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Backbone dynamics of a free and phosphopeptide-complexed Src homology 2 domain studied by 15N NMR relaxation

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2070	Structural and dynamic characterization of an SH2 domain-phosphopeptide complex by NMR approaches. 1995 , 23, 729-33		5
2069	Chapter 24. SH2 and SH3 Domains: Choreographers of Multiple Signaling Pathways. 1995 , 30, 227-237		23
2068	Solution structure of the C-terminal SH2 domain of the human tyrosine kinase Syk complexed with a phosphotyrosine pentapeptide. <i>Structure</i> , 1995 , 3, 1061-73	5.2	50
2067	Larmor frequency selective model free analysis of protein NMR relaxation. 1995 , 6, 366-74		16
2066	Application of the quasi-spectral density function of (15)N nuclei to the selection of a motional model for model-free analysis. 1995 , 6, 423-6		6
2065	Internal motions of apo-neocarzinostatin as studied by 13C NMR methine relaxation at natural abundance. 1995 , 5, 233-44		29
2064	Spectral density function mapping using 15N relaxation data exclusively. 1995 , 6, 153-62		454
2063	Direct demonstration of an intramolecular SH2-phosphotyrosine interaction in the Crk protein. <i>Nature</i> , 1995 , 374, 477-9	50.4	128
2062	Flexibility and function in HIV-1 protease. 1995 , 2, 274-80		216

2061	Pulsed field gradient multi-dimensional NMR methods for the study of protein structure and dynamics in solution. 1995 , 63, 277-99		126
2060	SH2 domain structure and function. 1995 , 1242, 61-75		14
2059	The effects of interhelical electrostatic repulsions between glutamic acid residues in controlling the dimerization and stability of two-stranded alpha-helical coiled-coils. <i>Journal of Biological Chemistry</i> , 1995 , 270, 25495-506	5.4	73
2058	Solution Structure of a Cellulose-Binding Domain from Cellulomonas fimi by Nuclear Magnetic Resonance Spectroscopy. <i>Biochemistry</i> , 1995 , 34, 6993-7009	3.2	217
2057	Solution structure of the human pp60c-src SH2 domain complexed with a phosphorylated tyrosine pentapeptide. <i>Biochemistry</i> , 1995 , 34, 2107-21	3.2	87
2056	1H and 15N NMR sequential assignment, secondary structure, and tertiary fold of [2Fe-2S] ferredoxin from Synechocystis sp. PCC 6803. <i>Biochemistry</i> , 1995 , 34, 14462-73	3.2	41
2055	Backbone dynamics of trp repressor studied by 15N NMR relaxation. <i>Biochemistry</i> , 1995 , 34, 5212-23	3.2	68
2054	Cell regulation. 1995 , 7, 239-98		
2053	Folding and binding. 1995 , 5, 131-54		
2052	Field gradient techniques in NMR spectroscopy. 1995 , 5, 674-81		60
2052	Field gradient techniques in NMR spectroscopy. 1995, 5, 674-81 Backbone dynamics of Escherichia coli ribonuclease HI: correlations with structure and function in an active enzyme. <i>Journal of Molecular Biology</i> , 1995, 246, 144-63	6.5	907
	Backbone dynamics of Escherichia coli ribonuclease HI: correlations with structure and function in	6.5 6.5	
2051	Backbone dynamics of Escherichia coli ribonuclease HI: correlations with structure and function in an active enzyme. <i>Journal of Molecular Biology</i> , 1995 , 246, 144-63 Molecular dynamics simulation of E. coli ribonuclease H1 in solution: correlation with NMR and		907
2051 2050 2049	Backbone dynamics of Escherichia coli ribonuclease HI: correlations with structure and function in an active enzyme. <i>Journal of Molecular Biology</i> , 1995 , 246, 144-63 Molecular dynamics simulation of E. coli ribonuclease H1 in solution: correlation with NMR and X-ray data and insights into biological function. <i>Journal of Molecular Biology</i> , 1995 , 254, 771-92 Characterization of the dynamic properties of Rhodobacter capsulatus ferricytochrome cL-a 28 kDa		907
2051 2050 2049	Backbone dynamics of Escherichia coli ribonuclease HI: correlations with structure and function in an active enzyme. <i>Journal of Molecular Biology</i> , 1995 , 246, 144-63 Molecular dynamics simulation of E. coli ribonuclease H1 in solution: correlation with NMR and X-ray data and insights into biological function. <i>Journal of Molecular Biology</i> , 1995 , 254, 771-92 Characterization of the dynamic properties of Rhodobacter capsulatus ferricytochrome cL-a 28 kDa paramagnetic heme protein. 1995 , 368, 519-22		907 52 3
2051 2050 2049 2048	Backbone dynamics of Escherichia coli ribonuclease HI: correlations with structure and function in an active enzyme. <i>Journal of Molecular Biology</i> , 1995 , 246, 144-63 Molecular dynamics simulation of E. coli ribonuclease H1 in solution: correlation with NMR and X-ray data and insights into biological function. <i>Journal of Molecular Biology</i> , 1995 , 254, 771-92 Characterization of the dynamic properties of Rhodobacter capsulatus ferricytochrome cL-a 28 kDa paramagnetic heme protein. 1995 , 368, 519-22 Theory and practice of nuclear spin relaxation in proteins. 1996 , 47, 243-82		907 52 3
2051 2050 2049 2048 2047	Backbone dynamics of Escherichia coli ribonuclease HI: correlations with structure and function in an active enzyme. <i>Journal of Molecular Biology</i> , 1995 , 246, 144-63 Molecular dynamics simulation of E. coli ribonuclease H1 in solution: correlation with NMR and X-ray data and insights into biological function. <i>Journal of Molecular Biology</i> , 1995 , 254, 771-92 Characterization of the dynamic properties of Rhodobacter capsulatus ferricytochrome cL-a 28 kDa paramagnetic heme protein. 1995 , 368, 519-22 Theory and practice of nuclear spin relaxation in proteins. 1996 , 47, 243-82 Nuclear Magnetic Resonance Studies of Biopolymer Dynamics. 1996 , 100, 13293-13310 Correlation between dynamics and high affinity binding in an SH2 domain interaction. <i>Biochemistry</i> ,	6.5	907 52 3 134 295

2043	Backbone dynamics of the C-terminal domain of Escherichia coli topoisomerase I in the absence and presence of single-stranded DNA. <i>Biochemistry</i> , 1996 , 35, 9661-6	3.2	75
2042	Three-dimensional solution structure of the N-terminal domain of DNA polymerase beta and mapping of the ssDNA interaction interface. <i>Biochemistry</i> , 1996 , 35, 6188-200	3.2	52
2041	Structure and dynamics of bacteriophage IKe major coat protein in MPG micelles by solution NMR. <i>Biochemistry</i> , 1996 , 35, 5145-57	3.2	75
2040	Alternative modes of tyrosyl phosphopeptide binding to a Src family SH2 domain: implications for regulation of tyrosine kinase activity. <i>Biochemistry</i> , 1996 , 35, 11062-9	3.2	41
2039	Assignment of 15N, 13C∄13C∄ and HN Resonances in an 15N,13C,2H Labeled 64 kDa Trp RepressorФperator Complex Using Triple-Resonance NMR Spectroscopy and 2H-Decoupling. 1996 , 118, 6570-6579		127
2038	The three-dimensional solution structure of the SH2 domain from p55blk kinase. <i>Biochemistry</i> , 1996 , 35, 6201-11	3.2	26
2037	Structural Characterization of the Phosphotyrosine Binding Region of a High-Affinity SH2 Domain B hosphopeptide Complex by Molecular Dynamics Simulation and Chemical Shift Calculations. 1996 , 118, 11265-11277		42
2036	Three-dimensional solution structure and backbone dynamics of a variant of human interleukin-3. Journal of Molecular Biology, 1996 , 259, 524-41	6.5	61
2035	Accretion of structure in staphylococcal nuclease: an 15N NMR relaxation study. <i>Journal of Molecular Biology</i> , 1996 , 260, 570-87	6.5	46
2034	Contributions to conformational entropy arising from bond vector fluctuations measured from NMR-derived order parameters: application to protein folding. <i>Journal of Molecular Biology</i> , 1996 , 263, 369-82	6.5	403
2033	15N NMR relaxation studies of free and inhibitor-bound 4-oxalocrotonate tautomerase: backbone dynamics and entropy changes of an enzyme upon inhibitor binding. <i>Biochemistry</i> , 1996 , 35, 16036-47	3.2	102
2032	The Grb2-mSos1 complex binds phosphopeptides with higher affinity than Grb2. <i>Journal of Biological Chemistry</i> , 1996 , 271, 30472-8	5.4	57
2031	Protein dynamics and conformational transitions in allosteric proteins. 1996 , 65, 171-219		78
2030	NMR and protein dynamics. 1996 , 59, 315-332		9
2029	An (H)C(CO)NH-TOCSY pulse scheme for sequential assignment of protonated methyl groups in otherwise deuterated (15)N, (13)C-labeled proteins. 1996 , 8, 351-6		85
2028	Backbone dynamics of an alamethicin in methanol and aqueous detergent solution determined by heteronuclear (1)H- (15)N NMR spectroscopy. 1996 , 7, 283-94		16
2027	Solution studies of the SH2 domain from the fyn tyrosine kinase: secondary structure, backbone dynamics and protein association. 1996 , 24, 371-80		19
2026	Dynamic studies of a fibronectin type I module pair at three frequencies: Anisotropic modelling and direct determination of conformational exchange. 1996 , 8, 369-78		59

2025	1H, 15N and 13C resonance assignments and secondary structure determination of the RNA-binding domain of E.coli rho protein. 1996 , 8, 429-44		17
2024	Yeast heat shock transcription factor N-terminal activation domains are unstructured as probed by heteronuclear NMR spectroscopy. <i>Protein Science</i> , 1996 , 5, 262-9	6.3	45
2023	Structural coupling of the inhibitory regions flanking the ETS domain of murine Ets-1. <i>Protein Science</i> , 1996 , 5, 296-309	6.3	57
2022	Ca(2+)-binding domain VI of rat calpain is a homodimer in solution: hydrodynamic, crystallization and preliminary X-ray diffraction studies. <i>Protein Science</i> , 1996 , 5, 535-7	6.3	25
2021	Contribution of the tyrosines to the structure and function of the human U1A N-terminal RNA binding domain. <i>Protein Science</i> , 1996 , 5, 1567-83	6.3	34
2020	NMR characterization of structure, backbone dynamics, and glutathione binding of the human macrophage migration inhibitory factor (MIF). <i>Protein Science</i> , 1996 , 5, 2095-103	6.3	41
2019	NMR studies of structure, hydrogen exchange, and main-chain dynamics in a disrupted-core mutant of thioredoxin. <i>Protein Science</i> , 1996 , 5, 2552-65	6.3	21
2018	X-ray and NMR structure of human Bcl-xL, an inhibitor of programmed cell death. <i>Nature</i> , 1996 , 381, 335-41	50.4	1303
2017	Protein complexes studied by NMR spectroscopy. 1996 , 7, 403-8		32
2016	Demonstration of coiled-coil interactions within the kinesin neck region using synthetic peptides. Implications for motor activity. <i>Journal of Biological Chemistry</i> , 1997 , 272, 8946-56	5.4	72
2015	Solution structure of the carboxyl-terminal LIM domain from quail cysteine-rich protein CRP2. Journal of Biological Chemistry, 1997 , 272, 12001-7	5.4	36
2014	Attenuated T2 relaxation by mutual cancellation of dipole-dipole coupling and chemical shift anisotropy indicates an avenue to NMR structures of very large biological macromolecules in solution. 1997 , 94, 12366-71		2051
2013	Structure of the recombinant full-length hamster prion protein PrP(29-231): the N terminus is highly flexible. 1997 , 94, 13452-7		626
2012	Chapter 16 Measurements of relaxation rates for low natural abundance l=1/2 nuclei. 1997 , 8, 325-347		Ο
2011	Backbone structure and dynamics of a hemolymph protein from the mealworm beetle Tenebrio molitor. <i>Biochemistry</i> , 1997 , 36, 13791-801	3.2	14
2010	Backbone dynamics of the major coat protein of bacteriophage M13 in detergent micelles by 15N nuclear magnetic resonance relaxation measurements using the model-free approach and reduced spectral density mapping. <i>Biochemistry</i> , 1997 , 36, 4015-26	3.2	56
2009	Structure of the carboxy-terminal fragment of the apo-biotin carboxyl carrier subunit of Escherichia coli acetyl-CoA carboxylase. <i>Biochemistry</i> , 1997 , 36, 15089-100	3.2	68
2008	Chemical shift mapping of the RNA-binding interface of the multiple-RBD protein sex-lethal. <i>Biochemistry</i> , 1997 , 36, 14306-17	3.2	44

2007	Structures of the reduced and mercury-bound forms of MerP, the periplasmic protein from the bacterial mercury detoxification system. <i>Biochemistry</i> , 1997 , 36, 6885-95	3.2	186
2006	Anisotropic molecular rotational diffusion in 15N spin relaxation studies of protein mobility. <i>Biochemistry</i> , 1997 , 36, 7305-12	3.2	68
2005	Global folds of highly deuterated, methyl-protonated proteins by multidimensional NMR. <i>Biochemistry</i> , 1997 , 36, 1389-401	3.2	231
2004	Properly oriented heparin-decasaccharide-induced dimers are the biologically active form of basic fibroblast growth factor. <i>Biochemistry</i> , 1997 , 36, 4782-91	3.2	104
2003	Changes in the NMR-derived motional parameters of the insulin receptor substrate 1 phosphotyrosine binding domain upon binding to an interleukin 4 receptor phosphopeptide. <i>Biochemistry</i> , 1997 , 36, 4118-24	3.2	48
2002	Comparison of backbone dynamics of reduced and oxidized Escherichia coli glutaredoxin-1 using 15N NMR relaxation measurements. <i>Biochemistry</i> , 1997 , 36, 5029-44	3.2	41
2001	Characterization of the backbone dynamics of folded and denatured states of an SH3 domain. <i>Biochemistry</i> , 1997 , 36, 2390-402	3.2	148
2000	Tertiary structure of RBD2 and backbone dynamics of RBD1 and RBD2 of the human U1A protein determined by NMR spectroscopy. <i>Biochemistry</i> , 1997 , 36, 10393-405	3.2	38
1999	Conformation of the trypanocidal pharmaceutical suramin in its free and bound forms: transferred nuclear overhauser studies. <i>Biochemistry</i> , 1997 , 36, 14202-17	3.2	11
1998	Escherichia coli diacylglycerol kinase: a case study in the application of solution NMR methods to an integral membrane protein. <i>Biophysical Journal</i> , 1997 , 72, 2688-701	2.9	61
1997	Backbone dynamics and structural characterization of the partially folded A state of ubiquitin by 1H, 13C, and 15N nuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , 1997 , 36, 13043-53	3.2	165
1996	Flexible linker in the RNA polymerase alpha subunit facilitates the independent motion of the C-terminal activator contact domain. <i>Journal of Molecular Biology</i> , 1997 , 267, 953-62	6.5	72
1995	Characterization of NADP+ binding to perdeuterated MurB: backbone atom NMR assignments and chemical-shift changes. <i>Journal of Molecular Biology</i> , 1997 , 267, 1223-46	6.5	46
1994	Enhanced protein flexibility caused by a destabilizing amino acid replacement in BPTI. <i>Journal of Molecular Biology</i> , 1997 , 269, 154-64	6.5	54
1993	Contributions to protein entropy and heat capacity from bond vector motions measured by NMR spin relaxation. <i>Journal of Molecular Biology</i> , 1997 , 272, 790-804	6.5	134
1992	PDZ-like domains mediate binding specificity in the Clp/Hsp100 family of chaperones and protease regulatory subunits. 1997 , 91, 939-47		106
1991	NMR structural characterization of the CDK inhibitor p19INK4d. 1997 , 401, 127-32		23
1990	Solution structure of the ribosomal RNA binding protein S15 from Thermus thermophilus. 1997 , 4, 20-3		57

1989	The repeating segments of the F-actin cross-linking gelation factor (ABP-120) have an immunoglobulin-like fold. 1997 , 4, 223-30	6	59
1988	Structure and mobility of the PUT3 dimer. 1997 , 4, 744-50	4	1 7
1987	Assignments, secondary structure and dynamics of the inhibitor-free catalytic fragment of human fibroblast collagenase. 1997 , 10, 9-19	2	28
1986	Rotational diffusion anisotropy of proteins from simultaneous analysis of 15N and 13C alpha nuclear spin relaxation. 1997 , 9, 287-98	2	246
1985	The counterreceptor binding site of human CD2 exhibits an extended surface patch with multiple conformations fluctuating with millisecond to microsecond motions. <i>Protein Science</i> , 1997 , 6, 534-42	4	43
1984	pH titration studies of an SH2 domain-phosphopeptide complex: unusual histidine and phosphate pKa values. <i>Protein Science</i> , 1997 , 6, 1910-9	3	37
1983	NMR Relaxation Mechanisms for Backbone Carbonyl Carbons in a 13 C, 15 N-Labeled Protein. 1997 , 126, 48-57	3	30
1982	Internal and overall motions of the translation factor eIF4E: cap binding and insertion in a CHAPS detergent micelle. 1998 , 12, 73-88	1	19
1981	HMQC and HSQC experiments with water flip-back optimized for large proteins. 1998, 11, 279-88	1	15
1980	NMR studies of Borrelia burgdorferi OspA, a 28 kDa protein containing a single-layer beta-sheet. 1998 , 11, 407-14	2	24
1979	Practical model fitting approaches to the direct extraction of NMR parameters simultaneously from all dimensions of multidimensional NMR spectra. 1998 , 12, 277-97	1	18
1978	A Sensitive Pulse Scheme for Measuring the Backbone Dihedral Angle psi Based on Cross-correlation Between (13)C (alpha)- (1)Halpha Dipolar and Carbonyl Chemical Shift Anisotropy Relaxation Interactions. 1998 , 11, 213-20	3	39
1977	Solvent exchange rates of side-chain amide protons in proteins. 1998 , 11, 205-12	ϵ	5
1976	Local mobility of 15N labeled biomolecules characterized through cross-correlation rates: Applications to paramagnetic proteins. 1998 , 12, 509-21	1	18
1975	Structure of the IGF-binding domain of the insulin-like growth factor-binding protein-5 (IGFBP-5): implications for IGF and IGF-I receptor interactions. 1998 , 17, 6558-72	1	131
1974	Solution structure and backbone dynamics of the photoactive yellow protein. <i>Biochemistry</i> , 1998 , 37, 12689-99	1	121
1973	A novel DNA-binding motif shares structural homology to DNA replication and repair nucleases and polymerases. 1998 , 5, 959-64	4	4 1
1972	Structure of interleukin 16 resembles a PDZ domain with an occluded peptide binding site. 1998 , 5, 682-6	3	35

