIDQLLDS	2.70
3DI2	DFDLHLLKVSEGTTILLK	2.70
3DVE	MGKVYAALMIFDFYKQN	2.35
3DVU	TMENLSRRLKVTGDLFDI	2.50
3E95	RSFRLLDELERGQKG	2.50
3EAB	SMEAERVRVFHKQAFEYISIALRIDEDE	2.50
3EAB	GSVGTSVASAEQDELSQRL	2.50
3EX7	PEGLRVFYYLVQDLKCLVFSLIGLHFK	2.30
3EX7	DIRILRDIEQYY	2.30
3EZQ	KKEAYDTLIKDLKKANLCTLAEKIQTIILKDI	2.73
3FAL	PLMFPRMLMKLVSLRTLSSVHSEQVFALRL	2.36
3FWB	EANYRKDFIDTMTRELYDAFLHERLYLIYMDSRAELKRNSTLKKKFFEKWQA	2.50
3G9V	PYITNRTFMLAKEASLA	2.76
3GJX	WKFLKTVVNKLFEF	2.50
3GJX	SMEELSQALAS	2.50
3GJX	EEDEKRFLVTVIKDLLGLCEQK	2.50
3H6P	YAGTLQSLGADIASEQAVL	1.91
3HHR	LSRLFDNAMLRAHRLHQLAFDTYQEFEE	2.80
3HJW	GEYRRRWKREVL	2.35

Table S4. Dataset of Weak Interface HIPP interactions

Description of Entries

A. PDB code of predicted target.
B. Chains in the complex featuring a helix at the interface.
C. Candidate helix to be mimicked is part of the indicated chain.
D. Title of PDB entry.
E. Function of protein complex.
F. $\Delta\Delta G_{avg}$/helix is derived from Rosetta computational alanine mutagenesis studies and indicates the average free energy penalty for mutating two or more key residues in the helix at the interface to alanine.
G. $\Delta\Delta G_{sum}$/helix is derived from Rosetta computational alanine mutagenesis studies and indicates the average free energy penalty for mutating two or more key residues at the interface to alanine.
H. Number of hot spot residues in helix.
I. Length of candidate helix to be mimicked
J. First residue of the candidate helix segment.
K. Last residue of the candidate helix segment.
L. Sequence of candidate helix to be mimicked.
M. Resolution of PDB structure (NOT APP indicates NMR structure).

TABLE S4

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1A02	F J	F	STRUCTURE OF THE DNA BINDING DOMAINS OF NFAT, FOS AND JUN BOUND TO DNA
1A02	F J	J	STRUCTURE OF THE DNA BINDING DOMAINS OF NFAT, FOS AND JUN BOUND TO DNA
1A0O	C D	C	CHEY-BINDING DOMAIN OF CHEA IN COMPLEX WITH CHEY
1A93	A B	A	NMR SOLUTION STRUCTURE OF THE C-MYC-MAX HETERODIMERIC LEUCINE ZIPPER, NMR, MINIMIZED
1A9N	C D	D	CRYSTAL STRUCTURE OF THE SPLICEOSOMAL U2B''-U2A' PROTEIN COMPLEX BOUND TO A FRAGMENT
1AGR	A E	A	COMPLEX OF ALF4-ACTIVATED GI-ALPHA-1 WITH RGS4
1AGR	D H	H	COMPLEX OF ALF4-ACTIVATED GI-ALPHA-1 WITH RGS4
1AKH	A B	B	MAT A1/ALPHA2/DNA TERNARY COMPLEX
1AOK	A B	B	VIPOXIN COMPLEX
1APY	C B	B	HUMAN ASPARTYLGLUCOSAMINIDASE
1APY	C D	C	HUMAN ASPARTYLGLUCOSAMINIDASE
1AVO	A B	A	PROTEASOME ACTIVATOR REG(ALPHA)
1AVO	A B	B	PROTEASOME ACTIVATOR REG(ALPHA)
1AVO	C D	D	PROTEASOME ACTIVATOR REG(ALPHA)
1AVO	G H	H	PROTEASOME ACTIVATOR REG(ALPHA)
1AVO	I J	J	PROTEASOME ACTIVATOR REG(ALPHA)
1AVO	K L	K	PROTEASOME ACTIVATOR REG(ALPHA)
1AVO	K L	L	PROTEASOME ACTIVATOR REG(ALPHA)
1AVO	K L	L	PROTEASOME ACTIVATOR REG(ALPHA)
1AVO	M N	N	PROTEASOME ACTIVATOR REG(ALPHA)
1AWC	A B	A	MOUSE GABP ALPHA/BETA DOMAIN BOUND TO DNA
1AWC	A B	A	MOUSE GABP ALPHA/BETA DOMAIN BOUND TO DNA
1AWC	A B	B	MOUSE GABP ALPHA/BETA DOMAIN BOUND TO DNA
1AYY	A B	A	GLYCOSYLASPARAGINASE
1AYY	C D	C	GLYCOSYLASPARAGINASE
1B4U	A B	A	PROTOCATECHUATE 4,5-DIOXYGENASE (LIGAB) IN COMPLEX WITH PROTOCATECHUATE (PCA)
1B4U	A B	A	PROTOCATECHUATE 4,5-DIOXYGENASE (LIGAB) IN COMPLEX WITH PROTOCATECHUATE (PCA)
1B4U	A B	A	PROTOCATECHUATE 4,5-DIOXYGENASE (LIGAB) IN COMPLEX WITH PROTOCATECHUATE (PCA)
1B4U	A B	B	PROTOCATECHUATE 4,5-DIOXYGENASE (LIGAB) IN COMPLEX WITH PROTOCATECHUATE (PCA)
1B4U	A D	D	PROTOCATECHUATE 4,5-DIOXYGENASE (LIGAB) IN COMPLEX WITH PROTOCATECHUATE (PCA)
1B4U	C D	C	PROTOCATECHUATE 4,5-DIOXYGENASE (LIGAB) IN COMPLEX WITH PROTOCATECHUATE (PCA)
1B4U	C D	D	PROTOCATECHUATE 4,5-DIOXYGENASE (LIGAB) IN COMPLEX WITH PROTOCATECHUATE (PCA)
1B6C	A B	B	CRYSTAL STRUCTURE OF THE CYTOPLASMIC DOMAIN OF THE TYPE I TGF-BETA RECEPTOR IN COMPLE
1B6C	A B	B	CRYSTAL STRUCTURE OF THE CYTOPLASMIC DOMAIN OF THE TYPE I TGF-BETA RECEPTOR IN COMPLE
1B9X	A B	A	STRUCTURAL ANALYSIS OF PHOSDUCIN AND ITS PHOSPHORYLATION- REGULATED INTERACTION WIT
1B9X	A C	C	STRUCTURAL ANALYSIS OF PHOSDUCIN AND ITS PHOSPHORYLATION- REGULATED INTERACTION WIT
1BB1	A B	A	CRYSTAL STRUCTURE OF A DESIGNED, THERMOSTABLE HETEROTRIMERIC COILED COIL
1BB1	A C	A	CRYSTAL STRUCTURE OF A DESIGNED, THERMOSTABLE HETEROTRIMERIC COILED COIL
1BB1	A C	C	CRYSTAL STRUCTURE OF A DESIGNED, THERMOSTABLE HETEROTRIMERIC COILED COIL
1BB1	B C	C	CRYSTAL STRUCTURE OF A DESIGNED, THERMOSTABLE HETEROTRIMERIC COILED COIL
1BCC	A B	B	CYTOCHROME BC1 COMPLEX FROM CHICKEN
1BCC	D F	F	CYTOCHROME BC1 COMPLEX FROM CHICKEN
1BCC	D J	D	CYTOCHROME BC1 COMPLEX FROM CHICKEN
1BCC	D J	J	CYTOCHROME BC1 COMPLEX FROM CHICKEN
1BCC	E J	E	CYTOCHROME BC1 COMPLEX FROM CHICKEN
1BCC	E J	J	CYTOCHROME BC1 COMPLEX FROM CHICKEN
1BCC	G H	H	CYTOCHROME BC1 COMPLEX FROM CHICKEN
1BCP	A E	A	BINARY COMPLEX OF PERTUSSIS TOXIN AND ATP
1BCP	B F	B	BINARY COMPLEX OF PERTUSSIS TOXIN AND ATP
1BCP	C E	C	BINARY COMPLEX OF PERTUSSIS TOXIN AND ATP
1BCP	E F	E	BINARY COMPLEX OF PERTUSSIS TOXIN AND ATP
1BCP	E F	F	BINARY COMPLEX OF PERTUSSIS TOXIN AND ATP
1BCP	I K	I	BINARY COMPLEX OF PERTUSSIS TOXIN AND ATP
1BH8	A B	A	HTAFII18/HTAFII28 HETERODIMER CRYSTAL STRUCTURE
1BI4	A B	A	CATALYTIC DOMAIN OF HIV-1 INTEGRASE
1BI4	A B	B	CATALYTIC DOMAIN OF HIV-1 INTEGRASE
1BIQ	A B	A	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 1 BETA CHAIN MUTANT E238A
1BIQ	A B	A	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 1 BETA CHAIN MUTANT E238A
1BIQ	A B	A	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 1 BETA CHAIN MUTANT E238A
1BIQ	A B	B	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE 1 BETA CHAIN MUTANT E238A
1BP3	A B	A	THE XRAY STRUCTURE OF A GROWTH HORMONE-PROLACTIN RECEPTOR COMPLEX
1BPL	A B	A	GLYCOSYLTRANSFERASE
1BPL	A B	B	GLYCOSYLTRANSFERASE

TABLE S4

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
1A02	TRANSCRIPTION/DNA	1.7	9.9	6	52
1A02	TRANSCRIPTION/DNA	1.5	10.4	7	50
1A0O	CHEMOTAXIS	1.0	2.0	2	11
1A93	LEUCINE ZIPPER	1.4	4.1	3	29
1A9N	RNA BINDING PROTEIN/RNA	1.7	5.0	3	12
1AGR	COMPLEX (SIGNAL TRANSDUCTION/REGULATOR)	1.6	4.7	3	10
1AGR	COMPLEX (SIGNAL TRANSDUCTION/REGULATOR)	1.7	3.3	2	15
1AKH	DNA BINDING PROTEIN/DNA	1.6	3.2	2	9
1AOK	HYDROLASE	1.6	4.8	3	13
1APY	HYDROLASE	1.2	2.3	2	7
1APY	HYDROLASE	1.6	3.1	2	13
1AVO	PROTEASOME ACTIVATOR	1.8	10.5	6	15
1AVO	PROTEASOME ACTIVATOR	1.6	6.2	4	32
1AVO	PROTEASOME ACTIVATOR	1.5	5.9	4	32
1AVO	PROTEASOME ACTIVATOR	1.5	7.4	5	32
1AVO	PROTEASOME ACTIVATOR	1.6	10.9	7	32
1AVO	PROTEASOME ACTIVATOR	1.8	14.2	8	38
1AVO	PROTEASOME ACTIVATOR	1.6	6.5	4	32
1AVO	PROTEASOME ACTIVATOR	1.9	7.4	4	39
1AVO	PROTEASOME ACTIVATOR	1.5	4.6	3	32
1AWC	TRANSCRIPTION/DNA	1.1	2.1	2	19
1AWC	TRANSCRIPTION/DNA	1.5	2.9	2	10
1AWC	TRANSCRIPTION/DNA	1.9	3.7	2	8
1AYY	HYDROLASE	1.7	5.0	3	15
1AYY	HYDROLASE	1.5	4.4	3	15
1B4U	DIOXYGENASE	1.9	3.8	2	10
1B4U	DIOXYGENASE	1.4	2.8	2	11
1B4U	DIOXYGENASE	1.4	4.2	3	10
1B4U	DIOXYGENASE	1.6	4.7	3	8
1B4U	DIOXYGENASE	1.4	4.2	3	14
1B4U	DIOXYGENASE	1.6	3.2	2	10
1B4U	DIOXYGENASE	1.2	4.9	4	8
1B6C	COMPLEX (ISOMERASE/PROTEIN KINASE)	1.8	3.6	2	14
1B6C	COMPLEX (ISOMERASE/PROTEIN KINASE)	1.9	7.5	4	10
1B9X	SIGNALING PROTEIN	1.3	3.9	3	22
1B9X	SIGNALING PROTEIN	1.8	7.0	4	13
1BB1	DE NOVO PROTEIN DESIGN	1.4	4.3	3	33
1BB1	DE NOVO PROTEIN DESIGN	1.4	4.1	3	33
1BB1	DE NOVO PROTEIN DESIGN	1.6	4.9	3	32
1BB1	DE NOVO PROTEIN DESIGN	1.4	5.6	4	32
1BCC	OXIDOREDUCTASE	1.5	3.0	2	17
1BCC	OXIDOREDUCTASE	1.7	5.1	3	20
1BCC	OXIDOREDUCTASE	1.4	4.3	3	35
1BCC	OXIDOREDUCTASE	1.6	3.2	2	23
1BCC	OXIDOREDUCTASE	1.8	3.5	2	35
1BCC	OXIDOREDUCTASE	1.9	3.7	2	23
1BCC	OXIDOREDUCTASE	1.4	2.8	2	23
1BCP	TOXIN	1.2	2.4	2	21
1BCP	TOXIN	1.6	3.2	2	13
1BCP	TOXIN	1.7	6.9	4	13
1BCP	TOXIN	1.4	2.7	2	13
1BCP	TOXIN	1.5	4.5	3	16
1BCP	TOXIN	1.5	6.1	4	14
1BH8	TRANSCRIPTION REGULATION COMPLEX	1.5	7.6	5	25
1BI4	DNA INTEGRATION	1.4	4.3	3	15
1BI4	DNA INTEGRATION	1.6	3.1	2	14
1BIQ	OXIDOREDUCTASE	1.4	4.2	3	13
1BIQ	OXIDOREDUCTASE	1.9	9.4	5	27
1BIQ	OXIDOREDUCTASE	1.6	3.2	2	11
1BIQ	OXIDOREDUCTASE	1.9	7.7	4	19
1BP3	HORMONE/GROWTH FACTOR	1.6	7.9	5	31
1BPL	GLYCOSYLTRANSFERASE	1.4	4.3	3	14
1BPL	GLYCOSYLTRANSFERASE	1.5	3.0	2	13

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
1A02	141	192
1A02	268	317
1A0O	92	102
1A93	6	34
1A9N	23	34
1AGR	205	214
1AGR	86	100
1AKH	194	202
1AOK	2	14
1APY	237	243
1APY	126	138
1AVO	31	45
1AVO	108	139
1AVO	108	139
1AVO	108	139
1AVO	108	139
1AVO	8	45
1AVO	108	139
1AVO	195	233
1AVO	108	139
1AWC	411	429
1AWC	322	331
1AWC	107	114
1AYY	31	45
1AYY	31	45
1B4U	10	19
1B4U	89	99
1B4U	35	44
1B4U	229	236
1B4U	100	113
1B4U	115	124
1B4U	229	236
1B6C	239	252
1B6C	195	204
1B9X	4	25
1B9X	22	34
1BB1	2	34
1BB1	2	34
1BB1	3	34
1BB1	3	34
1BCC	355	371
1BCC	52	71
1BCC	199	233
1BCC	24	46
1BCC	25	59
1BCC	24	46
1BCC	55	77
1BCP	57	77
1BCP	146	158
1BCP	146	158
1BCP	63	75
1BCP	51	66
1BCP	146	159
1BH8	51	75
1BI4	172	186
1BI4	172	185
1BIQ	34	46
1BIQ	102	128
1BIQ	133	143
1BIQ	153	171
1BP3	155	185
1BPL	80	93
1BPL	381	393

TABLE S4

A. PDB CODE	L. HELIX SEQUENCE
1A02	RIRRERNKMAAAKSRNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKEK
1A02	KRMRNRIAASKSRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQ
1A0O	KENIIAAAQAG
1A93	VQAEEQKLISEEDLLRKRREQLKHKLEQL
1A9N	KEELKRSLYALF
1AGR	RSERKKWIHC
1AGR	EENIDFWISCEEYKK
1AKH	PELADLLSG
1AOK	LFQFAKMINGKLG
1APY	GDILMRF
1APY	SASQALHSDWLAR
1AVO	SYFPKKISELDAFLK
1AVO	EKIVVLLQRLKPEIKDVIEQLNLVTTWLQLQI
1AVO	EKIVVLLQRLKPEIKDVIEQLNLVTTWLQLQI
1AVO	EKIVVLLQRLKPEIKDVIEQLNLVTTWLQLQI
1AVO	EKIVVLLQRLKPEIKDVIEQLNLVTTWLQLQI
1AVO	PEAQAKVDVFREDLCTKTENLLGSYFPKKISELDAFLK
1AVO	EKIVVLLQRLKPEIKDVIEQLNLVTTWLQLQI
1AVO	GDYRQLVHELDEAEYRDIRLMVMEIRNAYAVLYDIILKN
1AVO	EKIVVLLQRLKPEIKDVIEQLNLVTTWLQLQI
1AWC	AAELNRLVIECEQKKLARM
1AWC	LWQFLLELLT
1AWC	ALHWATEH
1AYY	ALDAVEKGVRLVEDD
1AYY	ALDAVEKGVRLVEDD
1B4U	VHAYLAEFDD
1B4U	VYFLSKLFSTD
1B4U	YNLNQFAMSL
1B4U	HIQYLRES
1B4U	PDLAWHIAQSLILD
1B4U	QEEYAQMMID
1B4U	HIQYLRES
1B6C	ERSWFREAEIYQTV
1B6C	LLVQRTIART
1B9X	LDQLRQEAEQLKNQIRDARKAC
1B9X	PKGVINDWRKFKL
1BB1	EIAAIEYEQAAIKEEIAAIKDKIAAIKEYIAAI
1BB1	EIAAIEYEQAAIKEEIAAIKDKIAAIKEYIAAI
1BB1	IAAIKYKQAAIKNEIAAIKQEIAAIEQMIAAI
1BB1	IAAIKYKQAAIKNEIAAIKQEIAAIEQMIAAI
1BCC	ENVQAAKNKLKAKYLMS
1BCC	ENLYDDRMFRIKRALDLNMR
1BCC	DHRKRMGLKMLLMMGLLVPLVYYMKRHKWSVLKSR
1BCC	IVVGALLFERAFDQGADAIYEHI
1BCC	SRESDPSRKGFSYLVTAVTTLGVAYAAKNVVTQFV
1BCC	IVVGALLFERAFDQGADAIYEHI
1BCC	TEELFDFLHARDHCVAHKLFNSL
1BCP	RRYTEVYLEHRMQEAVEAERA
1BCP	YSRLRKMLYLIYV
1BCP	YDALRRLLYMIYM
1BCP	PMEVMLRAVFMQQ
1BCP	TWFDTMLGFAISAYAL
1BCP	YDALRRLLYMIYMS
1BH8	TESVDILEDLVIEFITEMTHKAMSI
1BI4	LKTAVQMAVFIHNHK
1BI4	LKTAVQMAVFIHNH
1BIQ	DIFEKLIEKQLSF
1BIQ	PELETWVETWAFSETIHSRSFTHIIRN
1BIQ	PSVVFDDIVTN
1BIQ	ISSYYDELIEMTSYWHLLG
1BP3	ALLKNYGLLYCFRKDMDKVETFLRIVQCRSV
1BPL	KGELQSAIKSLHSR
1BPL	KHKIEPILKARKQ

A. PDB CODE	M. RESOLUTION
1A02	2.7
1A02	2.7
1A0O	2.95
1A93	NOT APP
1A9N	2.38
1AGR	2.8
1AGR	2.8
1AKH	2.5
1AOK	2
1APY	2
1APY	2
1AVO	2.8
1AVO	2.8
1AVO	2.8
1AVO	2.8
1AVO	2.8
1AVO	2.8
1AVO	2.8
1AVO	2.8
1AVO	2.8
1AWC	2.15
1AWC	2.15
1AWC	2.15
1AYY	2.32
1AYY	2.32
1B4U	2.2
1B4U	2.2
1B4U	2.2
1B4U	2.2
1B4U	2.2
1B4U	2.2
1B4U	2.2
1B6C	2.6
1B6C	2.6
1B9X	3
1B9X	3
1BB1	1.8
1BB1	1.8
1BB1	1.8
1BB1	1.8
1BCC	3.16
1BCC	3.16
1BCC	3.16
1BCC	3.16
1BCC	3.16
1BCC	3.16
1BCC	3.16
1BCP	2.7
1BCP	2.7
1BCP	2.7
1BCP	2.7
1BCP	2.7
1BCP	2.7
1BH8	3
1BI4	2.5
1BI4	2.5
1BIQ	2.05
1BIQ	2.05
1BIQ	2.05
1BIQ	2.05
1BP3	2.9
1BPL	2.2
1BPL	2.2

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1BSX	A X	X	STRUCTURE AND SPECIFICITY OF NUCLEAR RECEPTOR-COACTIVATOR INTERACTIONS
1BSX	B Y	Y	STRUCTURE AND SPECIFICITY OF NUCLEAR RECEPTOR-COACTIVATOR INTERACTIONS
1BTH	J K	J	STRUCTURE OF THROMBIN COMPLEXED WITH BOVINE PANCREATIC TRYPSIN INHIBITOR
1BUH	A B	A	CRYSTAL STRUCTURE OF THE HUMAN CDK2 KINASE COMPLEX WITH CELL CYCLE-REGULATORY PROT
1BVK	D F	F	HUMANIZED ANTI-LYSOZYME FV COMPLEXED WITH LYSOZYME
1BVY	A F	F	COMPLEX OF THE HEME AND FMN-BINDING DOMAINS OF THE CYTOCHROME P450(BM-3)
1BX2	A C	A	CRYSTAL STRUCTURE OF HLA-DR2 (DRA*0101,DRB1*1501) COMPLEXED WITH A PEPTIDE FROM HUMAN
1BX2	B C	B	CRYSTAL STRUCTURE OF HLA-DR2 (DRA*0101,DRB1*1501) COMPLEXED WITH A PEPTIDE FROM HUMAN
1BX2	D E	D	CRYSTAL STRUCTURE OF HLA-DR2 (DRA*0101,DRB1*1501) COMPLEXED WITH A PEPTIDE FROM HUMAN
1BX2	D E	E	CRYSTAL STRUCTURE OF HLA-DR2 (DRA*0101,DRB1*1501) COMPLEXED WITH A PEPTIDE FROM HUMAN
1BX2	E F	E	CRYSTAL STRUCTURE OF HLA-DR2 (DRA*0101,DRB1*1501) COMPLEXED WITH A PEPTIDE FROM HUMAN
1C0G	S A	S	CRYSTAL STRUCTURE OF 1:1 COMPLEX BETWEEN GELSOLIN SEGMENT 1 AND A DICTYOSTELIUM/TETR
1CAX	E B	E	DETERMINATION OF THREE CRYSTAL STRUCTURES OF CANAVALIN BY MOLECULAR REPLACEMENT
1CB7	A B	A	GLUTAMATE MUTASE FROM CLOSTRIDIUM COCHLEARIUM RECONSTITUTED WITH METHYL-COBALAM
1CB7	A B	A	GLUTAMATE MUTASE FROM CLOSTRIDIUM COCHLEARIUM RECONSTITUTED WITH METHYL-COBALAM
1CB7	C D	C	GLUTAMATE MUTASE FROM CLOSTRIDIUM COCHLEARIUM RECONSTITUTED WITH METHYL-COBALAM
1CC0	A E	A	CRYSTAL STRUCTURE OF THE RHOA.GDP-RHOGDI COMPLEX
1CDL	A E	A	TARGET ENZYME RECOGNITION BY CALMODULIN: 2.4 ANGSTROMS STRUCTURE OF A CALMODULIN-PE
1CDL	A E	A	TARGET ENZYME RECOGNITION BY CALMODULIN: 2.4 ANGSTROMS STRUCTURE OF A CALMODULIN-PE
1CDL	A E	A	TARGET ENZYME RECOGNITION BY CALMODULIN: 2.4 ANGSTROMS STRUCTURE OF A CALMODULIN-PE
1CDL	A E	A	TARGET ENZYME RECOGNITION BY CALMODULIN: 2.4 ANGSTROMS STRUCTURE OF A CALMODULIN-PE
1CDL	B F	B	TARGET ENZYME RECOGNITION BY CALMODULIN: 2.4 ANGSTROMS STRUCTURE OF A CALMODULIN-PE
1CDL	B F	B	TARGET ENZYME RECOGNITION BY CALMODULIN: 2.4 ANGSTROMS STRUCTURE OF A CALMODULIN-PE
1CDL	D G	G	TARGET ENZYME RECOGNITION BY CALMODULIN: 2.4 ANGSTROMS STRUCTURE OF A CALMODULIN-PE
1CDL	D H	D	TARGET ENZYME RECOGNITION BY CALMODULIN: 2.4 ANGSTROMS STRUCTURE OF A CALMODULIN-PE
1CDL	D H	D	TARGET ENZYME RECOGNITION BY CALMODULIN: 2.4 ANGSTROMS STRUCTURE OF A CALMODULIN-PE
1CDL	D H	H	TARGET ENZYME RECOGNITION BY CALMODULIN: 2.4 ANGSTROMS STRUCTURE OF A CALMODULIN-PE
1CFF	A B	A	NMR SOLUTION STRUCTURE OF A COMPLEX OF CALMODULIN WITH A BINDING PEPTIDE OF THE CA2+-
1CFF	A B	A	NMR SOLUTION STRUCTURE OF A COMPLEX OF CALMODULIN WITH A BINDING PEPTIDE OF THE CA2+-
1CFF	A B	A	NMR SOLUTION STRUCTURE OF A COMPLEX OF CALMODULIN WITH A BINDING PEPTIDE OF THE CA2+-
1CI6	A B	A	TRANSCRIPTION FACTOR ATF4-C/EBP BETA BZIP HETERODIMER
1CM1	A B	A	MOTIONS OF CALMODULIN-SINGLE-CONFORMER REFINEMENT
1CM1	A B	B	MOTIONS OF CALMODULIN-SINGLE-CONFORMER REFINEMENT
1CP9	A B	A	CRYSTAL STRUCTURE OF PENICILLIN G ACYLASE FROM THE BRO1 MUTANT STRAIN OF PROVIDENCIA
1CP9	A B	A	CRYSTAL STRUCTURE OF PENICILLIN G ACYLASE FROM THE BRO1 MUTANT STRAIN OF PROVIDENCIA
1CP9	A B	A	CRYSTAL STRUCTURE OF PENICILLIN G ACYLASE FROM THE BRO1 MUTANT STRAIN OF PROVIDENCIA
1CP9	A B	A	CRYSTAL STRUCTURE OF PENICILLIN G ACYLASE FROM THE BRO1 MUTANT STRAIN OF PROVIDENCIA
1CSE	E I	E	THE HIGH-RESOLUTION X-RAY CRYSTAL STRUCTURE OF THE COMPLEX FORMED BETWEEN SUBTILISI
1CUL	A B	B	COMPLEX OF GS-ALPHA WITH THE CATALYTIC DOMAINS OF MAMMALIAN ADENYLYL CYCLASE: COMP
1CUL	B C	B	COMPLEX OF GS-ALPHA WITH THE CATALYTIC DOMAINS OF MAMMALIAN ADENYLYL CYCLASE: COMP
1CXZ	A B	B	CRYSTAL STRUCTURE OF HUMAN RHOA COMPLEXED WITH THE EFFECTOR DOMAIN OF THE PROTEIN K
1D2Z	A B	A	THREE-DIMENSIONAL STRUCTURE OF A COMPLEX BETWEEN THE DEATH DOMAINS OF PELLE AND TUB
1D2Z	C B	C	THREE-DIMENSIONAL STRUCTURE OF A COMPLEX BETWEEN THE DEATH DOMAINS OF PELLE AND TUB
1D2Z	C D	C	THREE-DIMENSIONAL STRUCTURE OF A COMPLEX BETWEEN THE DEATH DOMAINS OF PELLE AND TUB
1D3B	C D	C	CRYSTAL STRUCTURE OF THE D3B SUBCOMPLEX OF THE HUMAN CORE SNRNP DOMAIN AT 2.0A RESOL
1D8D	A B	A	CO-CRYSTAL STRUCTURE OF RAT PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH A K-RAS4B PEP
1D8D	A B	A	CO-CRYSTAL STRUCTURE OF RAT PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH A K-RAS4B PEP
1D8D	A B	B	CO-CRYSTAL STRUCTURE OF RAT PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH A K-RAS4B PEP
1DAN	L H	H	COMPLEX OF ACTIVE SITE INHIBITED HUMAN BLOOD COAGULATION FACTOR VIIA WITH HUMAN REC
1DE4	A C	A	HEMOCHROMATOSIS PROTEIN HFE COMPLEXED WITH TRANSFERRIN RECEPTOR
1DE4	A C	C	HEMOCHROMATOSIS PROTEIN HFE COMPLEXED WITH TRANSFERRIN RECEPTOR
1DE4	D F	D	HEMOCHROMATOSIS PROTEIN HFE COMPLEXED WITH TRANSFERRIN RECEPTOR
1DEV	A B	B	CRYSTAL STRUCTURE OF SMAD2 MH2 DOMAIN BOUND TO THE SMAD- BINDING DOMAIN OF SARA
1DKD	C G	C	CRYSTAL STRUCTURE OF A GROEL (APICAL DOMAIN) AND A DODECAMERIC PEPTIDE COMPLEX
1DKF	A B	B	CRYSTAL STRUCTURE OF A HETERODIMERIC COMPLEX OF RAR AND RXR LIGAND-BINDING DOMAINS
1DKF	A B	B	CRYSTAL STRUCTURE OF A HETERODIMERIC COMPLEX OF RAR AND RXR LIGAND-BINDING DOMAINS
1DKG	A D	D	CRYSTAL STRUCTURE OF THE NUCLEOTIDE EXCHANGE FACTOR GRPE BOUND TO THE ATPASE DOMAIN
1DML	A F	F	CRYSTAL STRUCTURE OF HERPES SIMPLEX UL42 BOUND TO THE C- TERMINUS OF HSV POL
1DML	E F	F	CRYSTAL STRUCTURE OF HERPES SIMPLEX UL42 BOUND TO THE C- TERMINUS OF HSV POL
1DML	G H	H	CRYSTAL STRUCTURE OF HERPES SIMPLEX UL42 BOUND TO THE C- TERMINUS OF HSV POL
1DOW	A B	A	CRYSTAL STRUCTURE OF A CHIMERA OF BETA-CATENIN AND ALPHA- CATENIN
1DOW	A B	B	CRYSTAL STRUCTURE OF A CHIMERA OF BETA-CATENIN AND ALPHA- CATENIN
1DS6	A B	B	CRYSTAL STRUCTURE OF A RAC-RHOGDI COMPLEX

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM,\ HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
1BSX	HORMONE/GROWTH FACTOR	1.5	4.6	3	6
1BSX	HORMONE/GROWTH FACTOR	1.5	4.6	3	6
1BTH	COMPLEX (SERINE PROTEASE/INHIBITOR)	1.7	6.9	4	9
1BUH	TRANSFERASE	1.6	4.7	3	12
1BVK	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE)	1.6	3.1	2	6
1BVY	OXIDOREDUCTASE	1.4	2.7	2	20
1BX2	IMMUNE SYSTEM	1.2	5.8	5	23
1BX2	IMMUNE SYSTEM	1.3	5.2	4	24
1BX2	IMMUNE SYSTEM	1.5	2.9	2	23
1BX2	IMMUNE SYSTEM	1.1	2.2	2	13
1BX2	IMMUNE SYSTEM	1.7	6.7	4	22
1C0G	CONTRACTILE PROTEIN	1.9	7.4	4	18
1CAX	SEED STORAGE PROTEIN	1.1	2.2	2	9
1CB7	ISOMERASE	1.5	3.0	2	15
1CB7	ISOMERASE	1.5	4.4	3	6
1CB7	ISOMERASE	1.5	2.9	2	14
1CC0	SIGNALING PROTEIN	1.3	2.6	2	19
1CDL	CALCIUM-BINDING PROTEIN	1.4	2.8	2	12
1CDL	CALCIUM-BINDING PROTEIN	1.5	4.4	3	16
1CDL	CALCIUM-BINDING PROTEIN	1.5	4.5	3	15
1CDL	CALCIUM-BINDING PROTEIN	1.4	4.2	3	10
1CDL	CALCIUM-BINDING PROTEIN	1.5	3.0	2	15
1CDL	CALCIUM-BINDING PROTEIN	1.7	3.3	2	9
1CDL	CALCIUM-BINDING PROTEIN	1.8	3.5	2	17
1CDL	CALCIUM-BINDING PROTEIN	1.5	4.5	3	15
1CDL	CALCIUM-BINDING PROTEIN	1.3	4.0	3	9
1CDL	CALCIUM-BINDING PROTEIN	1.8	16.2	9	17
1CFF	CALMODULIN	1.9	3.7	2	11
1CFF	CALMODULIN	1.6	4.8	3	12
1CFF	CALMODULIN	1.1	2.2	2	10
1CI6	TRANSCRIPTION	1.6	13.1	8	55
1CM1	COMPLEX (CALCIUM-BINDING/TRANSFERASE)	1.5	2.9	2	9
1CM1	COMPLEX (CALCIUM-BINDING/TRANSFERASE)	1.6	11.3	7	16
1CP9	HYDROLASE	1.4	4.3	3	10
1CP9	HYDROLASE	1.6	3.2	2	6
1CP9	HYDROLASE	1.3	2.5	2	11
1CP9	HYDROLASE	1.4	5.6	4	24
1CSE	COMPLEX(SERINE PROTEINASE-INHIBITOR)	1.3	2.6	2	14
1CUL	LYASE/LYASE/SIGNALING PROTEIN	1.8	11.0	6	19
1CUL	LYASE/LYASE/SIGNALING PROTEIN	1.4	2.8	2	19
1CXZ	SIGNALING PROTEIN	1.7	3.3	2	27
1D2Z	APOPTOSIS	1.4	2.7	2	13
1D2Z	APOPTOSIS	1.5	3.0	2	15
1D2Z	APOPTOSIS	1.5	2.9	2	13
1D3B	RNA BINDING PROTEIN	1.6	3.1	2	9
1D8D	TRANSFERASE	1.8	3.5	2	15
1D8D	TRANSFERASE	1.7	3.4	2	15
1D8D	TRANSFERASE	1.2	2.4	2	12
1DAN	COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND)	1.4	2.7	2	10
1DE4	METAL TRANSPORT INHIBITOR/RECEPTOR	1.9	3.7	2	12
1DE4	METAL TRANSPORT INHIBITOR/RECEPTOR	1.8	5.5	3	23
1DE4	METAL TRANSPORT INHIBITOR/RECEPTOR	1.8	7.0	4	28
1DEV	SIGNALING PROTEIN	1.0	2.0	2	6
1DKD	CHAPERONE	1.4	2.8	2	15
1DKF	HORMONE/GROWTH FACTOR RECEPTOR	1.0	2.0	2	23
1DKF	HORMONE/GROWTH FACTOR RECEPTOR	1.3	2.5	2	9
1DKG	COMPLEX (HSP24/HSP70)	1.2	2.3	2	18
1DML	DNA BINDING PROTEIN/TRANSFERASE	1.9	3.8	2	15
1DML	DNA BINDING PROTEIN/TRANSFERASE	1.6	4.9	3	15
1DML	DNA BINDING PROTEIN/TRANSFERASE	1.7	12.0	7	15
1DOW	CELL ADHESION	1.8	5.4	3	26
1DOW	CELL ADHESION	1.6	4.8	3	10
1DS6	SIGNALING PROTEIN	1.7	8.6	5	12

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
1BSX	689	694
1BSX	689	694
1BTH	14	14
1BUH	208	219
1BVK	120	125
1BVY	609	628
1BX2	56	78
1BX2	66	89
1BX2	56	78
1BX2	52	64
1BX2	65	86
1C0G	73	90
1CAX	192	200
1CB7	17	31
1CB7	67	72
1CB7	17	30
1CC0	89	107
1CDL	118	129
1CDL	78	93
1CDL	6	20
1CDL	65	74
1CDL	6	20
1CDL	138	146
1CDL	797	813
1CDL	6	20
1CDL	65	73
1CDL	799	815
1CFF	103	113
1CFF	118	129
1CFF	138	147
1CI6	287	341
1CM1	138	146
1CM1	295	310
1CP9	61	70
1CP9	115	120
1CP9	38	48
1CP9	85	108
1CSE	104	117
1CUL	909	927
1CUL	909	927
1CXZ	71	97
1D2Z	82	94
1D2Z	39	53
1D2Z	82	94
1D3B	6	14
1D8D	274	288
1D8D	166	180
1D8D	270	281
1DAN	126	129
1DE4	140	151
1DE4	640	662
1DE4	59	86
1DEV	686	691
1DKD	230	244
1DKF	345	367
1DKF	371	379
1DKG	256	273
1DML	1220	1234
1DML	1220	1234
1DML	1220	1234
1DOW	58	83
1DOW	133	142
1DS6	43	54

A. PDB CODE	L. HELIX SEQUENCE
1BSX	ILHRLL
1BSX	ILHRLL
1BTH	ERELLESYI
1BUH	EIDQLFRIFRTL
1BVK	VQAWIR
1BVY	FEGTYEEWREHMWSDVAAYF
1BX2	AQGALANIAVDKANLEIMTKRSN
1BX2	DILEQARAAVDTYCRHNYGVVESF
1BX2	AQGALANIAVDKANLEIMTKRSN
1BX2	ELGRPDAEYWNSQ
1BX2	KDILEQARAAVDTYCRHNYGVV
1C0G	QDESGAAAIFTVQLDDYL
1CAX	KNFLEASYD
1CB7	AVGNKILDHAFTNAG
1CB7	GEIDCK
1CB7	AVGNKILDHAFTNA
1CC0	PDSLENIPEKWTPEVKHFC
1CDL	DEEVDEMIREAD
1CDL	DTDSEEEIREAFRVFD
1CDL	EEQIAEFKEAFSLFD
1CDL	FPEFLTMMAR
1CDL	EEQIAEFKEAFSLFD
1CDL	YEEFVQMMT
1CDL	RRKWQKTGHAVRAIGRL
1CDL	EEQIAEFKEAFSLFD
1CDL	FPEFLTMMA
1CDL	KWQKTGHAVRAIGRLSS
1CFF	AELRHVMTNLG
1CFF	DEEVDEMIREAD
1CFF	YEEFVQMMTA
1CI6	QNKTAATRYRQKKRAEQEALTGECKELEKKNEALKERADSLAKEIQYLKDLIEEV
1CM1	YEEFVQMMT
1CM1	ARRKLKGAILTTMLAT
1CP9	ISFDKEIRNN
1CP9	KQFIDY
1CP9	LFQMEMAKRST
1CP9	SQEQDILRGYADGMNAWIKQINTK
1CSE	YSGIVSGIEWATTN
1CUL	LECLRLLNEIIADFDDLLS
1CUL	LECLRLLNEIIADFDDLLS
1CXZ	GPVELLLRGSSRRLDLLHQQLQELHAH
1D2Z	ASNEFLNIWGGQY
1D2Z	LPVRAQLCAHLDALD
1D2Z	ASNEFLNIWGGQY
1D3B	PIKVLHEAE
1D8D	ESAWNYLKGILQDRG
1D8D	YQVWHHRRVLVEWLK
1D8D	LKSLLQWVTSRQ
1DAN	RTFSERTLAF
1DE4	AWPTKLEWERHK
1DE4	QWLYSARGDFFRATSRLTTDFGN
1DE4	SQMWLQLSQSLKGWDHMFTVDFWTIMEN
1DEV	PLQQAQ
1DKD	IREMLPVLEAVAKAG
1DKF	PDRVDMLQEPLLEALKVYVRKRR
1DKF	PHMFPKMLM
1DKG	PLAMQRLKEAAEKAKIEL
1DML	AEETRRMLHRAFDTL
1DML	AEETRRMLHRAFDTL
1DML	AEETRRMLHRAFDTL
1DOW	AHVLAASVEQATENFLEKGDKIAKES
1DOW	KHAVVNLINY
1DS6	ESLIKYKKTLLG

A. PDB CODE	M. RESOLUTION
1BSX	3.7
1BSX	3.7
1BTH	2.3
1BUH	2.6
1BVK	2.7
1BVY	2.03
1BX2	2.6
1BX2	2.6
1BX2	2.6
1BX2	2.6
1BX2	2.6
1C0G	2
1CAX	2.6
1CB7	2
1CB7	2
1CB7	2
1CC0	5
1CDL	2
1CDL	2
1CDL	2
1CDL	2
1CDL	2
1CDL	2
1CDL	2
1CDL	2
1CDL	2
1CDL	2
1CFF	NOT APP
1CFF	NOT APP
1CFF	NOT APP
1CI6	2.6
1CM1	2
1CM1	2
1CP9	2.5
1CP9	2.5
1CP9	2.5
1CP9	2.5
1CSE	1.2
1CUL	2.4
1CUL	2.4
1CXZ	2.2
1D2Z	2
1D2Z	2
1D2Z	2
1D3B	2
1D8D	2
1D8D	2
1D8D	2
1DAN	2
1DE4	2.8
1DE4	2.8
1DE4	2.8
1DEV	2.2
1DKD	2.1
1DKF	2.5
1DKF	2.5
1DKG	2.8
1DML	2.7
1DML	2.7
1DML	2.7
1DOW	1.8
1DOW	1.8
1DS6	2.35

TABLE S4

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1DX5	C O	O	CRYSTAL STRUCTURE OF THE THROMBIN-THROMBOMODULIN COMPLEX
1DX5	D P	P	CRYSTAL STRUCTURE OF THE THROMBIN-THROMBOMODULIN COMPLEX
1E3A	A B	A	A SLOW PROCESSING PRECURSOR PENICILLIN ACYLASE FROM ESCHERICHIA COLI
1E3A	A B	A	A SLOW PROCESSING PRECURSOR PENICILLIN ACYLASE FROM ESCHERICHIA COLI
1E3A	A B	B	A SLOW PROCESSING PRECURSOR PENICILLIN ACYLASE FROM ESCHERICHIA COLI
1E6E	A B	B	ADRENODOXIN REDUCTASE/ADRENODOXIN COMPLEX OF MITOCHONDRIAL P450 SYSTEMS
1E7P	A B	A	QUINOL:FUMARATE REDUCTASE FROM WOLINELLA SUCCINOGENES
1E7P	A B	A	QUINOL:FUMARATE REDUCTASE FROM WOLINELLA SUCCINOGENES
1E7P	B C	C	QUINOL:FUMARATE REDUCTASE FROM WOLINELLA SUCCINOGENES
1E7P	D E	E	QUINOL:FUMARATE REDUCTASE FROM WOLINELLA SUCCINOGENES
1E7P	G H	H	QUINOL:FUMARATE REDUCTASE FROM WOLINELLA SUCCINOGENES
1E7P	J K	K	QUINOL:FUMARATE REDUCTASE FROM WOLINELLA SUCCINOGENES
1E8O	A B	A	CORE OF THE ALU DOMAIN OF THE MAMMALIAN SRP
1E8O	C D	C	CORE OF THE ALU DOMAIN OF THE MAMMALIAN SRP
1E8O	C D	D	CORE OF THE ALU DOMAIN OF THE MAMMALIAN SRP
1EAY	A C	A	CHEY-BINDING (P2) DOMAIN OF CHEA IN COMPLEX WITH CHEY FROM ESCHERICHIA COLI
1EAY	A C	C	CHEY-BINDING (P2) DOMAIN OF CHEA IN COMPLEX WITH CHEY FROM ESCHERICHIA COLI
1EBD	B C	C	DIHYDROLIPOAMIDE DEHYDROGENASE COMPLEXED WITH THE BINDING DOMAIN OF THE DIHYDROLI
1EER	A C	A	CRYSTAL STRUCTURE OF HUMAN ERYTHROPOIETIN COMPLEXED TO ITS RECEPTOR AT 1.9 ANGSTROMS
1EJH	A E	E	EIF4E/EIF4G PEPTIDE/7-METHYL-GDP
1EJH	B F	B	EIF4E/EIF4G PEPTIDE/7-METHYL-GDP
1EJR	C A	A	CRYSTAL STRUCTURE OF THE D221A VARIANT OF KLEBSIELLA AEROGENES UREASE
1EM8	C D	D	CRYSTAL STRUCTURE OF CHI AND PSI SUBUNIT HETERODIMER FROM DNA POL III
1EMU	A B	B	STRUCTURE OF THE AXIN RGS-HOMOLOGOUS DOMAIN IN COMPLEX WITH A SAMP REPEAT FROM APC
1F51	A E	A	A TRANSIENT INTERACTION BETWEEN TWO PHOSPHORELAY PROTEINSTRAPPED IN A CRYSTAL LATTIC
1F51	D H	H	A TRANSIENT INTERACTION BETWEEN TWO PHOSPHORELAY PROTEINSTRAPPED IN A CRYSTAL LATTIC
1F5Q	A B	A	CRYSTAL STRUCTURE OF MURINE GAMMA HERPESVIRUS CYCLIN COMPLEXED TO HUMAN CYCLIN DE
1F5Q	A B	B	CRYSTAL STRUCTURE OF MURINE GAMMA HERPESVIRUS CYCLIN COMPLEXED TO HUMAN CYCLIN DE
1F5Q	C D	C	CRYSTAL STRUCTURE OF MURINE GAMMA HERPESVIRUS CYCLIN COMPLEXED TO HUMAN CYCLIN DE
1F5Q	C D	D	CRYSTAL STRUCTURE OF MURINE GAMMA HERPESVIRUS CYCLIN COMPLEXED TO HUMAN CYCLIN DE
1F60	A B	A	CRYSTAL STRUCTURE OF THE YEAST ELONGATION FACTOR COMPLEX EEF1A:EEF1BA
1F80	A E	E	HOLO-(ACYL CARRIER PROTEIN) SYNTHASE IN COMPLEX WITH HOLO- (ACYL CARRIER PROTEIN)
1F80	A E	E	HOLO-(ACYL CARRIER PROTEIN) SYNTHASE IN COMPLEX WITH HOLO- (ACYL CARRIER PROTEIN)
1F80	B D	B	HOLO-(ACYL CARRIER PROTEIN) SYNTHASE IN COMPLEX WITH HOLO- (ACYL CARRIER PROTEIN)
1F80	C F	C	HOLO-(ACYL CARRIER PROTEIN) SYNTHASE IN COMPLEX WITH HOLO- (ACYL CARRIER PROTEIN)
1F93	A F	F	CRYSTAL STRUCTURE OF A COMPLEX BETWEEN THE DIMERIZATION DOMAIN OF HNF-1 ALPHA AND TH
1F9E	A B	B	CASPASE-8 SPECIFICITY PROBED AT SUBSITE S4: CRYSTAL STRUCTURE OF THE CASPASE-8-Z-DEVD-CHO
1FAV	A C	C	THE STRUCTURE OF AN HIV-1 SPECIFIC CELL ENTRY INHIBITOR IN COMPLEX WITH THE HIV-1 GP41 TRIM
1FBV	A C	C	STRUCTURE OF A CBL-UBCH7 COMPLEX: RING DOMAIN FUNCTION IN UBIQUITIN-PROTEIN LIGASES
1FG9	A C	A	3:1 COMPLEX OF INTERFERON-GAMMA RECEPTOR WITH INTERFERON- GAMMA DIMER
1FM6	A D	D	THE 2.1 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HETERODIMER OF THE HUMAN RXRAL
1FM6	D E	E	THE 2.1 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HETERODIMER OF THE HUMAN RXRAL
1FM6	U V	U	THE 2.1 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HETERODIMER OF THE HUMAN RXRAL
1FM6	U X	U	THE 2.1 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HETERODIMER OF THE HUMAN RXRAL
1FM6	U X	U	THE 2.1 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HETERODIMER OF THE HUMAN RXRAL
1FM6	X Y	Y	THE 2.1 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HETERODIMER OF THE HUMAN RXRAL
1FOE	A B	B	CRYSTAL STRUCTURE OF RAC1 IN COMPLEX WITH THE GUANINE NUCLEOTIDE EXCHANGE REGION OF
1FOE	A D	D	CRYSTAL STRUCTURE OF RAC1 IN COMPLEX WITH THE GUANINE NUCLEOTIDE EXCHANGE REGION OF
1FOE	E F	E	CRYSTAL STRUCTURE OF RAC1 IN COMPLEX WITH THE GUANINE NUCLEOTIDE EXCHANGE REGION OF
1FOE	E F	F	CRYSTAL STRUCTURE OF RAC1 IN COMPLEX WITH THE GUANINE NUCLEOTIDE EXCHANGE REGION OF
1FOE	G H	H	CRYSTAL STRUCTURE OF RAC1 IN COMPLEX WITH THE GUANINE NUCLEOTIDE EXCHANGE REGION OF
1FOS	E F	E	TWO HUMAN C-FOS:C-JUN:DNA COMPLEXES
1FOS	E F	F	TWO HUMAN C-FOS:C-JUN:DNA COMPLEXES
1FQ1	A B	B	CRYSTAL STRUCTURE OF KINASE ASSOCIATED PHOSPHATASE (KAP) IN COMPLEX WITH PHOSPHO-CDK2
1FQJ	A B	B	CRYSTAL STRUCTURE OF THE HETEROTRIMERIC COMPLEX OF THE RGS DOMAIN OF RGS9, THE GAMMA
1FQJ	A C	A	CRYSTAL STRUCTURE OF THE HETEROTRIMERIC COMPLEX OF THE RGS DOMAIN OF RGS9, THE GAMMA
1FQJ	A C	A	CRYSTAL STRUCTURE OF THE HETEROTRIMERIC COMPLEX OF THE RGS DOMAIN OF RGS9, THE GAMMA
1FQJ	A C	C	CRYSTAL STRUCTURE OF THE HETEROTRIMERIC COMPLEX OF THE RGS DOMAIN OF RGS9, THE GAMMA
1FQJ	D E	E	CRYSTAL STRUCTURE OF THE HETEROTRIMERIC COMPLEX OF THE RGS DOMAIN OF RGS9, THE GAMMA
1FQV	A B	B	INSIGHTS INTO SCF UBIQUITIN LIGASES FROM THE STRUCTURE OF THE SKP1-SKP2 COMPLEX
1FQV	A B	B	INSIGHTS INTO SCF UBIQUITIN LIGASES FROM THE STRUCTURE OF THE SKP1-SKP2 COMPLEX
1FQV	C D	C	INSIGHTS INTO SCF UBIQUITIN LIGASES FROM THE STRUCTURE OF THE SKP1-SKP2 COMPLEX

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
1DX5	SERINE PROTEINASE	1.5	2.9	2	11
1DX5	SERINE PROTEINASE	1.1	2.1	2	11
1E3A	ANTIBIOTIC RESISTANCE	1.3	4.0	3	22
1E3A	ANTIBIOTIC RESISTANCE	1.9	5.8	3	10
1E3A	ANTIBIOTIC RESISTANCE	1.5	8.9	6	13
1E6E	OXIDOREDUCTASE	1.8	5.3	3	9
1E7P	OXIDOREDUCTASE	1.3	2.6	2	9
1E7P	OXIDOREDUCTASE	1.5	4.5	3	17
1E7P	OXIDOREDUCTASE	1.2	3.5	3	15
1E7P	OXIDOREDUCTASE	1.2	2.3	2	13
1E7P	OXIDOREDUCTASE	1.0	2.0	2	13
1E7P	OXIDOREDUCTASE	1.1	2.1	2	13
1E8O	ALU RIBONUCLEOPROTEIN PARTICLE	1.9	7.6	4	19
1E8O	ALU RIBONUCLEOPROTEIN PARTICLE	1.7	5.1	3	17
1E8O	ALU RIBONUCLEOPROTEIN PARTICLE	1.0	2.0	2	16
1EAY	SIGNAL TRANSDUCTION COMPLEX	1.4	4.1	3	16
1EAY	SIGNAL TRANSDUCTION COMPLEX	1.2	2.3	2	13
1EBD	COMPLEX (OXIDOREDUCTASE/TRANSFERASE)	1.5	2.9	2	10
1EER	COMPLEX (CYTOKINE/RECEPTOR)	1.1	2.2	2	18
1EJH	TRANSLATION	1.7	5.2	3	7
1EJH	TRANSLATION	1.9	5.6	3	10
1EJR	HYDROLASE	1.1	2.2	2	19
1EM8	GENE REGULATION	1.1	2.1	2	10
1EMU	SIGNALING PROTEIN	1.9	3.8	2	11
1F51	TRANSFERASE	1.3	5.1	4	31
1F51	TRANSFERASE	1.3	2.6	2	11
1F5Q	TRANSFERASE	1.8	5.4	3	13
1F5Q	TRANSFERASE	1.8	3.5	2	20
1F5Q	TRANSFERASE	1.3	2.6	2	13
1F5Q	TRANSFERASE	1.8	3.5	2	20
1F60	TRANSLATION	1.7	3.3	2	15
1F80	TRANSFERASE	1.5	3.0	2	7
1F80	TRANSFERASE	1.9	9.5	5	13
1F80	TRANSFERASE	1.2	2.3	2	11
1F80	TRANSFERASE	1.5	2.9	2	9
1F93	TRANSCRIPTION	1.1	2.1	2	13
1F9E	APOPTOSIS	1.4	4.3	3	16
1FAV	VIRAL PROTEIN	1.3	2.6	2	11
1FBV	LIGASE	1.7	10.4	6	12
1FG9	IMMUNE SYSTEM	1.7	3.3	2	13
1FM6	TRANSCRIPTION	1.8	3.5	2	30
1FM6	TRANSCRIPTION	1.4	5.5	4	10
1FM6	TRANSCRIPTION	1.8	3.6	2	6
1FM6	TRANSCRIPTION	1.6	3.2	2	7
1FM6	TRANSCRIPTION	1.1	2.2	2	23
1FM6	TRANSCRIPTION	1.8	5.4	3	9
1FOE	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALI	1.8	3.6	2	5
1FOE	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALI	1.9	5.7	3	19
1FOE	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALI	1.0	2.0	2	12
1FOE	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALI	1.6	3.2	2	5
1FOE	SIGNALING PROTEIN, IMMUNE SYSTEM/SIGNALI	1.8	5.3	3	5
1FOS	TRANSCRIPTION/DNA	1.3	8.8	7	58
1FOS	TRANSCRIPTION/DNA	1.9	11.6	6	56
1FQ1	HYDROLASE/TRANSFERASE	1.2	2.3	2	12
1FQJ	SIGNALING PROTEIN	1.2	2.4	2	21
1FQJ	SIGNALING PROTEIN	1.0	2.0	2	14
1FQJ	SIGNALING PROTEIN	1.9	5.7	3	10
1FQJ	SIGNALING PROTEIN	1.8	3.6	2	7
1FQJ	SIGNALING PROTEIN	1.3	2.6	2	22
1FQV	LIGASE	1.3	2.6	2	10
1FQV	LIGASE	1.5	2.9	2	8
1FQV	LIGASE	1.5	2.9	2	8

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
1DX5	235	245
1DX5	235	245
1E3A	87	108
1E3A	63	72
1E3A	410	422
1E6E	72	80
1E7P	346	354
1E7P	156	172
1E7P	105	119
1E7P	36	48
1E7P	36	48
1E7P	36	48
1E8O	56	74
1E8O	59	75
1E8O	76	91
1EAY	113	128
1EAY	171	183
1EBD	133	142
1EER	9	26
1EJH	626	632
1EJH	69	78
1EJR	3032	3050
1EM8	52	61
1EMU	2037	2047
1F51	15	45
1F51	1413	1423
1F5Q	46	58
1F5Q	17	36
1F5Q	46	58
1F5Q	17	36
1F60	56	70
1F80	56	62
1F80	38	50
1F80	12	22
1F80	22	30
1F93	7	19
1F9E	348	362
1FAV	128	138
1FBV	1006	1017
1FG9	3	15
1FM6	431	460
1FM6	688	697
1FM6	449	454
1FM6	414	420
1FM6	421	443
1FM6	688	696
1FOE	65	69
1FOE	87	105
1FOE	1195	1206
1FOE	65	69
1FOE	65	69
1FOS	140	197
1FOS	267	322
1FQ1	208	219
1FQJ	386	406
1FQJ	238	251
1FQJ	201	210
1FQJ	78	84
1FQJ	386	407
1FQV	147	156
1FQV	132	139
1FQV	137	144

A. PDB CODE	L. HELIX SEQUENCE
1DX5	KKWIQKVIDQF
1DX5	KKWIQKVIDQF
1E3A	PEDMSILQGYADGMNAWIDKVN
1E3A	VKFDKDIRRN
1E3A	EVASLLAWTHQMK
1E6E	DEENDMLDL
1E7P	QEICEYFAG
1E7P	TGHTMLFAVANECLKLG
1E7P	YRQYLTFKTHKDLMR
1E7P	IFIVLNMIRETYD
1E7P	IFIVLNMIRETYD
1E7P	IFIVLNMIRETYD
1E8O	AQDVKKIEKFHSQLMRLMV
1E8O	VKKIEKFHSQLMRLMVA
1E8O	VNKFQMAYSNLLRANM
1EAY	AATLEEKLNKIFEKLG
1EAY	EVDLLEEELGHLT
1EBD	PSVRKYAREK
1EER	SRVLERYLLEAKEAEKIT
1EJH	REFLLDF
1EJH	VEDFWALYNH
1EJR	YPESVALISAFIMEGARDG
1EM8	PLVSDVLRAL
1EMU	DDLLQECISSA
1F51	TALTNELIHLLGHSRHDWMNKLQLIKGNLSL
1F51	SGIRILLNEVF
1F5Q	STAIREISLLKEL
1F5Q	EEDCRQMIYRSEREHDARMV
1F5Q	STAIREISLLKEL
1F5Q	EEDCRQMIYRSEREHDARMV
1F60	YAWVLDKLKAERERG
1F80	DEDAEKI
1F80	DVVELVMELEDEF
1F80	LKRIASMAGRQ
1F80	QKRFAERIL
1F93	QLQTELLAALLES
1F9E	WYIQSLCQSLRERCPR
1FAV	TSLIHSLIEES
1FBV	RLMKELEEIRKC
1FG9	PYVKEAENLKKYF
1FM6	LFAKLLQKMTDLRQIVTEHVQLLQVIKKTE
1FM6	KILHRLLQEG
1FM6	TFLMEM
1FM6	RFAKLLL
1FM6	RLPALRSIGLKCLEHLFFFKLIG
1FM6	KILHRLLQE
1FOE	DRLRP
1FOE	PASFENVRAKWYPEVRHHC
1FOE	KYPLLLRELFAL
1FOE	DRLRP
1FOE	DRLRP
1FOS	RRIRRERNKMAAAKSRNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKEKLEFIL
1FOS	KRMRNRIAASKSRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQLKQKVM
1FQ1	EIDQLFRIFRTL
1FQJ	DAAQTHIYMLMKKDSYARYLK
1FQJ	RMHESMKLFDSICN
1FQJ	RSERKKWIHC
1FQJ	LHELAQY
1FQJ	DAAQTHIYMLMKKDSYARYLKS
1FQV	EEEEAQVRKE
1FQV	PEEIRKTF
1FQV	KRWYRLAS

A. PDB CODE	M. RESOLUTION
1DX5	2.3
1DX5	2.3
1E3A	1.8
1E3A	1.8
1E3A	1.8
1E6E	2.3
1E7P	3.1
1E7P	3.1
1E7P	3.1
1E7P	3.1
1E7P	3.1
1E7P	3.1
1E8O	3.2
1E8O	3.2
1E8O	3.2
1EAY	2
1EAY	2
1EBD	2.6
1EER	1.9
1EJH	2.2
1EJH	2.2
1EJR	2
1EM8	2.1
1EMU	1.9
1F51	3
1F51	3
1F5Q	2.5
1F5Q	2.5
1F5Q	2.5
1F5Q	2.5
1F60	1.67
1F80	2.3
1F80	2.3
1F80	2.3
1F80	2.3
1F93	2.6
1F9E	2.9
1FAV	3
1FBV	2.9
1FG9	2.9
1FM6	2.1
1FM6	2.1
1FM6	2.1
1FM6	2.1
1FM6	2.1
1FM6	2.1
1FOE	2.8
1FOE	2.8
1FOE	2.8
1FOE	2.8
1FOE	2.8
1FOS	3.05
1FOS	3.05
1FQ1	3
1FQJ	2.02
1FQJ	2.02
1FQJ	2.02
1FQJ	2.02
1FQJ	2.02
1FQV	2.8
1FQV	2.8
1FQV	2.8

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1FQV	C D	D	INSIGHTS INTO SCF UBIQUITIN LIGASES FROM THE STRUCTURE OF THE SKP1-SKP2 COMPLEX
1FQV	I J	I	INSIGHTS INTO SCF UBIQUITIN LIGASES FROM THE STRUCTURE OF THE SKP1-SKP2 COMPLEX
1FQV	I J	J	INSIGHTS INTO SCF UBIQUITIN LIGASES FROM THE STRUCTURE OF THE SKP1-SKP2 COMPLEX
1FQV	K L	K	INSIGHTS INTO SCF UBIQUITIN LIGASES FROM THE STRUCTURE OF THE SKP1-SKP2 COMPLEX
1FQV	M N	M	INSIGHTS INTO SCF UBIQUITIN LIGASES FROM THE STRUCTURE OF THE SKP1-SKP2 COMPLEX
1FS1	A B	A	INSIGHTS INTO SCF UBIQUITIN LIGASES FROM THE STRUCTURE OF THE SKP1-SKP2 COMPLEX
1FS1	C D	D	INSIGHTS INTO SCF UBIQUITIN LIGASES FROM THE STRUCTURE OF THE SKP1-SKP2 COMPLEX
1FS2	A B	A	INSIGHTS INTO SCF UBIQUITIN LIGASES FROM THE STRUCTURE OF THE SKP1-SKP2 COMPLEX
1FS2	A B	B	INSIGHTS INTO SCF UBIQUITIN LIGASES FROM THE STRUCTURE OF THE SKP1-SKP2 COMPLEX
1FS2	A B	B	INSIGHTS INTO SCF UBIQUITIN LIGASES FROM THE STRUCTURE OF THE SKP1-SKP2 COMPLEX
1FYH	D E	D	1:1 COMPLEX BETWEEN AN INTERFERON GAMMA SINGLE-CHAIN VARIANT AND ITS RECEPTOR
1G1E	A B	A	NMR STRUCTURE OF THE HUMAN MAD1 TRANSREPRESSION DOMAIN SID IN COMPLEX WITH MAMMAL
1G1X	F B	B	STRUCTURE OF RIBOSOMAL PROTEINS S15, S6, S18, AND 16S RIBOSOMAL RNA
1G3I	C I	I	CRYSTAL STRUCTURE OF THE HSLUV PROTEASE-CHAPERONE COMPLEX
1G3N	A C	A	STRUCTURE OF A P18(INK4C)-CDK6-K-CYCLIN TERNARY COMPLEX
1G3N	A C	C	STRUCTURE OF A P18(INK4C)-CDK6-K-CYCLIN TERNARY COMPLEX
1G3N	E G	G	STRUCTURE OF A P18(INK4C)-CDK6-K-CYCLIN TERNARY COMPLEX
1G3N	E G	G	STRUCTURE OF A P18(INK4C)-CDK6-K-CYCLIN TERNARY COMPLEX
1G4U	S R	S	CRYSTAL STRUCTURE OF THE SALMONELLA TYROSINE PHOSPHATASE AND GTPASE ACTIVATING PROT
1G4Y	B R	B	1.60 A CRYSTAL STRUCTURE OF THE GATING DOMAIN FROM SMALL CONDUCTANCE POTASSIUM CHAN
1G4Y	B R	R	1.60 A CRYSTAL STRUCTURE OF THE GATING DOMAIN FROM SMALL CONDUCTANCE POTASSIUM CHAN
1G73	B D	B	CRYSTAL STRUCTURE OF SMAC BOUND TO XIAP-BIR3 DOMAIN
1GH6	A B	B	RETINOBLASTOMA POCKET COMPLEXED WITH SV40 LARGE T ANTIGEN
1GHQ	A B	A	CR2-C3D COMPLEX STRUCTURE
1GPQ	A D	A	STRUCTURE OF IVY COMPLEXED WITH ITS TARGET, HEWL
1GX7	A D	A	BEST MODEL OF THE ELECTRON TRANSFER COMPLEX BETWEEN CYTOCHROME C3 AND [FE]-HYDROGE
1GZL	B D	B	CRYSTAL STRUCTURE OF C14LINKMID/IQN17: A CROSS-LINKED INHIBITOR OF HIV-1 ENTRY BOUND TO
1GZL	B D	D	CRYSTAL STRUCTURE OF C14LINKMID/IQN17: A CROSS-LINKED INHIBITOR OF HIV-1 ENTRY BOUND TO
1GZS	B A	A	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE GEF DOMAIN OF THE SALMONELLA TYPHIMUR
1GZS	B A	B	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE GEF DOMAIN OF THE SALMONELLA TYPHIMUR
1GZS	D C	C	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE GEF DOMAIN OF THE SALMONELLA TYPHIMUR
1H1V	G A	G	GELSOLIN G4-G6/ACTIN COMPLEX
1H2M	A S	A	FACTOR INHIBITING HIF-1 ALPHA IN COMPLEX WITH HIF-1 ALPHA FRAGMENT PEPTIDE
1H2S	A B	A	MOLECULAR BASIS OF TRANSMENBRANE SIGNALLING BY SENSORY RHODOPSIN II-TRANSDUCER COM
1H2S	A B	B	MOLECULAR BASIS OF TRANSMENBRANE SIGNALLING BY SENSORY RHODOPSIN II-TRANSDUCER COM
1H3O	A B	A	CRYSTAL STRUCTURE OF THE HUMAN TAF4-TAF12 (TAFII135-TAFII20) COMPLEX
1H3O	A B	A	CRYSTAL STRUCTURE OF THE HUMAN TAF4-TAF12 (TAFII135-TAFII20) COMPLEX
1H3O	C D	C	CRYSTAL STRUCTURE OF THE HUMAN TAF4-TAF12 (TAFII135-TAFII20) COMPLEX
1H3O	C D	D	CRYSTAL STRUCTURE OF THE HUMAN TAF4-TAF12 (TAFII135-TAFII20) COMPLEX
1H4L	B E	B	STRUCTURE AND REGULATION OF THE CDK5-P25(NCK5A) COMPLEX
1H59	A B	A	COMPLEX OF IGFBP-5 WITH IGF-I
1H6K	A X	X	NUCLEAR CAP BINDING COMPLEX
1H6K	B Y	Y	NUCLEAR CAP BINDING COMPLEX
1H6K	B Y	Y	NUCLEAR CAP BINDING COMPLEX
1HBX	B G	B	TERNARY COMPLEX OF SAP-1 AND SRF WITH SPECIFIC SRE DNA
1HE1	A C	A	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE GAP DOMAIN OF THE PSEUDOMONAS AERUGI
1HE1	A C	A	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE GAP DOMAIN OF THE PSEUDOMONAS AERUGI
1HE1	B D	B	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE GAP DOMAIN OF THE PSEUDOMONAS AERUGI
1HE1	B D	B	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE GAP DOMAIN OF THE PSEUDOMONAS AERUGI
1HH4	A D	D	RAC1-RHOGDI COMPLEX INVOLVED IN NADPH OXIDASE ACTIVATION
1HIA	X Y	Y	KALLIKREIN COMPLEXED WITH HIRUSTASIN
1HL6	A B	B	A NOVEL MODE OF RBD-PROTEIN RECOGNITION IN THE Y14-MAGO COMPLEX
1HL6	C D	C	A NOVEL MODE OF RBD-PROTEIN RECOGNITION IN THE Y14-MAGO COMPLEX
1HLU	A P	A	STRUCTURE OF BOVINE BETA-ACTIN-PROFILIN COMPLEX WITH ACTIN BOUND ATP PHOSPHATES SOLVE
1HLU	A P	P	STRUCTURE OF BOVINE BETA-ACTIN-PROFILIN COMPLEX WITH ACTIN BOUND ATP PHOSPHATES SOLVE
1HT1	B F	B	NUCLEOTIDE-DEPENDENT CONFORMATIONAL CHANGES IN A PROTEASE- ASSOCIATED ATPASE HSLU
1HWM	A B	A	EBULIN,ORTHORHOMBIC CRYSTAL FORM MODEL
1HX1	A B	B	CRYSTAL STRUCTURE OF A BAG DOMAIN IN COMPLEX WITH THE HSC70 ATPASE DOMAIN
1HYR	B C	C	CRYSTAL STRUCTURE OF HUMAN MICA IN COMPLEX WITH NATURAL KILLER CELL RECEPTOR NKG2D
1I2M	A B	A	RAN-RCC1-SO4 COMPLEX
1I3O	A B	A	CRYSTAL STRUCTURE OF THE COMPLEX OF XIAP-BIR2 AND CASPASE 3
1I4D	A D	A	CRYSTAL STRUCTURE ANALYSIS OF RAC1-GDP COMPLEXED WITH ARFAPTIN (P21)
1I51	A B	A	CRYSTAL STRUCTURE OF CASPASE-7 COMPLEXED WITH XIAP

TABLE S4

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM,\ HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
1FQV	LIGASE	1.1	2.2	2	16
1FQV	LIGASE	1.7	5.1	3	8
1FQV	LIGASE	1.9	3.7	2	14
1FQV	LIGASE	1.4	4.2	3	8
1FQV	LIGASE	1.7	5.0	3	7
1FS1	LIGASE	1.6	3.1	2	9
1FS1	LIGASE	1.2	2.3	2	8
1FS2	LIGASE	1.3	2.6	2	8
1FS2	LIGASE	1.3	2.5	2	16
1FS2	LIGASE	1.3	2.6	2	8
1FYH	IMMUNE SYSTEM	1.2	2.3	2	7
1G1E	TRANSCRIPTION	1.4	2.8	2	13
1G1X	RIBOSOME	1.4	2.8	2	11
1G3I	CHAPERONE/HYDROLASE	1.1	2.2	2	11
1G3N	CELL CYCLE, SIGNALING PROTEIN	1.7	5.1	3	17
1G3N	CELL CYCLE, SIGNALING PROTEIN	1.2	2.4	2	17
1G3N	CELL CYCLE, SIGNALING PROTEIN	1.3	2.5	2	17
1G3N	CELL CYCLE, SIGNALING PROTEIN	1.8	5.4	3	15
1G4U	SIGNALING PROTEIN	1.1	2.2	2	14
1G4Y	SIGNALING PROTEIN	1.3	4.0	3	44
1G4Y	SIGNALING PROTEIN	1.9	3.8	2	11
1G73	APOPTOSIS/APOPTOSIS INHIBITOR	1.6	4.7	3	48
1GH6	ANTITUMOR PROTEIN	1.5	3.0	2	11
1GHQ	IMMUNE SYSTEM/VIRAL PROTEIN RECEPTOR	1.5	4.4	3	15
1GPQ	HYDROLASE/INHIBITOR	1.9	3.7	2	5
1GX7	OXIDOREDUCTASE	1.7	3.4	2	11
1GZL	GLYCOPROTEIN	1.7	5.1	3	44
1GZL	GLYCOPROTEIN	1.6	3.1	2	11
1GZS	TOXIN/CELL CYCLE	1.5	5.8	4	9
1GZS	TOXIN/CELL CYCLE	1.7	5.1	3	30
1GZS	TOXIN/CELL CYCLE	1.7	3.4	2	9
1H1V	ACTIN-BINDING	1.3	2.5	2	18
1H2M	TRANSCRIPTION ACTIVATOR/INHIBITOR	1.7	3.4	2	9
1H2S	MEMBRANE PROTEIN	1.2	2.4	2	28
1H2S	MEMBRANE PROTEIN	1.4	2.7	2	27
1H3O	TRANSCRIPTION/TBP-ASSOCIATED FACTORS	1.3	3.8	3	14
1H3O	TRANSCRIPTION/TBP-ASSOCIATED FACTORS	1.6	11.4	7	22
1H3O	TRANSCRIPTION/TBP-ASSOCIATED FACTORS	1.7	6.9	4	24
1H3O	TRANSCRIPTION/TBP-ASSOCIATED FACTORS	1.9	3.7	2	10
1H4L	KINASE/KINASE ACTIVATOR	1.5	3.0	2	14
1H59	INSULIN	1.3	2.5	2	7
1H6K	NUCLEAR PROTEIN	1.8	3.6	2	11
1H6K	NUCLEAR PROTEIN	1.8	3.6	2	11
1H6K	NUCLEAR PROTEIN	1.5	3.0	2	12
1HBX	GENE REGULATION	1.4	2.7	2	26
1HE1	SIGNALING PROTEIN	1.8	3.5	2	16
1HE1	SIGNALING PROTEIN	1.7	6.7	4	25
1HE1	SIGNALING PROTEIN	1.8	3.5	2	15
1HE1	SIGNALING PROTEIN	1.6	3.2	2	24
1HH4	SIGNALING PROTEIN/INHIBITOR	1.9	3.7	2	12
1HIA	COMPLEX (PROTEASE/INHIBITOR)	1.9	5.8	3	11
1HL6	SIGNAL PROTEIN	1.2	3.6	3	15
1HL6	SIGNAL PROTEIN	1.6	6.3	4	13
1HLU	COMPLEX (ACETYLATION/ACTIN-BINDING)	1.5	3.0	2	5
1HLU	COMPLEX (ACETYLATION/ACTIN-BINDING)	1.5	5.8	4	18
1HT1	CHAPERONE	1.3	4.0	3	12
1HWM	HYDROLASE	1.7	5.1	3	13
1HX1	CHAPERONE/CHAPERONE INHIBITOR	1.7	3.3	2	19
1HYR	IMMUNE SYSTEM	1.1	2.1	2	21
1I2M	CELL CYCLE	1.9	7.7	4	13
1I3O	APOPTOSIS	1.7	3.3	2	15
1I4D	SIGNALING PROTEIN	1.6	3.2	2	50
1I51	HYDROLASE/HYDROLASE INHIBITOR	1.5	4.5	3	16

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
1FQV	113	128
1FQV	137	144
1FQV	97	110
1FQV	137	144
1FQV	137	143
1FS1	114	122
1FS1	132	139
1FS2	137	144
1FS2	113	128
1FS2	132	139
1FYH	313	319
1G1E	9	21
1G1X	4	14
1G3I	71	81
1G3N	56	72
1G3N	93	109
1G3N	93	109
1G3N	128	142
1G4U	207	220
1G4Y	446	490
1G4Y	45	55
1G73	72	119
1GH6	721	731
1GHQ	104	118
1GPQ	118	122
1GX7	108	118
1GZL	2	45
1GZL	629	639
1GZS	65	73
1GZS	104	133
1GZS	65	73
1H1V	473	490
1H2M	156	164
1H2S	154	181
1H2S	25	51
1H3O	873	886
1H3O	896	917
1H3O	894	917
1H3O	60	69
1H4L	44	57
1H59	54	60
1H6K	53	63
1H6K	53	63
1H6K	91	102
1HBX	154	179
1HE1	144	159
1HE1	96	120
1HE1	144	158
1HE1	97	120
1HH4	346	357
1HIA	235	245
1HL6	55	69
1HL6	17	29
1HLU	370	374
1HLU	120	137
1HT1	55	66
1HWM	168	180
1HX1	204	222
1HYR	154	174
1I2M	101	113
1I3O	182	196
1I4D	29	78
1I51	90	105

A. PDB CODE	L. HELIX SEQUENCE
1FQV	KGLLDVTCKTVANMIK
1FQV	KRWYRLAS
1FQV	QGTLFELILAANYL
1FQV	KRWYRLAS
1FQV	KRWYRLA
1FS1	DELLLGIFS
1FS1	PEEIRKTF
1FS2	KRWYRLAS
1FS2	KGLLDVTCKTVANMIK
1FS2	PEEIRKTF
1FYH	LIQVMAE
1G1E	IQMLLEAADYLER
1G1X	KEEKQKVIQEF
1G3I	LLKSAVELAKD
1G3N	LSTIREVAVLRHLETFE
1G3N	FQKTGSACLLVASKLRS
1G3N	FQKTGSACLLVASKLRS
1G3N	RQELIDQEKELLEKL
1G4U	PLRSLMTNLQNLNK
1G4Y	HAKVRKHQRKFLQAIHQLRSVKMEQRKLNDQANTLVDLAKTQLH
1G4Y	EAELQDMINEV
1G73	EEEDEVWQVIIGARAEMTSKHQEYLKLETTWMTAVGLSEMAAEAAYQT
1GH6	FKIIVTAYKDL
1GHQ	SQVLCGAVKWLILEK
1GPQ	SLENH
1GX7	PAVRYALGDAF
1GZL	MKQIEDKIEEIESKQKKIENEIARIKKLLQLTVWGIKQLQARIL
1GZL	EEWDREIENYT
1GZS	DRLRPLSYP
1GZS	PAYASQTREAILSAVYSKNKDQCCNLLISK
1GZS	DRLRPLSYP
1H1V	QDEVAASAILTAQLDEEL
1H2M	RKIVMDFLG
1H2S	SGIKSLYVRLRNLTVILWAIYPFIWLLG
1H2S	VFIFVGALTVLFGAIAYGEVTAAAATG
1H3O	QAPLQRRILEIGKK
1H3O	VVSYVSHATQQRLQNLVEKISE
1H3O	PDVVSYVSHATQQRLQNLVEKISE
1H3O	KKKLQDLVRE
1H4L	VPSSALREICLLKE
1H59	LRRLEMY
1H6K	EEQIYELFSKS
1H6K	EEQIYELFSKS
1H6K	RADAENAMRYIN
1HBX	KLRRYTTFSKRKTGIMKKAYELSTLT
1HE1	ALRSLSTALAGIRAGS
1HE1	SSAVVFKQMVLQQALPMTLKGLDKA
1HE1	ALRSLSTALAGIRAG
1HE1	SAVVFKQMVLQQALPMTLKGLDKA
1HH4	ESLRKYKEALLG
1HIA	LDWIDDTITEN
1HL6	QSVMEELKRIIIDSE
1HL6	EDGDQGIVRLKEK
1HLU	VHRKC
1HLU	GGMINKKCYEMASHLRRS
1HT1	TLFELFERKLEM
1HWM	RYIEQEVRRSLQQ
1HX1	DRRVKATIEQFMKILEEID
1HYR	KTHYHAMHADCLQELRRYLKS
1I2M	VPNWHRDLVRVCE
1I3O	TDVDAANLRETFRNL
1I4D	ELELQIELLRETKRKYESVLQLGRALTAHLYSLLQTQHALGDAFADLSQK
1I51	TDKDAEALFKCFRSLG

A. PDB CODE	M. RESOLUTION
1FQV	2.8
1FQV	2.8
1FQV	2.8
1FQV	2.8
1FQV	2.8
1FS1	1.8
1FS1	1.8
1FS2	2.9
1FS2	2.9
1FS2	2.9
1FYH	2.04
1G1E	NOT APP
1G1X	2.6
1G3I	3.41
1G3N	2.9
1G3N	2.9
1G3N	2.9
1G3N	2.9
1G4U	2.3
1G4Y	1.6
1G4Y	1.6
1G73	2
1GH6	3.2
1GHQ	2.04
1GPQ	1.6
1GX7	NOT APP
1GZL	1.8
1GZL	1.8
1GZS	2.3
1GZS	2.3
1GZS	2.3
1H1V	3
1H2M	2.5
1H2S	1.93
1H2S	1.93
1H3O	2.3
1H3O	2.3
1H3O	2.3
1H3O	2.3
1H4L	2.65
1H59	2.1
1H6K	2
1H6K	2
1H6K	2
1HBX	3.15
1HE1	2
1HE1	2
1HE1	2
1HE1	2
1HH4	2.7
1HIA	2.4
1HL6	2.5
1HL6	2.5
1HLU	2.65
1HLU	2.65
1HT1	2.8
1HWM	2.8
1HX1	1.9
1HYR	2.7
1I2M	1.76
1I3O	2.7
1I4D	2.5
1I51	2.45

