	Database Field	Example	Description
IDENTITY	investigator	Bertone	Experimentalist
	protein_name	HSP60	Common name, gene
	orf_id	APP30	Open reading frame ID
	pdb_id	1DA7	Protein Data Bank ID
	nesgc_id	HY5	Primary Identifier
	creation_date	2000-12-31	Record instantiated
	modify_date	2000-12-31	Last modified
	entry_type	Valid	Allows "test" entries
	access	Restricted	Entry protection
	laboratory	Gerstein	Principal investigator
	institution	Yale	University, national lab, etc.
	target_org	Human (Hsap)	Protein origin
CLONING & EXPRESSION	vector	pet15	Cloning vector used
	tag	hexaHis	Type of sequence tag
	cloned_comment	[text]	Cloning notes
	expr_comment	[text]	Expression notes
	homolog_seqid	YGL043W	Homolog protein, ORF, etc.
	homolog_org	Scer	Homolog protein origin
	insert_type	Subsequence	Nature of construct sequence
	insert_begin	42	Sequence start coordinate
	insert_end	210	Sequence end coordinate
	tag_sequence	MGSSHHH...	Construct tag sequence
	terminal	N	Amino or carboxyl terminus
	cloned_date	2000-12-31	Date cloned
	seq_verified	One direction	Sequence confirmation
	sequence	MKREILKH...	Construct sequence
	expression	4	Expression level
SOLUBILITY & PURIFICATION	soluble_comment	[text]	Solubility notes
	purified_comment	[text]	Purification notes
	purified_date	2000-12-31	Date protein was purified
	purified_yield	2.0 mg/l	Quantity of purified protein
	phase	Inclusion body	Phase of cell extract
	concentratable	4	Degree of concentrability [1-5]
	soluble_yield	2.0 mg/ml	Quantity of solubilized protein
	soluble	4	Solubility in cell extract [1-5]
BIOPHYSICAL CHARACTERIZATION	cd_url	http://...	Link to CD data
	cd_comment	[text]	CD notes
	hsqc_url	http://...	Link to HSQC spectra
	hsqc_comment	[text]	HSQC notes
	oligo_state	Dimer	Oligomerization of target
	oligo_method	Sedimentation	Method of determination
	hsqc_quality	5	Quality of 15N-1H HSQC spectra
	cd_melt	Alpha+Beta	CD secondary structure
	cd_assignment	Coop+Rev	Biophysical characterization
NMR	nmr_url	http://...	Link to spectoscopy data
	nmr_comment	[text]	NMR notes
	nmr_assignment	Backbone	Resonance assignments
	nmr_struct	Tertiary	NMR structural data
CRYSTALLOGRAPHY	xray_resolution	3.2 Å	Refinement resolution
	xray_rfactor	20.0	R-factor
	xray_free_rfactor	25.0	Free R-factor
	xray_url	http://...	Link to diffraction data
	xray_comment	[text]	Crystallography notes
	xray_data	Have Crystal	Diffraction progress
	xray_struct	Refined	Structure determination state
MISCELLANEOUS	num_binding_partners	2	Target-binding proteins
	binding_partners	YAL002C	Binding protein identifiers
	function	AA synthesis	Target gene/protein function
	globular	Y	Globular protein
	general_comment	[text]	Additional notes
	rank1	50	Computed rank on attribute 1
	rank2	50	Computed rank on attribute 2
	rank3	50	Computed rank on attribute 3

Legend:
- Record keeping field, standardized or free text
- Standardized alphanumerical field
- Standardized field, useful data mining feature
- Data mining feature and predictable property