1971	NMR structure of human erythropoietin and a comparison with its receptor bound conformation. 1998 , 5, 861-6		146
1970	Conformational switching in an aspartic proteinase. 1998 , 5, 866-71		90
1969	Eukaryotic RNA polymerase subunit RPB8 is a new relative of the OB family. 1998 , 5, 110-4		20
1968	Structural and dynamic characterization of partially folded states of apomyoglobin and implications for protein folding. 1998 , 5, 148-55		318
1967	Correlation between binding and dynamics at SH2 domain interfaces. 1998 , 5, 156-63		97
1966	Protein NMR relaxation: theory, applications and outlook. 1998 , 33, 207-272		104
1965	How a protein prepares for B12 binding: structure and dynamics of the B12-binding subunit of glutamate mutase from Clostridium tetanomorphum. <i>Structure</i> , 1998 , 6, 1021-33	5.2	63
1964	Gradient- and sensitivity-enhanced TOCSY experiments. 1998 , 130, 162-8		34
1963	Improved Estimation of Protein Rotational Correlation Times from 15N Relaxation Measurements. 1998 , 131, 347-50		12
1962	An adiabatic multiple spin-echo pulse sequence: removal of systematic errors due to pulse imperfections and off-resonance effects. 1998 , 133, 134-47		37
1961	15N backbone dynamics of the S-peptide from ribonuclease A in its free and S-protein bound forms: toward a site-specific analysis of entropy changes upon folding. <i>Protein Science</i> , 1998 , 7, 389-402	6.3	33
1960	Solution structure and dynamics of a designed monomeric variant of the lambda Cro repressor. <i>Protein Science</i> , 1998 , 7, 983-93	6.3	9
1959	The interaction of eIF4E with 4E-BP1 is an induced fit to a completely disordered protein. <i>Protein Science</i> , 1998 , 7, 1639-42	6.3	70
1958	Effects of proline cis-trans isomerization on TB domain secondary structure. <i>Protein Science</i> , 1998 , 7, 2127-35	6.3	27
1957	15N NMR relaxation studies of calcium-loaded parvalbumin show tight dynamics compared to those of other EF-hand proteins. <i>Biochemistry</i> , 1998 , 37, 9964-75	3.2	26
1956	Solution structure and backbone dynamics of Mason-Pfizer monkey virus (MPMV) nucleocapsid protein. <i>Protein Science</i> , 1998 , 7, 2265-80	6.3	29
1955	Solution structure and backbone dynamics of component IV Glycera dibranchiata monomeric hemoglobin-CO. <i>Biochemistry</i> , 1998 , 37, 10906-19	3.2	25
1954	Structure and intramodular dynamics of the amino-terminal LIM domain from quail cysteine- and glycine-rich protein CRP2. <i>Biochemistry</i> , 1998 , 37, 7127-34	3.2	29

(1998-1998)

1953	Main-chain dynamics of cardiotoxin II from Taiwan cobra (Naja naja atra) as studied by carbon-13 NMR at natural abundance: delineation of the role of functionally important residues. <i>Biochemistry</i> , 1998 , 37, 155-64	3.2	21	
1952	Backbone and side chain dynamics of uncomplexed human adipocyte and muscle fatty acid-binding proteins. <i>Biochemistry</i> , 1998 , 37, 7965-80	3.2	82	
1951	Dynamics and thermodynamics of the regulatory domain of human cardiac troponin C in the apoand calcium-saturated states. <i>Biochemistry</i> , 1998 , 37, 18032-44	3.2	51	
1950	Significantly Improved Resolution for NOE Correlations from Valine and Isoleucine (C[2) Methyl Groups in 15N,13C- and 15N,13C,2H-Labeled Proteins. 1998 , 120, 4825-4831		28	
1949	Determination of the Protein Backbone Dihedral Angle Ifrom a Combination of NMR-Derived Cross-Correlation Spin Relaxation Rates. 1998 , 120, 9880-9887		51	
1948	Sequence specific collective motions in a winged helix DNA binding domain detected by 15N relaxation NMR. <i>Biochemistry</i> , 1998 , 37, 6179-87	3.2	39	
1947	Inadequacies of the Point-Dipole Approximation for Describing Electron Nuclear Interactions in Paramagnetic Proteins: Hybrid Density Functional Calculations and the Analysis of NMR Relaxation of High-Spin Iron(III) Rubredoxin. 1998, 102, 8300-8305		26	
1946	An NMR Experiment for Measuring Methyl Methyl NOEs in 13C-Labeled Proteins with High Resolution. 1998 , 120, 7617-7625		77	
1945	Tertiary structure of the major house dust mite allergen Der p 2: sequential and structural homologies. <i>Biochemistry</i> , 1998 , 37, 12707-14	3.2	75	
1944	Characterization of a buried neutral histidine in Bacillus circulans xylanase: internal dynamics and interaction with a bound water molecule. <i>Biochemistry</i> , 1998 , 37, 1810-8	3.2	18	
1943	Human general transcription factor TFIIB: conformational variability and interaction with VP16 activation domain. <i>Biochemistry</i> , 1998 , 37, 7941-51	3.2	41	
1942	Solution structure of the SH3 domain from BrutonIs tyrosine kinase. <i>Biochemistry</i> , 1998 , 37, 2912-24	3.2	68	
1941	Solution NMR Studies of a 42 KDa Escherichia Coli Maltose Binding Protein/ Cyclodextrin Complex: Chemical Shift Assignments and Analysis. 1998 , 120, 11738-11748		130	
1940	Relationship between enzyme specificity and the backbone dynamics of free and inhibited alpha-lytic protease. <i>Biochemistry</i> , 1998 , 37, 7696-707	3.2	27	
1939	Self-association and backbone dynamics of the hck SH2 domain in the free and phosphopeptide-complexed forms. <i>Biochemistry</i> , 1998 , 37, 7119-26	3.2	28	
1938	Precision and Uncertainty in the Characterization of Anisotropic Rotational Diffusion by 15N Relaxation. 1998 , 120, 4538-4539		66	
1937	Nuclear magnetic resonance shows asymmetric loss of triple helix in peptides modeling a collagen mutation in brittle bone disease. <i>Biochemistry</i> , 1998 , 37, 15528-33	3.2	49	
1936	The origin of differences in the physical properties of the equilibrium forms of cytochrome b5 revealed through high-resolution NMR structures and backbone dynamic analyses. <i>Biochemistry</i> , 1998, 37, 8289-302	3.2	42	

1935	NMR structural studies on antifreeze proteins. 1998 , 76, 284-293		16
1934	Backbone and methyl dynamics of the regulatory domain of troponin C: anisotropic rotational diffusion and contribution of conformational entropy to calcium affinity. <i>Journal of Molecular Biology</i> , 1998 , 278, 667-86	6.5	118
1933	Heteronuclear relaxation study of the PH domain of beta-spectrin: restriction of loop motions upon binding inositol trisphosphate. <i>Journal of Molecular Biology</i> , 1998 , 280, 879-96	6.5	33
1932	Dynamical behavior of the HIV-1 nucleocapsid protein. <i>Journal of Molecular Biology</i> , 1998 , 279, 633-49	6.5	129
1931	A disorder-to-order transition coupled to DNA binding in the essential zinc-finger DNA-binding domain of yeast ADR1. <i>Journal of Molecular Biology</i> , 1998 , 279, 929-43	6.5	32
1930	High-resolution solution structure of the retinoid X receptor DNA-binding domain. <i>Journal of Molecular Biology</i> , 1998 , 281, 271-84	6.5	54
1929	The NMR solution structure of human glutaredoxin in the fully reduced form. <i>Journal of Molecular Biology</i> , 1998 , 280, 687-701	6.5	78
1928	An investigation of the dynamics of ribosomal protein L9 using heteronuclear NMR relaxation measurements. <i>Journal of Molecular Biology</i> , 1998 , 281, 539-51	6.5	11
1927	Solution structure, rotational diffusion anisotropy and local backbone dynamics of Rhodobacter capsulatus cytochrome c2. <i>Journal of Molecular Biology</i> , 1998 , 281, 341-61	6.5	62
1926	The dependence of chemical exchange on boundary selection in a fibronectin type III domain from human tenascin. <i>Journal of Molecular Biology</i> , 1998 , 282, 181-94	6.5	22
1925	Backbone dynamics of the CDK inhibitor p19(INK4d) studied by 15N NMR relaxation experiments at two field strengths. <i>Journal of Molecular Biology</i> , 1998 , 283, 221-9	6.5	20
1924	Determinants of backbone dynamics in native BPTI: cooperative influence of the 14-38 disulfide and the Tyr35 side-chain. <i>Journal of Molecular Biology</i> , 1998 , 284, 1581-96	6.5	34
1923	Effect of N-terminal truncation and solution conditions on chemokine dimer stability: nuclear magnetic resonance structural analysis of macrophage inflammatory protein 1 beta mutants. <i>Biochemistry</i> , 1998 , 37, 9346-54	3.2	37
1922	Longitudinal and Transverse 1H🛮5N Dipolar/15N Chemical Shift Anisotropy Relaxation Interference: Unambiguous Determination of Rotational Diffusion Tensors and Chemical Exchange Effects in Biological Macromolecules. 1998 , 120, 7905-7915		237
1921	Structure of the Ets-1 pointed domain and mitogen-activated protein kinase phosphorylation site. 1998 , 95, 12129-34		122
1920	The amino-terminal domain of human STAT4. Overproduction, purification, and biophysical characterization. <i>Journal of Biological Chemistry</i> , 1998 , 273, 17109-14	5.4	12
1919	Yeast transcript elongation factor (TFIIS), structure and function. I: NMR structural analysis of the minimal transcriptionally active region. <i>Journal of Biological Chemistry</i> , 1998 , 273, 22589-94	5.4	42
1918	High-resolution NMR of encapsulated proteins dissolved in low-viscosity fluids. 1998 , 95, 15299-302		103

1917	Structure of cysteine- and glycine-rich protein CRP2. Backbone dynamics reveal motional freedom and independent spatial orientation of the lim domains. <i>Journal of Biological Chemistry</i> , 1998 , 273, 2323 3-40	36
1916	Overexpression, purification, and biophysical characterization of the heterodimerization domain of the core-binding factor beta subunit. <i>Journal of Biological Chemistry</i> , 1998 , 273, 2480-7	19
1915	The solution structure of the DNA-binding domain of Skn-1. 1998 , 95, 8455-60	14
1914	Identification of the single-stranded DNA binding surface of the transcriptional coactivator PC4 by NMR. <i>Journal of Biological Chemistry</i> , 1999 , 274, 3693-9	23
1913	Solution structure and peptide binding studies of the C-terminal src homology 3-like domain of the diphtheria toxin repressor protein. 1999 , 96, 6119-24	34
1912	Effects of troponin I phosphorylation on conformational exchange in the regulatory domain of cardiac troponin C. <i>Journal of Biological Chemistry</i> , 1999 , 274, 16681-4	63
1911	The dimerization domain of the b subunit of the Escherichia coli F(1)F(0)-ATPase. <i>Journal of Biological Chemistry</i> , 1999 , 274, 31094-101	51
1910	Variability of the 15N Chemical Shift Anisotropy in Escherichia coli Ribonuclease H in Solution. 1999 , 121, 10119-10125	126
1909	The effect of matrix metalloproteinase complex formation on the conformational mobility of tissue inhibitor of metalloproteinases-2 (TIMP-2). <i>Journal of Biological Chemistry</i> , 1999 , 274, 37226-32	17
1908	Study of dynamic processes in liquids using off-resonance rf irradiation. 1999 , 35, 295-340	58
1907	Inherent flexibility in a potent inhibitor of blood coagulation, recombinant nematode anticoagulant protein c2. 1999 , 265, 539-48	36
1906	Identification of the core domain and the secondary structure of the transcriptional coactivator MBF1. 1999 , 4, 415-24	15
1905	Millisecond-timescale motions contribute to the function of the bacterial response regulator protein Spo0F. <i>Nature</i> , 1999 , 400, 289-93	200
1904	The IdynamicsLin the thermodynamics of binding. 1999 , 6, 1086-7	73
1903	Increased protein backbone conformational entropy upon hydrophobic ligand binding. 1999 , 6, 1118-21	200
1902	Assessing potential bias in the determination of rotational correlation times of proteins by NMR relaxation. 1999 , 13, 101-12	64
1901	Induced alignment and measurement of dipolar couplings of an SH2 domain through direct binding with filamentous phage. 1999 , 14, 175-9	17
1900	Heteronuclear relaxation in time-dependent spin systems: (15)N-T1 (rho) dispersion during adiabatic fast passage. 1999 , 13, 213-21	11

1899	Improved 1HN-detected triple resonance TROSY-based experiments. 1999 , 13, 3-10		122
1898	Effect of hydrophobic core packing on sidechain dynamics. 1999 , 15, 135-43		16
1897	Sequential assignment and secondary structure analysis of the NADP(H)-binding domain of Escherichia coli transhydrogenase. 1999 , 14, 295-6		8
1896	Resonance assignments, secondary structure and 15N relaxation data of the human transcriptional coactivator hMBF1 (57-148). 1999 , 14, 373-6		9
1895	1H-15N NMR dynamic study of an isolated Ehelical peptide (1B6)- bacteriorhodopsin reveals the equilibrium helix-coil transitions. 1999 , 14, 345-356		24
1894	Human replication protein A: global fold of the N-terminal RPA-70 domain reveals a basic cleft and flexible C-terminal linker. 1999 , 14, 321-31		74
1893	Backbone dynamics of the human CC-chemokine eotaxin. 1999 , 15, 115-24		28
1892	Improved lineshape and sensitivity in the HNCO-family of triple resonance experiments. 1999 , 14, 273-2	76	23
1891	Letter to the Editor: Resonance assignment and topology of a 22 kDa C-terminal fragment of the polypyrimidine tract binding protein (PTB) containing two RNA binding domains. 1999 , 14, 383-384		1
1890	Dynamics of stromelysin/inhibitor interactions studied by 15N NMR relaxation measurements: comparison of ligand binding to the S1-S3 and SL1-SL3 subsites. 1999 , 15, 55-64		31
1889	Backbone dynamics of the human CC chemokine eotaxin: fast motions, slow motions, and implications for receptor binding. <i>Protein Science</i> , 1999 , 8, 2041-54	6.3	37
1888	Structure and interactions of the translation initiation factor eIF1. 1999 , 18, 2631-7		125
1887	NMR structure and metal interactions of the CopZ copper chaperone. <i>Journal of Biological Chemistry</i> , 1999 , 274, 22597-603	5.4	104
1886	Solution structure of a pair of modules from the gelatin-binding domain of fibronectin. <i>Structure</i> , 1999 , 7, 1451-60	5.2	19
1885	Structure and dynamics of the B12-binding subunit of glutamate mutase from Clostridium cochlearium. 1999 , 263, 178-88		23
1884	Quantitative measurement of transverse and longitudinal cross-correlation between 13C-1H dipolar interaction and 13C chemical shift anisotropy: application to a 13C-labeled DNA duplex. 1999 , 136, 169-75		16
1883	Estimation of dynamic parameters from NMR relaxation data using the Lipari-Szabo model-free approach and Bayesian statistical methods. 1999 , 139, 408-21		51
1882	A 500-ps molecular dynamics simulation trajectory of cardiotoxin II from Taiwan cobra venom in solution: Correlation with NMR and X-ray crystallography data. 1999 , 20, 546-562		1

1881	A preliminary CD and NMR study of the Escherichia coli DNA polymerase III theta subunit. 1999 , 36, 111	-6	6
1880	Solution structures of the C-terminal domain of cardiac troponin C free and bound to the N-terminal domain of cardiac troponin I. <i>Biochemistry</i> , 1999 , 38, 8313-22	3.2	46
1879	Circular permutation of granulocyte colony-stimulating factor. <i>Biochemistry</i> , 1999 , 38, 4553-63	3.2	20
1878	One of two unstructured domains of Ii becomes ordered in complexes with MHC class II molecules. 1999 , 10, 761-8		31
1877	Interactions of human nucleotide excision repair protein XPA with DNA and RPA70 Delta C327: chemical shift mapping and 15N NMR relaxation studies. <i>Biochemistry</i> , 1999 , 38, 15116-28	3.2	68
1876	Secondary structure of the C-terminal domain of the tyrosyl-transfer RNA synthetase from Bacillus stearothermophilus: a novel type of anticodon binding domain?. 1999 , 446, 81-5		7
1875	NMR characterization of the NADP(H)-binding domain of Escherichia coli transhydrogenase: sequential assignment and global fold. 1999 , 458, 180-4		22
1874	Solution structure of BID, an intracellular amplifier of apoptotic signaling. 1999 , 96, 615-24		425
1873	Solution structure of Syrian hamster prion protein rPrP(90-231). <i>Biochemistry</i> , 1999 , 38, 5362-77	3.2	172
1872	Comparison of backbone dynamics of oxidized and reduced putidaredoxin by 15N NMR relaxation measurements. <i>Biochemistry</i> , 1999 , 38, 9862-71	3.2	26
1871	TROSY Triple-Resonance Four-Dimensional NMR Spectroscopy of a 46 ns Tumbling Protein. 1999 , 121, 2571-2575		139
1870	Solution structure of the N-terminal F1 module pair from human fibronectin. <i>Biochemistry</i> , 1999 , 38, 8304-12	3.2	35
1869	1Hfl3C DipoleDipole Cross-Correlated Spin Relaxation As a Probe of Dynamics in Unfolded Proteins: Application to the DrkN SH3 Domain. 1999 , 121, 3555-3556		40
1868	Identification and dynamics of a heparin-binding site in hepatocyte growth factor. <i>Biochemistry</i> , 1999 , 38, 14793-802	3.2	53
1867	Hydrogen exchange shows peptide binding stabilizes motions in Hck SH2. <i>Biochemistry</i> , 1999 , 38, 8926-	35,2	72
1866	Backbone dynamics of the N-terminal domain in E. coli DnaJ determined by 15N- and 13CO-relaxation measurements. <i>Biochemistry</i> , 1999 , 38, 10567-77	3.2	25
1865	Backbone dynamics of inactive, active, and effector-bound Cdc42Hs from measurements of (15)N relaxation parameters at multiple field strengths. <i>Biochemistry</i> , 1999 , 38, 12547-57	3.2	44
1864	Conformational flexibility of a ubiquitin conjugation enzyme (E2). <i>Biochemistry</i> , 1999 , 38, 1415-25	3.2	28