TABLE S4

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1I51	A B	B	CRYSTAL STRUCTURE OF CASPASE-7 COMPLEXED WITH XIAP
1I51	C D	D	CRYSTAL STRUCTURE OF CASPASE-7 COMPLEXED WITH XIAP
1I5K	A D	D	STRUCTURE AND BINDING DETERMINANTS OF THE RECOMBINANT KRINGLE-2 DOMAIN OF HUMAN PL
1I5K	B C	C	STRUCTURE AND BINDING DETERMINANTS OF THE RECOMBINANT KRINGLE-2 DOMAIN OF HUMAN PL
1I7W	A B	A	BETA-CATENIN/PHOSPHORYLATED E-CADHERIN COMPLEX
1I7W	C D	C	BETA-CATENIN/PHOSPHORYLATED E-CADHERIN COMPLEX
1I7W	C D	D	BETA-CATENIN/PHOSPHORYLATED E-CADHERIN COMPLEX
1IB1	A E	A	CRYSTAL STRUCTURE OF THE 14-3-3 ZETA:SEROTONIN N- ACETYLTRANSFERASE COMPLEX
1IB1	A E	A	CRYSTAL STRUCTURE OF THE 14-3-3 ZETA:SEROTONIN N- ACETYLTRANSFERASE COMPLEX
1IB1	C G	C	CRYSTAL STRUCTURE OF THE 14-3-3 ZETA:SEROTONIN N- ACETYLTRANSFERASE COMPLEX
1IB1	D H	D	CRYSTAL STRUCTURE OF THE 14-3-3 ZETA:SEROTONIN N- ACETYLTRANSFERASE COMPLEX
1IBR	A B	A	COMPLEX OF RAN WITH IMPORTIN BETA
1IBR	A B	B	COMPLEX OF RAN WITH IMPORTIN BETA
1IBR	A B	B	COMPLEX OF RAN WITH IMPORTIN BETA
1IBR	C D	C	COMPLEX OF RAN WITH IMPORTIN BETA
1IBR	C D	D	COMPLEX OF RAN WITH IMPORTIN BETA
1IHF	A B	A	INTEGRATION HOST FACTOR/DNA COMPLEX
1IHF	A B	B	INTEGRATION HOST FACTOR/DNA COMPLEX
1II8	A B	A	CRYSTAL STRUCTURE OF THE P. FURIOSUS RAD50 ATPASE DOMAIN
1II8	A B	B	CRYSTAL STRUCTURE OF THE P. FURIOSUS RAD50 ATPASE DOMAIN
1IQ5	A B	A	CALMODULIN/NEMATODE CA2+/CALMODULIN DEPENDENT KINASE KINASE FRAGMENT
1IQ5	A B	A	CALMODULIN/NEMATODE CA2+/CALMODULIN DEPENDENT KINASE KINASE FRAGMENT
1IQ5	A B	B	CALMODULIN/NEMATODE CA2+/CALMODULIN DEPENDENT KINASE KINASE FRAGMENT
1IWQ	A B	A	CRYSTAL STRUCTURE OF MARCKS CALMODULIN BINDING DOMAIN PEPTIDE COMPLEXED WITH CA2+/
1IWQ	A B	A	CRYSTAL STRUCTURE OF MARCKS CALMODULIN BINDING DOMAIN PEPTIDE COMPLEXED WITH CA2+/
1IXR	B C	B	RUVA-RUVB COMPLEX
1IXS	A B	A	STRUCTURE OF RUVB COMPLEXED WITH RUVA DOMAIN III
1IYJ	A B	A	STRUCTURE OF A BRCA2-DSS1 COMPLEX
1IYJ	C D	C	STRUCTURE OF A BRCA2-DSS1 COMPLEX
1IYJ	C D	D	STRUCTURE OF A BRCA2-DSS1 COMPLEX
1IYJ	C D	D	STRUCTURE OF A BRCA2-DSS1 COMPLEX
1J19	A B	A	CRYSTAL STRUCTURE OF THE RADXIN FERM DOMAIN COMPLEXED WITH THE ICAM-2 CYTOPLASMIC P
1J1D	A B	A	CRYSTAL STRUCTURE OF THE 46KDA DOMAIN OF HUMAN CARDIAC TROPONIN IN THE CA2+ SATURATE
1J1D	A B	B	CRYSTAL STRUCTURE OF THE 46KDA DOMAIN OF HUMAN CARDIAC TROPONIN IN THE CA2+ SATURATE
1J1D	A C	A	CRYSTAL STRUCTURE OF THE 46KDA DOMAIN OF HUMAN CARDIAC TROPONIN IN THE CA2+ SATURATE
1J1D	A C	C	CRYSTAL STRUCTURE OF THE 46KDA DOMAIN OF HUMAN CARDIAC TROPONIN IN THE CA2+ SATURATE
1J1D	B C	B	CRYSTAL STRUCTURE OF THE 46KDA DOMAIN OF HUMAN CARDIAC TROPONIN IN THE CA2+ SATURATE
1J1D	B C	B	CRYSTAL STRUCTURE OF THE 46KDA DOMAIN OF HUMAN CARDIAC TROPONIN IN THE CA2+ SATURATE
1J1D	B C	C	CRYSTAL STRUCTURE OF THE 46KDA DOMAIN OF HUMAN CARDIAC TROPONIN IN THE CA2+ SATURATE
1J1D	D E	D	CRYSTAL STRUCTURE OF THE 46KDA DOMAIN OF HUMAN CARDIAC TROPONIN IN THE CA2+ SATURATE
1J1D	D F	D	CRYSTAL STRUCTURE OF THE 46KDA DOMAIN OF HUMAN CARDIAC TROPONIN IN THE CA2+ SATURATE
1J1D	D F	D	CRYSTAL STRUCTURE OF THE 46KDA DOMAIN OF HUMAN CARDIAC TROPONIN IN THE CA2+ SATURATE
1J1D	D F	F	CRYSTAL STRUCTURE OF THE 46KDA DOMAIN OF HUMAN CARDIAC TROPONIN IN THE CA2+ SATURATE
1J1D	D F	F	CRYSTAL STRUCTURE OF THE 46KDA DOMAIN OF HUMAN CARDIAC TROPONIN IN THE CA2+ SATURATE
1J1D	E F	E	CRYSTAL STRUCTURE OF THE 46KDA DOMAIN OF HUMAN CARDIAC TROPONIN IN THE CA2+ SATURATE
1J1D	E F	F	CRYSTAL STRUCTURE OF THE 46KDA DOMAIN OF HUMAN CARDIAC TROPONIN IN THE CA2+ SATURATE
1J34	A B	A	CRYSTAL STRUCTURE OF MG(II)-AND CA(II)-BOUND GLA DOMAIN OF FACTOR IX COMPLEXED WITH BI
1JCH	A B	B	CRYSTAL STRUCTURE OF COLICIN E3 IN COMPLEX WITH ITS IMMUNITY PROTEIN
1JCH	C D	D	CRYSTAL STRUCTURE OF COLICIN E3 IN COMPLEX WITH ITS IMMUNITY PROTEIN
1JEK	A B	A	VISNA TM CORE STRUCTURE
1JEY	A B	A	CRYSTAL STRUCTURE OF THE KU HETERODIMER BOUND TO DNA
1JEY	A B	A	CRYSTAL STRUCTURE OF THE KU HETERODIMER BOUND TO DNA
1JEY	A B	A	CRYSTAL STRUCTURE OF THE KU HETERODIMER BOUND TO DNA
1JEY	A B	A	CRYSTAL STRUCTURE OF THE KU HETERODIMER BOUND TO DNA
1JEY	A B	B	CRYSTAL STRUCTURE OF THE KU HETERODIMER BOUND TO DNA
1JFI	A B	A	CRYSTAL STRUCTURE OF THE NC2-TBP-DNA TERNARY COMPLEX
1JFI	A B	B	CRYSTAL STRUCTURE OF THE NC2-TBP-DNA TERNARY COMPLEX
1JFI	A B	B	CRYSTAL STRUCTURE OF THE NC2-TBP-DNA TERNARY COMPLEX
1JIW	P I	P	CRYSTAL STRUCTURE OF THE APR-APRIN COMPLEX
1JMO	H A	A	CRYSTAL STRUCTURE OF THE HEPARIN COFACTOR II-S195A THROMBIN COMPLEX
1JMO	L H	L	CRYSTAL STRUCTURE OF THE HEPARIN COFACTOR II-S195A THROMBIN COMPLEX
1JMU	B G	G	CRYSTAL STRUCTURE OF THE REOVIRUS MU1/SIGMA3 COMPLEX
1JMU	E F	F	CRYSTAL STRUCTURE OF THE REOVIRUS MU1/SIGMA3 COMPLEX

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
1I51	HYDROLASE/HYDROLASE INHIBITOR	1.2	3.7	3	13
1I51	HYDROLASE/HYDROLASE INHIBITOR	1.6	3.1	2	13
1I5K	BLOOD CLOTTING	1.2	2.4	2	22
1I5K	BLOOD CLOTTING	1.7	5.2	3	22
1I7W	CELL ADHESION	1.7	3.3	2	17
1I7W	CELL ADHESION	1.2	3.5	3	10
1I7W	CELL ADHESION	1.2	2.4	2	10
1IB1	SIGNALING PROTEIN/TRANSFERASE	1.7	3.3	2	19
1IB1	SIGNALING PROTEIN/TRANSFERASE	1.9	3.8	2	14
1IB1	SIGNALING PROTEIN/TRANSFERASE	1.4	2.7	2	31
1IB1	SIGNALING PROTEIN/TRANSFERASE	1.3	2.5	2	21
1IBR	CELL CYCLE,TRANSLATION	1.2	2.3	2	10
1IBR	CELL CYCLE,TRANSLATION	1.6	3.1	2	18
1IBR	CELL CYCLE,TRANSLATION	1.4	2.8	2	18
1IBR	CELL CYCLE,TRANSLATION	1.6	3.1	2	14
1IBR	CELL CYCLE,TRANSLATION	1.3	2.6	2	27
1IHF	TRANSCRIPTION/DNA	1.9	3.8	2	9
1IHF	TRANSCRIPTION/DNA	1.5	3.0	2	12
1II8	REPLICATION	1.5	9.2	6	32
1II8	REPLICATION	1.4	2.8	2	11
1IQ5	METAL BINDING PROTEIN/PROTEIN BINDING	1.9	3.8	2	11
1IQ5	METAL BINDING PROTEIN/PROTEIN BINDING	1.2	2.4	2	15
1IQ5	METAL BINDING PROTEIN/PROTEIN BINDING	1.8	10.9	6	13
1IWQ	METAL BINDING PROTEIN/PROTEIN BINDING	1.8	7.3	4	12
1IWQ	METAL BINDING PROTEIN/PROTEIN BINDING	1.4	4.3	3	15
1IXR	HYDROLASE	1.4	2.7	2	11
1IXS	HYDROLASE	1.2	2.4	2	10
1IYJ	GENE REGULATION/ANTITUMOR PROTEIN	1.4	2.8	2	5
1IYJ	GENE REGULATION/ANTITUMOR PROTEIN	1.6	3.2	2	5
1IYJ	GENE REGULATION/ANTITUMOR PROTEIN	1.2	3.5	3	18
1IYJ	GENE REGULATION/ANTITUMOR PROTEIN	1.0	2.0	2	22
1J19	CELL ADHESION	1.2	2.3	2	21
1J1D	CONTRACTILE PROTEIN	1.5	4.6	3	12
1J1D	CONTRACTILE PROTEIN	1.6	3.1	2	45
1J1D	CONTRACTILE PROTEIN	1.6	3.1	2	12
1J1D	CONTRACTILE PROTEIN	1.4	6.9	5	20
1J1D	CONTRACTILE PROTEIN	1.8	21.6	12	45
1J1D	CONTRACTILE PROTEIN	1.8	3.6	2	21
1J1D	CONTRACTILE PROTEIN	1.6	13.1	8	47
1J1D	CONTRACTILE PROTEIN	1.3	2.5	2	12
1J1D	CONTRACTILE PROTEIN	1.4	2.8	2	11
1J1D	CONTRACTILE PROTEIN	1.5	3.0	2	12
1J1D	CONTRACTILE PROTEIN	1.3	2.5	2	6
1J1D	CONTRACTILE PROTEIN	1.8	10.8	6	37
1J1D	CONTRACTILE PROTEIN	1.8	20.3	11	46
1J1D	CONTRACTILE PROTEIN	1.7	27.5	16	48
1J34	PROTEIN BINDING/BLOOD CLOTTING	1.5	2.9	2	10
1JCH	RIBOSOME INHIBITOR, HYDROLASE	1.6	4.8	3	8
1JCH	RIBOSOME INHIBITOR, HYDROLASE	1.6	4.8	3	8
1JEK	VIRAL PROTEIN	1.8	5.4	3	39
1JEY	DNA BINDING PROTEIN/DNA	1.4	4.2	3	10
1JEY	DNA BINDING PROTEIN/DNA	1.7	6.6	4	14
1JEY	DNA BINDING PROTEIN/DNA	1.6	4.7	3	15
1JEY	DNA BINDING PROTEIN/DNA	1.7	8.3	5	15
1JEY	DNA BINDING PROTEIN/DNA	1.6	8.2	5	14
1JFI	TRANSCRIPTION/DNA	1.8	12.7	7	27
1JFI	TRANSCRIPTION/DNA	1.1	2.1	2	12
1JFI	TRANSCRIPTION/DNA	1.5	3.0	2	12
1JIW	HYDROLASE/HYROLASE INHIBITOR	1.9	5.6	3	15
1JMO	BLOOD CLOTTING	1.6	4.7	3	7
1JMO	BLOOD CLOTTING	1.5	4.6	3	8
1JMU	VIRAL PROTEIN	1.7	3.3	2	5
1JMU	VIRAL PROTEIN	1.1	2.2	2	12

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
1I51	240	252
1I51	240	252
1I5K	406	427
1I5K	306	327
1I7W	375	391
1I7W	152	161
1I7W	657	666
1IB1	165	183
1IB1	215	228
1IB1	38	68
1IB1	112	132
1IBR	101	110
1IBR	144	161
1IBR	15	32
1IBR	157	170
1IBR	273	299
1IHF	85	93
1IHF	3	14
1II8	164	195
1II8	710	720
1IQ5	83	93
1IQ5	6	20
1IQ5	337	349
1IWQ	118	129
1IWQ	6	20
1IXR	179	189
1IXS	179	188
1IYJ	58	62
1IYJ	58	62
1IYJ	2579	2596
1IYJ	2547	2568
1J19	274	294
1J1D	94	105
1J1D	226	270
1J1D	130	141
1J1D	43	62
1J1D	226	270
1J1D	204	224
1J1D	90	136
1J1D	94	105
1J1D	131	141
1J1D	94	105
1J1D	151	156
1J1D	44	80
1J1D	226	271
1J1D	90	137
1J34	23	32
1JCH	53	60
1JCH	53	60
1JEK	547	585
1JEY	521	530
1JEY	456	469
1JEY	481	495
1JEY	378	392
1JEY	448	461
1JFI	32	58
1JFI	168	179
1JFI	115	126
1JIW	169	183
1JMO	63	69
1JMO	14	14
1JMU	331	335
1JMU	212	223

A. PDB CODE	L. HELIX SEQUENCE
1I51	WFVQALCSILEEH
1I51	WFVQALCSILEEH
1I5K	ADAELQRLKNERHEEAELERLK
1I5K	ADAELQRLKNERHEEAELERLK
1I7W	QRLVQNCLWTLRNLSDA
1I7W	AIPELTKLLN
1I7W	IDENLKAADS
1IB1	PIRLGLALNFSVFYYEILN
1IB1	TLIMQLLRDNLTLW
1IB1	NEERNLLSVAYKNVVGARRSSWRVVSSIEQK
1IB1	AESKVFYLKMKGDYYRYLAEV
1IBR	VPNWHRDLVR
1IBR	EHMKESTLEAIGYICQDI
1IBR	RLELEAAQKFLERAAVEN
1IBR	FEKPFLWLARKLIG
1IBR	DEVALQGIEFWSNVCDEEMDLAIEASE
1IHF	QKLKSRVEN
1IHF	KSELIERLATQQ
1II8	DKFETAYKKLSELKKTINNRIKEYRDILARTE
1II8	ERVKKEIKDLE
1IQ5	EEIREAFRVFD
1IQ5	EEQIAEFKEAFSLFD
1IQ5	LDTLILVKAMGHR
1IWQ	DEEVDEMIREAD
1IWQ	EEQIAEFKEAFSLFD
1IXR	AQDLIKEALKR
1IXS	AQDLIKEALK
1IYJ	AELEK
1IYJ	AELEK
1IYJ	PERVLLQLKYRYDVEIDN
1IYJ	SVWVSNHYRWIVWKLAAMEFAF
1J19	LRINKRILALCMGNHELYMRR
1J1D	EEELSDLFRMFD
1J1D	EDQLREKAKELWQTIYNLEAEKFDLQEKFKQQKYEINVLRNRIND
1J1D	EDDIEELMKDGD
1J1D	ASRKLQLKTLLLQIAKQELE
1J1D	EDQLREKAKELWQTIYNLEAEKFDLQEKFKQQKYEINVLRNRIND
1J1D	EREKKKKILAERRKVLAIDHL
1J1D	FAELQDLARQLHARVDKVDEERYDIEAKVTKNITEIADLTQKIFDLR
1J1D	EEELSDLFRMFD
1J1D	DDIEELMKDGD
1J1D	EEELSDLFRMFD
1J1D	ADAMMQ
1J1D	SRKLQLKTLLLQIAKQELEREAEERRGEKGRALSTRA
1J1D	EDQLREKAKELWQTIYNLEAEKFDLQEKFKQQKYEINVLRNRINDN
1J1D	FAELQDLARQLHARVDKVDEERYDIEAKVTKNITEIADLTQKIFDLRG
1J34	WDDAERFCTE
1JCH	EWVPLLQP
1JCH	EWVPLLQP
1JEK	SLANATAAQQEVLEASYAMVQHIAKGIRILEARVARVEA
1JEY	LVDEFKELVY
1JEY	PEQVGKMKAIVEKL
1JEY	PVLQQHFRNLEALAL
1JEY	SSTLFSALLIKCLEK
1JEY	EAQLNAVDALIDSM
1JFI	AAVPVIISRALELFLESLLKKACQVTQ
1JFI	PEHVIQALESLG
1JFI	RAAINKMIKETL
1JIW	YGRQTLTHEIGHTLG
1JMO	LEKIFSE
1JMO	ERELLESY
1JMU	APIVL
1JMU	MQSVVKLLDDQL

A. PDB CODE	M. RESOLUTION
1I51	2.45
1I51	2.45
1I5K	2.7
1I5K	2.7
1I7W	2
1I7W	2
1I7W	2
1IB1	2.7
1IB1	2.7
1IB1	2.7
1IB1	2.7
1IBR	2.3
1IBR	2.3
1IBR	2.3
1IBR	2.3
1IBR	2.3
1IHF	2.2
1IHF	2.2
1II8	3.02
1II8	3.02
1IQ5	1.8
1IQ5	1.8
1IQ5	1.8
1IWQ	2
1IWQ	2
1IXR	3.3
1IXS	3.2
1IYJ	3.4
1IYJ	3.4
1IYJ	3.4
1IYJ	3.4
1J19	2.4
1J1D	2.61
1J1D	2.61
1J1D	2.61
1J1D	2.61
1J1D	2.61
1J1D	2.61
1J1D	2.61
1J1D	2.61
1J1D	2.61
1J1D	2.61
1J1D	2.61
1J1D	2.61
1J1D	2.61
1J1D	2.61
1J34	1.55
1JCH	3.02
1JCH	3.02
1JEK	1.5
1JEY	2.5
1JEY	2.5
1JEY	2.5
1JEY	2.5
1JEY	2.5
1JFI	2.62
1JFI	2.62
1JFI	2.62
1JIW	1.74
1JMO	2.2
1JMO	2.2
1JMU	2.8
1JMU	2.8

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1JN5	A B	A	STRUCTURAL BASIS FOR THE RECOGNITION OF A NUCLEOPORIN FG- REPEAT BY THE NTF2-LIKE DOMA
1JOW	A B	A	CRYSTAL STRUCTURE OF A COMPLEX OF HUMAN CDK6 AND A VIRAL CYCLIN
1JPW	A D	A	CRYSTAL STRUCTURE OF A HUMAN TCF-4 / BETA-CATENIN COMPLEX
1JPW	A D	D	CRYSTAL STRUCTURE OF A HUMAN TCF-4 / BETA-CATENIN COMPLEX
1JPW	B E	B	CRYSTAL STRUCTURE OF A HUMAN TCF-4 / BETA-CATENIN COMPLEX
1JPW	B E	B	CRYSTAL STRUCTURE OF A HUMAN TCF-4 / BETA-CATENIN COMPLEX
1JPW	C F	C	CRYSTAL STRUCTURE OF A HUMAN TCF-4 / BETA-CATENIN COMPLEX
1JSU	A B	B	P27(KIP1)/CYCLIN A/CDK2 COMPLEX
1JSU	B C	B	P27(KIP1)/CYCLIN A/CDK2 COMPLEX
1JSU	B C	B	P27(KIP1)/CYCLIN A/CDK2 COMPLEX
1JSU	B C	C	P27(KIP1)/CYCLIN A/CDK2 COMPLEX
1JTH	A B	A	CRYSTAL STRUCTURE AND BIOPHYSICAL PROPERTIES OF A COMPLEX BETWEEN THE N-TERMINAL REG
1JTH	A B	B	CRYSTAL STRUCTURE AND BIOPHYSICAL PROPERTIES OF A COMPLEX BETWEEN THE N-TERMINAL REG
1JTH	A D	A	CRYSTAL STRUCTURE AND BIOPHYSICAL PROPERTIES OF A COMPLEX BETWEEN THE N-TERMINAL REG
1JTH	A D	D	CRYSTAL STRUCTURE AND BIOPHYSICAL PROPERTIES OF A COMPLEX BETWEEN THE N-TERMINAL REG
1JTH	C B	B	CRYSTAL STRUCTURE AND BIOPHYSICAL PROPERTIES OF A COMPLEX BETWEEN THE N-TERMINAL REG
1JTH	C B	C	CRYSTAL STRUCTURE AND BIOPHYSICAL PROPERTIES OF A COMPLEX BETWEEN THE N-TERMINAL REG
1JTH	C D	C	CRYSTAL STRUCTURE AND BIOPHYSICAL PROPERTIES OF A COMPLEX BETWEEN THE N-TERMINAL REG
1JTH	C D	D	CRYSTAL STRUCTURE AND BIOPHYSICAL PROPERTIES OF A COMPLEX BETWEEN THE N-TERMINAL REG
1K3Z	A D	A	X-RAY CRYSTAL STRUCTURE OF THE IKBB/NF-KB P65 HOMODIMER COMPLEX
1K5D	A B	A	CRYSTAL STRUCTURE OF RAN-GPPNHP-RANBP1-RANGAP COMPLEX
1K74	A D	A	THE 2.3 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HETERODIMER OF THE HUMAN PPARG
1K74	A D	D	THE 2.3 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HETERODIMER OF THE HUMAN PPARG
1K74	D E	D	THE 2.3 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HETERODIMER OF THE HUMAN PPARG
1K74	D E	E	THE 2.3 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HETERODIMER OF THE HUMAN PPARG
1K7L	C D	D	THE 2.5 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HUMAN PPARALPHA LIGAND BINDING
1K7L	C F	F	THE 2.5 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HUMAN PPARALPHA LIGAND BINDING
1K7L	G H	H	THE 2.5 ANGSTROM RESOLUTION CRYSTAL STRUCTURE OF THE HUMAN PPARALPHA LIGAND BINDING
1KBH	A B	A	MUTUAL SYNERGISTIC FOLDING IN THE INTERACTION BETWEEN NUCLEAR RECEPTOR COACTIVATORS
1KBH	A B	B	MUTUAL SYNERGISTIC FOLDING IN THE INTERACTION BETWEEN NUCLEAR RECEPTOR COACTIVATORS
1KCG	A C	C	NKG2D IN COMPLEX WITH ULBP3
1KCG	B C	C	NKG2D IN COMPLEX WITH ULBP3
1KDX	A B	A	KIX DOMAIN OF MOUSE CBP (CREB BINDING PROTEIN) IN COMPLEX WITH PHOSPHORYLATED KINASE I
1KDX	A B	A	KIX DOMAIN OF MOUSE CBP (CREB BINDING PROTEIN) IN COMPLEX WITH PHOSPHORYLATED KINASE I
1KDX	A B	B	KIX DOMAIN OF MOUSE CBP (CREB BINDING PROTEIN) IN COMPLEX WITH PHOSPHORYLATED KINASE I
1KDX	A B	B	KIX DOMAIN OF MOUSE CBP (CREB BINDING PROTEIN) IN COMPLEX WITH PHOSPHORYLATED KINASE I
1KF9	A B	A	PHAGE DISPLAY DERIVED VARIANT OF HUMAN GROWTH HORMONE COMPLEXED WITH TWO COPIES O
1KF9	A C	A	PHAGE DISPLAY DERIVED VARIANT OF HUMAN GROWTH HORMONE COMPLEXED WITH TWO COPIES O
1KF9	D F	D	PHAGE DISPLAY DERIVED VARIANT OF HUMAN GROWTH HORMONE COMPLEXED WITH TWO COPIES O
1KIL	A B	A	THREE-DIMENSIONAL STRUCTURE OF THE COMPLEXIN/SNARE COMPLEX
1KIL	A B	B	THREE-DIMENSIONAL STRUCTURE OF THE COMPLEXIN/SNARE COMPLEX
1KIL	A B	B	THREE-DIMENSIONAL STRUCTURE OF THE COMPLEXIN/SNARE COMPLEX
1KIL	A D	A	THREE-DIMENSIONAL STRUCTURE OF THE COMPLEXIN/SNARE COMPLEX
1KIL	A D	D	THREE-DIMENSIONAL STRUCTURE OF THE COMPLEXIN/SNARE COMPLEX
1KIL	A E	A	THREE-DIMENSIONAL STRUCTURE OF THE COMPLEXIN/SNARE COMPLEX
1KIL	B C	B	THREE-DIMENSIONAL STRUCTURE OF THE COMPLEXIN/SNARE COMPLEX
1KIL	B C	B	THREE-DIMENSIONAL STRUCTURE OF THE COMPLEXIN/SNARE COMPLEX
1KIL	B C	C	THREE-DIMENSIONAL STRUCTURE OF THE COMPLEXIN/SNARE COMPLEX
1KIL	C D	C	THREE-DIMENSIONAL STRUCTURE OF THE COMPLEXIN/SNARE COMPLEX
1KIL	C D	D	THREE-DIMENSIONAL STRUCTURE OF THE COMPLEXIN/SNARE COMPLEX
1KJY	C D	C	CRYSTAL STRUCTURE OF HUMAN G[ALPHA]I1 BOUND TO THE GOLOCO MOTIF OF RGS14
1KJY	C D	D	CRYSTAL STRUCTURE OF HUMAN G[ALPHA]I1 BOUND TO THE GOLOCO MOTIF OF RGS14
1KKL	A I	A	L.CASEI HPRK/P IN COMPLEX WITH B.SUBTILIS HPR
1KKL	B J	B	L.CASEI HPRK/P IN COMPLEX WITH B.SUBTILIS HPR
1KKL	C H	C	L.CASEI HPRK/P IN COMPLEX WITH B.SUBTILIS HPR
1KKQ	D H	H	CRYSTAL STRUCTURE OF THE HUMAN PPAR-ALPHA LIGAND-BINDING DOMAIN IN COMPLEX WITH AN
1KMI	Y Z	Z	CRYSTAL STRUCTURE OF AN E.COLI CHEMOTAXIS PROTEIN, CHEZ
1KPE	A B	A	PKCI-TRANSITION STATE ANALOG
1KPE	A B	B	PKCI-TRANSITION STATE ANALOG
1KXP	A D	D	CRYSTAL STRUCTURE OF HUMAN VITAMIN D-BINDING PROTEIN IN COMPLEX WITH SKELETAL ACTIN
1KXP	A D	D	CRYSTAL STRUCTURE OF HUMAN VITAMIN D-BINDING PROTEIN IN COMPLEX WITH SKELETAL ACTIN
1KZ7	A B	A	CRYSTAL STRUCTURE OF THE DH/PH FRAGMENT OF MURINE DBS IN COMPLEX WITH THE PLACENTAL
1KZ7	A B	B	CRYSTAL STRUCTURE OF THE DH/PH FRAGMENT OF MURINE DBS IN COMPLEX WITH THE PLACENTAL

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
1JN5	TRANSPORT PROTEIN	1.5	4.6	3	25
1JOW	CELL CYCLE/TRANSFERASE	1.9	3.8	2	21
1JPW	CELL ADHESION	1.6	3.1	2	18
1JPW	CELL ADHESION	1.4	2.7	2	6
1JPW	CELL ADHESION	1.3	4.0	3	18
1JPW	CELL ADHESION	1.7	3.3	2	16
1JPW	CELL ADHESION	1.9	5.7	3	18
1JSU	COMPLEX (TRANSFERASE/CYCLIN/INHIBITOR)	1.7	6.7	4	15
1JSU	COMPLEX (TRANSFERASE/CYCLIN/INHIBITOR)	1.6	4.7	3	15
1JSU	COMPLEX (TRANSFERASE/CYCLIN/INHIBITOR)	1.8	3.6	2	17
1JSU	COMPLEX (TRANSFERASE/CYCLIN/INHIBITOR)	1.6	3.1	2	13
1JTH	ENDOCYTOSIS/EXOCYTOSIS	1.3	9.4	7	61
1JTH	ENDOCYTOSIS/EXOCYTOSIS	1.4	8.6	6	66
1JTH	ENDOCYTOSIS/EXOCYTOSIS	1.5	14.7	10	61
1JTH	ENDOCYTOSIS/EXOCYTOSIS	1.9	13.0	7	44
1JTH	ENDOCYTOSIS/EXOCYTOSIS	1.6	12.8	8	66
1JTH	ENDOCYTOSIS/EXOCYTOSIS	1.6	9.8	6	68
1JTH	ENDOCYTOSIS/EXOCYTOSIS	1.3	7.7	6	68
1JTH	ENDOCYTOSIS/EXOCYTOSIS	1.5	10.2	7	44
1K3Z	TRANSCRIPTION	1.5	4.5	3	12
1K5D	SIGNALING PROTEIN/SIGNALING ACTIVATOR	1.9	3.8	2	9
1K74	TRANSCRIPTION	1.2	2.4	2	17
1K74	TRANSCRIPTION	1.3	5.3	4	29
1K74	TRANSCRIPTION	1.1	2.2	2	8
1K74	TRANSCRIPTION	1.5	4.5	3	10
1K7L	TRANSCRIPTION	1.2	3.6	3	10
1K7L	TRANSCRIPTION	1.4	2.7	2	10
1K7L	TRANSCRIPTION	1.6	3.2	2	10
1KBH	TRANSCRIPTION	1.8	3.5	2	14
1KBH	TRANSCRIPTION	1.9	9.5	5	17
1KCG	IMMUNE SYSTEM	1.1	2.1	2	23
1KCG	IMMUNE SYSTEM	1.9	3.7	2	23
1KDX	TRANSCRIPTION REGULATION COMPLEX	1.8	3.5	2	16
1KDX	TRANSCRIPTION REGULATION COMPLEX	1.7	5.0	3	21
1KDX	TRANSCRIPTION REGULATION COMPLEX	1.3	2.6	2	11
1KDX	TRANSCRIPTION REGULATION COMPLEX	1.4	4.1	3	11
1KF9	HORMONE/GROWTH FACTOR	1.3	3.8	3	47
1KF9	HORMONE/GROWTH FACTOR	1.3	2.6	2	28
1KF9	HORMONE/GROWTH FACTOR	1.4	2.7	2	28
1KIL	MEMBRANE PROTEIN	1.5	10.6	7	50
1KIL	MEMBRANE PROTEIN	1.4	2.8	2	17
1KIL	MEMBRANE PROTEIN	1.8	9.2	5	39
1KIL	MEMBRANE PROTEIN	1.5	13.4	9	50
1KIL	MEMBRANE PROTEIN	1.4	13.8	10	62
1KIL	MEMBRANE PROTEIN	1.5	3.0	2	50
1KIL	MEMBRANE PROTEIN	1.4	2.8	2	17
1KIL	MEMBRANE PROTEIN	1.4	8.3	6	39
1KIL	MEMBRANE PROTEIN	1.7	8.6	5	70
1KIL	MEMBRANE PROTEIN	1.3	6.4	5	70
1KIL	MEMBRANE PROTEIN	1.3	10.7	8	62
1KJY	SIGNALING PROTEIN	1.3	2.6	2	14
1KJY	SIGNALING PROTEIN	1.3	7.7	6	12
1KKL	TRANSFERASE,HYDROLASE/TRANSPORT PROTEIN	1.5	4.5	3	17
1KKL	TRANSFERASE,HYDROLASE/TRANSPORT PROTEIN	1.6	3.2	2	14
1KKL	TRANSFERASE,HYDROLASE/TRANSPORT PROTEIN	1.4	4.1	3	17
1KKQ	TRANSCRIPTION	1.5	3.0	2	6
1KMI	SIGNALING PROTEIN	1.9	3.7	2	49
1KPE	PROTEIN KINASE INHIBITOR	1.6	3.1	2	17
1KPE	PROTEIN KINASE INHIBITOR	1.5	4.4	3	18
1KXP	CONTRACTILE PROTEIN/PROTEIN BINDING	1.7	3.4	2	11
1KXP	CONTRACTILE PROTEIN/PROTEIN BINDING	1.7	6.8	4	33
1KZ7	SIGNALING PROTEIN	1.2	2.3	2	13
1KZ7	SIGNALING PROTEIN	1.7	3.3	2	8

TABLE S4

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
1JN5	6	30
1JOW	167	187
1JPW	249	266
1JPW	42	47
1JPW	249	266
1JPW	291	306
1JPW	249	266
1JSU	179	193
1JSU	288	302
1JSU	253	269
1JSU	38	50
1JTH	12	72
1JTH	192	257
1JTH	12	72
1JTH	196	239
1JTH	192	257
1JTH	11	78
1JTH	11	78
1JTH	196	239
1K3Z	294	305
1K5D	23	31
1K74	421	437
1K74	431	459
1K74	467	474
1K74	688	697
1K7L	688	697
1K7L	688	697
1K7L	688	697
1KBH	4	17
1KBH	84	100
1KCG	65	87
1KCG	65	87
1KDX	597	612
1KDX	646	666
1KDX	120	130
1KDX	135	145
1KF9	109	182
1KF9	6	33
1KF9	1006	1033
1KIL	39	88
1KIL	232	248
1KIL	193	231
1KIL	39	88
1KIL	141	202
1KIL	39	88
1KIL	232	248
1KIL	193	231
1KIL	11	80
1KIL	11	80
1KIL	141	202
1KJY	1242	1255
1KJY	1497	1508
1KKL	293	309
1KKL	293	306
1KKL	293	309
1KKQ	686	691
1KMI	104	152
1KPE	71	87
1KPE	71	88
1KXP	305	315
1KXP	195	227
1KZ7	761	773
1KZ7	66	73

A. PDB CODE	L. HELIX SEQUENCE
1JN5	FKTYVDQACRAAEEFVNVYYTTMDK
1JOW	EDLWPQLYEAASTTICKALIQ
1JPW	DSVLFYAITTLHNLLLHQ
1JPW	ADVKSS
1JPW	DSVLFYAITTLHNLLLHQ
1JPW	VKFLAITTDCLQILAY
1JPW	DSVLFYAITTLHNLLLHQ
1JSU	HEDIHTYLREMEVKC
1JSU	KKQVLRMEHLVLKVL
1JSU	LQLVGTAAMLLASKFEE
1JSU	HEELTRDLEKHCR
1JTH	EEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERIEEGMDQINKDMK
1JTH	LSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAVSDTKKAVKY
1JTH	EEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERIEEGMDQINKDMK
1JTH	ETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEH
1JTH	LSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAVSDTKKAVKY
1JTH	LEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERIEEGMDQINKDMKEAEKNL
1JTH	LEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLERIEEGMDQINKDMKEAEKNL
1JTH	ETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEH
1K3Z	DRHRIEEKRKRT
1K5D	KTTFVKRHL
1K74	RLPALRSIGLKCLEHLF
1K74	LFAKLLQKMTDLRQIVTEHVQLLQVIKKT
1K74	PLLQEIYK
1K74	KILHRLLQEG
1K7L	KILHRLLQEG
1K7L	KILHRLLQEG
1K7L	KILHRLLQEG
1KBH	SDERALLDQLHTLL
1KBH	PQLMAAFIKQRTAKYVA
1KCG	DAWGKQLEMLREVGQRLRLELAD
1KCG	DAWGKQLEMLREVGQRLRLELAD
1KDX	QDLRSHLVHKLVQAIF
1KDX	RDEYYHLLAEKIYKIQKELEE
1KDX	DSQKRREILSR
1KDX	RKILNDLSSDA
1KF9	NVYDLLKDLEEGIQTLMGRLLLKNYGLLYCFNKDMSKVSTYLRTVQC
1KF9	LSRLADNAWLRADRLNQLAFDTYQEFEE
1KF9	LSRLADNAWLRADRLNQLAFDTYQEFEE
1KIL	VDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFETSAAKLKRKY
1KIL	RIEYNVEHAVDYVERAV
1KIL	SEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMID
1KIL	VDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFETSAAKLKRKY
1KIL	ARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKM
1KIL	VDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFETSAAKLKRKY
1KIL	RIEYNVEHAVDYVERAV
1KIL	SEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMID
1KIL	LEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNLKD
1KIL	LEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNLKD
1KIL	ARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKM
1KJY	RMHESMKLFDSICN
1KJY	IEGLVELLNRVQ
1KKL	ATKTFEKNLNHLIEHNE
1KKL	ATKTFEKNLNHLIE
1KKL	ATKTFEKNLNHLIEHNE
1KKQ	EAIIRK
1KMI	LADARELVTDTRQFLADVPAHTSFTNAQLLKIMMAQDFQDLTGQVIKRM
1KPE	ESLLGHLMIVGKKCAAD
1KPE	ESLLGHLMIVGKKCAADL
1KXP	AMDVFVCTYFM
1KXP	PTVCFLKERLQLKHLSLLTTLSNRVCSQYAAYG
1KZ7	LDSYLLKPVQRIT
1KZ7	RLRPLSYP

A. PDB CODE	M. RESOLUTION
1JN5	2.8
1JOW	3.1
1JPW	2.5
1JPW	2.5
1JPW	2.5
1JPW	2.5
1JPW	2.5
1JSU	2.3
1JSU	2.3
1JSU	2.3
1JSU	2.3
1JTH	2
1JTH	2
1JTH	2
1JTH	2
1JTH	2
1JTH	2
1JTH	2
1JTH	2
1K3Z	2.5
1K5D	2.7
1K74	2.3
1K74	2.3
1K74	2.3
1K74	2.3
1K7L	2.5
1K7L	2.5
1K7L	2.5
1KBH	NOT APP
1KBH	NOT APP
1KCG	2.6
1KCG	2.6
1KDX	NOT APP
1KDX	NOT APP
1KDX	NOT APP
1KDX	NOT APP
1KF9	2.6
1KF9	2.6
1KF9	2.6
1KIL	2.3
1KIL	2.3
1KIL	2.3
1KIL	2.3
1KIL	2.3
1KIL	2.3
1KIL	2.3
1KIL	2.3
1KIL	2.3
1KIL	2.3
1KIL	2.3
1KJY	2.7
1KJY	2.7
1KKL	2.8
1KKL	2.8
1KKL	2.8
1KKQ	3
1KMI	2.9
1KPE	1.8
1KPE	1.8
1KXP	2.1
1KXP	2.1
1KZ7	2.4
1KZ7	2.4

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1KZ7	C D	C	CRYSTAL STRUCTURE OF THE DH/PH FRAGMENT OF MURINE DBS IN COMPLEX WITH THE PLACENTAL I
1KZ7	C D	D	CRYSTAL STRUCTURE OF THE DH/PH FRAGMENT OF MURINE DBS IN COMPLEX WITH THE PLACENTAL I
1L2I	A C	A	HUMAN ESTROGEN RECEPTOR ALPHA LIGAND-BINDING DOMAIN IN COMPLEX WITH (R,R)-5,11-CIS-DIE
1L2I	A C	C	HUMAN ESTROGEN RECEPTOR ALPHA LIGAND-BINDING DOMAIN IN COMPLEX WITH (R,R)-5,11-CIS-DIE
1L2W	B I	B	CRYSTAL STRUCTURE OF THE YERSINIA VIRULENCE EFFECTOR YOPE CHAPERONE-BINDING DOMAIN I
1L2W	B I	I	CRYSTAL STRUCTURE OF THE YERSINIA VIRULENCE EFFECTOR YOPE CHAPERONE-BINDING DOMAIN I
1L2W	C J	J	CRYSTAL STRUCTURE OF THE YERSINIA VIRULENCE EFFECTOR YOPE CHAPERONE-BINDING DOMAIN I
1L2W	D J	J	CRYSTAL STRUCTURE OF THE YERSINIA VIRULENCE EFFECTOR YOPE CHAPERONE-BINDING DOMAIN I
1L2W	E K	K	CRYSTAL STRUCTURE OF THE YERSINIA VIRULENCE EFFECTOR YOPE CHAPERONE-BINDING DOMAIN I
1L2W	H L	L	CRYSTAL STRUCTURE OF THE YERSINIA VIRULENCE EFFECTOR YOPE CHAPERONE-BINDING DOMAIN I
1L8C	A B	A	STRUCTURAL BASIS FOR HIF-1ALPHA/CBP RECOGNITION IN THE CELLULAR HYPOXIC RESPONSE
1L8C	A B	A	STRUCTURAL BASIS FOR HIF-1ALPHA/CBP RECOGNITION IN THE CELLULAR HYPOXIC RESPONSE
1LB1	A B	B	CRYSTAL STRUCTURE OF THE DBL AND PLECKSTRIN HOMOLOGY DOMAINS OF DBS IN COMPLEX WITH
1LB1	A B	B	CRYSTAL STRUCTURE OF THE DBL AND PLECKSTRIN HOMOLOGY DOMAINS OF DBS IN COMPLEX WITH
1LDK	A B	B	STRUCTURE OF THE CUL1-RBX1-SKP1-F BOXSKP2 SCF UBIQUITIN LIGASE COMPLEX
1LJ2	A D	A	RECOGNITION OF EIF4G BY ROTAVIRUS NSP3 REVEALS A BASIS FOR MRNA CIRCULARIZATION
1LJ2	A D	D	RECOGNITION OF EIF4G BY ROTAVIRUS NSP3 REVEALS A BASIS FOR MRNA CIRCULARIZATION
1LOT	A B	A	CRYSTAL STRUCTURE OF THE COMPLEX OF ACTIN WITH VITAMIN D- BINDING PROTEIN
1LOT	A B	A	CRYSTAL STRUCTURE OF THE COMPLEX OF ACTIN WITH VITAMIN D- BINDING PROTEIN
1LP1	A B	A	PROTEIN Z IN COMPLEX WITH AN IN VITRO SELECTED AFFIBODY
1LQM	E F	E	ESCHERICHIA COLI URACIL-DNA GLYCOSYLASE COMPLEX WITH URACIL- DNA GLYCOSYLASE INHIBIT
1LQS	R M	M	CRYSTAL STRUCTURE OF HUMAN CYTOMEGALOVIRUS IL-10 BOUND TO SOLUBLE HUMAN IL-10R1
1LTX	A B	B	STRUCTURE OF RAB ESCORT PROTEIN-1 IN COMPLEX WITH RAB GERANYLGERANYL TRANSFERASE AN
1LTX	A R	R	STRUCTURE OF RAB ESCORT PROTEIN-1 IN COMPLEX WITH RAB GERANYLGERANYL TRANSFERASE AN
1LZW	A B	A	STRUCTURAL BASIS OF CLPS-MEDIATED SWITCH IN CLPA SUBSTRATE RECOGNITION
1M1E	A B	B	BETA-CATENIN ARMADILLO REPEAT DOMAIN BOUND TO ICAT
1M2O	A B	B	CRYSTAL STRUCTURE OF THE SEC23-SAR1 COMPLEX
1M2O	C D	D	CRYSTAL STRUCTURE OF THE SEC23-SAR1 COMPLEX
1M2Z	A B	A	CRYSTAL STRUCTURE OF A DIMER COMPLEX OF THE HUMAN GLUCOCORTICOID RECEPTOR LIGAND-BI
1M2Z	A B	B	CRYSTAL STRUCTURE OF A DIMER COMPLEX OF THE HUMAN GLUCOCORTICOID RECEPTOR LIGAND-BI
1M45	A B	A	CRYSTAL STRUCTURE OF MLC1P BOUND TO IQ2 OF MYO2P, A CLASS V MYOSIN
1M45	A B	B	CRYSTAL STRUCTURE OF MLC1P BOUND TO IQ2 OF MYO2P, A CLASS V MYOSIN
1M63	A B	B	CRYSTAL STRUCTURE OF CALCINEURIN-CYCLOPHILIN-CYCLOSPORIN SHOWS COMMON BUT DISTINCT
1M63	A B	B	CRYSTAL STRUCTURE OF CALCINEURIN-CYCLOPHILIN-CYCLOSPORIN SHOWS COMMON BUT DISTINCT
1M63	E F	F	CRYSTAL STRUCTURE OF CALCINEURIN-CYCLOPHILIN-CYCLOSPORIN SHOWS COMMON BUT DISTINCT
1M63	E F	F	CRYSTAL STRUCTURE OF CALCINEURIN-CYCLOPHILIN-CYCLOSPORIN SHOWS COMMON BUT DISTINCT
1MDU	D E	D	CRYSTAL STRUCTURE OF THE CHICKEN ACTIN TRIMER COMPLEXED WITH HUMAN GELSOLIN SEGMEN
1MJE	B A	B	STRUCTURE OF A BRCA2-DSS1-SSDNA COMPLEX
1MKW	L H	L	THE CO-CRYSTAL STRUCTURE OF UNLIGANDED BOVINE ALPHA- THROMBIN AND PRETHROMBIN-2: MO
1MWA	A B	B	2C/H-2KBM3/DEV8 ALLOGENEIC COMPLEX
1MXE	A E	A	STRUCTURE OF THE COMPLEX OF CALMODULIN WITH THE TARGET SEQUENCE OF CAMKI
1MXE	A E	A	STRUCTURE OF THE COMPLEX OF CALMODULIN WITH THE TARGET SEQUENCE OF CAMKI
1MXE	A E	A	STRUCTURE OF THE COMPLEX OF CALMODULIN WITH THE TARGET SEQUENCE OF CAMKI
1MXE	A E	A	STRUCTURE OF THE COMPLEX OF CALMODULIN WITH THE TARGET SEQUENCE OF CAMKI
1MXE	B F	B	STRUCTURE OF THE COMPLEX OF CALMODULIN WITH THE TARGET SEQUENCE OF CAMKI
1MXE	B F	B	STRUCTURE OF THE COMPLEX OF CALMODULIN WITH THE TARGET SEQUENCE OF CAMKI
1MXE	B F	B	STRUCTURE OF THE COMPLEX OF CALMODULIN WITH THE TARGET SEQUENCE OF CAMKI
1MZN	A B	A	CRYSTAL STRUCTURE AT 1.9 ANGSTROEMS RESOLUTION OF THE HOMODIMER OF HUMAN RXR ALPHA I
1MZN	A B	A	CRYSTAL STRUCTURE AT 1.9 ANGSTROEMS RESOLUTION OF THE HOMODIMER OF HUMAN RXR ALPHA I
1MZN	A B	B	CRYSTAL STRUCTURE AT 1.9 ANGSTROEMS RESOLUTION OF THE HOMODIMER OF HUMAN RXR ALPHA I
1MZN	E F	F	CRYSTAL STRUCTURE AT 1.9 ANGSTROEMS RESOLUTION OF THE HOMODIMER OF HUMAN RXR ALPHA I
1N0W	A B	A	CRYSTAL STRUCTURE OF A RAD51-BRCA2 BRC REPEAT COMPLEX
1N2D	B C	B	TERNARY COMPLEX OF MLC1P BOUND TO IQ2 AND IQ3 OF MYO2P, A CLASS V MYOSIN
1N4M	B E	B	STRUCTURE OF RB TUMOR SUPPRESSOR BOUND TO THE TRANSACTIVATION DOMAIN OF E2F-2
1N4Q	A B	A	PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A KKKSKT
1N4Q	A B	A	PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A KKKSKT
1N4Q	A B	A	PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A KKKSKT
1N4Q	C D	C	PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A KKKSKT
1N4Q	C D	D	PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A KKKSKT
1N4Q	E F	E	PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A KKKSKT
1N4Q	E F	E	PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A KKKSKT
1N4Q	G H	G	PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A KKKSKT
1N4Q	G H	H	PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A KKKSKT

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
1KZ7	SIGNALING PROTEIN	1.0	2.0	2	13
1KZ7	SIGNALING PROTEIN	1.7	5.1	3	7
1L2I	TRANSCRIPTION RECEPTOR/COACTIVATOR	1.1	2.2	2	10
1L2I	TRANSCRIPTION RECEPTOR/COACTIVATOR	1.7	3.4	2	9
1L2W	CHAPERONE	1.8	3.5	2	16
1L2W	CHAPERONE	1.7	3.3	2	10
1L2W	CHAPERONE	1.6	3.2	2	10
1L2W	CHAPERONE	1.9	3.8	2	8
1L2W	CHAPERONE	1.3	2.5	2	10
1L2W	CHAPERONE	1.5	2.9	2	10
1L8C	GENE REGULATION	1.6	4.7	3	16
1L8C	GENE REGULATION	1.5	7.7	5	27
1LB1	SIGNALING PROTEIN	1.3	2.5	2	7
1LB1	SIGNALING PROTEIN	1.7	3.3	2	19
1LDK	LIGASE	1.2	2.3	2	15
1LJ2	VIRAL PROTEIN/ TRANSLATION	1.0	2.0	2	33
1LJ2	VIRAL PROTEIN/ TRANSLATION	1.3	2.6	2	6
1LOT	TRANSPORT PROTEIN, STRUCTURAL PROTEIN	1.4	2.7	2	11
1LOT	TRANSPORT PROTEIN, STRUCTURAL PROTEIN	1.7	5.1	3	33
1LP1	IMMUNE SYSTEM	1.7	6.7	4	14
1LQM	HYDROLASE/HYDROLASE INHIBITOR	1.0	2.0	2	12
1LQS	IMMUNE SYSTEM	1.5	3.0	2	15
1LTX	TRANSFERASE/PROTEIN BINDING	1.8	5.4	3	12
1LTX	TRANSFERASE/PROTEIN BINDING	1.7	3.4	2	16
1LZW	CHAPERONE	1.7	6.6	4	18
1M1E	STRUCTURAL PROTEIN	1.3	2.6	2	19
1M2O	PROTEIN TRANSPORT/SIGNALING PROTEIN	1.2	2.3	2	6
1M2O	PROTEIN TRANSPORT/SIGNALING PROTEIN	1.2	2.4	2	10
1M2Z	HORMONE/HORMONE ACTIVATOR	1.5	2.9	2	10
1M2Z	HORMONE/HORMONE ACTIVATOR	1.5	4.4	3	7
1M45	CELL CYCLE PROTEIN	1.4	2.7	2	8
1M45	CELL CYCLE PROTEIN	1.9	14.9	8	24
1M63	HYDROLASE/ISOMERASE	1.4	8.5	6	16
1M63	HYDROLASE/ISOMERASE	1.4	4.3	3	13
1M63	HYDROLASE/ISOMERASE	1.6	4.8	3	14
1M63	HYDROLASE/ISOMERASE	1.6	3.1	2	11
1MDU	STRUCTURAL PROTEIN	1.5	4.4	3	18
1MJE	GENE REGULATION/ANTITUMOR PROTEIN/DNA	1.9	3.8	2	5
1MKW	COMPLEX (BLOOD COAGULATION/PROENZYME)	1.9	5.6	3	9
1MWA	IMMUNE SYSTEM	1.4	2.8	2	7
1MXE	METAL BINDING PROTEIN	1.6	4.7	3	12
1MXE	METAL BINDING PROTEIN	1.7	3.3	2	15
1MXE	METAL BINDING PROTEIN	1.3	2.5	2	13
1MXE	METAL BINDING PROTEIN	1.6	3.2	2	10
1MXE	METAL BINDING PROTEIN	1.9	3.8	2	12
1MXE	METAL BINDING PROTEIN	1.6	3.2	2	12
1MXE	METAL BINDING PROTEIN	1.5	6.1	4	15
1MZN	TRANSCRIPTION	1.7	3.4	2	11
1MZN	TRANSCRIPTION	1.5	2.9	2	22
1MZN	TRANSCRIPTION	1.9	11.5	6	9
1MZN	TRANSCRIPTION	1.9	7.7	4	9
1N0W	GENE REGULATION/ANTITUMOR PROTEIN	1.4	2.7	2	13
1N2D	CELL CYCLE	1.8	5.3	3	11
1N4M	CELL CYCLE	1.6	3.1	2	13
1N4Q	TRANSFERASE	1.6	3.2	2	16
1N4Q	TRANSFERASE	1.3	2.5	2	10
1N4Q	TRANSFERASE	1.6	3.2	2	14
1N4Q	TRANSFERASE	1.7	5.0	3	10
1N4Q	TRANSFERASE	1.9	7.7	4	15
1N4Q	TRANSFERASE	1.2	2.4	2	13
1N4Q	TRANSFERASE	1.2	2.4	2	17
1N4Q	TRANSFERASE	1.9	5.7	3	10
1N4Q	TRANSFERASE	1.9	7.5	4	13

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
1KZ7	1761	1773
1KZ7	1065	1071
1L2I	538	547
1L2I	688	696
1L2W	102	117
1L2W	68	77
1L2W	68	77
1L2W	38	45
1L2W	68	77
1L2W	68	77
1L8C	62	77
1L8C	3	29
1LB1	69	75
1LB1	89	107
1LDK	417	431
1LJ2	274	306
1LJ2	153	158
1LOT	125	135
1LOT	179	211
1LP1	24	37
1LQM	87	98
1LQS	143	157
1LTX	212	223
1LTX	286	301
1LZW	63	80
1M1E	11	29
1M2O	82	87
1M2O	36	45
1M2Z	589	598
1M2Z	743	749
1M45	27	34
1M45	807	830
1M63	125	140
1M63	108	120
1M63	125	138
1M63	110	120
1MDU	71	88
1MJE	50	54
1MKW	14	14
1MWA	134	140
1MXE	118	129
1MXE	6	20
1MXE	81	93
1MXE	138	147
1MXE	118	129
1MXE	45	56
1MXE	6	20
1MZN	294	304
1MZN	264	285
1MZN	473	481
1MZN	2473	2481
1N0W	197	209
1N2D	83	93
1N4M	752	764
1N4Q	94	109
1N4Q	274	283
1N4Q	131	144
1N4Q	274	283
1N4Q	242	256
1N4Q	234	246
1N4Q	309	325
1N4Q	274	283
1N4Q	242	254

A. PDB CODE	L. HELIX SEQUENCE
1KZ7	LDSYLLKPVQRIT
1KZ7	DRLRPLS
1L2I	DLLLEMLDAH
1L2I	KILHRLLQD
1L2W	SLYTQLEMLVQGAERL
1L2W	HSVIGFIQRM
1L2W	HSVIGFIQRM
1L2W	QYANNLAG
1L2W	HSVIGFIQRM
1L2W	HSVIGFIQRM
1L8C	AHCASSRQIISHWKNC
1L8C	PEKRKLIQQQLVLLLHAHKCQRREQAN
1LB1	LRPLSYP
1LB1	PDSLENIPEKWTPEVKHFC
1LDK	KSPELLARYCDSLLK
1LJ2	PLHAFDDLESVIRNLISDYDKLFLMFKGLIQRS
1LJ2	TEEIMS
1LOT	NDEICEAFRKD
1LOT	PTVCFLKERLQLKHLSLLTTLSNRVCSQYAAYG
1LP1	DPQKKAFIFSLWDD
1LQM	PSLLNMYKELEN
1LQS	LDTLFSRLEEYLHSR
1LTX	SDLLGWWLCERQ
1LTX	MVEKRMLMKFLTFCVE
1LZW	AEVAETKVAMVNKYAREN
1M1E	PEEMYIQQKVRVLLMLRKM
1M2O	RLWKDY
1M2O	KTTLLHMLKN
1M2Z	LDDQMTLLQY
1M2Z	ALLRYLL
1M45	LGDYLRAI
1M45	ISQAIKYLQNNIKGFIIRQRVNDE
1M63	DTQLQQIVDKTIINAD
1M63	NGELFQVLKMMVG
1M63	DTQLQQIVDKTIIN
1M63	ELFQVLKMMVG
1MDU	QDESGAAAIFTVQLDDYL
1MJE	DDFSN
1MKW	EKELFESYI
1MWA	KAEIANK
1MXE	DEEVDEMIREAD
1MXE	EEQIAEFKEAFSLFD
1MXE	SEEEIREAFRVFD
1MXE	YEEFVTMMTS
1MXE	DEEVDEMIREAD
1MXE	EAELQDMINEVD
1MXE	EEQIAEFKEAFSLFD
1MZN	LDDQVILLRAG
1MZN	PVTNICQAADKQLFTLVEWAKR
1MZN	KILHRLLQD
1MZN	KILHRLLQD
1N0W	TDHQTQLLYQASA
1N2D	TEDFVKAFQVF
1N4M	IIVFYNSVFMQRL
1N4Q	EKFRDVYDYFRAVLQR
1N4Q	ESAWNYLKGI
1N4Q	YTVWHFRRVLLRSL
1N4Q	ESAWNYLKGI
1N4Q	EKELNRIKRWCIMRQ
1N4Q	NSVWNQRHFVISN
1N4Q	PYLIAFLVDIYEDMLEN
1N4Q	ESAWNYLKGI
1N4Q	EKELNRIKRWCIM

A. PDB CODE	M. RESOLUTION
1KZ7	2.4
1KZ7	2.4
1L2I	1.95
1L2I	1.95
1L2W	2
1L2W	2
1L2W	2
1L2W	2
1L2W	2
1L2W	2
1L8C	NOT APP
1L8C	NOT APP
1LB1	2.81
1LB1	2.81
1LDK	3.1
1LJ2	2.38
1LJ2	2.38
1LOT	2.5
1LOT	2.5
1LP1	2.3
1LQM	3.2
1LQS	2.7
1LTX	2.7
1LTX	2.7
1LZW	2.5
1M1E	2.1
1M2O	2.5
1M2O	2.5
1M2Z	2.5
1M2Z	2.5
1M45	1.65
1M45	1.65
1M63	2.8
1M63	2.8
1M63	2.8
1M63	2.8
1MDU	2.2
1MJE	3.5
1MKW	2.3
1MWA	2.4
1MXE	1.7
1MXE	1.7
1MXE	1.7
1MXE	1.7
1MXE	1.7
1MXE	1.7
1MXE	1.7
1MZN	1.9
1MZN	1.9
1MZN	1.9
1MZN	1.9
1N0W	1.7
1N2D	2
1N4M	2.2
1N4Q	2.4
1N4Q	2.4
1N4Q	2.4
1N4Q	2.4
1N4Q	2.4
1N4Q	2.4
1N4Q	2.4
1N4Q	2.4
1N4Q	2.4

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1N4Q	I J	I	PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A KKKSKT
1N4Q	K L	L	PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A KKKSKT
1NEX	A B	A	CRYSTAL STRUCTURE OF SCSKP1-SCCDC4-CPD PEPTIDE COMPLEX
1NEX	C D	C	CRYSTAL STRUCTURE OF SCSKP1-SCCDC4-CPD PEPTIDE COMPLEX
1NEX	C D	C	CRYSTAL STRUCTURE OF SCSKP1-SCCDC4-CPD PEPTIDE COMPLEX
1NF3	B D	B	STRUCTURE OF CDC42 IN A COMPLEX WITH THE GTPASE-BINDING DOMAIN OF THE CELL POLARITY PR
1NF5	A B	A	CRYSTAL STRUCTURE OF LACTOSE SYNTHASE, COMPLEX WITH GLUCOSE
1NGM	E F	F	CRYSTAL STRUCTURE OF A YEAST BRF1-TBP-DNA TERNARY COMPLEX
1NGM	I J	I	CRYSTAL STRUCTURE OF A YEAST BRF1-TBP-DNA TERNARY COMPLEX
1NGM	M N	M	CRYSTAL STRUCTURE OF A YEAST BRF1-TBP-DNA TERNARY COMPLEX
1NH2	B D	D	CRYSTAL STRUCTURE OF A YEAST TFIIA/TBP/DNA COMPLEX
1NIW	A B	B	CRYSTAL STRUCTURE OF ENDOTHELIAL NITRIC OXIDE SYNTHASE PEPTIDE BOUND TO CALMODULIN
1NIW	C D	C	CRYSTAL STRUCTURE OF ENDOTHELIAL NITRIC OXIDE SYNTHASE PEPTIDE BOUND TO CALMODULIN
1NIW	C D	C	CRYSTAL STRUCTURE OF ENDOTHELIAL NITRIC OXIDE SYNTHASE PEPTIDE BOUND TO CALMODULIN
1NIW	C D	D	CRYSTAL STRUCTURE OF ENDOTHELIAL NITRIC OXIDE SYNTHASE PEPTIDE BOUND TO CALMODULIN
1NIW	E F	E	CRYSTAL STRUCTURE OF ENDOTHELIAL NITRIC OXIDE SYNTHASE PEPTIDE BOUND TO CALMODULIN
1NIW	E F	F	CRYSTAL STRUCTURE OF ENDOTHELIAL NITRIC OXIDE SYNTHASE PEPTIDE BOUND TO CALMODULIN
1NIW	G H	G	CRYSTAL STRUCTURE OF ENDOTHELIAL NITRIC OXIDE SYNTHASE PEPTIDE BOUND TO CALMODULIN
1NKP	A B	A	CRYSTAL STRUCTURE OF MYC-MAX RECOGNIZING DNA
1NKP	A B	B	CRYSTAL STRUCTURE OF MYC-MAX RECOGNIZING DNA
1NKP	A B	B	CRYSTAL STRUCTURE OF MYC-MAX RECOGNIZING DNA
1NKP	D E	D	CRYSTAL STRUCTURE OF MYC-MAX RECOGNIZING DNA
1NKP	D E	D	CRYSTAL STRUCTURE OF MYC-MAX RECOGNIZING DNA
1NKP	D E	E	CRYSTAL STRUCTURE OF MYC-MAX RECOGNIZING DNA
1NLW	A B	A	CRYSTAL STRUCTURE OF MAD-MAX RECOGNIZING DNA
1NLW	A B	A	CRYSTAL STRUCTURE OF MAD-MAX RECOGNIZING DNA
1NLW	A B	B	CRYSTAL STRUCTURE OF MAD-MAX RECOGNIZING DNA
1NLW	A B	B	CRYSTAL STRUCTURE OF MAD-MAX RECOGNIZING DNA
1NLW	D E	D	CRYSTAL STRUCTURE OF MAD-MAX RECOGNIZING DNA
1NLW	D E	E	CRYSTAL STRUCTURE OF MAD-MAX RECOGNIZING DNA
1NLW	D E	E	CRYSTAL STRUCTURE OF MAD-MAX RECOGNIZING DNA
1NMU	C B	B	MBP-L30
1NRL	A C	A	CRYSTAL STRUCTURE OF THE HUMAN PXR-LBD IN COMPLEX WITH AN SRC-1 COACTIVATOR PEPTIDE A
1NRL	A C	C	CRYSTAL STRUCTURE OF THE HUMAN PXR-LBD IN COMPLEX WITH AN SRC-1 COACTIVATOR PEPTIDE A
1NRO	L H	L	CRYSTALLOGRAPHIC STRUCTURES OF THROMBIN COMPLEXED WITH THROMBIN RECEPTOR PEPTIDES:
1NU7	A B	A	STAPHYLOCOAGULASE-THROMBIN COMPLEX
1NU7	B D	D	STAPHYLOCOAGULASE-THROMBIN COMPLEX
1NU7	F H	H	STAPHYLOCOAGULASE-THROMBIN COMPLEX
1NVM	A B	A	CRYSTAL STRUCTURE OF A BIFUNCTIONAL ALDOLASE-DEHYDROGENASE : SEQUESTERING A REACTIV
1NVM	E F	F	CRYSTAL STRUCTURE OF A BIFUNCTIONAL ALDOLASE-DEHYDROGENASE : SEQUESTERING A REACTIV
1O9U	A B	A	GLYCOGEN SYNTHASE KINASE 3 BETA COMPLEXED WITH AXIN PEPTIDE
1O9U	A B	B	GLYCOGEN SYNTHASE KINASE 3 BETA COMPLEXED WITH AXIN PEPTIDE
1OC0	A B	A	PLASMINOGEN ACTIVATOR INHIBITOR-1 COMPLEX WITH SOMATOMEDIN B DOMAIN OF VITRONECTIN
1OHZ	A B	B	COHESIN-DOCKERIN COMPLEX FROM THE CELLULOSOME OF CLOSTRIDIUM THERMOCELLUM
1OQD	B L	L	CRYSTAL STRUCTURE OF STALL-1 AND BCMA
1OR0	A B	A	CRYSTAL STRUCTURES OF GLUTARYL 7-AMINOCEPHALOSPORANIC ACID ACYLASE: INSIGHT INTO AUT
1OR0	A B	B	CRYSTAL STRUCTURES OF GLUTARYL 7-AMINOCEPHALOSPORANIC ACID ACYLASE: INSIGHT INTO AUT
1OR0	A B	B	CRYSTAL STRUCTURES OF GLUTARYL 7-AMINOCEPHALOSPORANIC ACID ACYLASE: INSIGHT INTO AUT
1OR0	C D	C	CRYSTAL STRUCTURES OF GLUTARYL 7-AMINOCEPHALOSPORANIC ACID ACYLASE: INSIGHT INTO AUT
1OR7	B F	F	CRYSTAL STRUCTURE OF ESCHERICHIA COLI SIGMAE WITH THE CYTOPLASMIC DOMAIN OF ITS ANTI-S
1OSV	A C	A	STRUCTURAL BASIS FOR BILE ACID BINDING AND ACTIVATION OF THE NUCLEAR RECEPTOR FXR
1OSV	A C	C	STRUCTURAL BASIS FOR BILE ACID BINDING AND ACTIVATION OF THE NUCLEAR RECEPTOR FXR
1OSV	B D	B	STRUCTURAL BASIS FOR BILE ACID BINDING AND ACTIVATION OF THE NUCLEAR RECEPTOR FXR
1OW3	A B	A	CRYSTAL STRUCTURE OF RHOA.GDP.MGF3-IN COMPLEX WITH RHOGAP
1OW3	A B	B	CRYSTAL STRUCTURE OF RHOA.GDP.MGF3-IN COMPLEX WITH RHOGAP
1OW7	B E	E	PAXILLIN LD4 MOTIF BOUND TO THE FOCAL ADHESION TARGETING (FAT) DOMAIN OF THE FOCAL ADH
1OXK	A B	A	COMPLEX BETWEEN YPD1 AND SLN1 RESPONSE REGULATOR DOMAIN IN SPACE GROUP P3(2)
1OXK	C D	D	COMPLEX BETWEEN YPD1 AND SLN1 RESPONSE REGULATOR DOMAIN IN SPACE GROUP P3(2)
1OXK	E F	F	COMPLEX BETWEEN YPD1 AND SLN1 RESPONSE REGULATOR DOMAIN IN SPACE GROUP P3(2)
1OXK	G H	G	COMPLEX BETWEEN YPD1 AND SLN1 RESPONSE REGULATOR DOMAIN IN SPACE GROUP P3(2)
1OXK	I J	J	COMPLEX BETWEEN YPD1 AND SLN1 RESPONSE REGULATOR DOMAIN IN SPACE GROUP P3(2)
1P22	A B	B	STRUCTURE OF A BETA-TRCP1-SKP1-BETA-CATENIN COMPLEX: DESTRUCTION MOTIF BINDING AND LY
1P27	A B	A	CRYSTAL STRUCTURE OF THE HUMAN Y14/MAGOH COMPLEX

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
1N4Q	TRANSFERASE	1.5	3.0	2	10
1N4Q	TRANSFERASE	1.9	5.6	3	13
1NEX	LIGASE, CELL CYCLE	1.3	2.5	2	8
1NEX	LIGASE, CELL CYCLE	1.2	2.4	2	13
1NEX	LIGASE, CELL CYCLE	1.0	2.0	2	10
1NF3	SIGNALING PROTEIN	1.2	2.3	2	15
1NF5	TRANSFERASE/TRANSFERASE	1.5	2.9	2	12
1NGM	TRANSCRIPTION/DNA	1.3	2.5	2	5
1NGM	TRANSCRIPTION/DNA	1.9	5.6	3	17
1NGM	TRANSCRIPTION/DNA	1.4	2.8	2	19
1NH2	TRANSCRIPTION/DNA	1.6	4.8	3	22
1NIW	SIGNALING PROTEIN/OXIDOREDUCTASE	1.7	8.4	5	12
1NIW	SIGNALING PROTEIN/OXIDOREDUCTASE	1.4	2.7	2	15
1NIW	SIGNALING PROTEIN/OXIDOREDUCTASE	1.8	3.6	2	13
1NIW	SIGNALING PROTEIN/OXIDOREDUCTASE	1.9	9.3	5	14
1NIW	SIGNALING PROTEIN/OXIDOREDUCTASE	1.9	3.7	2	15
1NIW	SIGNALING PROTEIN/OXIDOREDUCTASE	1.8	12.9	7	13
1NIW	SIGNALING PROTEIN/OXIDOREDUCTASE	1.1	2.1	2	15
1NKP	TRANSCRIPTION/DNA	1.6	14.1	9	44
1NKP	TRANSCRIPTION/DNA	1.9	3.8	2	27
1NKP	TRANSCRIPTION/DNA	1.9	14.9	8	42
1NKP	TRANSCRIPTION/DNA	1.7	15.1	9	43
1NKP	TRANSCRIPTION/DNA	1.8	3.6	2	28
1NKP	TRANSCRIPTION/DNA	1.8	14.3	8	42
1NLW	TRANSCRIPTION/DNA	1.8	16.2	9	41
1NLW	TRANSCRIPTION/DNA	1.2	2.3	2	23
1NLW	TRANSCRIPTION/DNA	1.5	3.0	2	24
1NLW	TRANSCRIPTION/DNA	1.6	8.2	5	40
1NLW	TRANSCRIPTION/DNA	1.8	10.7	6	40
1NLW	TRANSCRIPTION/DNA	1.7	3.4	2	22
1NLW	TRANSCRIPTION/DNA	1.5	9.1	6	40
1NMU	SUGAR BINDING PROTEIN/RIBOSOME	1.3	4.0	3	11
1NRL	TRANSCRIPTION	1.8	3.6	2	7
1NRL	TRANSCRIPTION	1.3	5.1	4	8
1NRO	SERINE PROTEINASE/RECEPTOR	1.5	3.0	2	10
1NU7	HYDROLASE/PROTEIN BINDING	1.5	4.4	3	8
1NU7	HYDROLASE/PROTEIN BINDING	1.2	2.3	2	24
1NU7	HYDROLASE/PROTEIN BINDING	1.4	4.3	3	40
1NVM	LYASE/OXIDOREDUCTASE	1.4	2.7	2	11
1NVM	LYASE/OXIDOREDUCTASE	1.8	3.5	2	17
1O9U	KINASE	1.2	3.5	3	13
1O9U	KINASE	1.8	5.4	3	17
1OC0	HYDROLASE/INHIBITOR	1.8	3.5	2	15
1OHZ	CELL ADHESION	1.7	6.7	4	12
1OQD	IMMUNE RESPONSE	1.4	4.1	3	7
1OR0	HYDROLASE	1.9	3.7	2	10
1OR0	HYDROLASE	1.1	2.2	2	5
1OR0	HYDROLASE	1.8	3.6	2	7
1OR0	HYDROLASE	1.5	4.5	3	13
1OR7	TRANSCRIPTION	1.8	7.0	4	10
1OSV	DNA BINDING PROTEIN	1.0	2.0	2	25
1OSV	DNA BINDING PROTEIN	1.6	4.9	3	8
1OSV	DNA BINDING PROTEIN	1.8	3.6	2	10
1OW3	GENE REGULATION/SIGNALING PROTEIN	1.9	3.8	2	13
1OW3	GENE REGULATION/SIGNALING PROTEIN	1.8	5.4	3	9
1OW7	TRANSFERASE	1.3	3.8	3	10
1OXK	SIGNALING PROTEIN	1.8	3.6	2	26
1OXK	SIGNALING PROTEIN	1.3	2.5	2	14
1OXK	SIGNALING PROTEIN	1.4	2.8	2	14
1OXK	SIGNALING PROTEIN	1.7	6.8	4	26
1OXK	SIGNALING PROTEIN	1.4	5.6	4	14
1P22	SIGNALING PROTEIN	1.2	3.5	3	8
1P27	RNA BINDING PROTEIN	1.4	2.7	2	15

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
1N4Q	274	283
1N4Q	242	254
1NEX	163	170
1NEX	144	156
1NEX	132	141
1NF3	165	179
1NF5	23	34
1NGM	468	472
1NGM	131	147
1NGM	129	147
1NH2	34	55
1NIW	496	507
1NIW	6	20
1NIW	81	93
1NIW	496	509
1NIW	6	20
1NIW	496	508
1NIW	6	20
1NKP	939	982
1NKP	203	229
1NKP	239	280
1NKP	539	581
1NKP	500	527
1NKP	739	780
1NLW	40	80
1NLW	5	27
1NLW	204	227
1NLW	239	278
1NLW	539	578
1NLW	706	727
1NLW	739	778
1NMU	53	63
1NRL	423	429
1NRL	688	695
1NRO	14	14
1NU7	14	14
1NU7	24	47
1NU7	56	95
1NVM	123	133
1NVM	172	188
1O9U	262	274
1O9U	384	400
1OC0	129	143
1OHZ	45	56
1OQD	17	23
1OR0	74	83
1OR0	151	155
1OR0	505	511
1OR0	51	63
1OR7	55	64
1OSV	277	301
1OSV	3	10
1OSV	310	319
1OW3	192	204
1OW3	67	75
1OW7	3	12
1OXK	27	52
1OXK	1097	1110
1OXK	1097	1110
1OXK	27	52
1OXK	1097	1110
1P22	111	118
1P27	54	68

A. PDB CODE	L. HELIX SEQUENCE
1N4Q	ESAWNYLKGI
1N4Q	EKELNRIKRWCIM
1NEX	PEEIRRTF
1NEX	KPLLDAGCKVVAE
1NEX	YEIILAANYL
1NF3	LKNVFDEAILAALEP
1NF5	LLEWACVLFHTS
1NGM	EELNA
1NGM	DSKLASRKYARIIQKIG
1NGM	EDDSKLASRKYARIIQKIG
1NH2	ASLAMRVLETFDKVVAETLKDN
1NIW	FKEVANAVKISA
1NIW	EEQIAEFKEAFSLFD
1NIW	SEEEIREAFRVFD
1NIW	FKEVANAVKISASL
1NIW	EEQIAEFKEAFSLFD
1NIW	FKEVANAVKISAS
1NIW	EEQIAEFKEAFSLFD
1NKP	KVVILKKATAYILSVQAEEQKLISEEDLLRKRREQLKHKLEQLG
1NKP	KRAHHNALERKRRDHIKDSFHSLRDSV
1NKP	RAQILDKATEYIQYMRRKNHTHQQDIDDLKRQNALLEQQVRA
1NKP	KVVILKKATAYILSVQAEEQKLISEEDLLRKRREQLKHKLEQL
1NKP	NVKRRTHNVLERQRRNELKRSFFALRDQ
1NKP	RAQILDKATEYIQYMRRKNHTHQQDIDDLKRQNALLEQQVRA
1NLW	LSLLTKAKLHIKKLEDSDRKAVHQIDQLQREQRHLKRQLEK
1NLW	THNEMEKNRRAHLRLSLEKLKGL
1NLW	RAHHNALERKRRDHIKDSFHSLRD
1NLW	RAQILDKATEYIQYMRRKNHTHQQDIDDLKRQNALLEQQV
1NLW	TLSLLTKAKLHIKKLEDSDRKAVHQIDQLQREQRHLKRQL
1NLW	HHNALERKRRDHIKDSFHSLRD
1NLW	RAQILDKATEYIQYMRRKNHTHQQDIDDLKRQNALLEQQV
1NMU	KSELEYYAMLS
1NRL	PLMQELF
1NRL	KILHRLLQ
1NRO	TERELLESYI
1NU7	ERELLESY
1NU7	DWYLKGRLTSLESQFINALGILET
1NU7	KDAKDKLMTRILGEDQYLLERKKVQYEEYKKLYKKYKEEN
1NVM	KQHIEYARNLG
1NVM	IDEFTETTSKAIEVIGG
1O9U	GVDQLVEIIKVLG
1O9U	EPQKFAEELIHRLEAVQ
1OC0	VERARFIINDWVKTH
1OHZ	STDVLLLSRYLL
1OQD	CQLRCSS
1OR0	EQTTVWLLTN
1OR0	EQYFD
1OR0	REQVEAA
1OR0	GDNILRLYGEARG
1OR7	ISSRVMAAIE
1OSV	AEENFLILTEMATSHVQILVEFTKR
1OSV	ALLRYLLD
1OSV	HEDQIALLKG
1OW3	NTNLAVVFGPNLL
1OW3	DRLRPLSYP
1OW7	RELDELMASL
1OXK	FSKGLIIQFIDQAQTTFAQMQRQLDG
1OXK	HVNQEVIKRMLNLE
1OXK	HVNQEVIKRMLNLE
1OXK	FSKGLIIQFIDQAQTTFAQMQRQLDG
1OXK	HVNQEVIKRMLNLE
1P22	PEEIRKTF
1P27	KSVMEELKRIIDDSE

A. PDB CODE	M. RESOLUTION
1N4Q	2.4
1N4Q	2.4
1NEX	2.7
1NEX	2.7
1NEX	2.7
1NF3	2.1
1NF5	2
1NGM	2.95
1NGM	2.95
1NGM	2.95
1NH2	1.9
1NIW	2.05
1NIW	2.05
1NIW	2.05
1NIW	2.05
1NIW	2.05
1NIW	2.05
1NIW	2.05
1NKP	1.8
1NKP	1.8
1NKP	1.8
1NKP	1.8
1NKP	1.8
1NKP	1.8
1NLW	2
1NLW	2
1NLW	2
1NLW	2
1NLW	2
1NLW	2
1NLW	2
1NMU	2.31
1NRL	2
1NRL	2
1NRO	3.1
1NU7	2.2
1NU7	2.2
1NU7	2.2
1NVM	1.7
1NVM	1.7
1O9U	2.4
1O9U	2.4
1OC0	2.28
1OHZ	2.2
1OQD	2.6
1OR0	2
1OR0	2
1OR0	2
1OR0	2
1OR7	2
1OSV	2.5
1OSV	2.5
1OSV	2.5
1OW3	1.8
1OW3	1.8
1OW7	2.6
1OXK	2.1
1OXK	2.1
1OXK	2.1
1OXK	2.1
1OXK	2.1
1P22	2.95
1P27	2

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1P4Q	A B	B	SOLUTION STRUCTURE OF THE CITED2 TRANSACTIVATION DOMAIN IN COMPLEX WITH THE P300 CH1 D
1P8V	B C	B	CRYSTAL STRUCTURE OF THE COMPLEX OF PLATELET RECEPTOR GPIB- ALPHA AND ALPHA-THROMBIN
1P9M	A B	B	CRYSTAL STRUCTURE OF THE HEXAMERIC HUMAN IL-6/IL-6 ALPHA RECEPTOR/GP130 COMPLEX
1PCQ	F T	F	CRYSTAL STRUCTURE OF GROEL-GROES
1PD7	A B	A	EXTENDED SID OF MAD1 BOUND TO THE PAH2 DOMAIN OF MSIN3B
1PD7	A B	B	EXTENDED SID OF MAD1 BOUND TO THE PAH2 DOMAIN OF MSIN3B
1PGR	A B	A	2:2 COMPLEX OF G-CSF WITH ITS RECEPTOR
1PK1	A B	B	HETERO SAM DOMAIN STRUCTURE OF PH AND SCM.
1PQ1	A B	A	CRYSTAL STRUCTURE OF BCL-XL/BIM
1PSB	A C	A	SOLUTION STRUCTURE OF CALCIUM LOADED S100B COMPLEXED TO A PEPTIDE FROM N-TERMINAL RE
1PSB	A C	C	SOLUTION STRUCTURE OF CALCIUM LOADED S100B COMPLEXED TO A PEPTIDE FROM N-TERMINAL RE
1PSB	B D	D	SOLUTION STRUCTURE OF CALCIUM LOADED S100B COMPLEXED TO A PEPTIDE FROM N-TERMINAL RE
1PZL	A B	A	CRYSTAL STRUCTURE OF HNF4A LBD IN COMPLEX WITH THE LIGAND AND THE COACTIVATOR SRC-1 P
1QO0	A D	A	AMIDE RECEPTOR OF THE AMIDASE OPERON OF PSEUDOMONAS AERUGINOSA (AMIC) COMPLEXED WI
1QO0	B E	B	AMIDE RECEPTOR OF THE AMIDASE OPERON OF PSEUDOMONAS AERUGINOSA (AMIC) COMPLEXED WI
1QS7	A B	A	THE 1.8 ANGSTROM STRUCTURE OF CALMODULIN RS20 PEPTIDE COMPLEX
1QS7	A B	A	THE 1.8 ANGSTROM STRUCTURE OF CALMODULIN RS20 PEPTIDE COMPLEX
1QS7	A B	B	THE 1.8 ANGSTROM STRUCTURE OF CALMODULIN RS20 PEPTIDE COMPLEX
1QTY	S T	S	VASCULAR ENDOTHELIAL GROWTH FACTOR IN COMPLEX WITH DOMAIN 2 OF THE FLT-1 RECEPTOR
1QTY	V Y	V	VASCULAR ENDOTHELIAL GROWTH FACTOR IN COMPLEX WITH DOMAIN 2 OF THE FLT-1 RECEPTOR
1R0N	A B	B	CRYSTAL STRUCTURE OF HETERODIMERIC ECDSYONE RECEPTOR DNA BINDING COMPLEX
1R1K	D A	A	CRYSTAL STRUCTURE OF THE LIGAND-BINDING DOMAINS OF THE HETERODIMER ECR/USP BOUND TO
1R1K	D A	D	CRYSTAL STRUCTURE OF THE LIGAND-BINDING DOMAINS OF THE HETERODIMER ECR/USP BOUND TO
1R4M	A B	A	APPBP1-UBA3-NEDD8, AN E1-UBIQUITIN-LIKE PROTEIN COMPLEX
1R4M	A B	B	APPBP1-UBA3-NEDD8, AN E1-UBIQUITIN-LIKE PROTEIN COMPLEX
1R4M	A I	I	APPBP1-UBA3-NEDD8, AN E1-UBIQUITIN-LIKE PROTEIN COMPLEX
1R4M	C D	C	APPBP1-UBA3-NEDD8, AN E1-UBIQUITIN-LIKE PROTEIN COMPLEX
1R4M	C D	C	APPBP1-UBA3-NEDD8, AN E1-UBIQUITIN-LIKE PROTEIN COMPLEX
1R4M	C D	D	APPBP1-UBA3-NEDD8, AN E1-UBIQUITIN-LIKE PROTEIN COMPLEX
1R4M	E F	E	APPBP1-UBA3-NEDD8, AN E1-UBIQUITIN-LIKE PROTEIN COMPLEX
1R4M	E F	F	APPBP1-UBA3-NEDD8, AN E1-UBIQUITIN-LIKE PROTEIN COMPLEX
1R4M	F K	F	APPBP1-UBA3-NEDD8, AN E1-UBIQUITIN-LIKE PROTEIN COMPLEX
1R4M	G H	G	APPBP1-UBA3-NEDD8, AN E1-UBIQUITIN-LIKE PROTEIN COMPLEX
1R4M	G H	G	APPBP1-UBA3-NEDD8, AN E1-UBIQUITIN-LIKE PROTEIN COMPLEX
1R4M	G H	H	APPBP1-UBA3-NEDD8, AN E1-UBIQUITIN-LIKE PROTEIN COMPLEX
1R4M	H L	H	APPBP1-UBA3-NEDD8, AN E1-UBIQUITIN-LIKE PROTEIN COMPLEX
1R6O	A C	A	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA/ATP- DEPENDENT CLP PROTEASE ADAPT
1R6O	A C	C	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA/ATP- DEPENDENT CLP PROTEASE ADAPT
1R6O	A D	A	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA/ATP- DEPENDENT CLP PROTEASE ADAPT
1R6O	A D	D	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA/ATP- DEPENDENT CLP PROTEASE ADAPT
1R6O	B D	D	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA/ATP- DEPENDENT CLP PROTEASE ADAPT
1R8Q	A E	E	FULL-LENGTH ARF1-GDP-MG IN COMPLEX WITH BREFELDIN A AND A SEC7 DOMAIN
1R8Q	A F	F	FULL-LENGTH ARF1-GDP-MG IN COMPLEX WITH BREFELDIN A AND A SEC7 DOMAIN
1R8U	A B	B	NMR STRUCTURE OF CBP TAZ1/CITED2 COMPLEX
1R8U	A B	B	NMR STRUCTURE OF CBP TAZ1/CITED2 COMPLEX
1RDT	A D	A	CRYSTAL STRUCTURE OF A NEW REXINOID BOUND TO THE RXRALPHA LIGAND BINDING DOAMIN IN T
1RDT	A D	D	CRYSTAL STRUCTURE OF A NEW REXINOID BOUND TO THE RXRALPHA LIGAND BINDING DOAMIN IN T
1RDT	A D	D	CRYSTAL STRUCTURE OF A NEW REXINOID BOUND TO THE RXRALPHA LIGAND BINDING DOAMIN IN T
1RE0	A B	A	STRUCTURE OF ARF1-GDP BOUND TO SEC7 DOMAIN COMPLEXED WITH BREFELDIN A
1RE0	A B	B	STRUCTURE OF ARF1-GDP BOUND TO SEC7 DOMAIN COMPLEXED WITH BREFELDIN A
1RH5	A B	A	THE STRUCTURE OF A PROTEIN CONDUCTING CHANNEL
1RH5	A B	A	THE STRUCTURE OF A PROTEIN CONDUCTING CHANNEL
1RH5	A B	A	THE STRUCTURE OF A PROTEIN CONDUCTING CHANNEL
1RH5	A B	B	THE STRUCTURE OF A PROTEIN CONDUCTING CHANNEL
1RH5	A B	B	THE STRUCTURE OF A PROTEIN CONDUCTING CHANNEL
1RH5	A C	C	THE STRUCTURE OF A PROTEIN CONDUCTING CHANNEL
1RIW	B C	B	THROMBIN IN COMPLEX WITH NATURAL PRODUCT INHIBITOR OSCILLARIN
1RK8	A B	B	STRUCTURE OF THE CYTOSOLIC PROTEIN PYM BOUND TO THE MAGO- Y14 CORE OF THE EXON JUNCTI
1RKE	A B	A	HUMAN VINCULIN HEAD (1-258) IN COMPLEX WITH HUMAN VINCULIN TAIL (879-1066)
1RKE	A B	B	HUMAN VINCULIN HEAD (1-258) IN COMPLEX WITH HUMAN VINCULIN TAIL (879-1066)
1RKE	A B	B	HUMAN VINCULIN HEAD (1-258) IN COMPLEX WITH HUMAN VINCULIN TAIL (879-1066)
1RM1	B C	C	STRUCTURE OF A YEAST TFIIA/TBP/TATA-BOX DNA COMPLEX
1RM1	B C	C	STRUCTURE OF A YEAST TFIIA/TBP/TATA-BOX DNA COMPLEX

TABLE S4

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM,\ HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
1P4Q	TRANSCRIPTION/TRANSFERASE	1.2	2.4	2	14
1P8V	MEMBRANE PROTEIN/HYDROLASE	1.7	5.2	3	8
1P9M	SIGNALING PROTEIN/CYTOKINE	1.2	2.3	2	18
1PCQ	CHAPERONE	1.3	3.9	3	13
1PD7	TRANSCRIPTION	1.5	4.5	3	17
1PD7	TRANSCRIPTION	1.6	6.4	4	20
1PGR	CYTOKINE	1.6	4.7	3	29
1PK1	TRANSCRIPTION REPRESSION	1.7	5.0	3	14
1PQ1	APOPTOSIS	1.2	2.4	2	13
1PSB	METAL BINDING PROTEIN	1.4	4.3	3	12
1PSB	METAL BINDING PROTEIN	1.9	5.8	3	16
1PSB	METAL BINDING PROTEIN	1.8	9.1	5	16
1PZL	TRANSCRIPTION	1.9	7.4	4	11
1QO0	BINDING PROTEIN	1.1	2.1	2	16
1QO0	BINDING PROTEIN	1.8	3.5	2	17
1QS7	METAL BINDING PROTEIN/PEPTIDE	1.4	2.8	2	16
1QS7	METAL BINDING PROTEIN/PEPTIDE	1.8	3.5	2	10
1QS7	METAL BINDING PROTEIN/PEPTIDE	1.9	11.4	6	14
1QTY	HORMONE/GROWTH FACTOR RECEPTOR	1.7	3.3	2	9
1QTY	HORMONE/GROWTH FACTOR RECEPTOR	1.8	3.5	2	9
1R0N	TRANSCRIPTION/DNA	1.3	2.5	2	5
1R1K	HORMONE/GROWTH FACTOR RECEPTOR	1.6	4.8	3	22
1R1K	HORMONE/GROWTH FACTOR RECEPTOR	1.7	3.4	2	30
1R4M	CELL CYCLE	1.3	2.6	2	11
1R4M	CELL CYCLE	1.4	2.7	2	21
1R4M	CELL CYCLE	1.5	2.9	2	13
1R4M	CELL CYCLE	1.3	2.5	2	11
1R4M	CELL CYCLE	1.7	5.2	3	21
1R4M	CELL CYCLE	1.7	5.1	3	21
1R4M	CELL CYCLE	1.2	3.6	3	11
1R4M	CELL CYCLE	1.7	6.7	4	21
1R4M	CELL CYCLE	1.3	2.5	2	15
1R4M	CELL CYCLE	1.4	2.7	2	11
1R4M	CELL CYCLE	1.7	5.0	3	21
1R4M	CELL CYCLE	1.6	7.8	5	21
1R4M	CELL CYCLE	1.4	2.8	2	15
1R6O	HYDROLASE	1.6	3.1	2	17
1R6O	HYDROLASE	1.3	6.6	5	18
1R6O	HYDROLASE	1.1	2.2	2	17
1R6O	HYDROLASE	1.3	3.8	3	15
1R6O	HYDROLASE	1.8	7.3	4	18
1R8Q	PROTEIN TRANSPORT/EXCHANGE FACTOR	1.7	10.0	6	19
1R8Q	PROTEIN TRANSPORT/EXCHANGE FACTOR	1.5	2.9	2	14
1R8U	TRANSCRIPTION/TRANSCRIPTION ACTIVATOR	1.8	10.7	6	27
1R8U	TRANSCRIPTION/TRANSCRIPTION ACTIVATOR	1.3	2.6	2	16
1RDT	HORMONE/GROWTH FACTOR	1.9	3.8	2	23
1RDT	HORMONE/GROWTH FACTOR	1.5	4.4	3	29
1RDT	HORMONE/GROWTH FACTOR	1.1	2.1	2	23
1RE0	PROTEIN TRANSPORT	1.6	4.9	3	6
1RE0	PROTEIN TRANSPORT	1.6	6.5	4	19
1RH5	PROTEIN TRANSPORT	1.2	2.4	2	34
1RH5	PROTEIN TRANSPORT	1.9	3.8	2	17
1RH5	PROTEIN TRANSPORT	1.5	4.5	3	19
1RH5	PROTEIN TRANSPORT	1.4	8.2	6	37
1RH5	PROTEIN TRANSPORT	1.4	4.1	3	13
1RH5	PROTEIN TRANSPORT	1.9	5.8	3	20
1RIW	HYDROLASE/BLOOD CLOTTING	1.6	3.1	2	8
1RK8	TRANSLATION	1.5	4.6	3	15
1RKE	CELL ADHESION, STRUCTURAL PROTEIN	1.6	4.9	3	28
1RKE	CELL ADHESION, STRUCTURAL PROTEIN	1.7	5.0	3	20
1RKE	CELL ADHESION, STRUCTURAL PROTEIN	1.4	2.8	2	28
1RM1	TRANSCRIPTION/DNA	1.9	9.3	5	18
1RM1	TRANSCRIPTION/DNA	1.8	3.6	2	19

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
1P4Q	171	184
1P8V	20	27
1P9M	27	44
1PCQ	230	242
1PD7	5	21
1PD7	202	221
1PGR	12	40
1PK1	66	79
1PQ1	119	131
1PSB	50	61
1PSB	72	87
1PSB	72	87
1PZL	204	214
1QO0	151	166
1QO0	151	167
1QS7	78	93
1QS7	65	74
1QS7	6	19
1QTY	17	25
1QTY	17	25
1R0N	247	251
1R1K	385	406
1R1K	481	510
1R4M	476	486
1R4M	293	313
1R4M	123	135
1R4M	476	486
1R4M	491	511
1R4M	293	313
1R4M	476	486
1R4M	293	313
1R4M	148	162
1R4M	476	486
1R4M	491	511
1R4M	293	313
1R4M	148	162
1R6O	82	98
1R6O	78	95
1R6O	4	20
1R6O	55	69
1R6O	78	95
1R8Q	182	200
1R8Q	228	241
1R8U	348	374
1R8U	382	397
1RDT	386	408
1RDT	431	459
1RDT	403	425
1RE0	78	83
1RE0	248	266
1RH5	363	396
1RH5	169	185
1RH5	402	420
1RH5	30	66
1RH5	12	24
1RH5	30	49
1RIW	159	166
1RK8	55	69
1RKE	7	34
1RKE	986	1005
1RKE	944	971
1RM1	4	21
1RM1	32	50

A. PDB CODE	L. HELIX SEQUENCE
1P4Q	CASSRQIISHWKNC
1P8V	ERELLESY
1P9M	KQIRYILDGISALRKETC
1PCQ	IREMLPVLEAVAK
1PD7	VEFNNAISYVNKIKTRF
1PD7	IQMLLEAADYLERREREAEH
1PGR	QSFLLKCLEQVRKIQGDGAALQEKLCATY
1PK1	LGPALKICNLVNKV
1PQ1	AYQSFEQVVNELF
1PSB	QEVVDKVMETLD
1PSB	KETEFLRLKRTRLGLE
1PSB	KETEFLRLKRTRLGLE
1PZL	LDDQVALLRAH
1QO0	IYPRESNHVMRHLYRQ
1QO0	IYPRESNHVMRHLYRQH
1QS7	DTDSEEELKEAFRVFD
1QS7	FPEFLNLMAR
1QS7	KTGHAVRAIGRLSS
1QTY	FMDVYQRSY
1QTY	FMDVYQRSY
1R0N	MYMRR
1R1K	RQEVEVLREKMFLCLDEYCRRS
1R1K	PRCAVIFGKILGILTEIRTLGMQNSNMCIS
1R4M	DDYVHEFCRYG
1R4M	ASTNAVIAAVCATEVFKIATS
1R4M	VERIKERVEEKEG
1R4M	DDYVHEFCRYG
1R4M	HTIAAFLGGAAAQEVIKIITK
1R4M	ASTNAVIAAVCATEVFKIATS
1R4M	DDYVHEFCRYG
1R4M	ASTNAVIAAVCATEVFKIATS
1R4M	IIARRWINGMLISLL
1R4M	DDYVHEFCRYG
1R4M	HTIAAFLGGAAAQEVIKIITK
1R4M	ASTNAVIAAVCATEVFKIATS
1R4M	IIARRWINGMLISLL
1R6O	LSFQRVLQRAVFHVQSS
1R6O	AEVAETKVAMVNKYAREN
1R6O	QELELSLNMAFARAREH
1R6O	VERATQLMLAVHYQG
1R6O	AEVAETKVAMVNKYAREN
1R8Q	TDTCYVLSYSVIMLNTDLH
1R8Q	EELLRNLYDSIRNE
1R8U	EKRKLIQQQLVLLLHAHKCQRREQANG
1R8U	PHCRTMKNVLNHMTHC
1RDT	PAEVEALREKVYASLEAYCKHKY
1RDT	LFAKLLQKMTDLRQIVTEHVQLLQVIKKT
1RDT	VKPIEDIQDNLLQALELQLKLNH
1RE0	WRHYFQ
1RE0	ADSVFVLSYSIIMLNTDSH
1RH5	EKAIEHRLKRYIPPLTVMSSAFVGFLATIANFIG
1RH5	GIGLFIAAGVSQTIFVG
1RH5	TGVLLTVSIVYRMYEQLLR
1RH5	KDEYLAVAKVTALGISLLGIIGYIIHVPATYIKGILK
1RH5	KEFIEECRRVWLV
1RH5	PEHVIGVTVAFVIIEAILTY
1RIW	RETAASLL
1RK8	QSVMEELKRIIIDSE
1RKE	RTIESILEPVAQQISHLVIMHEEGEVDG
1RKE	ERIPTISTQLKILSTVKATM
1RKE	KRALIQCAKDIAKASDEVTRLAKEVAKQ
1RM1	AEASRVYEIIVESVVNEV
1RM1	EQTLQDLKNIWQKKLTETK

A. PDB CODE	M. RESOLUTION
1P4Q	NOT APP
1P8V	2.6
1P9M	3.65
1PCQ	2.81
1PD7	NOT APP
1PD7	NOT APP
1PGR	3.5
1PK1	1.8
1PQ1	1.65
1PSB	NOT APP
1PSB	NOT APP
1PSB	NOT APP
1PZL	2.1
1QO0	2.25
1QO0	2.25
1QS7	1.8
1QS7	1.8
1QS7	1.8
1QTY	2.7
1QTY	2.7
1R0N	2.6
1R1K	2.9
1R1K	2.9
1R4M	3
1R4M	3
1R4M	3
1R4M	3
1R4M	3
1R4M	3
1R4M	3
1R4M	3
1R4M	3
1R4M	3
1R4M	3
1R4M	3
1R4M	3
1R6O	2.25
1R6O	2.25
1R6O	2.25
1R6O	2.25
1R6O	2.25
1R8Q	1.86
1R8Q	1.86
1R8U	NOT APP
1R8U	NOT APP
1RDT	2.4
1RDT	2.4
1RDT	2.4
1RE0	2.4
1RE0	2.4
1RH5	3.2
1RH5	3.2
1RH5	3.2
1RH5	3.2
1RH5	3.2
1RH5	3.2
1RIW	2.04
1RK8	1.9
1RKE	2.35
1RKE	2.35
1RKE	2.35
1RM1	2.5
1RM1	2.5

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1RM1	B C	C	STRUCTURE OF A YEAST TFIIA/TBP/TATA-BOX DNA COMPLEX
1RP3	A B	A	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	A B	A	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	A B	A	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	A B	A	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	A B	A	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	A B	B	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	A B	B	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	C D	C	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	C D	C	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	C D	C	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	C D	D	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	C D	D	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	C D	D	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	E F	E	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	E F	F	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	E F	F	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	E F	F	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	G H	G	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	G H	G	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	G H	G	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RP3	G H	H	COCRYSTAL STRUCTURE OF THE FLAGELLAR SIGMA/ANTI-SIGMA COMPLEX, SIGMA-28/FLGM
1RSO	C D	C	HETERO-TETRAMERIC L27 (LIN-2, LIN-7) DOMAIN COMPLEXES AS ORGANIZATION PLATFORMS OF SUPR
1RSO	C D	C	HETERO-TETRAMERIC L27 (LIN-2, LIN-7) DOMAIN COMPLEXES AS ORGANIZATION PLATFORMS OF SUPR
1RSO	C D	D	HETERO-TETRAMERIC L27 (LIN-2, LIN-7) DOMAIN COMPLEXES AS ORGANIZATION PLATFORMS OF SUPR
1RTD	A B	B	STRUCTURE OF A CATALYTIC COMPLEX OF HIV-1 REVERSE TRANSCRIPTASE: IMPLICATIONS FOR NUCLE
1RY1	C D	C	STRUCTURE OF THE SIGNAL RECOGNITION PARTICLE INTERACTING WITH THE ELONGATION-ARRESTE
1RZR	A D	D	CRYSTAL STRUCTURE OF TRANSCRIPTIONAL REGULATOR- PHOSPHOPROTEIN-DNA COMPLEX
1S1C	A X	X	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE HUMAN RHOA AND RHO-BINDING DOMAIN OF
1S1C	A Y	Y	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE HUMAN RHOA AND RHO-BINDING DOMAIN OF
1S5E	A G	G	CHOLERA HOLOTOXIN, CRYSTAL FORM 1
1S5E	B K	K	CHOLERA HOLOTOXIN, CRYSTAL FORM 1
1S5E	B L	L	CHOLERA HOLOTOXIN, CRYSTAL FORM 1
1S5R	A B	A	SOLUTION STRUCTURE OF HBP1 SID-MSIN3A PAH2 COMPLEX
1S5R	A B	B	SOLUTION STRUCTURE OF HBP1 SID-MSIN3A PAH2 COMPLEX
1S9K	D E	D	CRYSTAL STRUCTURE OF HUMAN NFAT1 AND FOS-JUN ON THE IL-2 ARRE1 SITE
1S9K	D E	E	CRYSTAL STRUCTURE OF HUMAN NFAT1 AND FOS-JUN ON THE IL-2 ARRE1 SITE
1SA0	C D	D	TUBULIN-COLCHICINE: STATHMIN-LIKE DOMAIN COMPLEX
1SB0	A B	A	SOLUTION STRUCTURE OF THE KIX DOMAIN OF CBP BOUND TO THE TRANSACTIVATION DOMAIN OF C-
1SFC	A B	A	NEURONAL SYNAPTIC FUSION COMPLEX
1SFC	A B	B	NEURONAL SYNAPTIC FUSION COMPLEX
1SFC	A D	A	NEURONAL SYNAPTIC FUSION COMPLEX
1SFC	A D	D	NEURONAL SYNAPTIC FUSION COMPLEX
1SFC	B C	B	NEURONAL SYNAPTIC FUSION COMPLEX
1SFC	B C	C	NEURONAL SYNAPTIC FUSION COMPLEX
1SFC	C D	C	NEURONAL SYNAPTIC FUSION COMPLEX
1SFC	E C	E	NEURONAL SYNAPTIC FUSION COMPLEX
1SFC	E F	E	NEURONAL SYNAPTIC FUSION COMPLEX
1SFC	E F	F	NEURONAL SYNAPTIC FUSION COMPLEX
1SFC	E H	E	NEURONAL SYNAPTIC FUSION COMPLEX
1SFC	E H	H	NEURONAL SYNAPTIC FUSION COMPLEX
1SFC	G H	G	NEURONAL SYNAPTIC FUSION COMPLEX
1SFC	G H	H	NEURONAL SYNAPTIC FUSION COMPLEX
1SFC	I J	J	NEURONAL SYNAPTIC FUSION COMPLEX
1SFC	J K	J	NEURONAL SYNAPTIC FUSION COMPLEX
1SFC	J K	K	NEURONAL SYNAPTIC FUSION COMPLEX
1SFC	J K	K	NEURONAL SYNAPTIC FUSION COMPLEX
1SFC	K L	K	NEURONAL SYNAPTIC FUSION COMPLEX
1SFC	K L	K	NEURONAL SYNAPTIC FUSION COMPLEX
1SHZ	A F	F	CRYSTAL STRUCTURE OF THE P115RHOGEF RGRGS DOMAIN IN A COMPLEX WITH GALPHA(13):GALPHA(
1SHZ	D C	D	CRYSTAL STRUCTURE OF THE P115RHOGEF RGRGS DOMAIN IN A COMPLEX WITH GALPHA(13):GALPHA(
1SQ0	A B	A	CRYSTAL STRUCTURE OF THE COMPLEX OF THE WILD-TYPE VON WILLEBRAND FACTOR A1 DOMAIN AN
1SQK	A B	B	CRYSTAL STRUCTURE OF CIBOULOT IN COMPLEX WITH SKELETAL ACTIN

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
1RM1	TRANSCRIPTION/DNA	1.7	3.3	2	7
1RP3	TRANSCRIPTION	1.9	7.6	4	14
1RP3	TRANSCRIPTION	1.5	3.0	2	18
1RP3	TRANSCRIPTION	1.8	3.6	2	14
1RP3	TRANSCRIPTION	1.4	4.2	3	21
1RP3	TRANSCRIPTION	1.5	4.6	3	15
1RP3	TRANSCRIPTION	1.5	3.0	2	11
1RP3	TRANSCRIPTION	1.6	4.7	3	16
1RP3	TRANSCRIPTION	1.4	4.1	3	18
1RP3	TRANSCRIPTION	1.7	3.4	2	27
1RP3	TRANSCRIPTION	1.1	2.2	2	20
1RP3	TRANSCRIPTION	1.6	3.1	2	13
1RP3	TRANSCRIPTION	1.7	3.3	2	15
1RP3	TRANSCRIPTION	1.4	4.2	3	19
1RP3	TRANSCRIPTION	1.6	3.1	2	17
1RP3	TRANSCRIPTION	1.6	3.2	2	13
1RP3	TRANSCRIPTION	1.6	3.2	2	12
1RP3	TRANSCRIPTION	1.5	2.9	2	14
1RP3	TRANSCRIPTION	1.3	5.3	4	18
1RP3	TRANSCRIPTION	1.9	9.5	5	14
1RP3	TRANSCRIPTION	1.7	3.4	2	18
1RP3	TRANSCRIPTION	1.9	3.7	2	10
1RSO	NEUROPEPTIDE/MEMBRANE PROTEIN	1.6	3.2	2	12
1RSO	NEUROPEPTIDE/MEMBRANE PROTEIN	1.4	2.7	2	15
1RSO	NEUROPEPTIDE/MEMBRANE PROTEIN	1.5	7.5	5	17
1RTD	TRANSFERASE/DNA	1.6	3.1	2	7
1RY1	TRANSLATION	1.4	4.2	3	17
1RZR	TRANSCRIPTION/TRANSPORT PROTEIN/DNA	1.6	4.7	3	15
1S1C	SIGNALING PROTEIN	1.5	3.0	2	30
1S1C	SIGNALING PROTEIN	1.2	2.3	2	21
1S5E	TRANSERASE,TOXIN	1.8	3.6	2	20
1S5E	TRANSERASE,TOXIN	1.2	2.3	2	20
1S5E	TRANSERASE,TOXIN	1.6	3.1	2	20
1S5R	TRANSCRIPTION	1.3	5.3	4	12
1S5R	TRANSCRIPTION	1.5	4.5	3	17
1S9K	TRANSCRIPTION/DNA	1.4	7.1	5	51
1S9K	TRANSCRIPTION/DNA	1.7	8.5	5	48
1SA0	CELL CYCLE	1.5	2.9	2	8
1SB0	TRANSCRIPTION	1.3	2.6	2	16
1SFC	TRANSPORT PROTEIN	1.5	13.1	9	63
1SFC	TRANSPORT PROTEIN	1.7	14.9	9	68
1SFC	TRANSPORT PROTEIN	1.4	8.2	6	63
1SFC	TRANSPORT PROTEIN	1.5	8.7	6	59
1SFC	TRANSPORT PROTEIN	1.5	13.5	9	68
1SFC	TRANSPORT PROTEIN	1.4	10.1	7	73
1SFC	TRANSPORT PROTEIN	1.4	9.6	7	73
1SFC	TRANSPORT PROTEIN	1.6	3.1	2	64
1SFC	TRANSPORT PROTEIN	1.4	11.5	8	64
1SFC	TRANSPORT PROTEIN	1.6	3.1	2	30
1SFC	TRANSPORT PROTEIN	1.5	9.2	6	64
1SFC	TRANSPORT PROTEIN	1.5	4.4	3	47
1SFC	TRANSPORT PROTEIN	1.4	6.9	5	45
1SFC	TRANSPORT PROTEIN	1.7	5.2	3	47
1SFC	TRANSPORT PROTEIN	1.9	11.1	6	65
1SFC	TRANSPORT PROTEIN	1.7	15.6	9	65
1SFC	TRANSPORT PROTEIN	1.8	3.5	2	13
1SFC	TRANSPORT PROTEIN	1.5	6.1	4	48
1SFC	TRANSPORT PROTEIN	1.2	3.6	3	13
1SFC	TRANSPORT PROTEIN	1.4	10.9	8	48
1SHZ	SIGNALING PROTEIN	1.8	5.3	3	19
1SHZ	SIGNALING PROTEIN	1.1	2.2	2	12
1SQ0	BLOOD CLOTTING	1.3	5.3	4	13
1SQK	STRUCTURAL PROTEIN/PROTEIN BINDING	1.8	3.5	2	13

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
1RM1	22	28
1RP3	187	200
1RP3	39	56
1RP3	19	32
1RP3	164	184
1RP3	4	18
1RP3	5	15
1RP3	32	47
1RP3	39	56
1RP3	126	152
1RP3	165	184
1RP3	36	48
1RP3	4	18
1RP3	51	69
1RP3	39	55
1RP3	5	17
1RP3	36	47
1RP3	56	69
1RP3	167	184
1RP3	187	200
1RP3	39	56
1RP3	38	47
1RSO	47	58
1RSO	31	45
1RSO	120	136
1RTD	395	401
1RY1	59	75
1RZR	73	87
1S1C	983	1012
1S1C	991	1011
1S5E	59	78
1S5E	59	78
1S5E	59	78
1S5R	366	377
1S5R	302	318
1S9K	141	191
1S9K	269	316
1SA0	253	260
1SB0	12	27
1SFC	30	92
1SFC	190	257
1SFC	30	92
1SFC	144	202
1SFC	190	257
1SFC	10	82
1SFC	10	82
1SFC	32	95
1SFC	32	95
1SFC	232	261
1SFC	32	95
1SFC	157	203
1SFC	38	82
1SFC	157	203
1SFC	194	258
1SFC	194	258
1SFC	22	34
1SFC	35	82
1SFC	22	34
1SFC	35	82
1SHZ	145	163
1SHZ	113	124
1SQ0	594	606
1SQK	12	24

TABLE S4

A. PDB CODE	L. HELIX SEQUENCE
1RM1	REDFENA
1RP3	EREKLVIQLIFYEE
1RP3	IRDLISYGVIGLIKAVDN
1RP3	LPLVKAIATNIKKH
1RP3	NVEEEVIKRELTEKVKEAVSK
1RP3	PYSNQIEREELILKY
1RP3	IELSRLIGLLL
1RP3	KIEDKVTLSKIAQELS
1RP3	IRDLISYGVIGLIKAVDN
1RP3	TEELFKTLDKINFSYILSLEEVFRDFA
1RP3	VEEEVIKRELTEKVKEAVSK
1RP3	KVTLSKIAQELSK
1RP3	RIELSRLIGLLLETE
1RP3	VEEKDLEKKVKELKEKIEK
1RP3	IRDLISYGVIGLIKAVD
1RP3	IELSRLIGLLLET
1RP3	KVTLSKIAQELS
1RP3	LEKKVKELKEKIEK
1RP3	EEVIKRELTEKVKEAVSK
1RP3	EREKLVIQLIFYEE
1RP3	IRDLISYGVIGLIKAVDN
1RP3	TLSKIAQELS
1RSO	NLFQALIDIQEF
1RSO	RQLRSSIERVISIFQ
1RSO	QHLHTLLDLYDKINTKS
1RTD	KETWETW
1RY1	VKKIEKFHSQLMRLMVA
1RZR	IFYAELARGIEDIAT
1S1C	NLKAAFEKNINTERTLKTQAVNKLAEIMNR
1S1C	NINTERTLKTQAVNKLAEIMN
1S5E	DSQKKAIERMKDTLRIAYLT
1S5E	DSQKKAIERMKDTLRIAYLT
1S5E	DSQKKAIERMKDTLRIAYLT
1S5R	AVYVLSSMARQR
1S5R	VEFNHAINYVNKIKNRF
1S9K	RIRRERNKMAAAKCRNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKE
1S9K	RMRNRIAASKCRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVA
1SA0	RKLAVNMV
1SB0	QDLRSHLVHKLVQAIF
1SFC	RRLQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFETSAAKLKRKYWWKN
1SFC	QALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAVSDTKKAVKY
1SFC	RRLQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFETSAAKLKRKYWWKN
1SFC	NEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKM
1SFC	QALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAVSDTKKAVKY
1SFC	ELEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNLKDLG
1SFC	ELEEMQRRADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNLKDLG
1SFC	LQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFETSAAKLKRKYWWKNLKM
1SFC	LQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFETSAAKLKRKYWWKNLKM
1SFC	RIEYNVEHAVDYVERAVSDTKKAVKYQSKA
1SFC	LQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQFETSAAKLKRKYWWKNLKM
1SFC	IGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKML
1SFC	ESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNLKDLG
1SFC	IGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKML
1SFC	EIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAVSDTKKAVKYQ
1SFC	EIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAVSDTKKAVKYQ
1SFC	ADESLESTRRMLQ
1SFC	LVEESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNLKDLG
1SFC	ADESLESTRRMLQ
1SFC	LVEESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNLKDLG
1SHZ	SQQVAVGRQLEDFRSKRLM
1SHZ	NKNQLHGDKLMA
1SQ0	TSEVLKYTLFQIF
1SQK	PKVAENLKSQLEG

A. PDB CODE	M. RESOLUTION
1RM1	2.5
1RP3	2.3
1RP3	2.3
1RP3	2.3
1RP3	2.3
1RP3	2.3
1RP3	2.3
1RP3	2.3
1RP3	2.3
1RP3	2.3
1RP3	2.3
1RP3	2.3
1RP3	2.3
1RP3	2.3
1RP3	2.3
1RP3	2.3
1RP3	2.3
1RP3	2.3
1RP3	2.3
1RP3	2.3
1RP3	2.3
1RP3	2.3
1RSO	NOT APP
1RSO	NOT APP
1RSO	NOT APP
1RTD	3.2
1RY1	2
1RZR	2.8
1S1C	2.6
1S1C	2.6
1S5E	1.9
1S5E	1.9
1S5E	1.9
1S5R	NOT APP
1S5R	NOT APP
1S9K	3.1
1S9K	3.1
1SA0	3.58
1SB0	NOT APP
1SFC	2.4
1SFC	2.4
1SFC	2.4
1SFC	2.4
1SFC	2.4
1SFC	2.4
1SFC	2.4
1SFC	2.4
1SFC	2.4
1SFC	2.4
1SFC	2.4
1SFC	2.4
1SFC	2.4
1SFC	2.4
1SFC	2.4
1SFC	2.4
1SFC	2.4
1SFC	2.4
1SFC	2.4
1SFC	2.4
1SHZ	2.85
1SHZ	2.85
1SQ0	2.6
1SQK	2.5

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1SVF	A B	A	PARAMYXOVIRUS SV5 FUSION PROTEIN CORE
1SVF	C D	C	PARAMYXOVIRUS SV5 FUSION PROTEIN CORE
1SVX	A B	B	CRYSTAL STRUCTURE OF A DESIGNED SELECTED ANKYRIN REPEAT PROTEIN IN COMPLEX WITH THE M
1SYQ	A B	A	HUMAN VINCULIN HEAD DOMAIN VH1, RESIDUES 1-258, IN COMPLEX WITH HUMANTALIN'S VINCULIN
1SYQ	A B	A	HUMAN VINCULIN HEAD DOMAIN VH1, RESIDUES 1-258, IN COMPLEX WITH HUMANTALIN'S VINCULIN
1SYQ	A B	A	HUMAN VINCULIN HEAD DOMAIN VH1, RESIDUES 1-258, IN COMPLEX WITH HUMANTALIN'S VINCULIN
1T0F	A C	A	CRYSTAL STRUCTURE OF THE TNSA/TNSC(504-555) COMPLEX
1T0F	A C	A	CRYSTAL STRUCTURE OF THE TNSA/TNSC(504-555) COMPLEX
1T0F	A C	C	CRYSTAL STRUCTURE OF THE TNSA/TNSC(504-555) COMPLEX
1T0F	B D	B	CRYSTAL STRUCTURE OF THE TNSA/TNSC(504-555) COMPLEX
1T0F	B D	D	CRYSTAL STRUCTURE OF THE TNSA/TNSC(504-555) COMPLEX
1T0F	B D	D	CRYSTAL STRUCTURE OF THE TNSA/TNSC(504-555) COMPLEX
1T2K	C D	C	STRUCTURE OF THE DNA BINDING DOMAINS OF IRF3, ATF-2 AND JUN BOUND TO DNA
1T2K	C D	D	STRUCTURE OF THE DNA BINDING DOMAINS OF IRF3, ATF-2 AND JUN BOUND TO DNA
1TA3	A B	A	CRYSTAL STRUCTURE OF XYLANASE (GH10) IN COMPLEX WITH INHIBITOR (XIP)
1TA3	A B	A	CRYSTAL STRUCTURE OF XYLANASE (GH10) IN COMPLEX WITH INHIBITOR (XIP)
1TB6	L H	L	2.5A CRYSTAL STRUCTURE OF THE ANTITHROMBIN-THROMBIN-HEPARIN TERNARY COMPLEX
1TCO	A B	B	TERNARY COMPLEX OF A CALCINEURIN A FRAGMENT, CALCINEURIN B, FKBP12 AND THE IMMUNOSUP
1TCO	A B	B	TERNARY COMPLEX OF A CALCINEURIN A FRAGMENT, CALCINEURIN B, FKBP12 AND THE IMMUNOSUP
1TFC	A C	C	CRYSTAL STRUCTURE OF THE LIGAND-BINDING DOMAIN OF THE ESTROGEN-RELATED RECEPTOR GAM
1TH1	A C	A	BETA-CATENIN IN COMPLEX WITH A PHOSPHORYLATED APC 20AA REPEAT FRAGMENT
1TH1	A C	A	BETA-CATENIN IN COMPLEX WITH A PHOSPHORYLATED APC 20AA REPEAT FRAGMENT
1TH1	A C	A	BETA-CATENIN IN COMPLEX WITH A PHOSPHORYLATED APC 20AA REPEAT FRAGMENT
1TH1	B D	B	BETA-CATENIN IN COMPLEX WITH A PHOSPHORYLATED APC 20AA REPEAT FRAGMENT
1TH1	B D	B	BETA-CATENIN IN COMPLEX WITH A PHOSPHORYLATED APC 20AA REPEAT FRAGMENT
1TH1	B D	B	BETA-CATENIN IN COMPLEX WITH A PHOSPHORYLATED APC 20AA REPEAT FRAGMENT
1TI2	A B	A	CRYSTAL STRUCTURE OF PYROGALLOL-PHLOROGLUCINOL TRANSHYDROXYLASE FROM PELOBACTER
1TI2	C D	C	CRYSTAL STRUCTURE OF PYROGALLOL-PHLOROGLUCINOL TRANSHYDROXYLASE FROM PELOBACTER
1TI2	C D	D	CRYSTAL STRUCTURE OF PYROGALLOL-PHLOROGLUCINOL TRANSHYDROXYLASE FROM PELOBACTER
1TI2	E F	E	CRYSTAL STRUCTURE OF PYROGALLOL-PHLOROGLUCINOL TRANSHYDROXYLASE FROM PELOBACTER
1TI2	G H	G	CRYSTAL STRUCTURE OF PYROGALLOL-PHLOROGLUCINOL TRANSHYDROXYLASE FROM PELOBACTER
1TI2	K L	K	CRYSTAL STRUCTURE OF PYROGALLOL-PHLOROGLUCINOL TRANSHYDROXYLASE FROM PELOBACTER
1TIL	A B	A	CRYSTAL STRUCTURES OF THE ADP AND ATP BOUND FORMS OF THE CRYSTAL STRUCTURES OF THE A
1TIL	A B	B	CRYSTAL STRUCTURES OF THE ADP AND ATP BOUND FORMS OF THE CRYSTAL STRUCTURES OF THE A
1TIL	C D	D	CRYSTAL STRUCTURES OF THE ADP AND ATP BOUND FORMS OF THE CRYSTAL STRUCTURES OF THE A
1TN6	A B	A	PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH A RAP2A PEPTIDE SUBSTRATE AND A FPP ANALO
1TN6	A B	A	PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH A RAP2A PEPTIDE SUBSTRATE AND A FPP ANALO
1TOC	C D	C	STRUCTURE OF SERINE PROTEINASE
1TQE	P X	X	MECHANISM OF RECRUITMENT OF CLASS II HISTONE DEACETYLASES BY MYOCYTE ENHANCER FACT
1TQY	A B	A	THE ACTINORHODIN KETOSYNTHASE/CHAIN LENGTH FACTOR
1TQY	A B	A	THE ACTINORHODIN KETOSYNTHASE/CHAIN LENGTH FACTOR
1TQY	A B	B	THE ACTINORHODIN KETOSYNTHASE/CHAIN LENGTH FACTOR
1TQY	A B	B	THE ACTINORHODIN KETOSYNTHASE/CHAIN LENGTH FACTOR
1TQY	C D	C	THE ACTINORHODIN KETOSYNTHASE/CHAIN LENGTH FACTOR
1TQY	G H	H	THE ACTINORHODIN KETOSYNTHASE/CHAIN LENGTH FACTOR
1TU3	A F	F	CRYSTAL STRUCTURE OF RAB5 COMPLEX WITH RABAPTIN5 C-TERMINAL DOMAIN
1TU3	C H	H	CRYSTAL STRUCTURE OF RAB5 COMPLEX WITH RABAPTIN5 C-TERMINAL DOMAIN
1TU3	D I	D	CRYSTAL STRUCTURE OF RAB5 COMPLEX WITH RABAPTIN5 C-TERMINAL DOMAIN
1TU3	E J	E	CRYSTAL STRUCTURE OF RAB5 COMPLEX WITH RABAPTIN5 C-TERMINAL DOMAIN
1TU3	E J	J	CRYSTAL STRUCTURE OF RAB5 COMPLEX WITH RABAPTIN5 C-TERMINAL DOMAIN
1TUE	D E	D	THE X-RAY STRUCTURE OF THE PAPILLOMAVIRUS HELICASE IN COMPLEX WITH ITS MOLECULAR MAT
1TUE	D E	D	THE X-RAY STRUCTURE OF THE PAPILLOMAVIRUS HELICASE IN COMPLEX WITH ITS MOLECULAR MAT
1TUE	D E	E	THE X-RAY STRUCTURE OF THE PAPILLOMAVIRUS HELICASE IN COMPLEX WITH ITS MOLECULAR MAT
1TUE	F G	F	THE X-RAY STRUCTURE OF THE PAPILLOMAVIRUS HELICASE IN COMPLEX WITH ITS MOLECULAR MAT
1TUE	K L	K	THE X-RAY STRUCTURE OF THE PAPILLOMAVIRUS HELICASE IN COMPLEX WITH ITS MOLECULAR MAT
1TX4	A B	B	RHO/RHOGAP/GDP(DOT)ALF4 COMPLEX
1TY4	A C	A	CRYSTAL STRUCTURE OF A CED-9/EGL-1 COMPLEX
1TY4	B D	B	CRYSTAL STRUCTURE OF A CED-9/EGL-1 COMPLEX
1TYE	E F	F	STRUCTURAL BASIS FOR ALLOSTERY IN INTEGRINS AND BINDING OF LIGAND-MIMETIC THERAPEUTIC
1U0S	Y A	Y	CHEMOTAXIS KINASE CHEA P2 DOMAIN IN COMPLEX WITH RESPONSE REGULATOR CHEY FROM THE T
1U54	A B	B	CRYSTAL STRUCTURES OF THE PHOSPHORYLATED AND UNPHOSPHORYLATED KINASE DOMAINS OF TH
1U5T	A B	B	STRUCTURE OF THE ESCRT-II ENDOSOMAL TRAFFICKING COMPLEX
1U6G	A C	C	CRYSTAL STRUCTURE OF THE CAND1-CUL1-ROC1 COMPLEX

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
1SVF	VIRAL PROTEIN	1.6	3.2	2	61
1SVF	VIRAL PROTEIN	1.7	3.3	2	59
1SVX	DE NOVO PROTEIN/SUGAR BINDING PROTEIN	1.1	2.1	2	14
1SYQ	CELL ADHESION	1.5	7.4	5	21
1SYQ	CELL ADHESION	1.4	5.5	4	23
1SYQ	CELL ADHESION	1.3	5.1	4	49
1T0F	DNA BINDING PROTEIN	1.4	2.7	2	13
1T0F	DNA BINDING PROTEIN	1.7	5.1	3	17
1T0F	DNA BINDING PROTEIN	1.9	5.8	3	7
1T0F	DNA BINDING PROTEIN	1.4	4.3	3	17
1T0F	DNA BINDING PROTEIN	1.9	3.8	2	5
1T0F	DNA BINDING PROTEIN	1.8	3.5	2	8
1T2K	TRANSCRIPTION/DNA	1.3	7.7	6	61
1T2K	TRANSCRIPTION/DNA	1.3	6.3	5	60
1TA3	HYDROLASE INHIBITOR/HYDROLASE	1.6	6.5	4	13
1TA3	HYDROLASE INHIBITOR/HYDROLASE	1.0	2.0	2	9
1TB6	HYDROLASE/BLOOD CLOTTING	1.6	4.7	3	8
1TCO	COMPLEX (HYDROLASE/ISOMERASE)	1.4	4.1	3	16
1TCO	COMPLEX (HYDROLASE/ISOMERASE)	1.8	3.6	2	10
1TFC	TRANSCRIPTION	1.6	4.9	3	10
1TH1	CELL ADHESION/ANTITUMOR PROTEIN	1.5	2.9	2	18
1TH1	CELL ADHESION/ANTITUMOR PROTEIN	1.6	3.2	2	16
1TH1	CELL ADHESION/ANTITUMOR PROTEIN	1.7	5.2	3	16
1TH1	CELL ADHESION/ANTITUMOR PROTEIN	1.3	2.5	2	17
1TH1	CELL ADHESION/ANTITUMOR PROTEIN	1.1	3.4	3	16
1TH1	CELL ADHESION/ANTITUMOR PROTEIN	1.1	2.2	2	17
1TI2	OXIDOREDUCTASE	1.6	4.8	3	6
1TI2	OXIDOREDUCTASE	1.3	2.5	2	14
1TI2	OXIDOREDUCTASE	1.6	7.9	5	12
1TI2	OXIDOREDUCTASE	1.2	2.4	2	6
1TI2	OXIDOREDUCTASE	1.9	3.8	2	6
1TI2	OXIDOREDUCTASE	1.5	2.9	2	6
1TIL	TRANSCRIPTION	1.1	2.1	2	9
1TIL	TRANSCRIPTION	1.7	3.3	2	11
1TIL	TRANSCRIPTION	1.8	3.6	2	18
1TN6	TRANSFERASE	1.9	7.4	4	13
1TN6	TRANSFERASE	1.8	3.5	2	15
1TOC	COMPLEX (HYDROLASE/INHIBITOR)	1.3	2.5	2	7
1TQE	TRANSCRIPTION/PROTEIN BINDING/DNA	1.4	4.1	3	14
1TQY	TRANSFERASE	1.9	5.7	3	12
1TQY	TRANSFERASE	1.0	2.0	2	15
1TQY	TRANSFERASE	1.8	3.5	2	11
1TQY	TRANSFERASE	1.6	3.2	2	12
1TQY	TRANSFERASE	1.8	3.5	2	10
1TQY	TRANSFERASE	1.6	3.1	2	18
1TU3	PROTEIN TRANSPORT	1.2	3.7	3	33
1TU3	PROTEIN TRANSPORT	1.2	2.4	2	31
1TU3	PROTEIN TRANSPORT	1.1	2.1	2	6
1TU3	PROTEIN TRANSPORT	1.5	3.0	2	8
1TU3	PROTEIN TRANSPORT	1.6	4.7	3	31
1TUE	REPLICATION	1.4	2.8	2	13
1TUE	REPLICATION	1.5	5.8	4	11
1TUE	REPLICATION	1.8	3.6	2	23
1TUE	REPLICATION	1.9	3.8	2	13
1TUE	REPLICATION	1.9	3.8	2	14
1TX4	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE)	1.7	3.3	2	9
1TY4	APOPTOSIS	1.9	3.8	2	17
1TY4	APOPTOSIS	1.4	4.3	3	13
1TYE	CELL ADHESION	1.8	3.5	2	11
1U0S	SIGNALING PROTEIN	1.4	4.3	3	12
1U54	TRANSFERASE	1.4	2.8	2	6
1U5T	TRANSPORT PROTEIN	1.6	3.1	2	9
1U6G	LIGASE	1.4	2.8	2	19

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
1SVF	123	183
1SVF	123	181
1SVX	129	142
1SYQ	7	27
1SYQ	41	63
1SYQ	102	150
1T0F	61	73
1T0F	140	156
1T0F	521	527
1T0F	140	156
1T0F	547	551
1T0F	534	541
1T2K	254	314
1T2K	337	396
1TA3	233	245
1TA3	266	274
1TB6	14	14
1TCO	125	140
1TCO	149	158
1TFC	688	697
1TH1	249	266
1TH1	649	664
1TH1	375	390
1TH1	249	265
1TH1	649	664
1TH1	608	624
1TI2	254	259
1TI2	329	342
1TI2	18	29
1TI2	254	259
1TI2	254	259
1TI2	254	259
1TIL	108	116
1TIL	85	95
1TIL	24	41
1TN6	234	246
1TN6	166	180
1TOC	14	14
1TQE	111	124
1TQY	111	122
1TQY	171	185
1TQY	193	203
1TQY	137	148
1TQY	202	211
1TQY	161	178
1TU3	805	837
1TU3	807	837
1TU3	85	90
1TU3	83	90
1TU3	807	837
1TUE	460	472
1TUE	446	456
1TUE	4	26
1TUE	460	472
1TUE	460	473
1TX4	67	75
1TY4	168	184
1TY4	146	158
1TYE	315	325
1U0S	108	119
1U54	299	304
1U5T	457	465
1U6G	1077	1095

A. PDB CODE	L. HELIX SEQUENCE
1SVF	AAVALVKANENAAAILNLKNAIQKTNAAVADVVQATQSLGTAVQAVQDHINSVVSPAITAA
1SVF	AAVALVKANENAAAILNLKNAIQKTNAAVADVVQATQSLGTAVQAVQDHINSVVSPAIT
1SVX	WEEIPALDKELKAK
1SYQ	RTIESILEPVAQQISHLVIMH
1SYQ	TAPVAAVQAAVSNLVRVGKETVQ
1SYQ	VPARDYLIDGSRGILSGTSDLLLTFDEAEVRKIIRVCKGILEYLTVAEV
1T0F	DLELAVFLSLEWE
1T0F	ERTLEKLELERRYWQQK
1T0F	LRYIYSQ
1T0F	ERTLEKLELERRYWQQK
1T0F	MASLF
1T0F	MHERLKGK
1T2K	KAERKRMRNRIAASKSRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQLKQKVMN
1T2K	RRKFLERNRAAASRSRQKRKVWVQSLEKKAEDLSSLNGQLQSEVTLLRNEVAQLKQLLLA
1TA3	PKNVYYGVAPVAQ
1TA3	YSSLIKYYA
1TB6	ERELLESY
1TCO	DTQLQQIVDKTIINAD
1TCO	FEEFCAVVGG
1TFC	KILHRLLQEG
1TH1	DSVLFYAITTLHNLLLHQ
1TH1	EGVATYAAAVLFRMSE
1TH1	QRLVQNCLWTLRNLSD
1TH1	DSVLFYAITTLHNLLLH
1TH1	EGVATYAAAVLFRMSE
1TH1	ENIQRVAAGVLCELAQD
1TI2	HTARLV
1TI2	ACEIRALARQWAKK
1TI2	NCFMGCMDEHEL
1TI2	HTARLV
1TI2	HTARLV
1TI2	HTARLV
1TIL	MGFTIMENF
1TIL	PAVKRLFDMSG
1TIL	HHTAEELREQVTDVLENR
1TN6	NSVWNQRYFVISN
1TN6	YQVWHHRRVLVEWLR
1TOC	EKELFES
1TQE	TEVKQKLQEFLLSK
1TQY	ATSLEREYLLLS
1TQY	SGLDSVGNAVRAIEE
1TQY	PWGWVSQIASG
1TQY	YAVNTGQISIRH
1TQY	PIVVACFDAI
1TQY	QAGGLDALGHARRTIRRG
1TU3	QRLQTELDVSEQVQRDFVKLSQTLQVQLERIRQ
1TU3	LQTELDVSEQVQRDFVKLSQTLQVQLERIRQ
1TU3	LAPMYY
1TU3	HSLAPMYY
1TU3	LQTELDVSEQVQRDFVKLSQTLQVQLERIRQ
1TUE	FITFLGALKSFLK
1TUE	WRPIVQFLRYQ
1TUE	PKETLSERLSALQDKIIDHYEND
1TUE	FITFLGALKSFLK
1TUE	FITFLGALKSFLKG
1TX4	DRLRPLSYP
1TY4	YGRLIGLISFGGFVAAK
1TY4	FSPYQDVVRTVGN
1TYE	VNLYQNYSELI
1U0S	PSRVVEALNKVS
1U54	x
1U5T	PMEMREACE
1U6G	DGLDIRKAAFECMYTLLDS

A. PDB CODE	M. RESOLUTION
1SVF	1.4
1SVF	1.4
1SVX	2.24
1SYQ	2.42
1SYQ	2.42
1SYQ	2.42
1T0F	1.85
1T0F	1.85
1T0F	1.85
1T0F	1.85
1T0F	1.85
1T0F	1.85
1T2K	3
1T2K	3
1TA3	1.7
1TA3	1.7
1TB6	2.5
1TCO	2.5
1TCO	2.5
1TFC	2.4
1TH1	2.5
1TH1	2.5
1TH1	2.5
1TH1	2.5
1TH1	2.5
1TH1	2.5
1TI2	2.35
1TI2	2.35
1TI2	2.35
1TI2	2.35
1TI2	2.35
1TI2	2.35
1TIL	2.7
1TIL	2.7
1TIL	2.7
1TN6	1.8
1TN6	1.8
1TOC	3.1
1TQE	2.7
1TQY	2
1TQY	2
1TQY	2
1TQY	2
1TQY	2
1TQY	2
1TU3	2.31
1TU3	2.31
1TU3	2.31
1TU3	2.31
1TU3	2.31
1TUE	2.1
1TUE	2.1
1TUE	2.1
1TUE	2.1
1TUE	2.1
1TX4	1.65
1TY4	2.2
1TY4	2.2
1TYE	2.9
1U0S	1.9
1U54	2.8
1U5T	3.6
1U6G	3.1

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1U6G	A C	C	CRYSTAL STRUCTURE OF THE CAND1-CUL1-ROC1 COMPLEX
1U6H	A B	A	VINCULIN HEAD (0-258) IN COMPLEX WITH THE TALIN VINCULIN BINDING SITE 2 (849-879)
1U6H	A B	A	VINCULIN HEAD (0-258) IN COMPLEX WITH THE TALIN VINCULIN BINDING SITE 2 (849-879)
1U6H	A B	B	VINCULIN HEAD (0-258) IN COMPLEX WITH THE TALIN VINCULIN BINDING SITE 2 (849-879)
1U7F	C B	B	CRYSTAL STRUCTURE OF THE PHOSPHORYLATED SMAD3/SMAD4 HETEROTRIMERIC COMPLEX
1U8T	A E	E	CRYSTAL STRUCTURE OF CHEY D13K Y106W ALONE AND IN COMPLEX WITH A FLIM PEPTIDE
1UB4	A C	A	CRYSTAL STRUCTURE OF MAZEF COMPLEX
1UEA	C D	C	MMP-3/TIMP-1 COMPLEX
1UEL	A B	B	SOLUTION STRUCTURE OF UBIQUITIN-LIKE DOMAIN OF HHR23B COMPLEXED WITH UBIQUITIN-INTERA
1UHL	A B	A	CRYSTAL STRUCTURE OF THE LXRALFA-RXRBETA LBD HETERODIMER
1UJW	A B	B	STRUCTURE OF THE COMPLEX BETWEEN BTUB AND COLICIN E3 RECEPTOR BINDING DOMAIN
1UKL	A D	D	CRYSTAL STRUCTURE OF IMPORTIN-BETA AND SREBP-2 COMPLEX
1URQ	A D	A	CRYSTAL STRUCTURE OF NEURONAL Q-SNARES IN COMPLEX WITH R-SNARE MOTIF OF TOMOSYN
1URQ	A D	D	CRYSTAL STRUCTURE OF NEURONAL Q-SNARES IN COMPLEX WITH R-SNARE MOTIF OF TOMOSYN
1URQ	B C	B	CRYSTAL STRUCTURE OF NEURONAL Q-SNARES IN COMPLEX WITH R-SNARE MOTIF OF TOMOSYN
1URQ	C D	C	CRYSTAL STRUCTURE OF NEURONAL Q-SNARES IN COMPLEX WITH R-SNARE MOTIF OF TOMOSYN
1URQ	C D	D	CRYSTAL STRUCTURE OF NEURONAL Q-SNARES IN COMPLEX WITH R-SNARE MOTIF OF TOMOSYN
1USV	C D	C	THE STRUCTURE OF THE COMPLEX BETWEEN AHA1 AND HSP90
1USV	G H	G	THE STRUCTURE OF THE COMPLEX BETWEEN AHA1 AND HSP90
1UW4	D C	D	THE STRUCTURAL BASIS OF THE INTERACTION BETWEEN NONSENSE MEDIATED DECAY FACTORS UPF2
1VCB	B C	C	THE VHL-ELONGINC-ELONGINB STRUCTURE
1VCB	E F	E	THE VHL-ELONGINC-ELONGINB STRUCTURE
1VCB	H I	H	THE VHL-ELONGINC-ELONGINB STRUCTURE
1VF6	A C	A	2.1 ANGSTROM CRYSTAL STRUCTURE OF THE PALS-1-L27N AND PATJ L27 HETERODIMER COMPLEX
1VF6	A C	C	2.1 ANGSTROM CRYSTAL STRUCTURE OF THE PALS-1-L27N AND PATJ L27 HETERODIMER COMPLEX
1VF6	B D	B	2.1 ANGSTROM CRYSTAL STRUCTURE OF THE PALS-1-L27N AND PATJ L27 HETERODIMER COMPLEX
1VF6	B D	B	2.1 ANGSTROM CRYSTAL STRUCTURE OF THE PALS-1-L27N AND PATJ L27 HETERODIMER COMPLEX
1VF6	B D	D	2.1 ANGSTROM CRYSTAL STRUCTURE OF THE PALS-1-L27N AND PATJ L27 HETERODIMER COMPLEX
1VF6	B D	D	2.1 ANGSTROM CRYSTAL STRUCTURE OF THE PALS-1-L27N AND PATJ L27 HETERODIMER COMPLEX
1VF6	B D	D	2.1 ANGSTROM CRYSTAL STRUCTURE OF THE PALS-1-L27N AND PATJ L27 HETERODIMER COMPLEX
1VG0	A B	A	THE CRYSTAL STRUCTURES OF THE REP-1 PROTEIN IN COMPLEX WITH MONOPRENYLATED RAB7 PROT
1VG9	A B	A	THE CRYSTAL STRUCTURES OF THE REP-1 PROTEIN IN COMPLEX WITH C-TERMINALLY TRUNCATED RA
1VYW	A B	A	STRUCTURE OF CDK2/CYCLIN A WITH PNU-292137
1VYW	A B	B	STRUCTURE OF CDK2/CYCLIN A WITH PNU-292137
1VYW	C D	D	STRUCTURE OF CDK2/CYCLIN A WITH PNU-292137
1W1I	A F	F	CRYSTAL STRUCTURE OF DIPEPTIDYL PEPTIDASE IV (DPPIV OR CD26) IN COMPLEX WITH ADENOSINE D
1W1I	A F	F	CRYSTAL STRUCTURE OF DIPEPTIDYL PEPTIDASE IV (DPPIV OR CD26) IN COMPLEX WITH ADENOSINE D
1W7P	A D	A	THE CRYSTAL STRUCTURE OF ENDOSOMAL COMPLEX ESCRT-II (VPS22/VPS25/VPS36)
1WMH	A B	A	CRYSTAL STRUCTURE OF A PB1 DOMAIN COMPLEX OF PROTEIN KINASE C IOTA AND PAR6 ALPHA
1WPX	A B	A	CRYSTAL STRUCTURE OF CARBOXYPEPTIDASE Y INHIBITOR COMPLEXED WITH THE COGNATE PROTEI
1WQ1	R G	G	RAS-RASGAP COMPLEX
1WQ1	R G	R	RAS-RASGAP COMPLEX
1WRD	A B	A	CRYSTAL STRUCTURE OF TOM1 GAT DOMAIN IN COMPLEX WITH UBIQUITIN
1WRD	A B	A	CRYSTAL STRUCTURE OF TOM1 GAT DOMAIN IN COMPLEX WITH UBIQUITIN
1WX5	A B	A	CRYSTAL STRUCTURE OF THE COPPER-FREE STREPTOMYCES CASTANEOGLOBISPORUS TYROSINASE C
1X3Z	A B	A	STRUCTURE OF A PEPTIDE:N-GLYCANASE-RAD23 COMPLEX
1X3Z	A B	B	STRUCTURE OF A PEPTIDE:N-GLYCANASE-RAD23 COMPLEX
1X3Z	A B	B	STRUCTURE OF A PEPTIDE:N-GLYCANASE-RAD23 COMPLEX
1X79	A B	B	CRYSTAL STRUCTURE OF HUMAN GGA1 GAT DOMAIN COMPLEXED WITH THE GAT-BINDING DOMAIN O
1X79	A C	C	CRYSTAL STRUCTURE OF HUMAN GGA1 GAT DOMAIN COMPLEXED WITH THE GAT-BINDING DOMAIN O
1X86	A B	A	CRYSTAL STRUCTURE OF THE DH/PH DOMAINS OF LEUKEMIA- ASSOCIATED RHOGEF IN COMPLEX WIT
1X86	A B	B	CRYSTAL STRUCTURE OF THE DH/PH DOMAINS OF LEUKEMIA- ASSOCIATED RHOGEF IN COMPLEX WIT
1X86	G H	G	CRYSTAL STRUCTURE OF THE DH/PH DOMAINS OF LEUKEMIA- ASSOCIATED RHOGEF IN COMPLEX WIT
1XCG	A B	A	CRYSTAL STRUCTURE OF HUMAN RHOA IN COMPLEX WITH DH/PH FRAGMENT OF PDZRHOGEF
1XCG	A B	A	CRYSTAL STRUCTURE OF HUMAN RHOA IN COMPLEX WITH DH/PH FRAGMENT OF PDZRHOGEF
1XCG	E F	E	CRYSTAL STRUCTURE OF HUMAN RHOA IN COMPLEX WITH DH/PH FRAGMENT OF PDZRHOGEF
1XCG	E F	F	CRYSTAL STRUCTURE OF HUMAN RHOA IN COMPLEX WITH DH/PH FRAGMENT OF PDZRHOGEF
1XD2	A C	A	CRYSTAL STRUCTURE OF A TERNARY RAS:SOS:RAS*GDP COMPLEX
1XD2	B C	B	CRYSTAL STRUCTURE OF A TERNARY RAS:SOS:RAS*GDP COMPLEX
1XD2	B C	C	CRYSTAL STRUCTURE OF A TERNARY RAS:SOS:RAS*GDP COMPLEX
1XDK	A B	A	CRYSTAL STRUCTURE OF THE RARBETA/RXRALPHA LIGAND BINDING DOMAIN HETERODIMER IN COM
1XDK	A B	A	CRYSTAL STRUCTURE OF THE RARBETA/RXRALPHA LIGAND BINDING DOMAIN HETERODIMER IN COM
1XDK	E F	F	CRYSTAL STRUCTURE OF THE RARBETA/RXRALPHA LIGAND BINDING DOMAIN HETERODIMER IN COM

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
1U6G	LIGASE	1.3	2.6	2	15
1U6H	CELL ADHESION	1.2	2.4	2	24
1U6H	CELL ADHESION	1.1	2.1	2	46
1U6H	CELL ADHESION	1.9	7.5	4	21
1U7F	SIGNALING PROTEIN	1.2	3.7	3	13
1U8T	SIGNALING PROTEIN	1.6	3.1	2	9
1UB4	DNA BINDING PROTEIN	1.5	3.0	2	15
1UEA	COMPLEX (METALLOPROTEASE/INHIBITOR)	1.5	3.0	2	13
1UEL	GENE REGULATION/PROTEIN BINDING	1.3	5.0	4	16
1UHL	DNA BINDING PROTEIN	1.7	3.3	2	17
1UJW	TRANSPORT PROTEIN/HYDROLASE	1.7	3.3	2	32
1UKL	PROTEIN TRANSPORT/DNA BINDING PROTEIN	1.9	3.7	2	21
1URQ	TRANSPORT PROTEIN	1.4	4.1	3	56
1URQ	TRANSPORT PROTEIN	1.5	10.7	7	60
1URQ	TRANSPORT PROTEIN	1.7	16.9	10	61
1URQ	TRANSPORT PROTEIN	1.7	16.9	10	65
1URQ	TRANSPORT PROTEIN	1.9	15.2	8	60
1USV	CHAPERONE	1.2	2.4	2	24
1USV	CHAPERONE	1.4	4.2	3	22
1UW4	RNA-BINDING PROTEIN	1.5	7.6	5	22
1VCB	TRANSCRIPTION	1.7	3.4	2	13
1VCB	TRANSCRIPTION	1.9	3.7	2	18
1VCB	TRANSCRIPTION	1.8	3.6	2	15
1VF6	PROTEIN BINDING/PROTEIN TRANSPORT	1.4	4.2	3	15
1VF6	PROTEIN BINDING/PROTEIN TRANSPORT	1.7	3.3	2	15
1VF6	PROTEIN BINDING/PROTEIN TRANSPORT	1.7	5.1	3	24
1VF6	PROTEIN BINDING/PROTEIN TRANSPORT	1.0	3.1	3	16
1VF6	PROTEIN BINDING/PROTEIN TRANSPORT	1.5	4.5	3	14
1VF6	PROTEIN BINDING/PROTEIN TRANSPORT	1.7	5.1	3	16
1VF6	PROTEIN BINDING/PROTEIN TRANSPORT	1.9	3.8	2	13
1VG0	PROTEIN BINDING/PROTEIN TRANSPORT	1.9	5.8	3	15
1VG9	PROTEIN BINDING/PROTEIN TRANSPORT	1.7	3.4	2	15
1VYW	TRANSFERASE	1.4	2.8	2	13
1VYW	TRANSFERASE	1.3	2.6	2	15
1VYW	TRANSFERASE	1.4	4.3	3	15
1W1I	HYDROLASE	1.4	4.2	3	19
1W1I	HYDROLASE	1.9	3.8	2	18
1W7P	PROTEIN TRANSPORT	1.7	5.2	3	24
1WMH	TRANSFERASE/CELL CYCLE	1.7	6.6	4	14
1WPX	HYDROLASE	1.4	2.7	2	8
1WQ1	COMPLEX (GTP-BINDING/GTPASE ACTIVATION)	1.4	2.8	2	14
1WQ1	COMPLEX (GTP-BINDING/GTPASE ACTIVATION)	1.3	2.6	2	18
1WRD	PROTEIN TRANSPORT/SIGNALING PROTEIN	1.2	2.4	2	25
1WRD	PROTEIN TRANSPORT/SIGNALING PROTEIN	1.6	4.7	3	28
1WX5	OXIDOREDUCTASE/METAL TRANSPORT	1.5	3.0	2	10
1X3Z	HYDROLASE	1.9	7.6	4	20
1X3Z	HYDROLASE	1.5	2.9	2	10
1X3Z	HYDROLASE	1.9	3.7	2	12
1X79	PROTEIN TRANSPORT	1.3	3.9	3	88
1X79	PROTEIN TRANSPORT	1.3	3.9	3	81
1X86	SIGNALING PROTEIN/MEMBRANE PROTEIN	1.8	3.6	2	10
1X86	SIGNALING PROTEIN/MEMBRANE PROTEIN	1.5	2.9	2	9
1X86	SIGNALING PROTEIN/MEMBRANE PROTEIN	1.9	3.8	2	13
1XCG	SIGNALING PROTEIN ACTIVATOR/SIGNALING PR	1.9	3.8	2	38
1XCG	SIGNALING PROTEIN ACTIVATOR/SIGNALING PR	1.4	2.7	2	19
1XCG	SIGNALING PROTEIN ACTIVATOR/SIGNALING PR	1.2	3.5	3	38
1XCG	SIGNALING PROTEIN ACTIVATOR/SIGNALING PR	1.6	4.7	3	9
1XD2	SIGNALING PROTEIN	1.1	3.3	3	11
1XD2	SIGNALING PROTEIN	1.9	3.8	2	8
1XD2	SIGNALING PROTEIN	1.1	2.1	2	13
1XDK	HORMONE/GROWTH FACTOR RECEPTOR	1.8	7.2	4	21
1XDK	HORMONE/GROWTH FACTOR RECEPTOR	1.3	2.5	2	7
1XDK	HORMONE/GROWTH FACTOR RECEPTOR	1.8	5.5	3	7

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
1U6G	348	362
1U6H	40	63
1U6H	101	146
1U6H	854	874
1U7F	530	542
1U8T	8	16
1UB4	96	110
1UEA	195	207
1UEL	283	298
1UHL	457	473
1UJW	386	417
1UKL	369	389
1URQ	1053	1108
1URQ	140	199
1URQ	197	257
1URQ	17	81
1URQ	140	199
1USV	387	410
1USV	387	408
1UW4	839	860
1VCB	158	170
1VCB	67	84
1VCB	97	111
1VF6	13	27
1VF6	122	136
1VF6	45	68
1VF6	11	26
1VF6	157	170
1VF6	141	156
1VF6	124	136
1VG0	377	391
1VG9	377	391
1VYW	46	58
1VYW	288	302
1VYW	288	302
1W1I	126	144
1W1I	76	93
1W7P	87	110
1WMH	74	87
1WPX	301	308
1WQ1	793	806
1WQ1	87	104
1WRD	217	241
1WRD	248	275
1WX5	189	198
1X3Z	12	31
1X3Z	276	285
1X3Z	259	270
1X79	553	640
1X79	554	634
1X86	932	941
1X86	67	75
1X86	785	797
1XCG	730	767
1XCG	877	895
1XCG	901	938
1XCG	67	75
1XD2	65	75
1XD2	68	75
1XD2	930	942
1XDK	391	411
1XDK	419	425
1XDK	366	372

A. PDB CODE	L. HELIX SEQUENCE
1U6G	KVRRAAAKCLDAVVS
1U6H	TAPVSAVQAAVSNLVRVGKETVQT
1U6H	VPARDYLIDGSRGILSGTSDLLLTFDEAEVRKIIRVCKGILEYLTV
1U6H	RKLLSAAKILADATAKMVEAA
1U7F	HRALQLLDEVLHT
1U8T	QAEIDALLN
1UB4	PEELQLIKAKINVLI
1UEA	LFLVAAHEIGHSL
1UEL	EEEQIAYAMQMSLQGA
1UHL	PSEVEVLREKVYASLET
1UJW	GHRMWQMAGLKAQRAQTDVNNKQAAFDAAAKE
1UKL	VLRKAIDYIKYLQQVNHKLRQ
1URQ	EGVKGAASGVVGELARARLALDERGQKLSDLEERTAAMMSSADSFSKHAHEMMLKY
1URQ	SRENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRAT
1URQ	TRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAVSDTKKAVKY
1URQ	RADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNLKDL
1URQ	SRENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRAT
1USV	KIMKVIRKNIVKKLIEAFNEIAED
1USV	KIMKVIRKNIVKKLIEAFNEIA
1UW4	EDVGIHVVDGVLEDIRLGMEVN
1VCB	LKERCLQVVRSLV
1VCB	SHVLSKVCMYFTYKVRYT
1VCB	PEIALELLMAANFLD
1VF6	LQVLDRLKMKLQEKG
1VF6	PDVEDLFSSLKHIQH
1VF6	PLFNQILTLQQSIKQLKGQLNHIL
1VF6	QVLQVLDRLKMKLQEK
1VF6	RDFQNAFKIHNAVT
1VF6	SQSQEDISLLLQLVQN
1VF6	VEDLFSSLKHIQH
1VG0	QGELPQCFCRMCAVF
1VG9	QGELPQCFCRMCAVF
1VYW	STAIREISLLKEL
1VYW	KKQVLRMEHLVLKVL
1VYW	KKQVLRMEHLVLKVL
1W1I	PDEVVSLVNQGLQEGERDF
1W1I	RDAIKRIAYEFVEMKAKD
1W7P	TVNDFYYEVCLKVIEICRQTKDMN
1WMH	QLELEEAFRLYELN
1WPX	DINRNFLF
1WQ1	LASTLMEQYMKATA
1WQ1	TKSFEDIHQYREQIKRVK
1WRD	IGKLRSELEMVSGNVRVMSEMLTEL
1WRD	PADLELLQELNRTCRAMQQRVLELIPQI
1WX5	LHNRVHVWVG
1X3Z	FDSIAKMLLIKYKDFILSKF
1X3Z	LAPLLENISA
1X3Z	VEDLLSLRQVVS
1X79	TRDQVKKLQLMLRQANDQLEKTMKDKQELEDFIKQSSEDSSHQISALVLRAQASEILLEELQQGLSQAKRDVQEQMAVLMQSREQVSE
1X79	RDQVKKLQLMLRQANDQLEKTMKDKQELEDFIKQSSEDSSHQISALVLRAQASEILLEELQQGLSQAKRDVQEQMAVLMQS
1X86	TQMQRLTKYP
1X86	DRLRPLSYP
1X86	EIKRQEVINELFY
1XCG	QREIDRQEVINELFVTEASHLRTLRVLDLIFYQRMKKE
1XCG	SEMQRLTKYPLLLESIIKH
1XCG	SEHEKLCRARDQCREILKYVNEAVKQTENRHRLEGYQK
1XCG	DRLRPLSYP
1XD2	SAMRDQYMRTG
1XD2	RDQYMRTG
1XD2	FGIYLTNILKTEE
1XDK	PAEVEALREKVYASLEAYCKH
1XDK	RFAKLLL
1XDK	MFPKILM

A. PDB CODE	M. RESOLUTION
1U6G	3.1
1U6H	2.38
1U6H	2.38
1U6H	2.38
1U7F	2.6
1U8T	1.5
1UB4	1.7
1UEA	2.8
1UEL	NOT APP
1UHL	2.9
1UJW	2.75
1UKL	3
1URQ	2
1URQ	2
1URQ	2
1URQ	2
1URQ	2
1USV	2.7
1USV	2.7
1UW4	1.95
1VCB	2.7
1VCB	2.7
1VCB	2.7
1VF6	2.1
1VF6	2.1
1VF6	2.1
1VF6	2.1
1VF6	2.1
1VF6	2.1
1VF6	2.1
1VG0	2.2
1VG9	2.5
1VYW	2.3
1VYW	2.3
1VYW	2.3
1W1I	3.03
1W1I	3.03
1W7P	3.6
1WMH	1.5
1WPX	2.7
1WQ1	2.5
1WQ1	2.5
1WRD	1.75
1WRD	1.75
1WX5	2.02
1X3Z	2.8
1X3Z	2.8
1X3Z	2.8
1X79	2.41
1X79	2.41
1X86	3.22
1X86	3.22
1X86	3.22
1XCG	2.5
1XCG	2.5
1XCG	2.5
1XCG	2.5
1XD2	2.7
1XD2	2.7
1XD2	2.7
1XDK	2.9
1XDK	2.9
1XDK	2.9

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1XFU	A O	A	CRYSTAL STRUCTURE OF ANTHRAX EDEMA FACTOR (EF) TRUNCATION MUTANT, EF-DELTA 64 IN COMP
1XFU	A O	O	CRYSTAL STRUCTURE OF ANTHRAX EDEMA FACTOR (EF) TRUNCATION MUTANT, EF-DELTA 64 IN COMP
1XFU	C Q	C	CRYSTAL STRUCTURE OF ANTHRAX EDEMA FACTOR (EF) TRUNCATION MUTANT, EF-DELTA 64 IN COMP
1XFU	C Q	Q	CRYSTAL STRUCTURE OF ANTHRAX EDEMA FACTOR (EF) TRUNCATION MUTANT, EF-DELTA 64 IN COMP
1XFU	E S	E	CRYSTAL STRUCTURE OF ANTHRAX EDEMA FACTOR (EF) TRUNCATION MUTANT, EF-DELTA 64 IN COMP
1XFU	F T	T	CRYSTAL STRUCTURE OF ANTHRAX EDEMA FACTOR (EF) TRUNCATION MUTANT, EF-DELTA 64 IN COMP
1XG2	A B	B	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN PECTIN METHYLESTERASE AND ITS INHIBITOR PRO
1XIU	A E	A	CRYSTAL STRUCTURE OF THE AGONIST-BOUND LIGAND-BINDING DOMAIN OF BIOMPHALARIA GLABR
1XL3	A C	C	COMPLEX STRUCTURE OF Y.PESTIS VIRULENCE FACTORS YOPN AND TYEA
1XLS	A E	A	CRYSTAL STRUCTURE OF THE MOUSE CAR/RXR LBD HETERODIMER BOUND TO TCPOBOP AND 9CRA AN
1XLS	A E	E	CRYSTAL STRUCTURE OF THE MOUSE CAR/RXR LBD HETERODIMER BOUND TO TCPOBOP AND 9CRA AN
1XLS	A I	I	CRYSTAL STRUCTURE OF THE MOUSE CAR/RXR LBD HETERODIMER BOUND TO TCPOBOP AND 9CRA AN
1XLS	D L	L	CRYSTAL STRUCTURE OF THE MOUSE CAR/RXR LBD HETERODIMER BOUND TO TCPOBOP AND 9CRA AN
1XLS	E M	E	CRYSTAL STRUCTURE OF THE MOUSE CAR/RXR LBD HETERODIMER BOUND TO TCPOBOP AND 9CRA AN
1XLS	F N	N	CRYSTAL STRUCTURE OF THE MOUSE CAR/RXR LBD HETERODIMER BOUND TO TCPOBOP AND 9CRA AN
1XLS	H P	P	CRYSTAL STRUCTURE OF THE MOUSE CAR/RXR LBD HETERODIMER BOUND TO TCPOBOP AND 9CRA AN
1XOU	A B	A	CRYSTAL STRUCTURE OF THE CESA-ESPA COMPLEX
1XOU	A B	A	CRYSTAL STRUCTURE OF THE CESA-ESPA COMPLEX
1XOU	A B	A	CRYSTAL STRUCTURE OF THE CESA-ESPA COMPLEX
1XOU	A B	B	CRYSTAL STRUCTURE OF THE CESA-ESPA COMPLEX
1XOU	A B	B	CRYSTAL STRUCTURE OF THE CESA-ESPA COMPLEX
1XPK	D C	C	CRYSTAL STRUCTURE OF STAPHYLOCOCCUS AUREUS HMG-COA SYNTHASE WITH HMG-COA AND WITH
1XPK	D C	D	CRYSTAL STRUCTURE OF STAPHYLOCOCCUS AUREUS HMG-COA SYNTHASE WITH HMG-COA AND WITH
1XQ5	A D	D	MET-PERCH HEMOGLOBIN AT 1.9A
1XQ5	C D	C	MET-PERCH HEMOGLOBIN AT 1.9A
1XQ5	C D	D	MET-PERCH HEMOGLOBIN AT 1.9A
1XQS	A C	A	CRYSTAL STRUCTURE OF THE HSPBP1 CORE DOMAIN COMPLEXED WITH THE FRAGMENT OF HSP70 ATP
1XQS	A C	C	CRYSTAL STRUCTURE OF THE HSPBP1 CORE DOMAIN COMPLEXED WITH THE FRAGMENT OF HSP70 ATP
1XQS	B D	D	CRYSTAL STRUCTURE OF THE HSPBP1 CORE DOMAIN COMPLEXED WITH THE FRAGMENT OF HSP70 ATP
1XQS	B D	D	CRYSTAL STRUCTURE OF THE HSPBP1 CORE DOMAIN COMPLEXED WITH THE FRAGMENT OF HSP70 ATP
1XTG	A B	A	CRYSTAL STRUCTURE OF NEUROTOXIN BONT/A COMPLEXED WITH SYNAPTOSOMAL-ASSOCIATED PRO
1XTG	A B	A	CRYSTAL STRUCTURE OF NEUROTOXIN BONT/A COMPLEXED WITH SYNAPTOSOMAL-ASSOCIATED PRO
1XTG	A B	B	CRYSTAL STRUCTURE OF NEUROTOXIN BONT/A COMPLEXED WITH SYNAPTOSOMAL-ASSOCIATED PRO
1XV9	A B	B	CRYSTAL STRUCTURE OF CAR/RXR HETERODIMER BOUND WITH SRC1 PEPTIDE, FATTY ACID, AND 5B-P
1XV9	A B	B	CRYSTAL STRUCTURE OF CAR/RXR HETERODIMER BOUND WITH SRC1 PEPTIDE, FATTY ACID, AND 5B-P
1XV9	C D	C	CRYSTAL STRUCTURE OF CAR/RXR HETERODIMER BOUND WITH SRC1 PEPTIDE, FATTY ACID, AND 5B-P
1XV9	C G	C	CRYSTAL STRUCTURE OF CAR/RXR HETERODIMER BOUND WITH SRC1 PEPTIDE, FATTY ACID, AND 5B-P
1XZP	A B	A	STRUCTURE OF THE GTP-BINDING PROTEIN TRME FROM THERMOTOGA MARITIMA
1XZP	A B	B	STRUCTURE OF THE GTP-BINDING PROTEIN TRME FROM THERMOTOGA MARITIMA
1Y74	A D	A	SOLUTION STRUCTURE OF MLIN-2/MLIN-7 L27 DOMAIN COMPLEX
1Y76	C B	C	SOLUTION STRUCTURE OF PATJ/PALS1 L27 DOMAIN COMPLEX
1Y8R	A B	A	SUMO E1 ACTIVATING ENZYME SAE1-SAE2-SUMO1-MG-ATP COMPLEX
1Y8R	A B	A	SUMO E1 ACTIVATING ENZYME SAE1-SAE2-SUMO1-MG-ATP COMPLEX
1Y8R	A B	B	SUMO E1 ACTIVATING ENZYME SAE1-SAE2-SUMO1-MG-ATP COMPLEX
1Y8R	A B	B	SUMO E1 ACTIVATING ENZYME SAE1-SAE2-SUMO1-MG-ATP COMPLEX
1Y8R	D E	D	SUMO E1 ACTIVATING ENZYME SAE1-SAE2-SUMO1-MG-ATP COMPLEX
1Y8R	D E	D	SUMO E1 ACTIVATING ENZYME SAE1-SAE2-SUMO1-MG-ATP COMPLEX
1Y8R	D E	E	SUMO E1 ACTIVATING ENZYME SAE1-SAE2-SUMO1-MG-ATP COMPLEX
1Y8X	A B	B	STRUCTURAL BASIS FOR RECRUITMENT OF UBC12 BY AN E2-BINDING DOMAIN IN NEDD8'S E1
1YD8	U H	H	COMPLEX OF HUMAN GGA3 GAT DOMAIN AND UBIQUITIN
1YD8	V G	G	COMPLEX OF HUMAN GGA3 GAT DOMAIN AND UBIQUITIN
1YDI	A B	A	HUMAN VINCULIN HEAD DOMAIN (VH1, 1-258) IN COMPLEX WITH HUMAN ALPHA-ACTININ'S VINCULIN
1YDI	A B	A	HUMAN VINCULIN HEAD DOMAIN (VH1, 1-258) IN COMPLEX WITH HUMAN ALPHA-ACTININ'S VINCULIN
1YKE	A B	A	STRUCTURE OF THE MEDIATOR MED7/MED21 SUBCOMPLEX
1YKE	A B	A	STRUCTURE OF THE MEDIATOR MED7/MED21 SUBCOMPLEX
1YKE	A B	A	STRUCTURE OF THE MEDIATOR MED7/MED21 SUBCOMPLEX
1YKE	A B	B	STRUCTURE OF THE MEDIATOR MED7/MED21 SUBCOMPLEX
1YKE	A B	B	STRUCTURE OF THE MEDIATOR MED7/MED21 SUBCOMPLEX
1YKE	C D	C	STRUCTURE OF THE MEDIATOR MED7/MED21 SUBCOMPLEX
1YKE	C D	C	STRUCTURE OF THE MEDIATOR MED7/MED21 SUBCOMPLEX
1YKE	C D	D	STRUCTURE OF THE MEDIATOR MED7/MED21 SUBCOMPLEX
1YOK	A B	A	CRYSTAL STRUCTURE OF HUMAN LRH-1 BOUND WITH TIF-2 PEPTIDE AND PHOSPHATIDYLGLYCEROL
1YOV	A B	A	INSIGHTS INTO THE UBIQUITIN TRANSFER CASCADE FROM THE REFINED STRUCTURE OF THE ACTIVAT