1863	Assignment of 15N chemical shifts and 15N relaxation measurements for oxidized and reduced iso-1-cytochrome c. <i>Biochemistry</i> , 1999 , 38, 4480-92	3.2	72
1862	Dynamics of palmitic acid complexed with rat intestinal fatty acid binding protein. <i>Biochemistry</i> , 1999 , 38, 1554-61	3.2	11
1861	Dynamics study on the anti-human immunodeficiency virus chemokine viral macrophage-inflammatory protein-II (VMIP-II) reveals a fully monomeric protein. <i>Biochemistry</i> , 1999 , 38, 442-53	3.2	45
1860	Investigation of the local structure and dynamics of the H subunit of the mitochondrial glycine decarboxylase using heteronuclear NMR spectroscopy. <i>Biochemistry</i> , 1999 , 38, 8334-46	3.2	22
1859	NMR solution structure of a complex of calmodulin with a binding peptide of the Ca2+ pump. <i>Biochemistry</i> , 1999 , 38, 12320-32	3.2	182
1858	RNA recognition by the human U1A protein is mediated by a network of local cooperative interactions that create the optimal binding surface. <i>Journal of Molecular Biology</i> , 1999 , 285, 215-31	6.5	60
1857	Solution structure of the carboxyl terminus of a human class Mu glutathione S-transferase: NMR assignment strategies in large proteins. <i>Journal of Molecular Biology</i> , 1999 , 285, 2119-32	6.5	18
1856	Structure, backbone dynamics and interactions with RNA of the C-terminal RNA-binding domain of a mouse neural RNA-binding protein, Musashi1. <i>Journal of Molecular Biology</i> , 1999 , 287, 315-30	6.5	43
1855	Structure and interactions with RNA of the N-terminal UUAG-specific RNA-binding domain of hnRNP D0. <i>Journal of Molecular Biology</i> , 1999 , 287, 221-37	6.5	42
1854	The cellulose-binding domains from Cellulomonas fimi beta-1, 4-glucanase CenC bind nitroxide spin-labeled cellooligosaccharides in multiple orientations. <i>Journal of Molecular Biology</i> , 1999 , 287, 609	-25	48
1853	Backbone dynamics and energetics of a calmodulin domain mutant exchanging between closed and open conformations. <i>Journal of Molecular Biology</i> , 1999 , 289, 603-17	6.5	116
1852	Conformational dynamics and molecular recognition: backbone dynamics of the estrogen receptor DNA-binding domain. <i>Journal of Molecular Biology</i> , 1999 , 289, 963-79	6.5	32
1851	NMR hydrogen exchange of the OB-fold protein LysN as a function of denaturant: the most conserved elements of structure are the most stable to unfolding. <i>Journal of Molecular Biology</i> , 1999 , 289, 1041-54	6.5	25
1850	Dynamic DNA contacts observed in the NMR structure of winged helix protein-DNA complex. Journal of Molecular Biology, 1999 , 289, 683-90	6.5	93
1849	An NMR investigation of solution aggregation reactions preceding the misassembly of acid-denatured cold shock protein A into fibrils. <i>Journal of Molecular Biology</i> , 1999 , 291, 1191-206	6.5	41
1848	Mutational analysis and NMR spectroscopy of quail cysteine and glycine-rich protein CRP2 reveal an intrinsic segmental flexibility of LIM domains. <i>Journal of Molecular Biology</i> , 1999 , 292, 893-908	6.5	19
1847	Solution structure of the ribosomal protein S19 from Thermus thermophilus. <i>Journal of Molecular Biology</i> , 1999 , 292, 1071-81	6.5	9
1846	Backbone dynamics of a short PU.1 ETS domain. <i>Journal of Molecular Biology</i> , 1999 , 292, 1083-93	6.5	20

(2000-1999)

1845	Solution structure of the DNA-binding domain of NtrC with three alanine substitutions. <i>Journal of Molecular Biology</i> , 1999 , 292, 1095-110	6.5	71
1844	Structural dynamics in the C-terminal domain of calmodulin at low calcium levels. <i>Journal of Molecular Biology</i> , 1999 , 293, 883-99	6.5	140
1843	Changes in side-chain and backbone dynamics identify determinants of specificity in RNA recognition by human U1A protein. <i>Journal of Molecular Biology</i> , 1999 , 294, 967-79	6.5	65
1842	Nuclear magnetic resonance spectroscopy of peptide ion channel ligands: cloning and expression as aid to evaluation of structural and dynamic properties. 1999 , 294, 92-117		3
1841	Determination of the solution structure of the N-domain plus linker of Antarctic eel pout antifreeze protein RD3. 1999 , 126, 387-94		10
1840	Nuclear Magnetic Resonance of Biomolecules. 2000,		
1839	NMR structures of thioredoxin m from the green alga Chlamydomonas reinhardtii. 2000 , 41, 334-349		25
1838	Backbone dynamics of barstar: a (15)N NMR relaxation study. 2000 , 41, 460-74		23
1837	Photomodulation of conformational states. II. Mono- and bicyclic peptides with (4-aminomethyl)phenylazobenzoic acid as backbone constituent. 2000 , 54, 501-14		55
1836	Novel relaxation compensated method to measure proton exchange rates in biomolecules based on decorrelation of heteronuclear two-spin order. 2000 , 38, 789-794		1
1835	Simple and accurate determination of global tau(R) in proteins using (13)C or (15)N relaxation data. 2000 , 143, 229-32		8
1834	Protein dynamics measurements by TROSY-based NMR experiments. 2000 , 143, 423-6		160
1833	Separation of anisotropy and exchange broadening using (15)N CSA-(15)N-(1)H dipole-dipole relaxation cross-correlation experiments. 2000 , 145, 192-200		9
1832	Peptide internal motions on nanosecond time scale derived from direct fitting of (13)C and (15)N NMR spectral density functions. 2000 , 146, 188-95		13
1831	Structure of a novel leech carboxypeptidase inhibitor determined free in solution and in complex with human carboxypeptidase A2. 2000 , 7, 322-8		60
1830	Design of single-layer beta-sheets without a hydrophobic core. <i>Nature</i> , 2000 , 403, 456-60	50.4	54
1829	Autoinhibition and activation mechanisms of the Wiskott-Aldrich syndrome protein. <i>Nature</i> , 2000 , 404, 151-8	50.4	616
1828	Solution structure of PCP, a prototype for the peptidyl carrier domains of modular peptide synthetases. <i>Structure</i> , 2000 , 8, 407-18	5.2	157

1827	Structure and self-association of the Rous sarcoma virus capsid protein. Structure, 2000 , 8, 617-28	5.2	104
1826	Localization and characterization of the hyaluronan-binding site on the link module from human TSG-6. <i>Structure</i> , 2000 , 8, 763-74	5.2	91
1825	Another piece of the ribosome: solution structure of S16 and its location in the 30S subunit. <i>Structure</i> , 2000 , 8, 875-82	5.2	14
1824	Structure of a PH domain from the C. elegans muscle protein UNC-89 suggests a novel function. <i>Structure</i> , 2000 , 8, 1079-87	5.2	25
1823	Efficient analysis of macromolecular rotational diffusion from heteronuclear relaxation data. 2000 , 16, 23-8		435
1822	Backbone dynamics of free barnase and its complex with barstar determined by 15N NMR relaxation study. 2000 , 18, 107-18		21
1821	Backbone dynamics of a bacterially expressed peptide from the receptor binding domain of Pseudomonas aeruginosa pilin strain PAK from heteronuclear 1H-15N NMR spectroscopy. 2000 , 17, 23	9-55	23
1820	Intensity modulated HSQC and HMQC: two simple methods to measure 3J(HNH)alpha in proteins. 2000 , 16, 29-37		17
1819	Refinement of the protein backbone angle psi in NMR structure calculations. 2000 , 16, 47-58		25
1818	Pressure effect on the dynamics of an isolated alpha-helix studied by 15N-1H NMR relaxation. 2000 , 17, 257-63		21
1817	Off-resonance effects in 15N T2 CPMG measurements. 2000 , 17, 231-7		47
1816	Internal motional amplitudes and correlated bond rotations in an alpha-helical peptide derived from 13C and 15N NMR relaxation. <i>Protein Science</i> , 2000 , 9, 2118-27	6.3	11
1815	The role of backbone conformational heat capacity in protein stability: temperature dependent dynamics of the B1 domain of Streptococcal protein G. <i>Protein Science</i> , 2000 , 9, 1177-93	6.3	84
1814	Overall rotational diffusion and internal mobility in domain II of protein G from Streptococcus determined from 15N relaxation data. <i>Protein Science</i> , 2000 , 9, 1210-6	6.3	12
1813	Structure of tandem RNA recognition motifs from polypyrimidine tract binding protein reveals novel features of the RRM fold. 2000 , 19, 3132-41		125
1812	A dynamically tuned double-stranded RNA binding mechanism for the activation of antiviral kinase PKR. 2000 , 19, 5567-74		133
1811	RNA recognition by a Staufen double-stranded RNA-binding domain. 2000 , 19, 997-1009		291
1810	Regulatory domain conformational exchange and linker region flexibility in cardiac troponin C bound to cardiac troponin I. <i>Journal of Biological Chemistry</i> , 2000 , 275, 20610-7	5.4	43

(2000-2000)

1809	Local structural elements in the mostly unstructured transcriptional activation domain of human p53. <i>Journal of Biological Chemistry</i> , 2000 , 275, 29426-32	5.4	257
1808	15N NMR relaxation studies of free and ligand-bound human acidic fibroblast growth factor. <i>Journal of Biological Chemistry</i> , 2000 , 275, 39444-50	5.4	24
1807	NMR structure of the bovine prion protein. 2000 , 97, 8334-9		335
1806	Solution structure and backbone dynamics of long-[Arg(3)]insulin-like growth factor-I. <i>Journal of Biological Chemistry</i> , 2000 , 275, 10009-15	5.4	19
1805	Zinc-bundle structure of the essential RNA polymerase subunit RPB10 from Methanobacterium thermoautotrophicum. 2000 , 97, 6316-21		26
1804	Solution structure and backbone dynamics of the second PDZ domain of postsynaptic density-95. Journal of Molecular Biology, 2000 , 295, 225-37	6.5	94
1803	NMR structure of the sterol carrier protein-2: implications for the biological role. <i>Journal of Molecular Biology</i> , 2000 , 295, 595-603	6.5	55
1802	NMR solution structure of the inserted domain of human leukocyte function associated antigen-1. <i>Journal of Molecular Biology</i> , 2000 , 295, 1251-64	6.5	65
1801	Relationships between protein structure and dynamics from a database of NMR-derived backbone order parameters. <i>Journal of Molecular Biology</i> , 2000 , 295, 963-78	6.5	73
1800	Backbone dynamics and refined solution structure of the N-terminal domain of DNA polymerase beta. Correlation with DNA binding and dRP lyase activity. <i>Journal of Molecular Biology</i> , 2000 , 296, 229-	- 5 3 ^{.5}	67
1799	Solution structure and dynamics of the DNA-binding domain of the adipocyte-transcription factor FREAC-11. <i>Journal of Molecular Biology</i> , 2000 , 296, 351-9	6.5	49
1798	Backbone dynamics of the C-terminal SH2 domain of the p85alpha subunit of phosphoinositide 3-kinase: effect of phosphotyrosine-peptide binding and characterization of slow conformational exchange processes. <i>Journal of Molecular Biology</i> , 2000 , 299, 771-88	6.5	31
1797	Binding of retinol induces changes in rat cellular retinol-binding protein II conformation and backbone dynamics. <i>Journal of Molecular Biology</i> , 2000 , 300, 619-32	6.5	43
1796	Solution structure of the cysteine-rich domain of the Escherichia coli chaperone protein DnaJ. <i>Journal of Molecular Biology</i> , 2000 , 300, 805-18	6.5	102
1795	The effects of ligand binding on the backbone dynamics of the kringle 1 domain of human plasminogen. <i>Journal of Molecular Biology</i> , 2000 , 301, 333-47	6.5	15
1794	Tissue inhibitor of metalloproteinases-1 undergoes microsecond to millisecond motions at sites of matrix metalloproteinase-induced fit. <i>Journal of Molecular Biology</i> , 2000 , 301, 537-52	6.5	23
1793	High-resolution solution structure of the catalytic fragment of human collagenase-3 (MMP-13) complexed with a hydroxamic acid inhibitor. <i>Journal of Molecular Biology</i> , 2000 , 302, 671-89	6.5	54
1792	The three-dimensional structure of the Nudix enzyme diadenosine tetraphosphate hydrolase from Lupinus angustifolius L. <i>Journal of Molecular Biology</i> , 2000 , 302, 1165-77	6.5	43

1791	Arginine side-chain dynamics in the HIV-1 rev-RRE complex. Journal of Molecular Biology, 2000, 303, 515	5-83	30
1790	Formation of nNOS/PSD-95 PDZ dimer requires a preformed beta-finger structure from the nNOS PDZ domain. <i>Journal of Molecular Biology</i> , 2000 , 303, 359-70	6.5	103
1789	Identification of the phospholipid-binding site of human beta(2)-glycoprotein I domain V by heteronuclear magnetic resonance. <i>Journal of Molecular Biology</i> , 2000 , 304, 927-39	6.5	43
1788	Expression, purification, refolding, and characterization of recombinant human interleukin-13: utilization of intracellular processing. 2000 , 20, 186-95		23
1787	Transferred13CT1Relaxation at Natural Isotopic Abundance: A Practical Method for Determining Site-Specific Changes in Ligand Flexibility upon Binding to a Macromolecule. 2000 , 122, 12530-12535		26
1786	Relative Orientation of Peptide Planes in Proteins Is Reflected in Carbonyl arbonyl Chemical Shift Anisotropy Cross-Correlated Spin Relaxation. 2000 , 122, 7059-7071		19
1785	Solution structure of the interacting domains of the Mad-Sin3 complex: implications for recruitment of a chromatin-modifying complex. 2000 , 103, 655-65		83
1784	Rapid internal dynamics of BPTI is insensitive to pressure. (15)N spin relaxation at 2 kbar. 2000 , 470, 11	-4	19
1783	NMR analysis of secondary structure and dynamics of a recombinant peptide from the N-terminal region of human erythroid alpha-spectrin. 2000 , 485, 81-6		14
1782	NMR solution structure of the human prion protein. 2000 , 97, 145-50		914
1782 1781	NMR solution structure of the human prion protein. 2000 , 97, 145-50 Dynamics of cellular retinoic acid binding protein I on multiple time scales with implications for ligand binding. <i>Biochemistry</i> , 2000 , 39, 9119-29	3.2	914
ĺ	Dynamics of cellular retinoic acid binding protein I on multiple time scales with implications for	3.2	
1781	Dynamics of cellular retinoic acid binding protein I on multiple time scales with implications for ligand binding. <i>Biochemistry</i> , 2000 , 39, 9119-29 Changes in dynamical behavior of the retinoid X receptor DNA-binding domain upon binding to a 14		44
1781 1780	Dynamics of cellular retinoic acid binding protein I on multiple time scales with implications for ligand binding. <i>Biochemistry</i> , 2000 , 39, 9119-29 Changes in dynamical behavior of the retinoid X receptor DNA-binding domain upon binding to a 14 base-pair DNA half site. <i>Biochemistry</i> , 2000 , 39, 8747-57 Dynamics of the metallo-beta-lactamase from Bacteroides fragilis in the presence and absence of a	3.2	15
1781 1780 1779	Dynamics of cellular retinoic acid binding protein I on multiple time scales with implications for ligand binding. <i>Biochemistry</i> , 2000 , 39, 9119-29 Changes in dynamical behavior of the retinoid X receptor DNA-binding domain upon binding to a 14 base-pair DNA half site. <i>Biochemistry</i> , 2000 , 39, 8747-57 Dynamics of the metallo-beta-lactamase from Bacteroides fragilis in the presence and absence of a tight-binding inhibitor. <i>Biochemistry</i> , 2000 , 39, 13356-64 Restricted motion of the lipoyl-lysine swinging arm in the pyruvate dehydrogenase complex of	3.2	441553
1781 1780 1779	Dynamics of cellular retinoic acid binding protein I on multiple time scales with implications for ligand binding. <i>Biochemistry</i> , 2000 , 39, 9119-29 Changes in dynamical behavior of the retinoid X receptor DNA-binding domain upon binding to a 14 base-pair DNA half site. <i>Biochemistry</i> , 2000 , 39, 8747-57 Dynamics of the metallo-beta-lactamase from Bacteroides fragilis in the presence and absence of a tight-binding inhibitor. <i>Biochemistry</i> , 2000 , 39, 13356-64 Restricted motion of the lipoyl-lysine swinging arm in the pyruvate dehydrogenase complex of Escherichia coli. <i>Biochemistry</i> , 2000 , 39, 8448-59 Structural understanding of the allosteric conformational change of cyclic AMP receptor protein by	3.2 3.2 3.2	44155353
1781 1780 1779 1778	Dynamics of cellular retinoic acid binding protein I on multiple time scales with implications for ligand binding. <i>Biochemistry</i> , 2000 , 39, 9119-29 Changes in dynamical behavior of the retinoid X receptor DNA-binding domain upon binding to a 14 base-pair DNA half site. <i>Biochemistry</i> , 2000 , 39, 8747-57 Dynamics of the metallo-beta-lactamase from Bacteroides fragilis in the presence and absence of a tight-binding inhibitor. <i>Biochemistry</i> , 2000 , 39, 13356-64 Restricted motion of the lipoyl-lysine swinging arm in the pyruvate dehydrogenase complex of Escherichia coli. <i>Biochemistry</i> , 2000 , 39, 8448-59 Structural understanding of the allosteric conformational change of cyclic AMP receptor protein by cyclic AMP binding. <i>Biochemistry</i> , 2000 , 39, 13953-62 Ligand-induced changes in the structure and dynamics of a human class Mu glutathione	3.2 3.2 3.2	4415535354

(2001-2000)

1773	interaction of a bacterially expressed peptide from the receptor binding domain of Pseudomonas aeruginosa pili strain PAK with a cross-reactive antibody: conformation of the bound peptide. Biochemistry, 2000, 39, 14847-64	3.2	15	
1772	Conformational changes in the PBX homeodomain and C-terminal extension upon binding DNA and HOX-derived YPWM peptides. <i>Biochemistry</i> , 2000 , 39, 9943-50	3.2	21	
1771	NMR Analysis of Polyester Urethane End Groups and Solid-Phase Hydrolysis Kinetics. 2000 , 33, 3569-35	576	14	
1770	Structure and dynamics of an acid-denatured protein G mutant. <i>Biochemistry</i> , 2000 , 39, 965-77	3.2	38	
1769	Rotational Diffusion Anisotropy and Local Backbone Dynamics of Carbon Monoxide-Bound Rhodobactercapsulatus Cytochrome c[] 2000 , 122, 5603-5612		32	
1768	Elucidation of the Paramagnetic R1 Relaxation of Heteronuclei and Protons in Cu(II) Plastocyanin from Anabaena variabilis. 2000 , 122, 9473-9485		40	
1767	Characterization of the EGF-like module pair 3-4 from vitamin K-dependent protein S using NMR spectroscopy reveals dynamics on three separate time scales and extensive effects from calcium binding. <i>Biochemistry</i> , 2000 , 39, 15742-56	3.2	10	
1766	CC chemokine MIP-1 beta can function as a monomer and depends on Phe13 for receptor binding. <i>Biochemistry</i> , 2000 , 39, 3401-9	3.2	105	
1765	15N R1[Measurements Allow the Determination of Ultrafast Protein Folding Rates. 2000, 122, 5387-53	88	38	
1764	Three-dimensional solution structure of oryzacystatin-I, a cysteine proteinase inhibitor of the rice, Oryza sativa L. japonica. <i>Biochemistry</i> , 2000 , 39, 14753-60	3.2	97	
1763	Flexibility and ligand exchange in a buried cavity mutant of T4 lysozyme studied by multinuclear NMR. <i>Biochemistry</i> , 2000 , 39, 12614-22	3.2	87	
1762	Sequential calcium binding to the regulatory domain of calcium vector protein reveals functional asymmetry and a novel mode of structural rearrangement. <i>Biochemistry</i> , 2000 , 39, 7920-6	3.2	18	
1761	Site-specific NMR monitoring of cis-trans isomerization in the folding of the proline-rich collagen triple helix. <i>Biochemistry</i> , 2000 , 39, 4299-308	3.2	53	
1760	NMR solution structure and receptor peptide binding of the CC chemokine eotaxin-2. <i>Biochemistry</i> , 2000 , 39, 8382-95	3.2	57	
1759	The NMR structure of the nucleocapsid protein from the mouse mammary tumor virus reveals unusual folding of the C-terminal zinc knuckle. <i>Biochemistry</i> , 2000 , 39, 1604-12	3.2	33	
1758	Nuclear magnetic resonance methods for high molecular weight proteins: a study involving a complex of maltose binding protein and beta-cyclodextrin. 2001 , 339, 174-203		47	
1757	Two folded conformers of ubiquitin revealed by high-pressure NMR. <i>Biochemistry</i> , 2001 , 40, 13556-63	3.2	61	
1756	NMR structural and dynamic characterization of the acid-unfolded state of apomyoglobin provides insights into the early events in protein folding. <i>Biochemistry</i> , 2001 , 40, 3561-71	3.2	203	