TABLE S4

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
1XFU	LYASE/METAL BINDING PROTEIN	1.3	2.6	2	15
1XFU	LYASE/METAL BINDING PROTEIN	1.2	3.7	3	13
1XFU	LYASE/METAL BINDING PROTEIN	1.6	3.2	2	23
1XFU	LYASE/METAL BINDING PROTEIN	1.3	2.5	2	10
1XFU	LYASE/METAL BINDING PROTEIN	1.6	3.2	2	13
1XFU	LYASE/METAL BINDING PROTEIN	1.4	2.7	2	9
1XG2	HYDROLASE/HYDROLASE INHIBITOR	1.8	11.0	6	22
1XIU	TRANSCRIPTION/TRANSFERASE	1.6	6.5	4	24
1XL3	CELL INVASION	1.6	6.5	4	13
1XLS	TRANSCRIPTION	1.5	2.9	2	23
1XLS	TRANSCRIPTION	1.7	3.3	2	25
1XLS	TRANSCRIPTION	1.5	4.6	3	7
1XLS	TRANSCRIPTION	1.2	2.3	2	7
1XLS	TRANSCRIPTION	1.5	4.5	3	7
1XLS	TRANSCRIPTION	1.3	2.6	2	9
1XLS	TRANSCRIPTION	1.9	9.4	5	9
1XOU	STRUCTURAL PROTEIN/CHAPERONE	1.8	7.0	4	13
1XOU	STRUCTURAL PROTEIN/CHAPERONE	1.9	5.7	3	12
1XOU	STRUCTURAL PROTEIN/CHAPERONE	1.3	2.5	2	11
1XOU	STRUCTURAL PROTEIN/CHAPERONE	1.4	8.4	6	19
1XOU	STRUCTURAL PROTEIN/CHAPERONE	1.9	13.1	7	29
1XPK	TRANSFERASE	1.5	3.0	2	16
1XPK	TRANSFERASE	1.5	3.0	2	15
1XQ5	OXYGEN STORAGE/TRANSPORT	1.5	3.0	2	7
1XQ5	OXYGEN STORAGE/TRANSPORT	1.3	2.6	2	19
1XQ5	OXYGEN STORAGE/TRANSPORT	1.8	5.3	3	16
1XQS	CHAPERONE	1.3	2.5	2	18
1XQS	CHAPERONE	1.9	5.6	3	20
1XQS	CHAPERONE	1.4	2.7	2	20
1XQS	CHAPERONE	1.5	2.9	2	18
1XTG	TOXIN	1.6	3.1	2	13
1XTG	TOXIN	1.1	3.2	3	15
1XTG	TOXIN	1.8	7.2	4	20
1XV9	DNA BINDING PROTEIN	1.7	3.4	2	23
1XV9	DNA BINDING PROTEIN	1.3	2.5	2	18
1XV9	DNA BINDING PROTEIN	1.2	3.6	3	29
1XV9	DNA BINDING PROTEIN	1.2	2.3	2	10
1XZP	HYDROLASE	1.5	3.0	2	12
1XZP	HYDROLASE	1.8	3.6	2	14
1Y74	TRANSPORT PROTEIN	1.4	2.7	2	20
1Y76	TRANSPORT PROTEIN	1.2	3.5	3	20
1Y8R	LIGASE	1.2	3.7	3	20
1Y8R	LIGASE	1.3	2.6	2	14
1Y8R	LIGASE	1.9	3.7	2	20
1Y8R	LIGASE	1.7	3.4	2	14
1Y8R	LIGASE	1.9	3.7	2	21
1Y8R	LIGASE	1.4	2.8	2	14
1Y8R	LIGASE	1.8	3.6	2	21
1Y8X	LIGASE	1.5	3.0	2	6
1YD8	PROTEIN TRANSPORT, CHROMOSOMAL PROTEIN	1.2	2.4	2	25
1YD8	PROTEIN TRANSPORT, CHROMOSOMAL PROTEIN	1.6	3.1	2	25
1YDI	CELL ADHESION, STRUCTURAL PROTEIN	1.5	4.4	3	25
1YDI	CELL ADHESION, STRUCTURAL PROTEIN	1.1	3.4	3	49
1YKE	GENE REGULATION	1.4	4.2	3	22
1YKE	GENE REGULATION	1.6	6.2	4	39
1YKE	GENE REGULATION	1.9	5.7	3	24
1YKE	GENE REGULATION	1.3	5.0	4	42
1YKE	GENE REGULATION	1.5	3.0	2	16
1YKE	GENE REGULATION	1.7	5.0	3	22
1YKE	GENE REGULATION	1.8	10.7	6	39
1YKE	GENE REGULATION	1.0	2.0	2	10
1YOK	TRANSCRIPTION	1.4	2.7	2	22
1YOV	SIGNALING PROTEIN	1.2	4.8	4	21

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
1XFU	522	536
1XFU	81	93
1XFU	715	737
1XFU	138	147
1XFU	660	672
1XFU	121	129
1XG2	97	118
1XIU	268	291
1XL3	5	17
1XLS	386	408
1XLS	318	342
1XLS	743	749
1XLS	743	749
1XLS	351	357
1XLS	743	751
1XLS	743	751
1XOU	35	47
1XOU	165	176
1XOU	179	189
1XOU	66	84
1XOU	3	31
1XPK	112	127
1XPK	113	127
1XQ5	36	42
1XQ5	96	114
1XQ5	20	35
1XQS	244	261
1XQS	230	249
1XQS	230	249
1XQS	257	274
1XTG	102	114
1XTG	335	349
1XTG	148	167
1XV9	308	330
1XV9	236	253
1XV9	414	442
1XV9	294	303
1XZP	135	146
1XZP	85	98
1Y74	54	73
1Y76	45	64
1Y8R	300	319
1Y8R	46	59
1Y8R	388	407
1Y8R	27	40
1Y8R	300	320
1Y8R	46	59
1Y8R	388	408
1Y8X	398	403
1YD8	210	234
1YD8	210	234
1YDI	41	65
1YDI	102	150
1YKE	143	164
1YKE	166	204
1YKE	112	135
1YKE	87	128
1YKE	4	19
1YKE	141	162
1YKE	165	203
1YKE	97	106
1YOK	341	362
1YOV	491	511

A. PDB CODE	L. HELIX SEQUENCE
1XFU	SLEKQKGVTNLLIKY
1XFU	SEEEIREAFRVFD
1XFU	EKKRKISIFRGIQAYNEIENVLK
1XFU	YEEFVQMMTA
1XFU	SAEFIKNLSSIRR
1XFU	VDQMIREAD
1XG2	YNSLNIYASAAFDGAGTCEDSF
1XIU	LEDQVILLRAGWNELLIAGFSHRS
1XL3	LSEFMGDIVALVD
1XLS	PAEVEALREKVYASLEAYCKHKY
1XLS	LYAKLMGLLADLRSINNAYSYELQR
1XLS	ALLRYLL
1XLS	ALLRYLL
1XLS	PLLGEIC
1XLS	ALLRYLLDK
1XLS	ALLRYLLDK
1XOU	LFNKLGVFQAAIL
1XOU	NTLNLLTSARSD
1XOU	SLQYRTISGIS
1XOU	EERKLYDSALSKIEKLIET
1XOU	IVSQTRNKELLDKKIRSEIEAIKKIIAEF
1XPK	YAATPAIQLAKDYLAT
1XPK	AATPAIQLAKDYLAT
1XQ5	PWTQRYF
1XQ5	PANFKILSHCILVLLAVKF
1XQ5	YEAVGGATLARCLIVY
1XQS	QKLKVKSAFLLQNLLVGH
1XQS	GEDFDNRLVNHFVEEFKRKH
1XQS	GEDFDNRLVNHFVEEFKRKH
1XQS	KRAVRRLRTACERAKRTL
1XTG	DLGRMLLTSIVRG
1XTG	KLKFDKLYKMLTEIY
1XTG	ENLEQVSGIIGNLRHMALDM
1XV9	LYAKLLGLLAELRSINEAYGYQI
1XV9	VEFLELLFHFHGTLRKLQ
1XV9	RFAKLLLRLPALRSIGLKCLEHLFFFKLI
1XV9	LDDQVILLRA
1XZP	ETSLKLSLRNLK
1XZP	PLVVKKLLDLFLKS
1Y74	RFCSAIREVYEQLYDTLDIT
1Y76	PLFNQILTLQQSIKQLKGQL
1Y8R	APVCAVVGGILAQEIVKALS
1Y8R	GLGAEIAKNLILAG
1Y8R	ATTNAVIAGLIVLEGLKILS
1Y8R	GIGCELLKNLVLTG
1Y8R	APVCAVVGGILAQEIVKALSQ
1Y8R	GLGAEIAKNLILAG
1Y8R	ATTNAVIAGLIVLEGLKILSG
1Y8X	TSIEER
1YD8	KVTKRLHTLEEVNNNVRLLSEMLLH
1YD8	KVTKRLHTLEEVNNNVRLLSEMLLH
1YDI	TAPVAAVQAAVSNLVRVGKETVQTT
1YDI	VPARDYLIDGSRGILSGTSDLLLTFDEAEVRKIIRVCKGILEYLTVAEV
1YKE	MYERKVENIRTILVNIHHLLNE
1YKE	RPHQSRESLIMLLEEQLEYKRGEIREIEQVCKQVHDKLT
1YKE	YQYKIQELRKLLKSLLLNYLELIG
1YKE	AEEQLRKIDMLQKKLVEVEDEKIEAIKKKEKLLRHVDSLIED
1YKE	RLTQLQICLDQMTEQF
1YKE	PDMYERKVENIRTILVNIHHLL
1YKE	YRPHQSRESLIMLLEEQLEYKRGEIREIEQVCKQVHDKL
1YKE	LQKKLVEVED
1YOK	TFGLMCKMADQTLFSIVEWARS
1YOV	HTIAAFLGGAAAQEVIKIITK

A. PDB CODE	M. RESOLUTION
1XFU	3.35
1XFU	3.35
1XFU	3.35
1XFU	3.35
1XFU	3.35
1XFU	3.35
1XG2	1.9
1XIU	2.5
1XL3	2.2
1XLS	2.96
1XLS	2.96
1XLS	2.96
1XLS	2.96
1XLS	2.96
1XLS	2.96
1XLS	2.96
1XOU	2.8
1XOU	2.8
1XOU	2.8
1XOU	2.8
1XOU	2.8
1XPK	2
1XPK	2
1XQ5	1.9
1XQ5	1.9
1XQ5	1.9
1XQS	2.9
1XQS	2.9
1XQS	2.9
1XQS	2.9
1XTG	2.1
1XTG	2.1
1XTG	2.1
1XV9	2.7
1XV9	2.7
1XV9	2.7
1XV9	2.7
1XZP	2.3
1XZP	2.3
1Y74	NOT APP
1Y76	NOT APP
1Y8R	2.75
1Y8R	2.75
1Y8R	2.75
1Y8R	2.75
1Y8R	2.75
1Y8R	2.75
1Y8R	2.75
1Y8X	2.4
1YD8	2.8
1YD8	2.8
1YDI	1.8
1YDI	1.8
1YKE	3.3
1YKE	3.3
1YKE	3.3
1YKE	3.3
1YKE	3.3
1YKE	3.3
1YKE	3.3
1YKE	3.3
1YOK	2.5
1YOV	2.6

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1YOV	A B	A	INSIGHTS INTO THE UBIQUITIN TRANSFER CASCADE FROM THE REFINED STRUCTURE OF THE ACTIVAT
1YOV	A B	A	INSIGHTS INTO THE UBIQUITIN TRANSFER CASCADE FROM THE REFINED STRUCTURE OF THE ACTIVAT
1YOV	A B	B	INSIGHTS INTO THE UBIQUITIN TRANSFER CASCADE FROM THE REFINED STRUCTURE OF THE ACTIVAT
1YOV	A B	B	INSIGHTS INTO THE UBIQUITIN TRANSFER CASCADE FROM THE REFINED STRUCTURE OF THE ACTIVAT
1YOV	C D	C	INSIGHTS INTO THE UBIQUITIN TRANSFER CASCADE FROM THE REFINED STRUCTURE OF THE ACTIVAT
1YOV	C D	C	INSIGHTS INTO THE UBIQUITIN TRANSFER CASCADE FROM THE REFINED STRUCTURE OF THE ACTIVAT
1YOV	C D	C	INSIGHTS INTO THE UBIQUITIN TRANSFER CASCADE FROM THE REFINED STRUCTURE OF THE ACTIVAT
1YOV	C D	D	INSIGHTS INTO THE UBIQUITIN TRANSFER CASCADE FROM THE REFINED STRUCTURE OF THE ACTIVAT
1YOV	C D	D	INSIGHTS INTO THE UBIQUITIN TRANSFER CASCADE FROM THE REFINED STRUCTURE OF THE ACTIVAT
1YQ3	A B	A	AVIAN RESPIRATORY COMPLEX II WITH OXALOACETATE AND UBIQUINONE
1YQ3	B D	B	AVIAN RESPIRATORY COMPLEX II WITH OXALOACETATE AND UBIQUINONE
1YQ3	C D	C	AVIAN RESPIRATORY COMPLEX II WITH OXALOACETATE AND UBIQUINONE
1YQ3	C D	C	AVIAN RESPIRATORY COMPLEX II WITH OXALOACETATE AND UBIQUINONE
1YQ3	C D	D	AVIAN RESPIRATORY COMPLEX II WITH OXALOACETATE AND UBIQUINONE
1YQ3	C D	D	AVIAN RESPIRATORY COMPLEX II WITH OXALOACETATE AND UBIQUINONE
1YR5	A B	B	1.7-A STRUCTURE OF CALMODULIN BOUND TO A PEPTIDE FROM DAP KINASE
1YUC	A C	A	HUMAN NUCLEAR RECEPTOR LIVER RECEPTOR HOMOLOGUE-1, LRH-1, BOUND TO PHOSPHOLIPID AND
1YUC	A C	C	HUMAN NUCLEAR RECEPTOR LIVER RECEPTOR HOMOLOGUE-1, LRH-1, BOUND TO PHOSPHOLIPID AND
1YUC	B D	B	HUMAN NUCLEAR RECEPTOR LIVER RECEPTOR HOMOLOGUE-1, LRH-1, BOUND TO PHOSPHOLIPID AND
1YUC	B D	D	HUMAN NUCLEAR RECEPTOR LIVER RECEPTOR HOMOLOGUE-1, LRH-1, BOUND TO PHOSPHOLIPID AND
1Z00	A B	A	SOLUTION STRUCTURE OF THE C-TERMINAL DOMAIN OF ERCC1 COMPLEXED WITH THE C-TERMINAL D
1Z00	A B	A	SOLUTION STRUCTURE OF THE C-TERMINAL DOMAIN OF ERCC1 COMPLEXED WITH THE C-TERMINAL D
1Z0J	A B	B	STRUCTURE OF GTP-BOUND RAB22Q64L GTPASE IN COMPLEX WITH THE MINIMAL RAB BINDING DOMA
1Z0J	A B	B	STRUCTURE OF GTP-BOUND RAB22Q64L GTPASE IN COMPLEX WITH THE MINIMAL RAB BINDING DOMA
1Z0K	A B	B	STRUCTURE OF GTP-BOUND RAB4Q67L GTPASE IN COMPLEX WITH THE CENTRAL RAB BINDING DOMAI
1Z0K	C D	D	STRUCTURE OF GTP-BOUND RAB4Q67L GTPASE IN COMPLEX WITH THE CENTRAL RAB BINDING DOMAI
1Z2C	A B	A	CRYSTAL STRUCTURE OF MDIA1 GBD-FH3 IN COMPLEX WITH RHOC- GMPPNP
1Z2C	A B	B	CRYSTAL STRUCTURE OF MDIA1 GBD-FH3 IN COMPLEX WITH RHOC- GMPPNP
1Z2C	C D	C	CRYSTAL STRUCTURE OF MDIA1 GBD-FH3 IN COMPLEX WITH RHOC- GMPPNP
1Z5S	A C	A	CRYSTAL STRUCTURE OF A COMPLEX BETWEEN UBC9, SUMO-1, RANGAP1 AND NUP358/RANBP2
1Z5S	A D	A	CRYSTAL STRUCTURE OF A COMPLEX BETWEEN UBC9, SUMO-1, RANGAP1 AND NUP358/RANBP2
1Z5X	U E	E	HEMIPTERAN ECDYSONE RECEPTOR LIGAND-BINDING DOMAIN COMPLEXED WITH PONASTERONE A
1Z5X	U E	U	HEMIPTERAN ECDYSONE RECEPTOR LIGAND-BINDING DOMAIN COMPLEXED WITH PONASTERONE A
1Z7M	B G	G	ATP PHOSPHORIBOSYL TRANSFERASE (HISZG ATP-PRTASE) FROM LACTOCOCCUS LACTIS
1Z8U	A B	A	CRYSTAL STRUCTURE OF OXIDIZED ALPHA HEMOGLOBIN BOUND TO AHSP
1Z8U	A B	B	CRYSTAL STRUCTURE OF OXIDIZED ALPHA HEMOGLOBIN BOUND TO AHSP
1Z92	A B	A	STRUCTURE OF INTERLEUKIN-2 WITH ITS ALPHA RECEPTOR
1ZAV	A U	A	RIBOSOMAL PROTEIN L10-L12(NTD) COMPLEX, SPACE GROUP P21
1ZAV	A U	U	RIBOSOMAL PROTEIN L10-L12(NTD) COMPLEX, SPACE GROUP P21
1ZAV	A V	A	RIBOSOMAL PROTEIN L10-L12(NTD) COMPLEX, SPACE GROUP P21
1ZAV	A V	V	RIBOSOMAL PROTEIN L10-L12(NTD) COMPLEX, SPACE GROUP P21
1ZAV	A W	A	RIBOSOMAL PROTEIN L10-L12(NTD) COMPLEX, SPACE GROUP P21
1ZAV	A W	W	RIBOSOMAL PROTEIN L10-L12(NTD) COMPLEX, SPACE GROUP P21
1ZAV	A X	A	RIBOSOMAL PROTEIN L10-L12(NTD) COMPLEX, SPACE GROUP P21
1ZAV	A X	X	RIBOSOMAL PROTEIN L10-L12(NTD) COMPLEX, SPACE GROUP P21
1ZAV	A Y	A	RIBOSOMAL PROTEIN L10-L12(NTD) COMPLEX, SPACE GROUP P21
1ZAV	A Z	A	RIBOSOMAL PROTEIN L10-L12(NTD) COMPLEX, SPACE GROUP P21
1ZAV	A Z	Z	RIBOSOMAL PROTEIN L10-L12(NTD) COMPLEX, SPACE GROUP P21
1ZC4	C B	B	CRYSTAL STRUCTURE OF THE RAL-BINDING DOMAIN OF EXO84 IN COMPLEX WITH THE ACTIVE RALA
1ZDT	A P	A	THE CRYSTAL STRUCTURE OF HUMAN STEROIDOGENIC FACTOR-1
1ZE3	C D	C	CRYSTAL STRUCTURE OF THE TERNARY COMPLEX OF FIMD (N- TERMINAL DOMAIN) WITH FIMC AND T
1ZE3	C D	D	CRYSTAL STRUCTURE OF THE TERNARY COMPLEX OF FIMD (N- TERMINAL DOMAIN) WITH FIMC AND T
1ZHI	A B	A	COMPLEX OF THE S. CEREVISIAE ORC1 AND SIR1 INTERACTING DOMAINS
1ZM2	A B	A	STRUCTURE OF ADP-RIBOSYLATED EEF2 IN COMPLEX WITH CATALYTIC FRAGMENT OF ETA
1ZNV	A B	A	HOW A HIS-METAL FINGER ENDONUCLEASE COLE7 BINDS AND CLEAVES DNA WITH A TRANSITION MET
1ZOQ	A C	C	IRF3-CBP COMPLEX
1ZOQ	B D	B	IRF3-CBP COMPLEX
1ZOQ	B D	B	IRF3-CBP COMPLEX
1ZOQ	B D	D	IRF3-CBP COMPLEX
1ZUZ	A B	A	CALMODULIN IN COMPLEX WITH A MUTANT PEPTIDE FROM HUMAN DRP- 1 KINASE
1ZVV	A W	W	CRYSTAL STRUCTURE OF A CCPA-CRH-DNA COMPLEX
1ZW3	A B	A	VINCULIN HEAD (0-258) IN COMPLEX WITH THE TALIN ROD RESIDUES 1630-1652
1ZY3	A B	A	STRUCTURAL MODEL OF COMPLEX OF BCL-W PROTEIN WITH BID BH3- PEPTIDE

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
1YOV	SIGNALING PROTEIN	1.6	3.1	2	5
1YOV	SIGNALING PROTEIN	1.1	2.2	2	32
1YOV	SIGNALING PROTEIN	1.6	4.7	3	21
1YOV	SIGNALING PROTEIN	1.6	3.2	2	9
1YOV	SIGNALING PROTEIN	1.6	4.8	3	7
1YOV	SIGNALING PROTEIN	1.4	5.7	4	21
1YOV	SIGNALING PROTEIN	1.4	2.8	2	5
1YOV	SIGNALING PROTEIN	1.5	8.9	6	21
1YOV	SIGNALING PROTEIN	1.6	3.2	2	13
1YQ3	OXIDOREDUCTASE	1.6	3.2	2	15
1YQ3	OXIDOREDUCTASE	1.9	3.7	2	15
1YQ3	OXIDOREDUCTASE	1.6	4.7	3	30
1YQ3	OXIDOREDUCTASE	1.4	4.2	3	30
1YQ3	OXIDOREDUCTASE	1.1	2.1	2	26
1YQ3	OXIDOREDUCTASE	1.8	5.5	3	29
1YR5	METAL BINDING PROTEIN/TRANSFERASE	1.7	11.9	7	16
1YUC	TRANSCRIPTION REGULATION	1.0	3.1	3	22
1YUC	TRANSCRIPTION REGULATION	1.8	7.0	4	9
1YUC	TRANSCRIPTION REGULATION	1.3	2.5	2	11
1YUC	TRANSCRIPTION REGULATION	1.8	3.5	2	9
1Z00	HYDROLASE	1.8	3.6	2	7
1Z00	HYDROLASE	1.3	2.5	2	17
1Z0J	PROTEIN TRANSPORT	1.4	4.3	3	21
1Z0J	PROTEIN TRANSPORT	1.4	4.3	3	22
1Z0K	PROTEIN TRANSPORT	1.5	4.6	3	19
1Z0K	PROTEIN TRANSPORT	1.4	2.8	2	23
1Z2C	SIGNALING PROTEIN	1.6	3.2	2	13
1Z2C	SIGNALING PROTEIN	1.3	2.6	2	9
1Z2C	SIGNALING PROTEIN	1.5	3.0	2	7
1Z5S	LIGASE	1.3	2.6	2	10
1Z5S	LIGASE	1.4	2.8	2	15
1Z5X	HORMONE/GROWTH FACTOR RECEPTOR	1.2	3.5	3	32
1Z5X	HORMONE/GROWTH FACTOR RECEPTOR	1.4	2.7	2	7
1Z7M	TRANSFERASE	1.5	4.4	3	6
1Z8U	ELECTRON TRANSPORT	1.7	6.8	4	19
1Z8U	ELECTRON TRANSPORT	1.3	3.8	3	12
1Z92	IMMUNE SYSTEM	1.3	2.5	2	10
1ZAV	STRUCTURAL PROTEIN	1.6	7.8	5	41
1ZAV	STRUCTURAL PROTEIN	1.9	5.7	3	16
1ZAV	STRUCTURAL PROTEIN	1.5	6.1	4	41
1ZAV	STRUCTURAL PROTEIN	1.5	5.9	4	15
1ZAV	STRUCTURAL PROTEIN	1.3	3.8	3	41
1ZAV	STRUCTURAL PROTEIN	1.3	4.0	3	16
1ZAV	STRUCTURAL PROTEIN	1.3	2.5	2	41
1ZAV	STRUCTURAL PROTEIN	1.4	4.1	3	15
1ZAV	STRUCTURAL PROTEIN	1.6	4.9	3	41
1ZAV	STRUCTURAL PROTEIN	1.4	2.8	2	41
1ZAV	STRUCTURAL PROTEIN	1.2	2.4	2	13
1ZC4	SIGNALING PROTEIN	1.1	2.2	2	24
1ZDT	TRANSCRIPTION	1.3	2.5	2	11
1ZE3	CHAPERONE/STRUCTURAL/MEMBRANE PROTEIN	1.4	2.7	2	5
1ZE3	CHAPERONE/STRUCTURAL/MEMBRANE PROTEIN	1.9	3.8	2	5
1ZHI	TRANSCRIPTION/REPLICATION	1.2	2.4	2	12
1ZM2	BIOSYNTHETIC PROTEIN/TRANSFERASE	1.1	2.2	2	19
1ZNV	HYDROLASE/PROTEIN BINDING	1.4	2.7	2	6
1ZOQ	TRANSCRIPTION/TRANSFERASE	1.7	3.4	2	12
1ZOQ	TRANSCRIPTION/TRANSFERASE	1.3	2.5	2	13
1ZOQ	TRANSCRIPTION/TRANSFERASE	1.9	3.7	2	13
1ZOQ	TRANSCRIPTION/TRANSFERASE	1.4	4.2	3	13
1ZUZ	METAL BINDING PROTEIN/TRANSFERASE	1.9	5.7	3	10
1ZVV	TRANSCRIPTION/DNA	1.4	2.7	2	8
1ZW3	PROTEIN BINDING	1.7	3.4	2	22
1ZY3	APOPTOSIS	1.6	4.8	3	14

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
1YOV	49	53
1YOV	336	367
1YOV	293	313
1YOV	278	286
1YOV	14	20
1YOV	491	511
1YOV	49	53
1YOV	293	313
1YOV	103	115
1YQ3	153	167
1YQ3	231	245
1YQ3	34	63
1YQ3	81	110
1YQ3	5	30
1YQ3	62	90
1YR5	304	319
1YUC	341	362
1YUC	19	27
1YUC	371	381
1YUC	19	27
1Z00	260	266
1Z00	224	240
1Z0J	736	756
1Z0J	759	780
1Z0K	458	476
1Z0K	479	501
1Z2C	95	107
1Z2C	98	106
1Z2C	69	75
1Z5S	131	140
1Z5S	5	19
1Z5X	369	400
1Z5X	449	455
1Z7M	185	190
1Z8U	34	52
1Z8U	119	130
1Z92	63	72
1ZAV	137	177
1ZAV	15	30
1ZAV	137	177
1ZAV	15	29
1ZAV	137	177
1ZAV	15	30
1ZAV	137	177
1ZAV	15	29
1ZAV	137	177
1ZAV	137	177
1ZAV	15	27
1ZC4	258	281
1ZDT	291	301
1ZE3	95	99
1ZE3	20	24
1ZHI	116	127
1ZM2	702	720
1ZNV	51	56
1ZOQ	2094	2105
1ZOQ	322	334
1ZOQ	370	382
1ZOQ	2080	2092
1ZUZ	138	147
1ZVV	47	54
1ZW3	6	27
1ZY3	75	88

A. PDB CODE	L. HELIX SEQUENCE
1YOV	LVLPG
1YOV	SGKYIKLQNVYREKAKKDAAAVGNHVAKLLQS
1YOV	ASTNAVIAAVCATEVFKIATS
1YOV	YRLTQGVVK
1YOV	DRQLRLW
1YOV	HTIAAFLGGAAAQEVIKIITK
1YOV	LVLPG
1YOV	ASTNAVIAAVCATEVFKIATS
1YOV	KAEVAAEFLNDRV
1YQ3	TGHSLLHTLYGRSLR
1YQ3	PGKAIAEIKKMMATY
1YQ3	LPMAMSITHRGTGVALSLGVSLFSLAALLL
1YQ3	PALIYSAKFALVFPLSYHTWNGIRHLVWDM
1YQ3	AASLHWTSERAVSALLLGLLPAAYLY
1YQ3	DTPIKVANTGLYVLSAITFTGLCYFNYYD
1YR5	KWKQSVRLISLCQRLS
1YUC	TFGLMCKMADQTLFSIVEWARS
1YUC	AILYALLSS
1YUC	VDDQMKLLQNC
1YUC	AILYALLSS
1Z00	LEQLIAA
1Z00	MEKLEQDFVSRVTECLT
1Z0J	EELLLQQIDNIKAYIFDAKQC
1Z0J	LDEVEVLTENLRELKHTLAKQK
1Z0K	PLLQQIHNITSFIRQAKAA
1Z0K	MDEVRTLQENLRQLQDEYDQQQT
1Z2C	IPEKWTPEVKHFC
1Z2C	EEKQQPLRE
1Z2C	LRPLSYP
1Z5S	AEAYTIYCQN
1Z5S	ALSRLAQERKAWRKD
1Z5X	ATTIFAKLLSVLTELRTLGNMNSETCFSLKLK
1Z5X	RFAKLLL
1Z7M	KSSFKF
1Z8U	EEDMVTVVEDWMNFYINYY
1Z8U	PAVHASLDKFLA
1Z92	LKPLEEVLNL
1ZAV	KEELYAMLVGRVKAPITGLVFALSGILRNLVYVLNAIKEKK
1ZAV	VSELAELVKKLEDKFG
1ZAV	KEELYAMLVGRVKAPITGLVFALSGILRNLVYVLNAIKEKK
1ZAV	VSELAELVKKLEDKF
1ZAV	KEELYAMLVGRVKAPITGLVFALSGILRNLVYVLNAIKEKK
1ZAV	VSELAELVKKLEDKFG
1ZAV	KEELYAMLVGRVKAPITGLVFALSGILRNLVYVLNAIKEKK
1ZAV	VSELAELVKKLEDKF
1ZAV	KEELYAMLVGRVKAPITGLVFALSGILRNLVYVLNAIKEKK
1ZAV	KEELYAMLVGRVKAPITGLVFALSGILRNLVYVLNAIKEKK
1ZAV	VSELAELVKKLED
1ZC4	AKIKREWLEVLEETKRALSDKRRR
1ZDT	VADQMTLLQNC
1ZE3	KSKLT
1ZE3	SRFEN
1ZHI	LNYYNKLFSETA
1ZM2	GGQIIPTMRRATYAGFLLA
1ZNV	TDLIYY
1ZOQ	PQLMAAFIKQRT
1ZOQ	LGPFIVDLITFTE
1ZOQ	TCLRALVEMARVG
1ZOQ	PQQQQQVLNILKS
1ZUZ	YEEFVQMMTA
1ZVV	IMGLMSLA
1ZW3	RTIESILEPVAQQISHLVIMHE
1ZY3	QQRFTQVSDELFQG

A. PDB CODE	M. RESOLUTION
1YOV	2.6
1YOV	2.6
1YOV	2.6
1YOV	2.6
1YOV	2.6
1YOV	2.6
1YOV	2.6
1YOV	2.6
1YOV	2.6
1YQ3	2.2
1YQ3	2.2
1YQ3	2.2
1YQ3	2.2
1YQ3	2.2
1YQ3	2.2
1YR5	1.7
1YUC	1.9
1YUC	1.9
1YUC	1.9
1YUC	1.9
1Z00	NOT APP
1Z00	NOT APP
1Z0J	1.32
1Z0J	1.32
1Z0K	1.92
1Z0K	1.92
1Z2C	3
1Z2C	3
1Z2C	3
1Z5S	3.01
1Z5S	3.01
1Z5X	3.07
1Z5X	3.07
1Z7M	2.9
1Z8U	2.4
1Z8U	2.4
1Z92	2.8
1ZAV	1.9
1ZAV	1.9
1ZAV	1.9
1ZAV	1.9
1ZAV	1.9
1ZAV	1.9
1ZAV	1.9
1ZAV	1.9
1ZAV	1.9
1ZAV	1.9
1ZAV	1.9
1ZC4	2.5
1ZDT	2.1
1ZE3	1.84
1ZE3	1.84
1ZHI	2.7
1ZM2	3.07
1ZNV	2
1ZOQ	2.37
1ZOQ	2.37
1ZOQ	2.37
1ZOQ	2.37
1ZUZ	1.91
1ZVV	2.98
1ZW3	3.3
1ZY3	NOT APP

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
1ZY3	A B	B	STRUCTURAL MODEL OF COMPLEX OF BCL-W PROTEIN WITH BID BH3- PEPTIDE
2A1J	A B	A	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE C-TERMINAL DOMAINS OF HUMAN XPF AND E
2A1J	A B	A	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE C-TERMINAL DOMAINS OF HUMAN XPF AND E
2A1J	A B	B	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE C-TERMINAL DOMAINS OF HUMAN XPF AND E
2A1J	A B	B	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE C-TERMINAL DOMAINS OF HUMAN XPF AND E
2A1T	D S	D	STRUCTURE OF THE HUMAN MCAD:ETF E165BETAA COMPLEX
2A1T	R S	S	STRUCTURE OF THE HUMAN MCAD:ETF E165BETAA COMPLEX
2A1T	R S	S	STRUCTURE OF THE HUMAN MCAD:ETF E165BETAA COMPLEX
2A3I	A B	A	STRUCTURAL AND BIOCHEMICAL MECHANISMS FOR THE SPECIFICITY OF HORMONE BINDING AND CO
2A3I	A B	B	STRUCTURAL AND BIOCHEMICAL MECHANISMS FOR THE SPECIFICITY OF HORMONE BINDING AND CO
2A40	A C	C	TERNARY COMPLEX OF THE WH2 DOMAIN OF WAVE WITH ACTIN-DNASE I
2A40	D F	F	TERNARY COMPLEX OF THE WH2 DOMAIN OF WAVE WITH ACTIN-DNASE I
2A45	G H	G	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THROMBIN AND THE CENTRAL "E" REGION OF FIBR
2A45	G I	G	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THROMBIN AND THE CENTRAL "E" REGION OF FIBR
2A4J	A B	A	SOLUTION STRUCTURE OF THE C-TERMINAL DOMAIN (T94-Y172) OF THE HUMAN CENTRIN 2 IN COMPL
2A78	A B	B	CRYSTAL STRUCTURE OF THE C3BOT-RALA COMPLEX REVEALS A NOVEL TYPE OF ACTION OF A BACTE
2ACL	A B	A	LIVER X-RECEPTOR ALPHA LIGAND BINDING DOMAIN WITH SB313987
2ACL	A B	A	LIVER X-RECEPTOR ALPHA LIGAND BINDING DOMAIN WITH SB313987
2ACL	A B	B	LIVER X-RECEPTOR ALPHA LIGAND BINDING DOMAIN WITH SB313987
2ACL	A B	B	LIVER X-RECEPTOR ALPHA LIGAND BINDING DOMAIN WITH SB313987
2ACL	C D	C	LIVER X-RECEPTOR ALPHA LIGAND BINDING DOMAIN WITH SB313987
2ACL	C D	D	LIVER X-RECEPTOR ALPHA LIGAND BINDING DOMAIN WITH SB313987
2ACL	C H	C	LIVER X-RECEPTOR ALPHA LIGAND BINDING DOMAIN WITH SB313987
2ACL	E B	E	LIVER X-RECEPTOR ALPHA LIGAND BINDING DOMAIN WITH SB313987
2ACL	E F	E	LIVER X-RECEPTOR ALPHA LIGAND BINDING DOMAIN WITH SB313987
2ACL	G D	G	LIVER X-RECEPTOR ALPHA LIGAND BINDING DOMAIN WITH SB313987
2ACL	G H	H	LIVER X-RECEPTOR ALPHA LIGAND BINDING DOMAIN WITH SB313987
2ACL	G H	H	LIVER X-RECEPTOR ALPHA LIGAND BINDING DOMAIN WITH SB313987
2AGH	A B	A	STRUCTURAL BASIS FOR COOPERATIVE TRANSCRIPTION FACTOR BINDING TO THE CBP COACTIVATOR
2AGH	A B	B	STRUCTURAL BASIS FOR COOPERATIVE TRANSCRIPTION FACTOR BINDING TO THE CBP COACTIVATOR
2AGH	A B	B	STRUCTURAL BASIS FOR COOPERATIVE TRANSCRIPTION FACTOR BINDING TO THE CBP COACTIVATOR
2AQ1	A B	B	CRYSTAL STRUCTURE OF T-CELL RECEPTOR V BETA DOMAIN VARIANT COMPLEXED WITH SUPERANTI
2AST	A B	B	CRYSTAL STRUCTURE OF SKP1-SKP2-CKS1 IN COMPLEX WITH A P27 PEPTIDE
2AST	A B	B	CRYSTAL STRUCTURE OF SKP1-SKP2-CKS1 IN COMPLEX WITH A P27 PEPTIDE
2AUH	A B	A	CRYSTAL STRUCTURE OF THE GRB14 BPS REGION IN COMPLEX WITH THE INSULIN RECEPTOR TYROSIN
2AUS	A B	B	CRYSTAL STRUCTURE OF THE ARCHAEAL BOX H/ACA SRNP NOP10-CBF5 COMPLEX
2AUS	C D	D	CRYSTAL STRUCTURE OF THE ARCHAEAL BOX H/ACA SRNP NOP10-CBF5 COMPLEX
2AVU	B E	B	STRUCTURE OF THE ESCHERICHIA COLI FLHDC COMPLEX, A PROKARYOTIC HETEROMERIC REGULATO
2AVU	B E	E	STRUCTURE OF THE ESCHERICHIA COLI FLHDC COMPLEX, A PROKARYOTIC HETEROMERIC REGULATO
2AVU	D F	D	STRUCTURE OF THE ESCHERICHIA COLI FLHDC COMPLEX, A PROKARYOTIC HETEROMERIC REGULATO
2AYO	A B	A	STRUCTURE OF USP14 BOUND TO UBQUITIN ALDEHYDE
2AZE	A B	A	STRUCTURE OF THE RB C-TERMINAL DOMAIN BOUND TO AN E2F1-DP1 HETERODIMER
2AZE	A B	B	STRUCTURE OF THE RB C-TERMINAL DOMAIN BOUND TO AN E2F1-DP1 HETERODIMER
2B59	A B	B	THE TYPE II COHESIN DOCKERIN COMPLEX
2B5I	A B	A	CYTOKINE RECEPTOR COMPLEX
2B5I	A B	A	CYTOKINE RECEPTOR COMPLEX
2B5L	B D	D	CRYSTAL STRUCTURE OF DDB1 IN COMPLEX WITH SIMIAN VIRUS 5 V PROTEIN
2B5T	A B	A	2.1 ANGSTROM STRUCTURE OF A NONPRODUCTIVE COMPLEX BETWEEN ANTITHROMBIN, SYNTHETIC
2B5T	C D	C	2.1 ANGSTROM STRUCTURE OF A NONPRODUCTIVE COMPLEX BETWEEN ANTITHROMBIN, SYNTHETIC
2B87	A B	A	STRUCTURAL BASIS FOR MOLECULAR RECOGNITION IN AN AFFIBODY:AFFIBODY COMPLEX
2B87	A B	B	STRUCTURAL BASIS FOR MOLECULAR RECOGNITION IN AN AFFIBODY:AFFIBODY COMPLEX
2B9S	A B	A	CRYSTAL STRUCTURE OF HETERODIMERIC L. DONOVANI TOPOISOMERASE I-VANADATE-DNA COMPLE
2B9S	A B	A	CRYSTAL STRUCTURE OF HETERODIMERIC L. DONOVANI TOPOISOMERASE I-VANADATE-DNA COMPLE
2B9S	A B	B	CRYSTAL STRUCTURE OF HETERODIMERIC L. DONOVANI TOPOISOMERASE I-VANADATE-DNA COMPLE
2BBM	A B	A	SOLUTION STRUCTURE OF A CALMODULIN-TARGET PEPTIDE COMPLEX BY MULTIDIMENSIONAL NMR
2BBM	A B	A	SOLUTION STRUCTURE OF A CALMODULIN-TARGET PEPTIDE COMPLEX BY MULTIDIMENSIONAL NMR
2BBM	A B	B	SOLUTION STRUCTURE OF A CALMODULIN-TARGET PEPTIDE COMPLEX BY MULTIDIMENSIONAL NMR
2BCJ	A Q	A	CRYSTAL STRUCTURE OF G PROTEIN-COUPLED RECEPTOR KINASE 2 IN COMPLEX WITH GALPHA-Q AN
2BCJ	A Q	Q	CRYSTAL STRUCTURE OF G PROTEIN-COUPLED RECEPTOR KINASE 2 IN COMPLEX WITH GALPHA-Q AN
2BCJ	B G	B	CRYSTAL STRUCTURE OF G PROTEIN-COUPLED RECEPTOR KINASE 2 IN COMPLEX WITH GALPHA-Q AN
2BCJ	B G	B	CRYSTAL STRUCTURE OF G PROTEIN-COUPLED RECEPTOR KINASE 2 IN COMPLEX WITH GALPHA-Q AN
2BCJ	B G	G	CRYSTAL STRUCTURE OF G PROTEIN-COUPLED RECEPTOR KINASE 2 IN COMPLEX WITH GALPHA-Q AN
2BE6	A D	A	2.0 A CRYSTAL STRUCTURE OF THE CAV1.2 IQ DOMAIN-CA/CAM COMPLEX

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
1ZY3	APOPTOSIS	1.5	2.9	2	16
2A1J	DNA BINDING PROTEIN	1.9	3.8	2	12
2A1J	DNA BINDING PROTEIN	1.7	3.4	2	6
2A1J	DNA BINDING PROTEIN	1.4	2.8	2	20
2A1J	DNA BINDING PROTEIN	1.1	2.1	2	13
2A1T	OXIDOREDUCTASE/ELECTRON TRANSPORT	1.7	6.6	4	21
2A1T	OXIDOREDUCTASE/ELECTRON TRANSPORT	1.4	2.7	2	6
2A1T	OXIDOREDUCTASE/ELECTRON TRANSPORT	1.6	4.8	3	10
2A3I	TRANSFERASE	1.2	2.4	2	11
2A3I	TRANSFERASE	1.8	5.3	3	7
2A40	STRUCTURAL PROTEIN	1.6	4.7	3	12
2A40	STRUCTURAL PROTEIN	1.6	3.1	2	12
2A45	BLOOD CLOTTING	1.7	3.3	2	25
2A45	BLOOD CLOTTING	1.5	3.0	2	25
2A4J	STRUCTURAL PROTEIN	1.4	2.8	2	10
2A78	PROTEIN BINDING/TRANSFERASE	1.6	3.2	2	16
2ACL	TRANSCRIPTION	1.6	3.2	2	23
2ACL	TRANSCRIPTION	1.5	2.9	2	7
2ACL	TRANSCRIPTION	1.6	7.9	5	29
2ACL	TRANSCRIPTION	1.7	3.4	2	23
2ACL	TRANSCRIPTION	1.5	4.5	3	9
2ACL	TRANSCRIPTION	1.4	4.3	3	25
2ACL	TRANSCRIPTION	1.3	2.6	2	11
2ACL	TRANSCRIPTION	1.1	2.2	2	23
2ACL	TRANSCRIPTION	1.1	2.2	2	13
2ACL	TRANSCRIPTION	1.3	2.6	2	23
2ACL	TRANSCRIPTION	1.8	7.3	4	26
2ACL	TRANSCRIPTION	1.6	3.2	2	10
2AGH	TRANSCRIPTION	1.7	8.7	5	19
2AGH	TRANSCRIPTION	1.3	5.1	4	16
2AGH	TRANSCRIPTION	1.5	7.5	5	23
2AQ1	IMMUNE SYSTEM	1.3	2.5	2	9
2AST	CELL CYCLE/LIGASE/PROTEIN TURNOVER	1.3	2.5	2	8
2AST	CELL CYCLE/LIGASE/PROTEIN TURNOVER	1.0	2.0	2	10
2AUH	TRANSFERASE/SIGNALING PROTEIN	1.1	2.1	2	16
2AUS	ISOMERASE/STRUCTURAL PROTEIN	1.7	5.1	3	12
2AUS	ISOMERASE/STRUCTURAL PROTEIN	1.1	2.2	2	13
2AVU	TRANSCRIPTION ACTIVATOR	1.9	7.7	4	22
2AVU	TRANSCRIPTION ACTIVATOR	1.4	2.7	2	16
2AVU	TRANSCRIPTION ACTIVATOR	1.5	7.5	5	21
2AYO	HYDROLASE	1.7	3.4	2	16
2AZE	CELL CYCLE, TRANSCRIPTION	1.7	8.6	5	48
2AZE	CELL CYCLE, TRANSCRIPTION	1.6	11.3	7	35
2B59	HYDROLASE/STRUCTURAL PROTEIN	1.6	6.2	4	10
2B5I	CYTOKINE/CYTOKINE RECEPTOR	1.5	4.6	3	17
2B5I	CYTOKINE/CYTOKINE RECEPTOR	1.8	10.8	6	23
2B5L	PROTEIN BINDING/VIRAL PROTEIN	1.6	3.2	2	11
2B5T	BLOOD CLOTTING	1.5	4.6	3	8
2B5T	BLOOD CLOTTING	1.2	3.6	3	7
2B87	PROTEIN BINDING	1.9	3.8	2	14
2B87	PROTEIN BINDING	1.4	2.8	2	14
2B9S	ISOMERASE/DNA	1.9	5.6	3	19
2B9S	ISOMERASE/DNA	1.5	9.1	6	20
2B9S	ISOMERASE/DNA	1.3	5.2	4	9
2BBM	CALCIUM-BINDING PROTEIN	1.1	2.2	2	12
2BBM	CALCIUM-BINDING PROTEIN	1.7	3.3	2	9
2BBM	CALCIUM-BINDING PROTEIN	1.6	9.6	6	17
2BCJ	TRANSFERASE/HYDROLASE	1.7	8.7	5	22
2BCJ	TRANSFERASE/HYDROLASE	1.2	3.7	3	9
2BCJ	TRANSFERASE/HYDROLASE	1.8	5.4	3	10
2BCJ	TRANSFERASE/HYDROLASE	1.8	3.5	2	14
2BCJ	TRANSFERASE/HYDROLASE	1.8	7.3	4	20
2BE6	MEMBRANE PROTEIN	1.3	2.6	2	12

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
1ZY3	203	218
2A1J	880	891
2A1J	838	843
2A1J	221	240
2A1J	279	291
2A1T	18	38
2A1T	243	248
2A1T	133	142
2A3I	795	805
2A3I	1434	1440
2A40	435	446
2A40	435	446
2A45	48	72
2A45	48	72
2A4J	159	168
2A78	102	117
2ACL	386	408
2ACL	414	420
2ACL	399	427
2ACL	373	395
2ACL	449	457
2ACL	401	425
2ACL	294	304
2ACL	294	316
2ACL	421	433
2ACL	264	286
2ACL	400	425
2ACL	281	290
2AGH	292	310
2AGH	597	612
2AGH	646	668
2AQ1	21	29
2AST	2125	2132
2AST	2149	2158
2AUH	1038	1053
2AUS	42	53
2AUS	42	54
2AVU	85	106
2AVU	91	106
2AVU	85	105
2AYO	199	214
2AZE	199	246
2AZE	202	236
2B59	144	153
2B5I	82	98
2B5I	7	29
2B5L	24	34
2B5T	14	14
2B5T	14	14
2B87	24	37
2B87	6	19
2B9S	406	424
2B9S	433	452
2B9S	215	223
2BBM	118	129
2BBM	138	146
2BBM	5	21
2BCJ	98	119
2BCJ	210	218
2BCJ	3	12
2BCJ	13	26
2BCJ	5	24
2BE6	118	129

A. PDB CODE	L. HELIX SEQUENCE
1ZY3	KNIARHLAQVGDSMDR
2A1J	AANAKQLYDFIH
2A1J	QDFLLK
2A1J	DLLMEKLEQDFVSRVTECLT
2A1J	PQKARRLFDVLHE
2A1T	EQQKEFQATARKFAREEIIPV
2A1T	EDLVAK
2A1T	QTGQMTAGFL
2A3I	LEDQITLIQYS
2A3I	LLQQLLT
2A40	ARSDLLSAIRQG
2A40	ARSDLLSAIRQG
2A45	GCRMKGLIDEVNQDFTNRINKLKNS
2A45	GCRMKGLIDEVNQDFTNRINKLKNS
2A4J	EQEFLRIMKK
2A78	SNLIKQVELLDKSFNK
2ACL	PAEVEALREKVYASLEAYCKHKY
2ACL	RFAKLLL
2ACL	PLMFPRMLMKLVSLRTLSSVHSEQVFALR
2ACL	QLQVERLQHTYVEALHAYVSINH
2ACL	TFLMEMLEA
2ACL	MFPRMLMKLVSLRTLSSVHSEQVFA
2ACL	LDDQVILLRAG
2ACL	LDDQVILLRAGWNELLIASFSHR
2ACL	RLPALRSIGLKCL
2ACL	PVTNICQAADKQLFTLVEWAKRI
2ACL	LMFPRMLMKLVSLRTLSSVHSEQVFA
2ACL	REDQIALLKT
2AGH	EKRIKELELLLMSTENELK
2AGH	QDLRSHLVHKLVQAIF
2AGH	RDEYYHLLAEKIYKIQKELEEKR
2AQ1	MGNMKYLYD
2AST	KRWYRLAS
2AST	PDVTGRLLSQ
2AUH	LRERIEFLNEASVMKG
2AUS	GEYRRRLKRELL
2AUS	GEYRRRLKRELLG
2AVU	DDLQQIHTGIMLSTRLLNDVNQ
2AVU	GVDAVIKAYRLYLEQC
2AVU	DDLQQIHTGIMLSTRLLNDVN
2AYO	ANECWIQMMRVLQQKL
2AZE	AQECQNLEVERQRRLERIKQKQSQLQELILQQIAFKNLVQRNRHAEQQ
2AZE	RLEGLTQDLRQLQESEQQLDHLMNICTTQLRLLSE
2B59	MQDIMIVHKH
2B5I	PRDLISNINVIVLELKG
2B5I	TKKTQLQLEHLLLDLQMILNGIN
2B5L	VEYFTSQQVTG
2B5T	ERELLESY
2B5T	ERELLES
2B87	GVQVKAFIDSLRDD
2B87	NKERVIAIGEIMRL
2B9S	AKVFRTYNASITLDRWFKE
2B9S	TADKLAYFNKANTEVAILCN
2B9S	LGTSKINYI
2BBM	DEEVDEMIREAD
2BBM	YEEFVTMMT
2BBM	KKNFIAVSAANRFKKIS
2BCJ	EEERLVCSREIFDTYIMKELLA
2BCJ	RSERRKWIH
2BCJ	ELDQLRQEAE
2BCJ	QLKNQIRDARKACA
2BCJ	NTASIAQARKLVEQLKMEAN
2BE6	DEEVDEMIREAD

A. PDB CODE	M. RESOLUTION
1ZY3	NOT APP
2A1J	2.7
2A1J	2.7
2A1J	2.7
2A1J	2.7
2A1T	2.8
2A1T	2.8
2A1T	2.8
2A3I	1.95
2A3I	1.95
2A40	1.8
2A40	1.8
2A45	3.65
2A45	3.65
2A4J	NOT APP
2A78	1.81
2ACL	2.8
2ACL	2.8
2ACL	2.8
2ACL	2.8
2ACL	2.8
2ACL	2.8
2ACL	2.8
2ACL	2.8
2ACL	2.8
2ACL	2.8
2ACL	2.8
2ACL	2.8
2AGH	NOT APP
2AGH	NOT APP
2AGH	NOT APP
2AQ1	2.1
2AST	2.3
2AST	2.3
2AUH	3.2
2AUS	2.1
2AUS	2.1
2AVU	3
2AVU	3
2AVU	3
2AYO	3.5
2AZE	2.55
2AZE	2.55
2B59	2.11
2B5I	2.3
2B5I	2.3
2B5L	2.85
2B5T	2.1
2B5T	2.1
2B87	NOT APP
2B87	NOT APP
2B9S	2.27
2B9S	2.27
2B9S	2.27
2BBM	NOT APP
2BBM	NOT APP
2BBM	NOT APP
2BCJ	3.06
2BCJ	3.06
2BCJ	3.06
2BCJ	3.06
2BCJ	3.06
2BE6	2

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
2BE6	A D	A	2.0 A CRYSTAL STRUCTURE OF THE CAV1.2 IQ DOMAIN-CA/CAM COMPLEX
2BE6	B E	B	2.0 A CRYSTAL STRUCTURE OF THE CAV1.2 IQ DOMAIN-CA/CAM COMPLEX
2BE6	C F	C	2.0 A CRYSTAL STRUCTURE OF THE CAV1.2 IQ DOMAIN-CA/CAM COMPLEX
2BE6	C F	C	2.0 A CRYSTAL STRUCTURE OF THE CAV1.2 IQ DOMAIN-CA/CAM COMPLEX
2BEC	A B	B	CRYSTAL STRUCTURE OF CHP2 IN COMPLEX WITH ITS BINDING REGION IN NHE1 AND INSIGHTS INTO
2BEX	B D	D	CRYSTAL STRUCTURE OF PLACENTAL RIBONUCLEASE INHIBITOR IN COMPLEX WITH HUMAN EOSINO
2BEZ	C F	C	STRUCTURE OF A PROTEOLITICALLY RESISTANT CORE FROM THE SEVERE ACUTE RESPIRATORY SYND
2BEZ	C F	F	STRUCTURE OF A PROTEOLITICALLY RESISTANT CORE FROM THE SEVERE ACUTE RESPIRATORY SYND
2BGN	C G	G	HIV-1 TAT PROTEIN DERIVED N-TERMINAL NONAPEPTIDE TRP2-TAT (1-9) BOUND TO THE ACTIVE SITE O
2BKR	A B	A	NEDD8 NEDP1 COMPLEX
2BOV	A B	A	MOLECULAR RECOGNITION OF AN ADP-RIBOSYLATING CLOSTRIDIUM BOTULINUM C3 EXOENZYME BY
2BYK	B C	B	HISTONE FOLD HETERODIMER OF THE CHROMATIN ACCESSIBILITY COMPLEX
2BZW	A B	A	THE CRYSTAL STRUCTURE OF BCL-XL IN COMPLEX WITH FULL-LENGTH BAD
2C0L	A B	A	TPR DOMAIN OF HUMAN PEX5P IN COMPLEX WITH HUMAN MSCP2
2C0L	A B	B	TPR DOMAIN OF HUMAN PEX5P IN COMPLEX WITH HUMAN MSCP2
2C4F	T U	U	CRYSTAL STRUCTURE OF FACTOR VII.STF COMPLEXED WITH PD0297121
2C52	A B	A	STRUCTURAL DIVERSITY IN CBP P160 COMPLEXES
2C5I	T P	T	N-TERMINAL DOMAIN OF TLG1 COMPLEXED WITH N-TERMINUS OF VPS51 IN DISTORTED CONFORMATI
2C9W	A C	A	CRYSTAL STRUCTURE OF SOCS-2 IN COMPLEX WITH ELONGIN-B AND ELONGIN-C AT 1.9A RESOLUTION
2CCI	A B	A	CRYSTAL STRUCTURE OF PHOSPHO-CDK2 CYCLIN A IN COMPLEX WITH A PEPTIDE CONTAINING BOTH
2CCI	A B	B	CRYSTAL STRUCTURE OF PHOSPHO-CDK2 CYCLIN A IN COMPLEX WITH A PEPTIDE CONTAINING BOTH
2CCI	B F	B	CRYSTAL STRUCTURE OF PHOSPHO-CDK2 CYCLIN A IN COMPLEX WITH A PEPTIDE CONTAINING BOTH
2CG9	B Y	B	CRYSTAL STRUCTURE OF AN HSP90-SBA1 CLOSED CHAPERONE COMPLEX
2CLY	A B	A	SUBCOMPLEX OF THE STATOR OF BOVINE MITOCHONDRIAL ATP SYNTHASE
2CLY	A B	B	SUBCOMPLEX OF THE STATOR OF BOVINE MITOCHONDRIAL ATP SYNTHASE
2CLY	A B	B	SUBCOMPLEX OF THE STATOR OF BOVINE MITOCHONDRIAL ATP SYNTHASE
2CLY	A C	A	SUBCOMPLEX OF THE STATOR OF BOVINE MITOCHONDRIAL ATP SYNTHASE
2CLY	D E	D	SUBCOMPLEX OF THE STATOR OF BOVINE MITOCHONDRIAL ATP SYNTHASE
2CLY	D F	D	SUBCOMPLEX OF THE STATOR OF BOVINE MITOCHONDRIAL ATP SYNTHASE
2CNW	B D	B	GDPALF4 COMPLEX OF THE SRP GTPASES FFH AND FTSY
2CNW	C F	F	GDPALF4 COMPLEX OF THE SRP GTPASES FFH AND FTSY
2D1P	A B	A	CRYSTAL STRUCTURE OF HETEROHEXAMERIC TUSBCD PROTEINS, WHICH ARE CRUCIAL FOR THE TRN
2D1P	A C	C	CRYSTAL STRUCTURE OF HETEROHEXAMERIC TUSBCD PROTEINS, WHICH ARE CRUCIAL FOR THE TRN
2D1P	A H	H	CRYSTAL STRUCTURE OF HETEROHEXAMERIC TUSBCD PROTEINS, WHICH ARE CRUCIAL FOR THE TRN
2D1P	H I	H	CRYSTAL STRUCTURE OF HETEROHEXAMERIC TUSBCD PROTEINS, WHICH ARE CRUCIAL FOR THE TRN
2D26	A B	A	ACTIVE SITE DISTORTION IS SUFFICIENT FOR PROTEINASE INHIBIT SECOND CRYSTAL STRUCTURE OF
2D3G	A P	P	DOUBLE SIDED UBIQUITIN BINDING OF HRS-UIM
2D7D	A B	B	STRUCTURAL INSIGHTS INTO THE CRYPTIC DNA DEPENDENT ATP-ASE ACTIVITY OF UVRB
2DF4	A B	A	STRUCTURE OF TRNA-DEPENDENT AMIDOTRANSFERASE GATCAB COMPLEXED WITH MN2+
2DF4	A C	A	STRUCTURE OF TRNA-DEPENDENT AMIDOTRANSFERASE GATCAB COMPLEXED WITH MN2+
2DF4	A C	A	STRUCTURE OF TRNA-DEPENDENT AMIDOTRANSFERASE GATCAB COMPLEXED WITH MN2+
2DF4	A C	C	STRUCTURE OF TRNA-DEPENDENT AMIDOTRANSFERASE GATCAB COMPLEXED WITH MN2+
2DF4	A C	C	STRUCTURE OF TRNA-DEPENDENT AMIDOTRANSFERASE GATCAB COMPLEXED WITH MN2+
2DFK	C D	C	CRYSTAL STRUCTURE OF THE CDC42-COLLYBISTIN II COMPLEX
2DFK	C D	D	CRYSTAL STRUCTURE OF THE CDC42-COLLYBISTIN II COMPLEX
2DSQ	C H	C	STRUCTURAL BASIS FOR THE INHIBITION OF INSULIN-LIKE GROWTH FACTORS BY IGF BINDING PROTE
2DSQ	I G	I	STRUCTURAL BASIS FOR THE INHIBITION OF INSULIN-LIKE GROWTH FACTORS BY IGF BINDING PROTE
2DSR	B I	B	STRUCTURAL BASIS FOR THE INHIBITION OF INSULIN-LIKE GROWTH FACTORS BY IGF BINDING PROTE
2DSR	G I	G	STRUCTURAL BASIS FOR THE INHIBITION OF INSULIN-LIKE GROWTH FACTORS BY IGF BINDING PROTE
2DSR	G I	I	STRUCTURAL BASIS FOR THE INHIBITION OF INSULIN-LIKE GROWTH FACTORS BY IGF BINDING PROTE
2DT7	A B	A	SOLUTION STRUCTURE OF THE SECOND SURP DOMAIN OF HUMAN SPLICING FACTOR SF3A120 IN COMP
2DWZ	C D	D	STRUCTURE OF THE ONCOPROTEIN GANKYRIN IN COMPLEX WITH S6 ATPASE OF THE 26S PROTEASOME
2DYM	A B	A	THE CRYSTAL STRUCTURE OF SACCHAROMYCES CEREVISIAE ATG5- ATG16(1-46) COMPLEX
2DYM	A B	B	THE CRYSTAL STRUCTURE OF SACCHAROMYCES CEREVISIAE ATG5- ATG16(1-46) COMPLEX
2DYM	C D	C	THE CRYSTAL STRUCTURE OF SACCHAROMYCES CEREVISIAE ATG5- ATG16(1-46) COMPLEX
2DYM	E F	E	THE CRYSTAL STRUCTURE OF SACCHAROMYCES CEREVISIAE ATG5- ATG16(1-46) COMPLEX
2DZN	C D	C	CRYSTAL STRUCTURE ANALYSIS OF YEAST NAS6P COMPLEXED WITH THE PROTEASOME SUBUNIT, RPT
2E2D	A C	A	FLEXIBILITY AND VARIABILITY OF TIMP BINDING: X-RAY STRUCTURE OF THE COMPLEX BETWEEN CO
2E32	C D	C	STRUCTURAL BASIS FOR SELECTION OF GLYCOSYLATED SUBSTRATE BY SCFFBS1 UBIQUITIN LIGASE
2E9X	A C	A	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	A D	A	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	A D	A	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	A F	A	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
2BE6	MEMBRANE PROTEIN	1.6	4.9	3	15
2BE6	MEMBRANE PROTEIN	1.2	4.8	4	14
2BE6	MEMBRANE PROTEIN	1.8	5.4	3	12
2BE6	MEMBRANE PROTEIN	1.4	5.7	4	12
2BEC	METAL BINDING PROTEIN/TRANSPORT PROTEIN	1.5	4.6	3	22
2BEX	HYDROLASE/INHIBITOR	1.4	4.3	3	9
2BEZ	VIRAL PROTEIN	1.4	7.0	5	74
2BEZ	VIRAL PROTEIN	1.8	3.5	2	14
2BGN	HYDROLASE	1.7	3.3	2	19
2BKR	PROTEIN-BINDING/HYDROLASE	1.4	2.8	2	9
2BOV	TRANSFERASE	1.4	2.8	2	11
2BYK	DNA-BINDING PROTEIN	1.3	2.5	2	29
2BZW	TRANSCRIPTION	1.4	4.1	3	13
2C0L	TRANSPORT PROTEIN/RECEPTOR	1.8	3.6	2	14
2C0L	TRANSPORT PROTEIN/RECEPTOR	1.8	3.6	2	12
2C4F	HYDROLASE	1.7	3.3	2	5
2C52	TRANSFERASE	1.1	3.3	3	13
2C5I	PROTEIN TRANSPORT	1.8	7.3	4	23
2C9W	TRANSCRIPTION REGULATION	1.9	7.5	4	13
2CCI	CELL CYCLE	1.2	2.3	2	13
2CCI	CELL CYCLE	1.4	4.1	3	17
2CCI	CELL CYCLE	1.9	5.7	3	8
2CG9	CHAPERONE	1.1	3.2	3	23
2CLY	HYDROLASE	1.9	25.9	14	62
2CLY	HYDROLASE	1.1	2.2	2	23
2CLY	HYDROLASE	1.2	2.3	2	10
2CLY	HYDROLASE	1.6	7.9	5	62
2CLY	HYDROLASE	1.9	25.2	13	64
2CLY	HYDROLASE	1.5	5.9	4	64
2CNW	SIGNAL RECOGNITION	1.1	3.4	3	17
2CNW	SIGNAL RECOGNITION	1.7	5.1	3	12
2D1P	TRANSLATION	1.6	3.2	2	11
2D1P	TRANSLATION	1.9	9.4	5	11
2D1P	TRANSLATION	1.2	2.4	2	11
2D1P	TRANSLATION	1.1	2.1	2	11
2D26	HYDROLASE/HYDROLASE INHIBITOR	1.2	2.4	2	5
2D3G	PROTEIN TRANSPORT	1.1	2.2	2	17
2D7D	HYDROLASE/DNA	1.3	4.0	3	19
2DF4	LIGASE	1.3	2.5	2	6
2DF4	LIGASE	1.4	2.7	2	14
2DF4	LIGASE	1.7	12.0	7	26
2DF4	LIGASE	1.5	4.4	3	21
2DF4	LIGASE	1.9	3.8	2	11
2DFK	CELL CYCLE	1.2	2.4	2	29
2DFK	CELL CYCLE	1.5	4.6	3	5
2DSQ	PROTEIN BINDING/HORMONE/GROWTH FACTOR	1.8	3.5	2	12
2DSQ	PROTEIN BINDING/HORMONE/GROWTH FACTOR	1.6	3.1	2	9
2DSR	PROTEIN BINDING/HORMONE/GROWTH FACTOR	1.8	5.5	3	7
2DSR	PROTEIN BINDING/HORMONE/GROWTH FACTOR	1.4	2.7	2	16
2DSR	PROTEIN BINDING/HORMONE/GROWTH FACTOR	1.3	2.6	2	7
2DT7	RNA BINDING PROTEIN	1.9	7.5	4	18
2DWZ	ONCOPROTEIN	1.5	2.9	2	6
2DYM	PROTEIN TURNOVER/PROTEIN TURNOVER	1.3	2.6	2	12
2DYM	PROTEIN TURNOVER/PROTEIN TURNOVER	1.8	12.8	7	18
2DYM	PROTEIN TURNOVER/PROTEIN TURNOVER	1.4	2.8	2	11
2DYM	PROTEIN TURNOVER/PROTEIN TURNOVER	1.6	3.1	2	11
2DZN	PROTEIN BINDING	1.5	3.0	2	8
2E2D	HYDROLASE/HYDROLASE INHIBITOR	1.8	3.6	2	13
2E32	LIGASE	1.6	4.7	3	11
2E9X	REPLICATION	1.9	3.8	2	13
2E9X	REPLICATION	1.7	5.0	3	25
2E9X	REPLICATION	1.2	6.2	5	37
2E9X	REPLICATION	1.6	3.2	2	6

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
2BE6	6	20
2BE6	65	78
2BE6	118	129
2BE6	82	93
2BEC	518	539
2BEX	7	15
2BEZ	899	972
2BEZ	1162	1175
2BGN	126	144
2BKR	56	64
2BOV	139	149
2BYK	31	59
2BZW	119	131
2C0L	556	569
2C0L	28	39
2C4F	102	106
2C52	38	50
2C5I	7	29
2C9W	163	175
2CCI	46	58
2CCI	253	269
2CCI	275	282
2CG9	387	409
2CLY	121	182
2CLY	101	123
2CLY	65	74
2CLY	121	182
2CLY	119	182
2CLY	119	182
2CNW	70	86
2CNW	145	156
2D1P	112	122
2D1P	79	89
2D1P	103	113
2D1P	103	113
2D26	54	58
2D3G	258	274
2D7D	623	641
2DF4	319	324
2DF4	305	318
2DF4	370	395
2DF4	24	44
2DF4	6	16
2DFK	212	240
2DFK	65	69
2DSQ	8	19
2DSQ	43	51
2DSR	68	74
2DSR	152	167
2DSR	43	49
2DT7	80	97
2DWZ	360	365
2DYM	0	11
2DYM	24	41
2DYM	0	10
2DYM	0	10
2DZN	39	46
2E2D	216	228
2E32	56	66
2E9X	4	16
2E9X	26	50
2E9X	58	94
2E9X	100	105

A. PDB CODE	L. HELIX SEQUENCE
2BE6	EEQIAEFKEAFSLFD
2BE6	FPEFLTMMARKMKD
2BE6	DEEVDEMIREAD
2BE6	EEEIREAFRVFD
2BEC	INEEIHTQFLDHLLTGIEDICG
2BEX	WAQWFETQH
2BEZ	YENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAE
2BEZ	QKEIDRLNEVAKNL
2BGN	PDEVVSLVNQGLQEGERDF
2BKR	PEVTQFIKC
2BOV	VEEAKNRAEQW
2BYK	KEARAAIARAASVFAIFVTSSSTALAHKQ
2BZW	AYQSFEQVVNELF
2C0L	IRSRYNLGISCINL
2C0L	KANLVFKEIEKK
2C4F	PYLET
2C52	PQLMAAFIKQRTA
2C5I	PFQQVVKDTKEQLNRINNYITRH
2C9W	LQHLCRLTINKCT
2CCI	STAIREISLLKEL
2CCI	LQLVGTAAMLLASKFEE
2CCI	VAEFVYIT
2CG9	KIMKVIRKNIVKKLIEAFNEIAE
2CLY	RHYLFDVQRNNIAMALEVTYRERLHRVYREVKNRLDYHISVQNMMRQKEQEHMINWVEKRVV
2CLY	AEFLTQSKTRIQEYEKELEKMRN
2CLY	LVDDFEKKFN
2CLY	RHYLFDVQRNNIAMALEVTYRERLHRVYREVKNRLDYHISVQNMMRQKEQEHMINWVEKRVV
2CLY	QKRHYLFDVQRNNIAMALEVTYRERLHRVYREVKNRLDYHISVQNMMRQKEQEHMINWVEKRVV
2CLY	QKRHYLFDVQRNNIAMALEVTYRERLHRVYREVKNRLDYHISVQNMMRQKEQEHMINWVEKRVV
2CNW	PAEVILATVYEALKEAL
2CNW	GGTQLSEWGKRL
2D1P	LGALAEASLTC
2D1P	YTDFVRLTVKH
2D1P	ADALRRELANY
2D1P	ADALRRELANY
2D26	PVSIA
2D3G	QEEEELQLALALSQSEA
2D7D	ERQKVVEQMEHEMKEAAKA
2DF4	SNLSRF
2DF4	GIPSYYVIASSEAS
2DF4	YYDAYYKKSQKVRTLIKNDFDKVFEN
2DF4	ETEEMANTLESILDFAKQNDS
2DF4	REEVEHIANLA
2DFK	SDYRYVAAALAVMRNVTQQINERKRRLEN
2DFK	DRLRP
2DSQ	AELVDALQFVCG
2DSQ	IVDECCFRS
2DSR	PLHTLMH
2DSR	SCQSELHRALERLAAS
2DSR	IVDECCF
2DT7	EFAEFYNRLKQIKEFHRK
2DWZ	LEDYVA
2DYM	HMNDIKQLLWNG
2DYM	MDDLLIRRLTDRNDKEAH
2DYM	HMNDIKQLLWN
2DYM	HMNDIKQLLWN
2DZN	PLHWSVSF
2E2D	LFLVAAHEFGHSL
2E32	EPLLLRVLAEL
2E9X	EKAMELIRELHRA
2E9X	EDGLRQVLEEMKALYEQNQSDVNEA
2E9X	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRWEY
2E9X	NALRFH

A. PDB CODE	M. RESOLUTION
2BE6	2
2BE6	2
2BE6	2
2BE6	2
2BEC	2.7
2BEX	1.99
2BEZ	1.6
2BEZ	1.6
2BGN	3.15
2BKR	1.9
2BOV	2.66
2BYK	2.4
2BZW	2.3
2C0L	2.3
2C0L	2.3
2C4F	1.72
2C52	NOT APP
2C5I	2.3
2C9W	1.9
2CCI	2.7
2CCI	2.7
2CCI	2.7
2CG9	3.1
2CLY	2.8
2CLY	2.8
2CLY	2.8
2CLY	2.8
2CLY	2.8
2CLY	2.8
2CNW	2.39
2CNW	2.39
2D1P	2.15
2D1P	2.15
2D1P	2.15
2D1P	2.15
2D26	3.3
2D3G	1.7
2D7D	2.1
2DF4	3.2
2DF4	3.2
2DF4	3.2
2DF4	3.2
2DF4	3.2
2DFK	2.15
2DFK	2.15
2DSQ	2.8
2DSQ	2.8
2DSR	2.1
2DSR	2.1
2DSR	2.1
2DT7	NOT APP
2DWZ	2.4
2DYM	2.2
2DYM	2.2
2DYM	2.2
2DYM	2.2
2DZN	2.2
2E2D	2
2E32	3.52
2E9X	2.3
2E9X	2.3
2E9X	2.3
2E9X	2.3

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
2E9X	A F	F	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	B C	C	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	B D	B	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	B D	B	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	B D	B	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	B D	D	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	E G	E	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	E H	E	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	E H	E	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	E H	H	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	F G	F	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	F H	F	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2E9X	F H	H	THE CRYSTAL STRUCTURE OF HUMAN GINS CORE COMPLEX
2EFC	A B	A	ARA7-GDP/ATVPS9A
2EFC	C D	D	ARA7-GDP/ATVPS9A
2EHO	A B	A	CRYSTAL STRUCTURE OF HUMAN GINS COMPLEX
2EHO	A B	A	CRYSTAL STRUCTURE OF HUMAN GINS COMPLEX
2EHO	A B	B	CRYSTAL STRUCTURE OF HUMAN GINS COMPLEX
2EHO	A C	A	CRYSTAL STRUCTURE OF HUMAN GINS COMPLEX
2EHO	E F	F	CRYSTAL STRUCTURE OF HUMAN GINS COMPLEX
2EHO	F H	F	CRYSTAL STRUCTURE OF HUMAN GINS COMPLEX
2EHO	G H	G	CRYSTAL STRUCTURE OF HUMAN GINS COMPLEX
2EHO	G H	H	CRYSTAL STRUCTURE OF HUMAN GINS COMPLEX
2EHO	G H	H	CRYSTAL STRUCTURE OF HUMAN GINS COMPLEX
2EHO	I J	I	CRYSTAL STRUCTURE OF HUMAN GINS COMPLEX
2EHO	I J	J	CRYSTAL STRUCTURE OF HUMAN GINS COMPLEX
2EHO	I K	I	CRYSTAL STRUCTURE OF HUMAN GINS COMPLEX
2EHO	I K	K	CRYSTAL STRUCTURE OF HUMAN GINS COMPLEX
2EHO	J L	J	CRYSTAL STRUCTURE OF HUMAN GINS COMPLEX
2EKV	A C	C	THE CRYSTAL STRUCTURE OF RIGOR LIKE SQUID MYOSIN S1 IN THE ABSENCE OF NUCLEOTIDE
2EQB	A C	A	CRYSTAL STRUCTURE OF THE RAB GTPASE SEC4P, THE SEC2P GEF DOMAIN, AND PHOSPHATE COMPLEX
2EQB	A C	C	CRYSTAL STRUCTURE OF THE RAB GTPASE SEC4P, THE SEC2P GEF DOMAIN, AND PHOSPHATE COMPLEX
2ERJ	B D	D	CRYSTAL STRUCTURE OF THE HETEROTRIMERIC INTERLEUKIN-2 RECEPTOR IN COMPLEX WITH INTER
2ERJ	B D	D	CRYSTAL STRUCTURE OF THE HETEROTRIMERIC INTERLEUKIN-2 RECEPTOR IN COMPLEX WITH INTER
2ERJ	E H	H	CRYSTAL STRUCTURE OF THE HETEROTRIMERIC INTERLEUKIN-2 RECEPTOR IN COMPLEX WITH INTER
2ES4	A D	A	CRYSTAL STRUCTURE OF THE BURKHOLDERIA GLUMAE LIPASE- SPECIFIC FOLDASE IN COMPLEX WITH
2ES4	A D	D	CRYSTAL STRUCTURE OF THE BURKHOLDERIA GLUMAE LIPASE- SPECIFIC FOLDASE IN COMPLEX WITH
2ES4	A D	D	CRYSTAL STRUCTURE OF THE BURKHOLDERIA GLUMAE LIPASE- SPECIFIC FOLDASE IN COMPLEX WITH
2ES4	B E	E	CRYSTAL STRUCTURE OF THE BURKHOLDERIA GLUMAE LIPASE- SPECIFIC FOLDASE IN COMPLEX WITH
2EY4	A C	A	CRYSTAL STRUCTURE OF A CBF5-NOP10-GAR1 COMPLEX
2EY4	B D	B	CRYSTAL STRUCTURE OF A CBF5-NOP10-GAR1 COMPLEX
2EY4	B F	B	CRYSTAL STRUCTURE OF A CBF5-NOP10-GAR1 COMPLEX
2EY4	B F	F	CRYSTAL STRUCTURE OF A CBF5-NOP10-GAR1 COMPLEX
2F49	A C	A	CRYSTAL STRUCTURE OF FUS3 IN COMPLEX WITH A STE5 PEPTIDE
2F4O	A B	A	THE MOUSE PNGASE-HR23 COMPLEX REVEALS A COMPLETE REMODULATION OF THE PROTEIN-PROTE
2F4O	A B	B	THE MOUSE PNGASE-HR23 COMPLEX REVEALS A COMPLETE REMODULATION OF THE PROTEIN-PROTE
2F66	A B	A	STRUCTURE OF THE ESCRT-I ENDOSOMAL TRAFFICKING COMPLEX
2F66	A B	B	STRUCTURE OF THE ESCRT-I ENDOSOMAL TRAFFICKING COMPLEX
2F66	A E	A	STRUCTURE OF THE ESCRT-I ENDOSOMAL TRAFFICKING COMPLEX
2F66	A E	E	STRUCTURE OF THE ESCRT-I ENDOSOMAL TRAFFICKING COMPLEX
2F66	D B	B	STRUCTURE OF THE ESCRT-I ENDOSOMAL TRAFFICKING COMPLEX
2F93	A B	A	K INTERMEDIATE STRUCTURE OF SENSORY RHODOPSIN II/TRANSDUCER COMPLEX IN COMBINATION
2F93	A B	B	K INTERMEDIATE STRUCTURE OF SENSORY RHODOPSIN II/TRANSDUCER COMPLEX IN COMBINATION
2F9D	A P	P	2.5 ANGSTROM RESOLUTION STRUCTURE OF THE SPLICEOSOMAL PROTEIN P14 BOUND TO REGION OF
2FCW	A B	A	STRUCTURE OF A COMPLEX BETWEEN THE PAIR OF THE LDL RECEPTOR LIGAND-BINDING MODULES 3-
2FCW	A B	A	STRUCTURE OF A COMPLEX BETWEEN THE PAIR OF THE LDL RECEPTOR LIGAND-BINDING MODULES 3-
2FEP	A S	S	STRUCTURE OF TRUNCATED CCPA IN COMPLEX WITH P-SER-HPR AND SULFATE IONS
2FF6	G A	G	CRYSTAL STRUCTURE OF GELSOLIN DOMAIN 1:CIBOULOT DOMAIN 2 HYBRID IN COMPLEX WITH ACTI
2FHO	A B	A	NMR SOLUTION STRUCTURE OF THE HUMAN SPLICEOSOMAL PROTEIN COMPLEX P14-SF3B155
2FHW	B A	B	SOLUTION STRUCTURE OF HUMAN RELAXIN-3
2FIF	A B	B	CRYSTAL STRUCTURE OF A BOVINE RABEX-5 FRAGMENT COMPLEXED WITH UBIQUITIN
2FK0	A B	B	CRYSTAL STRUCTURE OF A H5N1 INFLUENZA VIRUS HEMAGGLUTININ.
2FK0	C D	D	CRYSTAL STRUCTURE OF A H5N1 INFLUENZA VIRUS HEMAGGLUTININ.

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
2E9X	REPLICATION	1.0	2.0	2	29
2E9X	REPLICATION	1.3	4.0	3	15
2E9X	REPLICATION	1.9	5.7	3	9
2E9X	REPLICATION	1.1	2.2	2	22
2E9X	REPLICATION	1.3	2.6	2	10
2E9X	REPLICATION	1.5	7.5	5	18
2E9X	REPLICATION	1.5	10.4	7	38
2E9X	REPLICATION	1.7	5.0	3	27
2E9X	REPLICATION	1.2	4.7	4	38
2E9X	REPLICATION	1.7	8.4	5	25
2E9X	REPLICATION	1.7	3.3	2	29
2E9X	REPLICATION	1.2	3.6	3	9
2E9X	REPLICATION	1.7	10.4	6	31
2EFC	TRANSPORT PROTEIN	1.6	4.8	3	16
2EFC	TRANSPORT PROTEIN	1.5	2.9	2	8
2EHO	REPLICATION	1.3	2.6	2	13
2EHO	REPLICATION	1.8	5.4	3	14
2EHO	REPLICATION	1.1	2.1	2	35
2EHO	REPLICATION	1.5	3.0	2	7
2EHO	REPLICATION	1.1	3.4	3	37
2EHO	REPLICATION	1.9	11.2	6	37
2EHO	REPLICATION	1.8	3.6	2	10
2EHO	REPLICATION	1.8	7.0	4	19
2EHO	REPLICATION	1.6	4.8	3	18
2EHO	REPLICATION	1.5	4.4	3	14
2EHO	REPLICATION	1.3	2.5	2	12
2EHO	REPLICATION	1.8	5.4	3	14
2EHO	REPLICATION	1.6	4.7	3	10
2EHO	REPLICATION	1.8	3.6	2	35
2EKV	CONTRACTILE PROTEIN	1.5	3.0	2	11
2EQB	ENDOCYTOSIS/EXOCYTOSIS	1.9	3.8	2	6
2EQB	ENDOCYTOSIS/EXOCYTOSIS	1.4	2.7	2	46
2ERJ	IMMUNE SYSTEM/CYTOKINE	1.2	3.5	3	17
2ERJ	IMMUNE SYSTEM/CYTOKINE	1.5	4.5	3	26
2ERJ	IMMUNE SYSTEM/CYTOKINE	1.5	3.0	2	7
2ES4	HYDROLASE	1.8	5.5	3	15
2ES4	HYDROLASE	1.2	3.7	3	10
2ES4	HYDROLASE	1.5	3.0	2	26
2ES4	HYDROLASE	1.2	3.6	3	11
2EY4	ISOMERASE/BIOSYNTHETIC PROTEIN	1.5	3.0	2	12
2EY4	ISOMERASE/BIOSYNTHETIC PROTEIN	1.8	3.5	2	13
2EY4	ISOMERASE/BIOSYNTHETIC PROTEIN	1.8	9.0	5	14
2EY4	ISOMERASE/BIOSYNTHETIC PROTEIN	1.3	2.5	2	13
2F49	TRANSFERASE	1.3	2.6	2	21
2F4O	HYDROLASE	1.9	5.8	3	19
2F4O	HYDROLASE	1.3	2.6	2	12
2F66	TRANSPORT PROTEIN	1.2	2.4	2	29
2F66	TRANSPORT PROTEIN	1.3	2.6	2	29
2F66	TRANSPORT PROTEIN	1.5	4.4	3	29
2F66	TRANSPORT PROTEIN	1.7	3.4	2	10
2F66	TRANSPORT PROTEIN	1.3	2.5	2	10
2F93	MEMBRANE PROTEIN	1.6	4.9	3	33
2F93	MEMBRANE PROTEIN	1.5	2.9	2	22
2F9D	RNA BINDING PROTEIN	1.3	2.6	2	16
2FCW	LIPID TRANSPORT/ENDOCYTOSIS/CHAPERONE	1.9	5.7	3	41
2FCW	LIPID TRANSPORT/ENDOCYTOSIS/CHAPERONE	1.0	2.0	2	41
2FEP	TRANSCRIPTION	1.3	2.6	2	8
2FF6	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN	1.8	7.3	4	18
2FHO	RNA BINDING PROTEIN	1.8	3.5	2	8
2FHW	SIGNALING PROTEIN	1.6	3.2	2	12
2FIF	PROTEIN TURNOVER/ENDOCYTOSIS	1.5	2.9	2	36
2FK0	VIRAL PROTEIN	1.2	3.6	3	52
2FK0	VIRAL PROTEIN	1.4	2.7	2	23

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
2E9X	110	138
2E9X	1131	1145
2E9X	3	11
2E9X	150	171
2E9X	46	55
2E9X	23	40
2E9X	58	95
2E9X	26	52
2E9X	58	95
2E9X	124	148
2E9X	110	138
2E9X	3	11
2E9X	73	103
2EFC	184	199
2EFC	73	80
2EHO	136	148
2EHO	84	97
2EHO	58	92
2EHO	73	79
2EHO	58	94
2EHO	58	94
2EHO	157	166
2EHO	131	149
2EHO	173	190
2EHO	84	97
2EHO	113	124
2EHO	84	97
2EHO	46	55
2EHO	58	92
2EKV	84	94
2EQB	49	54
2EQB	91	136
2ERJ	82	98
2ERJ	4	29
2ERJ	35	41
2ES4	303	317
2ES4	320	329
2ES4	221	246
2ES4	320	330
2EY4	183	194
2EY4	183	195
2EY4	220	233
2EY4	42	54
2F49	111	131
2F4O	424	442
2F4O	283	294
2F66	323	351
2F66	31	59
2F66	323	351
2F66	108	117
2F66	108	117
2F93	190	222
2F93	30	51
2F9D	380	395
2FCW	237	277
2FCW	280	320
2FEP	47	54
2FF6	95	112
2FHO	401	408
2FHW	12	23
2FIF	36	71
2FK0	75	126
2FK0	38	60

TABLE S4

A. PDB CODE	L. HELIX SEQUENCE
2E9X	ADEIRTLVKDMWDTRIAKLRVSADSFVRQ
2E9X	NADISQSLLQTFIGR
2E9X	AAEVEFLAE
2E9X	LMEINTSGTFLTQALNHMYKLR
2E9X	LWLAINLKQR
2E9X	PAELIERLEQAWMNEKFA
2E9X	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRWEYG
2E9X	EDGLRQVLEEMKALYEQNQSDVNEAKS
2E9X	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRWEYG
2E9X	PEELAFAREFMANTESYLKNVALKH
2E9X	ADEIRTLVKDMWDTRIAKLRVSADSFVRQ
2E9X	AAEVEFLAE
2E9X	LKVSIHQMEMERIRYVLSSYLRCRLMKIEKF
2EFC	ADEFLPVLIYVTIKAN
2EFC	HSLAPMYY
2EHO	NTESYLKNVALKH
2EHO	RIRYVLSSYLRCRL
2EHO	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRW
2EHO	LKVSIHQ
2EHO	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRWEY
2EHO	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRWEY
2EHO	GTFLTQALNH
2EHO	NADISQSLLQTFIGRFRRI
2EHO	RGLFQTGQKGLNDFQCWE
2EHO	RIRYVLSSYLRCRL
2EHO	WFNNYKRSLATY
2EHO	RIRYVLSSYLRCRL
2EHO	LWLAINLKQR
2EHO	LIPTIKFRHCSLLRNRRCTVAYLYDRLLRIRALRW
2EKV	ADEFMEAFKTF
2EQB	FITTIG
2EQB	EEEADKLNKEVEDLTASLFDEANNMVADARKEKYAIEILNKRLTEQ
2ERJ	PRDLISNINVIVLELKG
2ERJ	SSSTKKTQLQLEHLLLDLQMILNGIN
2ERJ	KLTRMLT
2ES4	PVAVIRTHVNRLKLQ
2ES4	EAIRAASLDR
2ES4	PDERAQQAALHAQQDAVTKIADLQKA
2ES4	EAIRAASLDRG
2EY4	IRSLIHHIGLAL
2EY4	IRSLIHHIGLALG
2EY4	LHDLVDYYYFWKED
2EY4	GEYRRRWKREVLG
2F49	DDHIQYFIYQTLRAVKVLHGS
2F4O	ESRRKELLQRIIVELVEFI
2F4O	PQFQQMRQIIQQ
2F66	DGLNQLYNLVAQDYALTDTIEALSRMLHR
2F66	SKDKEVIETLSEIYSIVITLDHVEKAYLK
2F66	DGLNQLYNLVAQDYALTDTIEALSRMLHR
2F66	ASNAITRLER
2F66	ASNAITRLER
2F93	PTVDVALIVYLDLVTKVGFGFIALDAAATLRAE
2F93	GALTVLFGAIAYGEVTAAAATG
2F9D	PEQLQAWRWEREIDER
2FCW	DKELEAFREELKHFEAKIEKHNHYQKQLEIAHEKLRHAESV
2FCW	GERVSRSREKHALLEGRTKELGYTVKKHLQDLSGRISRARH
2FEP	IMGVMSLG
2FF6	QDESGAAAIFTVQLDDYL
2FHO	DEELDAMF
2FHW	REFIRAVIFTCG
2FIF	SKCWREEYHKARQKQIQEDWELAERLQREEEEAFAS
2FK0	RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQL
2FK0	KESTQKAIDGVTNKVNSIIDKMN

A. PDB CODE	M. RESOLUTION
2E9X	2.3
2E9X	2.3
2E9X	2.3
2E9X	2.3
2E9X	2.3
2E9X	2.3
2E9X	2.3
2E9X	2.3
2E9X	2.3
2E9X	2.3
2E9X	2.3
2E9X	2.3
2E9X	2.3
2EFC	2.09
2EFC	2.09
2EHO	3
2EHO	3
2EHO	3
2EHO	3
2EHO	3
2EHO	3
2EHO	3
2EHO	3
2EHO	3
2EHO	3
2EHO	3
2EHO	3
2EHO	3
2EHO	3
2EKV	3.4
2EQB	2.7
2EQB	2.7
2ERJ	3
2ERJ	3
2ERJ	3
2ES4	1.85
2ES4	1.85
2ES4	1.85
2ES4	1.85
2EY4	2.11
2EY4	2.11
2EY4	2.11
2EY4	2.11
2F49	1.9
2F4O	2.26
2F4O	2.26
2F66	2.8
2F66	2.8
2F66	2.8
2F66	2.8
2F66	2.8
2F93	2
2F93	2
2F9D	2.5
2FCW	1.26
2FCW	1.26
2FEP	2.45
2FF6	2.05
2FHO	NOT APP
2FHW	NOT APP
2FIF	2.49
2FK0	2.95
2FK0	2.95

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
2FK0	C F	C	CRYSTAL STRUCTURE OF A H5N1 INFLUENZA VIRUS HEMAGGLUTININ.
2FK0	E F	F	CRYSTAL STRUCTURE OF A H5N1 INFLUENZA VIRUS HEMAGGLUTININ.
2FK0	G H	H	CRYSTAL STRUCTURE OF A H5N1 INFLUENZA VIRUS HEMAGGLUTININ.
2FK0	I J	J	CRYSTAL STRUCTURE OF A H5N1 INFLUENZA VIRUS HEMAGGLUTININ.
2FK0	K L	L	CRYSTAL STRUCTURE OF A H5N1 INFLUENZA VIRUS HEMAGGLUTININ.
2FKW	A B	B	STRUCTURE OF LH2 FROM RPS. ACIDOPHILA CRYSTALLIZED IN LIPIDIC MESOPHASES
2FKW	E F	F	STRUCTURE OF LH2 FROM RPS. ACIDOPHILA CRYSTALLIZED IN LIPIDIC MESOPHASES
2FKW	O P	P	STRUCTURE OF LH2 FROM RPS. ACIDOPHILA CRYSTALLIZED IN LIPIDIC MESOPHASES
2FKW	R S	S	STRUCTURE OF LH2 FROM RPS. ACIDOPHILA CRYSTALLIZED IN LIPIDIC MESOPHASES
2FM8	B C	B	CRYSTAL STRUCTURE OF THE SALMONELLA SECRETION CHAPERONE INVB IN COMPLEX WITH SIPA
2FNJ	B C	C	CRYSTAL STRUCTURE OF A B30.2/SPRY DOMAIN-CONTAINING PROTEIN GUSTAVUS IN COMPLEX WITH E
2FO1	A D	D	CRYSTAL STRUCTURE OF THE CSL-NOTCH-MASTERMIND TERNARY COMPLEX BOUND TO DNA
2FOI	A C	A	SYNTHESIS, BIOLOGICAL ACTIVITY, AND X-RAY CRYSTAL STRUCTURAL ANALYSIS OF DIARYL ETHER I
2FOI	A C	C	SYNTHESIS, BIOLOGICAL ACTIVITY, AND X-RAY CRYSTAL STRUCTURAL ANALYSIS OF DIARYL ETHER I
2FRV	A B	A	CRYSTAL STRUCTURE OF THE OXIDIZED FORM OF NI-FE HYDROGENASE
2FRV	A B	B	CRYSTAL STRUCTURE OF THE OXIDIZED FORM OF NI-FE HYDROGENASE
2FRV	A B	B	CRYSTAL STRUCTURE OF THE OXIDIZED FORM OF NI-FE HYDROGENASE
2FRV	C D	C	CRYSTAL STRUCTURE OF THE OXIDIZED FORM OF NI-FE HYDROGENASE
2FRV	C D	D	CRYSTAL STRUCTURE OF THE OXIDIZED FORM OF NI-FE HYDROGENASE
2FRV	E F	E	CRYSTAL STRUCTURE OF THE OXIDIZED FORM OF NI-FE HYDROGENASE
2FRV	E F	F	CRYSTAL STRUCTURE OF THE OXIDIZED FORM OF NI-FE HYDROGENASE
2FRV	G H	G	CRYSTAL STRUCTURE OF THE OXIDIZED FORM OF NI-FE HYDROGENASE
2FRV	G H	H	CRYSTAL STRUCTURE OF THE OXIDIZED FORM OF NI-FE HYDROGENASE
2FRV	I J	I	CRYSTAL STRUCTURE OF THE OXIDIZED FORM OF NI-FE HYDROGENASE
2FRV	I J	J	CRYSTAL STRUCTURE OF THE OXIDIZED FORM OF NI-FE HYDROGENASE
2FRV	S L	L	CRYSTAL STRUCTURE OF THE OXIDIZED FORM OF NI-FE HYDROGENASE
2FRV	S L	S	CRYSTAL STRUCTURE OF THE OXIDIZED FORM OF NI-FE HYDROGENASE
2FTK	B F	B	BERYLLOFLOURIDE SPO0F COMPLEX WITH SPO0B
2FUG	4 5	5	CRYSTAL STRUCTURE OF THE HYDROPHILIC DOMAIN OF RESPIRATORY COMPLEX I FROM THERMUS T
2FUG	4 9	4	CRYSTAL STRUCTURE OF THE HYDROPHILIC DOMAIN OF RESPIRATORY COMPLEX I FROM THERMUS T
2FUG	9 7	7	CRYSTAL STRUCTURE OF THE HYDROPHILIC DOMAIN OF RESPIRATORY COMPLEX I FROM THERMUS T
2FUG	A B	B	CRYSTAL STRUCTURE OF THE HYDROPHILIC DOMAIN OF RESPIRATORY COMPLEX I FROM THERMUS T
2FUG	A C	A	CRYSTAL STRUCTURE OF THE HYDROPHILIC DOMAIN OF RESPIRATORY COMPLEX I FROM THERMUS T
2FUG	D E	E	CRYSTAL STRUCTURE OF THE HYDROPHILIC DOMAIN OF RESPIRATORY COMPLEX I FROM THERMUS T
2FUG	S U	S	CRYSTAL STRUCTURE OF THE HYDROPHILIC DOMAIN OF RESPIRATORY COMPLEX I FROM THERMUS T
2FUG	T U	T	CRYSTAL STRUCTURE OF THE HYDROPHILIC DOMAIN OF RESPIRATORY COMPLEX I FROM THERMUS T
2FUG	U V	V	CRYSTAL STRUCTURE OF THE HYDROPHILIC DOMAIN OF RESPIRATORY COMPLEX I FROM THERMUS T
2FV4	A B	A	NMR SOLUTION STRUCTURE OF THE YEAST KINETOCHORE SPC24/SPC25 GLOBULAR DOMAIN
2FV4	A B	B	NMR SOLUTION STRUCTURE OF THE YEAST KINETOCHORE SPC24/SPC25 GLOBULAR DOMAIN
2G2U	A B	A	CRYSTAL STRUCTURE OF THE SHV-1 BETA-LACTAMASE/BETA- LACTAMASE INHIBITOR PROTEIN (BLIP)
2G38	A B	B	A PE/PPE PROTEIN COMPLEX FROM MYCOBACTERIUM TUBERCULOSIS
2G38	C D	C	A PE/PPE PROTEIN COMPLEX FROM MYCOBACTERIUM TUBERCULOSIS
2G38	C D	D	A PE/PPE PROTEIN COMPLEX FROM MYCOBACTERIUM TUBERCULOSIS
2G38	C D	D	A PE/PPE PROTEIN COMPLEX FROM MYCOBACTERIUM TUBERCULOSIS
2G4D	A B	A	CRYSTAL STRUCTURE OF HUMAN SENP1 MUTANT (C603S) IN COMPLEX WITH SUMO-1
2G4D	C D	C	CRYSTAL STRUCTURE OF HUMAN SENP1 MUTANT (C603S) IN COMPLEX WITH SUMO-1
2G77	A B	A	CRYSTAL STRUCTURE OF GYP1 TBC DOMAIN IN COMPLEX WITH RAB33 GTPASE BOUND TO GDP AND A
2GEZ	A B	A	CRYSTAL STRUCTURE OF POTASSIUM-INDEPENDENT PLANT ASPARAGINASE
2GEZ	A D	D	CRYSTAL STRUCTURE OF POTASSIUM-INDEPENDENT PLANT ASPARAGINASE
2GEZ	C D	C	CRYSTAL STRUCTURE OF POTASSIUM-INDEPENDENT PLANT ASPARAGINASE
2GGM	A C	A	HUMAN CENTRIN 2 XERODERMA PIGMENTOSUM GROUP C PROTEIN COMPLEX
2GGM	B D	B	HUMAN CENTRIN 2 XERODERMA PIGMENTOSUM GROUP C PROTEIN COMPLEX
2GGP	A B	A	SOLUTION STRUCTURE OF THE ATX1-CU(I)-CCC2A COMPLEX
2GL7	A B	A	CRYSTAL STRUCTURE OF A BETA-CATENIN/BCL9/TCF4 COMPLEX
2GL7	A B	B	CRYSTAL STRUCTURE OF A BETA-CATENIN/BCL9/TCF4 COMPLEX
2GL7	A C	C	CRYSTAL STRUCTURE OF A BETA-CATENIN/BCL9/TCF4 COMPLEX
2GL7	D E	D	CRYSTAL STRUCTURE OF A BETA-CATENIN/BCL9/TCF4 COMPLEX
2GL7	D E	D	CRYSTAL STRUCTURE OF A BETA-CATENIN/BCL9/TCF4 COMPLEX
2GL7	D E	D	CRYSTAL STRUCTURE OF A BETA-CATENIN/BCL9/TCF4 COMPLEX
2GL7	D F	F	CRYSTAL STRUCTURE OF A BETA-CATENIN/BCL9/TCF4 COMPLEX
2GOO	A B	A	TERNARY COMPLEX OF BMP-2 BOUND TO BMPR-IA-ECD AND ACTRII-ECD
2GOX	A B	B	CRYSTAL STRUCTURE OF EFB-C / C3D COMPLEX
2GPP	B D	B	ESTROGEN RELATED RECEPTOR-GAMMA LIGAND BINDING DOMAIN COMPLEXED WITH A RIP140 PEPTI

TABLE S4

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
2FK0	VIRAL PROTEIN	1.7	3.4	2	8
2FK0	VIRAL PROTEIN	1.3	4.0	3	23
2FK0	VIRAL PROTEIN	1.1	2.1	2	23
2FK0	VIRAL PROTEIN	1.4	2.8	2	23
2FK0	VIRAL PROTEIN	1.6	4.7	3	23
2FKW	MEMBRANE PROTEIN, PHOTOSYNTHESIS	1.9	3.8	2	32
2FKW	MEMBRANE PROTEIN, PHOTOSYNTHESIS	1.7	3.3	2	32
2FKW	MEMBRANE PROTEIN, PHOTOSYNTHESIS	1.5	2.9	2	32
2FKW	MEMBRANE PROTEIN, PHOTOSYNTHESIS	1.8	3.6	2	32
2FM8	CHAPERONE/CELL INVASION	1.4	2.8	2	22
2FNJ	PROTEIN TRANSPORT/SIGNALING PROTEIN	1.8	7.3	4	17
2FO1	GENE REGULATION/SIGNALLING PROTEIN/DNA	1.7	3.4	2	22
2FOI	OXIDOREDUCTASE	1.3	3.9	3	12
2FOI	OXIDOREDUCTASE	1.8	3.6	2	13
2FRV	OXIDOREDUCTASE	1.2	2.3	2	9
2FRV	OXIDOREDUCTASE	1.2	2.4	2	29
2FRV	OXIDOREDUCTASE	1.6	4.9	3	10
2FRV	OXIDOREDUCTASE	1.2	2.3	2	9
2FRV	OXIDOREDUCTASE	1.2	2.4	2	29
2FRV	OXIDOREDUCTASE	1.2	2.4	2	9
2FRV	OXIDOREDUCTASE	1.2	2.3	2	29
2FRV	OXIDOREDUCTASE	1.2	2.4	2	9
2FRV	OXIDOREDUCTASE	1.2	2.4	2	29
2FRV	OXIDOREDUCTASE	1.7	3.4	2	9
2FRV	OXIDOREDUCTASE	1.2	2.4	2	29
2FRV	OXIDOREDUCTASE	1.2	2.4	2	29
2FRV	OXIDOREDUCTASE	1.2	2.3	2	9
2FTK	TRANSFERASE	1.2	2.4	2	31
2FUG	OXIDOREDUCTASE	1.4	4.3	3	11
2FUG	OXIDOREDUCTASE	1.4	2.7	2	14
2FUG	OXIDOREDUCTASE	1.3	2.6	2	5
2FUG	OXIDOREDUCTASE	1.6	3.2	2	5
2FUG	OXIDOREDUCTASE	1.1	2.1	2	16
2FUG	OXIDOREDUCTASE	1.5	6.0	4	11
2FUG	OXIDOREDUCTASE	1.1	2.2	2	19
2FUG	OXIDOREDUCTASE	1.1	3.2	3	11
2FUG	OXIDOREDUCTASE	1.8	8.8	5	10
2FV4	STRUCTURAL PROTEIN, PROTEIN BINDING	1.2	3.7	3	16
2FV4	STRUCTURAL PROTEIN, PROTEIN BINDING	1.7	3.4	2	13
2G2U	HYDROLASE/HYDROLASE INHIBITOR	1.1	2.2	2	6
2G38	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	1.8	3.6	2	35
2G38	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	1.4	2.7	2	28
2G38	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	1.9	5.6	3	31
2G38	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	1.3	4.0	3	45
2G4D	HYDROLASE/PROTEIN BINDING	1.7	3.4	2	7
2G4D	HYDROLASE/PROTEIN BINDING	1.6	3.1	2	15
2G77	HYDROLASE ACTIVATOR/PROTEIN TRANSPORT	1.9	3.7	2	10
2GEZ	HYDROLASE	1.5	5.9	4	15
2GEZ	HYDROLASE	1.4	2.7	2	7
2GEZ	HYDROLASE	1.9	7.5	4	24
2GGM	CELL CYCLE	1.2	2.3	2	11
2GGM	CELL CYCLE	1.0	2.0	2	11
2GGP	CHAPERONE, METAL TRANSPORT	1.2	2.4	2	12
2GL7	TRANSCRIPTION	1.8	3.5	2	16
2GL7	TRANSCRIPTION	1.8	7.3	4	11
2GL7	TRANSCRIPTION	1.6	4.9	3	22
2GL7	TRANSCRIPTION	1.7	3.4	2	17
2GL7	TRANSCRIPTION	1.6	3.1	2	17
2GL7	TRANSCRIPTION	1.1	2.1	2	17
2GL7	TRANSCRIPTION	1.3	2.5	2	14
2GOO	TRANSFERASE	1.4	2.8	2	13
2GOX	CELL ADHESION/TOXIN	1.6	6.4	4	14
2GPP	TRANSCRIPTION	1.5	2.9	2	8

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
2FK0	105	112
2FK0	38	60
2FK0	38	60
2FK0	38	60
2FK0	38	60
2FKW	5	36
2FKW	5	36
2FKW	5	36
2FKW	5	36
2FM8	112	133
2FNJ	67	83
2FO1	85	106
2FOI	111	122
2FOI	368	380
2FRV	19	27
2FRV	186	214
2FRV	54	63
2FRV	19	27
2FRV	186	214
2FRV	19	27
2FRV	186	214
2FRV	19	27
2FRV	186	214
2FRV	19	27
2FRV	186	214
2FRV	186	214
2FRV	19	27
2FTK	215	245
2FUG	115	125
2FUG	151	164
2FUG	38	42
2FUG	86	90
2FUG	381	396
2FUG	115	125
2FUG	357	375
2FUG	57	67
2FUG	324	333
2FV4	206	221
2FV4	200	212
2G2U	107	112
2G38	69	103
2G38	10	37
2G38	22	52
2G38	59	103
2G4D	454	460
2G4D	468	482
2G77	595	604
2GEZ	48	62
2GEZ	246	252
2GEZ	21	44
2GGM	123	133
2GGM	123	133
2GGP	53	64
2GL7	291	306
2GL7	39	49
2GL7	353	374
2GL7	249	265
2GL7	375	391
2GL7	504	520
2GL7	356	369
2GOO	59	71
2GOX	127	140
2GPP	448	455

A. PDB CODE	L. HELIX SEQUENCE
2FK0	YEELKHLL
2FK0	KESTQKAIDGVTNKVNSIIDKMN
2FK0	KESTQKAIDGVTNKVNSIIDKMN
2FK0	KESTQKAIDGVTNKVNSIIDKMN
2FK0	KESTQKAIDGVTNKVNSIIDKMN
2FKW	AEQSEELHKYVIDGTRVFLGLALVAHFLAFSA
2FKW	AEQSEELHKYVIDGTRVFLGLALVAHFLAFSA
2FKW	AEQSEELHKYVIDGTRVFLGLALVAHFLAFSA
2FKW	AEQSEELHKYVIDGTRVFLGLALVAHFLAFSA
2FM8	GEKFSTALNGFYNYLEVFSRSL
2FNJ	SHVLSKVCMYFTYKVRY
2FO1	RPEMIANQRAVTAHLFNRYTED
2FOI	YGWGIAKELSKR
2FOI	FIDYAIEYSEKYA
2FRV	GCSESVLRT
2FRV	AEVDLIATAHYLEALRVQVKAARAMAIFG
2FRV	PRDAQHFTQR
2FRV	GCSESVLRT
2FRV	AEVDLIATAHYLEALRVQVKAARAMAIFG
2FRV	GCSESVLRT
2FRV	AEVDLIATAHYLEALRVQVKAARAMAIFG
2FRV	GCSESVLRT
2FRV	AEVDLIATAHYLEALRVQVKAARAMAIFG
2FRV	GCSESVLRT
2FRV	AEVDLIATAHYLEALRVQVKAARAMAIFG
2FRV	AEVDLIATAHYLEALRVQVKAARAMAIFG
2FRV	GCSESVLRT
2FTK	TALTNELIHLLGHSRHDWMNKLQLIKGNLSL
2FUG	EREVYDLFGIV
2FUG	RERETILDLFEWVT
2FUG	PDFIY
2FUG	LSCKL
2FUG	EKDVENLEALLPLIEG
2FUG	EREVYDLFGIV
2FUG	TPCREGVAGFMVNLFAKIG
2FUG	PTEVMGVASFY
2FUG	VIYHFKHYTE
2FV4	LAAFLVVARDMLLASL
2FV4	DFYKTKYIWERLG
2G2U	PVSEKH
2G38	KPFVRWLTDLCVQLSEVERQIHEIVRAYEWAHHDM
2G38	ALTVAATEVRRIRDRAIQSDAQVAPMTT
2G38	DSMLAAARAWRSLDVEMTAVQRSFNRTLLSL
2G38	PVVMQLMEAAKPFVRWLTDLCVQLSEVERQIHEIVRAYEWAHHDM
2G4D	RKDIQTL
2G4D	DEIINFYMNMLMERS
2G77	FQETITFLQN
2GEZ	PLDVVELVVRELENI
2GEZ	GEEIIRA
2GEZ	PERRKPREEGLRHCLQIGVEALKA
2GGM	FKNLKRVAKEL
2GGM	FKNLKRVAKEL
2GGP	YDFILEKIKKTG
2GL7	VKFLAITTDCLQILAY
2GL7	RDLADVKSSLV
2GL7	QEQLEHRERSLQTLRDIQRMLF
2GL7	DSVLFYAITTLHNLLLH
2GL7	QRLVQNCLWTLRNLSDA
2GL7	WPLIKATVGLIRNLALC
2GL7	LEHRERSLQTLRDI
2GOO	NHAIVQTLVNSVN
2GOX	VSAHRKAQKAVNLV
2GPP	KLFLEMLE

A. PDB CODE	M. RESOLUTION
2FK0	2.95
2FK0	2.95
2FK0	2.95
2FK0	2.95
2FK0	2.95
2FKW	2.45
2FKW	2.45
2FKW	2.45
2FKW	2.45
2FM8	2.2
2FNJ	1.8
2FO1	3.12
2FOI	2.5
2FOI	2.5
2FRV	2.54
2FRV	2.54
2FRV	2.54
2FRV	2.54
2FRV	2.54
2FRV	2.54
2FRV	2.54
2FRV	2.54
2FRV	2.54
2FRV	2.54
2FRV	2.54
2FRV	2.54
2FRV	2.54
2FTK	3.05
2FUG	3.3
2FUG	3.3
2FUG	3.3
2FUG	3.3
2FUG	3.3
2FUG	3.3
2FUG	3.3
2FUG	3.3
2FUG	3.3
2FV4	NOT APP
2FV4	NOT APP
2G2U	1.6
2G38	2.2
2G38	2.2
2G38	2.2
2G38	2.2
2G4D	2.8
2G4D	2.8
2G77	2.26
2GEZ	2.6
2GEZ	2.6
2GEZ	2.6
2GGM	2.35
2GGM	2.35
2GGP	NOT APP
2GL7	2.6
2GL7	2.6
2GL7	2.6
2GL7	2.6
2GL7	2.6
2GL7	2.6
2GL7	2.6
2GOO	2.2
2GOX	2.2
2GPP	2.6

TABLE S4

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
2GPP	B D	B	ESTROGEN RELATED RECEPTOR-GAMMA LIGAND BINDING DOMAIN COMPLEXED WITH A RIP140 PEPTII
2GPP	B D	D	ESTROGEN RELATED RECEPTOR-GAMMA LIGAND BINDING DOMAIN COMPLEXED WITH A RIP140 PEPTII
2GPV	B H	H	ESTROGEN RELATED RECEPTOR-GAMMA LIGAND BINDING DOMAIN COMPLEXED WITH 4-HYDROXY-TA
2GTP	A D	D	CRYSTAL STRUCTURE OF THE HETERODIMERIC COMPLEX OF HUMAN RGS1 AND ACTIVATED GI ALPHA
2GTP	B C	B	CRYSTAL STRUCTURE OF THE HETERODIMERIC COMPLEX OF HUMAN RGS1 AND ACTIVATED GI ALPHA
2GTP	B C	C	CRYSTAL STRUCTURE OF THE HETERODIMERIC COMPLEX OF HUMAN RGS1 AND ACTIVATED GI ALPHA
2GV5	A C	A	CRYSTAL STRUCTURE OF SFI1P/CDC31P COMPLEX
2GV5	B C	B	CRYSTAL STRUCTURE OF SFI1P/CDC31P COMPLEX
2GV5	B C	C	CRYSTAL STRUCTURE OF SFI1P/CDC31P COMPLEX
2GV5	B C	C	CRYSTAL STRUCTURE OF SFI1P/CDC31P COMPLEX
2GV5	D F	D	CRYSTAL STRUCTURE OF SFI1P/CDC31P COMPLEX
2GV5	D F	F	CRYSTAL STRUCTURE OF SFI1P/CDC31P COMPLEX
2GV5	E F	E	CRYSTAL STRUCTURE OF SFI1P/CDC31P COMPLEX
2GV5	E F	F	CRYSTAL STRUCTURE OF SFI1P/CDC31P COMPLEX
2GWF	A B	A	STRUCTURE OF A USP8-NRDP1 COMPLEX
2GWF	A B	B	STRUCTURE OF A USP8-NRDP1 COMPLEX
2GWW	A B	A	HUMAN VINCULIN (HEAD DOMAIN, VH1, RESIDUES 1-258) IN COMPLEX WITH SHIGELLA'S IPAA VINCULI
2GWW	A B	A	HUMAN VINCULIN (HEAD DOMAIN, VH1, RESIDUES 1-258) IN COMPLEX WITH SHIGELLA'S IPAA VINCULI
2GWW	A B	B	HUMAN VINCULIN (HEAD DOMAIN, VH1, RESIDUES 1-258) IN COMPLEX WITH SHIGELLA'S IPAA VINCULI
2GYK	E F	E	CRYSTAL STRUCTURE OF THE COMPLEX OF THE COLICIN E9 DNASE DOMAIN WITH A MUTANT IMMUNI
2GZD	A C	C	CRYSTAL STRUCTURE OF RAB11 IN COMPLEX WITH RAB11-FIP2
2H0D	A B	A	STRUCTURE OF A BMI-1-RING1B POLYCOMB GROUP UBIQUITIN LIGASE COMPLEX
2H0D	A B	A	STRUCTURE OF A BMI-1-RING1B POLYCOMB GROUP UBIQUITIN LIGASE COMPLEX
2H0D	A B	A	STRUCTURE OF A BMI-1-RING1B POLYCOMB GROUP UBIQUITIN LIGASE COMPLEX
2H0D	A B	B	STRUCTURE OF A BMI-1-RING1B POLYCOMB GROUP UBIQUITIN LIGASE COMPLEX
2H1L	B N	B	THE STRUCTURE OF THE ONCOPROTEIN SV40 LARGE T ANTIGEN AND P53 TUMOR SUPPRESSOR COMPLI
2H1L	C O	C	THE STRUCTURE OF THE ONCOPROTEIN SV40 LARGE T ANTIGEN AND P53 TUMOR SUPPRESSOR COMPLI
2H1L	F R	R	THE STRUCTURE OF THE ONCOPROTEIN SV40 LARGE T ANTIGEN AND P53 TUMOR SUPPRESSOR COMPLI
2H1O	A E	E	STRUCTURE OF FITAB BOUND TO IR36 DNA FRAGMENT
2H1O	B F	B	STRUCTURE OF FITAB BOUND TO IR36 DNA FRAGMENT
2H1O	C G	C	STRUCTURE OF FITAB BOUND TO IR36 DNA FRAGMENT
2H4M	A C	A	KARYOPHERIN BETA2/TRANSPORTIN-M9NLS
2H4M	A C	A	KARYOPHERIN BETA2/TRANSPORTIN-M9NLS
2H62	B C	B	CRYSTAL STRUCTURE OF A TERNARY LIGAND-RECEPTOR COMPLEX OF BMP-2
2H7V	A C	A	CO-CRYSTAL STRUCTURE OF YPKA-RAC1
2H7V	B D	B	CO-CRYSTAL STRUCTURE OF YPKA-RAC1
2HL5	A C	A	CRYSTAL STRUCTURE OF THE C-TERMINAL DOMAIN OF HUMAN EB1 IN COMPLEX WITH THE A49M MUT
2HL5	B D	B	CRYSTAL STRUCTURE OF THE C-TERMINAL DOMAIN OF HUMAN EB1 IN COMPLEX WITH THE A49M MUT
2HQW	A B	A	CRYSTAL STRUCTURE OF CA2+/CALMODULIN BOUND TO NMDA RECEPTOR NR1C1 PEPTIDE
2HQW	A B	A	CRYSTAL STRUCTURE OF CA2+/CALMODULIN BOUND TO NMDA RECEPTOR NR1C1 PEPTIDE
2HRK	A B	A	STRUCTURAL BASIS OF YEAST AMINOACYL-TRNA SYNTHETASE COMPLEX FORMATION REVEALED BY
2HWN	A E	A	CRYSTAL STRUCTURE OF RII ALPHA DIMERIZATION/DOCKING DOMAIN OF PKA BOUND TO THE D-AKAP
2HWN	B E	E	CRYSTAL STRUCTURE OF RII ALPHA DIMERIZATION/DOCKING DOMAIN OF PKA BOUND TO THE D-AKAP
2HWN	D F	F	CRYSTAL STRUCTURE OF RII ALPHA DIMERIZATION/DOCKING DOMAIN OF PKA BOUND TO THE D-AKAP
2I2R	A E	E	CRYSTAL STRUCTURE OF THE KCHIP1/KV4.3 T1 COMPLEX
2I2R	B F	F	CRYSTAL STRUCTURE OF THE KCHIP1/KV4.3 T1 COMPLEX
2I2R	B F	F	CRYSTAL STRUCTURE OF THE KCHIP1/KV4.3 T1 COMPLEX
2I2R	C G	G	CRYSTAL STRUCTURE OF THE KCHIP1/KV4.3 T1 COMPLEX
2I2R	D H	H	CRYSTAL STRUCTURE OF THE KCHIP1/KV4.3 T1 COMPLEX
2I2R	J M	M	CRYSTAL STRUCTURE OF THE KCHIP1/KV4.3 T1 COMPLEX
2I2R	L O	O	CRYSTAL STRUCTURE OF THE KCHIP1/KV4.3 T1 COMPLEX
2I2R	L P	P	CRYSTAL STRUCTURE OF THE KCHIP1/KV4.3 T1 COMPLEX
2I3S	C D	D	BUB3 COMPLEX WITH BUB1 GLEBS MOTIF
2I3S	E F	F	BUB3 COMPLEX WITH BUB1 GLEBS MOTIF
2I3T	A B	B	BUB3 COMPLEX WITH MAD3 (BUBR1) GLEBS MOTIF
2I3T	E F	F	BUB3 COMPLEX WITH MAD3 (BUBR1) GLEBS MOTIF
2IBF	A B	A	HUMAN VINCULIN'S HEAD DOMAIN (VH1, RESIDUES 1-258) IN COMPLEX WITH TWO VINCULIN BINDING
2IHB	A B	B	CRYSTAL STRUCTURE OF THE HETERODIMERIC COMPLEX OF HUMAN RGS10 AND ACTIVATED GI ALPH
2IHS	B D	D	CRYSTAL STRUCTURE OF THE B30.2/SPRY DOMAIN OF GUSTAVUS IN COMPLEX WITH A 20-RESIDUE VAS
2IK8	A B	B	CRYSTAL STRUCTURE OF THE HETERODIMERIC COMPLEX OF HUMAN RGS16 AND ACTIVATED GI ALPH
2IK8	C D	D	CRYSTAL STRUCTURE OF THE HETERODIMERIC COMPLEX OF HUMAN RGS16 AND ACTIVATED GI ALPH
2IK8	C D	D	CRYSTAL STRUCTURE OF THE HETERODIMERIC COMPLEX OF HUMAN RGS16 AND ACTIVATED GI ALPH
2IO1	A B	A	CRYSTAL STRUCTURE OF HUMAN SENP2 IN COMPLEX WITH PRESUMO-3

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM,\ HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
2GPP	TRANSCRIPTION	1.9	5.7	3	11
2GPP	TRANSCRIPTION	1.6	6.4	4	8
2GPV	TRANSCRIPTION	1.8	5.4	3	11
2GTP	SIGNALING PROTEIN	1.3	2.6	2	21
2GTP	SIGNALING PROTEIN	1.2	2.4	2	10
2GTP	SIGNALING PROTEIN	1.3	2.6	2	21
2GV5	CELL CYCLE	1.7	3.3	2	13
2GV5	CELL CYCLE	1.1	3.3	3	14
2GV5	CELL CYCLE	1.3	5.2	4	50
2GV5	CELL CYCLE	1.5	5.8	4	16
2GV5	CELL CYCLE	1.4	2.8	2	8
2GV5	CELL CYCLE	1.8	19.6	11	50
2GV5	CELL CYCLE	1.2	2.4	2	14
2GV5	CELL CYCLE	1.9	5.6	3	50
2GWF	HYDROLASE/LIGASE	1.4	2.8	2	9
2GWF	HYDROLASE/LIGASE	1.8	3.5	2	7
2GWW	CELL ADHESION, STRUCTURAL PROTEIN	1.6	3.1	2	20
2GWW	CELL ADHESION, STRUCTURAL PROTEIN	1.3	4.0	3	25
2GWW	CELL ADHESION, STRUCTURAL PROTEIN	1.8	5.5	3	15
2GYK	ANTIBIOTIC/ANTIBIOTIC INHIBITOR	1.8	5.4	3	16
2GZD	PROTEIN TRANSPORT	1.3	3.9	3	19
2H0D	METAL BINDING PROTEIN/LIGASE	1.5	4.5	3	7
2H0D	METAL BINDING PROTEIN/LIGASE	1.4	4.1	3	11
2H0D	METAL BINDING PROTEIN/LIGASE	1.9	5.6	3	16
2H0D	METAL BINDING PROTEIN/LIGASE	1.8	3.5	2	11
2H1L	VIRAL PROTEIN	1.8	3.5	2	14
2H1L	VIRAL PROTEIN	1.8	5.5	3	15
2H1L	VIRAL PROTEIN	1.5	3.0	2	5
2H1O	GENE REGULATION/DNA COMPLEX	1.9	5.6	3	12
2H1O	GENE REGULATION/DNA COMPLEX	1.4	2.7	2	18
2H1O	GENE REGULATION/DNA COMPLEX	1.6	3.2	2	18
2H4M	PROTEIN TRANSPORT	1.9	5.6	3	19
2H4M	PROTEIN TRANSPORT	1.7	3.3	2	19
2H62	HORMONE/GROWTH FACTOR	1.1	2.1	2	13
2H7V	SIGNALING PROTEIN	1.7	6.6	4	9
2H7V	SIGNALING PROTEIN	1.4	5.5	4	10
2HL5	STRUCTURAL PROTEIN	1.9	7.7	4	37
2HL5	STRUCTURAL PROTEIN	1.9	5.6	3	35
2HQW	METAL BINDING PROTEIN	1.7	3.3	2	12
2HQW	METAL BINDING PROTEIN	1.2	2.4	2	12
2HRK	LIGASE/RNA BINDING PROTEIN	1.6	3.1	2	13
2HWN	TRANSFERASE	1.3	3.8	3	16
2HWN	TRANSFERASE	1.4	4.2	3	17
2HWN	TRANSFERASE	1.4	2.7	2	18
2I2R	TRANSPORT PROTEIN	1.0	3.1	3	15
2I2R	TRANSPORT PROTEIN	1.4	2.8	2	12
2I2R	TRANSPORT PROTEIN	1.5	2.9	2	8
2I2R	TRANSPORT PROTEIN	1.2	2.4	2	12
2I2R	TRANSPORT PROTEIN	1.3	2.6	2	12
2I2R	TRANSPORT PROTEIN	1.5	4.6	3	15
2I2R	TRANSPORT PROTEIN	1.9	7.7	4	15
2I2R	TRANSPORT PROTEIN	1.3	3.9	3	12
2I3S	CELL CYCLE	1.5	2.9	2	5
2I3S	CELL CYCLE	1.3	2.6	2	5
2I3T	CELL CYCLE	1.8	7.1	4	8
2I3T	CELL CYCLE	1.3	2.5	2	5
2IBF	CELL ADHESION, STRUCTURAL PROTEIN	1.8	5.4	3	47
2IHB	SIGNALING PROTEIN	1.4	5.6	4	21
2IHS	PEPTIDE BINDING PROTEIN	1.6	3.2	2	6
2IK8	SIGNALING PROTEIN	1.0	3.0	3	13
2IK8	SIGNALING PROTEIN	1.5	2.9	2	21
2IK8	SIGNALING PROTEIN	1.2	2.3	2	13
2IO1	PROTEIN BINDING, HYDROLASE	1.6	3.1	2	10

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
2GPP	294	304
2GPP	379	386
2GPV	1320	1330
2GTP	159	179
2GTP	205	214
2GTP	159	179
2GV5	94	106
2GV5	19	32
2GV5	643	692
2GV5	695	710
2GV5	151	158
2GV5	643	692
2GV5	19	32
2GV5	643	692
2GWF	241	249
2GWF	262	268
2GWW	7	26
2GWW	41	65
2GWW	611	625
2GYK	30	45
2GZD	470	488
2H0D	9	15
2H0D	73	83
2H0D	86	101
2H0D	104	114
2H1L	609	622
2H1L	593	607
2H1L	177	181
2H1O	48	59
2H1O	54	71
2H1O	54	71
2H4M	722	740
2H4M	494	512
2H62	59	71
2H7V	62	70
2H7V	64	73
2HL5	195	231
2HL5	197	231
2HQW	118	129
2HQW	45	56
2HRK	162	174
2HWN	9	24
2HWN	4	20
2HWN	4	21
2I2R	50	64
2I2R	71	82
2I2R	174	181
2I2R	71	82
2I2R	71	82
2I2R	50	64
2I2R	50	64
2I2R	71	82
2I3S	323	327
2I3S	323	327
2I3T	381	388
2I3T	362	366
2IBF	102	148
2IHB	120	140
2IHS	195	200
2IK8	134	146
2IK8	153	173
2IK8	134	146
2IO1	440	449

A. PDB CODE	L. HELIX SEQUENCE
2GPP	LADQMSLLQSA
2GPP	LLLHLLKS
2GPV	LEAIIRKALMG
2GTP	DEAQKVIYTLMEKDSYPRFLK
2GTP	RSERKKWIHC
2GTP	DEAQKVIYTLMEKDSYPRFLK
2GV5	PLDEIKRAFQLFD
2GV5	EEQKQEIYEAFSLF
2GV5	KLNDILHVYEKSKERELQSQLFNAWRNRFCFYTEECNIQAISKRNYQLEK
2GV5	LKKFRERLLEIVKSEE
2GV5	ENEFIAIC
2GV5	KLNDILHVYEKSKERELQSQLFNAWRNRFCFYTEECNIQAISKRNYQLEK
2GV5	EEQKQEIYEAFSLF
2GV5	KLNDILHVYEKSKERELQSQLFNAWRNRFCFYTEECNIQAISKRNYQLEK
2GWF	DDSKDTWKK
2GWF	LETRQMN
2GWW	RTIESILEPVAQQISHLVIM
2GWW	TAPVAAVQAAVSNLVRVGKETVQTT
2GWW	NIYKAAKDVTTSLSK
2GYK	EEELVKLVTHFEEMTE
2GZD	KDTHIRELEDYIDNLLVRV
2H0D	ITELNPH
2H0D	KTLQDIVYKLV
2H0D	LFKNEMKRRRDFYAAH
2H0D	PNFDALISKIY
2H1L	LSVYQKMKFNVAMG
2H1L	QSRIVEWKERLDKEF
2H1L	PHHER
2H1O	LGSMLASIGQEI
2H1O	KKKNVLHERMEQSILPLF
2H1O	KKKNVLHERMEQSILPLF
2H4M	ISVCNNATWAIGEISIQMG
2H4M	KRVQEAACSAFATLEEEAC
2H62	NHAIVQTLVNSVN
2H7V	EDYDRLRPL
2H7V	YDRLRPLSYP
2HL5	ELMQQVNVLKLTVEDLEKERDFYFGKLRNIELICQEN
2HL5	MQQVNVLKLTVEDLEKERDFYFGKLRNIELICQEN
2HQW	DEEVDEMIREAD
2HQW	EAELQDMINEVD
2HRK	VNVSRWYTLLEMD
2HWN	LTELLQGYTVEVLRQQ
2HWN	LAWKIAKMIVSDVMQQC
2HWN	LAWKIAKMIVSDVMQQCK
2I2R	KRELQVLYRGFKNEC
2I2R	EDTFKQIYAQFF
2I2R	HVDVFFQK
2I2R	EDTFKQIYAQFF
2I2R	EDTFKQIYAQFF
2I2R	KRELQVLYRGFKNEC
2I2R	KRELQVLYRGFKNEC
2I2R	EDTFKQIYAQFF
2I3S	FNLIY
2I3S	FNLIY
2I3T	LEEVLAIS
2I3T	FKLIY
2IBF	VPARDYLIDGSRGILSGTSDLLLTFDEAEVRKIIRVCKGILEYLTVA
2IHB	QKLQDQIFNLMKYDSYSRFLK
2IHS	VERKRE
2IK8	HETRELTRMNLQT
2IK8	DAAQGKTRTLMEKDSYPRFLK
2IK8	HETRELTRMNLQT
2IO1	TFFYPKLKSG

A. PDB CODE	M. RESOLUTION
2GPP	2.6
2GPP	2.6
2GPV	2.85
2GTP	2.55
2GTP	2.55
2GTP	2.55
2GV5	3
2GV5	3
2GV5	3
2GV5	3
2GV5	3
2GV5	3
2GV5	3
2GV5	3
2GWF	2.3
2GWF	2.3
2GWW	2.72
2GWW	2.72
2GWW	2.72
2GYK	1.6
2GZD	2.44
2H0D	2.5
2H0D	2.5
2H0D	2.5
2H0D	2.5
2H1L	3.16
2H1L	3.16
2H1L	3.16
2H1O	3
2H1O	3
2H1O	3
2H4M	3.05
2H4M	3.05
2H62	1.85
2H7V	2.6
2H7V	2.6
2HL5	1.93
2HL5	1.93
2HQW	1.9
2HQW	1.9
2HRK	2.05
2HWN	1.6
2HWN	1.6
2HWN	1.6
2I2R	3.35
2I2R	3.35
2I2R	3.35
2I2R	3.35
2I2R	3.35
2I2R	3.35
2I2R	3.35
2I2R	3.35
2I3S	1.9
2I3S	1.9
2I3T	2.8
2I3T	2.8
2IBF	3.2
2IHB	2.71
2IHS	2.2
2IK8	2.71
2IK8	2.71
2IK8	2.71
2IO1	2.6

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
2IO5	A B	B	CRYSTAL STRUCTURE OF THE CIA- HISTONE H3-H4 COMPLEX
2IO5	B C	B	CRYSTAL STRUCTURE OF THE CIA- HISTONE H3-H4 COMPLEX
2IO5	B C	C	CRYSTAL STRUCTURE OF THE CIA- HISTONE H3-H4 COMPLEX
2IO5	B C	C	CRYSTAL STRUCTURE OF THE CIA- HISTONE H3-H4 COMPLEX
2IZV	A C	A	CRYSTAL STRUCTURE OF SOCS-4 IN COMPLEX WITH ELONGIN-B AND ELONGIN-C AT 2.55A RESOLUTION
2IZV	A C	C	CRYSTAL STRUCTURE OF SOCS-4 IN COMPLEX WITH ELONGIN-B AND ELONGIN-C AT 2.55A RESOLUTION
2IZX	A C	C	MOLECULAR BASIS OF AKAP SPECIFICITY FOR PKA REGULATORY SUBUNITS
2IZX	B C	B	MOLECULAR BASIS OF AKAP SPECIFICITY FOR PKA REGULATORY SUBUNITS
2IZX	B C	C	MOLECULAR BASIS OF AKAP SPECIFICITY FOR PKA REGULATORY SUBUNITS
2J0Q	A C	A	THE CRYSTAL STRUCTURE OF THE EXON JUNCTION COMPLEX AT 3.2 A RESOLUTION
2J0Q	A T	A	THE CRYSTAL STRUCTURE OF THE EXON JUNCTION COMPLEX AT 3.2 A RESOLUTION
2J0Q	B D	D	THE CRYSTAL STRUCTURE OF THE EXON JUNCTION COMPLEX AT 3.2 A RESOLUTION
2J0Q	B I	B	THE CRYSTAL STRUCTURE OF THE EXON JUNCTION COMPLEX AT 3.2 A RESOLUTION
2J0Q	B I	B	THE CRYSTAL STRUCTURE OF THE EXON JUNCTION COMPLEX AT 3.2 A RESOLUTION
2J0Q	C D	C	THE CRYSTAL STRUCTURE OF THE EXON JUNCTION COMPLEX AT 3.2 A RESOLUTION
2J0T	C F	C	CRYSTAL STRUCTURE OF THE CATALYTIC DOMAIN OF MMP-1 IN COMPLEX WITH THE INHIBITORY DOM
2J3R	A B	A	THE CRYSTAL STRUCTURE OF THE BET3-TRS31 HETERODIMER.
2J3R	A B	A	THE CRYSTAL STRUCTURE OF THE BET3-TRS31 HETERODIMER.
2J3R	A B	B	THE CRYSTAL STRUCTURE OF THE BET3-TRS31 HETERODIMER.
2J3W	C F	F	THE CRYSTAL STRUCTURE OF THE BET3-TRS31-SEDLIN COMPLEX.
2J59	B N	N	CRYSTAL STRUCTURE OF THE ARF1:ARHGAP21-ARFBD COMPLEX
2J59	C O	O	CRYSTAL STRUCTURE OF THE ARF1:ARHGAP21-ARFBD COMPLEX
2J59	D P	P	CRYSTAL STRUCTURE OF THE ARF1:ARHGAP21-ARFBD COMPLEX
2J59	E Q	Q	CRYSTAL STRUCTURE OF THE ARF1:ARHGAP21-ARFBD COMPLEX
2J59	F R	R	CRYSTAL STRUCTURE OF THE ARF1:ARHGAP21-ARFBD COMPLEX
2J9U	A B	A	2 ANGSTROM X-RAY STRUCTURE OF THE YEAST ESCRT-I VPS28 C- TERMINUS IN COMPLEX WITH THE N
2JBY	A B	A	A VIRAL PROTEIN UNEXPECTEDLY MIMICS THE STRUCTURE AND FUNCTION OF PRO-SURVIVAL BCL-2
2JBY	A B	A	A VIRAL PROTEIN UNEXPECTEDLY MIMICS THE STRUCTURE AND FUNCTION OF PRO-SURVIVAL BCL-2
2JBY	A B	B	A VIRAL PROTEIN UNEXPECTEDLY MIMICS THE STRUCTURE AND FUNCTION OF PRO-SURVIVAL BCL-2
2JDQ	B D	B	C-TERMINAL DOMAIN OF INFLUENZA A VIRUS POLYMERASE PB2 SUBUNIT IN COMPLEX WITH HUMAN I
2JF9	A P	A	ESTROGEN RECEPTOR ALPHA LBD IN COMPLEX WITH A TAMOXIFEN- SPECIFIC PEPTIDE ANTAGONIST
2JF9	A P	P	ESTROGEN RECEPTOR ALPHA LBD IN COMPLEX WITH A TAMOXIFEN- SPECIFIC PEPTIDE ANTAGONIST
2JF9	B Q	B	ESTROGEN RECEPTOR ALPHA LBD IN COMPLEX WITH A TAMOXIFEN- SPECIFIC PEPTIDE ANTAGONIST
2JFA	A B	A	ESTROGEN RECEPTOR ALPHA LBD IN COMPLEX WITH AN AFFINITY- SELECTED COREPRESSOR PEPTIDE
2JFA	A B	B	ESTROGEN RECEPTOR ALPHA LBD IN COMPLEX WITH AN AFFINITY- SELECTED COREPRESSOR PEPTIDE
2JFA	A P	A	ESTROGEN RECEPTOR ALPHA LBD IN COMPLEX WITH AN AFFINITY- SELECTED COREPRESSOR PEPTIDE
2JFA	B Q	Q	ESTROGEN RECEPTOR ALPHA LBD IN COMPLEX WITH AN AFFINITY- SELECTED COREPRESSOR PEPTIDE
2JGZ	A B	B	CRYSTAL STRUCTURE OF PHOSPHO-CDK2 IN COMPLEX WITH CYCLIN B
2JKI	A S	A	COMPLEX OF HSP90 N-TERMINAL AND SGT1 CS DOMAIN
2JKI	B S	B	COMPLEX OF HSP90 N-TERMINAL AND SGT1 CS DOMAIN
2JKI	C T	C	COMPLEX OF HSP90 N-TERMINAL AND SGT1 CS DOMAIN
2JM6	A B	A	SOLUTION STRUCTURE OF MCL-1 COMPLEXED WITH NOXAB
2JQ9	A B	A	VPS4A MIT-CHMP1A COMPLEX
2JQ9	A B	B	VPS4A MIT-CHMP1A COMPLEX
2JQK	A B	B	VPS4B MIT-CHMP2B COMPLEX
2JTT	A C	A	SOLUTION STRUCTURE OF CALCIUM LOADED S100A6 BOUND TO C- TERMINAL SIAH-1 INTERACTING PR
2JTT	A D	D	SOLUTION STRUCTURE OF CALCIUM LOADED S100A6 BOUND TO C- TERMINAL SIAH-1 INTERACTING PR
2JTT	A D	D	SOLUTION STRUCTURE OF CALCIUM LOADED S100A6 BOUND TO C- TERMINAL SIAH-1 INTERACTING PR
2JTT	B C	B	SOLUTION STRUCTURE OF CALCIUM LOADED S100A6 BOUND TO C- TERMINAL SIAH-1 INTERACTING PR
2JTT	B D	D	SOLUTION STRUCTURE OF CALCIUM LOADED S100A6 BOUND TO C- TERMINAL SIAH-1 INTERACTING PR
2JXC	A B	A	STRUCTURE OF THE EPS15-EH2 STONIN2 COMPLEX
2JZB	A B	A	SOLUTION STRUCTURE OF THE COMPLEX BETWEEN E.COLI NUSA-AR2 AND RNAP-ACTD
2K2I	A B	A	NMR SOLUTION STRUCTURE OF THE C-TERMINAL DOMAIN (T94-Y172) OF THE HUMAN CENTRIN 2 IN CC
2K2I	A B	A	NMR SOLUTION STRUCTURE OF THE C-TERMINAL DOMAIN (T94-Y172) OF THE HUMAN CENTRIN 2 IN CC
2K2I	A B	A	NMR SOLUTION STRUCTURE OF THE C-TERMINAL DOMAIN (T94-Y172) OF THE HUMAN CENTRIN 2 IN CC
2K2I	A B	A	NMR SOLUTION STRUCTURE OF THE C-TERMINAL DOMAIN (T94-Y172) OF THE HUMAN CENTRIN 2 IN CC
2K3S	A B	A	HADDOCK-DERIVED STRUCTURE OF THE CH-DOMAIN OF THE SMOOTHELIN-LIKE 1 COMPLEXED WITH
2K7W	A B	B	BAX ACTIVATION IS INITIATED AT A NOVEL INTERACTION SITE
2K8F	A B	A	STRUCTURAL BASIS FOR THE REGULATION OF P53 FUNCTION BY P300
2K9J	A B	B	INTEGRIN ALPHAIIB-BETA3 TRANSMEMBRANE COMPLEX
2KA6	A B	A	NMR STRUCTURE OF THE CBP-TAZ2/STAT1-TAD COMPLEX
2KA6	A B	A	NMR STRUCTURE OF THE CBP-TAZ2/STAT1-TAD COMPLEX
2KBR	A B	A	SOLUTION STRUCTURE OF HARMONIN N TERMINAL DOMAIN IN COMPLEX WITH A INTERNAL PEPTIDE

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
2IO5	CHAPERONE/STRUCTURAL PROTEIN	1.5	3.0	2	12
2IO5	CHAPERONE/STRUCTURAL PROTEIN	1.4	7.0	5	16
2IO5	CHAPERONE/STRUCTURAL PROTEIN	1.8	11.0	6	27
2IO5	CHAPERONE/STRUCTURAL PROTEIN	1.1	2.1	2	11
2IZV	TRANSCRIPTION	1.9	7.6	4	13
2IZV	TRANSCRIPTION	1.6	3.2	2	11
2IZX	KINASE	1.7	5.2	3	17
2IZX	KINASE	1.1	2.1	2	16
2IZX	KINASE	1.2	2.4	2	17
2J0Q	HYDROLASE	1.3	2.6	2	12
2J0Q	HYDROLASE	1.7	5.2	3	14
2J0Q	HYDROLASE	1.7	3.3	2	12
2J0Q	HYDROLASE	1.6	4.8	3	14
2J0Q	HYDROLASE	1.5	2.9	2	14
2J0Q	HYDROLASE	1.8	3.6	2	25
2J0T	HYDROLASE	1.2	2.4	2	13
2J3R	TRANSPORT	1.3	2.6	2	26
2J3R	TRANSPORT	1.5	7.7	5	19
2J3R	TRANSPORT	1.5	9.0	6	18
2J3W	TRANSPORT	1.3	2.5	2	11
2J59	HYDROLASE	1.8	3.6	2	22
2J59	HYDROLASE	1.8	5.3	3	20
2J59	HYDROLASE	1.6	4.9	3	21
2J59	HYDROLASE	1.5	5.8	4	22
2J59	HYDROLASE	1.2	3.7	3	22
2J9U	PROTEIN TRANSPORT	1.7	5.0	3	19
2JBY	APOPTOSIS	1.7	3.3	2	11
2JBY	APOPTOSIS	1.6	3.2	2	22
2JBY	APOPTOSIS	1.8	5.5	3	13
2JDQ	PROTEIN TRANSPORT	1.8	3.5	2	16
2JF9	TRANSCRIPTION	1.6	6.4	4	24
2JF9	TRANSCRIPTION	1.7	5.1	3	8
2JF9	TRANSCRIPTION	1.8	3.5	2	22
2JFA	TRANSCRIPTION	1.4	6.9	5	33
2JFA	TRANSCRIPTION	1.3	9.2	7	32
2JFA	TRANSCRIPTION	1.2	2.4	2	24
2JFA	TRANSCRIPTION	1.9	5.8	3	14
2JGZ	TRANSFERASE	1.7	3.4	2	15
2JKI	CHAPERONE	1.6	6.4	4	8
2JKI	CHAPERONE	1.2	2.4	2	12
2JKI	CHAPERONE	1.4	2.8	2	12
2JM6	APOPTOSIS	1.2	4.9	4	24
2JQ9	PROTEIN TRANSPORT	1.5	3.0	2	26
2JQ9	PROTEIN TRANSPORT	1.2	2.3	2	12
2JQK	PROTEIN TRANSPORT	1.3	2.6	2	11
2JTT	CALCIUM BINDING PROTEIN/ANTITUMOR PROTEI	1.8	3.6	2	22
2JTT	CALCIUM BINDING PROTEIN/ANTITUMOR PROTEI	1.3	2.5	2	13
2JTT	CALCIUM BINDING PROTEIN/ANTITUMOR PROTEI	1.8	7.3	4	10
2JTT	CALCIUM BINDING PROTEIN/ANTITUMOR PROTEI	1.8	3.5	2	15
2JTT	CALCIUM BINDING PROTEIN/ANTITUMOR PROTEI	1.4	2.7	2	13
2JXC	ENDOCYTOSIS/PROTEIN BINDING	1.3	2.5	2	12
2JZB	TRANSFERASE/TRANSCRIPTION	1.7	3.3	2	14
2K2I	CELL CYCLE	1.5	2.9	2	10
2K2I	CELL CYCLE	1.7	3.4	2	9
2K2I	CELL CYCLE	1.5	4.4	3	12
2K2I	CELL CYCLE	1.9	3.7	2	13
2K3S	PROTEIN BINDING	1.3	2.6	2	18
2K7W	APOPTOSIS	1.5	2.9	2	16
2K8F	TRANSFERASE/TRANSCRIPTION	1.7	3.3	2	16
2K9J	MEMBRANE PROTEIN	1.3	5.0	4	33
2KA6	TRANSCRIPTION REGULATOR	1.9	5.7	3	13
2KA6	TRANSCRIPTION REGULATOR	1.7	5.1	3	17
2KBR	STRUCTURAL PROTEIN/CELL ADHESION	1.7	3.3	2	16

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
2IO5	121	132
2IO5	64	79
2IO5	50	76
2IO5	31	41
2IZV	389	401
2IZV	100	110
2IZX	5	21
2IZX	9	24
2IZX	5	21
2J0Q	385	396
2J0Q	195	208
2J0Q	124	135
2J0Q	195	208
2J0Q	287	300
2J0Q	116	140
2J0T	212	224
2J3R	37	62
2J3R	16	34
2J3R	26	43
2J3W	176	186
2J59	1042	1063
2J59	1042	1061
2J59	1042	1062
2J59	1042	1063
2J59	1042	1063
2J9U	174	192
2JBY	42	52
2JBY	77	98
2JBY	70	82
2JDQ	352	367
2JF9	372	395
2JF9	5	12
2JF9	342	363
2JFA	497	529
2JFA	497	528
2JFA	372	395
2JFA	2	15
2JGZ	279	293
2JKI	88	95
2JKI	189	200
2JKI	189	200
2JM6	71	94
2JQ9	50	75
2JQ9	116	127
2JQK	117	127
2JTT	3	24
2JTT	206	218
2JTT	192	201
2JTT	70	84
2JTT	206	218
2JXC	162	173
2JZB	297	310
2K2I	140	149
2K2I	159	167
2K2I	123	134
2K2I	102	114
2K3S	94	111
2K7W	146	161
2K8F	34	49
2K9J	693	725
2KA6	79	91
2KA6	55	71
2KBR	3	18

A. PDB CODE	L. HELIX SEQUENCE
2IO5	PKDIQLARRIRG
2IO5	KLPFQRLVREIAQDFK
2IO5	IYEETRGVLKVFLENVIRDAVTYTEHA
2IO5	KPAIRRLARRG
2IZV	LQHICRTVICNCT
2IZV	ALELLMAANFL
2IZX	IEYLAKQIVDNAIQQAK
2IZX	LTELLQGYTVEVLRQQ
2IZX	IEYLAKQIVDNAIQQAK
2J0Q	DIRILRDIEQYY
2J0Q	KGFKEQIYDVYRYL
2J0Q	YKEAQAAMEGLN
2J0Q	KGFKEQIYDVYRYL
2J0Q	KRKVDWLTEKMREA
2J0Q	PEGLRVFYYLVQDLKCLVFSLIGLH
2J0T	LHRVAAHELGHSL
2J3R	DEDVNKQLDRMGYNIGVRLIEDFLAR
2J3R	SELFTLTYGALVTQLCKDY
2J3R	VSAFALLFSEMVQYCQSR
2J3W	ESVIARDKALD
2J59	EEDTGVTNRDLISRRIKEYNNL
2J59	EEDTGVTNRDLISRRIKEYN
2J59	EEDTGVTNRDLISRRIKEYNN
2J59	EEDTGVTNRDLISRRIKEYNNL
2J59	EEDTGVTNRDLISRRIKEYNNL
2J9U	KDQLHPLLAELLISINRVT
2JBY	AKNYDTLYDIM
2JBY	PSVKLATLTLLASVIKKLNKIQ
2JBY	TMGQVGRQLAIIG
2JDQ	ESIKKEACWTISNITA
2JF9	LHDQVHLLECAWLEILMIGLVWRS
2JF9	REWFKDML
2JF9	MMGLLTNLADRELVHMINWAKR
2JFA	LQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMK
2JFA	LQQQHQRLAQLLLILSHIRHMSNKGMEHLYSM
2JFA	LHDQVHLLECAWLEILMIGLVWRS
2JFA	AFQLRQLILRGLQD
2JGZ	KHQIRQMEMKILRAL
2JKI	KSDLVNNL
2JKI	ERRIKDLVKRHS
2JKI	ERRIKDLVKRHS
2JM6	LKDECAQLRRIGDKVNLRQKLLNM
2JQ9	DKAKESIRAKCVQYLDRAEKLKDYLR
2JQ9	DQLSRRLAALRN
2JQK	EEIERQLKALG
2JTT	SPLDQAIGLLIGIFHKYSGKEG
2JTT	DMKRTINKAWVES
2JTT	LMNVLKKIYE
2JTT	FQEYITFLGALAMIY
2JTT	DMKRTINKAWVES
2JXC	VDILGRVWELSD
2JZB	KKSLTEIKDVLASR
2K2I	EELQEMIDEA
2K2I	EQEFLRIMK
2K2I	FKNLKRVAKELG
2K2I	TKEEILKAFKLFD
2K3S	SKCVYTYIQELYRSLVQK
2K7W	IWIAQELRRIGDEFNA
2K8F	PSCQKMKRVVQHTKGC
2K9J	ILVVLLSVMGAILLIGLAALLIWKLLITIHDRK
2KA6	PFCLNIKHKLRQQ
2KA6	PVCKQLIALCCYHAKHC
2KBR	RKVAREFRHKVDFLIE

A. PDB CODE	M. RESOLUTION
2IO5	2.7
2IO5	2.7
2IO5	2.7
2IO5	2.7
2IZV	2.55
2IZV	2.55
2IZX	1.3
2IZX	1.3
2IZX	1.3
2J0Q	3.2
2J0Q	3.2
2J0Q	3.2
2J0Q	3.2
2J0Q	3.2
2J0Q	3.2
2J0T	2.54
2J3R	2.6
2J3R	2.6
2J3R	2.6
2J3W	2.1
2J59	2.1
2J59	2.1
2J59	2.1
2J59	2.1
2J59	2.1
2J9U	2
2JBY	2.41
2JBY	2.41
2JBY	2.41
2JDQ	2.2
2JF9	2.1
2JF9	2.1
2JF9	2.1
2JFA	2.55
2JFA	2.55
2JFA	2.55
2JFA	2.55
2JGZ	2.9
2JKI	3.3
2JKI	3.3
2JKI	3.3
2JM6	NOT APP
2JQ9	NOT APP
2JQ9	NOT APP
2JQK	NOT APP
2JTT	NOT APP
2JTT	NOT APP
2JTT	NOT APP
2JTT	NOT APP
2JTT	NOT APP
2JXC	NOT APP
2JZB	NOT APP
2K2I	NOT APP
2K2I	NOT APP
2K2I	NOT APP
2K2I	NOT APP
2K3S	NOT APP
2K7W	NOT APP
2K8F	NOT APP
2K9J	NOT APP
2KA6	NOT APP
2KA6	NOT APP
2KBR	NOT APP

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
2KBR	A B	B	SOLUTION STRUCTURE OF HARMONIN N TERMINAL DOMAIN IN COMPLEX WITH A INTERNAL PEPTIDE
2KC8	A B	B	STRUCTURE OF E. COLI TOXIN RELE (R81A/R83A) MUTANT IN COMPLEX WITH ANTITOXIN RELBC (K47-L
2NLA	A B	A	CRYSTAL STRUCTURE OF THE MCL-1:MNOXAB BH3 COMPLEX
2NNU	A B	A	CRYSTAL STRUCTURE OF THE PAPILLOMAVIRUS DNA TETHERING COMPLEX E2:BRD4
2NNU	A B	A	CRYSTAL STRUCTURE OF THE PAPILLOMAVIRUS DNA TETHERING COMPLEX E2:BRD4
2NOJ	C D	C	CRYSTAL STRUCTURE OF EHP / C3D COMPLEX
2NOJ	C D	D	CRYSTAL STRUCTURE OF EHP / C3D COMPLEX
2NP0	A B	B	CRYSTAL STRUCTURE OF THE BOTULINUM NEUROTOXIN TYPE B COMPLEXED WITH SYNAPTOTAGAMI
2NPP	A B	A	STRUCTURE OF THE PROTEIN PHOSPHATASE 2A HOLOENZYME
2NPP	A C	A	STRUCTURE OF THE PROTEIN PHOSPHATASE 2A HOLOENZYME
2NPS	A B	A	CRYSTAL STRUCTURE OF THE EARLY ENDOSOMAL SNARE COMPLEX
2NPS	A B	B	CRYSTAL STRUCTURE OF THE EARLY ENDOSOMAL SNARE COMPLEX
2NPS	A D	D	CRYSTAL STRUCTURE OF THE EARLY ENDOSOMAL SNARE COMPLEX
2NPS	B C	B	CRYSTAL STRUCTURE OF THE EARLY ENDOSOMAL SNARE COMPLEX
2NPS	B C	C	CRYSTAL STRUCTURE OF THE EARLY ENDOSOMAL SNARE COMPLEX
2NPS	C D	C	CRYSTAL STRUCTURE OF THE EARLY ENDOSOMAL SNARE COMPLEX
2NPS	C D	D	CRYSTAL STRUCTURE OF THE EARLY ENDOSOMAL SNARE COMPLEX
2NS8	B H	B	HOW AN IN VITRO SELECTED PEPTIDE MIMICS THE ANTIBIOTIC TETRACYCLINE TO INDUCE TET REPRE
2NS8	B H	B	HOW AN IN VITRO SELECTED PEPTIDE MIMICS THE ANTIBIOTIC TETRACYCLINE TO INDUCE TET REPRE
2NTS	P A	A	CRYSTAL STRUCTURE OF SEK-HVB5.1
2NTY	B D	D	ROP4-GDP-PRONE8
2NUD	A C	A	THE STRUCTURE OF THE TYPE III EFFECTOR AVRB COMPLEXED WITH A HIGH-AFFINITY RIN4 PEPTIDE
2NVU	A B	A	STRUCTURE OF APPBP1-UBA3~NEDD8-NEDD8-MGATP-UBC12(C111A), A TRAPPED UBIQUITIN-LIKE PROT
2NVU	A B	A	STRUCTURE OF APPBP1-UBA3~NEDD8-NEDD8-MGATP-UBC12(C111A), A TRAPPED UBIQUITIN-LIKE PROT
2NVU	A B	B	STRUCTURE OF APPBP1-UBA3~NEDD8-NEDD8-MGATP-UBC12(C111A), A TRAPPED UBIQUITIN-LIKE PROT
2NVU	B C	B	STRUCTURE OF APPBP1-UBA3~NEDD8-NEDD8-MGATP-UBC12(C111A), A TRAPPED UBIQUITIN-LIKE PROT
2NVU	C J	C	STRUCTURE OF APPBP1-UBA3~NEDD8-NEDD8-MGATP-UBC12(C111A), A TRAPPED UBIQUITIN-LIKE PROT
2NZ8	A B	A	N-TERMINAL DHPH CASSETTE OF TRIO IN COMPLEX WITH NUCLEOTIDE- FREE RAC1
2NZ8	A B	B	N-TERMINAL DHPH CASSETTE OF TRIO IN COMPLEX WITH NUCLEOTIDE- FREE RAC1
2NZU	G L	L	STRUCTURAL MECHANISM FOR THE FINE-TUNING OF CCPA FUNCTION BY THE SMALL MOLECULE EFFE
2O26	B Y	B	STRUCTURE OF A CLASS III RTK SIGNALING ASSEMBLY
2O26	B Y	B	STRUCTURE OF A CLASS III RTK SIGNALING ASSEMBLY
2O2V	A B	A	CRYSTAL STRUCTURE OF THE COMPLEX OF HUMAN MITOGEN ACTIVATED PROTEIN KINASE KINASE 5
2O60	A B	A	CALMODULIN BOUND TO PEPTIDE FROM NEURONAL NITRIC OXIDE SYNTHASE
2O60	A B	A	CALMODULIN BOUND TO PEPTIDE FROM NEURONAL NITRIC OXIDE SYNTHASE
2O8F	A B	B	HUMAN MUTSALPHA (MSH2/MSH6) BOUND TO DNA WITH A SINGLE BASE T INSERT
2O8F	A B	B	HUMAN MUTSALPHA (MSH2/MSH6) BOUND TO DNA WITH A SINGLE BASE T INSERT
2O9I	A C	A	CRYSTAL STRUCTURE OF THE HUMAN PREGNANE X RECEPTOR LBD IN COMPLEX WITH AN SRC-1 COAC
2O9I	A C	A	CRYSTAL STRUCTURE OF THE HUMAN PREGNANE X RECEPTOR LBD IN COMPLEX WITH AN SRC-1 COAC
2O9I	B D	D	CRYSTAL STRUCTURE OF THE HUMAN PREGNANE X RECEPTOR LBD IN COMPLEX WITH AN SRC-1 COAC
2OBH	A C	A	CENTRIN-XPC PEPTIDE
2OBH	B D	B	CENTRIN-XPC PEPTIDE
2OCF	A D	A	HUMAN ESTROGEN RECEPTOR ALPHA LIGAND-BINDING DOMAIN IN COMPLEX WITH ESTRADIOL AND
2OCY	A C	A	COMPLEX OF THE GUANINE EXCHANGE FACTOR SEC2P AND THE RAB GTPASE SEC4P
2ODB	A B	A	THE CRYSTAL STRUCTURE OF HUMAN CDC42 IN COMPLEX WITH THE CRIB DOMAIN OF HUMAN P21-AC
2ODE	A B	B	CRYSTAL STRUCTURE OF THE HETERODIMERIC COMPLEX OF HUMAN RGS8 AND ACTIVATED GI ALPHA
2ODE	C B	B	CRYSTAL STRUCTURE OF THE HETERODIMERIC COMPLEX OF HUMAN RGS8 AND ACTIVATED GI ALPHA
2ODE	C D	D	CRYSTAL STRUCTURE OF THE HETERODIMERIC COMPLEX OF HUMAN RGS8 AND ACTIVATED GI ALPHA
2ODY	A B	A	THROMBIN-BOUND BOOPHILIN DISPLAYS A FUNCTIONAL AND ACCESSIBLE REACTIVE-SITE LOOP
2ODY	D F	F	THROMBIN-BOUND BOOPHILIN DISPLAYS A FUNCTIONAL AND ACCESSIBLE REACTIVE-SITE LOOP
2OF5	D J	D	OLIGOMERIC DEATH DOMAIN COMPLEX
2OF5	E J	J	OLIGOMERIC DEATH DOMAIN COMPLEX
2OF5	E K	E	OLIGOMERIC DEATH DOMAIN COMPLEX
2ONL	A C	C	CRYSTAL STRUCTURE OF THE P38A-MAPKAP KINASE 2 HETERODIMER
2ONL	B D	B	CRYSTAL STRUCTURE OF THE P38A-MAPKAP KINASE 2 HETERODIMER
2OOB	A B	A	CRYSTAL STRUCTURE OF THE UBA DOMAIN FROM CBL-B UBIQUITIN LIGASE IN COMPLEX WITH UBIQU
2OT3	A B	B	CRYSTAL STRUCTURE OF RABEX-5 VPS9 DOMAIN IN COMPLEX WITH NUCLEOTIDE FREE RAB21
2OV2	C K	C	THE CRYSTAL STRUCTURE OF THE HUMAN RAC3 IN COMPLEX WITH THE CRIB DOMAIN OF HUMAN P21-
2OV2	G O	G	THE CRYSTAL STRUCTURE OF THE HUMAN RAC3 IN COMPLEX WITH THE CRIB DOMAIN OF HUMAN P21-
2OVQ	A B	A	STRUCTURE OF THE SKP1-FBW7-CYCLINEDEGC COMPLEX
2OVQ	A B	B	STRUCTURE OF THE SKP1-FBW7-CYCLINEDEGC COMPLEX
2OZA	A B	A	STRUCTURE OF P38ALPHA COMPLEX
2OZB	A B	A	STRUCTURE OF A HUMAN PRP31-15.5K-U4 SNRNA COMPLEX

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
2KBR	STRUCTURAL PROTEIN/CELL ADHESION	1.7	3.3	2	14
2KC8	TOXIN/TOXIN REPRESSOR	1.6	6.4	4	15
2NLA	APOPTOSIS	1.9	3.8	2	21
2NNU	TRANSCRIPTION	1.5	3.0	2	23
2NNU	TRANSCRIPTION	1.9	5.6	3	24
2NOJ	IMMUNE SYSTEM	1.1	2.2	2	15
2NOJ	IMMUNE SYSTEM	1.8	3.6	2	14
2NP0	HYDROLASE	1.9	11.6	6	13
2NPP	SIGNALING PROTEIN,HYDROLASE	1.3	2.6	2	16
2NPP	SIGNALING PROTEIN,HYDROLASE	1.7	3.4	2	19
2NPS	TRANSPORT PROTEIN	1.1	3.4	3	52
2NPS	TRANSPORT PROTEIN	1.7	11.6	7	63
2NPS	TRANSPORT PROTEIN	1.4	13.7	10	58
2NPS	TRANSPORT PROTEIN	1.2	9.9	8	63
2NPS	TRANSPORT PROTEIN	1.8	10.7	6	57
2NPS	TRANSPORT PROTEIN	1.6	11.2	7	57
2NPS	TRANSPORT PROTEIN	1.5	13.1	9	58
2NS8	TRANSCRIPTION	1.3	2.5	2	31
2NS8	TRANSCRIPTION	1.5	4.4	3	14
2NTS	TOXIN/IMMUNE SYSTEM	1.8	5.3	3	11
2NTY	SIGNALING PROTEIN	1.4	2.7	2	19
2NUD	TOXIN/PROTEIN BINDING	1.3	2.5	2	16
2NVU	PROTEIN TURNOVER, LIGASE	1.9	5.7	3	7
2NVU	PROTEIN TURNOVER, LIGASE	1.7	5.0	3	21
2NVU	PROTEIN TURNOVER, LIGASE	1.7	3.4	2	21
2NVU	PROTEIN TURNOVER, LIGASE	1.5	2.9	2	10
2NVU	PROTEIN TURNOVER, LIGASE	1.7	3.3	2	14
2NZ8	SIGNALING PROTEIN,CELL CYCLE	1.8	3.6	2	9
2NZ8	SIGNALING PROTEIN,CELL CYCLE	1.2	3.6	3	25
2NZU	TRANSCRIPTION	1.5	2.9	2	8
2O26	CYTOKINE/SIGNALING PROTEIN	1.8	9.2	5	19
2O26	CYTOKINE/SIGNALING PROTEIN	1.9	3.8	2	22
2O2V	TRANSFERASE	1.2	2.3	2	21
2O60	METAL BINDING PROTEIN	1.8	3.5	2	12
2O60	METAL BINDING PROTEIN	1.2	2.4	2	15
2O8F	DNA BINDING PROTEIN/DNA	1.6	4.7	3	16
2O8F	DNA BINDING PROTEIN/DNA	1.7	3.3	2	13
2O9I	TRANSCRIPTION	1.8	3.6	2	22
2O9I	TRANSCRIPTION	1.7	3.3	2	7
2O9I	TRANSCRIPTION	1.5	4.5	3	9
2OBH	CELL CYCLE	1.2	2.3	2	11
2OBH	CELL CYCLE	1.3	2.6	2	11
2OCF	HORMONE/GROWTH FACTOR	1.7	3.4	2	9
2OCY	ENDOCYTOSIS/EXOCYTOSIS	1.7	8.7	5	22
2ODB	PROTEIN BINDING	1.3	2.6	2	14
2ODE	SIGNALING PROTEIN	1.5	4.5	3	21
2ODE	SIGNALING PROTEIN	1.3	2.5	2	17
2ODE	SIGNALING PROTEIN	1.6	4.7	3	21
2ODY	BLOOD CLOTTING/BLOOD CLOTTING INHIBITOR	1.8	9.2	5	11
2ODY	BLOOD CLOTTING/BLOOD CLOTTING INHIBITOR	1.5	6.1	4	8
2OF5	APOPTOSIS	1.4	4.2	3	10
2OF5	APOPTOSIS	1.5	3.0	2	11
2OF5	APOPTOSIS	1.9	3.8	2	16
2ONL	TRANSFERASE	1.4	2.8	2	12
2ONL	TRANSFERASE	1.8	3.6	2	6
2OOB	LIGASE	1.5	3.0	2	11
2OT3	PROTEIN TRANSPORT	1.4	4.3	3	7
2OV2	PROTEIN BINDING/TRANSFERASE	1.4	2.8	2	14
2OV2	PROTEIN BINDING/TRANSFERASE	1.5	3.0	2	14
2OVQ	TRANSCRIPTION/CELL CYCLE	1.9	3.8	2	8
2OVQ	TRANSCRIPTION/CELL CYCLE	1.3	2.6	2	10
2OZA	SIGNALING PROTEIN/TRANSFERASE	1.1	3.3	3	19
2OZB	RNA BINDING PROTEIN/RNA	1.1	2.2	2	10

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
2KBR	103	116
2KC8	54	68
2NLA	261	281
2NNU	62	84
2NNU	26	49
2NOJ	1018	1032
2NOJ	71	84
2NP0	47	59
2NPP	179	194
2NPP	417	435
2NPS	60	111
2NPS	184	246
2NPS	173	230
2NPS	184	246
2NPS	131	187
2NPS	131	187
2NPS	173	230
2NS8	127	157
2NS8	168	181
2NTS	4	14
2NTY	90	108
2NUD	184	199
2NVU	14	20
2NVU	491	511
2NVU	2293	2313
2NVU	2040	2049
2NVU	125	138
2NZ8	65	73
2NZ8	1359	1383
2NZU	47	54
2O26	72	90
2O26	41	62
2O2V	75	95
2O60	118	129
2O60	6	20
2O8F	1310	1325
2O8F	1189	1201
2O9I	240	261
2O9I	423	429
2O9I	1631	1639
2OBH	123	133
2OBH	123	133
2OCF	538	546
2OCY	93	114
2ODB	165	178
2ODE	144	164
2ODE	98	114
2ODE	144	164
2ODY	14	14
2ODY	132	139
2OF5	117	126
2OF5	814	824
2OF5	156	171
2ONL	381	392
2ONL	113	118
2OOB	932	942
2OT3	84	90
2OV2	165	178
2OV2	165	178
2OVQ	1132	1139
2OVQ	2286	2295
2OZA	346	364
2OZB	39	48