1755	Nuclear magnetic resonance methods for elucidation of structure and dynamics in disordered states. 2001 , 339, 258-70		137
1754	Temperature dependence of dynamics and thermodynamics of the regulatory domain of human cardiac troponin C. <i>Biochemistry</i> , 2001 , 40, 12541-51	3.2	39
1753	Chalcone derivatives antagonize interactions between the human oncoprotein MDM2 and p53. <i>Biochemistry</i> , 2001 , 40, 336-44	3.2	248
1752	Comparison of protein backbone entropy and beta-sheet stability: NMR-derived dynamics of protein G B1 domain mutants. 2001 , 123, 185-6		30
1751	Solution structure of a sweet protein: NMR study of MNEI, a single chain monellin. <i>Journal of Molecular Biology</i> , 2001 , 305, 505-14	6.5	61
1750	Solution structure of Grb2 reveals extensive flexibility necessary for target recognition. <i>Journal of Molecular Biology</i> , 2001 , 306, 527-37	6.5	52
1749	Self-association reaction of denatured staphylococcal nuclease fragments characterized by heteronuclear NMR. <i>Journal of Molecular Biology</i> , 2001 , 307, 309-22	6.5	9
1748	Solution structure and dynamics of the central CCP module pair of a poxvirus complement control protein. <i>Journal of Molecular Biology</i> , 2001 , 307, 323-39	6.5	52
1747	Solution structure of a type I dockerin domain, a novel prokaryotic, extracellular calcium-binding domain. <i>Journal of Molecular Biology</i> , 2001 , 307, 745-53	6.5	74
1746	Structure, function, and dynamics of the dimerization and DNA-binding domain of oncogenic transcription factor v-Myc. <i>Journal of Molecular Biology</i> , 2001 , 307, 1395-410	6.5	83
1745	Formation of the single-layer beta-sheet of Borrelia burgdorferi OspA in the absence of the C-terminal capping globular domain. <i>Journal of Molecular Biology</i> , 2001 , 308, 367-75	6.5	8
1744	Ligand-induced structural changes to maltodextrin-binding protein as studied by solution NMR spectroscopy. <i>Journal of Molecular Biology</i> , 2001 , 309, 961-74	6.5	114
1743	The B(12)-binding subunit of glutamate mutase from Clostridium tetanomorphum traps the nucleotide moiety of coenzyme B(12). <i>Journal of Molecular Biology</i> , 2001 , 309, 777-91	6.5	28
1742	Solution structure of the catalytic domain of gammadelta resolvase. Implications for the mechanism of catalysis. <i>Journal of Molecular Biology</i> , 2001 , 310, 1089-107	6.5	22
1741	Structure of the C-terminal RNA-binding domain of hnRNP D0 (AUF1), its interactions with RNA and DNA, and change in backbone dynamics upon complex formation with DNA. <i>Journal of Molecular Biology</i> , 2001 , 311, 973-88	6.5	35
1740	NMR structure and backbone dynamics of a concatemer of epidermal growth factor homology modules of the human low-density lipoprotein receptor. <i>Journal of Molecular Biology</i> , 2001 , 311, 341-56	6.5	29
1739	The role of backbone motions in ligand binding to the c-Src SH3 domain. <i>Journal of Molecular Biology</i> , 2001 , 313, 873-87	6.5	86
1738	Defining the molecular basis of Arf and Hdm2 interactions. <i>Journal of Molecular Biology</i> , 2001 , 314, 263-	-7675	112

(2001-2001)

1737	Solution structure and backbone dynamics of an engineered arginine-rich subdomain 2 of the hepatitis C virus NS3 RNA helicase. <i>Journal of Molecular Biology</i> , 2001 , 314, 543-61	6.5	16
1736	NMR relaxation studies of the role of conformational entropy in protein stability and ligand binding. 2001 , 34, 379-88		155
1735	Structure of type I antifreeze protein and mutants in supercooled water. <i>Biophysical Journal</i> , 2001 , 81, 1677-83	2.9	32
1734	Orientation and effects of mastoparan X on phospholipid bicelles. <i>Biophysical Journal</i> , 2001 , 80, 280-93	2.9	113
1733	Heteronuclear nuclear magnetic resonance assignments, structure and dynamics of SUMO-1, a human ubiquitin-like protein. 2001 , 28, 227-34		25
1732	Nmr probes of molecular dynamics: overview and comparison with other techniques. 2001 , 30, 129-55		307
1731	Backbone dynamics of the channel-forming antibiotic zervamicin IIB studied by 15N NMR relaxation. 2001 , 495, 52-5		15
1730	Backbone dynamics of receptor binding and antigenic regions of a Pseudomonas aeruginosa pilin monomer. <i>Biochemistry</i> , 2001 , 40, 3985-95	3.2	18
1729	Structure and backbone dynamics of Apo-CBFbeta in solution. <i>Biochemistry</i> , 2001 , 40, 11423-32	3.2	7
1728	NMR derived solution structure of an EF-hand calcium-binding protein from Entamoeba Histolytica. <i>Biochemistry</i> , 2001 , 40, 14392-403	3.2	40
1727	Solution structure of the DNA binding domain of the human forkhead transcription factor AFX (FOXO4). <i>Biochemistry</i> , 2001 , 40, 5861-9	3.2	66
1726	Dynamic characterization of the water binding loop in the P-type cardiotoxin: implication for the role of the bound water molecule. <i>Biochemistry</i> , 2001 , 40, 12782-94	3.2	18
1725	Concerted motion of a protein-peptide complex: backbone dynamics studies of an (15)N-labeled peptide derived from P(21)-activated kinase bound to Cdc42Hs.GMPPCP. <i>Biochemistry</i> , 2001 , 40, 14368-	· 3 5²	14
1724	Monomeric solution structure of the prototypical ICLchemokine lymphotactin. <i>Biochemistry</i> , 2001 , 40, 12486-96	3.2	47
1723	Main chain and side chain dynamics of a heme protein: 15N and 2H NMR relaxation studies of R. capsulatus ferrocytochrome c2. <i>Biochemistry</i> , 2001 , 40, 6559-69	3.2	40
1722	Backbone dynamics of the calcium-signaling protein apo-S100B as determined by 15N NMR relaxation. <i>Biochemistry</i> , 2001 , 40, 3439-48	3.2	30
1721	Structural characterization of proteins with an attached ATCUN motif by paramagnetic relaxation enhancement NMR spectroscopy. 2001 , 123, 9843-7		145
1720	15N NMR relaxation studies of backbone dynamics in free and steroid-bound Delta 5-3-ketosteroid isomerase from Pseudomonas testosteroni. <i>Biochemistry</i> , 2001 , 40, 3967-73	3.2	30

1719	Conversion of phospholamban into a soluble pentameric helical bundle. <i>Biochemistry</i> , 2001 , 40, 6636-45	3.2	33
1718	Solution Structure and Backbone Dynamics of the Defunct Domain of Calcium Vector Protein Biochemistry, 2001 , 40, 13888-13897	3.2	13
1717	Three-dimensional structure and dynamics of a brain specific growth inhibitory factor: metallothionein-3. <i>Biochemistry</i> , 2001 , 40, 11433-41	3.2	84
1716	Cross-correlated chemical shift modulation: a signature of slow internal motions in proteins. 2001 , 123, 4810-6		51
1715	Conformational and dynamic characterization of the molten globule state of an apomyoglobin mutant with an altered folding pathway. <i>Biochemistry</i> , 2001 , 40, 14459-67	3.2	43
1714	Dynamics of a de novo designed three-helix bundle protein studied by 15N, 13C, and 2H NMR relaxation methods. <i>Biochemistry</i> , 2001 , 40, 9560-9	3.2	42
1713	Slow motion in the CAA*TTG sequence of a DNA decamer duplex studied by NMR. <i>Biochemistry</i> , 2001 , 40, 7239-46	3.2	9
1712	Structure, dynamics, and thermodynamics of the structural domain of troponin C in complex with the regulatory peptide 1-40 of troponin I. <i>Biochemistry</i> , 2001 , 40, 10063-77	3.2	37
1711	Dynamics of the Mrf-2 DNA-binding domain free and in complex with DNA. <i>Biochemistry</i> , 2001 , 40, 9142	-3.0	31
1710	Role of the conserved acidic residue Asp21 in the structure of phosphatidylinositol 3-kinase Src homology 3 domain: circular dichroism and nuclear magnetic resonance studies. <i>Biochemistry</i> , 2001 , 40, 119-29	3.2	6
1709	Main chain and side chain dynamics of oxidized flavodoxin from Cyanobacterium anabaena. <i>Biochemistry</i> , 2001 , 40, 14744-53	3.2	35
1708	Conformational exchange on the microsecond time scale in alpha-helix and beta-hairpin peptides measured by 13C NMR transverse relaxation. <i>Biochemistry</i> , 2001 , 40, 2844-53	3.2	18
1707	Redox-dependent conformational selection in a Cys4Fe2S2 ferredoxin. <i>Biochemistry</i> , 2001 , 40, 5602-14	3.2	33
1706	Local structural plasticity of the prion protein. Analysis of NMR relaxation dynamics. <i>Biochemistry</i> , 2001 , 40, 2743-53	3.2	164
1705	Dynamic activation of protein function: a view emerging from NMR spectroscopy. 2001 , 8, 926-31		253
1704	Solution structure and dynamic character of the histidine-containing phosphotransfer domain of anaerobic sensor kinase ArcB from Escherichia coli. <i>Biochemistry</i> , 2001 , 40, 375-86	3.2	19
1703	NMR 15N relaxation of the insulin-like growth factor (IGF)-binding domain of IGF binding protein-5 (IGFBP-5) determined free in solution and in complex with IGF-II. 2001 , 268, 1058-65		14
1702	NMR studies of Brownian tumbling and internal motions in proteins. 2001 , 38, 197-266		163

1701	NMR spin relaxation methods for characterization of disorder and folding in proteins. 2001 , 19, 3-12	43
1700	Structural and biochemical characterization of neuronal calretinin domain I-II (residues 1-100). Comparison to homologous calbindin D28k domain I-II (residues 1-93). 2001 , 268, 6229-37	19
1699	Solution structure and dynamics of ribonuclease Sa. 2001 , 44, 200-11	24
1698	Separating structure and dynamics in CSA/DD cross-correlated relaxation: a case study on trehalose and ubiquitin. 2001 , 150, 137-46	14
1697	Analytical solution to the Lipari-Szabo model based on the reduced spectral density approximation offers a novel protocol for extracting motional parameters. 2001 , 151, 32-9	7
1696	A new approach to visualizing spectral density functions and deriving motional correlation time distributions: applications to an alpha-helix-forming peptide and to a well-folded protein. 2001 , 152, 132-48	7
1695	Improved measurement of (15)N-[(1)H] NOEs in the presence of H(N)-water proton chemical exchange. 2001 , 153, 138-43	12
1694	Design and synthesis of non-peptidic inhibitors for the Syk C-terminal SH2 domain based on structure-based in-silico screening. 2001 , 44, 4737-40	27
1693	Domain orientation in beta-cyclodextrin-loaded maltose binding protein: diffusion anisotropy measurements confirm the results of a dipolar coupling study. 2001 , 20, 83-8	38
1692	Backbone dynamics of the natively unfolded pro-peptide of subtilisin by heteronuclear NMR relaxation studies. 2001 , 20, 233-49	61
1691	NMR studies of the sporulation protein SpoIIAA: implications for the regulation of the transcription factor sigmaF in Bacillus subtilis. 2001 , 19, 293-304	8
1690	An improved method for distinguishing between anisotropic tumbling and chemical exchange in analysis of 15N relaxation parameters. 2001 , 20, 149-65	69
1689	Measurement of homonuclear three-bond J(H(N)Halpha) coupling constants in unlabeled peptides complexed with labeled proteins: application to a decapeptide inhibitor bound to the proteinase domain of the NS3 protein of hepatitis C virus (HCV). 2001 , 20, 23-9	1
1688	Anisotropic rotational diffusion in model-free analysis for a ternary DHFR complex. 2001 , 19, 209-30	42
1687	NMR-based structure of the conserved protein MTH865 from the archaeon Methanobacterium thermoautotrophicum. 2001 , 21, 63-6	1
1686	Potential bias in NMR relaxation data introduced by peak intensity analysis and curve fitting methods. 2001 , 21, 1-9	42
1685	CPMG sequences with enhanced sensitivity to chemical exchange. 2001 , 21, 361-6	63
1684	15N NMR relaxation as a probe for helical intrinsic propensity: the case of the unfolded D2 domain of annexin I. 2001 , 19, 3-18	22

1683	Solution structure and backbone dynamics of an omega-conotoxin precursor. <i>Protein Science</i> , 2001 , 10, 538-50	6.3	21
1682	NMR and SAXS characterization of the denatured state of the chemotactic protein CheY: implications for protein folding initiation. <i>Protein Science</i> , 2001 , 10, 1100-12	6.3	55
1681	Implications of SH3 domain structure and dynamics for protein regulation and drug design. 2001 , 35, 127-40		32
1680	The extracellular human melanoma inhibitory activity (MIA) protein adopts an SH3 domain-like fold. 2001 , 20, 340-9		62
1679	SMN tudor domain structure and its interaction with the Sm proteins. 2001 , 8, 27-31		247
1678	Peptide-triggered conformational switch in HIV-1 RRE RNA complexes. 2001 , 8, 146-50		53
1677	Structure of outer membrane protein A transmembrane domain by NMR spectroscopy. 2001 , 8, 334-8		331
1676	Dynamics of the transition between open and closed conformations in a calmodulin C-terminal domain mutant. <i>Structure</i> , 2001 , 9, 185-95	5.2	77
1675	Structure of Cdc4p, a contractile ring protein essential for cytokinesis in Schizosaccharomyces pombe. <i>Journal of Biological Chemistry</i> , 2001 , 276, 5943-51	5.4	19
1674	Backbone dynamics of a module pair from the ligand-binding domain of the LDL receptor. <i>Biochemistry</i> , 2001 , 40, 2808-15	3.2	44
1673	Molecular interactions of the Gbeta binding domain of the Ste20p/PAK family of protein kinases. An isolated but fully functional Gbeta binding domain from Ste20p is only partially folded as shown by heteronuclear NMR spectroscopy. <i>Journal of Biological Chemistry</i> , 2001 , 276, 41205-12	5.4	12
1672	Two different neurodegenerative diseases caused by proteins with similar structures. 2001 , 98, 2352-7		134
1671	Residual structure and dynamics in ParkinsonIs disease-associated mutants of alpha-synuclein. Journal of Biological Chemistry, 2001 , 276, 45996-6003	5.4	207
1670	Conformational heterogeneity in the C-terminal zinc fingers of human MTF-1: an NMR and zinc-binding study. <i>Journal of Biological Chemistry</i> , 2001 , 276, 42322-32	5.4	29
1669	Solution structure and dynamics of GCN4 cognate DNA: NMR investigations. <i>Nucleic Acids Research</i> , 2001 , 29, 499-505	20.1	5
1668	Solution structure, backbone dynamics, and stability of a double mutant single-chain monellin. structural origin of sweetness. <i>Journal of Biological Chemistry</i> , 2001 , 276, 19624-30	5.4	31
1667	Folding and stability of sweet protein single-chain monellin. An insight to protein engineering. Journal of Biological Chemistry, 2001 , 276, 44229-38	5.4	15
1666	Solution structure and dynamics of myeloid progenitor inhibitory factor-1 (MPIF-1), a novel monomeric CC chemokine. <i>Journal of Biological Chemistry</i> , 2001 , 276, 4909-16	5.4	26

1665	Production and characterization of recombinant tachycitin, the Cys-rich chitin-binding protein. 2002 , 15, 763-9		7
1664	Solution structure of the viral receptor domain of Tva and its implications in viral entry. 2002 , 76, 2848-	56	23
1663	PDZ7 of glutamate receptor interacting protein binds to its target via a novel hydrophobic surface area. <i>Journal of Biological Chemistry</i> , 2002 , 277, 41140-6	5.4	28
1662	Solution structure of human GABA(A) receptor-associated protein GABARAP: implications for biolgoical function and its regulation. <i>Journal of Biological Chemistry</i> , 2002 , 277, 13363-6	5.4	56
1661	Dynamics-modulated biological activity of transforming growth factor beta3. <i>Journal of Biological Chemistry</i> , 2002 , 277, 46273-9	5.4	34
1660	Solution structure and dynamics of the outer membrane enzyme PagP by NMR. 2002 , 99, 13560-5		282
1659	NMR structure and dynamics of a receptor-active apolipoprotein E peptide. <i>Journal of Biological Chemistry</i> , 2002 , 277, 29172-80	5.4	22
1658	Characterization of the structure and dynamics of a near-native equilibrium intermediate in the unfolding pathway of an all beta-barrel protein. <i>Journal of Biological Chemistry</i> , 2002 , 277, 47507-16	5.4	15
1657	Structural rearrangement of human lymphotactin, a C chemokine, under physiological solution conditions. <i>Journal of Biological Chemistry</i> , 2002 , 277, 17863-70	5.4	60
1656	Structure of a regulatory complex involving the Abl SH3 domain, the Crk SH2 domain, and a Crk-derived phosphopeptide. 2002 , 99, 14053-8		63
1655	Identification of protein surfaces by NMR measurements with a pramagnetic Gd(III) chelate. 2002 , 124, 372-3		182
1654	Molecular hinges in protein folding: the urea-denatured state of apomyoglobin. <i>Biochemistry</i> , 2002 , 41, 12681-6	3.2	123
1653	Functional consequences of preorganized helical structure in the intrinsically disordered cell-cycle inhibitor p27(Kip1). <i>Biochemistry</i> , 2002 , 41, 752-9	3.2	131
1652	Populating partially unfolded forms by hydrogen exchange-directed protein engineering. <i>Biochemistry</i> , 2002 , 41, 12308-12	3.2	34
1651	Solution structure and backbone dynamics of the functional cytoplasmic subdomain of human ephrin B2, a cell-surface ligand with bidirectional signaling properties. <i>Biochemistry</i> , 2002 , 41, 10942-9	3.2	27
1650	Deuterium spin probes of side-chain dynamics in proteins. 1. Measurement of five relaxation rates per deuteron in (13)C-labeled and fractionally (2)H-enriched proteins in solution. 2002 , 124, 6439-48		166
1649	Site-specific characterization of the association of xylooligosaccharides with the CBM13 lectin-like xylan binding domain from Streptomyces lividans xylanase 10A by NMR spectroscopy. <i>Biochemistry</i> , 2002 , 41, 4255-63	3.2	22
1648	NMR identification and characterization of the flexible regions in the 160 kDa molten globule-like aggregate of barstar at low pH. <i>Biochemistry</i> , 2002 , 41, 9885-99	3.2	29