A. PDB CODE	L. HELIX SEQUENCE
2KBR	RYLREAIQEYDNIA
2KC8	EDAELVEIVKERLRN
2NLA	WGRIVTLISFGAFVAKHLKTI
2NNU	LAVSKNKALQAIELQLTLETIYN
2NNU	LRDHIDYWKHMRLECAIYYKAREM
2NOJ	MTPTVIAVHYLDETE
2NOJ	VATHRKAQRAVNLI
2NP0	FAKLKEKFFNEIN
2NPP	PMVRRAAASKLGEFAK
2NPP	WRVRLAIIEYMPLLAGQLG
2NPS	QVDEVIDVMQENITKVIERGERLDELQDKSESLSDNATAFSNRSKQLRRQMW
2NPS	RETAIQQLEADILDVNQIFKDLAMMIHDQGDLIDSIEANVESSEVHVERASDQLQRAAYYQKK
2NPS	LELVSGSIGVLKNMSQRIGGELEEQAVMLEDFSHELESTQSRLDNVMKKLAKVSHMTS
2NPS	RETAIQQLEADILDVNQIFKDLAMMIHDQGDLIDSIEANVESSEVHVERASDQLQRAAYYQKK
2NPS	RLEAGYQIAVETEQIGQEMLENLSHDRERIQRARERLRETDANLGKSSRILTGMLRR
2NPS	RLEAGYQIAVETEQIGQEMLENLSHDRERIQRARERLRETDANLGKSSRILTGMLRR
2NPS	LELVSGSIGVLKNMSQRIGGELEEQAVMLEDFSHELESTQSRLDNVMKKLAKVSHMTS
2NS8	LENALYALSAVGHFTLGSVLEDQEHQVAKEE
2NS8	PLLRQAIELFDHQG
2NTS	IGIDNLRNFYT
2NTY	KASYENVAKKWIPELRHYA
2NUD	TEYLRDRVAHLRTELG
2NVU	DRQLRLW
2NVU	HTIAAFLGGAAAQEVIKIITK
2NVU	ASTNAVIAAVCATEVFKIATS
2NVU	ESLQFLLDTC
2NVU	INSIIYGLQYLFLE
2NZ8	DRLRPLSYP
2NZ8	ISSYLIKPVQRITKYQLLLKELLTC
2NZU	IMGVMSLG
2O26	NYSIIDKLGKIVDDLVLCM
2O26	SHCWLRDMVIQLSLSLTTLLDK
2O2V	DEEMKAMLSYYYSTVMEQQVN
2O60	DEEVDEMIREAD
2O60	EEQIAEFKEAFSLFD
2O8F	EEVIQKGHRKAREFEK
2O8F	TFFVELSETASIL
2O9I	LPHMADMSTYMFKGIISFAKVI
2O9I	PLMQELF
2O9I	KILHRLLQE
2OBH	FKNLKRVAKEL
2OBH	FKNLKRVAKEL
2OCF	DLLLEMLDA
2OCY	EADKLNKEVEDLTASLFDEANN
2ODB	LKNVFDEAILAALE
2ODE	DQAQGKVHSLMEKDSYPRFLR
2ODE	TAKLVSKAHRIFEEFVD
2ODE	DQAQGKVHSLMEKDSYPRFLR
2ODY	EKELFESYIEG
2ODY	EEECELVC
2OF5	DRQINQLAQR
2OF5	YREVQRIRHEF
2OF5	VQSQVVEAFIRWRQRF
2ONL	PLLLKRRKKARA
2ONL	LNNIVK
2OOB	VDAKIAKLMGE
2OT3	LGPIYYR
2OV2	LKTVFDEAIRAVLG
2OV2	LKTVFDEAIRAVLG
2OVQ	PEEIRKTF
2OVQ	KELALYVLSF
2OZA	KERWEDVKEEMTSALATMR
2OZB	ANEATKTLNR

A. PDB CODE	M. RESOLUTION
2KBR	NOT APP
2KC8	NOT APP
2NLA	2.8
2NNU	1.59
2NNU	1.59
2NOJ	2.7
2NOJ	2.7
2NP0	2.62
2NPP	3.3
2NPP	3.3
2NPS	2.5
2NPS	2.5
2NPS	2.5
2NPS	2.5
2NPS	2.5
2NPS	2.5
2NPS	2.5
2NS8	2.55
2NS8	2.55
2NTS	2.4
2NTY	3.1
2NUD	2.3
2NVU	2.8
2NVU	2.8
2NVU	2.8
2NVU	2.8
2NVU	2.8
2NZ8	2
2NZ8	2
2NZU	2.5
2O26	2.5
2O26	2.5
2O2V	1.83
2O60	1.55
2O60	1.55
2O8F	3.25
2O8F	3.25
2O9I	2.8
2O9I	2.8
2O9I	2.8
2OBH	1.8
2OBH	1.8
2OCF	2.95
2OCY	3.3
2ODB	2.4
2ODE	1.9
2ODE	1.9
2ODE	1.9
2ODY	2.35
2ODY	2.35
2OF5	3.2
2OF5	3.2
2OF5	3.2
2ONL	4
2ONL	4
2OOB	1.9
2OT3	2.1
2OV2	2.1
2OV2	2.1
2OVQ	2.6
2OVQ	2.6
2OZA	2.7
2OZB	2.6

TABLE S4

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
2P1L	C D	C	STRUCTURE OF THE BCL-XL:BECLIN 1 COMPLEX
2P1L	C D	C	STRUCTURE OF THE BCL-XL:BECLIN 1 COMPLEX
2P1L	C D	D	STRUCTURE OF THE BCL-XL:BECLIN 1 COMPLEX
2P1L	E F	E	STRUCTURE OF THE BCL-XL:BECLIN 1 COMPLEX
2P1L	G H	G	STRUCTURE OF THE BCL-XL:BECLIN 1 COMPLEX
2P1N	A B	A	MECHANISM OF AUXIN PERCEPTION BY THE TIR1 UBIQUTIN LIGASE
2P1N	A B	B	MECHANISM OF AUXIN PERCEPTION BY THE TIR1 UBIQUTIN LIGASE
2P1N	D E	D	MECHANISM OF AUXIN PERCEPTION BY THE TIR1 UBIQUTIN LIGASE
2P1N	D E	E	MECHANISM OF AUXIN PERCEPTION BY THE TIR1 UBIQUTIN LIGASE
2P22	A B	A	STRUCTURE OF THE YEAST ESCRT-I HETEROTETRAMER CORE
2P22	A B	B	STRUCTURE OF THE YEAST ESCRT-I HETEROTETRAMER CORE
2P22	A C	A	STRUCTURE OF THE YEAST ESCRT-I HETEROTETRAMER CORE
2P22	A C	A	STRUCTURE OF THE YEAST ESCRT-I HETEROTETRAMER CORE
2P22	A C	C	STRUCTURE OF THE YEAST ESCRT-I HETEROTETRAMER CORE
2P22	A C	C	STRUCTURE OF THE YEAST ESCRT-I HETEROTETRAMER CORE
2P22	A C	C	STRUCTURE OF THE YEAST ESCRT-I HETEROTETRAMER CORE
2P22	A C	C	STRUCTURE OF THE YEAST ESCRT-I HETEROTETRAMER CORE
2P22	A D	A	STRUCTURE OF THE YEAST ESCRT-I HETEROTETRAMER CORE
2P22	A D	A	STRUCTURE OF THE YEAST ESCRT-I HETEROTETRAMER CORE
2P22	C D	D	STRUCTURE OF THE YEAST ESCRT-I HETEROTETRAMER CORE
2P5T	A B	A	MOLECULAR AND STRUCTURAL CHARACTERIZATION OF THE PEZAT CHROMOSOMAL TOXIN-ANTITOXI
2P5T	A B	A	MOLECULAR AND STRUCTURAL CHARACTERIZATION OF THE PEZAT CHROMOSOMAL TOXIN-ANTITOXI
2P5T	A B	B	MOLECULAR AND STRUCTURAL CHARACTERIZATION OF THE PEZAT CHROMOSOMAL TOXIN-ANTITOXI
2P5T	C D	D	MOLECULAR AND STRUCTURAL CHARACTERIZATION OF THE PEZAT CHROMOSOMAL TOXIN-ANTITOXI
2P5T	C D	D	MOLECULAR AND STRUCTURAL CHARACTERIZATION OF THE PEZAT CHROMOSOMAL TOXIN-ANTITOXI
2P5T	E F	F	MOLECULAR AND STRUCTURAL CHARACTERIZATION OF THE PEZAT CHROMOSOMAL TOXIN-ANTITOXI
2P6A	A C	C	THE STRUCTURE OF THE ACTIVIN:FOLLISTATIN 315 COMPLEX
2P6A	A D	D	THE STRUCTURE OF THE ACTIVIN:FOLLISTATIN 315 COMPLEX
2P7V	A B	A	CRYSTAL STRUCTURE OF THE ESCHERICHIA COLI REGULATOR OF SIGMA 70, RSD, IN COMPLEX WITH SI
2P7V	A B	B	CRYSTAL STRUCTURE OF THE ESCHERICHIA COLI REGULATOR OF SIGMA 70, RSD, IN COMPLEX WITH SI
2PBD	A V	V	TERNARY COMPLEX OF PROFILIN-ACTIN WITH THE POLY-PRO-GAB DOMAIN OF VASP*
2PBI	A B	A	THE MULTIFUNCTIONAL NATURE OF GBETA5/RGS9 REVEALED FROM ITS CRYSTAL STRUCTURE
2PBI	A B	B	THE MULTIFUNCTIONAL NATURE OF GBETA5/RGS9 REVEALED FROM ITS CRYSTAL STRUCTURE
2PBI	C D	C	THE MULTIFUNCTIONAL NATURE OF GBETA5/RGS9 REVEALED FROM ITS CRYSTAL STRUCTURE
2PBI	C D	C	THE MULTIFUNCTIONAL NATURE OF GBETA5/RGS9 REVEALED FROM ITS CRYSTAL STRUCTURE
2PBI	C D	C	THE MULTIFUNCTIONAL NATURE OF GBETA5/RGS9 REVEALED FROM ITS CRYSTAL STRUCTURE
2PBI	C D	C	THE MULTIFUNCTIONAL NATURE OF GBETA5/RGS9 REVEALED FROM ITS CRYSTAL STRUCTURE
2PBI	C D	D	THE MULTIFUNCTIONAL NATURE OF GBETA5/RGS9 REVEALED FROM ITS CRYSTAL STRUCTURE
2PG1	D K	D	STRUCTURAL ANALYSIS OF A CYTOPLASMIC DYNEIN LIGHT CHAIN- INTERMEDIATE CHAIN COMPLEX
2PHG	A B	B	MODEL FOR VP16 BINDING TO TFIIB
2PJW	H V	H	THE VPS27/HSE1 COMPLEX IS A GAT DOMAIN-BASED SCAFFOLD FOR UBIQUITIN-DEPENDENT SORTING
2PJW	H V	V	THE VPS27/HSE1 COMPLEX IS A GAT DOMAIN-BASED SCAFFOLD FOR UBIQUITIN-DEPENDENT SORTING
2PK9	A B	A	STRUCTURE OF THE PHO85-PHO80 CDK-CYCLIN COMPLEX OF THE PHOSPHATE-RESPONSIVE SIGNAL TR
2PL9	A D	A	CRYSTAL STRUCTURE OF CHEY-MG(2+)-BEF(3)(-) IN COMPLEX WITH CHEZ(C19) PEPTIDE SOLVED FROM
2PL9	A D	D	CRYSTAL STRUCTURE OF CHEY-MG(2+)-BEF(3)(-) IN COMPLEX WITH CHEZ(C19) PEPTIDE SOLVED FROM
2PMS	B D	D	CRYSTAL STRUCTURE OF THE COMPLEX OF HUMAN LACTOFERRIN N- LOBE AND LACTOFERRIN-BINDI
2PMS	B D	D	CRYSTAL STRUCTURE OF THE COMPLEX OF HUMAN LACTOFERRIN N- LOBE AND LACTOFERRIN-BINDI
2PO6	G H	H	CRYSTAL STRUCTURE OF CD1D-LIPID-ANTIGEN COMPLEXED WITH BETA- 2-MICROGLOBULIN, NKT15 A
2PON	A B	B	SOLUTION STRUCTURE OF THE BCL-XL/BECLIN-1 COMPLEX
2PQ4	A B	B	NMR SOLUTION STRUCTURE OF NAPD IN COMPLEX WITH NAPA1-35 SIGNAL PEPTIDE
2PQR	A C	A	CRYSTAL STRUCTURE OF YEAST FIS1 COMPLEXED WITH A FRAGMENT OF YEAST CAF4
2PQR	A C	A	CRYSTAL STRUCTURE OF YEAST FIS1 COMPLEXED WITH A FRAGMENT OF YEAST CAF4
2PQR	A C	A	CRYSTAL STRUCTURE OF YEAST FIS1 COMPLEXED WITH A FRAGMENT OF YEAST CAF4
2PRG	B C	C	LIGAND-BINDING DOMAIN OF THE HUMAN PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR GAMM
2PSM	A F	A	CRYSTAL STRUCTURE OF INTERLEUKIN 15 IN COMPLEX WITH INTERLEUKIN 15 RECEPTOR ALPHA
2Q0O	A C	A	CRYSTAL STRUCTURE OF AN ANTI-ACTIVATION COMPLEX IN BACTERIAL QUORUM SENSING
2Q0O	A C	C	CRYSTAL STRUCTURE OF AN ANTI-ACTIVATION COMPLEX IN BACTERIAL QUORUM SENSING
2Q86	A B	B	STRUCTURE OF THE MOUSE INVARIANT NKT CELL RECEPTOR VALPHA14
2Q97	A T	T	COMPLEX OF MAMMALIAN ACTIN WITH TOXOFILIN FROM TOXOPLASMA GONDII
2Q97	A T	T	COMPLEX OF MAMMALIAN ACTIN WITH TOXOFILIN FROM TOXOPLASMA GONDII
2QCS	A B	B	A COMPLEX STRUCTURE BETWEEN THE CATALYTIC AND REGULATORY SUBUNIT OF PROTEIN KINASE A
2QFA	A B	B	CRYSTAL STRUCTURE OF A SURVIVIN-BOREALIN-INCENP CORE COMPLEX
2QFA	A C	A	CRYSTAL STRUCTURE OF A SURVIVIN-BOREALIN-INCENP CORE COMPLEX

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
2P1L	APOPTOSIS	1.3	3.9	3	13
2P1L	APOPTOSIS	1.7	3.4	2	24
2P1L	APOPTOSIS	1.8	11.0	6	21
2P1L	APOPTOSIS	1.3	2.6	2	13
2P1L	APOPTOSIS	1.2	3.6	3	16
2P1N	SIGNALING PROTEIN	1.8	8.8	5	16
2P1N	SIGNALING PROTEIN	1.6	8.1	5	9
2P1N	SIGNALING PROTEIN	1.3	2.6	2	16
2P1N	SIGNALING PROTEIN	1.3	2.6	2	7
2P22	TRANSPORT PROTEIN	1.7	10.2	6	28
2P22	TRANSPORT PROTEIN	1.7	3.4	2	28
2P22	TRANSPORT PROTEIN	1.7	5.2	3	34
2P22	TRANSPORT PROTEIN	1.7	10.2	6	35
2P22	TRANSPORT PROTEIN	1.8	7.1	4	29
2P22	TRANSPORT PROTEIN	1.3	2.5	2	10
2P22	TRANSPORT PROTEIN	1.8	3.5	2	11
2P22	TRANSPORT PROTEIN	1.8	9.0	5	38
2P22	TRANSPORT PROTEIN	1.3	2.6	2	30
2P22	TRANSPORT PROTEIN	1.3	3.8	3	34
2P22	TRANSPORT PROTEIN	1.5	9.2	6	27
2P5T	TRANSCRIPTION REGULATOR	1.5	16.8	11	31
2P5T	TRANSCRIPTION REGULATOR	1.6	3.1	2	14
2P5T	TRANSCRIPTION REGULATOR	1.5	2.9	2	12
2P5T	TRANSCRIPTION REGULATOR	1.0	2.0	2	17
2P5T	TRANSCRIPTION REGULATOR	1.9	3.7	2	12
2P5T	TRANSCRIPTION REGULATOR	1.3	2.6	2	13
2P6A	SIGNALING PROTEIN	1.5	4.4	3	9
2P6A	SIGNALING PROTEIN	1.1	2.1	2	12
2P7V	TRANSCRIPTION	1.5	5.9	4	27
2P7V	TRANSCRIPTION	1.7	3.3	2	15
2PBD	STRUCTURAL PROTEIN	1.8	3.5	2	7
2PBI	SIGNALING PROTEIN	1.6	3.1	2	21
2PBI	SIGNALING PROTEIN	1.6	6.4	4	24
2PBI	SIGNALING PROTEIN	1.2	2.4	2	14
2PBI	SIGNALING PROTEIN	1.0	2.0	2	13
2PBI	SIGNALING PROTEIN	1.9	3.8	2	14
2PBI	SIGNALING PROTEIN	1.8	8.8	5	15
2PBI	SIGNALING PROTEIN	1.4	4.1	3	22
2PG1	STRUCTURAL PROTEIN	1.9	5.7	3	16
2PHG	TRANSCRIPTION	1.6	4.9	3	9
2PJW	ENDOCYTOSIS/EXOCYTOSIS	1.6	4.8	3	15
2PJW	ENDOCYTOSIS/EXOCYTOSIS	1.6	6.4	4	32
2PK9	SIGNALING PROTEIN,TRANSFERASE/CELL CYCLE	1.7	8.6	5	12
2PL9	SIGNALING PROTIEN	1.6	3.2	2	10
2PL9	SIGNALING PROTIEN	1.6	8.2	5	11
2PMS	METAL TRANSPORT, HYDROLASE	1.2	2.3	2	38
2PMS	METAL TRANSPORT, HYDROLASE	1.9	7.6	4	19
2PO6	LIPID BINDING PROTEIN/IMMUNE SYSTEM	1.3	2.6	2	7
2PON	APOPTOSIS INHIBITOR	1.3	2.6	2	13
2PQ4	CHAPERONE/OXIDOREDUCTASE	1.9	3.8	2	17
2PQR	APOPTOSIS	1.9	3.7	2	14
2PQR	APOPTOSIS	1.4	2.7	2	15
2PQR	APOPTOSIS	1.5	5.9	4	18
2PRG	COMPLEX (THIAZOLIDINEDIONE/RECEPTOR)	1.3	3.8	3	9
2PSM	CYTOKINE	1.2	3.5	3	19
2Q0O	TRANSCRIPTION	1.6	4.7	3	12
2Q0O	TRANSCRIPTION	1.6	6.5	4	33
2Q86	IMMUNE SYSTEM	1.2	2.3	2	8
2Q97	STRUCTURAL PROTEIN/CELL INVASION	1.8	7.1	4	15
2Q97	STRUCTURAL PROTEIN/CELL INVASION	1.3	6.6	5	17
2QCS	TRANSFERASE/TRANSFERASE INHIBITOR	1.9	3.8	2	6
2QFA	CELL CYCLE/CELL CYCLE/CELL CYCLE	1.9	17.1	9	46
2QFA	CELL CYCLE/CELL CYCLE/CELL CYCLE	1.7	6.8	4	43

TABLE S4

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
2P1L	119	131
2P1L	26	105
2P1L	106	126
2P1L	119	131
2P1L	116	131
2P1N	111	126
2P1N	24	32
2P1N	111	126
2P1N	35	41
2P22	356	383
2P22	31	58
2P22	254	287
2P22	219	253
2P22	178	206
2P22	62	71
2P22	72	82
2P22	86	123
2P22	323	352
2P22	254	287
2P22	40	66
2P5T	69	99
2P5T	110	123
2P5T	45	56
2P5T	8	24
2P5T	45	56
2P5T	234	246
2P6A	45	53
2P6A	188	199
2P7V	52	78
2P7V	584	598
2PBD	225	231
2PBI	386	406
2PBI	10	33
2PBI	15	28
2PBI	52	64
2PBI	67	80
2PBI	240	254
2PBI	12	33
2PG1	35	50
2PHG	477	485
2PJW	296	310
2PJW	381	412
2PK9	48	59
2PL9	92	101
2PL9	202	212
2PMS	212	249
2PMS	174	192
2PO6	135	141
2PON	135	147
2PQ4	5	21
2PQR	39	52
2PQR	76	90
2PQR	55	72
2PRG	688	696
2PSM	36	54
2Q0O	178	189
2Q0O	64	96
2Q86	128	135
2Q97	104	118
2Q97	132	148
2QCS	200	205
2QFA	16	61
2QFA	98	140

A. PDB CODE	L. HELIX SEQUENCE
2P1L	AYQSFEQVVNELF
2P1L	QMAAVKQALREAGDEFELRYRRAF
2P1L	SGTMENLSRRLKVTGDLFDIM
2P1L	AYQSFEQVVNELF
2P1L	PGTAYQSFEQVVNELF
2P1N	KNLLDLTCQTVADMIK
2P1N	DKDRNSVSL
2P1N	KNLLDLTCQTVADMIK
2P1N	KSWYEIE
2P22	LDTFVKQGRELARQQFLVRWHIQRITSP
2P22	SKDKEVIETLSEIYSIVITLDHVEKAYL
2P22	MQESIARFHEIIAIDKNHLRAVEQAIEQTMHSLN
2P22	TNHHEMLQNLQTVVNELYREDVDYVADKILTRQTV
2P22	ADDLDQFIKNYLDIRTQYHLRREKLATWD
2P22	KEIIDLIQTH
2P22	RHQLELYVTKF
2P22	TDFAGKIHAFRDQFKQLEENFEDLHEQKDKVQALLENA
2P22	DGLNQLYNLVAQDYALTDTIECLSRMLHRG
2P22	MQESIARFHEIIAIDKNHLRAVEQAIEQTMHSLN
2P22	LQPTRDLLCPWYEECDNITKVCQLHDS
2P5T	PVEDYELTLKIEIVKERGANLLSRLYRYQDS
2P5T	PWILMSDDLSDLIH
2P5T	KTTIHRIKQKEF
2P5T	DSEFKHALARNLRSLTR
2P5T	KTTIHRIKQKEF
2P5T	QVEKEMLQVGEKR
2P6A	TLFKWMIFN
2P6A	ACHLRKATCLLG
2P7V	KALDDFCQSLVDYLSAGHFSIYERILH
2P7V	RERIRQIEAKALRKL
2PBD	LAAAIAG
2PBI	DAAQTHIYMLMKKDSYARYLK
2PBI	ETLASLKSEAESLKGKLEEERAKL
2PBI	AFLQKIEALVKDMQ
2PBI	GGDVLQWITQRLW
2PBI	NLEAQNLGNFIVKY
2PBI	SSVSLGGIVKYSEQF
2PBI	LASLKSEAESLKGKLEEERAKL
2PG1	EKDIAAYIKKEFDKKY
2PHG	QMFTDALGI
2PJW	KTTIDQLHNSLNAAS
2PJW	KLQNLAQRVFASKARLNYALNDKAQKYNTLIE
2PK9	STAIREISLMKE
2PL9	KENIIAAAQA
2PL9	QDQVDDLLDSL
2PMS	LQSKLDAKKAKLSKLEELSDKIDELDAEIAKLEDQLKA
2PMS	PQAKIAELENQVHRLEQEL
2PO6	EAEISHT
2PON	AYQSFEQVVNELF
2PQ4	RRSFMKANAVAAAAAAA
2PQR	IQSRFNYAWGLIKS
2PQR	RRECLYYLTIGCYKL
2PQR	VNDERLGVKILTDIYKEA
2PRG	KILHRLLQE
2PSM	KVTAMNCFLLELQVILHEY
2Q0O	PREMLCLVWASK
2Q0O	GPVLQTLQDEYVARQKRSEAQQEELSDILDALG
2Q86	KAEIANKQ
2Q97	PEQAKAALLDEILRA
2Q97	TEQQKAYEQVQRDLSQL
2QCS	ELALIY
2QFA	LRRRKLASFLKDFDREVEIRIKQIESDRQNLLKEVDNLYNIEILRL
2QFA	LGEFLKLDRERAKNKIAKETNNKKKEFEETAKKVRRAIEQLAA

A. PDB CODE	M. RESOLUTION
2P1L	2.5
2P1L	2.5
2P1L	2.5
2P1L	2.5
2P1L	2.5
2P1N	2.5
2P1N	2.5
2P1N	2.5
2P1N	2.5
2P22	2.7
2P22	2.7
2P22	2.7
2P22	2.7
2P22	2.7
2P22	2.7
2P22	2.7
2P22	2.7
2P22	2.7
2P22	2.7
2P22	2.7
2P5T	3.2
2P5T	3.2
2P5T	3.2
2P5T	3.2
2P5T	3.2
2P5T	3.2
2P6A	3.4
2P6A	3.4
2P7V	2.6
2P7V	2.6
2PBD	1.5
2PBI	1.95
2PBI	1.95
2PBI	1.95
2PBI	1.95
2PBI	1.95
2PBI	1.95
2PBI	1.95
2PG1	2.8
2PHG	NOT APP
2PJW	3.01
2PJW	3.01
2PK9	2.91
2PL9	2.6
2PL9	2.6
2PMS	2.91
2PMS	2.91
2PO6	3.2
2PON	NOT APP
2PQ4	NOT APP
2PQR	1.88
2PQR	1.88
2PQR	1.88
2PRG	2.3
2PSM	2.19
2Q0O	2
2Q0O	2
2Q86	1.85
2Q97	2.5
2Q97	2.5
2QCS	2.2
2QFA	1.4
2QFA	1.4

TABLE S4

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
2QFA	A C	C	CRYSTAL STRUCTURE OF A SURVIVIN-BOREALIN-INCENP CORE COMPLEX
2QFA	B C	B	CRYSTAL STRUCTURE OF A SURVIVIN-BOREALIN-INCENP CORE COMPLEX
2QKH	B A	A	CRYSTAL STRUCTURE OF THE EXTRACELLULAR DOMAIN OF HUMAN GIP RECEPTOR IN COMPLEX WIT
2QKH	B A	B	CRYSTAL STRUCTURE OF THE EXTRACELLULAR DOMAIN OF HUMAN GIP RECEPTOR IN COMPLEX WIT
2QL2	A B	A	CRYSTAL STRUCTURE OF THE BASIC-HELIX-LOOP-HELIX DOMAINS OF THE HETERODIMER E47/NEURO
2QL2	A B	A	CRYSTAL STRUCTURE OF THE BASIC-HELIX-LOOP-HELIX DOMAINS OF THE HETERODIMER E47/NEURO
2QL2	C D	C	CRYSTAL STRUCTURE OF THE BASIC-HELIX-LOOP-HELIX DOMAINS OF THE HETERODIMER E47/NEURO
2QL2	C D	D	CRYSTAL STRUCTURE OF THE BASIC-HELIX-LOOP-HELIX DOMAINS OF THE HETERODIMER E47/NEURO
2QL2	C D	D	CRYSTAL STRUCTURE OF THE BASIC-HELIX-LOOP-HELIX DOMAINS OF THE HETERODIMER E47/NEURO
2QL5	A B	A	CRYSTAL STRUCTURE OF CASPASE-7 WITH INHIBITOR AC-DMQD-CHO
2QL5	A B	B	CRYSTAL STRUCTURE OF CASPASE-7 WITH INHIBITOR AC-DMQD-CHO
2QL5	C D	D	CRYSTAL STRUCTURE OF CASPASE-7 WITH INHIBITOR AC-DMQD-CHO
2QLV	A B	A	CRYSTAL STRUCTURE OF THE HETEROTRIMER CORE OF THE S. CEREVISIAE AMPK HOMOLOG SNF1
2QLV	A C	A	CRYSTAL STRUCTURE OF THE HETEROTRIMER CORE OF THE S. CEREVISIAE AMPK HOMOLOG SNF1
2QLV	D E	D	CRYSTAL STRUCTURE OF THE HETEROTRIMER CORE OF THE S. CEREVISIAE AMPK HOMOLOG SNF1
2QNA	A B	B	CRYSTAL STRUCTURE OF HUMAN IMPORTIN-BETA (127-876) IN COMPLEX WITH THE IBB-DOMAIN OF SN
2QR1	C D	C	CRYSTAL STRUCTURE OF THE ADENYLATE SENSOR FROM AMP- ACTIVATED PROTEIN KINASE IN COMP
2QR1	C D	C	CRYSTAL STRUCTURE OF THE ADENYLATE SENSOR FROM AMP- ACTIVATED PROTEIN KINASE IN COMP
2QR1	C D	D	CRYSTAL STRUCTURE OF THE ADENYLATE SENSOR FROM AMP- ACTIVATED PROTEIN KINASE IN COMP
2QSH	A X	A	CRYSTAL STRUCTURE OF RAD4-RAD23 BOUND TO A MISMATCH DNA
2QSH	A X	X	CRYSTAL STRUCTURE OF RAD4-RAD23 BOUND TO A MISMATCH DNA
2QSH	A X	X	CRYSTAL STRUCTURE OF RAD4-RAD23 BOUND TO A MISMATCH DNA
2QSH	A X	X	CRYSTAL STRUCTURE OF RAD4-RAD23 BOUND TO A MISMATCH DNA
2QTV	A B	B	STRUCTURE OF SEC23-SAR1 COMPLEXED WITH THE ACTIVE FRAGMENT OF SEC31
2QYF	A B	A	CRYSTAL STRUCTURE OF THE MAD2/P31(COMET)/MAD2-BINDING PEPTIDE TERNARY COMPLEX
2QYF	A B	B	CRYSTAL STRUCTURE OF THE MAD2/P31(COMET)/MAD2-BINDING PEPTIDE TERNARY COMPLEX
2QYF	C D	D	CRYSTAL STRUCTURE OF THE MAD2/P31(COMET)/MAD2-BINDING PEPTIDE TERNARY COMPLEX
2R17	A C	C	FUNCTIONAL ARCHITECTURE OF THE RETROMER CARGO-RECOGNITION COMPLEX
2RAW	A B	A	CRYSTAL STRUCTURE OF THE BOREALIN-SURVIVIN COMPLEX
2RAX	A B	B	CRYSTAL STRUCTURE OF BOREALIN (20-78) BOUND TO SURVIVIN (1- 120)
2RAX	E F	F	CRYSTAL STRUCTURE OF BOREALIN (20-78) BOUND TO SURVIVIN (1- 120)
2RAX	X Y	X	CRYSTAL STRUCTURE OF BOREALIN (20-78) BOUND TO SURVIVIN (1- 120)
2RAX	X Y	Y	CRYSTAL STRUCTURE OF BOREALIN (20-78) BOUND TO SURVIVIN (1- 120)
2RAX	X Y	Y	CRYSTAL STRUCTURE OF BOREALIN (20-78) BOUND TO SURVIVIN (1- 120)
2RD0	A B	B	STRUCTURE OF A HUMAN P110ALPHA/P85ALPHA COMPLEX
2REX	C D	D	CRYSTAL STRUCTURE OF THE EFFECTOR DOMAIN OF PLXNB1 BOUND WITH RND1 GTPASE
2RGN	A B	A	CRYSTAL STRUCTURE OF P63RHOGEF COMPLEX WITH GALPHA-Q AND RHOA
2RGN	A B	B	CRYSTAL STRUCTURE OF P63RHOGEF COMPLEX WITH GALPHA-Q AND RHOA
2RGN	A B	B	CRYSTAL STRUCTURE OF P63RHOGEF COMPLEX WITH GALPHA-Q AND RHOA
2RGN	D E	E	CRYSTAL STRUCTURE OF P63RHOGEF COMPLEX WITH GALPHA-Q AND RHOA
2RGN	D E	E	CRYSTAL STRUCTURE OF P63RHOGEF COMPLEX WITH GALPHA-Q AND RHOA
2RMK	A B	B	RAC1/PRK1 COMPLEX
2RMS	A B	A	SOLUTION STRUCTURE OF THE MSIN3A PAH1-SAP25 SID COMPLEX
2ROC	A B	A	SOLUTION STRUCTURE OF MCL-1 COMPLEXED WITH PUMA
2ROC	A B	A	SOLUTION STRUCTURE OF MCL-1 COMPLEXED WITH PUMA
2ROD	A B	A	SOLUTION STRUCTURE OF MCL-1 COMPLEXED WITH NOXAA
2ROD	A B	A	SOLUTION STRUCTURE OF MCL-1 COMPLEXED WITH NOXAA
2SIV	A B	B	SIV GP41 CORE STRUCTURE
2SIV	C B	C	SIV GP41 CORE STRUCTURE
2SIV	E D	E	SIV GP41 CORE STRUCTURE
2SIV	E F	E	SIV GP41 CORE STRUCTURE
2UXN	A B	A	STRUCTURAL BASIS OF HISTONE DEMETHYLATION BY LSD1 REVEALED BY SUICIDE INACTIVATION
2UXN	A B	B	STRUCTURAL BASIS OF HISTONE DEMETHYLATION BY LSD1 REVEALED BY SUICIDE INACTIVATION
2UXN	A B	B	STRUCTURAL BASIS OF HISTONE DEMETHYLATION BY LSD1 REVEALED BY SUICIDE INACTIVATION
2UXN	A B	B	STRUCTURAL BASIS OF HISTONE DEMETHYLATION BY LSD1 REVEALED BY SUICIDE INACTIVATION
2UY1	A B	A	CRYSTAL STRUCTURE OF CSTF-77
2UY1	A B	A	CRYSTAL STRUCTURE OF CSTF-77
2UY1	A B	B	CRYSTAL STRUCTURE OF CSTF-77
2UY1	A B	B	CRYSTAL STRUCTURE OF CSTF-77
2UY1	A B	B	CRYSTAL STRUCTURE OF CSTF-77
2UZ6	A K	K	ACHBP-TARGETED A-CONOTOXIN CORRELATES DISTINCT BINDING ORIENTATIONS WITH NACHR SUBT
2V1D	A B	A	STRUCTURAL BASIS OF LSD1-COREST SELECTIVITY IN HISTONE H3 RECOGNITION
2V1D	A B	B	STRUCTURAL BASIS OF LSD1-COREST SELECTIVITY IN HISTONE H3 RECOGNITION

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
2QFA	CELL CYCLE/CELL CYCLE/CELL CYCLE	1.8	14.0	8	39
2QFA	CELL CYCLE/CELL CYCLE/CELL CYCLE	1.8	8.8	5	46
2QKH	SIGNALING PROTEIN/HORMONE	1.6	3.1	2	22
2QKH	SIGNALING PROTEIN/HORMONE	1.7	8.3	5	27
2QL2	TRANSCRIPTION/DNA	1.6	8.1	5	19
2QL2	TRANSCRIPTION/DNA	1.7	6.9	4	28
2QL2	TRANSCRIPTION/DNA	1.9	7.5	4	21
2QL2	TRANSCRIPTION/DNA	1.7	13.8	8	20
2QL2	TRANSCRIPTION/DNA	1.5	2.9	2	25
2QL5	HYDROLASE	1.7	5.2	3	16
2QL5	HYDROLASE	1.3	4.0	3	11
2QL5	HYDROLASE	1.2	2.4	2	13
2QLV	TRANSFERASE/PROTEIN BINDING	1.5	3.0	2	19
2QLV	TRANSFERASE/PROTEIN BINDING	1.2	2.4	2	12
2QLV	TRANSFERASE/PROTEIN BINDING	1.2	3.5	3	19
2QNA	TRANSPORT PROTEIN	1.8	8.8	5	27
2QR1	TRANSFERASE	1.5	2.9	2	15
2QR1	TRANSFERASE	1.6	3.2	2	14
2QR1	TRANSFERASE	1.9	3.8	2	6
2QSH	DNA BINDING PROTEIN/DNA	1.4	8.1	6	30
2QSH	DNA BINDING PROTEIN/DNA	1.3	2.5	2	11
2QSH	DNA BINDING PROTEIN/DNA	1.2	3.6	3	10
2QSH	DNA BINDING PROTEIN/DNA	1.7	3.4	2	10
2QTV	PROTEIN TRANSPORT	1.2	2.4	2	10
2QYF	CELL CYCLE	1.9	3.7	2	22
2QYF	CELL CYCLE	1.1	2.1	2	13
2QYF	CELL CYCLE	1.5	2.9	2	14
2R17	PROTEIN TRANSPORT	1.8	3.5	2	20
2RAW	CELL CYCLE	1.9	15.3	8	43
2RAX	CELL CYCLE	1.9	9.4	5	39
2RAX	CELL CYCLE	1.5	5.8	4	38
2RAX	CELL CYCLE	1.7	5.2	3	19
2RAX	CELL CYCLE	1.4	4.2	3	38
2RAX	CELL CYCLE	1.5	3.0	2	5
2RD0	TRANSFERASE/ONCOPROTEIN	1.4	4.2	3	50
2REX	SIGNALING PROTEIN/LIPOPROTEIN	1.1	2.1	2	9
2RGN	SIGNALING PROTEIN COMPLEX	1.3	2.5	2	10
2RGN	SIGNALING PROTEIN COMPLEX	1.3	2.6	2	10
2RGN	SIGNALING PROTEIN COMPLEX	1.8	5.5	3	26
2RGN	SIGNALING PROTEIN COMPLEX	1.7	5.1	3	7
2RGN	SIGNALING PROTEIN COMPLEX	1.2	2.4	2	13
2RMK	MEMBRANE PROTEIN/TRANSFERASE	1.3	2.5	2	34
2RMS	TRANSCRIPTION	1.1	2.1	2	16
2ROC	APOPTOSIS	1.1	2.1	2	15
2ROC	APOPTOSIS	1.8	3.6	2	21
2ROD	APOPTOSIS	1.2	2.4	2	11
2ROD	APOPTOSIS	1.7	3.3	2	21
2SIV	ENVELOPE GLYCOPROTEIN	1.3	3.8	3	33
2SIV	ENVELOPE GLYCOPROTEIN	1.4	4.2	3	35
2SIV	ENVELOPE GLYCOPROTEIN	1.2	4.7	4	35
2SIV	ENVELOPE GLYCOPROTEIN	1.5	4.5	3	35
2UXN	OXIDOREDUCTASE/TRANSCRIPTION REGULATOR	1.4	14.1	10	61
2UXN	OXIDOREDUCTASE/TRANSCRIPTION REGULATOR	1.2	4.7	4	34
2UXN	OXIDOREDUCTASE/TRANSCRIPTION REGULATOR	1.2	2.4	2	8
2UXN	OXIDOREDUCTASE/TRANSCRIPTION REGULATOR	1.9	3.8	2	15
2UY1	RNA-BINDING PROTEIN	1.3	3.9	3	17
2UY1	RNA-BINDING PROTEIN	1.3	2.5	2	16
2UY1	RNA-BINDING PROTEIN	1.1	2.1	2	13
2UY1	RNA-BINDING PROTEIN	1.5	2.9	2	17
2UY1	RNA-BINDING PROTEIN	1.7	3.4	2	14
2UZ6	RECEPTOR	1.1	3.4	3	7
2V1D	OXIDOREDUCTASE/REPRESSOR	1.3	10.5	8	59
2V1D	OXIDOREDUCTASE/REPRESSOR	1.2	3.5	3	34

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
2QFA	8	46
2QFA	16	61
2QKH	32	53
2QKH	6	32
2QL2	581	599
2QL2	544	571
2QL2	581	601
2QL2	139	158
2QL2	103	127
2QL5	90	105
2QL5	240	250
2QL5	540	552
2QLV	612	630
2QLV	475	486
2QLV	612	630
2QNA	38	64
2QR1	462	476
2QR1	562	575
2QR1	214	219
2QSH	134	163
2QSH	276	286
2QSH	298	307
2QSH	288	297
2QTV	78	87
2QYF	121	142
2QYF	183	195
2QYF	182	195
2R17	713	732
2RAW	98	140
2RAX	23	61
2RAX	24	61
2RAX	98	116
2RAX	24	61
2RAX	70	74
2RD0	450	499
2REX	75	83
2RGN	210	219
2RGN	210	219
2RGN	451	476
2RGN	470	476
2RGN	478	490
2RMK	160	193
2RMS	142	157
2ROC	221	235
2ROC	242	262
2ROD	206	216
2ROD	242	262
2SIV	629	661
2SIV	547	581
2SIV	547	581
2SIV	547	581
2UXN	408	468
2UXN	330	363
2UXN	318	325
2UXN	385	399
2UY1	400	416
2UY1	319	334
2UY1	435	447
2UY1	400	416
2UY1	384	397
2UZ6	6	12
2V1D	408	466
2V1D	330	363

A. PDB CODE	L. HELIX SEQUENCE
2QFA	PIHLLELCDQKLMEFLCNMDNKDLVWLEEIQEEAERMFT
2QFA	LRRRKLASFLKDFDREVEIRIKQIESDRQNLLKEVDNLYNIEILRL
2QKH	AGELYQRWERYRRECQETLAAA
2QKH	FISDYSIAMDKIHQQDFVNWLLAQKGK
2QL2	KLLILQQAVQVILGLEQQV
2QL2	RMANNARERVRVRDINEAFRELGRMCQL
2QL2	KLLILQQAVQVILGLEQQVRE
2QL2	KIETLRLAKNYIWALSEILR
2QL2	RMKANARERNRMHGLNAALDNLRKV
2QL5	TDKDAEALFKCFRSLG
2QL5	WFVQALCSILE
2QL5	WFVQALCSILEEH
2QLV	AYPFLHLTTKLIMELAVNS
2QLV	PQIHRANMLAQG
2QLV	AYPFLHLTTKLIMELAVNS
2QNA	LEQSERRRRLLELQKSKRLDYVNHARR
2QR1	APEILLAVYRALQRA
2QR1	FLDLCAMLVCKLFS
2QR1	AFLTSN
2QSH	NEERKRRKYFHMLYLVCLMVHGFIRNEWIN
2QSH	LAPLLENISAR
2QSH	PEVFVSMLLE
2QSH	PQLREHIMAN
2QTV	IQARRLWKDY
2QYF	QKAIQDEIRSVIRQITATVTFL
2QYF	TAACLRRLFRAIF
2QYF	STAACLRRLFRAIF
2R17	PSLQVQLFIEILNRYIYFYE
2RAW	LGEFLKLDRERAKNKIAKETNNKKKEFEETAKKVRRAIEQLAA
2RAX	SFLKDFDREVEIRIKQIESDRQNLLKEVDNLYNIEILRL
2RAX	FLKDFDREVEIRIKQIESDRQNLLKEVDNLYNIEILRL
2RAX	LGEFLKLDRERAKNKIAKE
2RAX	FLKDFDREVEIRIKQIESDRQNLLKEVDNLYNIEILRL
2RAX	WLDYF
2RD0	HEYNTQFQEKSREYDRLYEEYTRTSQEIQMKRTAIEAFNETIKIFEEQCQ
2REX	DNVRPLCYS
2RGN	RSERRKWIHC
2RGN	IQQIYEWHRD
2RGN	PAISQAWIKHVAQILESQRDFLNALQ
2RGN	DFLNALQ
2RGN	PIEYQRRESQTNS
2RMK	RKLLLTAQQMLQDSKTKIDIIRMQLRRALQADQL
2RMS	QVYNDFLDIMKEFKSQ
2ROC	EGDVKSFSRVMVHVF
2ROC	WGRIVTLISFGAFVAKHLKSV
2ROD	ETAFQGMLRKL
2ROD	WGRIVTLISFGAFVAKHLKSV
2SIV	QEWERKVDFLEENITALLEEAQIQQEKNMYELQ
2SIV	GIVQQQQLLDVVKRQQELLRLTVWGTKNLQTRVT
2SIV	GIVQQQQLLDVVKRQQELLRLTVWGTKNLQTRVT
2SIV	GIVQQQQLLDVVKRQQELLRLTVWGTKNLQTRVT
2UXN	LGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMVNLKEKIKELHQQYKEASEV
2UXN	AATTVLRQLDMELVSVKRQIQNIKQTNSALKEKL
2UXN	QEDVEAVS
2UXN	TEEQLLAVQAIRKYG
2UY1	MELFRELVDQKMDAIKA
2UY1	PHVFIYCAFIEYYATG
2UY1	ILGRYHCFLDSFN
2UY1	MELFRELVDQKMDAIKA
2UY1	SRMWDSMIEYEFMV
2UZ6	PPCILNN
2V1D	LGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMVNLKEKIKELHQQYKEAS
2V1D	AATTVLRQLDMELVSVKRQIQNIKQTNSALKEKL

A. PDB CODE	M. RESOLUTION
2QFA	1.4
2QFA	1.4
2QKH	1.9
2QKH	1.9
2QL2	2.5
2QL2	2.5
2QL2	2.5
2QL2	2.5
2QL2	2.5
2QL5	2.34
2QL5	2.34
2QL5	2.34
2QLV	2.6
2QLV	2.6
2QLV	2.6
2QNA	2.84
2QR1	2.7
2QR1	2.7
2QR1	2.7
2QSH	2.81
2QSH	2.81
2QSH	2.81
2QSH	2.81
2QTV	2.5
2QYF	2.3
2QYF	2.3
2QYF	2.3
2R17	2.8
2RAW	2.4
2RAX	3.3
2RAX	3.3
2RAX	3.3
2RAX	3.3
2RAX	3.3
2RD0	3.05
2REX	2.3
2RGN	3.5
2RGN	3.5
2RGN	3.5
2RGN	3.5
2RGN	3.5
2RMK	NOT APP
2RMS	NOT APP
2ROC	NOT APP
2ROC	NOT APP
2ROD	NOT APP
2ROD	NOT APP
2SIV	2.2
2SIV	2.2
2SIV	2.2
2SIV	2.2
2UXN	2.72
2UXN	2.72
2UXN	2.72
2UXN	2.72
2UY1	2
2UY1	2
2UY1	2
2UY1	2
2UY1	2
2UZ6	2.4
2V1D	3.1
2V1D	3.1

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
2V1D	A B	B	STRUCTURAL BASIS OF LSD1-COREST SELECTIVITY IN HISTONE H3 RECOGNITION
2V1S	A K	A	CRYSTAL STRUCTURE OF RAT TOM20-ALDH PRESEQUENCE COMPLEX
2V1S	A K	K	CRYSTAL STRUCTURE OF RAT TOM20-ALDH PRESEQUENCE COMPLEX
2V1S	E J	J	CRYSTAL STRUCTURE OF RAT TOM20-ALDH PRESEQUENCE COMPLEX
2V4I	A B	B	STRUCTURE OF A NOVEL N-ACYL-ENZYME INTERMEDIATE OF AN N- TERMINAL NUCLEOPHILE (NTN) H
2V4I	G F	F	STRUCTURE OF A NOVEL N-ACYL-ENZYME INTERMEDIATE OF AN N- TERMINAL NUCLEOPHILE (NTN) H
2V4Z	A B	A	THE CRYSTAL STRUCTURE OF THE HUMAN G-PROTEIN SUBUNIT ALPHA (GNAI3) IN COMPLEX WITH AN
2V4Z	A B	B	THE CRYSTAL STRUCTURE OF THE HUMAN G-PROTEIN SUBUNIT ALPHA (GNAI3) IN COMPLEX WITH AN
2V51	B F	F	STRUCTURE OF MAL-RPEL1 COMPLEXED TO ACTIN
2V6Q	A B	A	CRYSTAL STRUCTURE OF A BHRF-1 : BIM BH3 COMPLEX
2V6X	A B	A	STRACTURAL INSIGHT INTO THE INTERACTION BETWEEN ESCRT-III AND VPS4
2V6X	A B	B	STRACTURAL INSIGHT INTO THE INTERACTION BETWEEN ESCRT-III AND VPS4
2V8W	A B	B	CRYSTALLOGRAPHIC AND MASS SPECTROMETRIC CHARACTERISATION OF EIF4E WITH N7-CAP DERIVA
2VAS	A B	B	MYOSIN VI (MD-INSERT2-CAM, DELTA-INSERT1) POST-RIGOR STATE
2VAS	A B	B	MYOSIN VI (MD-INSERT2-CAM, DELTA-INSERT1) POST-RIGOR STATE
2VAS	A B	B	MYOSIN VI (MD-INSERT2-CAM, DELTA-INSERT1) POST-RIGOR STATE
2VDA	A B	B	SOLUTION STRUCTURE OF THE SECA-SIGNAL PEPTIDE COMPLEX
2VE7	A C	A	CRYSTAL STRUCTURE OF A BONSAI VERSION OF THE HUMAN NDC80 COMPLEX
2VE7	A C	A	CRYSTAL STRUCTURE OF A BONSAI VERSION OF THE HUMAN NDC80 COMPLEX
2VE7	A C	C	CRYSTAL STRUCTURE OF A BONSAI VERSION OF THE HUMAN NDC80 COMPLEX
2VE7	B D	B	CRYSTAL STRUCTURE OF A BONSAI VERSION OF THE HUMAN NDC80 COMPLEX
2VGO	A D	D	CRYSTAL STRUCTURE OF AURORA B KINASE IN COMPLEX WITH REVERSINE INHIBITOR
2VOF	A B	B	STRUCTURE OF MOUSE A1 BOUND TO THE PUMA BH3-DOMAIN
2VOG	A B	A	STRUCTURE OF MOUSE A1 BOUND TO THE BMF BH3-DOMAIN
2VOG	A B	A	STRUCTURE OF MOUSE A1 BOUND TO THE BMF BH3-DOMAIN
2VOG	A B	B	STRUCTURE OF MOUSE A1 BOUND TO THE BMF BH3-DOMAIN
2VOH	A B	A	STRUCTURE OF MOUSE A1 BOUND TO THE BAK BH3-DOMAIN
2VOH	A B	B	STRUCTURE OF MOUSE A1 BOUND TO THE BAK BH3-DOMAIN
2VPD	A B	B	DECODING OF METHYLATED HISTONE H3 TAIL BY THE PYGO-BCL9 WNT SIGNALING COMPLEX
2VPE	A B	A	DECODING OF METHYLATED HISTONE H3 TAIL BY THE PYGO-BCL9 WNT SIGNALING COMPLEX
2VPE	A B	B	DECODING OF METHYLATED HISTONE H3 TAIL BY THE PYGO-BCL9 WNT SIGNALING COMPLEX
2VPE	C D	C	DECODING OF METHYLATED HISTONE H3 TAIL BY THE PYGO-BCL9 WNT SIGNALING COMPLEX
2VRC	C D	C	CRYSTAL STRUCTURE OF THE CITROBACTER SP. TRIPHENYLMETHANE REDUCTASE COMPLEXED WITH
2VRW	A B	B	CRITICAL STRUCTURAL ROLE FOR THE PH AND C1 DOMAINS OF THE VAV1 EXCHANGE FACTOR
2VRW	A B	B	CRITICAL STRUCTURAL ROLE FOR THE PH AND C1 DOMAINS OF THE VAV1 EXCHANGE FACTOR
2VRW	A B	B	CRITICAL STRUCTURAL ROLE FOR THE PH AND C1 DOMAINS OF THE VAV1 EXCHANGE FACTOR
2VTB	A B	A	STRUCTURE OF CRYPTOCHROME 3 - DNA COMPLEX
2VTB	A B	B	STRUCTURE OF CRYPTOCHROME 3 - DNA COMPLEX
2VUS	E M	M	CRYSTAL STRUCTURE OF UNLIGANDED NMRA-AREA ZINC FINGER COMPLEX
2VZD	A C	C	CRYSTAL STRUCTURE OF THE C-TERMINAL CALPONIN HOMOLOGY DOMAIN OF ALPHA PARVIN IN COM
2VZD	B D	B	CRYSTAL STRUCTURE OF THE C-TERMINAL CALPONIN HOMOLOGY DOMAIN OF ALPHA PARVIN IN COM
2W2M	P A	A	WT PCSK9-DELTAC BOUND TO WT EGF-A OF LDLR
2W83	A C	C	CRYSTAL STRUCTURE OF THE ARF6 GTPASE IN COMPLEX WITH A SPECIFIC EFFECTOR, JIP4
2W83	B D	B	CRYSTAL STRUCTURE OF THE ARF6 GTPASE IN COMPLEX WITH A SPECIFIC EFFECTOR, JIP4
2WAX	A B	A	STRUCTURE OF THE HUMAN DDX6 C-TERMINAL DOMAIN IN COMPLEX WITH AN EDC3-FDF PEPTIDE
2WEL	A D	A	CRYSTAL STRUCTURE OF SU6656-BOUND CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE II DE
2WEL	A D	D	CRYSTAL STRUCTURE OF SU6656-BOUND CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE II DE
2WEL	A D	D	CRYSTAL STRUCTURE OF SU6656-BOUND CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE II DE
2WG3	A C	C	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN HUMAN HEDGEHOG- INTERACTING PROTEIN HIP A
2WG3	B D	D	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN HUMAN HEDGEHOG- INTERACTING PROTEIN HIP A
2WIN	B Q	Q	C3 CONVERTASE (C3BBB) STABILIZED BY SCIN
2WIN	D P	P	C3 CONVERTASE (C3BBB) STABILIZED BY SCIN
2WIN	F M	M	C3 CONVERTASE (C3BBB) STABILIZED BY SCIN
2WIN	F P	P	C3 CONVERTASE (C3BBB) STABILIZED BY SCIN
2WIN	L N	N	C3 CONVERTASE (C3BBB) STABILIZED BY SCIN
2WIU	A B	B	MERCURY-MODIFIED BACTERIAL PERSISTENCE REGULATOR HIPBA
2WME	B C	B	CRYSTALLOGRAPHIC STRUCTURE OF BETAINE ALDEHYDE DEHYDROGENASE FROM PSEUDOMONAS A
2WME	B C	C	CRYSTALLOGRAPHIC STRUCTURE OF BETAINE ALDEHYDE DEHYDROGENASE FROM PSEUDOMONAS A
2WME	D C	C	CRYSTALLOGRAPHIC STRUCTURE OF BETAINE ALDEHYDE DEHYDROGENASE FROM PSEUDOMONAS A
2WME	D C	D	CRYSTALLOGRAPHIC STRUCTURE OF BETAINE ALDEHYDE DEHYDROGENASE FROM PSEUDOMONAS A
2WME	F E	E	CRYSTALLOGRAPHIC STRUCTURE OF BETAINE ALDEHYDE DEHYDROGENASE FROM PSEUDOMONAS A
2WME	F E	F	CRYSTALLOGRAPHIC STRUCTURE OF BETAINE ALDEHYDE DEHYDROGENASE FROM PSEUDOMONAS A
2Z2S	A B	A	CRYSTAL STRUCTURE OF RHODOBACTER SPHAEROIDES SIGE IN COMPLEX WITH THE ANTI-SIGMA CHR

TABLE S4

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
2V1D	OXIDOREDUCTASE/REPRESSOR	1.3	2.5	2	15
2V1S	OXIDOREDUCTASE	1.6	3.2	2	19
2V1S	OXIDOREDUCTASE	1.9	3.8	2	9
2V1S	OXIDOREDUCTASE	1.8	3.5	2	10
2V4I	TRANSFERASE	1.9	3.7	2	14
2V4I	TRANSFERASE	1.3	3.8	3	11
2V4Z	CELL CYCLE	1.5	3.0	2	10
2V4Z	CELL CYCLE	1.3	4.0	3	21
2V51	STRUCTURAL PROTEIN/CONTRACTILE PROTEIN	1.6	4.7	3	9
2V6Q	APOPTOSIS	1.9	3.8	2	21
2V6X	PROTEIN TRANSPORT	1.5	5.8	4	18
2V6X	PROTEIN TRANSPORT	1.7	6.6	4	12
2V8W	TRANSLATION	1.3	3.9	3	7
2VAS	MOTOR PROTEIN	1.4	4.3	3	11
2VAS	MOTOR PROTEIN	1.8	3.6	2	14
2VAS	MOTOR PROTEIN	1.3	2.5	2	11
2VDA	PROTEIN TRANSPORT	1.5	3.0	2	7
2VE7	CELL CYCLE	1.9	5.8	3	16
2VE7	CELL CYCLE	1.6	4.8	3	19
2VE7	CELL CYCLE	1.7	5.2	3	12
2VE7	CELL CYCLE	1.6	4.9	3	15
2VGO	TRANSFERASE	1.5	3.0	2	8
2VOF	APOPTOSIS	1.9	13.0	7	21
2VOG	APOPTOSIS	1.4	2.8	2	16
2VOG	APOPTOSIS	1.3	2.5	2	21
2VOG	APOPTOSIS	1.9	11.2	6	20
2VOH	APOPTOSIS	1.1	2.2	2	16
2VOH	APOPTOSIS	1.8	14.6	8	20
2VPD	GENE REGULATION	1.7	3.4	2	13
2VPE	GENE REGULATION	1.6	3.2	2	10
2VPE	GENE REGULATION	1.5	3.0	2	13
2VPE	GENE REGULATION	1.5	3.0	2	10
2VRC	OXIDOREDUCTASE	1.9	3.8	2	17
2VRW	SIGNALING PROTEIN	1.3	2.5	2	40
2VRW	SIGNALING PROTEIN	1.9	3.8	2	36
2VRW	SIGNALING PROTEIN	1.4	2.7	2	13
2VTB	LYASE/DNA	1.7	5.0	3	17
2VTB	LYASE/DNA	1.8	5.3	3	18
2VUS	TRANSCRIPTION	1.5	3.0	2	11
2VZD	CELL ADHESION	1.3	2.6	2	9
2VZD	CELL ADHESION	1.8	3.6	2	15
2W2M	HYDROLASE/RECEPTOR	1.4	2.8	2	18
2W83	PROTEIN TRANSPORT	1.5	2.9	2	64
2W83	PROTEIN TRANSPORT	1.3	2.6	2	7
2WAX	HYDROLASE	1.9	9.6	5	12
2WEL	TRANSFERASE	1.7	13.3	8	16
2WEL	TRANSFERASE	1.3	2.5	2	12
2WEL	TRANSFERASE	1.3	3.8	3	15
2WG3	SIGNALING PROTEIN	1.4	2.7	2	7
2WG3	SIGNALING PROTEIN	1.1	2.1	2	7
2WIN	IMMUNE SYSTEM	1.8	3.6	2	24
2WIN	IMMUNE SYSTEM	1.8	3.6	2	24
2WIN	IMMUNE SYSTEM	1.9	5.7	3	24
2WIN	IMMUNE SYSTEM	1.4	2.7	2	21
2WIN	IMMUNE SYSTEM	1.6	3.2	2	8
2WIU	TRANSFERASE/TRANSCRIPTION	1.6	3.1	2	15
2WME	OXIDOREDUCTASE	1.6	3.2	2	18
2WME	OXIDOREDUCTASE	1.2	2.4	2	11
2WME	OXIDOREDUCTASE	1.6	3.2	2	11
2WME	OXIDOREDUCTASE	1.6	3.2	2	11
2WME	OXIDOREDUCTASE	1.5	3.0	2	10
2WME	OXIDOREDUCTASE	1.2	2.3	2	11
2Z2S	TRANSCRIPTION	1.6	3.2	2	11

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
2V1D	385	399
2V1S	65	83
2V1S	15	23
2V1S	14	23
2V4I	194	207
2V4I	303	313
2V4Z	205	214
2V4Z	171	191
2V51	72	80
2V6Q	98	118
2V6X	6	23
2V6X	219	230
2V8W	56	62
2VAS	118	128
2VAS	80	93
2VAS	45	55
2VDA	13	19
2VE7	244	259
2VE7	222	240
2VE7	1182	1193
2VE7	244	258
2VGO	821	828
2VOF	132	152
2VOG	64	79
2VOG	86	106
2VOG	130	149
2VOH	64	79
2VOH	67	86
2VPD	182	194
2VPE	376	385
2VPE	182	194
2VPE	376	385
2VRC	116	132
2VRW	350	389
2VRW	191	226
2VRW	335	347
2VTB	147	163
2VTB	147	164
2VUS	695	705
2VZD	3	11
2VZD	354	368
2W2M	261	278
2W83	389	452
2W83	71	77
2WAX	432	443
2WEL	296	311
2WEL	119	130
2WEL	7	21
2WG3	376	382
2WG3	376	382
2WIN	60	83
2WIN	60	83
2WIN	60	83
2WIN	38	58
2WIN	26	33
2WIU	10	24
2WME	65	82
2WME	424	434
2WME	424	434
2WME	424	434
2WME	424	433
2WME	424	434
2Z2S	48	58

A. PDB CODE	L. HELIX SEQUENCE
2V1D	TEEQLLAVQAIRKYG
2V1S	AVQKFFLEEIQLGEELLAQ
2V1S	LSRLLSYAG
2V1S	RLSRLLSYAG
2V4I	PAEQDRLFRRVMDR
2V4I	WGRVAMAIGKC
2V4Z	RSERKKWIHC
2V4Z	TTAQKRVYSLMENDSYPRFLK
2V51	NVLQLKLQQ
2V6Q	LGRALAWMAWCMHACRTLCCN
2V6X	FLTKGIELVQKAIDLDTA
2V6X	DDLQARLNTLKK
2V8W	RKFLMEC
2VAS	DEEVDEMIREA
2VAS	DSEEEIREAFRVFD
2VAS	EAELQDMINEV
2VDA	LAVAVAA
2VE7	DEMNAELQSKLKDLFN
2VE7	NKLFLDYTIKCYESFMSGA
2VE7	RKFISDYLWSLV
2VE7	DEMNAELQSKLKDLF
2VGO	VDRMYGTI
2VOF	EWAREIGAQLRRIADDLNAQY
2VOG	IDTARIIFNQVMEKEF
2VOG	WGRIVTIFAFGGVLLKKLKQE
2VOG	AEVQIARKLQCIADQFHRLH
2VOH	IDTARIIFNQVMEKEF
2VOH	ILGQVGRQLALIGDDINRRY
2VPD	TEMANKAAEAVLK
2VPE	ETAYGLLTAE
2VPE	TEMANKAAEAVLK
2VPE	ETAYGLLTAE
2VRC	PLAHVHLATEYAIRTTN
2VRW	ATEKENLRLALDAMRDLAQCVNEVKRDNETLRQITNFQLS
2VRW	EYDKRCCCLREIQQTEEKYTDTLGSIQQHFMKPLQR
2VRW	KYHLLLQELVKHT
2VTB	SEEVDVERLVNQGLKRV
2VTB	SEEVDVERLVNQGLKRVG
2VUS	NACGLFLKLHG
2VZD	DLDALLADL
2VZD	LKSTLRVLYNLFTKY
2W2M	VSGTLIGLEFIRKSQLVQ
2W83	PEFMGREVENLILENTQLLETKNALNIVKNDLIAKVDELTCEKDVLQGELEAVKQAKLKLEEKN
2W83	RPLWRHY
2WAX	RFNLKSIEEQLG
2WEL	ARRKLKGAILTTMLAT
2WEL	DEEVDEMIREAD
2WEL	EEQIAEFKEAFSLFD
2WG3	LDDMEEM
2WG3	LDDMEEM
2WIN	FKKMSEAKYQLQKIYNEIDEALKS
2WIN	FKKMSEAKYQLQKIYNEIDEALKS
2WIN	FKKMSEAKYQLQKIYNEIDEALKS
2WIN	TYYKRTIKISGQKAMYALKSK
2WIN	LNVNELAT
2WIU	PTQLANAMKLVRQQN
2WME	AMQRSRILRRAVDILRER
2WME	LARAHRAIHRL
2WME	LARAHRAIHRL
2WME	LARAHRAIHRL
2WME	LARAHRAIHR
2WME	LARAHRAIHRL
2Z2S	ASQAEECAQDV

A. PDB CODE	M. RESOLUTION
2V1D	3.1
2V1S	2.05
2V1S	2.05
2V1S	2.05
2V4I	2.2
2V4I	2.2
2V4Z	2.8
2V4Z	2.8
2V51	2.35
2V6Q	2.7
2V6X	1.98
2V6X	1.98
2V8W	2.3
2VAS	2.4
2VAS	2.4
2VAS	2.4
2VDA	NOT APP
2VE7	2.88
2VE7	2.88
2VE7	2.88
2VE7	2.88
2VGO	1.7
2VOF	1.8
2VOG	1.9
2VOG	1.9
2VOG	1.9
2VOH	1.9
2VOH	1.9
2VPD	2.77
2VPE	1.7
2VPE	1.7
2VPE	1.7
2VRC	2.5
2VRW	1.85
2VRW	1.85
2VRW	1.85
2VTB	2.01
2VTB	2.01
2VUS	2.6
2VZD	2.1
2VZD	2.1
2W2M	2.4
2W83	1.93
2W83	1.93
2WAX	2.3
2WEL	1.9
2WEL	1.9
2WEL	1.9
2WG3	2.6
2WG3	2.6
2WIN	3.9
2WIN	3.9
2WIN	3.9
2WIN	3.9
2WIN	3.9
2WIU	2.35
2WME	2.1
2WME	2.1
2WME	2.1
2WME	2.1
2WME	2.1
2WME	2.1
2Z2S	2.7

TABLE S4

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
2Z2S	A B	A	CRYSTAL STRUCTURE OF RHODOBACTER SPHAEROIDES SIGE IN COMPLEX WITH THE ANTI-SIGMA CHR
2Z2S	A B	B	CRYSTAL STRUCTURE OF RHODOBACTER SPHAEROIDES SIGE IN COMPLEX WITH THE ANTI-SIGMA CHR
2Z2S	A H	A	CRYSTAL STRUCTURE OF RHODOBACTER SPHAEROIDES SIGE IN COMPLEX WITH THE ANTI-SIGMA CHR
2Z2S	C D	C	CRYSTAL STRUCTURE OF RHODOBACTER SPHAEROIDES SIGE IN COMPLEX WITH THE ANTI-SIGMA CHR
2Z2S	C D	C	CRYSTAL STRUCTURE OF RHODOBACTER SPHAEROIDES SIGE IN COMPLEX WITH THE ANTI-SIGMA CHR
2Z2S	E F	E	CRYSTAL STRUCTURE OF RHODOBACTER SPHAEROIDES SIGE IN COMPLEX WITH THE ANTI-SIGMA CHR
2Z2S	E F	F	CRYSTAL STRUCTURE OF RHODOBACTER SPHAEROIDES SIGE IN COMPLEX WITH THE ANTI-SIGMA CHR
2Z2S	G H	G	CRYSTAL STRUCTURE OF RHODOBACTER SPHAEROIDES SIGE IN COMPLEX WITH THE ANTI-SIGMA CHR
2Z2S	G H	G	CRYSTAL STRUCTURE OF RHODOBACTER SPHAEROIDES SIGE IN COMPLEX WITH THE ANTI-SIGMA CHR
2Z2T	A F	A	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN GP41 FRAGMENT N36 AND FUSION INHIBITOR SC34E
2Z2T	A F	F	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN GP41 FRAGMENT N36 AND FUSION INHIBITOR SC34E
2Z2T	B E	E	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN GP41 FRAGMENT N36 AND FUSION INHIBITOR SC34E
2Z2T	C E	C	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN GP41 FRAGMENT N36 AND FUSION INHIBITOR SC34E
2Z2T	C E	E	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN GP41 FRAGMENT N36 AND FUSION INHIBITOR SC34E
2Z2T	C F	F	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN GP41 FRAGMENT N36 AND FUSION INHIBITOR SC34E
2Z3R	E H	E	CRYSTAL STRUCTURE OF THE IL-15/IL-15RA COMPLEX
2Z3R	K J	K	CRYSTAL STRUCTURE OF THE IL-15/IL-15RA COMPLEX
2ZET	A C	C	CRYSTAL STRUCTURE OF THE SMALL GTPASE RAB27B COMPLEXED WITH THE SLP HOMOLOGY DOMAIN
2ZET	A C	C	CRYSTAL STRUCTURE OF THE SMALL GTPASE RAB27B COMPLEXED WITH THE SLP HOMOLOGY DOMAIN
2ZET	B D	D	CRYSTAL STRUCTURE OF THE SMALL GTPASE RAB27B COMPLEXED WITH THE SLP HOMOLOGY DOMAIN
2ZET	B D	D	CRYSTAL STRUCTURE OF THE SMALL GTPASE RAB27B COMPLEXED WITH THE SLP HOMOLOGY DOMAIN
2ZFD	A B	A	THE CRYSTAL STRUCTURE OF PLANT SPECIFIC CALCIUM BINDING PROTEIN ATCBL2 IN COMPLEX WITH
2ZFD	A B	A	THE CRYSTAL STRUCTURE OF PLANT SPECIFIC CALCIUM BINDING PROTEIN ATCBL2 IN COMPLEX WITH
2ZFD	A B	A	THE CRYSTAL STRUCTURE OF PLANT SPECIFIC CALCIUM BINDING PROTEIN ATCBL2 IN COMPLEX WITH
2ZHX	G H	H	CRYSTAL STRUCTURE OF URACIL-DNA GLYCOSYLASE FROM MYCOBACTERIUM TUBERCULOSIS IN COM
2ZHX	M N	M	CRYSTAL STRUCTURE OF URACIL-DNA GLYCOSYLASE FROM MYCOBACTERIUM TUBERCULOSIS IN COM
2ZIV	A B	A	CRYSTAL STRUCTURE OF THE MUS81-EME1 COMPLEX
2ZIV	A B	A	CRYSTAL STRUCTURE OF THE MUS81-EME1 COMPLEX
2ZIV	A B	A	CRYSTAL STRUCTURE OF THE MUS81-EME1 COMPLEX
2ZIV	A B	B	CRYSTAL STRUCTURE OF THE MUS81-EME1 COMPLEX
2ZIV	A B	B	CRYSTAL STRUCTURE OF THE MUS81-EME1 COMPLEX
2ZIV	A B	B	CRYSTAL STRUCTURE OF THE MUS81-EME1 COMPLEX
2ZIX	A B	A	CRYSTAL STRUCTURE OF THE MUS81-EME1 COMPLEX
2ZME	A B	B	INTEGRATED STRUCTURAL AND FUNCTIONAL MODEL OF THE HUMAN ESCRT-II COMPLEX
2ZNL	A B	A	CRYSTAL STRUCTURE OF PA-PB1 COMPLEX FORM INFLUENZA VIRUS RNA POLYMERASE
2ZNV	A B	A	CRYSTAL STRUCTURE OF HUMAN AMSH-LP DUB DOMAIN IN COMPLEX WITH LYS63-LINKED UBIQUITIN
2ZSH	A B	A	STRUCTURAL BASIS OF GIBBERELLIN(GA3)-INDUCED DELLA RECOGNITION BY THE GIBBERELLIN RECE
2ZSH	A B	A	STRUCTURAL BASIS OF GIBBERELLIN(GA3)-INDUCED DELLA RECOGNITION BY THE GIBBERELLIN RECE
2ZVN	C H	H	NEMO COZI DOMAIN INCOMPLEX WITH DIUBIQUITIN IN P212121 SPACE GROUP
2ZVN	G D	D	NEMO COZI DOMAIN INCOMPLEX WITH DIUBIQUITIN IN P212121 SPACE GROUP
2ZXE	A B	A	CRYSTAL STRUCTURE OF THE SODIUM - POTASSIUM PUMP IN THE E2.2K+.PI STATE
2ZXE	A B	B	CRYSTAL STRUCTURE OF THE SODIUM - POTASSIUM PUMP IN THE E2.2K+.PI STATE
2ZXE	A G	G	CRYSTAL STRUCTURE OF THE SODIUM - POTASSIUM PUMP IN THE E2.2K+.PI STATE
2ZXX	A C	A	CRYSTAL STRUCTURE OF CDT1/GEMININ COMPLEX
2ZXX	B C	B	CRYSTAL STRUCTURE OF CDT1/GEMININ COMPLEX
2ZXX	B F	F	CRYSTAL STRUCTURE OF CDT1/GEMININ COMPLEX
2ZYZ	A D	A	PYROBACULUM AEROPHILUM SPLICING ENDONUCLEASE
2ZYZ	C B	C	PYROBACULUM AEROPHILUM SPLICING ENDONUCLEASE
2ZYZ	C D	C	PYROBACULUM AEROPHILUM SPLICING ENDONUCLEASE
3A1G	A B	A	HIGH-RESOLUTION CRYSTAL STRUCTURE OF RNA POLYMERASE PB1-PB2 SUBUNITS FROM INFLUENZA A
3A1G	A B	A	HIGH-RESOLUTION CRYSTAL STRUCTURE OF RNA POLYMERASE PB1-PB2 SUBUNITS FROM INFLUENZA A
3A1G	A B	B	HIGH-RESOLUTION CRYSTAL STRUCTURE OF RNA POLYMERASE PB1-PB2 SUBUNITS FROM INFLUENZA A
3A1G	C D	C	HIGH-RESOLUTION CRYSTAL STRUCTURE OF RNA POLYMERASE PB1-PB2 SUBUNITS FROM INFLUENZA A
3A1Q	D F	F	CRYSTAL STRUCTURE OF THE MOUSE RAP80 UIMS IN COMPLEX WITH LYS63-LINKED DI-UBIQUITIN
3B4V	E H	E	X-RAY STRUCTURE OF ACTIVIN IN COMPLEX WITH FSTL3
3B4V	E H	H	X-RAY STRUCTURE OF ACTIVIN IN COMPLEX WITH FSTL3
3B71	B E	E	CD4 ENDOCYTOSIS MOTIF BOUND TO THE FOCAL ADHESION TARGETING (FAT) DOMAIN OF THE FOCAL
3BC1	A B	A	CRYSTAL STRUCTURE OF THE COMPLEX RAB27A-SLP2A
3BC1	A F	F	CRYSTAL STRUCTURE OF THE COMPLEX RAB27A-SLP2A
3BC1	E B	B	CRYSTAL STRUCTURE OF THE COMPLEX RAB27A-SLP2A
3BC1	E F	F	CRYSTAL STRUCTURE OF THE COMPLEX RAB27A-SLP2A
3BEJ	B F	B	STRUCTURE OF HUMAN FXR IN COMPLEX WITH MFA-1 AND CO- ACTIVATOR PEPTIDE
3BEJ	B F	F	STRUCTURE OF HUMAN FXR IN COMPLEX WITH MFA-1 AND CO- ACTIVATOR PEPTIDE

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
2Z2S	TRANSCRIPTION	1.3	7.9	6	18
2Z2S	TRANSCRIPTION	1.5	2.9	2	17
2Z2S	TRANSCRIPTION	1.3	2.5	2	18
2Z2S	TRANSCRIPTION	1.8	9.1	5	19
2Z2S	TRANSCRIPTION	1.2	2.4	2	12
2Z2S	TRANSCRIPTION	1.9	5.6	3	16
2Z2S	TRANSCRIPTION	1.4	2.8	2	17
2Z2S	TRANSCRIPTION	1.7	3.3	2	11
2Z2S	TRANSCRIPTION	1.1	2.1	2	17
2Z2T	VIRAL PROTEIN/INHIBITOR	1.4	2.7	2	35
2Z2T	VIRAL PROTEIN/INHIBITOR	1.5	4.5	3	31
2Z2T	VIRAL PROTEIN/INHIBITOR	1.6	11.3	7	31
2Z2T	VIRAL PROTEIN/INHIBITOR	1.7	8.4	5	35
2Z2T	VIRAL PROTEIN/INHIBITOR	1.8	7.1	4	31
2Z2T	VIRAL PROTEIN/INHIBITOR	1.5	9.0	6	31
2Z3R	CYTOKINE/CYTOKINE RECEPTOR	1.3	2.5	2	20
2Z3R	CYTOKINE/CYTOKINE RECEPTOR	1.7	3.4	2	20
2ZET	SIGNALING PROTEIN	1.8	7.3	4	42
2ZET	SIGNALING PROTEIN	1.2	2.3	2	14
2ZET	SIGNALING PROTEIN	1.2	3.5	3	42
2ZET	SIGNALING PROTEIN	1.2	2.3	2	14
2ZFD	SIGNALING PROTEIN/TRANSFERASE	1.7	5.2	3	16
2ZFD	SIGNALING PROTEIN/TRANSFERASE	1.3	2.6	2	11
2ZFD	SIGNALING PROTEIN/TRANSFERASE	1.5	4.4	3	15
2ZHX	HYDROLASE/HYDROLASE INHIBITOR	1.7	6.7	4	9
2ZHX	HYDROLASE/HYDROLASE INHIBITOR	1.8	3.5	2	6
2ZIV	HYDROLASE	1.4	4.3	3	16
2ZIV	HYDROLASE	1.8	5.4	3	11
2ZIV	HYDROLASE	1.2	4.9	4	10
2ZIV	HYDROLASE	1.8	5.3	3	10
2ZIV	HYDROLASE	1.3	2.6	2	10
2ZIV	HYDROLASE	1.9	5.6	3	15
2ZIX	HYDROLASE	1.3	2.5	2	5
2ZME	PROTEIN TRANSPORT	1.5	4.5	3	22
2ZNL	TRANSCRIPTION	1.3	2.6	2	11
2ZNV	HYDROLASE/SIGNALING PROTEIN	1.9	5.7	3	14
2ZSH	HORMONE RECEPTOR	1.4	7.2	5	18
2ZSH	HORMONE RECEPTOR	1.9	5.7	3	8
2ZVN	SIGNALING PROTEIN/TRANSCRIPTION	1.6	4.9	3	51
2ZVN	SIGNALING PROTEIN/TRANSCRIPTION	1.1	2.2	2	46
2ZXE	HYDROLASE/TRANSPORT PROTEIN	1.4	4.3	3	30
2ZXE	HYDROLASE/TRANSPORT PROTEIN	1.9	13.6	7	31
2ZXE	HYDROLASE/TRANSPORT PROTEIN	1.8	9.1	5	24
2ZXX	CELL CYCLE/REPLICATION	1.7	3.3	2	44
2ZXX	CELL CYCLE/REPLICATION	1.7	5.0	3	38
2ZXX	CELL CYCLE/REPLICATION	1.6	3.1	2	30
2ZYZ	SPLICING	1.3	2.5	2	13
2ZYZ	SPLICING	1.6	3.1	2	14
2ZYZ	SPLICING	1.1	3.2	3	14
3A1G	TRANSFERASE	1.4	2.7	2	11
3A1G	TRANSFERASE	1.8	5.4	3	11
3A1G	TRANSFERASE	1.1	2.2	2	10
3A1G	TRANSFERASE	1.7	3.3	2	11
3A1Q	GENE REGULATION/SIGNALING PROTEIN	1.1	2.1	2	38
3B4V	HORMONE REGULATOR COMPLEX	1.6	3.2	2	13
3B4V	HORMONE REGULATOR COMPLEX	1.8	3.6	2	9
3B71	PROTEIN BINDING	1.9	3.8	2	10
3BC1	SIGNALING PROTEIN/TRANSPORT PROTEIN	1.0	2.0	2	19
3BC1	SIGNALING PROTEIN/TRANSPORT PROTEIN	1.4	2.8	2	29
3BC1	SIGNALING PROTEIN/TRANSPORT PROTEIN	1.9	11.1	6	29
3BC1	SIGNALING PROTEIN/TRANSPORT PROTEIN	1.9	13.0	7	29
3BEJ	TRANSCRIPTION REGULATOR	1.3	2.5	2	26
3BEJ	TRANSCRIPTION REGULATOR	1.8	3.5	2	8

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
2Z2S	162	179
2Z2S	36	52
2Z2S	162	179
2Z2S	23	41
2Z2S	121	132
2Z2S	163	178
2Z2S	36	52
2Z2S	48	58
2Z2S	163	179
2Z2T	1547	1581
2Z2T	3631	3661
2Z2T	2631	2661
2Z2T	3547	3581
2Z2T	2631	2661
2Z2T	3631	3661
2Z3R	36	55
2Z3R	57	76
2ZET	12	53
2ZET	105	118
2ZET	12	53
2ZET	105	118
2ZFD	161	176
2ZFD	185	195
2ZFD	141	155
2ZHX	26	34
2ZHX	194	199
2ZIV	441	456
2ZIV	407	417
2ZIV	532	541
2ZIV	478	487
2ZIV	507	516
2ZIV	405	419
2ZIX	392	396
2ZME	173	194
2ZNL	405	415
2ZNV	358	371
2ZSH	18	35
2ZSH	43	50
2ZVN	286	336
2ZVN	291	336
2ZXE	847	876
2ZXE	31	61
2ZXE	16	39
2ZXX	95	138
2ZXX	93	130
2ZXX	300	329
2ZYZ	3	15
2ZYZ	2	15
2ZYZ	49	62
3A1G	746	756
3A1G	690	700
3A1G	14	23
3A1G	746	756
3A1Q	81	118
3B4V	58	70
3B4V	54	62
3B71	407	416
3BC1	170	188
3BC1	7	35
3BC1	7	35
3BC1	7	35
3BEJ	280	305
3BEJ	688	695

A. PDB CODE	L. HELIX SEQUENCE
2Z2S	LGTIKSRIRLALDRLRQH
2Z2S	DECRARAGALDAVGGSL
2Z2S	LGTIKSRIRLALDRLRQH
2Z2S	EAAFAELFQHFAPKVKGFL
2Z2S	QENARLGRAIAR
2Z2S	GTIKSRIRLALDRLRQ
2Z2S	DECRARAGALDAVGGSL
2Z2S	ASQAEECAQDV
2Z2S	GTIKSRIRLALDRLRQH
2Z2T	DIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL
2Z2T	WDRKIEEYTKKIEELIKKSQEQQEKNEKELK
2Z2T	WDRKIEEYTKKIEELIKKSQEQQEKNEKELK
2Z2T	DIVQQQNNLLRAIEAQQHLLQLTVWGIKQLQARIL
2Z2T	WDRKIEEYTKKIEELIKKSQEQQEKNEKELK
2Z2T	WDRKIEEYTKKIEELIKKSQEQQEKNEKELK
2Z3R	KVTAMKCFLLELQVISLESG
2Z3R	ASIHDTVENLIILANNSLSS
2ZET	DEEAEHVWAVVQRDFDLRRREEERLQGLKGKIQKESSKRELL
2ZET	DPCHLARVVKIGSL
2ZET	DEEAEHVWAVVQRDFDLRRREEERLQGLKGKIQKESSKRELL
2ZET	DPCHLARVVKIGSL
2ZFD	DTVIEDIIDKTFEEAD
2ZFD	KEEWRSLVLRH
2ZFD	RQEVKQMVVATLAES
2ZHX	PEEVEEVIG
2ZHX	PLSASR
2ZIV	ESTLQQAIVNTQVVDG
2ZIV	RFREQKFRLKR
2ZIV	VREVFARQLM
2ZIV	LALVWRRQIQ
2ZIV	PQLLVQAYQQ
2ZIV	RVDAEEALVDLQLHT
2ZIX	QVIDG
2ZME	NISEAFEDLSKLMIKAKEMVEL
2ZNL	SWIQNEFNKAC
2ZNV	SVDLHTHCSYQLML
2ZSH	LNTWVLISNFKVAYNILR
2ZSH	RHLAEYLD
2ZVN	IVMETVPVLKAQADIYKADFQAERHAREKLVEKKEYLQEQLEQLQREFNKL
2ZVN	VPVLKAQADIYKADFQAERHAREKLVEKKEYLQEQLEQLQREFNKL
2ZXE	ERLISMAYGQIGMIQALGGFFSYFVILAEN
2ZXE	SSWFKIFLFYLIFYGCLAGIFIGTIQVLLLT
2ZXE	YYRLRVVGLIVAAVLCVIGIIILL
2ZXX	YWKEVAEQRRKALYEALKENEKLHKEIEQKDSEIARLRKENKDL
2ZXX	SQYWKEVAEQRRKALYEALKENEKLHKEIEQKDSEIAR
2ZXX	ATCLLQRRQVFRQNLVERVKEQHKVFLASL
2ZYZ	VLQEQVFKDLKSR
2ZYZ	DVLQEQVFKDLKSR
2ZYZ	IQTLLSVINMGETL
3A1G	ICSTIEELRRQ
3A1G	QRCCNLFEKFF
3A1G	SRTREILTKT
3A1G	ICSTIEELRRQ
3A1Q	EEEQFALALKMSEQEAREVNNQEEKEEELLRKAIAESL
3B4V	FHSTVINHYRMRG
3B4V	KINLLGFLG
3B71	MSQIKRLLSE
3BC1	ISHAIEMLLDLIMKRMERS
3BC1	PEFEEQEAIMKVLQRDAALKRAEEERVRH
3BC1	PEFEEQEAIMKVLQRDAALKRAEEERVRH
3BC1	PEFEEQEAIMKVLQRDAALKRAEEERVRH
3BEJ	AEENFLILTEMATNHVQVLVEFTKKL
3BEJ	KILHRLLQ

A. PDB CODE	M. RESOLUTION
2Z2S	2.7
2Z2S	2.7
2Z2S	2.7
2Z2S	2.7
2Z2S	2.7
2Z2S	2.7
2Z2S	2.7
2Z2S	2.7
2Z2S	2.7
2Z2T	2.1
2Z2T	2.1
2Z2T	2.1
2Z2T	2.1
2Z2T	2.1
2Z2T	2.1
2Z3R	2
2Z3R	2
2ZET	3
2ZET	3
2ZET	3
2ZET	3
2ZFD	1.2
2ZFD	1.2
2ZFD	1.2
2ZHX	3.1
2ZHX	3.1
2ZIV	2.7
2ZIV	2.7
2ZIV	2.7
2ZIV	2.7
2ZIV	2.7
2ZIV	2.7
2ZIX	3.5
2ZME	2.9
2ZNL	2.3
2ZNV	1.6
2ZSH	1.8
2ZSH	1.8
2ZVN	3
2ZVN	3
2ZXE	2.4
2ZXE	2.4
2ZXE	2.4
2ZXX	2.8
2ZXX	2.8
2ZXX	2.8
2ZYZ	1.7
2ZYZ	1.7
2ZYZ	1.7
3A1G	1.7
3A1G	1.7
3A1G	1.7
3A1G	1.7
3A1Q	2.2
3B4V	2.48
3B4V	2.48
3B71	2.82
3BC1	1.8
3BC1	1.8
3BC1	1.8
3BC1	1.8
3BEJ	1.9
3BEJ	1.9

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
3BG0	A B	B	ARCHITECTURE OF A COAT FOR THE NUCLEAR PORE MEMBRANE
3BIM	E N	E	CRYSTAL STRUCTURE OF THE BCL6 BTB DOMAIN DIMER IN COMPLEX WITH THE BCOR BBD COREPRES
3BJI	A D	A	STRUCTURAL BASIS OF PROMISCUOUS GUANINE NUCLEOTIDE EXCHANGE BY THE T-CELL ESSENTIAL
3BJI	B C	C	STRUCTURAL BASIS OF PROMISCUOUS GUANINE NUCLEOTIDE EXCHANGE BY THE T-CELL ESSENTIAL
3BL2	A C	A	CRYSTAL STRUCTURE OF M11, THE BCL-2 HOMOLOG OF MURINE GAMMA- HERPESVIRUS 68, COMPLEX
3BL2	B D	B	CRYSTAL STRUCTURE OF M11, THE BCL-2 HOMOLOG OF MURINE GAMMA- HERPESVIRUS 68, COMPLEX
3BL2	B D	B	CRYSTAL STRUCTURE OF M11, THE BCL-2 HOMOLOG OF MURINE GAMMA- HERPESVIRUS 68, COMPLEX
3BLH	A B	A	CRYSTAL STRUCTURE OF HUMAN CDK9/CYCLINT1
3BLH	A B	B	CRYSTAL STRUCTURE OF HUMAN CDK9/CYCLINT1
3BOW	A B	A	STRUCTURE OF M-CALPAIN IN COMPLEX WITH CALPASTATIN
3BOW	A B	B	STRUCTURE OF M-CALPAIN IN COMPLEX WITH CALPASTATIN
3BOW	A C	C	STRUCTURE OF M-CALPAIN IN COMPLEX WITH CALPASTATIN
3BOW	A C	C	STRUCTURE OF M-CALPAIN IN COMPLEX WITH CALPASTATIN
3BP8	B D	B	CRYSTAL STRUCTURE OF MLC/EIIB COMPLEX
3BPL	A B	A	CRYSTAL STRUCTURE OF THE IL4-IL4R-COMMON GAMMA TERNARY COMPLEX
3BPN	A B	A	CRYSTAL STRUCTURE OF THE IL4-IL4R-IL13RA TERNARY COMPLEX
3BPN	A C	A	CRYSTAL STRUCTURE OF THE IL4-IL4R-IL13RA TERNARY COMPLEX
3BPQ	A B	B	CRYSTAL STRUCTURE OF RELB-RELE ANTITOXIN-TOXIN COMPLEX FROM METHANOCOCCUS JANNASC
3BPQ	C B	B	CRYSTAL STRUCTURE OF RELB-RELE ANTITOXIN-TOXIN COMPLEX FROM METHANOCOCCUS JANNASC
3BPS	P A	A	PCSK9:EGF-A COMPLEX
3BPS	P A	A	PCSK9:EGF-A COMPLEX
3BRT	A D	D	NEMO/IKK ASSOCIATION DOMAIN STRUCTURE
3BRT	C B	B	NEMO/IKK ASSOCIATION DOMAIN STRUCTURE
3BRT	C B	C	NEMO/IKK ASSOCIATION DOMAIN STRUCTURE
3BRT	C D	C	NEMO/IKK ASSOCIATION DOMAIN STRUCTURE
3BRT	C D	D	NEMO/IKK ASSOCIATION DOMAIN STRUCTURE
3BRV	A D	D	NEMO/IKKB ASSOCIATION DOMAIN STRUCTURE
3BUA	A E	A	CRYSTAL STRUCTURE OF TRF2 TRFH DOMAIN AND APOLLO PEPTIDE COMPLEX
3BUA	A E	A	CRYSTAL STRUCTURE OF TRF2 TRFH DOMAIN AND APOLLO PEPTIDE COMPLEX
3BUA	B F	B	CRYSTAL STRUCTURE OF TRF2 TRFH DOMAIN AND APOLLO PEPTIDE COMPLEX
3BUA	C G	C	CRYSTAL STRUCTURE OF TRF2 TRFH DOMAIN AND APOLLO PEPTIDE COMPLEX
3BXK	C D	C	CRYSTAL STRUCTURE OF THE P/Q-TYPE CALCIUM CHANNEL (CAV2.1) IQ DOMAIN AND CA2+CALMODU
3BXK	C D	D	CRYSTAL STRUCTURE OF THE P/Q-TYPE CALCIUM CHANNEL (CAV2.1) IQ DOMAIN AND CA2+CALMODU
3BZL	A C	C	CRYSTAL STRUCTURAL OF NATIVE ESCU C-TERMINAL DOMAIN
3C3Q	A B	A	ALIX BRO1-DOMAIN:CHMIP4B CO-CRYSTAL STRUCTURE
3C4M	A C	A	STRUCTURE OF HUMAN PARATHYROID HORMONE IN COMPLEX WITH THE EXTRACELLULAR DOMAIN
3C4M	B D	B	STRUCTURE OF HUMAN PARATHYROID HORMONE IN COMPLEX WITH THE EXTRACELLULAR DOMAIN
3C59	A B	B	CRYSTAL STRUCTURE OF THE LIGAND-BOUND GLUCAGON-LIKE PEPTIDE- 1 RECEPTOR EXTRACELLUL
3C5W	A C	A	COMPLEX BETWEEN PP2A-SPECIFIC METHYLESTERASE PME-1 AND PP2A CORE ENZYME
3C5W	A C	A	COMPLEX BETWEEN PP2A-SPECIFIC METHYLESTERASE PME-1 AND PP2A CORE ENZYME
3C5W	A C	A	COMPLEX BETWEEN PP2A-SPECIFIC METHYLESTERASE PME-1 AND PP2A CORE ENZYME
3C5W	A C	A	COMPLEX BETWEEN PP2A-SPECIFIC METHYLESTERASE PME-1 AND PP2A CORE ENZYME
3C5W	C P	P	COMPLEX BETWEEN PP2A-SPECIFIC METHYLESTERASE PME-1 AND PP2A CORE ENZYME
3CDG	A J	A	HUMAN CD94/NKG2A IN COMPLEX WITH HLA-E
3CFV	A F	F	STRUCTURAL BASIS OF THE INTERACTION OF RBAP46/RBAP48 WITH HISTONE H4
3CFV	B E	E	STRUCTURAL BASIS OF THE INTERACTION OF RBAP46/RBAP48 WITH HISTONE H4
3CHW	P V	P	COMPLEX OF DICTYOSTELIUM DISCOIDEUM ACTIN WITH PROFILIN AND THE LAST POLY-PRO OF HUMA
3CJT	C D	D	RIBOSOMAL PROTEIN L11 METHYLTRANSFERASE (PRMA) IN COMPLEX WITH DIMETHYLATED RIBOSOM
3CJT	E F	E	RIBOSOMAL PROTEIN L11 METHYLTRANSFERASE (PRMA) IN COMPLEX WITH DIMETHYLATED RIBOSOM
3CJT	E F	F	RIBOSOMAL PROTEIN L11 METHYLTRANSFERASE (PRMA) IN COMPLEX WITH DIMETHYLATED RIBOSOM
3CJT	I J	I	RIBOSOMAL PROTEIN L11 METHYLTRANSFERASE (PRMA) IN COMPLEX WITH DIMETHYLATED RIBOSOM
3CL3	A D	D	CRYSTAL STRUCTURE OF A VFLIP-IKKGAMMA COMPLEX: INSIGHTS INTO VIRAL ACTIVATION OF THE IK
3CM8	A B	B	A RNA POLYMERASE SUBUNIT STRUCTURE FROM VIRUS
3CQC	A B	A	NUCLEOPORIN NUP107/NUP133 INTERACTION COMPLEX
3CQC	A B	B	NUCLEOPORIN NUP107/NUP133 INTERACTION COMPLEX
3CQC	A B	B	NUCLEOPORIN NUP107/NUP133 INTERACTION COMPLEX
3CQX	A D	A	CHAPERONE COMPLEX
3CQX	A D	D	CHAPERONE COMPLEX
3CQX	B C	C	CHAPERONE COMPLEX
3CUQ	A B	A	INTEGRATED STRUCTURAL AND FUNCTIONAL MODEL OF THE HUMAN ESCRT-II COMPLEX
3CUQ	A B	A	INTEGRATED STRUCTURAL AND FUNCTIONAL MODEL OF THE HUMAN ESCRT-II COMPLEX
3CUQ	A B	A	INTEGRATED STRUCTURAL AND FUNCTIONAL MODEL OF THE HUMAN ESCRT-II COMPLEX
3CUQ	A B	B	INTEGRATED STRUCTURAL AND FUNCTIONAL MODEL OF THE HUMAN ESCRT-II COMPLEX

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
3BG0	PROTEIN TRANSPORT, HYDROLASE	1.8	3.6	2	17
3BIM	TRANSCRIPTION REPRESSOR	1.2	3.6	3	15
3BJI	SIGNALING PROTEIN	1.1	2.2	2	13
3BJI	SIGNALING PROTEIN	1.9	5.8	3	5
3BL2	VIRAL PROTEIN/APOPTOSIS	1.5	2.9	2	9
3BL2	VIRAL PROTEIN/APOPTOSIS	1.8	5.3	3	22
3BL2	VIRAL PROTEIN/APOPTOSIS	1.7	3.3	2	13
3BLH	TRANSCRIPTION	1.4	4.2	3	13
3BLH	TRANSCRIPTION	1.4	2.7	2	21
3BOW	HYDROLASE/HYDROLASE INHIBITOR	1.5	3.0	2	9
3BOW	HYDROLASE/HYDROLASE INHIBITOR	1.8	9.0	5	11
3BOW	HYDROLASE/HYDROLASE INHIBITOR	1.6	6.3	4	12
3BOW	HYDROLASE/HYDROLASE INHIBITOR	1.7	5.1	3	8
3BP8	TRANSCRIPTION	1.3	2.6	2	16
3BPL	CYTOKINE/CYTOKINE RECEPTOR	1.8	7.0	4	16
3BPN	CYTOKINE/CYTOKINE RECEPTOR	1.7	3.3	2	26
3BPN	CYTOKINE/CYTOKINE RECEPTOR	1.4	2.7	2	16
3BPQ	TOXIN	1.6	4.9	3	8
3BPQ	TOXIN	1.7	3.4	2	8
3BPS	HYDROLASE/LIPID TRANSPORT	1.4	2.8	2	13
3BPS	HYDROLASE/LIPID TRANSPORT	1.8	5.3	3	18
3BRT	TRANSFERASE/TRANSCRIPTION	1.6	4.7	3	60
3BRT	TRANSFERASE/TRANSCRIPTION	1.2	3.7	3	60
3BRT	TRANSFERASE/TRANSCRIPTION	1.5	4.4	3	27
3BRT	TRANSFERASE/TRANSCRIPTION	1.2	3.7	3	27
3BRT	TRANSFERASE/TRANSCRIPTION	1.7	6.8	4	60
3BRV	TRANSFERASE/TRANSCRIPTION	1.2	4.8	4	60
3BUA	DNA BINDING PROTEIN	1.4	5.4	4	19
3BUA	DNA BINDING PROTEIN	1.7	3.3	2	17
3BUA	DNA BINDING PROTEIN	1.7	8.5	5	16
3BUA	DNA BINDING PROTEIN	1.1	2.2	2	15
3BXK	MEMBRANE PROTEIN, SIGNALING PROTEIN	1.2	2.4	2	15
3BXK	MEMBRANE PROTEIN, SIGNALING PROTEIN	1.9	13.2	7	18
3BZL	MEMBRANE PROTEIN, PROTEIN TRANSPORT	1.4	4.3	3	13
3C3Q	TRANSPORT PROTEIN	1.2	2.3	2	23
3C4M	MEMBRANE PROTEIN	1.7	3.3	2	21
3C4M	MEMBRANE PROTEIN	1.6	3.2	2	24
3C59	SIGNALING PROTEIN/SIGNALING PROTEIN	1.9	5.6	3	6
3C5W	HYDROLASE	1.4	2.7	2	17
3C5W	HYDROLASE	1.4	2.7	2	14
3C5W	HYDROLASE	1.7	3.3	2	19
3C5W	HYDROLASE	1.7	3.3	2	17
3C5W	HYDROLASE	1.1	2.1	2	9
3CDG	IMMUNE SYSTEM	1.7	3.3	2	29
3CFV	HISTONE/CHAPERONE	1.7	5.1	3	10
3CFV	HISTONE/CHAPERONE	1.4	4.3	3	9
3CHW	STRUCTURAL PROTEIN	1.2	2.4	2	18
3CJT	TRANSFERASE/RIBOSOMAL PROTEIN	1.4	2.7	2	8
3CJT	TRANSFERASE/RIBOSOMAL PROTEIN	1.8	3.6	2	10
3CJT	TRANSFERASE/RIBOSOMAL PROTEIN	1.9	3.8	2	9
3CJT	TRANSFERASE/RIBOSOMAL PROTEIN	1.6	4.7	3	8
3CL3	VIRAL PROTEIN/SIGNALING PROTEIN	1.8	5.3	3	53
3CM8	RNA BINDING PROTEIN/TRANSFERASE	1.9	5.8	3	5
3CQC	PROTEIN TRANSPORT	1.3	3.9	3	21
3CQC	PROTEIN TRANSPORT	1.8	5.5	3	18
3CQC	PROTEIN TRANSPORT	1.4	2.7	2	8
3CQX	CHAPERONE	1.8	5.5	3	18
3CQX	CHAPERONE	1.9	3.7	2	9
3CQX	CHAPERONE	1.5	3.0	2	24
3CUQ	PROTEIN TRANSPORT	1.2	2.4	2	15
3CUQ	PROTEIN TRANSPORT	1.4	4.3	3	19
3CUQ	PROTEIN TRANSPORT	1.8	7.0	4	23
3CUQ	PROTEIN TRANSPORT	1.7	5.0	3	21

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
3BG0	534	550
3BIM	14	28
3BJI	322	334
3BJI	65	69
3BL2	71	79
3BL2	35	56
3BL2	67	79
3BLH	61	73
3BLH	124	144
3BOW	640	648
3BOW	260	270
3BOW	573	584
3BOW	621	628
3BP8	124	139
3BPL	5	20
3BPN	70	95
3BPN	5	20
3BPQ	80	87
3BPQ	80	87
3BPS	295	307
3BPS	261	278
3BRT	51	110
3BRT	50	109
3BRT	705	731
3BRT	705	731
3BRT	51	110
3BRV	50	109
3BUA	94	112
3BUA	73	89
3BUA	97	112
3BUA	98	112
3BXK	6	20
3BXK	1961	1978
3BZL	289	301
3C3Q	143	165
3C4M	34	54
3C4M	34	57
3C59	23	28
3C5W	534	550
3C5W	573	586
3C5W	417	435
3C5W	495	511
3C5W	328	336
3CDG	57	85
3CFV	31	40
3CFV	31	39
3CHW	120	137
3CJT	22	29
3CJT	14	23
3CJT	22	30
3CJT	17	24
3CL3	195	247
3CM8	6	10
3CQC	894	914
3CQC	964	981
3CQC	936	943
3CQX	257	274
3CQX	153	161
3CQX	164	187
3CUQ	62	76
3CUQ	35	53
3CUQ	93	115
3CUQ	174	194

A. PDB CODE	L. HELIX SEQUENCE
3BG0	SQLIFNAQALKDRYEGN
3BIM	HASDVLLNLNRLRSR
3BJI	LRDLLMVPMQRVL
3BJI	DRLRP
3BL2	LSKLFTSLF
3BL2	LVDVSKIITLTQEFRRHYDSVY
3BL2	WKRDLSKLFTSLF
3BLH	ITALREIKILQLL
3BLH	EAYLQQVQDLVILESIILQTL
3BOW	CQLHQVIVA
3BOW	IQEWLQLTMYS
3BOW	DDALDELSDSLG
3BOW	PEYRHLLD
3BP8	LLDRIISHIDQFFIRH
3BPL	ITLQEIIKTLNSLTEQ
3BPN	AQQFHRHKQLIRFLKRLDRNLWGLAG
3BPN	ITLQEIIKTLNSLTEQ
3BPQ	RKSIYDYF
3BPQ	RKSIYDYF
3BPS	RVLNAACQRLARA
3BPS	VSGTLIGLEFIRKSQLVQ
3BRT	LQRCLEENQELRDAIRQSNQILRERCEELLHFQASQREEKEFLMCKFQEARKLVERLGLE
3BRT	TLQRCLEENQELRDAIRQSNQILRERCEELLHFQASQREEKEFLMCKFQEARKLVERLGL
3BRT	SEELVAEAHNLCTLLENAIQDTVREQG
3BRT	SEELVAEAHNLCTLLENAIQDTVREQG
3BRT	LQRCLEENQELRDAIRQSNQILRERCEELLHFQASQREEKEFLMCKFQEARKLVERLGLE
3BRV	TLQRCLEENQELRDAIRQSNQILRERCEELLHFQASQREEKEFLMCKFQEARKLVERLGL
3BUA	EHTVSRLLRVMQCLSRIEE
3BUA	YGDFRQIRDIMQALLVR
3BUA	VSRLLRVMQCLSRIEE
3BUA	SRLLRVMQCLSRIEE
3BXK	EEQIAEFKEAFSLFD
3BXK	IYAAMMIMEYYRQSKAKK
3BZL	AKALQIIKLAELY
3C3Q	DEGLKIAAKHYQFASGAFLHIKE
3C4M	KEEQIFLLHRAQAQCEKRLKE
3C4M	KEEQIFLLHRAQAQCEKRLKEVLQ
3C59	IEWLKN
3C5W	ANVRFNVAKSLQKIGPI
3C5W	VDVKYFAQEALTVL
3C5W	WRVRLAIIEYMPLLAGQLG
3C5W	YLHRMTTLFCINVLSEV
3C5W	KDLTIGQMQ
3CDG	SEYWDRETRSARDTAQIFRVNLRTLRGYY
3CFV	KPAIRRLARR
3CFV	KPAIRRLAR
3CHW	GGLINKKCYEMASHLRRS
3CJT	PVGPALGQ
3CJT	DPILPGLFDG
3CJT	PVGPALGQH
3CJT	LPGLFDGG
3CL3	HSVQVDQLRMQGQSVEAALRMERQAASEEKRKLAQLQVAYHQLFQEYDNHIKS
3CM8	PTLLF
3CQC	KEELRKLLQKLRESSLMLLDQ
3CQC	FAKKKTLLGLSKLAALAS
3CQC	SWLHEINS
3CQX	KRAVRRLRTACERAKRTL
3CQX	QKFQSIVIG
3CQX	LEDQKKIKRRLETLLRNIDNSDKA
3CUQ	PEFRVQFQDMCATIG
3CUQ	QMSKQLDMFKTNLEEFASK
3CUQ	VGDFYYELGVQIIEVCLALKHRN
3CUQ	ISEAFEDLSKLMIKAKEMVEL

TABLE S4

A. PDB CODE	M. RESOLUTION
3BG0	3.15
3BIM	2.6
3BJI	2.6
3BJI	2.6
3BL2	2.3
3BL2	2.3
3BL2	2.3
3BLH	2.48
3BLH	2.48
3BOW	2.4
3BOW	2.4
3BOW	2.4
3BOW	2.4
3BP8	2.85
3BPL	2.93
3BPN	3.02
3BPN	3.02
3BPQ	2.2
3BPQ	2.2
3BPS	2.41
3BPS	2.41
3BRT	2.25
3BRT	2.25
3BRT	2.25
3BRT	2.25
3BRT	2.25
3BRV	2.2
3BUA	2.5
3BUA	2.5
3BUA	2.5
3BUA	2.5
3BXK	2.55
3BXK	2.55
3BZL	1.71
3C3Q	2.1
3C4M	1.95
3C4M	1.95
3C59	2.3
3C5W	2.8
3C5W	2.8
3C5W	2.8
3C5W	2.8
3C5W	2.8
3CDG	3.4
3CFV	2.6
3CFV	2.6
3CHW	2.3
3CJT	2.3
3CJT	2.3
3CJT	2.3
3CJT	2.3
3CL3	3.2
3CM8	2.9
3CQC	2.53
3CQC	2.53
3CQC	2.53
3CQX	2.3
3CQX	2.3
3CQX	2.3
3CUQ	2.61
3CUQ	2.61
3CUQ	2.61
3CUQ	2.61

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
3CUQ	A B	B	INTEGRATED STRUCTURAL AND FUNCTIONAL MODEL OF THE HUMAN ESCRT-II COMPLEX
3CUQ	B C	C	INTEGRATED STRUCTURAL AND FUNCTIONAL MODEL OF THE HUMAN ESCRT-II COMPLEX
3CWZ	A B	B	STRUCURE OF RAB6(GTP)-R6IP1 COMPLEX
3D2E	A B	A	CRYSTAL STRUCTURE OF A COMPLEX OF SSE1P AND HSP70, SELENOMETHIONINE-LABELED CRYSTALS
3D2E	C D	C	CRYSTAL STRUCTURE OF A COMPLEX OF SSE1P AND HSP70, SELENOMETHIONINE-LABELED CRYSTALS
3D32	A C	A	COMPLEX OF GABA(A) RECEPTOR-ASSOCIATED PROTEIN (GABARAP) WITH A SYNTHETIC PEPTIDE
3D7V	A B	A	CRYSTAL STRUCTURE OF MCL-1 IN COMPLEX WITH AN MCL-1 SELECTIVE BH3 LIGAND
3DBH	A B	A	STRUCTURAL DISSECTION OF A GATING MECHANISM PREVENTING MISACTIVATION OF UBIQUITIN BY
3DBH	A B	B	STRUCTURAL DISSECTION OF A GATING MECHANISM PREVENTING MISACTIVATION OF UBIQUITIN BY
3DBH	C D	C	STRUCTURAL DISSECTION OF A GATING MECHANISM PREVENTING MISACTIVATION OF UBIQUITIN BY
3DBH	C D	C	STRUCTURAL DISSECTION OF A GATING MECHANISM PREVENTING MISACTIVATION OF UBIQUITIN BY
3DBH	C D	D	STRUCTURAL DISSECTION OF A GATING MECHANISM PREVENTING MISACTIVATION OF UBIQUITIN BY
3DBH	D J	D	STRUCTURAL DISSECTION OF A GATING MECHANISM PREVENTING MISACTIVATION OF UBIQUITIN BY
3DBH	E F	E	STRUCTURAL DISSECTION OF A GATING MECHANISM PREVENTING MISACTIVATION OF UBIQUITIN BY
3DCG	B F	B	CRYSTAL STRUCTURE OF THE HIV VIF BC-BOX IN COMPLEX WITH HUMAN ELONGINB AND ELONGINC
3DCG	B F	F	CRYSTAL STRUCTURE OF THE HIV VIF BC-BOX IN COMPLEX WITH HUMAN ELONGINB AND ELONGINC
3DCG	C D	D	CRYSTAL STRUCTURE OF THE HIV VIF BC-BOX IN COMPLEX WITH HUMAN ELONGINB AND ELONGINC
3DCT	A B	A	FXR WITH SRC1 AND GW4064
3DCT	A B	B	FXR WITH SRC1 AND GW4064
3DD7	A B	B	STRUCTURE OF DOCH66Y IN COMPLEX WITH THE C-TERMINAL DOMAIN OF PHD
3DD7	C D	C	STRUCTURE OF DOCH66Y IN COMPLEX WITH THE C-TERMINAL DOMAIN OF PHD
3DD7	C D	C	STRUCTURE OF DOCH66Y IN COMPLEX WITH THE C-TERMINAL DOMAIN OF PHD
3DGC	L S	L	STRUCTURE OF IL-22/IL-22R1
3DGC	M R	M	STRUCTURE OF IL-22/IL-22R1
3DGE	A C	A	STRUCTURE OF A HISTIDINE KINASE-RESPONSE REGULATOR COMPLEX REVEALS INSIGHTS INTO TWO-
3DGE	A C	C	STRUCTURE OF A HISTIDINE KINASE-RESPONSE REGULATOR COMPLEX REVEALS INSIGHTS INTO TWO-
3DGE	B D	B	STRUCTURE OF A HISTIDINE KINASE-RESPONSE REGULATOR COMPLEX REVEALS INSIGHTS INTO TWO-
3DI2	A B	A	CRYSTAL STRUCTURE OF THE COMPLEX OF HUMAN INTERLEUKIN-7 WITH UNGLYCOSYLATED HUMAN
3DI2	C D	C	CRYSTAL STRUCTURE OF THE COMPLEX OF HUMAN INTERLEUKIN-7 WITH UNGLYCOSYLATED HUMAN
3DOE	A B	A	COMPLEX OF ARL2 AND BART, CRYSTAL FORM 1
3DOE	A B	B	COMPLEX OF ARL2 AND BART, CRYSTAL FORM 1
3DQV	B D	D	STRUCTURAL INSIGHTS INTO NEDD8 ACTIVATION OF CULLIN-RING LIGASES: CONFORMATIONAL CONT
3DUH	A C	C	STRUCTURE OF INTERLEUKIN-23
3DUH	B D	D	STRUCTURE OF INTERLEUKIN-23
3DVE	A B	A	CRYSTAL STRUCTURE OF CA2+/CAM-CAV2.2 IQ DOMAIN COMPLEX
3DVE	A B	A	CRYSTAL STRUCTURE OF CA2+/CAM-CAV2.2 IQ DOMAIN COMPLEX
3DVE	A B	A	CRYSTAL STRUCTURE OF CA2+/CAM-CAV2.2 IQ DOMAIN COMPLEX
3DVE	A B	A	CRYSTAL STRUCTURE OF CA2+/CAM-CAV2.2 IQ DOMAIN COMPLEX
3DVU	A C	A	CRYSTAL STRUCTURE OF THE COMPLEX OF MURINE GAMMA- HERPESVIRUS 68 BCL-2 HOMOLOG M11 A
3DVU	A C	A	CRYSTAL STRUCTURE OF THE COMPLEX OF MURINE GAMMA- HERPESVIRUS 68 BCL-2 HOMOLOG M11 A
3DVU	A C	C	CRYSTAL STRUCTURE OF THE COMPLEX OF MURINE GAMMA- HERPESVIRUS 68 BCL-2 HOMOLOG M11 A
3DVU	B D	B	CRYSTAL STRUCTURE OF THE COMPLEX OF MURINE GAMMA- HERPESVIRUS 68 BCL-2 HOMOLOG M11 A
3DW8	A B	A	STRUCTURE OF A PROTEIN PHOSPHATASE 2A HOLOENZYME WITH B55 SUBUNIT
3DW8	A B	A	STRUCTURE OF A PROTEIN PHOSPHATASE 2A HOLOENZYME WITH B55 SUBUNIT
3DW8	A C	A	STRUCTURE OF A PROTEIN PHOSPHATASE 2A HOLOENZYME WITH B55 SUBUNIT
3DXC	A B	B	CRYSTAL STRUCTURE OF THE INTRACELLULAR DOMAIN OF HUMAN APP IN COMPLEX WITH FE65-PTB2
3DXC	A B	B	CRYSTAL STRUCTURE OF THE INTRACELLULAR DOMAIN OF HUMAN APP IN COMPLEX WITH FE65-PTB2
3DZU	A D	A	INTACT PPAR GAMMA - RXR ALPHA NUCLEAR RECEPTOR COMPLEX ON DNA BOUND WITH BVT.13, 9-CIS
3DZU	A D	D	INTACT PPAR GAMMA - RXR ALPHA NUCLEAR RECEPTOR COMPLEX ON DNA BOUND WITH BVT.13, 9-CIS
3E2K	A D	A	CRYSTAL STRUCTURE OF THE KPC-2 BETA-LACTAMASE/BETA-LACTAMASE INHIBITOR PROTEIN (BLIP)
3EA5	A B	A	KAP95P BINDING INDUCES THE SWITCH LOOPS OF RANGDP TO ADOPT THE GTP-BOUND CONFORMATIO
3EA5	A B	A	KAP95P BINDING INDUCES THE SWITCH LOOPS OF RANGDP TO ADOPT THE GTP-BOUND CONFORMATIO
3EA5	A B	A	KAP95P BINDING INDUCES THE SWITCH LOOPS OF RANGDP TO ADOPT THE GTP-BOUND CONFORMATIO
3EA5	A B	B	KAP95P BINDING INDUCES THE SWITCH LOOPS OF RANGDP TO ADOPT THE GTP-BOUND CONFORMATIO
3EA5	A B	B	KAP95P BINDING INDUCES THE SWITCH LOOPS OF RANGDP TO ADOPT THE GTP-BOUND CONFORMATIO
3EA5	C D	D	KAP95P BINDING INDUCES THE SWITCH LOOPS OF RANGDP TO ADOPT THE GTP-BOUND CONFORMATIO
3EAB	A G	A	CRYSTAL STRUCTURE OF SPASTIN MIT IN COMPLEX WITH ESCRT III
3EAB	A G	A	CRYSTAL STRUCTURE OF SPASTIN MIT IN COMPLEX WITH ESCRT III
3EAB	A G	G	CRYSTAL STRUCTURE OF SPASTIN MIT IN COMPLEX WITH ESCRT III
3EAB	B H	B	CRYSTAL STRUCTURE OF SPASTIN MIT IN COMPLEX WITH ESCRT III
3EAB	D J	D	CRYSTAL STRUCTURE OF SPASTIN MIT IN COMPLEX WITH ESCRT III
3EAB	E K	E	CRYSTAL STRUCTURE OF SPASTIN MIT IN COMPLEX WITH ESCRT III
3EAB	E K	K	CRYSTAL STRUCTURE OF SPASTIN MIT IN COMPLEX WITH ESCRT III

TABLE S4

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
3CUQ	PROTEIN TRANSPORT	1.9	3.7	2	11
3CUQ	PROTEIN TRANSPORT	1.0	2.0	2	22
3CWZ	TRANSPORT PROTEIN	1.3	2.5	2	32
3D2E	CHAPERONE	1.4	2.8	2	29
3D2E	CHAPERONE	1.4	5.6	4	29
3D32	TRANSPORT PROTEIN	1.9	5.8	3	12
3D7V	APOPTOSIS	1.4	5.4	4	11
3DBH	CELL CYCLE	1.7	3.3	2	11
3DBH	CELL CYCLE	1.1	2.2	2	21
3DBH	CELL CYCLE	1.2	2.3	2	11
3DBH	CELL CYCLE	1.1	2.1	2	20
3DBH	CELL CYCLE	1.3	2.6	2	21
3DBH	CELL CYCLE	1.1	2.2	2	15
3DBH	CELL CYCLE	1.3	2.5	2	21
3DCG	LIGASE/VIRAL PROTEIN	1.1	2.2	2	11
3DCG	LIGASE/VIRAL PROTEIN	1.9	7.5	4	11
3DCG	LIGASE/VIRAL PROTEIN	1.8	3.5	2	17
3DCT	TRANSCRIPTION/TRANSCRIPTION ACTIVATOR	1.5	2.9	2	26
3DCT	TRANSCRIPTION/TRANSCRIPTION ACTIVATOR	1.3	3.9	3	9
3DD7	RIBOSOME INHIBITOR	1.8	3.6	2	6
3DD7	RIBOSOME INHIBITOR	1.2	2.4	2	16
3DD7	RIBOSOME INHIBITOR	1.7	6.9	4	16
3DGC	CYTOKINE/SIGNALING PROTEIN	1.2	2.4	2	16
3DGC	CYTOKINE/SIGNALING PROTEIN	1.6	4.9	3	17
3DGE	TRANSFERASE/SIGNALING PROTEIN	1.9	3.8	2	32
3DGE	TRANSFERASE/SIGNALING PROTEIN	1.6	6.3	4	14
3DGE	TRANSFERASE/SIGNALING PROTEIN	1.3	3.9	3	15
3DI2	CYTOKINE/CYTOKINE RECEPTOR	1.9	3.8	2	16
3DI2	CYTOKINE/CYTOKINE RECEPTOR	1.9	3.7	2	17
3DOE	SIGNALING PROTEIN/HYDROLASE	1.5	3.0	2	8
3DOE	SIGNALING PROTEIN/HYDROLASE	1.5	2.9	2	10
3DQV	LIGASE	1.3	2.6	2	22
3DUH	IMMUNE SYSTEM/CYTOKINE	1.2	2.3	2	31
3DUH	IMMUNE SYSTEM/CYTOKINE	1.8	3.5	2	26
3DVE	MEMBRANE PROTEIN	1.2	2.3	2	12
3DVE	MEMBRANE PROTEIN	1.6	3.2	2	15
3DVE	MEMBRANE PROTEIN	1.5	4.4	3	13
3DVE	MEMBRANE PROTEIN	1.2	2.4	2	8
3DVU	VIRAL PROTEIN/APOPTOSIS	1.8	3.5	2	25
3DVU	VIRAL PROTEIN/APOPTOSIS	1.8	3.5	2	13
3DVU	VIRAL PROTEIN/APOPTOSIS	1.8	12.8	7	20
3DVU	VIRAL PROTEIN/APOPTOSIS	1.8	3.6	2	23
3DW8	HYDROLASE	1.4	2.8	2	12
3DW8	HYDROLASE	1.8	3.5	2	16
3DW8	HYDROLASE	1.5	5.8	4	17
3DXC	PROTEIN BINDING	1.7	5.0	3	13
3DXC	PROTEIN BINDING	1.9	7.7	4	9
3DZU	TRANSCRIPTION/DNA	1.4	2.7	2	23
3DZU	TRANSCRIPTION/DNA	1.5	2.9	2	29
3E2K	HYDROLASE/HYDROLASE INHIBITOR	1.2	2.3	2	6
3EA5	TRANSPORT PROTEIN	1.7	3.4	2	5
3EA5	TRANSPORT PROTEIN	1.0	3.0	3	14
3EA5	TRANSPORT PROTEIN	1.0	3.1	3	12
3EA5	TRANSPORT PROTEIN	1.3	2.6	2	25
3EA5	TRANSPORT PROTEIN	1.3	3.9	3	13
3EA5	TRANSPORT PROTEIN	1.4	2.8	2	28
3EAB	CELL CYCLE	1.8	3.5	2	28
3EAB	CELL CYCLE	1.9	5.7	3	28
3EAB	CELL CYCLE	1.6	4.7	3	22
3EAB	CELL CYCLE	1.9	3.7	2	25
3EAB	CELL CYCLE	1.5	4.4	3	26
3EAB	CELL CYCLE	1.6	4.8	3	28
3EAB	CELL CYCLE	1.9	11.6	6	20

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
3CUQ	266	276
3CUQ	23	44
3CWZ	718	749
3D2E	559	587
3D2E	559	587
3D32	59	70
3D7V	244	254
3DBH	476	486
3DBH	293	313
3DBH	476	486
3DBH	491	510
3DBH	293	313
3DBH	148	162
3DBH	491	511
3DCG	100	110
3DCG	145	155
3DCG	67	83
3DCT	313	338
3DCT	747	755
3DD7	64	69
3DD7	72	87
3DD7	6	21
3DGC	114	129
3DGC	113	129
3DGE	285	316
3DGE	12	25
3DGE	264	278
3DI2	74	89
3DI2	10	26
3DOE	3	10
3DOE	107	116
3DQV	1701	1722
3DUH	139	169
3DUH	143	168
3DVE	118	129
3DVE	6	20
3DVE	65	77
3DVE	138	145
3DVU	32	56
3DVU	67	79
3DVU	107	126
3DVU	35	57
3DW8	10	21
3DW8	179	194
3DW8	495	511
3DXC	669	681
3DXC	685	693
3DZU	386	408
3DZU	431	459
3E2K	107	112
3EA5	77	81
3EA5	157	170
3EA5	101	112
3EA5	563	587
3EA5	55	67
3EA5	280	307
3EAB	169	196
3EAB	110	137
3EAB	175	196
3EAB	169	193
3EAB	169	194
3EAB	169	196
3EAB	174	193

A. PDB CODE	L. HELIX SEQUENCE
3CUQ	LTEVYCLVNRA
3CUQ	VDTRQKQLAAWCSLVLSFCRLH
3CWZ	VIAQTNWKFVEGLLKECRNKTKRMLVEKMGRE
3D2E	AQDKLVAETEDRKNTLEEYIYTLRGKLEE
3D2E	AQDKLVAETEDRKNTLEEYIYTLRGKLEE
3D32	VGQFYFLIRKRI
3D7V	KSLSRVMIHVF
3DBH	DDYVHEFCRYG
3DBH	ASTNAVIAAVCATEVFKIATS
3DBH	DDYVHEFCRYG
3DBH	HTIAAFLGGAAAQEVIKIIT
3DBH	ASTNAVIAAVCATEVFKIATS
3DBH	IIARRWINGMLISLL
3DBH	HTIAAFLGGAAAQEVIKIITK
3DCG	ALELLMAANFL
3DCG	LQYLALAALIK
3DCG	SHVLSKVCMYFTYKVRY
3DCT	HEDQIALLKGSAVEAMFLRSAEIFNK
3DCT	QLLRYLLDK
3DD7	DSTNKE
3DD7	NKRTALNSALLFLRRN
3DD7	PEELIALHDANISRYG
3DGC	YMQEVVPFLARLSNRL
3DGC	PYMQEVVPFLARLSNRL
3DGE	LSTLKEFLEVIIDQSNHLENLLNELLDFSRLE
3DGE	AVLRKIVSFNLKKE
3DGE	TPLTAIKAYAETIYN
3DI2	DFDLHLLKVSEGTTIL
3DI2	KQYESVLMVSIDQLLDS
3DOE	LLTILKKM
3DOE	DIFDMLLTFT
3DQV	EEENEGIVQLRILRTQEAIIQI
3DUH	RLLLRFKILRSLQAFVAVAARVFAHGAATLS
3DUH	RFKILRSLQAFVAVAARVFAHGAATL
3DVE	DEEVDEMIREAD
3DVE	EEQIAEFKEAFSLFD
3DVE	FPEFLTMMARKMK
3DVE	YEEFVQMM
3DVU	SAVLVDVSKIITLTQEFRRHYDSVY
3DVU	WKRDLSKLFTSLF
3DVU	GTMENLSRRLKVTGDLFDIM
3DVU	LVDVSKIITLTQEFRRHYDSVYR
3DW8	LYPIAVLIDELR
3DW8	PMVRRAAASKLGEFAK
3DW8	YLHRMTTLFCINVLSEV
3DXC	PEERHLSKMQQNG
3DXC	PTYKFFEQM
3DZU	PAEVEALREKVYASLEAYCKHKY
3DZU	LFAKLLQKMTDLRQIVTEHVQLLQVIKKT
3E2K	PISEKY
3EA5	DGYYI
3EA5	FEKPFLWLARKLIG
3EA5	VPNWHRDLVRVC
3EA5	LEDAQSLQELQSNILTVLAAVIRKS
3EA5	LEGRILAALTLKN
3EA5	DKVASMTVEFWSTICEEEIDIAYELAQF
3EAB	EQCERARRLQAKMMTNLVMAKDRLQLLE
3EAB	SMEAERVRVFHKQAFEYISIALRIDEDE
3EAB	SVGTSVASAEQDELSQRLARLR
3EAB	EQCERARRLQAKMMTNLVMAKDRLQ
3EAB	EQCERARRLQAKMMTNLVMAKDRLQL
3EAB	EQCERARRLQAKMMTNLVMAKDRLQLLE
3EAB	GSVGTSVASAEQDELSQRLA

A. PDB CODE	M. RESOLUTION
3CUQ	2.61
3CUQ	2.61
3CWZ	3.2
3D2E	2.35
3D2E	2.35
3D32	1.3
3D7V	2.03
3DBH	2.85
3DBH	2.85
3DBH	2.85
3DBH	2.85
3DBH	2.85
3DBH	2.85
3DBH	2.85
3DCG	2.4
3DCG	2.4
3DCG	2.4
3DCT	2.5
3DCT	2.5
3DD7	1.7
3DD7	1.7
3DD7	1.7
3DGC	2.5
3DGC	2.5
3DGE	2.8
3DGE	2.8
3DGE	2.8
3DI2	2.7
3DI2	2.7
3DOE	2.25
3DOE	2.25
3DQV	3
3DUH	2.3
3DUH	2.3
3DVE	2.35
3DVE	2.35
3DVE	2.35
3DVE	2.35
3DVU	2.5
3DVU	2.5
3DVU	2.5
3DVU	2.5
3DW8	2.85
3DW8	2.85
3DW8	2.85
3DXC	2.1
3DXC	2.1
3DZU	3.2
3DZU	3.2
3E2K	2.1
3EA5	2.5
3EA5	2.5
3EA5	2.5
3EA5	2.5
3EA5	2.5
3EA5	2.5
3EAB	2.5
3EAB	2.5
3EAB	2.5
3EAB	2.5
3EAB	2.5
3EAB	2.5
3EAB	2.5

TABLE S4

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
3EAB	F L	F	CRYSTAL STRUCTURE OF SPASTIN MIT IN COMPLEX WITH ESCRT III
3ECH	A C	A	THE MARR-FAMILY REPRESSOR MEXR IN COMPLEX WITH ITS ANTIREPRESSOR ARMR
3ECH	B C	B	THE MARR-FAMILY REPRESSOR MEXR IN COMPLEX WITH ITS ANTIREPRESSOR ARMR
3ECH	B C	B	THE MARR-FAMILY REPRESSOR MEXR IN COMPLEX WITH ITS ANTIREPRESSOR ARMR
3EG5	A B	A	CRYSTAL STRUCTURE OF MDIA1-TSH GBD-FH3 IN COMPLEX WITH CDC42-GMPPNP
3EG5	A B	B	CRYSTAL STRUCTURE OF MDIA1-TSH GBD-FH3 IN COMPLEX WITH CDC42-GMPPNP
3EHU	A C	C	CRYSTAL STRUCTURE OF THE EXTRACELLULAR DOMAIN OF HUMAN CORTICOTROPIN RELEASING FAC
3EIQ	A C	C	CRYSTAL STRUCTURE OF PDCD4-EIF4A
3EJB	A B	A	CRYSTAL STRUCTURE OF P450BIOI IN COMPLEX WITH TETRADECANOIC ACID LIGATED ACYL CARRIER
3EUH	A C	A	CRYSTAL STRUCTURE OF THE MUKE-MUKF COMPLEX
3EUH	A C	A	CRYSTAL STRUCTURE OF THE MUKE-MUKF COMPLEX
3EUH	B E	B	CRYSTAL STRUCTURE OF THE MUKE-MUKF COMPLEX
3EUH	B E	E	CRYSTAL STRUCTURE OF THE MUKE-MUKF COMPLEX
3EX7	A B	A	THE CRYSTAL STRUCTURE OF EJC IN ITS TRANSITION STATE
3EX7	E H	H	THE CRYSTAL STRUCTURE OF EJC IN ITS TRANSITION STATE
3EX7	H I	H	THE CRYSTAL STRUCTURE OF EJC IN ITS TRANSITION STATE
3EZQ	A B	A	CRYSTAL STRUCTURE OF THE FAS/FADD DEATH DOMAIN COMPLEX
3EZQ	A B	B	CRYSTAL STRUCTURE OF THE FAS/FADD DEATH DOMAIN COMPLEX
3EZQ	E F	E	CRYSTAL STRUCTURE OF THE FAS/FADD DEATH DOMAIN COMPLEX
3EZQ	M N	M	CRYSTAL STRUCTURE OF THE FAS/FADD DEATH DOMAIN COMPLEX
3F1I	H S	H	HUMAN ESCRT-0 CORE COMPLEX
3F1I	H S	S	HUMAN ESCRT-0 CORE COMPLEX
3F1I	H S	S	HUMAN ESCRT-0 CORE COMPLEX
3F3P	B D	D	CRYSTAL STRUCTURE OF A NUCLEOPORIN COMPLEX, SPACE GROUP P21212
3F3P	F H	H	CRYSTAL STRUCTURE OF A NUCLEOPORIN COMPLEX, SPACE GROUP P21212
3F5C	A C	A	STRUCTURE OF DAX-1:LRH-1 COMPLEX
3F6Q	A B	B	CRYSTAL STRUCTURE OF INTEGRIN-LINKED KINASE ANKYRIN REPEAT DOMAIN IN COMPLEX WITH PIN
3F75	A P	A	ACTIVATED TOXOPLASMA GONDII CATHEPSIN L (TGCPL) IN COMPLEX WITH ITS PROPEPTIDE
3F75	A P	P	ACTIVATED TOXOPLASMA GONDII CATHEPSIN L (TGCPL) IN COMPLEX WITH ITS PROPEPTIDE
3F7P	A C	A	CRYSTAL STRUCTURE OF A COMPLEX BETWEEN INTEGRIN BETA4 AND PLECTIN
3F9K	A C	A	TWO DOMAIN FRAGMENT OF HIV-2 INTEGRASE IN COMPLEX WITH LEDGF IBD
3F9K	E G	E	TWO DOMAIN FRAGMENT OF HIV-2 INTEGRASE IN COMPLEX WITH LEDGF IBD
3F9K	g i	g	TWO DOMAIN FRAGMENT OF HIV-2 INTEGRASE IN COMPLEX WITH LEDGF IBD
3F9K	I K	I	TWO DOMAIN FRAGMENT OF HIV-2 INTEGRASE IN COMPLEX WITH LEDGF IBD
3F9K	I K	K	TWO DOMAIN FRAGMENT OF HIV-2 INTEGRASE IN COMPLEX WITH LEDGF IBD
3F9K	J K	J	TWO DOMAIN FRAGMENT OF HIV-2 INTEGRASE IN COMPLEX WITH LEDGF IBD
3F9K	M O	M	TWO DOMAIN FRAGMENT OF HIV-2 INTEGRASE IN COMPLEX WITH LEDGF IBD
3F9K	Q S	Q	TWO DOMAIN FRAGMENT OF HIV-2 INTEGRASE IN COMPLEX WITH LEDGF IBD
3F9K	Y a	a	TWO DOMAIN FRAGMENT OF HIV-2 INTEGRASE IN COMPLEX WITH LEDGF IBD
3F9K	Y a	Y	TWO DOMAIN FRAGMENT OF HIV-2 INTEGRASE IN COMPLEX WITH LEDGF IBD
3FAL	A B	A	HUMANRXR ALPHA & MOUSE LXR ALPHA COMPLEXED WITH RETENOIC ACID AND GSK2186
3FAL	A B	A	HUMANRXR ALPHA & MOUSE LXR ALPHA COMPLEXED WITH RETENOIC ACID AND GSK2186
3FAL	A B	B	HUMANRXR ALPHA & MOUSE LXR ALPHA COMPLEXED WITH RETENOIC ACID AND GSK2186
3FAL	A D	A	HUMANRXR ALPHA & MOUSE LXR ALPHA COMPLEXED WITH RETENOIC ACID AND GSK2186
3FAL	C B	C	HUMANRXR ALPHA & MOUSE LXR ALPHA COMPLEXED WITH RETENOIC ACID AND GSK2186
3FAL	C D	C	HUMANRXR ALPHA & MOUSE LXR ALPHA COMPLEXED WITH RETENOIC ACID AND GSK2186
3FDL	A B	A	BIM BH3 PEPTIDE IN COMPLEX WITH BCL-XL
3FHI	A B	A	CRYSTAL STRUCTURE OF A COMPLEX BETWEEN THE CATALYTIC AND REGULATORY (RI{ALPHA}) SUBU
3FMO	A B	B	CRYSTAL STRUCTURE OF THE NUCLEOPORIN NUP214 IN COMPLEX WITH THE DEAD-BOX HELICASE DD
3FMP	C D	D	CRYSTAL STRUCTURE OF THE NUCLEOPORIN NUP214 IN COMPLEX WITH THE DEAD-BOX HELICASE DD
3FSH	B C	C	CRYSTAL STRUCTURE OF THE UBIQUITIN CONJUGATING ENZYME UBE2G2 BOUND TO THE G2BR DOMA
3FUB	C D	C	CRYSTAL STRUCTURE OF GDNF-GFRALPHA1 COMPLEX
3FWB	A B	A	SAC3:SUS1:CDC31 COMPLEX
3FWB	A B	A	SAC3:SUS1:CDC31 COMPLEX
3FWB	A B	A	SAC3:SUS1:CDC31 COMPLEX
3FWB	B C	C	SAC3:SUS1:CDC31 COMPLEX
3FWB	B C	C	SAC3:SUS1:CDC31 COMPLEX
3G33	A D	A	CRYSTAL STRUCTURE OF CDK4/CYCLIN D3
3G33	A D	D	CRYSTAL STRUCTURE OF CDK4/CYCLIN D3
3G33	C B	B	CRYSTAL STRUCTURE OF CDK4/CYCLIN D3
3G33	C B	C	CRYSTAL STRUCTURE OF CDK4/CYCLIN D3
3G9V	C D	D	CRYSTAL STRUCTURE OF A SOLUBLE DECOY RECEPTOR IL-22BP BOUND TO INTERLEUKIN-22
3GCG	A B	A	CRYSTAL STRUCTURE OF MAP AND CDC42 COMPLEX

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM,\ HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
3EAB	CELL CYCLE	1.8	3.6	2	25
3ECH	TRANSCRIPTION, TRANSCRIPTION REGULATION	1.7	6.6	4	24
3ECH	TRANSCRIPTION, TRANSCRIPTION REGULATION	1.6	4.8	3	23
3ECH	TRANSCRIPTION, TRANSCRIPTION REGULATION	1.2	2.3	2	13
3EG5	SIGNALING PROTEIN	1.9	3.8	2	19
3EG5	SIGNALING PROTEIN	1.2	2.4	2	15
3EHU	MEMBRANE PROTEIN	1.5	3.0	2	15
3EIQ	HYDROLASE/ANTITUMOR PROTEIN	1.2	2.4	2	10
3EJB	OXIDOREDUCTASE/LIPID TRANSPORT	1.5	5.9	4	14
3EUH	CELL CYCLE	1.5	2.9	2	40
3EUH	CELL CYCLE	1.6	3.2	2	12
3EUH	CELL CYCLE	1.8	5.5	3	40
3EUH	CELL CYCLE	1.4	4.2	3	15
3EX7	HYDROLASE/RNA BINDING PROTEIN/RNA	1.2	2.3	2	15
3EX7	HYDROLASE/RNA BINDING PROTEIN/RNA	1.5	2.9	2	11
3EX7	HYDROLASE/RNA BINDING PROTEIN/RNA	1.3	2.6	2	14
3EZQ	APOPTOSIS	1.9	3.8	2	33
3EZQ	APOPTOSIS	1.3	3.9	3	16
3EZQ	APOPTOSIS	1.5	4.5	3	15
3EZQ	APOPTOSIS	1.6	8.2	5	32
3F1I	PROTEIN BINDING	1.5	6.0	4	26
3F1I	PROTEIN BINDING	1.9	5.7	3	13
3F1I	PROTEIN BINDING	1.9	18.8	10	50
3F3P	STRUCTURAL PROTEIN	1.6	3.2	2	14
3F3P	STRUCTURAL PROTEIN	1.9	3.7	2	7
3F5C	TRANSCRIPTION	1.5	3.0	2	18
3F6Q	SIGNALING PROTEIN/SIGNALING PROTEIN	1.7	6.6	4	9
3F75	HYDROLASE	1.4	2.8	2	5
3F75	HYDROLASE	1.4	2.8	2	23
3F7P	STRUCTURAL PROTEIN/CELL ADHESION	1.4	2.7	2	19
3F9K	VIRAL PROTEIN, RECOMBINATION	1.5	4.5	3	12
3F9K	VIRAL PROTEIN, RECOMBINATION	1.2	2.3	2	12
3F9K	VIRAL PROTEIN, RECOMBINATION	1.7	6.8	4	12
3F9K	VIRAL PROTEIN, RECOMBINATION	1.4	4.1	3	12
3F9K	VIRAL PROTEIN, RECOMBINATION	1.2	2.3	2	10
3F9K	VIRAL PROTEIN, RECOMBINATION	1.7	3.3	2	11
3F9K	VIRAL PROTEIN, RECOMBINATION	1.5	4.4	3	12
3F9K	VIRAL PROTEIN, RECOMBINATION	1.6	3.1	2	12
3F9K	VIRAL PROTEIN, RECOMBINATION	1.2	2.4	2	15
3F9K	VIRAL PROTEIN, RECOMBINATION	1.7	3.3	2	12
3FAL	SIGNALING PROTEIN	1.7	3.4	2	18
3FAL	SIGNALING PROTEIN	1.9	7.7	4	12
3FAL	SIGNALING PROTEIN	1.6	6.5	4	26
3FAL	SIGNALING PROTEIN	1.5	5.9	4	8
3FAL	SIGNALING PROTEIN	1.3	2.5	2	8
3FAL	SIGNALING PROTEIN	1.2	2.4	2	13
3FDL	APOPTOSIS	1.2	3.5	3	13
3FHI	TRANSFERASE	1.6	3.1	2	11
3FMO	ONCOPROTEIN/HYDROLASE	1.8	5.5	3	11
3FMP	ONCOPROTEIN/HYDROLASE	1.8	3.5	2	12
3FSH	LIGASE	1.7	6.6	4	17
3FUB	HORMONE	1.1	2.1	2	11
3FWB	CELL CYCLE, TRANSCRIPTION	1.4	2.7	2	11
3FWB	CELL CYCLE, TRANSCRIPTION	1.9	9.7	5	11
3FWB	CELL CYCLE, TRANSCRIPTION	1.9	3.7	2	13
3FWB	CELL CYCLE, TRANSCRIPTION	1.6	4.8	3	15
3FWB	CELL CYCLE, TRANSCRIPTION	1.5	4.6	3	15
3G33	CELL CYCLE	1.5	4.5	3	17
3G33	CELL CYCLE	1.4	2.8	2	15
3G33	CELL CYCLE	1.8	3.5	2	15
3G33	CELL CYCLE	1.8	7.0	4	17
3G9V	CYTOKINE/CYTOKINE RECEPTOR	1.1	4.3	4	12
3GCG	SIGNALING PROTEIN/TRANSCRIPTION	1.3	4.0	3	9

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
3EAB	169	193
3ECH	99	122
3ECH	9	31
3ECH	37	49
3EG5	87	105
3EG5	202	216
3EHU	27	41
3EIQ	181	190
3EJB	57	70
3EUH	252	291
3EUH	296	307
3EUH	247	286
3EUH	99	113
3EX7	54	68
3EX7	386	396
3EX7	287	300
3EZQ	287	319
3EZQ	171	186
3EZQ	225	239
3EZQ	287	318
3F1I	405	430
3F1I	304	316
3F1I	327	376
3F3P	532	545
3F3P	504	510
3F5C	525	542
3F6Q	60	68
3F75	147	151
3F75	131	153
3F7P	157	175
3F9K	5	16
3F9K	5	16
3F9K	5	16
3F9K	5	16
3F9K	394	403
3F9K	124	134
3F9K	5	16
3F9K	5	16
3F9K	348	362
3F9K	5	16
3FAL	343	360
3FAL	421	432
3FAL	399	424
3FAL	451	458
3FAL	451	458
3FAL	421	433
3FDL	119	131
3FHI	243	253
3FMO	253	263
3FMP	218	229
3FSH	582	598
3FUB	153	163
3FWB	151	161
3FWB	115	125
3FWB	94	106
3FWB	58	72
3FWB	38	52
3G33	56	72
3G33	24	38
3G33	24	38
3G33	56	72
3G9V	167	178
3GCG	65	73

A. PDB CODE	L. HELIX SEQUENCE
3EAB	EQCERARRLQAKMMTNLVMAKDRLQ
3ECH	DEGLAIHLHAELIMSRVHDELFAP
3ECH	LMPALMAVFQHVRTRIQSELDCQ
3ECH	PPDVHVLKLIDEQ
3EG5	PSSFENVKEKWVPEITHHC
3EG5	SRNQHEIIRCLKAFM
3EHU	LAQQAHSNRKLMEII
3EIQ	TNEVAEMLRD
3EJB	LDTVELVMALEEEF
3EUH	LVFDLQSKLDRIISWGQQSIDLWIGYDRHVHKFIRTAIDM
3EUH	VFAQRLRQSVQT
3EUH	HFVDRLVFDLQSKLDRIISWGQQSIDLWIGYDRHVHKFIR
3EUH	ELDMMVGKILCYLYL
3EX7	KSVMEELKRIIDDSE
3EX7	IRILRDIEQYY
3EX7	KRKVDWLTEKMREA
3EZQ	KKEAYDTLIKDLKKANLCTLAEKIQTIILKDIT
3EZQ	NLVADLVQEVQQARDL
3EZQ	SDVDLSKYITTIAGV
3EZQ	KKEAYDTLIKDLKKANLCTLAEKIQTIILKDI
3F1I	HEQFLKALQNAVTTFVNRMKSNHMRG
3F1I	EDKMDQLLQMLQS
3F1I	PELLHLEAMCHQMGPLIDEKLEDIDRKHSELSELNVKVMEALSLYTKLMN
3F3P	PEIAKEIYTTLGNQ
3F3P	IAELLPH
3F5C	LRAISKQAEDYLYYKHVN
3F6Q	EHDFQMLFA
3F75	MPFQF
3F75	EEEKQRRYAIFKNNLVYIHTHNQ
3F7P	PKLTLGLIWTIILHFQISD
3F9K	IEPAQEEHEKYH
3F9K	IEPAQEEHEKYH
3F9K	IEPAQEEHEKYH
3F9K	IEPAQEEHEKYH
3F9K	TEMITTLKKI
3F9K	QEVKMVAWWIG
3F9K	IEPAQEEHEKYH
3F9K	IEPAQEEHEKYH
3F9K	MDSRLQRIHAEIKNS
3F9K	IEPAQEEHEKYH
3FAL	GAIFDRVLTELVSKMRDM
3FAL	RLPALRSIGLKC
3FAL	PLMFPRMLMKLVSLRTLSSVHSEQVF
3FAL	FLMEMLEA
3FAL	FLMEMLEA
3FAL	RLPALRSIGLKCL
3FDL	AYQSFEQVVNELF
3FHI	PIQIYEKIVSG
3FMO	HQDQSIRIQRM
3FMP	PGTVLDWCSKLK
3FSH	LVQRKDELLQQARKRFL
3FUB	NCLDAAKACNL
3FWB	ENEFIAICTDS
3FWB	IKNLRRVAKEL
3FWB	PLDEIKRAFQLFD
3FWB	FTQILSTVEPKALEM
3FWB	WVDKVKDLTKSEMNI
3G33	ISTVREVALLRRLEAFE
3G33	DQRVLQSLLRLEERY
3G33	DQRVLQSLLRLEERY
3G33	ISTVREVALLRRLEAFE
3G9V	LDLLFMSLRNAC
3GCG	DRLRPLSYP

A. PDB CODE	M. RESOLUTION
3EAB	2.5
3ECH	1.8
3ECH	1.8
3ECH	1.8
3EG5	2.7
3EG5	2.7
3EHU	1.96
3EIQ	3.5
3EJB	2
3EUH	2.9
3EUH	2.9
3EUH	2.9
3EUH	2.9
3EX7	2.3
3EX7	2.3
3EX7	2.3
3EZQ	2.73
3EZQ	2.73
3EZQ	2.73
3EZQ	2.73
3F1I	2.3
3F1I	2.3
3F1I	2.3
3F3P	3.2
3F3P	3.2
3F5C	3
3F6Q	1.6
3F75	1.99
3F75	1.99
3F7P	2.75
3F9K	3.2
3F9K	3.2
3F9K	3.2
3F9K	3.2
3F9K	3.2
3F9K	3.2
3F9K	3.2
3F9K	3.2
3F9K	3.2
3F9K	3.2
3FAL	2.36
3FAL	2.36
3FAL	2.36
3FAL	2.36
3FAL	2.36
3FAL	2.36
3FDL	1.78
3FHI	2
3FMO	2.51
3FMP	3.19
3FSH	2.76
3FUB	2.35
3FWB	2.5
3FWB	2.5
3FWB	2.5
3FWB	2.5
3FWB	2.5
3G33	3
3G33	3
3G33	3
3G33	3
3G9V	2.76
3GCG	2.3

A. PDB CODE	B. INTERFACE CHAINS	C. CHAIN	D. TITLE
3GCG	A B	B	CRYSTAL STRUCTURE OF MAP AND CDC42 COMPLEX
3GJX	B A	A	CRYSTAL STRUCTURE OF THE NUCLEAR EXPORT COMPLEX CRM1- SNURPORTIN1-RANGTP
3GJX	C A	A	CRYSTAL STRUCTURE OF THE NUCLEAR EXPORT COMPLEX CRM1- SNURPORTIN1-RANGTP
3GJX	C A	A	CRYSTAL STRUCTURE OF THE NUCLEAR EXPORT COMPLEX CRM1- SNURPORTIN1-RANGTP
3GJX	C A	C	CRYSTAL STRUCTURE OF THE NUCLEAR EXPORT COMPLEX CRM1- SNURPORTIN1-RANGTP
3GJX	F D	D	CRYSTAL STRUCTURE OF THE NUCLEAR EXPORT COMPLEX CRM1- SNURPORTIN1-RANGTP
3GJX	F D	F	CRYSTAL STRUCTURE OF THE NUCLEAR EXPORT COMPLEX CRM1- SNURPORTIN1-RANGTP
3GM1	A E	E	CRYSTAL STRUCTURE OF THE FOCAL ADHESION TARGETING (FAT) DOMAIN OF PYK2 IN COMPLEX WITH
3GM1	A F	A	CRYSTAL STRUCTURE OF THE FOCAL ADHESION TARGETING (FAT) DOMAIN OF PYK2 IN COMPLEX WITH
3GM1	A F	A	CRYSTAL STRUCTURE OF THE FOCAL ADHESION TARGETING (FAT) DOMAIN OF PYK2 IN COMPLEX WITH
3GM1	A F	F	CRYSTAL STRUCTURE OF THE FOCAL ADHESION TARGETING (FAT) DOMAIN OF PYK2 IN COMPLEX WITH
3GM1	B C	C	CRYSTAL STRUCTURE OF THE FOCAL ADHESION TARGETING (FAT) DOMAIN OF PYK2 IN COMPLEX WITH
3GM1	B D	D	CRYSTAL STRUCTURE OF THE FOCAL ADHESION TARGETING (FAT) DOMAIN OF PYK2 IN COMPLEX WITH
3GMW	C D	C	CRYSTAL STRUCTURE OF BETA-LACTAMSE INHIBITORY PROTEIN-I (BLIP-I) IN COMPLEX WITH TEM-1 BE
3GNI	A B	A	STRUCTURE OF STRAD AND MO25
3GNI	A B	A	STRUCTURE OF STRAD AND MO25
3GNI	A B	A	STRUCTURE OF STRAD AND MO25
3H11	A B	A	ZYMOGEN CASPASE-8:C-FLIPL PROTEASE DOMAIN COMPLEX
3H11	A B	B	ZYMOGEN CASPASE-8:C-FLIPL PROTEASE DOMAIN COMPLEX
3H4S	A E	A	STRUCTURE OF THE COMPLEX OF A MITOTIC KINESIN WITH ITS CALCIUM BINDING REGULATOR
3H4S	A E	E	STRUCTURE OF THE COMPLEX OF A MITOTIC KINESIN WITH ITS CALCIUM BINDING REGULATOR
3H6P	A C	A	CRYSTAL STRUCTURE OF RV3019C-RV3020C FROM MYCOBACTERIUM TUBERCULOSIS
3H6P	A D	A	CRYSTAL STRUCTURE OF RV3019C-RV3020C FROM MYCOBACTERIUM TUBERCULOSIS
3H6P	A D	D	CRYSTAL STRUCTURE OF RV3019C-RV3020C FROM MYCOBACTERIUM TUBERCULOSIS
3H6P	B C	B	CRYSTAL STRUCTURE OF RV3019C-RV3020C FROM MYCOBACTERIUM TUBERCULOSIS
3H6P	B D	B	CRYSTAL STRUCTURE OF RV3019C-RV3020C FROM MYCOBACTERIUM TUBERCULOSIS
3H6P	B D	D	CRYSTAL STRUCTURE OF RV3019C-RV3020C FROM MYCOBACTERIUM TUBERCULOSIS
3H9R	A B	A	CRYSTAL STRUCTURE OF THE KINASE DOMAIN OF TYPE I ACTIVIN RECEPTOR (ACVR1) IN COMPLEX WI
3HD7	A B	A	HELICAL EXTENSION OF THE NEURONAL SNARE COMPLEX INTO THE MEMBRANE, SPACEGROUP C 1 2 1
3HD7	A B	A	HELICAL EXTENSION OF THE NEURONAL SNARE COMPLEX INTO THE MEMBRANE, SPACEGROUP C 1 2 1
3HD7	A B	B	HELICAL EXTENSION OF THE NEURONAL SNARE COMPLEX INTO THE MEMBRANE, SPACEGROUP C 1 2 1
3HD7	A D	A	HELICAL EXTENSION OF THE NEURONAL SNARE COMPLEX INTO THE MEMBRANE, SPACEGROUP C 1 2 1
3HD7	B C	B	HELICAL EXTENSION OF THE NEURONAL SNARE COMPLEX INTO THE MEMBRANE, SPACEGROUP C 1 2 1
3HD7	B C	C	HELICAL EXTENSION OF THE NEURONAL SNARE COMPLEX INTO THE MEMBRANE, SPACEGROUP C 1 2 1
3HD7	C D	C	HELICAL EXTENSION OF THE NEURONAL SNARE COMPLEX INTO THE MEMBRANE, SPACEGROUP C 1 2 1
3HD7	C D	D	HELICAL EXTENSION OF THE NEURONAL SNARE COMPLEX INTO THE MEMBRANE, SPACEGROUP C 1 2 1
3HD7	E F	E	HELICAL EXTENSION OF THE NEURONAL SNARE COMPLEX INTO THE MEMBRANE, SPACEGROUP C 1 2 1
3HD7	E F	E	HELICAL EXTENSION OF THE NEURONAL SNARE COMPLEX INTO THE MEMBRANE, SPACEGROUP C 1 2 1
3HD7	E F	F	HELICAL EXTENSION OF THE NEURONAL SNARE COMPLEX INTO THE MEMBRANE, SPACEGROUP C 1 2 1
3HD7	E H	E	HELICAL EXTENSION OF THE NEURONAL SNARE COMPLEX INTO THE MEMBRANE, SPACEGROUP C 1 2 1
3HD7	E H	E	HELICAL EXTENSION OF THE NEURONAL SNARE COMPLEX INTO THE MEMBRANE, SPACEGROUP C 1 2 1
3HD7	E H	H	HELICAL EXTENSION OF THE NEURONAL SNARE COMPLEX INTO THE MEMBRANE, SPACEGROUP C 1 2 1
3HD7	F G	F	HELICAL EXTENSION OF THE NEURONAL SNARE COMPLEX INTO THE MEMBRANE, SPACEGROUP C 1 2 1
3HD7	F G	G	HELICAL EXTENSION OF THE NEURONAL SNARE COMPLEX INTO THE MEMBRANE, SPACEGROUP C 1 2 1
3HD7	G H	H	HELICAL EXTENSION OF THE NEURONAL SNARE COMPLEX INTO THE MEMBRANE, SPACEGROUP C 1 2 1
3HGK	C G	G	CRYSTAL STRUCTURE OF EFFECT PROTEIN AVRPTOB COMPLEXED WITH KINASE PTO
3HH2	A D	D	CRYSTAL STRUCTURE OF THE MYOSTATIN:FOLLISTATIN 288 COMPLEX
3HHR	A B	A	HUMAN GROWTH HORMONE AND EXTRACELLULAR DOMAIN OF ITS RECEPTOR: CRYSTAL STRUCTURE
3HHZ	C M	M	COMPLEX OF THE VESICULAR STOMATITIS VIRUS NUCLEOCAPSID AND THE NUCLEOCAPSID-BINDING I
3HKI	D E	D	CRYSTAL STRUCTURE OF MURINE THROMBIN MUTANT W215A/E217A IN COMPLEX WITH THE EXTRACE
3HO5	B H	B	CRYSTAL STRUCTURE OF HEDGEHOG-INTERACTING PROTEIN (HHIP) AND SONIC HEDGEHOG (SHH) COM
3HUJ	A G	A	CRYSTAL STRUCTURE OF HUMAN CD1D-ALPHA-GALACTOSYLCERAMIDE IN COMPLEX WITH SEMI-INVA
3HUJ	G H	H	CRYSTAL STRUCTURE OF HUMAN CD1D-ALPHA-GALACTOSYLCERAMIDE IN COMPLEX WITH SEMI-INVA
3I1H	A B	A	CRYSTAL STRUCTURE OF HUMAN BFL-1 IN COMPLEX WITH BAK BH3 PEPTIDE
3I1H	A B	B	CRYSTAL STRUCTURE OF HUMAN BFL-1 IN COMPLEX WITH BAK BH3 PEPTIDE

(a) PDB code of predicted target. (b) Chains in the complex featuring a helix at the interface. (c) Candidate helix to be mim
for mutating two or more key residues in the helix at the interface to alanine. (g) ΔΔGsum/helix is derived from Rosetta co
(j) First residue of the candidate helix segment. (k) Last residue of the candidate helix segment. (l) Sequence of candidate h

A. PDB CODE	E. FUNCTION	F. $\Delta\Delta G_{AVG,HELIX}$ (KCAL/MOL)	G. $\Delta\Delta G_{SUM, HELIX}$ (KCAL/MOL)	H. # HOTSPOT RESIDUES	I. HELIX LENGTH
3GCG	SIGNALING PROTEIN/TRANSCRIPTION	1.3	2.6	2	28
3GJX	PROTEIN TRANSPORT	1.9	3.8	2	22
3GJX	PROTEIN TRANSPORT	1.5	2.9	2	20
3GJX	PROTEIN TRANSPORT	1.1	2.2	2	18
3GJX	PROTEIN TRANSPORT	1.5	4.4	3	6
3GJX	PROTEIN TRANSPORT	1.2	2.4	2	18
3GJX	PROTEIN TRANSPORT	1.5	3.0	2	6
3GM1	TRANSFERASE	1.3	3.9	3	9
3GM1	TRANSFERASE	1.6	8.2	5	28
3GM1	TRANSFERASE	1.4	2.7	2	31
3GM1	TRANSFERASE	1.8	3.5	2	6
3GM1	TRANSFERASE	1.8	5.4	3	10
3GM1	TRANSFERASE	1.7	5.0	3	10
3GMW	PROTEIN BINDING	1.6	3.1	2	5
3GNI	SIGNALING PROTEIN/SIGNALING PROTEIN	1.4	2.8	2	16
3GNI	SIGNALING PROTEIN/SIGNALING PROTEIN	1.3	2.6	2	10
3GNI	SIGNALING PROTEIN/SIGNALING PROTEIN	1.5	2.9	2	16
3H11	APOPTOSIS	1.3	5.2	4	17
3H11	APOPTOSIS	1.2	3.6	3	14
3H4S	MOTOR PROTEIN/CALCIUM BINDING PROTEIN	1.8	5.3	3	21
3H4S	MOTOR PROTEIN/CALCIUM BINDING PROTEIN	1.2	3.5	3	19
3H6P	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	1.7	5.1	3	58
3H6P	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	1.7	8.5	5	58
3H6P	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	1.7	8.3	5	23
3H6P	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	1.8	9.1	5	63
3H6P	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	1.7	3.3	2	63
3H6P	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	1.7	8.7	5	20
3H9R	ISOMERASE/PROTEIN KINASE	1.3	2.6	2	9
3HD7	EXOCYTOSIS	1.3	4.0	3	44
3HD7	EXOCYTOSIS	1.5	6.0	4	41
3HD7	EXOCYTOSIS	1.6	9.6	6	95
3HD7	EXOCYTOSIS	1.4	2.8	2	41
3HD7	EXOCYTOSIS	1.6	16.3	10	95
3HD7	EXOCYTOSIS	1.6	11.3	7	61
3HD7	EXOCYTOSIS	1.2	6.2	5	61
3HD7	EXOCYTOSIS	1.3	5.2	4	47
3HD7	EXOCYTOSIS	1.6	14.8	9	41
3HD7	EXOCYTOSIS	1.8	10.7	6	41
3HD7	EXOCYTOSIS	1.7	20.5	12	96
3HD7	EXOCYTOSIS	1.3	2.5	2	41
3HD7	EXOCYTOSIS	1.3	2.6	2	41
3HD7	EXOCYTOSIS	1.4	2.7	2	54
3HD7	EXOCYTOSIS	1.3	8.0	6	96
3HD7	EXOCYTOSIS	1.6	3.1	2	52
3HD7	EXOCYTOSIS	1.6	4.8	3	54
3HGK	TRANSFERASE	1.2	2.4	2	5
3HH2	SIGNALING PROTEIN/CYTOKINE	1.4	2.7	2	10
3HHR	HORMONE/RECEPTOR	1.3	2.6	2	31
3HHZ	VIRAL PROTEIN/RNA	1.6	3.1	2	11
3HKI	HYDROLASE	1.8	7.2	4	10
3HO5	SIGNALING PROTEIN	1.1	2.2	2	6
3HUJ	IMMUNE SYSTEM	1.6	3.1	2	29
3HUJ	IMMUNE SYSTEM	1.9	3.7	2	5
3I1H	APOPTOSIS	1.9	5.8	3	22
3I1H	APOPTOSIS	1.8	5.4	3	14

icked is part of the indicated chain. (d) Title of PDB entry. (e) Function of protein complex (f) ΔΔGavg/helix is derived from Rosetta com
mputational alanine mutagenesis studies and indicates the average free energy penalty for mutating two or more key residues at the interfa
elix to be mimicked. (m) Resolution of PDB structure (NOT APP indicates NMR structure).