1647	Folding and conformational consequences of glycine to alanine replacements at different positions in a collagen model peptide. <i>Biochemistry</i> , 2002 , 41, 6539-47	3.2	35
1646	Four-dimensional NMR spectroscopy of a 723-residue protein: chemical shift assignments and secondary structure of malate synthase g. 2002 , 124, 10025-35		205
1645	Direct structure determination using residual dipolar couplings: reaction-site conformation of methionine sulfoxide reductase in solution. 2002 , 124, 13709-15		21
1644	Insights into the structure and dynamics of unfolded proteins from nuclear magnetic resonance. 2002 , 62, 311-40		183
1643	Structure-function analysis of the heat shock factor-binding protein reveals a protein composed solely of a highly conserved and dynamic coiled-coil trimerization domain. <i>Journal of Biological Chemistry</i> , 2002 , 277, 735-45	5.4	33
1642	Solution NMR structure and backbone dynamics of the PsaE subunit of photosystem I from Synechocystis sp. PCC 6803. <i>Biochemistry</i> , 2002 , 41, 13902-14	3.2	15
1641	Structural mobility of the extracellular ligand-binding core of an ionotropic glutamate receptor. Analysis of NMR relaxation dynamics. <i>Biochemistry</i> , 2002 , 41, 10472-81	3.2	78
1640	An NMR experiment for the accurate measurement of heteronuclear spin-lock relaxation rates. 2002 , 124, 10743-53		114
1639	Effects of the N2144S mutation on backbone dynamics of a TB-cbEGF domain pair from human fibrillin-1. <i>Journal of Molecular Biology</i> , 2002 , 316, 113-25	6.5	27
1638	Solution structure and dynamics of Crh, the Bacillus subtilis catabolite repression HPr. <i>Journal of Molecular Biology</i> , 2002 , 317, 131-44	6.5	42
1637	Differences in backbone dynamics of two homologous bacterial albumin-binding modules: implications for binding specificity and bacterial adaptation. <i>Journal of Molecular Biology</i> , 2002 , 316, 1083-99	6.5	16
1636	Temperature dependence of the internal dynamics of a calmodulin-peptide complex. <i>Biochemistry</i> , 2002 , 41, 13814-25	3.2	83
1635	Structure and dynamics of a beta-helical antifreeze protein. <i>Biochemistry</i> , 2002 , 41, 5515-25	3.2	54
1634	Enzyme dynamics during catalysis. 2002 , 295, 1520-3		616
1633	Deuterium spin probes of side-chain dynamics in proteins. 2. Spectral density mapping and identification of nanosecond time-scale side-chain motions. 2002 , 124, 6449-60		115
1632	Structure comparison of two conserved HNF-3/fkh proteins HFH-1 and genesis indicates the existence of folding differences in their complexes with a DNA binding sequence. <i>Biochemistry</i> , 2002 , 41, 3286-93	3.2	15
1631	O2 penetration and proton burial depth in proteins: applicability to fold family recognition. 2002 , 124, 4463-72		44
1630	Structure of the N-WASP EVH1 domain-WIP complex: insight into the molecular basis of Wiskott-Aldrich Syndrome. 2002 , 111, 565-76		145

1629	The regions of securin and cyclin B proteins recognized by the ubiquitination machinery are natively unfolded. 2002 , 527, 303-8		34	
1628	Structural dynamics of the membrane translocation domain of colicin E9 and its interaction with TolB. <i>Journal of Molecular Biology</i> , 2002 , 318, 787-804	6.5	37	
1627	NMR studies of the backbone flexibility and structure of human growth hormone: a comparison of high and low pH conformations. <i>Journal of Molecular Biology</i> , 2002 , 318, 679-95	6.5	35	
1626	Olfactory marker protein (OMP) exhibits a beta-clam fold in solution: implications for target peptide interaction and olfactory signal transduction. <i>Journal of Molecular Biology</i> , 2002 , 319, 823-37	6.5	28	
1625	Redox-coupled conformational alternations in cytochrome c(3) from D. vulgaris Miyazaki F on the basis of its reduced solution structure. <i>Journal of Molecular Biology</i> , 2002 , 319, 767-78	6.5	33	
1624	The nuclease A inhibitor represents a new variation of the rare PR-1 fold. <i>Journal of Molecular Biology</i> , 2002 , 320, 771-82	6.5	18	
1623	Temperature-dependent dynamics of the villin headpiece helical subdomain, an unusually small thermostable protein. <i>Journal of Molecular Biology</i> , 2002 , 320, 841-54	6.5	62	
1622	Hsc70-interacting HPD loop of the J domain of polyomavirus T antigens fluctuates in ps to ns and micros to ms. <i>Journal of Molecular Biology</i> , 2002 , 321, 503-16	6.5	15	
1621	Intramolecular dynamics of low molecular weight protein tyrosine phosphatase in monomer-dimer equilibrium studied by NMR: a model for changes in dynamics upon target binding. <i>Journal of Molecular Biology</i> , 2002 , 322, 137-52	6.5	48	
1620	Solution structure of a luteoviral P1-P2 frameshifting mRNA pseudoknot. <i>Journal of Molecular Biology</i> , 2002 , 322, 621-33	6.5	73	
1619	Side-chain dynamics of the SAP SH2 domain correlate with a binding hot spot and a region with conformational plasticity. <i>Journal of Molecular Biology</i> , 2002 , 322, 605-20	6.5	46	
1618	A functional role for correlated motion in the N-terminal RNA-binding domain of human U1A protein. <i>Journal of Molecular Biology</i> , 2002 , 322, 533-42	6.5	39	
1617	Solution structure and ligand recognition of the WW domain pair of the yeast splicing factor Prp40. Journal of Molecular Biology, 2002 , 324, 807-22	6.5	68	
1616	Solution structure of a llama single-domain antibody with hydrophobic residues typical of the VH/VL interface. <i>Biochemistry</i> , 2002 , 41, 8570-9	3.2	40	
1615	Protein Dynamics Measurements by 3D HNCO Based NMR Experiments. 2002 , 16, 1-13		5	
1614	Comparative studies of frameshifting and nonframeshifting RNA pseudoknots: a mutational and NMR investigation of pseudoknots derived from the bacteriophage T2 gene 32 mRNA and the retroviral gag-pro frameshift site. 2002 , 8, 981-96		26	
1613	Structure and dynamics of the anticodon arm binding domain of Bacillus stearothermophilus Tyrosyl-tRNA synthetase. <i>Structure</i> , 2002 , 10, 311-7	5.2	16	
1612	SH3-SH2 domain orientation in Src kinases: NMR studies of Fyn. <i>Structure</i> , 2002 , 10, 901-11	5.2	33	

1611	Structure and interactions of PAS kinase N-terminal PAS domain: model for intramolecular kinase regulation. <i>Structure</i> , 2002 , 10, 1349-61	.2	127
1610	Heteronuclear multidimensional NMR spectroscopy of solubilized membrane proteins: resonance assignment of native bacteriorhodopsin. 2002 , 3, 1019-23		36
1609	The first orally active low molecular weight agonists for the LH receptor: thienopyr(im)idines with therapeutic potential for ovulation induction. 2002 , 3, 1023-6		73
1608	Ribosome-associated factor Y adopts a fold resembling a double-stranded RNA binding domain scaffold. 2002 , 269, 5182-91		23
1607	Solution structure and backbone dynamics of the catalytic domain of matrix metalloproteinase-2 complexed with a hydroxamic acid inhibitor. 2002 , 1598, 10-23		67
1606	The dynamic behavior of CheW from Thermotoga maritima in solution, as determined by nuclear magnetic resonance: implications for potential protein-protein interaction sites. 2002 , 101-102, 359-73		14
1605	NMR structure of the Escherichia coli protein YacG: a novel sequence motif in the zinc-finger family of proteins. 2002 , 49, 289-93		10
1604	Backbone dynamics of the CC-chemokine eotaxin-2 and comparison among the eotaxin group chemokines. 2003 , 50, 184-91		7
1603	Solution structure of the DNA-binding domain of MafG. 2002 , 9, 252-6		35
1602	Structural characterization of a proline-driven conformational switch within the Itk SH2 domain.		100
	2002 , 9, 900-5		100
1601	2002 , 9, 900-5 Practical aspects of the 2D 15N-[1h]-NOE experiment. 2002 , 23, 23-33		76
	2002, 9, 900-5		
	Practical aspects of the 2D 15N-[1h]-NOE experiment. 2002 , 23, 23-33		76
1600	Practical aspects of the 2D 15N-[1h]-NOE experiment. 2002 , 23, 23-33 Protein dynamics in supercooled water: the search for slow motional modes. 2002 , 23, 63-7 Backbone dynamics of the 8 kDa dynein light chain dimer reveals molecular basis of the proteinls		76 30
1600 1599	Practical aspects of the 2D 15N-[1h]-NOE experiment. 2002 , 23, 23-33 Protein dynamics in supercooled water: the search for slow motional modes. 2002 , 23, 63-7 Backbone dynamics of the 8 kDa dynein light chain dimer reveals molecular basis of the proteinls functional diversity. 2002 , 23, 103-14 NMR-based solution structure of the complex of Lactobacillus casei dihydrofolate reductase with		76 30 25
1600 1599 1598	Practical aspects of the 2D 15N-[1h]-NOE experiment. 2002, 23, 23-33 Protein dynamics in supercooled water: the search for slow motional modes. 2002, 23, 63-7 Backbone dynamics of the 8 kDa dynein light chain dimer reveals molecular basis of the proteinls functional diversity. 2002, 23, 103-14 NMR-based solution structure of the complex of Lactobacillus casei dihydrofolate reductase with trimethoprim and NADPH. 2002, 24, 67-70 Backbone dynamics of the cytotoxic ribonuclease alpha-sarcin by 15N NMR relaxation methods.		76 30 25 18
1600 1599 1598 1597	Practical aspects of the 2D 15N-[1h]-NOE experiment. 2002, 23, 23-33 Protein dynamics in supercooled water: the search for slow motional modes. 2002, 23, 63-7 Backbone dynamics of the 8 kDa dynein light chain dimer reveals molecular basis of the proteinls functional diversity. 2002, 23, 103-14 NMR-based solution structure of the complex of Lactobacillus casei dihydrofolate reductase with trimethoprim and NADPH. 2002, 24, 67-70 Backbone dynamics of the cytotoxic ribonuclease alpha-sarcin by 15N NMR relaxation methods. 2002, 24, 301-16		76 30 25 18

1593	Model selection for the interpretation of protein side chain methyl dynamics. 2003 , 25, 325-33		13
1592	Structure and dynamics of a membrane protein in micelles from three solution NMR experiments. 2003 , 26, 327-34		36
1591	Angular dependence of dipole-dipole-Curie-spin cross-correlation effects in high-spin and low-spin paramagnetic myoglobin. 2003 , 27, 115-32		28
1590	Characterization of the overall and local dynamics of a protein with intermediate rotational anisotropy: Differentiating between conformational exchange and anisotropic diffusion in the B3 domain of protein G. 2003 , 27, 261-75		107
1589	Detection of nano-second internal motion and determination of overall tumbling times independent of the time scale of internal motion in proteins from NMR relaxation data. 2003 , 27, 291-31.	2	16
1588	Solution structure of a PAN module from the apicomplexan parasite Eimeria tenella. 2003, 4, 227-34		14
1587	Backbone dynamics of the human MIA protein studied by (15)N NMR relaxation: implications for extended interactions of SH3 domains. <i>Protein Science</i> , 2003 , 12, 510-9	5.3	25
1586	Effects of denaturants and substitutions of hydrophobic residues on backbone dynamics of denatured staphylococcal nuclease. <i>Protein Science</i> , 2003 , 12, 1530-7	5.3	18
1585	Structural basis for the recognition of ldb1 by the N-terminal LIM domains of LMO2 and LMO4. 2003 , 22, 2224-33		57
1584	Solution structure of Vps27 UIM-ubiquitin complex important for endosomal sorting and receptor downregulation. 2003 , 22, 4597-606		172
1583	The use of model selection in the model-free analysis of protein dynamics. 2003 , 25, 25-39		113
1582	Backbone H(N), N, C(alpha) and C(beta) assignment of the GFPuv mutant. 2003, 25, 161-2		10
1581	Backbone dynamics and hydrogen exchange of Pseudomonas aeruginosa ferricytochrome c(551). 2003 , 8, 156-66		36
1580	Solution structure of Sco1: a thioredoxin-like protein Involved in cytochrome c oxidase assembly. Structure, 2003 , 11, 1431-43	5.2	115
1579	Application of the model-free approach to low molecular weight systems with hindered internal rotation: cinnamoylmesitylene. 2003 , 41, 989-995		
1578	Protein stabilization by compatible solutes. Effect of diglycerol phosphate on the dynamics of Desulfovibrio gigas rubredoxin studied by NMR. 2003 , 270, 4606-14		41
1577	Structure determination of human Lck unique and SH3 domains by nuclear magnetic resonance spectroscopy. 2003 , 3, 3		8
1576	Structure and dynamics of the potato carboxypeptidase inhibitor by 1H and 15N NMR. 2003 , 50, 410-22		17

1575	Solution structure of the highly acidic protein HI1450 from Haemophilus influenzae, a putative double-stranded DNA mimic. 2004 , 54, 375-83		19
1574	A dimeric viral SET domain methyltransferase specific to Lys27 of histone H3. 2003 , 10, 187-96		78
1573	Increased rigidity of eglin c at acidic pH: evidence from NMR spin relaxation and MD simulations. <i>Biochemistry</i> , 2003 , 42, 13856-68	3.2	29
1572	Electrostatic interactions in the reconstitution of an SH2 domain from constituent peptide fragments. <i>Protein Science</i> , 2003 , 12, 44-55	6.3	7
1571	Ligand-induced changes in dynamics in the RT loop of the C-terminal SH3 domain of Sem-5 indicate cooperative conformational coupling. <i>Protein Science</i> , 2003 , 12, 982-96	6.3	45
1570	Changes in structure and dynamics of the Fv fragment of a catalytic antibody upon binding of inhibitor. <i>Protein Science</i> , 2003 , 12, 1386-94	6.3	13
1569	Solution structure of the carboxyl-terminal domain of RAP74 and NMR characterization of the FCP1-binding sites of RAP74 and human TFIIB. <i>Biochemistry</i> , 2003 , 42, 1460-9	3.2	18
1568	NMR structure and dynamics of the second transmembrane domain of the neuronal acetylcholine receptor beta 2 subunit. <i>Biochemistry</i> , 2003 , 42, 13058-65	3.2	17
1567	Solution structure and backbone dynamics of the holo form of the frenolicin acyl carrier protein. <i>Biochemistry</i> , 2003 , 42, 4648-57	3.2	86
1566	High-resolution solution structure of the beryllofluoride-activated NtrC receiver domain. <i>Biochemistry</i> , 2003 , 42, 9081-90	3.2	58
1565	NMR structure and backbone dynamics of the extended second transmembrane domain of the human neuronal glycine receptor alpha1 subunit. <i>Biochemistry</i> , 2003 , 42, 3989-95	3.2	25
1564	Protein inhibitors of serine proteinases: role of backbone structure and dynamics in controlling the hydrolysis constant. <i>Biochemistry</i> , 2003 , 42, 5186-94	3.2	11
1563	Backbone dynamics of reduced plastocyanin from the cyanobacterium Anabaena variabilis: regions involved in electron transfer have enhanced mobility. <i>Biochemistry</i> , 2003 , 42, 320-30	3.2	17
1562	Side chain dynamics in unfolded protein states: an NMR based 2H spin relaxation study of delta131delta. 2003 , 125, 1748-58		43
1561	Characterization of the yeast peroxiredoxin Ahp1 in its reduced active and overoxidized inactive forms using NMR. <i>Biochemistry</i> , 2003 , 42, 14139-49	3.2	32
1560	NMR study of the interaction between Zn(II) ligated bleomycin and Streptoalloteichus hindustanus bleomycin resistance protein. <i>Biochemistry</i> , 2003 , 42, 651-63	3.2	10
1559	NMR studies of the interaction of a type II dihydrofolate reductase with pyridine nucleotides reveal unexpected phosphatase and reductase activity. <i>Biochemistry</i> , 2003 , 42, 11150-60	3.2	20
1558	Solution structure, dynamics, and thermodynamics of the native state ensemble of the Sem-5 C-terminal SH3 domain. <i>Biochemistry</i> , 2003 , 42, 5582-91	3.2	30

(2003-2003)