A. PDB CODE	J. HELIX START RESIDUE #	K. HELIX END RESIDUE #
3GCG	72	99
3GJX	510	531
3GJX	314	333
3GJX	124	141
3GJX	137	142
3GJX	124	141
3GJX	137	142
3GM1	266	274
3GM1	903	930
3GM1	933	963
3GM1	268	273
3GM1	265	274
3GM1	264	273
3GMW	107	111
3GNI	92	107
3GNI	299	308
3GNI	223	238
3H11	439	455
3H11	424	437
3H4S	1222	1242
3H4S	96	114
3H6P	18	75
3H6P	18	75
3H6P	51	73
3H6P	15	77
3H6P	15	77
3H6P	21	40
3H9R	198	206
3HD7	70	113
3HD7	29	69
3HD7	190	284
3HD7	29	69
3HD7	190	284
3HD7	18	78
3HD7	18	78
3HD7	139	185
3HD7	70	110
3HD7	29	69
3HD7	189	284
3HD7	70	110
3HD7	29	69
3HD7	147	200
3HD7	189	284
3HD7	29	80
3HD7	147	200
3HGK	176	180
3HH2	43	52
3HHR	155	185
3HHZ	375	385
3HKI	14	14
3HO5	376	381
3HUJ	60	88
3HUJ	135	139
3I1H	86	107
3I1H	74	87

putational alanine mutagenesis studies
ce to alanine. (h) Number of hot spot re

A. PDB CODE	L. HELIX SEQUENCE
3GCG	QQWFQQEQTTYISRTVNRTLDDYCRSNN
3GJX	EEDEKRFLVTVIKDLLGLCEQK
3GJX	DEQNFIQNLSLFLCTFLKEH
3GJX	KVYIGKLNMILVQILKQE
3GJX	VFHRKK
3GJX	KVYIGKLNMILVQILKQE
3GJX	VFHRKK
3GM1	LDELMASLS
3GM1	PEGYVVVVKNVGLTLRKLIGSVDDLLPS
3GM1	SSSRTEIEGTQKLLNKDLAELINKMRLAQQN
3GM1	ELMASL
3GM1	ELDELMASLS
3GM1	RELDELMASL
3GMW	PVTEK
3GNI	FEGKKDVAQIFNNILR
3GNI	QAKLIEFLSK
3GNI	YVTKRQSLKLLGELLL
3H11	LLDLHIELNGYMYDWNS
3H11	ILTILTEVNYEVSN
3H4S	EMVRLKKLVAYWKEQAGKKGE
3H4S	QTEFCVLMVRLSPEMMEDA
3H6P	FAAKAGLMRHTIGQAEQQAMSAQAFHQGESAAAFQGAHARFVAAAAKVNTLLDIAQAN
3H6P	FAAKAGLMRHTIGQAEQQAMSAQAFHQGESAAAFQGAHARFVAAAAKVNTLLDIAQAN
3H6P	YQGWQTQWNQALEDLVRAYQSMS
3H6P	HTAFAAKAGLMRHTIGQAEQQAMSAQAFHQGESAAAFQGAHARFVAAAAKVNTLLDIAQANLG
3H6P	HTAFAAKAGLMRHTIGQAEQQAMSAQAFHQGESAAAFQGAHARFVAAAAKVNTLLDIAQANLG
3H6P	YAGTLQSLGADIASEQAVLS
3H9R	FLVQRTVAR
3HD7	LQAGASQFETSAAKLKRKYWWKNLKMMIILGVICAIILIIIIVY
3HD7	MRRLQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADA
3HD7	QALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAVSDTKKAVKYQSKARRKKIMIIICCVILGIIIASTIG
3HD7	MRRLQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADA
3HD7	QALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAVSDTKKAVKYQSKARRKKIMIIICCVILGIIIASTIG
3HD7	ADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNL
3HD7	ADQLADESLESTRRMLQLVEESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNL
3HD7	HMARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKA
3HD7	LQAGASQFETSAAKLKRKYWWKNLKMMIILGVICAIILIII
3HD7	MRRLQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADA
3HD7	KQALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAVSDTKKAVKYQSKARRKKIMIIICCVILGIIIASTIG
3HD7	LQAGASQFETSAAKLKRKYWWKNLKMMIILGVICAIILIII
3HD7	MRRLQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADA
3HD7	DENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRAT
3HD7	KQALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAVSDTKKAVKYQSKARRKKIMIIICCVILGIIIASTIG
3HD7	TRRMLQLVEESKDAGIRTLVMLDEQGEQLDRVEEGMNHINQDMKEAEKNLKD
3HD7	DENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRAT
3HGK	MPMHG
3HH2	DNTLFKWMIF
3HHR	ALLKNYGLLYCFRKDMDKVETFLRIVQCRSV
3HHZ	VVEWLGWFEDQ
3HKI	EKELLDSYID
3HO5	LDDMEE
3HUJ	DQQWETLQHIFRVYRSSFTRDVKEFAKML
3HUJ	EAEIS
3I1H	WGRIVTIFAFEGILIKKLLRQQ
3I1H	VGRQLAIIGDDINR

and indicates the average free energy penalty
sidues in helix. (i) Length of candidate helix to be mimicked

A. PDB CODE	M. RESOLUTION
3GCG	2.3
3GJX	2.5
3GJX	2.5
3GJX	2.5
3GJX	2.5
3GJX	2.5
3GJX	2.5
3GM1	2.95
3GM1	2.95
3GM1	2.95
3GM1	2.95
3GM1	2.95
3GM1	2.95
3GMW	2.1
3GNI	2.35
3GNI	2.35
3GNI	2.35
3H11	1.9
3H11	1.9
3H4S	2.4
3H4S	2.4
3H6P	1.91
3H6P	1.91
3H6P	1.91
3H6P	1.91
3H6P	1.91
3H6P	1.91
3H9R	2.35
3HD7	3.4
3HD7	3.4
3HD7	3.4
3HD7	3.4
3HD7	3.4
3HD7	3.4
3HD7	3.4
3HD7	3.4
3HD7	3.4
3HD7	3.4
3HD7	3.4
3HD7	3.4
3HD7	3.4
3HD7	3.4
3HD7	3.4
3HD7	3.4
3HD7	3.4
3HGK	3.3
3HH2	2.15
3HHR	2.8
3HHZ	3.5
3HKI	2.2
3HO5	3.01
3HUJ	2.5
3HUJ	2.5
3I1H	2.2
3I1H	2.2

Table S5. Full Dataset of HIPP interactions

Description of Entries

A. PDB code of predicted target.
B. Title of PDB entry.
C. PDB Classification and function of protein complex.

A. PDB Code	B. Title	C. 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	COMPLEX (SERINE PROTEASE/INHIBITOR)

	BORONATE INHIBITOR BOROLOG2	
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 GLUTAMINE HYDROLYSIS	AMIDOTRANSFERASE
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	FAB 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	IGG-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	CRYSTAL 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 (GGRKKKYKL-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	HOTOSYNTHETIC REACTION CENTER FROM RHODOBACTER SPHAEROIDES IN THE D+QB-CHARGE SEPARATED STATE	PHOTOSYNTHETIC REACTION CENTER
1AIJ	HOTOSYNTHETIC 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 CYTOSOLIC ASPARTATE AMINOTRANSFERASE AND ITS COMPLEX WITH 2-METHYLASPARTATE	AMINOTRANSFERASE
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	UMAN ASPARTYLGLUCOSAMINIDASE COMPLEX WITH REACTION PRODUCT	COMPLEX (HYDROLASE/PEPTIDE)
1AQD	HLA-DR1 (DRA, DRB1 0101) HUMAN CLASS II HISTOCOMPATIBILITY PROTEIN (EXTRACELLULAR DOMAIN) COMPLEXED WITH ENDOGENOUS	COMPLEX (MHC PROTEIN/ANTIGEN)

	PEPTIDE	
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	COMPLEX (SERINE PROTEASE/INHIBITOR)

	MACROCYCLIC TRIPEPTIDE MOTIF	
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 INSULIN CRYSTALS (PH 6.16 COORDINATES)	HORMONE/GROWTH FACTOR
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	IMMUNE SYSTEM

	ANTIBODY	
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	'HENYLALANYL 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.	AMINOTRANSFERASE

	COLI IN COMPLEX WITH ALPHA-METHYL-L-GLUTAMATE	
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	THE 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	COMPLEX (ANTIBODY/ANTIGEN)

	BOBWHITE QUAIL LYSOZYME	
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	CRYSTAL 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	PHENYLALANINE 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	THE CRYSTAL STRUCTURE OF RUBISCO FROM ALCALIGENES EUTROPHUS TO 2.7 ANGSTROMS.	LYASE
1BXR	STRUCTURE 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	COMPLEX 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	CRYSTAL STRUCTURE OF 1:1 COMPLEX BETWEEN GELSOLIN SEGMENT 1 AND A DICTYOSTELIUM/TETRAHYMENA CHIMERA ACTIN (MUTANT 228: Q228K/T229A/A230Y/E360H)	CONTRACTILE PROTEIN
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	THREE-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	THREE-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 CONFORMATIONS	PHOSPHOTRANSFERASE
1CMX	STRUCTURAL BASIS FOR THE SPECIFICITY OF UBIQUITIN C-TERMINAL HYDROLASES	HYDROLASE
1CMY	THE MUTATION BETA99 ASP-TYR STABILIZES Y-A NEW, COMPOSITE	OXYGEN TRANSPORT

	QUATERNARY STATE OF HUMAN HEMOGLOBIN	
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	IUMAN P56LCK TYROSINE KINASE COMPLEXED WITH PHOSPHONOPEPTIDE	COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
1CWE	IUMAN 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	SPARTATE 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	CRYSTAL 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	CRYSTAL STRUCTURE OF RIBOSOMAL PROTEIN L12 FROM THERMOTOGA MARITIMA	RIBOSOME
1DD4	CRYSTAL 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	LIGAND-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	CRYSTAL 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	HOTOSYNTHETIC 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	HOTOSYNTHETIC REACTION CENTER FROM RHODOBACTER SPHAEROIDES IN THE CHARGE-SEPARATED D+QAQB-STATE WITH THE PROTON TRANSFER INHIBITOR CD2+	PHOTOSYNTHESIS
1DV6	HOTOSYNTHETIC 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 EXOSITE INHIBITOR E-76 AND COAGULATION FACTOR VIIA	HYDROLASE/HYDROLASE INHIBITOR
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	CRYSTAL 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	PHOTOSYNTHETIC 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	CRYSTAL 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-	COMPLEX (ANTIBODY/ANTIGEN)

	TGFALPHA ANTIBODY FAB-FRAGMENT	
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-EMD56133	HYDROLASE (ACID PROTEINASE)
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	TRANSPORT PROTEIN

	A COMPLEX WITH A C-MYC NLS PEPTIDE	
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	THE 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	CRYSTAL 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	CRYSTAL STRUCTURE OF WILD-TYPE KLEBSIELLA AEROGENES UREASE AT 298K	HYDROLASE
1EJX	CRYSTAL 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	STRUCTURE 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 COGNATE IMMUNITY PROTEIN IM9 (1.7 ANGSTROMS)	IMMUNE SYSTEM
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	IMMUNE SYSTEM

	ANTIGEN RECOGNITION BY IMMUNOGLOBULINS	
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	CRYSTAL STRUCTURE OF HUMAN COAGULATION FACTOR XA COMPLEXED WITH RPR128515	HYDROLASE
1EZS	CRYSTAL STRUCTURE OF ECOTIN MUTANT M84R, W67A, G68A, Y69A, D70A BOUND TO RAT ANIONIC TRYPSIN II	HYDROLASE/INHIBITOR
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	CRYSTAL STRUCTURE OF HUMAN COAGULATION FACTOR XA COMPLEXED WITH RPR208815	HYDROLASE
1F0S	CRYSTAL 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-	TRANSFERASE

	PHOSPHONACETYL-L-ASPARTATE	
1F1J	CRYSTAL STRUCTURE OF CASPASE-7 IN COMPLEX WITH ACETYL-ASP-GLU-VAL-ASP-CHO	HYDROLASE, APOPTOSIS
1F1W	SRC 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	CRYSTAL 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 HUMAN TFIIF	TRANSCRIPTION
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 BY GROUP IV WW DOMAINS	ISOMERASE
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	THE 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	CRYSTAL 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	THE 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	CRYSTAL 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 ANTIBODY FAB LA-2	IMMUNE SYSTEM
1FJG	STRUCTURE 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	THE 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	THE 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	PHOTOSYNTHESIS

	PRO L209-> PHE FROM THE PHOTOSYNTHETIC PURPLE BACTERIUM RHODOBACTER SPHAEROIDES	
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 DIPHOSPHATE	PRENYLTRANSFERASE
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	THE 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	METHANE MONOOXYGENASE HYDROXYLASE, FORM II COCRYSTALLIZED WITH DIBROMOMETHANE	OXIDOREDUCTASE
1FZ9	METHANE 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	CRYSTAL STRUCTURE OF FRAGMENT D FROM HUMAN FIBRINOGEN WITH THE PEPTIDE LIGAND GLY-HIS-ARG-PRO-AMIDE	BLOOD COAGULATION
1FZH	METHANE MONOOXYGENASE HYDROXYLASE, FORM II PRESSURIZED WITH XENON GAS	OXIDOREDUCTASE
1FZI	METHANE 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	MGATP-BOUND AND NUCLEOTIDE-FREE STRUCTURES OF A NITROGENASE PROTEIN COMPLEX BETWEEN LEU127DEL-FE PROTEIN AND THE MOFE PROTEIN	OXIDOREDUCTASE
1G21	MGATP-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	CRYSTAL 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-GLUCOSIDASE	IMMUNE SYSTEM
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 SITE	HYDROLASE/HYDROLASE INHIBITOR
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 GLUTARYLAMIDASE TO ALLOW SINGLE-STEP ENZYMATIC PRODUCTION OF 7-AMINOCEPHALOSPORANIC ACID FROM CEPHALOSPORIN C	HYDROLASE
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	STRUCTURE OF THE COMPLEX BETWEEN BOVINE ALPHA-CHYMOTRYPSIN AND PMP-D2V, AN INHIBITOR FROM THE INSECT LOCUSTA MIGRATORIA	COMPLEX (PROTEASE/INHIBITOR)
1GL1	STRUCTURE 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	SOLUTION 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	NUCLEAR RECEPTOR

	COMPLEX WITH 17BETA-OESTRADIOL AND TIF2 NRBOX3 PEPTIDE	
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	CRYSTAL 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	STRUCTURE OF HUMAN THR160-PHOSPHO CDK2/CYCLIN A COMPLEXED WITH THE INHIBITOR NU2058	TRANSFERASE
1H1Q	STRUCTURE OF HUMAN THR160-PHOSPHO CDK2/CYCLIN A COMPLEXED WITH THE INHIBITOR NU6094	TRANSFERASE
1H1R	STRUCTURE OF HUMAN THR160-PHOSPHO CDK2/CYCLIN A COMPLEXED WITH THE INHIBITOR NU6086	TRANSFERASE
1H1S	STRUCTURE OF HUMAN THR160-PHOSPHO CDK2/CYCLIN A COMPLEXED WITH THE INHIBITOR NU6102	TRANSFERASE
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	CELL CYCLE

	PEPTIDE FROM P53	
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	CRYSTAL 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	MOLYBDATE 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 INFRARED SPECTROSCOPY OF THE DISTAL BETA-HEME POCKET VALINE67(E11)-THREONINE MUTATION OF HEMOGLOBIN	OXYGEN TRANSPORT
1HDM	HISTOCOMPATIBILITY ANTIGEN HLA-DM	IMMUNE SYSTEM
1HDS	MACROMOLECULAR 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	CRYSTAL 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 HAEMOGLOBINS: 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 HAEMOGLOBINS: 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 HAEMOGLOBINS: 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	VIRAL PROTEIN

	NUCLEAR MAGNETIC RESONANCE SPECTROSCOPY AND X-RAY CRYSTALLOGRAPHY	
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 CELL-SURFACE RECEPTOR, SIALIC ACID: ANALYSIS BY PROTON NUCLEAR MAGNETIC RESONANCE SPECTROSCOPY AND X-RAY CRYSTALLOGRAPHY	VIRAL PROTEIN
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	IMMUNOGLOBULIN

	ANTIGEN-ANTIBODY RECOGNITION	
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	THE 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	STRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT IN COMPLEX WITH TETRACYCLINE	RIBOSOME
1HNX	STRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT IN COMPLEX WITH PACTAMYCIN	RIBOSOME
1HNZ	STRUCTURE 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	STRUCTURE OF PYRUVOYL-DEPENDENT HISTIDINE DECARBOXYLASE AT PH 8	LYASE
1HQE	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1	TRANSFERASE
1HQM	CRYSTAL 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	NUCLEOTIDE-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	NUCLEOTIDE-DEPENDENT CONFORMATIONAL CHANGES IN A PROTEASE-ASSOCIATED ATPASE HSLU	CHAPERONE
1HT2	NUCLEOTIDE-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	IMMUNE SYSTEM

	WITH BETA 2-MICROGLOBULIN AND HIV-RT VARIANT PEPTIDE I1Y	
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 PEPTIDE FROM A GROUP A STREPTOCOCCAL SURFACE PROTEIN	BLOOD CLOTTING
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	IUMAN 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	IUMAN 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	IUMAN S-ADENOSYLMETHIONINE DECARBOXYLASE WITH COVALENTLY BOUND PYRUVOYL GROUP AND COVALENTLY BOUND S-ADENOSYLMETHIONINE METHYL ESTER	LYASE
1I7C	IUMAN S-ADENOSYLMETHIONINE DECARBOXYLASE WITH COVALENTLY BOUND PYRUVOYL GROUP AND COMPLEXED WITH METHYLGLYOXAL BIS-(GUANYLHYDRAZONE)	LYASE
1I7M	IUMAN 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	CRYO-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	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
1I9C	GLUTAMATE MUTASE FROM CLOSTRIDIUM COCHLEARIUM: COMPLEX WITH ADENOSYLCOBALAMIN AND SUBSTRATE	ISOMERASE
1I9I	NATIVE 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	STRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT IN COMPLEX WITH THE ANTIBIOTIC PAROMOMYCIN	RIBOSOME
1IBL	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 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 SURFACE COMPLEMENTARITY	IMMUNOGLOBULIN

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 MEAN)	CYTOKINE
1IM3	CRYSTAL 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	IMMUNOGLOBULIN

	CHELATE	
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	CRYSTAL 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	OXYGEN STORAGE/TRANSPORT

	A RESOLUTION	
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	PYROCOCCUS FURIOSUS PCNA COMPLEXED WITH RFCL PIP-BOX PEPTIDE	DNA BINDING PROTEIN
1IVO	CRYSTAL STRUCTURE OF THE COMPLEX OF HUMAN EPIDERMAL GROWTH FACTOR AND RECEPTOR EXTRACELLULAR DOMAINS.	TRANSFERASE/SIGNALING PROTEIN
1IVP	THE CRYSTALLOGRAPHIC STRUCTURE OF THE PROTEASE FROM HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 WITH TWO SYNTHETIC PEPTIDIC TRANSITION STATE ANALOG INHIBITORS	HYDROLASE(ACID PROTEINASE)
1IVQ	THE 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	TRANSFERASE

	COMPLEXED WITH FARNESYL DIPHOSPHATE AND THE PEPTIDOMIMETIC INHIBITOR L-739,750	
1JCR	CRYSTAL STRUCTURE OF RAT PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH THE NON-SUBSTRATE TETRAPEPTIDE INHIBITOR CVFM AND FARNESYL DIPHOSPHATE SUBSTRATE	TRANSFERASE
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	STRUCTURE 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	OXIDOREDUCTASE

	HYPERTHERMOPHILIC ARCHAEOGLOBUS FULGIDUS AT 1.6 RESOLUTION	
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	CRYSTAL 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 COMPLEX WITH TEM-1 BETA-LACTAMASE	HYDROLASE/INHIBITOR
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	STRUCTURE 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	HOTOSYNETHETIC REACTION CENTER FROM RHODOBACTER SPHAEROIDES	PHOTOSYNTHESIS
1K6N	E(L212)A,D(L213)A DOUBLE MUTANT STRUCTURE OF PHOTOSYNTHETIC REACTION CENTER FROM RHODOBACTER SPHAEROIDES	PHOTOSYNTHESIS
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	TRANSCRIPTION

	HETERODIMER OF THE HUMAN PPARGAMMA AND RXRALPHA LIGAND BINDING DOMAINS RESPECTIVELY BOUND WITH GW409544 AND 9-CIS RETINOIC ACID AND CO-ACTIVATOR PEPTIDES.	
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	CRYSTAL STRUCTURE OF THE TRYPTOPHAN SYNTHASE BETA-SER178PRO MUTANT COMPLEXED WITH D,L-ALPHA-GLYCEROL-3-PHOSPHATE	LYASE
1K8Z	CRYSTAL 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 HETERODIMER ACID-D12IA16V BASE-D12LA16L	DE NOVO PROTEIN
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	PSEUDOMONAS 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	PSEUDOMONAS SERINE-CARBOXYL PROTEINASE COMPLEXED WITH THE INHIBITOR AIPF (THIS ENZYME RENAMED "SEDOLISIN" IN 2003)	HYDROLASE
1KDZ	PSEUDOMONAS SERINE-CARBOXYL PROTEINASE COMPLEXED WITH THE INHIBITOR TYROSTATIN (THIS ENZYME RENAMED "SEDOLISIN" IN 2003)	HYDROLASE
1KE1	PSEUDOMONAS SERINE-CARBOXYL PROTEINASE COMPLEXED WITH THE INHIBITOR PSEUDOTYROSTATIN (THIS ENZYME RENAMED "SEDOLISIN" IN 2003)	HYDROLASE
1KE2	PSEUDOMONAS SERINE-CARBOXYL PROTEINASE COMPLEXED WITH THE	HYDROLASE

	INHIBITOR CHYMOSTATIN (THIS ENZYME RENAMED "SEDOLISIN" IN 2003)	
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	IMMUNE SYSTEM/TOXIN

	(SEC3-3B2)	
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	CRYSTAL 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 CONFORMATION	CONTRACTILE PROTEIN
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	PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH FARNESYLATED K-RAS4B PEPTIDE PRODUCT AND FARNESYL DIPHOSPHATE SUBSTRATE BOUND SIMULTANEOUSLY	TRANSFERASE
1KZP	PROTEIN FARNESYLTRANSFERASE COMPLEXED WITH A FARNESYLATED K-RAS4B PEPTIDE PRODUCT	TRANSFERASE
1KZU	INTEGRAL 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	THE 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	COMPLEX (KINASE/PEPTIDE)

	PEPTIDE EPQPYEEIPIYL	
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	UMAN ALPHA-THROMBIN COMPLEXED WITH AC-(D)PHE-PRO-BOROARG-OH	COMPLEX (SERINE PROTEASE/INHIBITOR)
1LHD	IUMAN 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	CRYSTAL 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	HOTOSYNTHETIC 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	CRYSTAL 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	SIGNALING PROTEIN

	REELING SIGNALING	
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	CRYSTALLINE 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	CRYSTAL 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 LIGANDS	IMMUNOGLOBULIN
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	THREE-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	CRYSTAL 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-	COMPLEX (BLOOD COAGULATION/PROENZYME)

	THROMBIN AND PRETHROMBIN-2: MOVEMENT OF THE YPPW SEGMENT AND ACTIVE SITE RESIDUES UPON LIGAND BINDING	
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 CRH, THE BACILLUS SUBTILIS CATABOLITE REPRESSION CONTAINING PROTEIN CRH REVEALS AN UNEXPECTED SWAPPING DOMAIN AS AN UNTERTWINNED DIMER	TRANSPORT PROTEIN
1MOX	CRYSTAL 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	ENDOCYTOSIS/EXOCYTOSIS

	PEPTIDE OF SED5P	
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 COMPLEXES	IMMUNOGLOBULIN
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	METHANE 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	STRUCTURE 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	STRUCTURE 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 SITE WITH PAROMOMYCIN	RIBOSOME

1N34	STRUCTURE 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	STRUCTURE 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	CHARACTERIZATION 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	PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH GERANYLGERANYL DIPHOSPHATE	TRANSFERASE
1N4Q	PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A KKKSKTKCVIL PEPTIDE	TRANSFERASE
1N4R	PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GERANYLGERANYLATED KKKSKTKCVIL PEPTIDE PRODUCT	TRANSFERASE
1N4S	PROTEIN 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	IMMUNE SYSTEM

	SITE ON HEPATITIS C VIRUS PROTEIN BOUND TO MAB 19D9D6	
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 HETERODIMER FROM CANDIDA TROPICALIS	HYDROLASE
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	HYDROLASE

	IN ISOLATION AND IN COMPLEX WITH UBIQUITIN ALDEHYDE	
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	OXIDOREDUCTASE/ELECTRON TRANSPORT

	DINITROPHENOL-17 INHIBITOR CO-CRYSTALLIZED AT THE UBIQUINONE BINDING SITE	
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	CRYSTAL 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	CRYSTAL STRUCTURE OF HUMAN COAGULATION FACTOR XA COMPLEXED WITH RPR132747	HYDROLASE
1NFW	CRYSTAL STRUCTURE OF HUMAN COAGULATION FACTOR XA COMPLEXED WITH RPR209685	HYDROLASE
1NFX	CRYSTAL STRUCTURE OF HUMAN COAGULATION FACTOR XA COMPLEXED WITH RPR208944	HYDROLASE
1NFY	CRYSTAL STRUCTURE OF HUMAN COAGULATION FACTOR XA COMPLEXED WITH RPR200095	HYDROLASE
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	RIBOSOME

	SUBUNIT	
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	CHARACTERIZATION 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	THE 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	CRYSTAL STRUCTURE OF MITOCHONDRIAL CYTOCHROME BC1 COMPLEX AT 2.4 ANGSTROM	OXIDOREDUCTASE
1NTV	CRYSTAL STRUCTURE OF THE DISABLED-1 (DAB1) PTB DOMAIN-APOER2 PEPTIDE COMPLEX	SIGNALING PROTEIN
1NTZ	CRYSTAL STRUCTURE OF MITOCHONDRIAL CYTOCHROME BC1 COMPLEX	OXIDOREDUCTASE

	BOUND WITH UBIQUINONE	
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	CRYSTAL 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	CONTRACTILE PROTEIN

	TOMOGRAMS OF INSECT FLIGHT MUSCLE	
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 SOX2 TRANSCRIPTION FACTORS WITH A 19MER OLIGONUCLEOTIDE FROM THE HOXB1 REGULATORY ELEMENT	TRANSCRIPTION/DNA
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 METHYLOPHILUS METHYLOTROPHUS, RECOGNITION LOOP REMOVED BY LIMITED PROTEOLYSIS	ELECTRON TRANSFER
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	CRYSTAL 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	COMPLEX 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	STRUCTURE OF BOVINE HEART CYTOCHROME C OXIDASE AT THE FULLY OXIDIZED STATE	OXIDOREDUCTASE (CYTOCHROME(C)-OXYGEN)
1OCO	BOVINE HEART CYTOCHROME C OXIDASE IN CARBON MONOXIDE-BOUND STATE	OXIDOREDUCTASE
1OCR	BOVINE 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	STRUCTURE 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	CRYSTAL 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	OXIDOREDUCTASE

	WITH ALPHAKETOGLUTARATE	
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 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
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	CRYSTAL 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-TERMINAL SRC HOMOLOGY 2 DOMAIN OF PI3-KINASE COMPLEXED TO	PROTEIN BINDING

	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 COBRA REVEALS CARBOHYDRATE BINDING IN THE HYDROPHOBIC CHANNEL	HYDROLASE
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	SIGNALING PROTEIN

SPACE GROUP P3(2)

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-ANALOGUE HEXA-PEPTIDE INHIBITOR AT 2.2 ANGSTROMS RESOLUTION	HYDROLASE
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	CRYSTAL 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	HYDROLASE(SERINE PROTEINASE)

	CHLOROMETHYLKETONE AND SIGNIFICANCE OF THE TYR-PRO-PRO-TRP INSERTION SEGMENT	
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	COMPLEX (HYDROLASE/PEPTIDE)

	(DADEPYL-NH2)	
1PU9	CRYSTAL STRUCTURE OF TETRAHYMENA GCN5 WITH BOUND COENZYME A AND A 19-RESIDUE HISTONE H3 PEPTIDE	TRANSFERASE/STRUCTURAL PROTEIN
1PUA	CRYSTAL STRUCTURE OF TETRAHYMENA GCN5 WITH BOUND COENZYME A AND A PHOSPHORYLATED, 19-RESIDUE HISTONE H3 PEPTIDE	TRANSFERASE/STRUCTURAL PROTEIN
1PUF	CRYSTAL 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 DECARBOXYLASE FROM LACTOBACILLUS 30A	CARBOXY-LYASE
1PYO	CRYSTAL STRUCTURE OF HUMAN CASPASE-2 IN COMPLEX WITH ACETYL-LEU-ASP-GLU-SER-ASP-CHO	HYDROLASE
1PYT	TERNARY COMPLEX OF PROCARBOXYPEPTIDASE A, PROPROTEINASE E, AND CHYMOTRYPSINOGEN C	TERNARY COMPLEX (ZYMOGEN)
1PYU	PROCESSED 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	W314A-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	MOUSE IMPORTIN ALPHA- PHOSPHORYLATED SV40 CN PEPTIDE COMPLEX	PROTEIN TRANSPORT
1Q1T	MOUSE IMPORTIN ALPHA: NON-PHOSPHORYLATED SV40 CN PEPTIDE COMPLEX	PROTEIN TRANSPORT
1Q2C	CRYSTAL STRUCTURE OF TETRAHYMENA GCN5 WITH BOUND COENZYME A AND A 19-RESIDUE HISTONE H4 PEPTIDE	TRANSFERASE/STRUCTURAL PROTEIN
1Q2D	CRYSTAL 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	CRYSTAL 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	THE 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	IMMUNE SYSTEM

	NONAMER AND DECAMER HIV-1 EPITOPES CLEARLY REVEAL THE PRESENCE OF A MIDDLE ANCHOR RESIDUE	
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	DEOXYGENATED 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	CRYO-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	CRYSTAL 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	PLASMODIUM 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	IMMUNE SYSTEM

	HTLV-1 TAX PEPTIDE Y8A	
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	CRYSTAL 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-	CELL ADHESION

	CATENIN	
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 HETERODIMER ECR/USP BOUND TO PONASTERONE A	HORMONE/GROWTH FACTOR RECEPTOR
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	MEMBRANE PROTEIN

	TL+	
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	TRANSFERASE

	TRANSCARBAMOYLASE AT 2.5 ANGSTROMS RESOLUTION: IMPLICATIONS FOR ATCASE MUTANTS AND THE MECHANISM OF NEGATIVE COOPERATIVITY	
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	STRUCTURAL 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	STRUCTURE 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	CRYSTAL STRUCTURE OF THE COMPLEX BETWEEN THE HUMAN RHOA AND	SIGNALING PROTEIN

	RHO-BINDING DOMAIN OF HUMAN ROCKI	
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 ENDOPEPTIDASE FUNCTIONING IN PROGRAMMED CELL DEATH OF RICINUS COMMUNIS ENDOSPERM	HYDROLASE
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	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
1S5X	THE CRYSTAL STRUCTURE OF TREMATOMUS BERNACCHII HEMOGLOBIN OXIDIZED BY AIR	OXYGEN STORAGE/TRANSPORT
1S5Y	THE 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	RAT 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, IN COMPLEX WITH HLA-A2	IMMUNE SYSTEM
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	STRUCTURE 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 ESCHERICHIA COLI AT 2.5 ANGSTROMS RESOLUTION	LIGASE (ATP-BINDING)
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	CRYSTAL 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	CRYSTAL 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 COMPLEXED WITH STREPTOMYCES GRISEUS PROTEINASE B	COMPLEX (SERINE PROTEASE/INHIBITOR)
1SGY	TYR 18 VARIANT OF TURKEY OVOMUCOID INHIBITOR THIRD DOMAIN COMPLEXED WITH STREPTOMYCES GRISEUS PROTEINASE B AT PH 6.5	HYDROLASE/HYDROLASE INHIBITOR
1SHB	CRYSTAL 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	CRYSTAL 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	T7 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	CRYSTAL 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	TRUCTURE 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	CRYSTAL 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	SIGNALING PROTEIN

	ALPHA1C SUBUNIT	
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	CRYSTAL 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	CRYSTAL 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 CHYMOTRYPSIN COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
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	HYDROLASE INHIBITOR/HYDROLASE

	INHIBITOR (XIP)	
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 COMPLEXED WITH EGLIN-C	COMPLEX(SERINE PROTEINASE-INHIBITOR)
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-PHE-PRO-ARG-CHLOROMETHYLKETONE	SERINE PROTEASE
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	TRANSCRIPTION

	WITH ATP, CRYSTAL FORM II	
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 PHOSPHOLIPASE A2 AND DESIGNED PEPTIDE INHIBITOR CARBOBENZOXY-DEHYDRO-VAL-ALA-ARG-SER AT 1.2 A RESOLUTION	HYDROLASE
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	CRYSTALLOGRAPHIC 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	RAT PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A SUBSTRATE KKSKTKCVIF PEPTIDE DERIVED FROM TC21	TRANSFERASE
1TNO	RAT PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A KKKSKTKCVIM PEPTIDE DERIVED FROM K-RAS4B	TRANSFERASE
1TNU	RAT PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A GCINCCKVL PEPTIDE DERIVED FROM RHOB	TRANSFERASE

1TNY	RAT PROTEIN GERANYLGERANYLTRANSFERASE TYPE-I COMPLEXED WITH A GGPP ANALOG AND A FREKKFFCAIL PEPTIDE DERIVED FROM THE HETEROTRIMERIC G PROTEIN GAMMA-2 SUBUNIT	TRANSFERASE
1TNZ	RAT 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 COMPLEXED WITH N-(PHOSPHONACETYL-L-ASPARTATE) (PALA)	HYDROLASE/HYDROLASE REGULATOR
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	CARBON-OXYGEN LYASE

	POTASSIUM AT ROOM TEMPERATURE	
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	CRYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH WAY-338	TRANSCRIPTION
1U3S	CRYSTAL 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	ELECTRON 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 HETEROTRIMERIC COMPLEX	SIGNALING PROTEIN
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	CRYSTAL 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	THREE-DIMENSIONAL STRUCTURE OF THE CARBON MONOXIDE COMPLEX OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE
1UBJ	THREE-DIMENSIONAL STRUCTURE OF THE CARBON MONOXIDE COMPLEX OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE
1UBK	THREE-DIMENSIONAL STRUCTURE OF THE CARBON MONOXIDE COMPLEX OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE
1UBL	THREE-DIMENSIONAL STRUCTURE OF THE CARBON MONOXIDE COMPLEX OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI	OXIDOREDUCTASE

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1UBM	THREE-DIMENSIONAL STRUCTURE OF THE CARBON MONOXIDE COMPLEX OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE
1UBO	THREE-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	THREE-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	THREE-DIMENSIONAL STRUCTURE OF THE CARBON MONOXIDE COMPLEX OF [NIFE]HYDROGENASE FROM DESULUFOVIBRIO VULGARIS MIYAZAKI F	OXIDOREDUCTASE
1UBU	THREE-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	LYASE

	HYDRATASE	
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	MOLECULAR 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	A CHIMERIC CHLAMYDOMONAS, SYNECHOCOCCUS RUBISCO ENZYME	LYASE
1V02	CRYSTAL STRUCTURE OF THE SORGHUM BICOLOR DHURRINASE 1	HYDROLASE
1V11	CROSSTALK BETWEEN COFACTOR BINDING AND THE PHOSPHORYLATION LOOP CONFORMATION IN THE BCKD MACHINE	OXIDOREDUCTASE
1V16	CROSSTALK 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	CROSSTALK BETWEEN COFACTOR BINDING AND THE PHOSPHORYLATION LOOP CONFORMATION IN THE BCKD MACHINE	OXIDOREDUCTASE
1V1R	CROSSTALK 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	CRYSTAL 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	RYSTAL 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	RIBOSOME

	CONTAINS FIVE 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	
1VOU	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
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 SPARSOMYCIN BOUND TO THE LARGE RIBOSOMAL SUBUNIT OF HALOARCULA MARISMORTUI	RIBOSOME
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	THE 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 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
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	TRANSFERASE

	IIAMANNOSE AND IIBMANNOSE OF THE MANNOSE TRANSPORTER OF THE E. COLI PHOSPHOTRANSFERASE SYSTEM	
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,	ENDOCYTOSIS/EXOCYTOSIS

	FROM THE AP2 ADAPTOR COMPLEX, BOUND TO 2 PEPTIDES FROM SYNAPTOJANIN170	
1W85	THE 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 CPN60/CPN10/(ADP)7 FROM THERMUS THERMOPHILUS	CHAPERONE
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	CUMENE 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	CRYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH WAY-697	TRANSCRIPTION
1X78	CRYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH WAY-244	TRANSCRIPTION
1X79	CRYSTAL STRUCTURE OF HUMAN GGA1 GAT DOMAIN COMPLEXED WITH THE GAT-BINDING DOMAIN OF RABAPTIN5	PROTEIN TRANSPORT
1X7B	CRYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH ERB-041	TRANSCRIPTION
1X7E	CRYSTAL STRUCTURE OF ESTROGEN RECEPTOR ALPHA COMPLEXED WITH WAY-244	TRANSCRIPTION

1X7J	CRYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH GENISTEIN	TRANSCRIPTION
1X7Q	CRYSTAL STRUCTURE OF HLA-A*1101 WITH SARS NUCLEOCAPSID PEPTIDE	IMMUNE SYSTEM
1X7R	CRYSTAL 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	IMMUNE SYSTEM

	HEN EGG LYSOZYME	
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 IN COMPLEX WITH PROTEIN KINASE A AND MUTANTS	TRANSFERASE/TRANSFERASE INHIBITOR
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	CRYSTAL STRUCTURE OF APO METHANE MONOOXYGENASE HYDROXYLASE FROM M. CAPSULATUS (BATH)	OXIDOREDUCTASE
1XMH	STRUCTURE OF CO(II) RECONSTITUTED METHANE MONOOXYGENASE HYDROXYLASE FROM M. CAPSULATUS (BATH)	OXIDOREDUCTASE
1XMN	CRYSTAL STRUCTURE OF THROMBIN BOUND TO HEPARIN	BLOOD CLOTTING
1XMO	CRYSTAL 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	CRYSTAL 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	CHAPERONE

	THE FRAGMENT OF HSP70 ATPASE DOMAIN	
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	OLUBLE 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	LUBLE METHANE MONOOXYGENASE HYDROXYLASE: 6-BROMOHEXANOL SOAKED STRUCTURE	OXIDOREDUCTASE
1XVC	LUBLE METHANE MONOOXYGENASE HYDROXYLASE: 8-BROMOOCTANOL SOAKED STRUCTURE	OXIDOREDUCTASE
1XVD	LUBLE 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	LUBLE 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 PEPTIDE, FATTY ACID AND CITCO	DNA BINDING PROTEIN
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 DEOXYHEMOGLOBIN NO-SALT	TRANSPORT PROTEIN
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 TYPE I-GAMMA BINDING TO TALIN AT FOCAL ADHESIONS	STRUCTURAL PROTEIN, SIGNALING PROTEIN
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 CHYMOTRYPSIN INHIBITOR 2 M59R/E60S MUTANT	HYDROLASE/HYDROLASE INHIBITOR
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	COMPLEX (PHOSPHOTRANSFERASE/INHIBITOR)

	SUBUNIT IN COMPLEX WITH H89 PROTEIN KINASE INHIBITOR N-[2-(4-BROMOCINNAMYLAMINO)ETHYL]-5-ISOQUINOLINE	
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	OXYGEN STORAGE/TRANSPORT

	QUATERNARY STATES (R2 AND R3) IN ONE CRYSTAL	
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	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
1YK1	STRUCTURE 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	STRUCTURE 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	LAYSE, TOXIN

	PERTUSSIS IN PRESENCE OF C-TERMINAL CALMODULIN AND 1MM CALCIUM CHLORIDE	
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	CRYSTAL STRUCTURE OF THE SUBTILISIN CARLSBERG:OMTKY3 COMPLEX	HYDROLASE
1YUC	HUMAN 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	CRYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH 1-CHLORO-6-(4-HYDROXY-PHENYL)-NAPHTHALEN-2-OL	TRANSCRIPTION
1YY8	CRYSTAL 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	CRYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH	TRANSCRIPTION

	WAY-202196	
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	CRYSTAL 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	TRANSFERASE

	LACTOCOCCUS LACTIS	
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	CRYSTAL 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	HOTOSYNTHETIC REACTION CENTER FROM RHODOBACTER SPHAEROIDES	PHOTOSYNTHESIS
1Z9K	HOTOSYNTHETIC 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	THE STRUCTURE OF AN ANTITUMOR CH2-DOMAIN-DELETED HUMANIZED ANTIBODY	IMMUNE SYSTEM
1ZAF	CRYSTAL STRUCTURE OF ESTROGEN RECEPTOR BETA COMPLEXED WITH 3-BROMO-6-HYDROXY-2-(4-HYDROXY-PHENYL)-INDEN-1-ONE	TRANSCRIPTION/TRANSFERASE
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	THE 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	GROWTH 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	HORMONE/GROWTH FACTOR RECEPTOR

	INTERACTING PROTEIN 1 NR BOX II PEPTIDE	
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 OCTAPEPTIDE	IMMUNE SYSTEM
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	CRYSTAL 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	A 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	TRUCTURE 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 AT 2.7 ANGSTROMS RESOLUTION AND ITS COMPARISON WITH OTHER SERPINS	PROTEINASE INHIBITOR
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 STRUCTURE OF THE CARBAMYL PHOSPHATE AND L-ALANOSINE LIGATED ENZYME	TRANSFERASE
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 BINDING/VIRAL PROTEIN

	PROTEIN	
2B5R	1B LACTAMASE / B LACTAMASE INHIBITOR	HYDROLASE/HYDROLASE INHIBITOR
2B5T	2.1 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	CRYSTAL 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	RIBOSOME

	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
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	CRYSTAL 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	X-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	CRYSTAL 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	LIPIDIC 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	LIPIDIC 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	NEW 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	OXIDOREDUCTASE

	ACINETOBACTER SP. ADP1 MUTANT R457S- APO	
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 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	2.1 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	CRYSTAL 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	CRYSTAL 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-	OXIDOREDUCTASE

	KETOACID DEHYDROGENASE BY AN INTERNAL MOLECULAR SWITCH	
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	X-RAY STRUCTURE OF THE GENERAL SECRETION PATHWAY COMPLEX OF THE N-TERMINAL DOMAIN OF EPSE AND THE CYTOSOLIC DOMAIN OF	TRANSPORT PROTEIN

	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	CRYSTAL 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	LIPIDIC 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	LIPIDIC 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	NEW 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	PHOTOSYNTHESIS

	CHILENSIS.	
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
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	LAUE STRUCTURE OF PHYCOERYTHROCYANIN FROM MASTIGOCLADUS LAMINOSUS	ELECTRON TRANSPORT
2C7L	LOW TEMPERATURE STRUCTURE OF PHYCOERYTHROCYANIN FROM MASTIGOCLADUS LAMINOSUS	ELECTRON TRANSPORT

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 CD1D-ALPHA-GALACTOSYLCERAMIDE SPECIFIC T CELL RECEPTORS-INKT-TCR	CELL RECEPTOR
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	CRYSTAL 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	NCK1 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	COMPLEX (HYDROLASE-INHIBITOR)

	HIGH RESOLUTION X-RAY STRUCTURE ANALYSIS	
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	CRYSTAL STRUCTURE OF SUMO-3-MODIFIED THYMINE-DNA GLYCOSYLASE	HYDROLASE
2D0O	STRCUTURE 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	CRYSTAL STRUCTURE OF THE RADIXIN FERM DOMAIN COMPLEXED WITH THE NHERF-1 C-TERMINAL TAIL PEPTIDE	CELL ADHESION
2D11	CRYSTAL 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	CRYSTAL 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	CRYSTAL 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 PSEUDOMONAS FRAGI, FORM V	LYASE, OXIDOREDUCTASE/TRANSFERASE
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	CRYSTAL 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	HYDROLASE

	INHIBITOR, ANGIOSTATIN, BOUND A TO A PEPTIDE FROM THE GROUP A STREPTOCOCCAL SURFACE PROTEIN PAM	
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	CRYSTAL 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	CRYSTAL 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	CRYSTAL 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	CRYSTAL 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	CRYSTAL 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	STRUCTURAL BASIS FOR SELECTION OF GLYCOSYLATED SUBSTRATE BY SCFFBS1 UBIQUITIN LIGASE	LIGASE
2.00E+32	STRUCTURAL BASIS FOR SELECTION OF GLYCOSYLATED SUBSTRATE BY SCFFBS1 UBIQUITIN LIGASE	LIGASE
2.00E+33	STRUCTURAL BASIS FOR SELECTION OF GLYCOSYLATED SUBSTRATE BY SCFFBS1 UBIQUITIN LIGASE	LIGASE/HYDROLASE
2E3K	CRYSTAL STRUCTURE OF THE HUMAN BRD2 SECOND BROMODOMAIN IN COMPLEXED WITH THE ACETYLATED HISTONE H4 PEPTIDE	TRANSCRIPTION
2E3X	CRYSTAL 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	CRYSTAL 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	CRYSTAL 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 ITS YEAST ORTHOLOGS	HYDROLASE

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	CRYSTAL 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	CRYSTAL 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	2.9 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	CRYSTAL 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	THE 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	THE 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	PROTON TRANSPORT,MEMBRANE PROTEIN

	NABR	
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 ARABIDOPSIS THALIANA	HYDROLASE, PLANT PROTEIN
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	CRYSTAL STRUCTURE OF MYCOBACTERIAL TUBERCULOSIS PROTEASOME	HYDROLASE
2FHH	CRYSTAL 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	CRYSTAL 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	TRANSFERASE

	IN COMPLEX WITH ALPHA-LACTALBUMIN, GLUCOSE, MN, AND UDP-N-ACETYLGALACTOSAMINE	
2FYL	HADDOCK 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	CRYSTAL 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	IMMUNE SYSTEM

	(NITRO-STILBENE DERIVATIVE)	
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 WITH SUMO-1	HYDROLASE/PROTEIN BINDING
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	HORMONE/GROWTH FACTOR RECEPTOR

	GLUCOCORTICOID RECEPTOR INTERACTING PROTEIN 1 NR BOX II PEPTIDE	
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	CRYSTALLOGRAPHIC 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	TRANSCRIPTION

	COMPLEXED WITH A RIP140 PEPTIDE AND SYNTHETIC LIGAND GSK4716	
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 POTENT INHIBITORS FOR AKT: SYNTHESIS AND SAR STUDIES	SIGNALING PROTEIN,TRANSFERASE/INHIBITOR
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 IMMUNITY PROTEIN IM9 (Y55A)	ANTIBIOTIC/ANTIBIOTIC INHIBITOR
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	CRYSTAL STRUCTURE OF AN ELECTRON TRANSFER COMPLEX BETWEEN AROMATIC AMINE DEHYDROGENASE AND AZURIN FROM ALCALIGENES FAECALIS (FORM 3)	OXIDOREDUCTASE/ELECTRON TRANSPORT
2H43	CRYSTAL STRUCTURE OF HUMAN FRAGMENT D COMPLEXED WITH ALA-HIS-ARG-PRO-AMIDE	BLOOD CLOTTING
2H47	CRYSTAL 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	HYDROLASE

	COMPLEX WITH 3-[2-(2-BENZYLOXYCARBONYLAMINO-3-METHYL-BUTYRYLAMINO)-PROPIONYLAMINO]-4-OXO-PENTANOIC ACID (Z-VAD-FMK)	
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	CRYSTAL 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	THE 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-BUTYRYLAMINO)-PROPIONYLAMINO]-4-OXO-PENTANOIC ACID (Z-VAD-FMK)	HYDROLASE
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	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.	
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 COMPLEXED WITH DIBROMINATED PHOSPHATIDYLGLYCEROL	PHOTOSYNTHESIS/MEMBRANE PROTEIN
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	OXIOREDUCTASE

	MUTANT BOUND TO PHENANTHRENE.	
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	STRUCTURES OF THE NONCOVALENT COMPLEXES OF HUMAN AND BOVINE PROTHROMBIN FRAGMENT 2 WITH HUMAN PPACK-THROMBIN	HYDROLASE(SERINE PROTEINASE)
2HPQ	STRUCTURES 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	CRYSTAL 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	STRUCTURAL 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	STRUCTURAL BASIS OF YEAST AMINOACYL-TRNA SYNTHETASE COMPLEX FORMATION REVEALED BY CRYSTAL STRUCTURES OF TWO BINARY SUB-COMPLEXES	LIGASE/RNA BINDING PROTEIN
2HSN	STRUCTURAL 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 Y445H MUTANT AND FAB COMPLEX	MEMBRANE PROTEIN
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	CRYSTAL 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	STRUCTURE 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 OXIDIZED AND REDUCED STATES SHOW REDOX-CORRELATED STRUCTURAL CHANGES	ELECTRON TRANSPORT, OXIDOREDUCTASE
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 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
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	CRYSTAL 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	CRYSTAL 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 TRANSCRIPTASE (RT) IN COMPLEX WITH ATP	TRANSFERASE
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	CRYSTAL 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-SUMO-2	PROTEIN BINDING, HYDROLASE
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	CRYSTAL 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	STRUCTURE 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 THE EVH1 DOMAIN OF MENA	METAL-BINDING
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 PILUS TERMINATOR SUBUNIT PAPH AT 2.3 ANGSTROM RESOLUTION	CHAPERONE/SURFACE ACTIVE PROTEIN
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	CRYSTAL 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	CRYSTAL 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-101	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	TRANSFERASE

	KINASE I G	
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	STRUCTURE 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	STRUCTURE 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		
2KAU	THE CRYSTAL STRUCTURE OF UREASE FROM KLEBSIELLA AEROGENES AT 2.2 ANGSTROMS RESOLUTION	HYDROLASE (UREA AMIDO)
2KIN	KINESIN (MONOMERIC) FROM RATTUS NORVEGICUS	MOTOR PROTEIN
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	STRUCTURE 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	TRANSCRIPTION

	COMPLEX E2:BRD4	
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
2NP0	CRYSTAL STRUCTURE OF THE BOTULINUM NEUROTOXIN TYPE B COMPLEXED WITH SYNAPTOTAGAMIN-II ECTODOMAIN	HYDROLASE
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
		HYDROLASE

2NU1	MOLECULAR STRUCTURES OF THE COMPLEXES OF SGPB WITH OMTKY3 AROMATIC P1 VARIANTS TRP18I, HIS18I, PHE18I AND TYR18I	
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	CRYSTAL 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'-DUTP	TRANSCRIPTION/DNA/RNA
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, S334A, S375W) COMPLEXED WITH CD4 AND ANTIBODY 17B	VIRAL PROTEIN/IMMUNE SYSTEM
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	HYDROLASE

	BOUND TRP FRAGMENT OF DLWCF	
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
		VIRAL PROTEIN

2OC7	STRUCTURE OF HEPATITIS C VIRAL NS3 PROTEASE DOMAIN COMPLEXED WITH NS4A PEPTIDE AND KETOAMIDE SCH571696	
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	IMMUNE SYSTEM

	II MHC MOLECULE HLA-DR1/HA COMPLEX IN THE PRESENCE OF EDTA	
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
2OO5	STRUCTURE OF TRANSHYDROGENASE (DI.H2NADH)2(DIII.NADP+)1 ASYMMETRIC COMPLEX	OXIDOREDUCTASE
2OOB	CRYSTAL STRUCTURE OF THE UBA DOMAIN FROM CBL-B UBIQUITIN LIGASE IN COMPLEX WITH UBIQUITIN	LIGASE
		OXIDOREDUCTASE

2OOR	STRUCTURE OF TRANSHYDROGENASE (DI.NAD+)2(DIII.H2NADPH)1 ASYMMETRIC COMPLEX	
2OOV	CRYSTAL STRUCTURE OF HANSENULA POLYMORPHA AMINE OXIDASE TO 1.7 ANGSTROMS	OXIDOREDUCTASE
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	TRANSFERASE
2OP4	CRYSTAL STRUCTURE OF QUORUM-QUENCHING ANTIBODY 1G9	IMMUNE SYSTEM
2OPL	CRYSTAL STRUCTURE OF OSMC-LIKE PROTEIN FROM GEOBACTER SULFURREDUCENS AT 1.50 A RESOLUTION	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
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.	TRANSFERASE
2OPZ	AVPF BOUND TO BIR3-XIAP	APOPTOSIS INHIBITOR
2OQ1	TANDEM SH2 DOMAINS OF ZAP-70 WITH 19-MER ZETA1 PEPTIDE	TRANSFERASE
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	OXIDOREDUCTASE
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	IMMUNE SYSTEM
2OS2	CRYSTAL STRUCTURE OF JMJD2A COMPLEXED WITH HISTONE H3 PEPTIDE TRIMETHYLATED AT LYS36	OXIDOREDUCTASE
2OS8	RIGOR-LIKE STRUCTURES OF MUSCLE MYOSINS REVEAL KEY MECHANICAL ELEMENTS IN THE TRANSDUCTION PATHWAYS OF THIS ALLOSTERIC MOTOR	CONTRACTILE PROTEIN
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
		TRANSPORT PROTEIN

2OT8	KARYOPHERIN BETA2/TRANSPORTIN-HNRNPM NLS COMPLEX	
2OTG	RIGOR-LIKE STRUCTURES OF MUSCLE MYOSINS REVEAL KEY MECHANICAL ELEMENTS IN THE TRANSDUCTION PATHWAYS OF THIS ALLOSTERIC MOTOR	CONTRACTILE PROTEIN
2OTJ	13-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
		RNA BINDING PROTEIN/RNA

2OZB	STRUCTURE OF A HUMAN PRP31-15.5K-U4 SNRNA COMPLEX	
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
2P1Q	MECHANISM OF AUXIN PERCEPTION BY THE TIR1 UBIQUITIN LIGASE	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
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	HORMONE RECEPTOR
2P22	STRUCTURE OF THE YEAST ESCRT-I HETEROTETRAMER CORE	TRANSPORT PROTEIN
2P24	I-AU/MBP125-135	IMMUNE SYSTEM
2P28	STRUCTURE OF THE PHE2 AND PHE3 FRAGMENTS OF THE INTEGRIN BETA2 SUBUNIT	CELL ADHESION
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	HYDROLASE
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}	BLOOD CLOTTING
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	HYDROLASE/IMMUNE SYSTEM
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
		VIRAL PROTEIN

2P8M	CRYSTAL STRUCTURE OF THE HIV-1 CROSS NEUTRALIZING MONOCLONAL ANTIBODY 2F5 IN COMPLEX WITH GP41 PEPTIDE ELLELDKWASLWN IN NEW CRYSTAL FORM	
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 DOMAIN OF VASP*	STRUCTURAL PROTEIN

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	NON-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	CYTOKINE/CYTOKINE RECEPTOR

	SIGNALING COMPLEX	
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	CRYSTAL 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
2PMS	CRYSTAL STRUCTURE OF THE COMPLEX OF HUMAN LACTOFERRIN N-LOBE AND LACTOFERRIN-BINDING DOMAIN OF PNEUMOCOCCAL SURFACE PROTEIN A	METAL TRANSPORT, HYDROLASE
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	HYDROLASE/HYDROLASE

	COMPLEXED WITH CDP	
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
2PRC	PHOTOSYNTHETIC REACTION CENTER FROM RHODOPSEUDOMONAS VIRIDIS (UBIQUINONE-2 COMPLEX)	PHOTOSYNTHETIC REACTION CENTER
2PRG	LIGAND-BINDING DOMAIN OF THE HUMAN PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR GAMMA	COMPLEX (THIAZOLIDINEDIONE/RECEPTOR)
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	CRYSTAL SRTUCTURE OF THE BINARY COMPLEX BETWEEN FERREDOXIN: THIOREDOXIN REDUCTASE AND THIOREDOXIN F	ELECTRON TRANSPORT
2PUK	CRYSTAL SRTUCTURE OF THE BINARY COMPLEX BETWEEN FERREDOXIN: THIOREDOXIN REDUCTASE AND THIOREDOXIN M	ELECTRON TRANSPORT
2PUO	CRYSTAL SRTUCTURE OF THE NEM MODIFIED FERREDOXIN:THIOREDOXIN REDUCTASE	ELECTRON TRANSPORT
2PUQ	CRYSTAL STRUCTURE OF ACTIVE SITE INHIBITED COAGULATION FACTOR VIIA IN COMPLEX WITH SOLUBLE TISSUE FACTOR	BLOOD CLOTTING
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
2PV1	CRYSTALLOGRAPHIC STRUCTURE OF SURA FIRST PEPTIDYL-PROLYL	ISOMERASE

	ISOMERASE DOMAIN COMPLEXED WITH PEPTIDE WEYIPNV	
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	ISOMERASE
2PV9	CRYSTAL STRUCTURE OF MURINE THROMBIN IN COMPLEX WITH THE EXTRACELLULAR FRAGMENT OF MURINE PAR4	HYDROLASE
2PVC	DNMT3L RECOGNIZES UNMETHYLATED HISTONE H3 LYSINE 4	TRANSFERASE REGULATOR
2PVD	CRYSTAL SRTUCTURE OF THE REDUCED FERREDOXIN:THIOREDOXIN REDUCTASE	ELECTRON TRANSPORT
2PVF	CRYSTAL STRUCTURE OF TYROSINE PHOSPHORYLATED ACTIVATED FGF RECEPTOR 2 (FGFR2) KINASE DOMAIN IN COMPLEX WITH ATP ANALOG AND SUBSTRATE PEPTIDE	TRANSFERASE
2PVG	CRYSTAL 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	ELECTRON TRANSPORT
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
		VIRUS/RNA

2Q26	FHV VIRUS LIKE PARTICLE	
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	THE 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	CRYSTAL 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	THE ANDROGEN RECEPTOR PROSTATE CANCER MUTANT H874Y LIGAND BINDING DOMAIN BOUND WITH TESTOSTERONE AND AN AR 20-30 PEPTIDE	HORMONE
2Q7L	THE 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	OXIDOREDUCTASE

	WITH P-CHLOROBENZYLAMINE.	
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 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
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	RIBOSOME

	70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	
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	CRYSTAL 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. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES AND IS DESCRIBED IN REMARK 400.	RIBOSOME
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	RIBOSOME

	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.	
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 SUBUNIT OF PROTEIN KINASE A THAT REPRESENTS THE INHIBITED STATE	TRANSFERASE/TRANSFERASE INHIBITOR
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
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	TRANSFERASE/TRANSFERASE REGULATOR
		TRANSCRIPTION

2QGT	CRYSTAL STRUCTURE OF THE ESTROGEN RECEPTOR ALPHA LIGAND BINDING DOMAIN COMPLEXED TO AN ETHER ESTRADIOL COMPOUND	
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	TRANSCRIPTION
2QHO	CRYSTAL STRUCTURE OF THE UBA DOMAIN FROM EDD UBIQUITIN LIGASE IN COMPLEX WITH UBIQUITIN	PROTEIN BINDING/LIGASE
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
2QIE	STAPHYLOCOCCUS AUREUS MOLYBDOPTERIN SYNTHASE IN COMPLEX WITH PRECURSOR Z	TRANSFERASE
2QIU	STRUCTURE OF HUMAN ARG-INSULIN	HORMONE
2QIY	YEAST DEUBIQUITINASE UBP3 AND BRE5 COFACTOR COMPLEX	SIGNALING PROTEIN/HYDROLASE
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	CYTOKINE/RECEPTOR
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	CRYSTAL STRUCTURE OF WILD TYPE RHODOBACTER SPHAEROIDES WITH STIGMATELLIN AND ANTIMYCIN INHIBITED	ELECTRON TRANSPORT
2QJY	CRYSTAL 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
		HYDROLASE

2QL7	CRYSTAL STRUCTURE OF CASPASE-7 WITH INHIBITOR AC-IEPD-CHO	
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-GLUTAMYLTRANSPEPTIDASE IN COMPLEX WITH GLUTAMATE	TRANSFERASE
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	RIBOSOME

	SPECTINOMYCIN BOUND. THE ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES.	
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
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 ENTIRE CRYSTAL STRUCTURE CONTAINS TWO 70S RIBOSOMES.	RIBOSOME

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-4-CARBOXAMIDE 1-BETA-D-RIBOFURANOTIDE (ZMP)	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
2QSE	CRYSTAL STRUCTURE OF THE ESTROGEN RECEPTOR ALPHA LIGAND BINDING DOMAIN COMPLEXED WITH BURNED MEAT COMPOUND 4-OH-PHIP	TRANSCRIPTION
		DNA BINDING PROTEIN

2QSF	CRYSTAL STRUCTURE OF THE RAD4-RAD23 COMPLEX	
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 BOVINE HSC70 (1-394AA)R171C AND BOVINE AUXILIN (810-910AA) D876C IN THE AMPPNP HYDROLYZED FORM	CHAPERONE
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
		TRANSCRIPTION

2QZO	CRYSTAL STRUCTURE OF THE ESTROGEN RECEPTOR ALPHA LIGAND BINDING DOMAIN COMPLEXED WITH WAY-169916	
2R00	CRYSTAL 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
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
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-	CELL CYCLE

	120)	
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
2RD5	STRUCTURAL BASIS FOR THE REGULATION OF N-ACETYLGLUTAMATE KINASE BY PII IN ARABIDOPSIS THALIANA	PROTEIN BINDING
2RD7	IUMAN 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	X-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	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	VIRAL PROTEIN

	COMPLEX WITH LSTA RECEPTOR ANALOG	
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	COMPLEX (ISOMERASE/IMMUNOSUPPRESSANT)

	CYCLOSPORIN A AND N-METHYL-4-[(E)-2-BUTENYL]-4,4-DIMETHYLTHREONINE CYCLOSPORIN A	
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 WITH H187D MUTANT UDG AND WILD-TYPE UGI	REPLICATION, HYDROLASE
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
		TRANSFERASE/INHIBITOR COMPLEX

2UW0	STRUCTURE OF PKA-PKB CHIMERA COMPLEXED WITH 6-(4-(4-(4-CHLORO-PHENYL)-PIPERIDIN-4-YL)-PHENYL)-9H-PURINE	
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 TYPE III SECRETION NEEDLE FORMATION	CHAPERONE
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-	PHOTOSYNTHESIS

	SEPARATED STATE, 2ND DATASET	
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 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	PHOTOSYNTHESIS
2UXN	STRUCTURAL BASIS OF HISTONE DEMETHYLATION BY LSD1 REVEALED BY SUICIDE INACTIVATION	OXIDOREDUCTASE/REPRESSOR COMPLEX
2UXX	HUMAN LSD1 HISTONE DEMETHYLASE-COREST IN COMPLEX WITH AN FAD-TRANYLCYPROMINE ADDUCT	OXIDOREDUCTASE/REPRESSOR
2UY1	CRYSTAL STRUCTURE OF CSTF-77	RNA-BINDING PROTEIN
2UY6	CRYSTAL STRUCTURE OF THE P PILUS ROD SUBUNIT PAPA	CHAPERONE
2UY7	CRYSTAL STRUCTURE OF THE P PILUS ROD SUBUNIT PAPA	CHAPERONE
2UYL	CRYSTAL STRUCTURE OF A MONOCLONAL ANTIBODY DIRECTED AGAINST AN ANTIGENIC DETERMINANT COMMON TO OGAWA AND INABA SEROTYPES OF VIBRIO CHOLERAE O1	IMMUNE SYSTEM
2UYN	CRYSTAL STRUCTURE OF E. COLI TDCF WITH BOUND 2-KETOBUTYRATE	UNKNOWN FUNCTION
2UYZ	NON-COVALENT COMPLEX BETWEEN UBC9 AND SUMO1	LIGASE
2UZ1	1.65 ANGSTROM STRUCTURE OF BENZALDEHYDE LYASE COMPLEXED WITH 2-METHYL-2,4-PENTANEDIOL	LYASE
2UZ6	ACHBP-TARGETED A-CONOTOXIN CORRELATES DISTINCT BINDING ORIENTATIONS WITH NACHR SUBTYPE SELECTIVITY.	RECEPTOR
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	TRANSFERASE
2UZI	CRYSTAL STRUCTURE OF HRAS(G12V)- ANTI-RAS FV COMPLEX	SIGNALING PROTEIN/IMMUNE SYSTEM
2UZL	CRYSTAL STRUCTURE OF HUMAN CDK2 COMPLEXED WITH A THIAZOLIDINONE INHIBITOR	TRANSFERASE
2UZT	PKA STRUCTURES OF AKT, INDAZOLE-PYRIDINE INHIBITORS	TRANSFERASE
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 THERMUS THERMOPHILUS 70S RIBOSOME WITH MRNA, ASL-PHE AND	RIBOSOME

	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	CRYSTAL 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	CRYSTAL STRUCTURE OF CHLAMYDOMONAS REINHARDTII RUBISCO WITH A LARGE-SUBUNIT SUPRESSOR MUTATION T342I	OXIDOREDUCTASE
2V68	CRYSTAL STRUCTURE OF CHLAMYDOMONAS REINHARDTII RUBISCO WITH	OXIDOREDUCTASE

	LARGE-SUBUNIT MUTATIONS V331A, T342I	
2V69	CRYSTAL STRUCTURE OF CHLAMYDOMONAS REINHARDTII RUBISCO WITH A LARGE-SUBUNIT MUTATION D473E	OXIDOREDUCTASE
2V6A	CRYSTAL 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 ALLOPHYCOCYANIN AT 3.5 ANGSTROEMS.	ELECTRON TRANSPORT
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	CRYSTAL STRUCTURE OF THE REGULATORY FRAGMENT OF MAMMALIAN AMPK IN COMPLEXES WITH AMP	TRANSFERASE
2V8S	VTI1B HABC DOMAIN - EPSINR ENTH DOMAIN COMPLEX	PROTEIN TRANSPORT
2V8W	CRYSTALLOGRAPHIC AND MASS SPECTROMETRIC CHARACTERISATION OF EIF4E WITH N7-CAP DERIVATIVES	TRANSLATION
2V8X	CRYSTALLOGRAPHIC AND MASS SPECTROMETRIC CHARACTERISATION OF EIF4E WITH N7-CAP DERIVATIVES	TRANSLATION
2V8Y	CRYSTALLOGRAPHIC AND MASS SPECTROMETRIC CHARACTERISATION OF EIF4E WITH N7-CAP DERIVATIVES	TRANSLATION

2V92	CRYSTAL STRUCTURE OF THE REGULATORY FRAGMENT OF MAMMALIAN AMPK IN COMPLEXES WITH ATP-AMP	TRANSFERASE
2V9J	CRYSTAL 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	CRYSTAL STRUCTURE OF THE NS3 PROTEASE-HELICASE FROM DENGUE VIRUS	HYDROLASE
2VBJ	MOLECULAR BASIS OF HUMAN XPC GENE RECOGNITION AND CLEAVAGE BY ENGINEERED HOMING ENDONUCLEASE HETERODIMERS	HYDROLASE
2VBL	MOLECULAR BASIS OF HUMAN XPC GENE RECOGNITION AND CLEAVAGE BY ENGINEERED HOMING ENDONUCLEASE HETERODIMERS	HYDROLASE
2VBN	MOLECULAR 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	CRYSTAL STRUCTURE OF CHLAMYDOMONAS REINHARDTII RUBISCO WITH A LARGE-SUBUNIT C172S MUTATION	LYASE
2VDI	CRYSTAL 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	CELL ADHESION/IMMUNE SYSTEM COMPLEX

	ANTAGONIST EPTIFIBATIDE	
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 COMPLEX WITH A PHOTOCLEAVABLE PEPTIDE	IMMUNE SYSTEM
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	RIBOSOME

	(PART 1 OF 4)	
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	CRYSTAL STRUCTURE OF THE MDM2-MDMX RING DOMAIN HETERODIMER	LIGASE
2VJF	CRYSTAL STRUCTURE OF THE MDM2-MDMX RING DOMAIN HETERODIMER	LIGASE
2VJH	THE 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	IMMUNE SYSTEM

	T-CELL RECEPTOR ARE PROGRAMMED BY ITS VBETA DOMAIN	
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	THE 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 SIGNALING COMPLEX	GENE REGULATION
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	GENE REGULATION

	SIGNALING COMPLEX	
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 RECEPTOR BINDING DOMAIN	TRANSPORT PROTEIN/HYDROLASE
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	PEPTIDE BINDING PROTEIN

	OPPA WITH TRI-LYSINE LIGAND	
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 PEPTIDASE	HYDROLASE
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	RIBOSOME

	DESCRIBED IN REMARK 400.	
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
		TRANSFERASE

2Z8K	CRYSTAL STRUCTURE OF ESCHERICHIA COLI GAMMA-GLUTAMYLTRANSPEPTIDASE IN COMPLEX WITH ACIVICIN	
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 THERMOACETICA	OXIDOREDUCTASE/TRANSFERASE
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	CRYSTAL 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 COMPLEX WITH TMC278 (RILPIVIRINE), A NON-NUCLEOSIDE RT	TRANSFERASE, HYDROLASE

	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
2ZJR	REFINED NATIVE STRUCTURE OF THE LARGE RIBOSOMAL SUBUNIT (50S) FROM DEINOCOCCUS RADIODURANS	RIBOSOME
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
		HYDROLASE

2ZL4	CRYSTAL STRUCTURE OF H.PYLORI CLPP S99A IN COMPLEX WITH THE PEPTIDE AAAA	
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	HA3 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	CRYSTAL 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 RECOGNITION BY THE GIBBERELLIN RECEPTOR	HORMONE 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
		CELL ADHESION

3B3Q	CRYSTAL STRUCTURE OF A SYNAPTIC ADHESION COMPLEX	
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	HYDROLASE

	ALKALINE PHOSPHATASE	
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 SUBSTRATE ASF/SF2	TRANSFERASE/SPLICING
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	TRANSFERASE

	WITH THE INHIBITOR MERIOLIN 3	
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	STRUCTURAL 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 IN THE REGULATORY SUBUNITS	OXIDOREDUCTASE
3BLX	YEAST ISOCITRATE DEHYDROGENASE (APO FORM)	OXIDOREDUCTASE
3BMC	STRUCTURE OF PTERIDINE REDUCTASE 1 (PTR1) FROM TRYPANOSOMA BRUCEI IN TERNARY COMPLEX WITH COFACTOR (NADP+) AND	OXIDOREDUCTASE

	SUBSTRATE (FOLATE)	
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	IMMUNE SYSTEM

	COMPLEX WITH A CATHEPSIN A SIGNAL SEQUENCE PEPTIDE, PCATA	
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 THERMUS THERMOPHILUS UNDER XENON PRESSURE, 100PSI 5MIN	OXIDOREDUCTASE
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 DOMAIN	MEMBRANE PROTEIN, PROTEIN TRANSPORT
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
		TRANSPORT PROTEIN

3C3R	ALIX BRO1 CHMP4C COMPLEX	
3C4M	STRUCTURE 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
3C4P	CRYSTAL STRUCTURE OF THE SHV-1 BETA-LACTAMASE/BETA-LACTAMASE INHIBITOR PROTEIN (BLIP) E73M COMPLEX	HYDROLASE/HYDROLASE INHIBITOR
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 INHIBITOR	TRANSFERASE

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
3CB8	4FE-4S-PYRUVATE FORMATE-LYASE ACTIVATING ENZYME IN COMPLEX WITH ADOMET AND A PEPTIDE SUBSTRATE	OXIDOREDUCTASE
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
		TRANSFERASE/TRANSFERASE RECEPTOR

3CBM	SET7/9-ER-ADOMET COMPLEX	
3CBO	SET7/9-ER-ADOHCY COMPLEX	TRANSFERASE/TRANSFERASE RECEPTOR
3CBP	SET7/9-ER-SINEFUNGIN COMPLEX	TRANSFERASE/TRANSFERASE RECEPTOR
3CC2	THE 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: 23S RRNA MUTATION G2616A	RIBOSOME
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-	HYDROLASE

	PYRIDINYL) AMINO)SULFONYL)PHENYL)-4-(2-OXO-1(2H)-PYRIDINYL)BENZAMIDE	
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 H4	HISTONE/CHAPERONE
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	ANTITUMOR PROTEIN/LIGASE

	COMPLEX WITH A PHOSPHORYLATED PEPTIDE FROM HUMAN ACETYL-COA CARBOXYLASE 1	
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	TRANSPORT PROTEIN

	TO T. BRUCEI PHOSPHOGLUCOISOMERASE (PGI) PTS1 PEPTIDE	
3CVH	HOW TCR-LIKE ANTIBODY RECOGNIZES MHC-BOUND PEPTIDE	IMMUNE SYSTEM
3CVI	HOW TCR-LIKE ANTIBODY RECOGNIZES MHC-BOUND PEPTIDE	IMMUNE SYSTEM
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	CRYSTAL STRUCTURE OF HUMAN PROTO-ONCOGENE SERINE THREONINE KINASE (PIM1) IN COMPLEX WITH A CONSENSUS PEPTIDE AND A BETA CARBOLINE LIGAND I	TRANSFERASE
3CY2	CRYSTAL STRUCTURE OF HUMAN PROTO-ONCOGENE SERINE THREONINE KINASE (PIM1) IN COMPLEX WITH A CONSENSUS PEPTIDE AND A BETA CARBOLINE LIGAND II	TRANSFERASE
3CY3	CRYSTAL STRUCTURE OF HUMAN PROTO-ONCOGENE SERINE THREONINE	TRANSFERASE

	KINASE (PIM1) IN COMPLEX WITH A CONSENSUS PEPTIDE AND THE JNK INHIBITOR V	
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
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	HYDROLASE
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	IMMUNE SYSTEM
3D17	A TRIPLY LIGATED CRYSTAL STRUCTURE OF RELAXED STATE HUMAN HEMOGLOBIN	OXYGEN BINDING
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	TRANSFERASE, TRANSCRIPTION
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
3D29	PROTEASOME INHIBITION BY FELLUTAMIDE B	HYDROLASE
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	PHOTOSYNTHESIS

	REACTION CENTER FROM BLASTOCHLORIS VIRIDIS. CRYSTALS GROWN IN MICROFLUIDICS BY DETERGENT CAPTURE	
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 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
3D5R	CRYSTAL STRUCTURE OF EFB-C (N138A) / C3D COMPLEX	CELL ADHESION/TOXIN
3D5S	CRYSTAL STRUCTURE OF EFB-C (R131A) / C3D COMPLEX	CELL ADHESION/TOXIN
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	TRANSFERASE
3D7V	CRYSTAL STRUCTURE OF MCL-1 IN COMPLEX WITH AN MCL-1 SELECTIVE BH3 LIGAND	APOPTOSIS
3D7W	MISTLETOE LECTIN I IN COMPLEX WITH ZEATIN	HYDROLASE
3D81	SIR2-S-ALKYLAMIDATE COMPLEX CRYSTAL STRUCTURE	HYDROLASE
3D85	CRYSTAL STRUCTURE OF IL-23 IN COMPLEX WITH NEUTRALIZING FAB	IMMUNE SYSTEM/CYTOKINE
3D87	CRYSTAL STRUCTURE OF INTERLEUKIN-23	CYTOKINE

3D8A	CO-CRYSTAL STRUCTURE OF TRAM-TRAD COMPLEX.	DNA BINDING PROTEIN
3D8C	FACTOR INHIBITING HIF-1 ALPHA D201G MUTANT IN COMPLEX WITH ZN(II), ALPHA-KETOGLUTARATE AND HIF-1 ALPHA 19MER	TRANSCRIPTION REGULATOR, OXIDOREDUCTASE
3D9A	HIGH RESOLUTION CRYSTAL STRUCTURE STRUCTURE OF HYHEL10 FAB COMPLEXED TO HEN EGG LYSOZYME	HYDROLASE/IMMUNE SYSTEM
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	TRANSCRIPTION
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
		LIGASE/VIRAL PROTEIN

3DCG	CRYSTAL STRUCTURE OF THE HIV VIF BC-BOX IN COMPLEX WITH HUMAN ELONGINB AND ELONGINC	
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 NEUROTOXIN SEROTYPE A WITH A SNAP-25 PEPTIDE	HYDROLASE
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	ALCIUM-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	RYSTAL 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	THE 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-655KNEQELLELDKWASLWN671 SOAKED IN PEG/2-PROPANOL SOLUTION	IMMUNE SYSTEM

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
		IMMUNE SYSTEM

3DVN	CRYSTAL STRUCTURE OF K63-SPECIFIC FAB APU2.16 BOUND TO K63-LINKED DI-UBIQUITIN	
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 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
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
		CELL CYCLE

3.00E+22	TUBULIN-COLCHICINE-SOBLIDOTIN: STATHMIN-LIKE DOMAIN COMPLEX	
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 WITH ATP-COMPETITIVE INHIBITORS	TRANSFERASE
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
		SIGNALING PROTEIN

3EG5	CRYSTAL STRUCTURE OF MDIA1-TSH GBD-FH3 IN COMPLEX WITH CDC42-GMPPNP	
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	IMMUNE SYSTEM/CYTOKINE

	TRANSFORMING GROWTH FACTOR-BETA 3	
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-ADENOSYLMETHIONINE METHYL ESTER AND NO PUTRESCINE BOUND	LYASE
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
		IMMUNE SYSTEM

3EYF	CRYSTAL STRUCTURE OF ANTI-HUMAN CYTOMEGALOVIRUS ANTIBODY 8F9 PLUS GB PEPTIDE	
3EYO	CRYSTAL 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	STRUCTURE 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
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	CRYSTAL 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
		MOTOR PROTEIN

TABLE S5

3KIN	KINESIN (DIMERIC) FROM RATTUS NORVEGICUS	
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	STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 3,4-DIHYDROXYBENZOATE	DIOXYGENASE
3PCB	STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 3-HYDROXYBENZOATE	DIOXYGENASE
3PCC	STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 4-HYDROXYBENZOATE	DIOXYGENASE
3PCD	PROTOCATECHUATE 3,4-DIOXYGENASE Y447H MUTANT	DIOXYGENASE
3PCE	STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 3-HYDROXYPHENYLACETATE	DIOXYGENASE
3PCF	STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 3-FLURO-4-HYDROXYBENZOATE	DIOXYGENASE
3PCG	STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH THE INHIBITOR 4-HYDROXYPHENYLACETATE	DIOXYGENASE
3PCH	STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 3-CHLORO-4-HYDROXYBENZOATE	DIOXYGENASE
3PCI	STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 3-IODO-4-HYDROXYBENZOATE	DIOXYGENASE
3PCJ	STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 2-HYDROXYISONICOTINIC ACID N-OXIDE	DIOXYGENASE
3PCK	STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 6-HYDROXYNICOTINIC ACID N-OXIDE	DIOXYGENASE
3PCL	STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 2-HYDROXYISONICOTINIC ACID N-OXIDE AND CYANIDE	DIOXYGENASE
3PCM	STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 6-HYDROXYNICOTINIC ACID N-OXIDE AND CYANIDE	DIOXYGENASE
3PCN	STRUCTURE OF PROTOCATECHUATE 3,4-DIOXYGENASE COMPLEXED WITH 3,4-DIHYDROXYPHENYLACETATE	DIOXYGENASE
3PRC	PHOTOSYNTHETIC 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	RIBONUCLEOTIDE REDUCTASE R1 PROTEIN WITH AMPPNP OCCUPYING THE ACTIVITY SITE FROM ESCHERICHIA COLI	COMPLEX (OXIDOREDUCTASE/PEPTIDE)
		COMPLEX (ISOMERASE/DEOXYADENOSINE)

3REQ	METHYLMALONYL-COA MUTASE, SUBSTRATE-FREE STATE (POOR QUALITY STRUCTURE)	
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	STRUCTURE 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)
3TEC	CALCIUM BINDING TO THERMITASE. CRYSTALLOGRAPHIC STUDIES OF THERMITASE AT 0, 5 AND 100 MM CALCIUM	COMPLEX(SERINE PROTEINASE-INHIBITOR)
3TMN	THE BINDING OF L-VALYL-L-TRYPTOPHAN TO CRYSTALLINE THERMOLYSIN ILLUSTRATES THE MODE OF INTERACTION OF A PRODUCT OF PEPTIDE HYDROLYSIS	HYDROLASE (METALLOPROTEINASE)
3UBP	DIAMIDOPHOSPHATE INHIBITED BACILLUS PASTEURII UREASE	HYDROLASE
3VGC	GAMMA-CHYMOTRYPSIN L-NAPHTHYL-1-ACETAMIDO BORONIC ACID ACID INHIBITOR COMPLEX	SERINE PROTEASE
3YGS	APAF-1 CARD IN COMPLEX WITH PRODOMAIN OF PROCASPASE-9	APOPTOSIS
43C9	CRYSTALLOGRAPHIC STRUCTURE OF THE ESTEROLYTIC AND AMIDOLYTIC 43C9 ANTIBODY	IMMUNOGLOBULIN
4AAH	METHANOL DEHYDROGENASE FROM METHYLOPHILUS W3A1	OXIDOREDUCTASE (PQQ(A)-CHOH(D))
4AIY	R6 HUMAN INSULIN HEXAMER (SYMMETRIC), NMR, 'GREEN' SUBSTATE, AVERAGE STRUCTURE	HORMONE/GROWTH FACTOR
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	TRANSFERASE (CARBAMOYL-P,ASPARTATE)
4BJL	LOCW, A LAMBDA 1 TYPE LIGHT-CHAIN DIMER (BENCE-JONES PROTEIN) CRYSTALLIZED IN DISTILLED WATER	IMMUNOGLOBULIN
4CAA	CLEAVED ANTICHYMOTRYPSIN T345R	SERPIN
4CHA	STRUCTURE OF ALPHA-*CHYMOTRYPSIN REFINED AT 1.68 ANGSTROMS RESOLUTION	HYDROLASE (SERINE PROTEINASE)
4CPA	REFINED CRYSTAL STRUCTURE OF THE POTATO INHIBITOR COMPLEX	HYDROLASE (C-TERMINAL PEPTIDASE)

	OF CARBOXYPEPTIDASE A AT 2.5 ANGSTROMS RESOLUTION	
4FAB	THREE-DIMENSIONAL STRUCTURE OF A FLUORESCEIN-FAB COMPLEX CRYSTALLIZED IN 2-METHYL-2,4-PENTANEDIOL	IMMUNOGLOBULIN
4FAP	ATOMIC STRUCTURES OF THE RAPAMYCIN ANALOGS IN COMPLEX WITH BOTH HUMAN FKBP12 AND FRB DOMAIN OF FRAP	CELL CYCLE
4GCH	STRUCTURE AND ACTIVITY OF TWO PHOTOREVERSIBLE CINNAMATES BOUND TO CHYMOTRYPSIN	HYDROLASE (SERINE PROTEINASE)
4HHB	THE CRYSTAL STRUCTURE OF HUMAN DEOXYHAEMOGLOBIN AT 1.74 ANGSTROMS RESOLUTION	OXYGEN TRANSPORT
4HMG	REFINEMENT OF THE INFLUENZA VIRUS HEMAGGLUTININ BY SIMULATED ANNEALING	VIRAL PROTEIN
4HTC	THE REFINED STRUCTURE OF THE HIRUDIN-THROMBIN COMPLEX	HYDROLASE(SERINE PROTEASE)
4HVP	STRUCTURE OF COMPLEX OF SYNTHETIC HIV-1 PROTEASE WITH A STUBTRATE-BASED INHIBITOR AT 2.3 ANGSTROMS RESOLUTION	HYDROLASE(ACID PROTEINASE)
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	STRUCTURE 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)
		HYDROLASE (SERINE PROTEINASE)

6CHA	STRUCTURE OF A TETRAHEDRAL TRANSITION STATE COMPLEX OF ALPHA-*CHYMOTRYPSIN AT 1.8-*ANGSTROMS RESOLUTION	IMMUNOGLOBULIN
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	HYDROLASE (SERINE PROTEINASE)
6GCH	TRUCTURE OF CHYMOTRYPSIN-*TRIFLUOROMETHYL KETONE INHIBITOR COMPLEXES. COMPARISON OF SLOWLY AND RAPIDLY EQUILIBRATING INHIBITORS	OXYGEN STORAGE/TRANSPORT
6HBW	CRYSTAL STRUCTURE OF DEOXY-HUMAN HEMOGLOBIN BETA6 GLU->TRP	HYDROLASE (SULFHYDRYL PROTEINASE)
6PAD	BINDING OF CHLOROMETHYL KETONE SUBSTRATE ANALOGUES TO CRYSTALLINE PAPAIN	PHOTOSYNTHETIC REACTION CENTER
6PRC	PHOTOSYNTHETIC REACTION CENTER FROM RHODOPSEUDOMONAS VIRIDIS (DG-420314 (TRIAZINE) COMPLEX)	COMPLEX (OXIDOREDUCTASE/PEPTIDE)
6R1R	RIBONUCLEOTIDE REDUCTASE E441D MUTANT R1 PROTEIN FROM ESCHERICHIA COLI	ISOMERASE
6REQ	METHYLMALONYL-COA MUTASE, 3-CARBOXYPROPYL-COA INHIBITOR COMPLEX	HORMONE(MUSCLE RELAXANT)
6RLX	X-RAY STRUCTURE OF HUMAN RELAXIN AT 1.5 ANGSTROMS. COMPARISON TO INSULIN AND IMPLICATIONS FOR RECEPTOR BINDING DETERMINANTS	HYDROLASE (METALLOPROTEINASE)
6TMN	STRUCTURES OF TWO THERMOLYSIN-INHIBITOR COMPLEXES THAT DIFFER BY A SINGLE HYDROGEN BOND	PROTEINASE INHIBITOR
7API	THE S VARIANT OF HUMAN ALPHA1-ANTITRYPSIN, STRUCTURE AND IMPLICATIONS FOR FUNCTION AND METABOLISM	TRANSFERASE (CARBAMOYL-P,ASPARTATE)
7AT1	CRYSTAL STRUCTURES OF ASPARTATE CARBAMOYLTRANSFERASE LIGATED WITH PHOSPHONOACETAMIDE, MALONATE, AND CTP OR ATP AT 2.8-ANGSTROMS RESOLUTION AND NEUTRAL P*H	IMMUNE SYSTEM
7CEI	THE ENDONUCLEASE DOMAIN OF COLICIN E7 IN COMPLEX WITH ITS INHIBITOR IM7 PROTEIN	IMMUNOGLOBULIN
7FAB	RYSTAL STRUCTURE OF HUMAN IMMUNOGLOBULIN FRAGMENT FAB NEW REFINED AT 2.0 ANGSTROMS RESOLUTION	HYDROLASE (SERINE PROTEINASE)
7GCH	TRUCTURE OF CHYMOTRYPSIN-*TRIFLUOROMETHYL KETONE INHIBITOR COMPLEXES. COMPARISON OF SLOWLY AND RAPIDLY EQUILIBRATING INHIBITORS	HYDROLASE(ACID PROTEINASE)
7HVP	X-RAY CRYSTALLOGRAPHIC STRUCTURE OF A COMPLEX BETWEEN A SYNTHETIC PROTEASE OF HUMAN IMMUNODEFICIENCY VIRUS 1 AND A SUBSTRATE-BASED HYDROXYETHYLAMINE INHIBITOR	HORMONE
7INS	STRUCTURE OF PORCINE INSULIN COCRYSTALLIZED WITH CLUPEINE Z	HYDROLASE
7KME	CRYSTAL STRUCTURE OF HUMAN ALPHA-THROMBIN INHIBITED WITH SEL2711.	PHOTOSYNTHETIC REACTION CENTER
7PRC	PHOTOSYNTHETIC REACTION CENTER FROM RHODOPSEUDOMONAS VIRIDIS (DG-420315 (TRIAZINE) COMPLEX)	COMPLEX (OXIDOREDUCTASE/PEPTIDE)
7R1R	RIBONUCLEOTIDE REDUCTASE E441Q MUTANT R1 PROTEIN FROM ESCHERICHIA COLI	ISOMERASE

7REQ	METHYLMALONYL-COA MUTASE, 2-CARBOXYPROPYL-COA INHIBITOR COMPLEX	
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	STRUCTURAL 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