Interaction of a peptide from the receptor-binding domain of Pseudomonas aeruginosa pili strain PAK with a cross-reactive antibody: changes in backbone dynamics induced by binding. <i>Biochemistry</i> , 2003 , 42, 11334-46	3.2	9
Solution structure and dynamics of oxytetracycline polyketide synthase acyl carrier protein from Streptomyces rimosus. <i>Biochemistry</i> , 2003 , 42, 8423-33	3.2	65
Two conformational states of Turkey ovomucoid third domain at low pH: three-dimensional structures, internal dynamics, and interconversion kinetics and thermodynamics. <i>Biochemistry</i> , 2003 , 42, 6380-91	3.2	15
NMR and CD spectroscopy show that imino acid restriction of the unfolded state leads to efficient folding. <i>Biochemistry</i> , 2003 , 42, 8696-703	3.2	22
The swapping of terminal arms in ribonucleases: comparison of the solution structure of monomeric bovine seminal and pancreatic ribonucleases. <i>Biochemistry</i> , 2003 , 42, 8704-11	3.2	22
NMR structure of a bifunctional rhodamine labeled N-domain of troponin C complexed with the regulatory "switch" peptide from troponin I: implications for in situ fluorescence studies in muscle fibers. <i>Biochemistry</i> , 2003 , 42, 4333-48	3.2	32
A conserved histidine in vertebrate-type ferredoxins is critical for redox-dependent dynamics. <i>Biochemistry</i> , 2003 , 42, 8171-82	3.2	10
Structural rearrangements of the two domains of Azotobacter vinelandii rhodanese upon sulfane sulfur release: essential molecular dynamics, 15N NMR relaxation and deuterium exchange on the uniformly labeled protein. 2003 , 33, 193-201		5
Identification of a residue critical for maintaining the functional conformation of BPTI. <i>Journal of Molecular Biology</i> , 2003 , 333, 425-41	6.5	17
High-resolution X-ray and NMR structures of the SMN Tudor domain: conformational variation in the binding site for symmetrically dimethylated arginine residues. <i>Journal of Molecular Biology</i> , 2003 , 327, 507-20	6.5	142
Increased backbone mobility in beta-barrel enhances entropy gain driving binding of N-TIMP-1 to MMP-3. <i>Journal of Molecular Biology</i> , 2003 , 327, 719-34	6.5	73
Spruce budworm antifreeze protein: changes in structure and dynamics at low temperature. <i>Journal of Molecular Biology</i> , 2003 , 327, 1155-68	6.5	31
Quantitative NMR studies of high molecular weight proteins: application to domain orientation and ligand binding in the 723 residue enzyme malate synthase G. <i>Journal of Molecular Biology</i> , 2003 , 327, 1121-33	6.5	86
Dynamics and DNA substrate recognition by the catalytic domain of lambda integrase. <i>Journal of Molecular Biology</i> , 2003 , 329, 423-39	6.5	16
Towards an understanding of the poliovirus replication complex: the solution structure of the soluble domain of the poliovirus 3A protein. <i>Journal of Molecular Biology</i> , 2003 , 330, 225-34	6.5	53
Two homologous rat cellular retinol-binding proteins differ in local conformational flexibility. Journal of Molecular Biology, 2003 , 330, 799-812	6.5	28
A core mutation affecting the folding properties of a soluble domain of the ATPase protein CopA from Bacillus subtilis. <i>Journal of Molecular Biology</i> , 2003 , 331, 473-84	6.5	29
Anastellin, an FN3 fragment with fibronectin polymerization activity, resembles amyloid fibril precursors. <i>Journal of Molecular Biology</i> , 2003 , 332, 205-15	6.5	67
	PAK with a cross-reactive antibody: changes in backbone dynamics induced by binding. <i>Biochemistry</i> , 2003, 42, 11334-46 Solution structure and dynamics of oxytetracycline polyketide synthase acyl carrier protein from Streptomyces rimosus. <i>Biochemistry</i> , 2003, 42, 8423-33 Two conformational states of Turkey ovomucoid third domain at low pH: three-dimensional structures, internal dynamics, and interconversion kinetics and thermodynamics. <i>Biochemistry</i> , 2003, 42, 6390-91 NMR and CD spectroscopy show that imino acid restriction of the unfolded state leads to efficient folding. <i>Biochemistry</i> , 2003, 42, 8696-703 The swapping of terminal arms in ribonucleases: comparison of the solution structure of monomeric bovine seminal and pancreatic ribonucleases. <i>Biochemistry</i> , 2003, 42, 8704-11 NMR structure of a bifunctional rhodamine labeled N-domain of troponin C complexed with the regulatory "switch" peptide from troponin I: implications for in situ fluorescence studies in muscle fibers. <i>Biochemistry</i> , 2003, 42, 8171-82 A conserved histidine in vertebrate-type ferredoxins is critical for redox-dependent dynamics. <i>Biochemistry</i> , 2003, 42, 8171-82 Structural rearrangements of the two domains of Azotobacter vinelandii rhodanese upon sulfane sulfur release: essential molecular dynamics, 15N NMR relaxation and deuterium exchange on the uniformly labeled protein. 2003, 33, 193-201 Identification of a residue critical for maintaining the functional conformation of BPTI. <i>Journal of Molecular Biology</i> , 2003, 337, 507-20 Increased backbone mobility in beta-barrel enhances entropy gain driving binding of N-TIMP-1 to MMP-3. <i>Journal of Molecular Biology</i> , 2003, 327, 1155-68 Quantitative NMR studies of high molecular weight proteins: application to domain orientation and ligand binding in the 723 residue enzyme malate synthase G. <i>Journal of Molecular Biology</i> , 2003, 327, 2003, 327, 327, 327-339 Towards an understanding of the poliovirus replication complex: the solution structure of the soluble domain of the poliovir	PAK with a cross-reactive antibody: changes in backbone dynamics induced by binding. Biochemistry, 2003, 42, 11334-46 Solution structure and dynamics of oxytetracycline polyketide synthase acyl carrier protein from Streptomyces rimosus. Biochemistry, 2003, 42, 8423-33 Two conformational states of Turkey ovomucoid third domain at low pH: three-dimensional structures, internal dynamics, and interconversion kinetics and thermodynamics. Biochemistry, 2003, 42, 6380-91 NMR and CD spectroscopy show that imino acid restriction of the unfolded state leads to efficient folding. Biochemistry, 2003, 42, 8696-703 The swapping of terminal arms in ribonucleases: comparison of the solution structure of monomeric bovine seminal and pancreatic ribonucleases. Biochemistry, 2003, 42, 8704-11 NMR structure of a bifunctional rhodamine labeled N-domain of troponin C complexed with the regulatory "switch" peptide from troponin I: implications for in situ fluorescence studies in muscle fibers. Biochemistry, 2003, 42, 4333-48 A conserved histidine in vertebrate-type ferredoxins is critical for redox-dependent dynamics. Biochemistry, 2003, 42, 8171-82 Structural rearrangements of the two domains of Azotobacter vinelandii rhodanese upon sulfane sulfur release essential molecular dynamics, 15N NMR relaxation and deuterium exchange on the uniformly labeled protein. 2003, 33, 193-201 Identification of a residue critical for maintaining the functional conformation of BPTI. Journal of Molecular Biology, 2003, 333, 425-41 High-resolution X-ray and NMR structures of the SMN Tudor domain: conformational variation in the binding site for symmetrically dimethylated arginine residues. Journal of Molecular Biology, 2003, 327, 507-20 Increased backbone mobility in beta-barrel enhances entropy gain driving binding of N-TIMP-1 to MMP-3. Journal of Molecular Biology, 2003, 327, 1713-34 Spruce budworm antifreeze protein: changes in structure and dynamics at low temperature. Journal of Molecular Biology, 2003, 327, 1713-34 Spruce budworm antif

1539	The N-terminus is unstructured, but not dynamically disordered, in the complex between HK022 Nun protein and lambda-phage BoxB RNA hairpin. 2003 , 553, 95-8		7
1538	The small protein CP12: a protein linker for supramolecular complex assembly. <i>Biochemistry</i> , 2003 , 42, 8163-70	3.2	95
1537	Modular architecture of the bacteriophage T7 primase couples RNA primer synthesis to DNA synthesis. 2003 , 11, 1349-60		90
1536	Global structure and dynamics of human apolipoprotein CII in complex with micelles: evidence for increased mobility of the helix involved in the activation of lipoprotein lipase. <i>Biochemistry</i> , 2003 , 42, 1872-89	3.2	47
1535	Disulfide bond isomerization in basic pancreatic trypsin inhibitor: multisite chemical exchange quantified by CPMG relaxation dispersion and chemical shift modeling. 2003 , 125, 14324-35		127
1534	Mapping chemical exchange in proteins with MW > 50 kD. 2003 , 125, 8968-9		72
1533	Epitope mapping of antigenic MUC1 peptides to breast cancer antibody fragment B27.29: a heteronuclear NMR study. <i>Biochemistry</i> , 2003 , 42, 14293-305	3.2	30
1532	NMR analysis of methyl groups at 100-500 kDa: model systems and Arp2/3 complex. <i>Biochemistry</i> , 2003 , 42, 8579-86	3.2	19
1531	Relaxation-based structure refinement and backbone molecular dynamics of the dynein motor domain-associated light chain. <i>Biochemistry</i> , 2003 , 42, 57-71	3.2	31
1530	Structural basis for the function of the N-terminal domain of the ATPase CopA from Bacillus subtilis. <i>Journal of Biological Chemistry</i> , 2003 , 278, 50506-13	5.4	41
1529	A recombinant chimeric epidermal growth factor-like module with high binding affinity for integrins. <i>Journal of Biological Chemistry</i> , 2003 , 278, 19834-43	5.4	6
1528	Structure and dynamics of the C-domain of human cardiac troponin C in complex with the inhibitory region of human cardiac troponin I. <i>Journal of Biological Chemistry</i> , 2003 , 278, 27024-34	5.4	35
1527	Solution structure of the C-terminal domain of the ciliary neurotrophic factor (CNTF) receptor and ligand free associations among components of the CNTF receptor complex. <i>Journal of Biological Chemistry</i> , 2003 , 278, 23285-94	5.4	17
1526	Solution structure and function of the "tandem inactivation domain" of the neuronal A-type potassium channel Kv1.4. <i>Journal of Biological Chemistry</i> , 2003 , 278, 16142-50	5.4	34
1525	Correlation of the sweetness of variants of the protein brazzein with patterns of hydrogen bonds detected by NMR spectroscopy. <i>Journal of Biological Chemistry</i> , 2003 , 278, 31331-9	5.4	27
1524	A conserved structural motif at the N terminus of bacterial translation initiation factor IF2. <i>Journal of Biological Chemistry</i> , 2003 , 278, 16320-8	5.4	27
1523	NMR elucidation of early folding hierarchy in HIV-1 protease. <i>Journal of Biological Chemistry</i> , 2003 , 278, 19980-5	5.4	29
1522	Interaction of T4 endonuclease V with DNA: importance of the flexible loop regions in protein-DNA interaction. <i>Journal of Biological Chemistry</i> , 2003 , 278, 30985-92	5.4	1

1521	Induction of flexibility through protein-protein interactions. <i>Journal of Biological Chemistry</i> , 2003 , 278, 18581-7	5.4	35
1520	Solution structure of the plant disease resistance-triggering protein NIP1 from the fungus Rhynchosporium secalis shows a novel beta-sheet fold. <i>Journal of Biological Chemistry</i> , 2003 , 278, 4573	0 ⁵ 6 ⁴	19
1519	Lipid-bound structure of an apolipoprotein E-derived peptide. <i>Journal of Biological Chemistry</i> , 2003 , 278, 25998-6006	5.4	26
1518	NMR study of mersacidin and lipid II interaction in dodecylphosphocholine micelles. Conformational changes are a key to antimicrobial activity. <i>Journal of Biological Chemistry</i> , 2003 , 278, 13110-7	5.4	105
1517	NMR solution structure and dynamics of an exchangeable apolipoprotein, Locusta migratoria apolipophorin III. <i>Journal of Biological Chemistry</i> , 2003 , 278, 21212-20	5.4	44
1516	A single-nucleotide natural variation (U4 to C4) in an influenza A virus promoter exhibits a large structural change: implications for differential viral RNA synthesis by RNA-dependent RNA polymerase. <i>Nucleic Acids Research</i> , 2003 , 31, 1216-23	20.1	24
1515	Molecular structure and dynamics of proteins in solution: Insights derived from high-resolution NMR approaches. 2003 , 75, 1371-1381		9
1514	Solution structure of the flexible class II ubiquitin-conjugating enzyme Ubc1 provides insights for polyubiquitin chain assembly. <i>Journal of Biological Chemistry</i> , 2004 , 279, 47139-47	5.4	43
1513	TROSY-based NMR experiments for the study of macromolecular dynamics and hydrogen bonding. 2004 , 278, 161-84		3
1512	Solution structure of the tandem Src homology 3 domains of p47phox in an autoinhibited form. <i>Journal of Biological Chemistry</i> , 2004 , 279, 29752-60	5.4	44
1511	Coupling of folding and binding of thymosin beta4 upon interaction with monomeric actin monitored by nuclear magnetic resonance. <i>Journal of Biological Chemistry</i> , 2004 , 279, 23637-45	5.4	81
1510	Heteronuclear NMR investigations of dynamic regions of intact Escherichia coli ribosomes. 2004 , 101, 10949-54		80
1509	Solution structure and backbone dynamics of the non-receptor protein-tyrosine kinase-6 Src homology 2 domain. <i>Journal of Biological Chemistry</i> , 2004 , 279, 29700-8	5.4	19
1508	The Gly-Gly linker region of the insect cytokine growth-blocking peptide is essential for activity. Journal of Biological Chemistry, 2004 , 279, 51331-7	5.4	5
1507	Solution structure of a ubiquitin-like domain from tubulin-binding cofactor B. <i>Journal of Biological Chemistry</i> , 2004 , 279, 46787-93	5.4	26
1506	Affinity maturation of leukemia inhibitory factor and conversion to potent antagonists of signaling. Journal of Biological Chemistry, 2004 , 279, 2125-34	5.4	25
1505	Structural basis for the attachment of a paramyxoviral polymerase to its template. 2004 , 101, 8301-6		163
1504	Probing nucleotide-binding effects on backbone dynamics and folding of the nucleotide-binding domain of the sarcoplasmic/endoplasmic-reticulum Ca2+-ATPase. 2004 , 379, 235-42		11

1503	The NMR structure of dematin headpiece reveals a dynamic loop that is conformationally altered upon phosphorylation at a distal site. <i>Journal of Biological Chemistry</i> , 2004 , 279, 7909-16	5.4	21
1502	Solution structure of Cox11, a novel type of beta-immunoglobulin-like fold involved in CuB site formation of cytochrome c oxidase. <i>Journal of Biological Chemistry</i> , 2004 , 279, 34833-9	5.4	78
1501	Structure and DNA-binding sites of the SWI1 AT-rich interaction domain (ARID) suggest determinants for sequence-specific DNA recognition. <i>Journal of Biological Chemistry</i> , 2004 , 279, 16670-	6 ^{5.4}	33
1500	Structural and dynamic independence of isopeptide-linked RanGAP1 and SUMO-1. <i>Journal of Biological Chemistry</i> , 2004 , 279, 49131-7	5.4	24
1499	Identification of a SUMO-binding motif that recognizes SUMO-modified proteins. 2004 , 101, 14373-8		459
1498	Solution structures of a cyanobacterial metallochaperone: insight into an atypical copper-binding motif. <i>Journal of Biological Chemistry</i> , 2004 , 279, 27502-10	5.4	45
1497	From structure and dynamics of protein L7/L12 to molecular switching in ribosome. <i>Journal of Biological Chemistry</i> , 2004 , 279, 17697-706	5.4	79
1496	A novel zinc finger structure in the large subunit of human general transcription factor TFIIE. Journal of Biological Chemistry, 2004 , 279, 51395-403	5.4	28
1495	Protein NMR Techniques. 2004,		10
1494	Bacterial IscU is a well folded and functional single domain protein. 2004 , 271, 2093-100		37
1494 1493	Bacterial IscU is a well folded and functional single domain protein. 2004 , 271, 2093-100 Structure, dynamics and interactions of p47, a major adaptor of the AAA ATPase, p97. 2004 , 23, 1463-73	3	37 56
.,,		3	
1493	Structure, dynamics and interactions of p47, a major adaptor of the AAA ATPase, p97. 2004 , 23, 1463-73. Structure and DNA-binding properties of the cytolysin regulator CylR2 from Enterococcus faecalis.	3	56
1493 1492	Structure, dynamics and interactions of p47, a major adaptor of the AAA ATPase, p97. 2004 , 23, 1463-73. Structure and DNA-binding properties of the cytolysin regulator CylR2 from Enterococcus faecalis. 2004 , 23, 3632-42. CBFbeta allosterically regulates the Runx1 Runt domain via a dynamic conformational equilibrium.	5.2	56 32
1493 1492 1491	Structure, dynamics and interactions of p47, a major adaptor of the AAA ATPase, p97. 2004 , 23, 1463-73. Structure and DNA-binding properties of the cytolysin regulator CylR2 from Enterococcus faecalis. 2004 , 23, 3632-42. CBFbeta allosterically regulates the Runx1 Runt domain via a dynamic conformational equilibrium. 2004 , 11, 901-6. Solution structure of the C-terminal domain of Ku80 suggests important sites for protein-protein.	5.2	56 32 54
1493 1492 1491 1490	Structure, dynamics and interactions of p47, a major adaptor of the AAA ATPase, p97. 2004 , 23, 1463-73. Structure and DNA-binding properties of the cytolysin regulator CylR2 from Enterococcus faecalis. 2004 , 23, 3632-42. CBFbeta allosterically regulates the Runx1 Runt domain via a dynamic conformational equilibrium. 2004 , 11, 901-6. Solution structure of the C-terminal domain of Ku80 suggests important sites for protein-protein interactions. <i>Structure</i> , 2004 , 12, 495-502.	5.2	56325449
1493 1492 1491 1490	Structure, dynamics and interactions of p47, a major adaptor of the AAA ATPase, p97. 2004 , 23, 1463-73. Structure and DNA-binding properties of the cytolysin regulator CylR2 from Enterococcus faecalis. 2004 , 23, 3632-42 CBFbeta allosterically regulates the Runx1 Runt domain via a dynamic conformational equilibrium. 2004 , 11, 901-6 Solution structure of the C-terminal domain of Ku80 suggests important sites for protein-protein interactions. <i>Structure</i> , 2004 , 12, 495-502 The oxidized subunit B8 from human complex I adopts a thioredoxin fold. <i>Structure</i> , 2004 , 12, 1645-54	5.2	5632544928

1485	The response of internal dynamics to hydrophobic core mutations in the SH3 domain from the Fyn tyrosine kinase. <i>Protein Science</i> , 2004 , 13, 1088-99	34
1484	1H, 13C and 15N backbone resonance assignments of the dimeric yeast peroxiredoxin YLR109w. 2004 , 28, 95-6	1
1483	Temperature-dependent spectral density analysis applied to monitoring backbone dynamics of major urinary protein-I complexed with the pheromone 2- sec-butyl-4,5-dihydrothiazole. 2004 , 28, 369-84	47
1482	Characterization of threonine side chain dynamics in an antifreeze protein using natural abundance 13C NMR spectroscopy. 2004 , 29, 139-50	11
1481	Binding ability of a HHP-tagged protein towards Ni2+ studied by paramagnetic NMR relaxation: the possibility of obtaining long-range structure information. 2004 , 29, 175-85	25
1480	NMR structural characterization of the N-terminal domain of the adenylyl cyclase-associated protein (CAP) from Dictyostelium discoideum. 2004 , 29, 73-84	15
1479	Site-specific labelling with a metal chelator for protein-structure refinement. 2004 , 29, 351-61	75
1478	Characterisation of a mobile protein-binding epitope in the translocation domain of colicin E9. 2004 , 30, 81-96	16
1477	(1)H, (13)C and (15)N NMR assignment of the homodimeric poplar phloem type II peroxiredoxin. 2004 , 30, 105-6	5
1476	1H, 13C and 15N resonance assignments of poplar phloem glutaredoxin. 2004 , 30, 219-20	1
1475	Measurement of 15N csa/dipolar cross-correlation rates by means of Spin State Selective experiments. 2004 , 30, 133-42	2
1474	Alzheimerls disease: NMR studies of asialo (GM1) and trisialo (GT1b) ganglioside interactions with Abeta(1-40) peptide in a membrane mimic environment. 2004 , 29, 447-53	30
1473	Determination of protein rotational correlation time from NMR relaxation data at various solvent viscosities. 2004 , 30, 431-42	19
1472	Solution structure of hypothetical Nudix hydrolase DR0079 from extremely radiation-resistant Deinococcus radiodurans bacterium. 2004 , 56, 28-39	5
1471	Structure and dynamics of the human pleckstrin DEP domain: distinct molecular features of a novel DEP domain subfamily. 2005 , 58, 354-66	25
1470	Comparison of backbone dynamics of monomeric and domain-swapped stefin A. 2004 , 54, 500-12	13
1469	The solution structure of ChaB, a putative membrane ion antiporter regulator from Escherichia coli. 2004 , 4, 9	15
1468	Determination of the electron relaxation rates in paramagnetic metal complexes: applicability of available NMR methods. 2004 , 167, 169-77	8

1467	Product operator analysis of the influence of chemical exchange on relaxation rates. 2004, 171, 330-7		14
1466	The role of protein motions in molecular recognition: insights from heteronuclear NMR relaxation measurements. 2004 , 44, 141-187		42
1465	Changes in structural dynamics of the Grb2 adaptor protein upon binding of phosphotyrosine ligand to its SH2 domain. 2004 , 1700, 53-64		21
1464	Preliminary structural characterisation of the 33 kDa protein (PsbO) in solution studied by site-directed mutagenesis and NMR spectroscopy. 2004 , 6, 4878-4881		22
1463	The structure and dynamics of tandem WW domains in a negative regulator of notch signaling, Suppressor of deltex. <i>Journal of Biological Chemistry</i> , 2004 , 279, 34991-5000	5.4	33
1462	Long-range dynamic effects of point mutations propagate through side chains in the serine protease inhibitor eglin c. <i>Biochemistry</i> , 2004 , 43, 12448-58	3.2	71
1461	Consequences of binding an S-adenosylmethionine analogue on the structure and dynamics of the thiopurine methyltransferase protein backbone. <i>Biochemistry</i> , 2004 , 43, 12198-209	3.2	30
1460	Dynamic characterization of a DNA repair enzyme: NMR studies of [methyl-13C]methionine-labeled DNA polymerase beta. <i>Biochemistry</i> , 2004 , 43, 8911-22	3.2	50
1459	Transient aggregation and stable dimerization induced by introducing an Alzheimer sequence into a water-soluble protein. <i>Biochemistry</i> , 2004 , 43, 12964-78	3.2	16
1458	Characterization of micros-ms dynamics of proteins using a combined analysis of 15N NMR relaxation and chemical shift: conformational exchange in plastocyanin induced by histidine protonations. 2004 , 126, 753-65		36
1457	Solution structure and backbone dynamics of the K18G/R82E Alicyclobacillus acidocaldarius thioredoxin mutant: a molecular analysis of its reduced thermal stability. <i>Biochemistry</i> , 2004 , 43, 6043-5	8 ^{3.2}	21
1456	The N-terminal domain of the Drosophila histone mRNA binding protein, SLBP, is intrinsically disordered with nascent helical structure. <i>Biochemistry</i> , 2004 , 43, 9390-400	3.2	17
1455	NMR structural studies reveal a novel protein fold for MerB, the organomercurial lyase involved in the bacterial mercury resistance system. <i>Biochemistry</i> , 2004 , 43, 8322-32	3.2	33
1454	Solution structure and backbone dynamics of the N-terminal region of the calcium regulatory domain from soybean calcium-dependent protein kinase alpha. <i>Biochemistry</i> , 2004 , 43, 15131-40	3.2	4
1453	Same fold with different mobility: backbone dynamics of small protease inhibitors from the desert locust, Schistocerca gregaria. <i>Biochemistry</i> , 2004 , 43, 3376-84	3.2	25
1452	Effect of temperature on the structure of trout troponin C. <i>Biochemistry</i> , 2004 , 43, 4955-63	3.2	17
1451	Structure determination of membrane proteins by NMR spectroscopy. <i>Chemical Reviews</i> , 2004 , 104, 358	7860 6	368
1450	The N-terminal domain (IF2N) of bacterial translation initiation factor IF2 is connected to the conserved C-terminal domains by a flexible linker. <i>Protein Science</i> , 2004 , 13, 230-9	6.3	17

Biophysical characterization of Z(SPA-1)a phage-display selected binder to protein A. <i>Protein Science</i> , 2004 , 13, 2078-88	23
Solution structure of the human Grb14-SH2 domain and comparison with the structures of the human Grb7-SH2/erbB2 peptide complex and human Grb10-SH2 domain. <i>Protein Science</i> , 2004 , 13, 2541-63	3
C-terminal domain of insulin-like growth factor (IGF) binding protein 6: conformational exchange and its correlation with IGF-II binding. <i>Biochemistry</i> , 2004 , 43, 11187-95	15
(1)H/(15)N heteronuclear NMR spectroscopy shows four dynamic domains for phospholamban reconstituted in dodecylphosphocholine micelles. <i>Biophysical Journal</i> , 2004 , 87, 1205-14	68
1445 NMR R1 rho rotating-frame relaxation with weak radio frequency fields. 2004 , 126, 2247-56	128
Solution structure of coactosin reveals structural homology to ADF/cofilin family proteins. 2004 , 1444 576, 91-6	20
Diffusion and dynamics of penetratin in different membrane mimicking media. 2004 , 1661, 18-25	44
NMR evidence for independent domain structures in zoocin A, an antibacterial exoenzyme. 2004 , 317, 527-30	4
Distinctive features in the structure and dynamics of the DNA repeat sequence GGCGGG. 2004 , 317, 625-33	9
Human programmed cell death 5 protein has a helical-core and two dissociated structural regions. 2004 , 318, 391-6	13
An atomic resolution model for assembly, architecture, and function of the Dr adhesins. 2004 , 15, 647-57	97
Backbone dynamic properties of the central linker region of calcium-calmodulin in 35% trifluoroethanol. 2004 , 146, 272-80	14
1437 Backbone dynamics of oxidised and reduced forms of human atrial natriuretic peptide. 2004 , 148, 214-25	6
1436 Altering the RNA-binding mode of the U1A RBD1 protein. <i>Journal of Molecular Biology</i> , 2004 , 335, 465-8 % .5	31
Ligand-dependent dynamics and intramolecular signaling in a PDZ domain. <i>Journal of Molecular Biology</i> , 2004 , 335, 1105-15	193
The solution structure of ribosomal protein L18 from Bacillus stearothermophilus. <i>Journal of</i> Molecular Biology, 2004 , 335, 679-84 6.5	7
Insights into conformation and dynamics of protein GB1 during folding and unfolding by NMR. Journal of Molecular Biology, 2004 , 335, 1299-307 6.5	72
NMR studies on the substrate-binding domains of the thermosome: structural plasticity in the protrusion region. <i>Journal of Molecular Biology</i> , 2004 , 336, 717-29	16

1431	Structural basis for telomeric single-stranded DNA recognition by yeast Cdc13. <i>Journal of Molecular Biology</i> , 2004 , 338, 241-55	6.5	83
1430	Two homologous domains of similar structure but different stability in the yeast linker histone, Hho1p. <i>Journal of Molecular Biology</i> , 2004 , 338, 139-48	6.5	25
1429	Multiple time scale backbone dynamics of homologous thermophilic and mesophilic ribonuclease HI enzymes. <i>Journal of Molecular Biology</i> , 2004 , 339, 855-71	6.5	71
1428	Structural characterization of the RNase E S1 domain and identification of its oligonucleotide-binding and dimerization interfaces. <i>Journal of Molecular Biology</i> , 2004 , 341, 37-54	6.5	43
1427	The solution structure of the S.cerevisiae Ste11 MAPKKK SAM domain and its partnership with Ste50. <i>Journal of Molecular Biology</i> , 2004 , 342, 681-93	6.5	21
1426	Dynamics of ATP-binding cassette contribute to allosteric control, nucleotide binding and energy transduction in ABC transporters. <i>Journal of Molecular Biology</i> , 2004 , 342, 525-37	6.5	64
1425	The NMR solution structure of a mutant of the Max b/HLH/LZ free of DNA: insights into the specific and reversible DNA binding mechanism of dimeric transcription factors. <i>Journal of Molecular Biology</i> , 2004 , 342, 813-32	6.5	38
1424	Diversity in structure and function of the Ets family PNT domains. <i>Journal of Molecular Biology</i> , 2004 , 342, 1249-64	6.5	45
1423	Gated electron transfers and electron pathways in azurin: a NMR dynamic study at multiple fields and temperatures. <i>Journal of Molecular Biology</i> , 2004 , 342, 1599-611	6.5	29
1422	Solution NMR structure of the iron-sulfur cluster assembly protein U (IscU) with zinc bound at the active site. <i>Journal of Molecular Biology</i> , 2004 , 344, 567-83	6.5	121
1421	NMR characterization of full-length farnesylated and non-farnesylated H-Ras and its implications for Raf activation. <i>Journal of Molecular Biology</i> , 2004 , 343, 1391-408	6.5	93
1420	Solution structure of the dimeric SAM domain of MAPKKK Ste11 and its interactions with the adaptor protein Ste50 from the budding yeast: implications for Ste11 activation and signal transmission through the Ste50-Ste11 complex. <i>Journal of Molecular Biology</i> , 2004 , 344, 1071-87	6.5	32
1419	Solution structure of the ubiquitin-conjugating enzyme UbcH5B. <i>Journal of Molecular Biology</i> , 2004 , 344, 513-26	6.5	30
1418	The solution structure of the SODD BAG domain reveals additional electrostatic interactions in the HSP70 complexes of SODD subfamily BAG domains. 2004 , 558, 101-6		12
1417	The folding pathway of barnase: the rate-limiting transition state and a hidden intermediate under native conditions. <i>Biochemistry</i> , 2004 , 43, 3346-56	3.2	43
1416	Thermodynamics of binding of 2-methoxy-3-isopropylpyrazine and 2-methoxy-3-isobutylpyrazine to the major urinary protein. 2004 , 126, 1675-81		100
1415	Probing Zn2+-binding effects on the zinc-ribbon domain of human general transcription factor TFIIB. 2004 , 378, 317-24		15
1414	The N-terminal 26-residue fragment of human programmed cell death 5 protein can form a stable alpha-helix having unique electrostatic potential character. 2005 , 392, 47-54		15

1413 Protein Dynamics. **2005**, 245-262

	Binding of a diphosphorylated-ITAM peptide to spleen tyrosine kinase (Syk) induces distal		
1412	conformational changes: a hydrogen exchange mass spectrometry study. 2005 , 16, 1039-51		15
1411	Recent progress in the study of biomolecular structure and dynamics in solution from residual dipolar couplings. 2005 , 46, 23-61		247
1410	Solution structure and backbone dynamics of Calsensin, an invertebrate neuronal calcium-binding protein. <i>Protein Science</i> , 2005 , 14, 1894-901	6.3	5
1409	Solution structure of the ubiquitin-like domain of human DC-UbP from dendritic cells. <i>Protein Science</i> , 2005 , 14, 2044-50	6.3	7
1408	Solution structure of thioredoxin h1 from Arabidopsis thaliana. <i>Protein Science</i> , 2005 , 14, 2195-200	6.3	26
1407	Rapid and accurate structure determination of coiled-coil domains using NMR dipolar couplings: application to cGMP-dependent protein kinase Ialpha. <i>Protein Science</i> , 2005 , 14, 2421-8	6.3	41
1406	Structure and chromosomal DNA binding of the SWIRM domain. 2005 , 12, 1078-85		50
1405	The structure of the flock house virus B2 protein, a viral suppressor of RNA interference, shows a novel mode of double-stranded RNA recognition. 2005 , 6, 1149-55		107
1404	Solution structure and internal dynamics of NSCP, a compact calcium-binding protein. 2005 , 272, 2022-3	36	8
1403	Probing the supramodular architecture of a multidomain protein: the structure of syntenin in solution. <i>Structure</i> , 2005 , 13, 319-27	5.2	14
1402	The solution structure of a transient photoreceptor intermediate: Delta25 photoactive yellow protein. <i>Structure</i> , 2005 , 13, 953-62	5.2	68
1401	Structural and dynamic consequences of increasing repeats in a MUC1 peptide tumor antigen. 2005 , 77, 107-20		9
1400	Characterisation of disulfide-bond dynamics in non-native states of lysozyme and its disulfide deletion mutants by NMR. 2005 , 6, 1619-27		22
1399	Elucidation of the relationship between enzyme activity and internal motion using a lysozyme stabilized by cavity-filling mutations. <i>Cellular and Molecular Life Sciences</i> , 2005 , 62, 1047-55	10.3	10
1398	Temperature-dependent protein backbone dynamics from auto- and cross-correlated NMR relaxation rates. 2005 , 28, 147-163		
1397	Structure of calmodulin complexed with an olfactory CNG channel fragment and role of the central linker: residual dipolar couplings to evaluate calmodulin binding modes outside the kinase family. 2005 , 31, 185-99		40
1396	Residue specific ribose and nucleobase dynamics of the cUUCGg RNA tetraloop motif by MNMR 13C relaxation. 2005 , 32, 295-308		56

1395	Backbone chemical shift assignments of the LexA catalytic domain in its active conformation. 2005 , 31, 371-2		2
1394	Solution structure of an antifreeze protein CfAFP-501 from Choristoneura fumiferana. 2005 , 32, 251-6		11
1393	Helicobacter pylori protein HP0222 belongs to Arc/MetJ family of transcriptional regulators. 2005 , 59, 303-11		13
1392	Methyl dynamics for understanding hydrophobic core packing of dynamically different motifs of double-stranded RNA binding domain of protein kinase R. 2006 , 62, 501-8		5
1391	Folding regulates autoprocessing of HIV-1 protease precursor. <i>Journal of Biological Chemistry</i> , 2005 , 280, 11369-78	5.4	33
1390	Structural and functional characteristics of the Val44Met insulin-like growth factor I missense mutation: correlation with effects on growth and development. 2005 , 19, 711-21		60
1389	A novel galectin-like domain from Toxoplasma gondii micronemal protein 1 assists the folding, assembly, and transport of a cell adhesion complex. <i>Journal of Biological Chemistry</i> , 2005 , 280, 38583-91	₁ 5·4	62
1388	Comparison of structure and dynamics of micelle-bound human alpha-synuclein and Parkinson disease variants. <i>Journal of Biological Chemistry</i> , 2005 , 280, 43179-87	5.4	128
1387	The structural and dynamic basis of Ets-1 DNA binding autoinhibition. <i>Journal of Biological Chemistry</i> , 2005 , 280, 7088-99	5.4	80
1386	NMR structure of the first PHD finger of autoimmune regulator protein (AIRE1). Insights into autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED) disease. <i>Journal of Biological Chemistry</i> , 2005 , 280, 11505-12	5.4	69
1385	The serine-rich domain from Crk-associated substrate (p130cas) is a four-helix bundle. <i>Journal of Biological Chemistry</i> , 2005 , 280, 21908-14	5.4	23
1384	Calcium-dependent changes in the flexibility of the regulatory domain of troponin C in the troponin complex. <i>Journal of Biological Chemistry</i> , 2005 , 280, 21924-32	5.4	32
1383	Solution structures and backbone dynamics of arsenate reductase from Bacillus subtilis: reversible conformational switch associated with arsenate reduction. <i>Journal of Biological Chemistry</i> , 2005 , 280, 39601-8	5.4	15
1382	Protein-Protein Recognition in Phosphotyrosine-Mediated Intracellular Signaling. 2005, 165-184		10
1381	Proteomics and Protein-Protein Interactions. 2005,		10
1380	Structural characterization of the antimicrobial peptide pleurocidin from winter flounder. <i>Biochemistry</i> , 2005 , 44, 7282-93	3.2	51
1379	Dynamic properties of biologically active synthetic heparin-like hexasaccharides. 2005 , 15, 1008-15		33
1378	NMR structure and Mg2+ binding of an RNA segment that underlies the L7/L12 stalk in the E.coli 50S ribosomal subunit. <i>Nucleic Acids Research</i> , 2005 , 33, 3145-53	20.1	5

(2005-2005)

1377	Structure of the bundle-forming pilus from enteropathogenic Escherichia coli. <i>Journal of Biological Chemistry</i> , 2005 , 280, 40252-60	5.4	46
1376	High-resolution NMR studies of encapsulated proteins in liquid ethane. 2005 , 127, 10176-7		32
1375	Changes in calmodulin main-chain dynamics upon ligand binding revealed by cross-correlated NMR relaxation measurements. 2005 , 127, 828-9		37
1374	The structure of phospholamban pentamer reveals a channel-like architecture in membranes. 2005 , 102, 10870-5		286
1373	Serine 16 phosphorylation induces an order-to-disorder transition in monomeric phospholamban. <i>Biochemistry</i> , 2005 , 44, 4386-96	3.2	69
1372	NMR dynamics-derived insights into the binding properties of a peptide interacting with an SH2 domain. <i>Biochemistry</i> , 2005 , 44, 694-703	3.2	27
1371	NMR investigation of main-chain dynamics of the H80E mutant of bovine neurophysin-I: demonstration of dimerization-induced changes at the hormone-binding site. <i>Biochemistry</i> , 2005 , 44, 11766-76	3.2	3
1370	Backbone and side chain dynamics of mutant calmodulin-peptide complexes. <i>Biochemistry</i> , 2005 , 44, 12627-39	3.2	27
1369	Dynamics of hyaluronan oligosaccharides revealed by 15N relaxation. 2005 , 127, 1086-7		29
1368	Stability junction at a common mutation site in the collagenous domain of the mannose binding lectin. <i>Biochemistry</i> , 2005 , 44, 1793-9	3.2	9
1367	Solution structure and interactions of the Escherichia coli cell division activator protein CedA. <i>Biochemistry</i> , 2005 , 44, 6738-44	3.2	5
1366	Microsecond-to-millisecond conformational dynamics demarcate the GluR2 glutamate receptor bound to agonists glutamate, quisqualate, and AMPA. <i>Biochemistry</i> , 2005 , 44, 3410-7	3.2	36
1365	PhosphoThr peptide binding globally rigidifies much of the FHA domain from Arabidopsis receptor kinase-associated protein phosphatase. <i>Biochemistry</i> , 2005 , 44, 10119-34	3.2	21
1364	A copper(I) protein possibly involved in the assembly of CuA center of bacterial cytochrome c oxidase. 2005 , 102, 3994-9		80
1363	Limited variations in 15N CSA magnitudes and orientations in ubiquitin are revealed by joint analysis of longitudinal and transverse NMR relaxation. 2005 , 127, 1995-2005		36
1362	Main chain and side chain dynamics of the ubiquitin conjugating enzyme variant human Mms2 in the free and ubiquitin-bound States. <i>Biochemistry</i> , 2005 , 44, 8770-81	3.2	16
1361	Dissecting the domain structure of Cdc4p, a myosin essential light chain involved in Schizosaccharomyces pombe cytokinesis. <i>Biochemistry</i> , 2005 , 44, 12136-48	3.2	4
1360	Stability and flexibility in the structure of the hyperthermophile DNA-binding protein Sac7d. <i>Biochemistry</i> , 2005 , 44, 13500-9	3.2	8

1359	A new spin probe of protein dynamics: nitrogen relaxation in 15N-2H amide groups. 2005 , 127, 3220-9		12
1358	Protein dynamics in living cells. <i>Biochemistry</i> , 2005 , 44, 9275-9	3.2	41
1357	Solution structure of the ligand binding domain of the fibroblast growth factor receptor: role of heparin in the activation of the receptor. <i>Biochemistry</i> , 2005 , 44, 15787-98	3.2	27
1356	Structure and dynamics of micelle-bound human alpha-synuclein. <i>Journal of Biological Chemistry</i> , 2005 , 280, 9595-603	5.4	637
1355	The solution structure of the C-terminal domain of TonB and interaction studies with TonB box peptides. <i>Journal of Molecular Biology</i> , 2005 , 345, 1185-97	6.5	87
1354	Dynamics in the unfolded state of beta2-microglobulin studied by NMR. <i>Journal of Molecular Biology</i> , 2005 , 346, 279-94	6.5	88
1353	Protein and RNA dynamics play key roles in determining the specific recognition of GU-rich polyadenylation regulatory elements by human Cstf-64 protein. <i>Journal of Molecular Biology</i> , 2005 , 347, 719-33	6.5	51
1352	NMR snapshots of a fluctuating protein structure: ubiquitin at 30 bar-3 kbar. <i>Journal of Molecular Biology</i> , 2005 , 347, 277-85	6.5	138
1351	Molecular mechanism underlying the thermal stability and pH-induced unfolding of CHABII. <i>Journal of Molecular Biology</i> , 2005 , 348, 205-18	6.5	28
1350	Solution structure and backbone dynamics of the KH-QUA2 region of the Xenopus STAR/GSG quaking protein. <i>Journal of Molecular Biology</i> , 2005 , 348, 265-79	6.5	28
1349	The native energy landscape for interleukin-1beta. Modulation of the population ensemble through native-state topology. <i>Journal of Molecular Biology</i> , 2005 , 348, 335-47	6.5	30
1348	Engineering the structural stability and functional properties of the GI domain into the intrinsically unfolded GII domain of the yeast linker histone Hho1p. <i>Journal of Molecular Biology</i> , 2005 , 349, 608-20	6.5	8
1347	Dynamics and metal exchange properties of C4C4 RING domains from CNOT4 and the p44 subunit of TFIIH. <i>Journal of Molecular Biology</i> , 2005 , 349, 621-37	6.5	20
1346	13C NMR relaxation studies of RNA base and ribose nuclei reveal a complex pattern of motions in the RNA binding site for human U1A protein. <i>Journal of Molecular Biology</i> , 2005 , 349, 699-715	6.5	53
1345	Solution structure of the symmetric coiled coil tetramer formed by the oligomerization domain of hnRNP C: implications for biological function. <i>Journal of Molecular Biology</i> , 2005 , 350, 319-37	6.5	31
1344	Structure and inter-domain interactions of domain II from the blood-stage malarial protein, apical membrane antigen 1. <i>Journal of Molecular Biology</i> , 2005 , 350, 641-56	6.5	29
1343	NMR reveals a novel glutaredoxin-glutaredoxin interaction interface. <i>Journal of Molecular Biology</i> , 2005 , 353, 629-41	6.5	24
1342	The structure of the C5a receptor-blocking domain of chemotaxis inhibitory protein of Staphylococcus aureus is related to a group of immune evasive molecules. <i>Journal of Molecular Biology</i> , 2005 , 353, 859-72	6.5	53

(2006-2005)

1341	Structure, dynamics, and membrane topology of stannin: a mediator of neuronal cell apoptosis induced by trimethyltin chloride. <i>Journal of Molecular Biology</i> , 2005 , 354, 652-65	6.5	46
1340	The neural repressor NRSF/REST binds the PAH1 domain of the Sin3 corepressor by using its distinct short hydrophobic helix. <i>Journal of Molecular Biology</i> , 2005 , 354, 903-15	6.5	62
1339	Solution structure of isoform 1 of Roadblock/LC7, a light chain in the dynein complex. <i>Journal of Molecular Biology</i> , 2005 , 354, 1043-51	6.5	24
1338	Characterization of the PR domain of RIZ1 histone methyltransferase. 2005 , 333, 925-34		46
1337	Solution-state NMR investigation of DNA binding interactions in Escherichia coli formamidopyrimidine-DNA glycosylase (Fpg): a dynamic description of the DNA/protein interface. 2005 , 4, 327-39		21
1336	NMR structure and regulated expression in APL cell of human SH3BGRL3. 2005 , 579, 2788-94		18
1335	The solution structure of an N-terminally truncated version of the yeast CDC24p PB1 domain shows a different beta-sheet topology. 2005 , 579, 3534-8		3
1334	Crystal structure and solution NMR dynamics of a D (type II) peroxiredoxin glutaredoxin and thioredoxin dependent: a new insight into the peroxiredoxin oligomerism. <i>Biochemistry</i> , 2005 , 44, 1755	- <i>67</i>	48
1333	Dynamics of the fragment of thrombomodulin containing the fourth and fifth epidermal growth factor-like domains correlate with function. <i>Biochemistry</i> , 2005 , 44, 1225-33	3.2	8
1332	Microsecond timescale backbone conformational dynamics in ubiquitin studied with NMR R1rho relaxation experiments. <i>Protein Science</i> , 2005 , 14, 735-42	6.3	113
1331	Backbone dynamics of a symmetric calmodulin dimer in complex with the calmodulin-binding domain of the basic-helix-loop-helix transcription factor SEF2-1/E2-2: a highly dynamic complex. <i>Biophysical Journal</i> , 2005 , 89, 1214-26	2.9	13
1330	Direct determination of a membrane-peptide interface using the nuclear magnetic resonance cross-saturation method. <i>Biophysical Journal</i> , 2005 , 89, 4051-5	2.9	10
1329	NMR structure determination of a membrane protein with two transmembrane helices in micelles: MerF of the bacterial mercury detoxification system. <i>Biochemistry</i> , 2005 , 44, 5196-206	3.2	98
1328	Role of structural plasticity in signal transduction by the cryptochrome blue-light photoreceptor. <i>Biochemistry</i> , 2005 , 44, 3795-805	3.2	151
1327	Backbone dynamics of the olfactory marker protein as studied by 15N NMR relaxation measurements. <i>Biochemistry</i> , 2005 , 44, 9673-9	3.2	8
1326	Fast time scale dynamics of protein backbones: NMR relaxation methods, applications, and functional consequences. <i>Chemical Reviews</i> , 2006 , 106, 1624-71	68.1	327
1325	Structural plasticity of peptidyl-prolyl isomerase sFkpA is a key to its chaperone function as revealed by solution NMR. <i>Biochemistry</i> , 2006 , 45, 11983-91	3.2	29
1324	Structure, dynamics, and stability variation in bacterial albumin binding modules: implications for species specificity. <i>Biochemistry</i> , 2006 , 45, 10102-9	3.2	29

1323	Salt enhances calmodulin-target interaction. <i>Biophysical Journal</i> , 2006 , 90, 2903-10	2.9	19
1322	Local structural preferences and dynamics restrictions in the urea-denatured state of SUMO-1: NMR characterization. <i>Biophysical Journal</i> , 2006 , 90, 2498-509	2.9	15
1321	Dynamics of the C-terminal region of TnI in the troponin complex in solution. <i>Biophysical Journal</i> , 2006 , 90, 2436-44	2.9	45
1320	NMR solution structure and backbone dynamics of domain III of the E protein of tick-borne Langat flavivirus suggests a potential site for molecular recognition. <i>Protein Science</i> , 2006 , 15, 1342-55	6.3	20
1319	pH driven conformational dynamics and dimer-to-monomer transition in DLC8. <i>Protein Science</i> , 2006 , 15, 335-42	6.3	33
1318	Solution structure and backbone dynamics of an N-terminal ubiquitin-like domain in the GLUT4-regulating protein, TUG. <i>Protein Science</i> , 2006 , 15, 498-508	6.3	14
1317	A statistical thermodynamic model of the protein ensemble. <i>Chemical Reviews</i> , 2006 , 106, 1545-58	68.1	166
1316	The conformation of cyclo(-D-Pro-Ala4-) as a model for cyclic pentapeptides of the DL4 type. 2006 , 128, 13806-14		46
1315	Analysis and parametric optimization of 1H off-resonance relaxation NMR experiments designed to map polypeptide self-recognition and other noncovalent interactions. 2006 , 110, 20664-70		6
1314	Characterization of the dynamics of biomacromolecules using rotating-frame spin relaxation NMR spectroscopy. <i>Chemical Reviews</i> , 2006 , 106, 1700-19	68.1	256
1313	Probing methyl dynamics from 13C autocorrelated and cross-correlated relaxation. 2006 , 128, 5073-81		22
1312	Streptococcal M protein: structural studies of the hypervariable region, free and bound to human C4BP. <i>Biochemistry</i> , 2006 , 45, 4559-68	3.2	29
1311	Micelle-induced folding of spinach thylakoid soluble phosphoprotein of 9 kDa and its functional implications. <i>Biochemistry</i> , 2006 , 45, 15633-43	3.2	14
1310	Analysis of ligand binding and protein dynamics of human retinoid X receptor alpha ligand-binding domain by nuclear magnetic resonance. <i>Biochemistry</i> , 2006 , 45, 1629-39	3.2	35
1309	B-myc: N-terminal recognition of myc binding proteins. <i>Biochemistry</i> , 2006 , 45, 9857-65	3.2	12
1308	An isolated helix persists in a sparsely populated form of KIX under native conditions. <i>Biochemistry</i> , 2006 , 45, 8885-93	3.2	27
1307	Comparison between the backbone dynamics of an 11-amino acid peptide sequence in alpha-helical and beta-hairpin structural contexts. <i>Biochemistry</i> , 2006 , 45, 11179-89	3.2	1
1306	Chemical shift tensors of protonated base carbons in helical RNA and DNA from NMR relaxation and liquid crystal measurements. 2006 , 128, 11443-54		39

(2006-2006)

1305	Conformational dynamics of calmodulin in complex with the calmodulin-dependent kinase kinase alpha calmodulin-binding domain. <i>Biochemistry</i> , 2006 , 45, 8732-41	3.2	27
1304	A trade between similar but nonequivalent intrasubunit and intersubunit contacts in Cro dimer evolution. <i>Biochemistry</i> , 2006 , 45, 6379-91	3.2	11
1303	Solution structure and folding characteristics of the C-terminal SH3 domain of c-Crk-II. <i>Biochemistry</i> , 2006 , 45, 8874-84	3.2	37
1302	Solution structures of conformationally equilibrium forms of holo-acyl carrier protein (PfACP) from Plasmodium falciparum provides insight into the mechanism of activation of ACPs. <i>Biochemistry</i> , 2006 , 45, 6904-16	3.2	59
1301	Solution structure and dynamics of human metallothionein-3 (MT-3). 2006, 580, 795-800		61
1300	The HAMP domain structure implies helix rotation in transmembrane signaling. 2006 , 126, 929-40		326
1299	Effect of hsp70 chaperone on the folding and misfolding of polypeptides modeling an elongating protein chain. <i>Journal of Molecular Biology</i> , 2006 , 355, 809-20	6.5	27
1298	Characterizing a partially folded intermediate of the villin headpiece domain under non-denaturing conditions: contribution of His41 to the pH-dependent stability of the N-terminal subdomain. Journal of Molecular Biology, 2006 , 355, 1078-94	6.5	63
1297	Structural basis for metal binding specificity: the N-terminal cadmium binding domain of the P1-type ATPase CadA. <i>Journal of Molecular Biology</i> , 2006 , 356, 638-50	6.5	54
1296	A new solution structure of ATP synthase subunit c from thermophilic Bacillus PS3, suggesting a local conformational change for H+-translocation. <i>Journal of Molecular Biology</i> , 2006 , 358, 132-44	6.5	29
1295	Effects of calcium binding on the side-chain methyl dynamics of calbindin D9k: a 2H NMR relaxation study. <i>Journal of Molecular Biology</i> , 2006 , 357, 1237-52	6.5	19
1294	Structure and functional analysis of the MYND domain. <i>Journal of Molecular Biology</i> , 2006 , 358, 498-508	3 6.5	30
1293	Defining the intramembrane binding mechanism of sarcolipin to calcium ATPase using solution NMR spectroscopy. <i>Journal of Molecular Biology</i> , 2006 , 358, 420-9	6.5	48
1292	Residue-level NMR view of the urea-driven equilibrium folding transition of SUMO-1 (1-97): native preferences do not increase monotonously. <i>Journal of Molecular Biology</i> , 2006 , 361, 180-94	6.5	12
1291	The DICE-binding activity of KH domain 3 of hnRNP K is affected by c-Src-mediated tyrosine phosphorylation. <i>Journal of Molecular Biology</i> , 2006 , 361, 470-81	6.5	38
1290	A novel haem-binding interface in the 22 kDa haem-binding protein p22HBP. <i>Journal of Molecular Biology</i> , 2006 , 362, 287-97	6.5	8
1289	Binding site structure of one LRP-RAP complex: implications for a common ligand-receptor binding motif. <i>Journal of Molecular Biology</i> , 2006 , 362, 700-16	6.5	53
1288	Mis-translation of a computationally designed protein yields an exceptionally stable homodimer: implications for protein engineering and evolution. <i>Journal of Molecular Biology</i> , 2006 , 362, 1004-24	6.5	26

1287	Evaluation of energetic and dynamic coupling networks in a PDZ domain protein. <i>Journal of Molecular Biology</i> , 2006 , 364, 337-51	6.5	100
1286	Structure, dynamics and heparin binding of the C-terminal domain of insulin-like growth factor-binding protein-2 (IGFBP-2). <i>Journal of Molecular Biology</i> , 2006 , 364, 690-704	6.5	45
1285	Characterisation of the conformational properties of urea-unfolded Im7: implications for the early stages of protein folding. <i>Journal of Molecular Biology</i> , 2006 , 364, 824-35	6.5	38
1284	Abeta42 is more rigid than Abeta40 at the C terminus: implications for Abeta aggregation and toxicity. <i>Journal of Molecular Biology</i> , 2006 , 364, 853-62	6.5	214
1283	A mutation in the S-switch region of the Runt domain alters the dynamics of an allosteric network responsible for CBFbeta regulation. <i>Journal of Molecular Biology</i> , 2006 , 364, 1073-83	6.5	11
1282	Biomolecular Dynamics: Testing Microscopic Predictions against Macroscopic Experiments. 2006 , 156-1	69	1
1281	Modern High Resolution NMR for the Study of Structure, Dynamics and Interactions of Biological Macromolecules. 2006 , 220, 567-613		13
1280	Solution structure of Arabidopsis thaliana protein At5g39720.1, a member of the AIG2-like protein family. 2006 , 62, 490-3		6
1279	Effect of a mutation on the structure and dynamics of an alpha-helical antifreeze protein in water and ice. 2006 , 63, 603-10		6
1278	Accessibility of tobacco lipid transfer protein cavity revealed by 15N NMR relaxation studies and molecular dynamics simulations. 2006 , 64, 124-32		9
1277	Determination of dihedral Psi angles in large proteins by combining NH(N)/C(alpha)H(alpha) dipole/dipole cross-correlation and chemical shifts. 2006 , 64, 931-9		4
1276	The DC-module of doublecortin: dynamics, domain boundaries, and functional implications. 2006 , 64, 874-82		12
1275	NMR structure and binding studies confirm that PA4608 from Pseudomonas aeruginosa is a PilZ domain and a c-di-GMP binding protein. 2007 , 66, 266-71		63
1274	Local binding with globally distributed changes in a small protease inhibitor upon enzyme binding. 2006 , 273, 1831-42		5
1273	Monomeric solution structure of the helicase-binding domain of Escherichia coli DnaG primase. 2006 , 273, 4997-5009		25
1272	The solution structure of the invasive tip complex from Afa/Dr fibrils. 2006 , 62, 356-66		38
1271	The SPRY domain of SSB-2 adopts a novel fold that presents conserved Par-4-binding residues. 2006 , 13, 77-84		68
1270	NMR spectra of oligosaccharides at ultra-high field (900 MHz) have better resolution than expected due to favourable molecular tumbling. 2006 , 341, 1985-91		14

(2006-2006)

Solution structure of Asl1650, an acyl carrier protein from Anabaena sp. PCC 7120 with a variant phosphopantetheinylation-site sequence. <i>Protein Science</i> , 2006 , 15, 1030-41	6.3	18
Solution structure of GOPC PDZ domain and its interaction with the C-terminal motif of neuroligin. Protein Science, 2006 , 15, 2149-58	6.3	16
Increased mobility in the membrane targeting PX domain induced by phosphatidylinositol 3-phosphate. <i>Protein Science</i> , 2006 , 15, 1873-82	6.3	8
Comparative NMR study on the impact of point mutations on protein stability of Pseudomonas mendocina lipase. <i>Protein Science</i> , 2006 , 15, 1915-27	6.3	13
Nogo goes in the pure water: solution structure of Nogo-60 and design of the structured and buffer-soluble Nogo-54 for enhancing CNS regeneration. <i>Protein Science</i> , 2006 , 15, 1835-41	6.3	23
An inserted Gly residue fine tunes dynamics between mesophilic and thermophilic ribonucleases H. <i>Protein Science</i> , 2006 , 15, 2697-707	6.3	21
Dynamics of the SPRY domain-containing SOCS box protein 2: flexibility of key functional loops. Protein Science, 2006 , 15, 2761-72	6.3	12
NMR structure of the p63 SAM domain and dynamical properties of G534V and T537P pathological mutants, identified in the AEC syndrome. 2006 , 44, 475-89		15
Backbone dynamics of a biologically active human FGF-1 monomer, complexed to a hexasaccharide heparin-analogue, by 15N NMR relaxation methods. 2006 , 35, 225-39		17
Measurement of 15N relaxation in the detergent-solubilized tetrameric KcsA potassium channel. 2006 , 36, 123-36		76
A suite of Mathematica notebooks for the analysis of protein main chain 15N NMR relaxation data. 2006 , 36, 215-24		52
DYNAMOF : un programme pour llanalyse dynamique de donnês de relaxation obtenues 🛭 champs magnetiques multiples. 2006 , 9, 503-513		6
Solution structure of the X4 protein coded by the SARS related coronavirus reveals an immunoglobulin like fold and suggests a binding activity to integrin I domains. 2006 , 13, 281-93		28
1256 A phosphorylation-induced conformation change in dematin headpiece. <i>Structure</i> , 2006 , 14, 379-87	5.2	28
YfhJ, a molecular adaptor in iron-sulfur cluster formation or a frataxin-like protein?. <i>Structure</i> , 2006 , 14, 857-67	5.2	37
High-resolution structural validation of the computational redesign of human U1A protein. Structure, 2006 , 14, 847-56	5.2	19
Structural insights into the specific binding of huntingtin proline-rich region with the SH3 and WW domains. <i>Structure</i> , 2006 , 14, 1755-65	5.2	31
Carbon-13 chemical shift anisotropy in DNA bases from field dependence of solution NMR relaxation rates. 2006 , 44, 302-10		14

1251	Evaluation of two simplified 15N-NMR methods for determining micros-ms dynamics of proteins. 2006 , 44, 761-9		6
1250	Solution structure of the immunodominant domain of protective antigen GNA1870 of Neisseria meningitidis. <i>Journal of Biological Chemistry</i> , 2006 , 281, 7220-7	5.4	36
1249	Protein side-chain dynamics observed by solution- and solid-state NMR: comparative analysis of methyl 2H relaxation data. 2006 , 128, 12354-5		54
1248	The holo-form of the nucleotide binding domain of the KdpFABC complex from Escherichia coli reveals a new binding mode. <i>Journal of Biological Chemistry</i> , 2006 , 281, 9641-9	5.4	17
1247	NMR dynamic studies suggest that allosteric activation regulates ligand binding in chicken liver bile acid-binding protein. <i>Journal of Biological Chemistry</i> , 2006 , 281, 9697-709	5.4	45
1246	Human SOD1 before harboring the catalytic metal: solution structure of copper-depleted, disulfide-reduced form. <i>Journal of Biological Chemistry</i> , 2006 , 281, 2333-7	5.4	64
1245	Solution structure of a low-molecular-weight protein tyrosine phosphatase from Bacillus subtilis. 2006 , 188, 1509-17		31
1244	NMR structure of the R-module: a parallel beta-roll subunit from an Azotobacter vinelandii mannuronan C-5 epimerase. <i>Journal of Biological Chemistry</i> , 2006 , 281, 7350-6	5.4	31
1243	Sequence dependence of renucleation after a Gly mutation in model collagen peptides. <i>Journal of Biological Chemistry</i> , 2006 , 281, 36937-43	5.4	41
1242	The Bacillus subtilis YkuV is a thiol:disulfide oxidoreductase revealed by its redox structures and activity. <i>Journal of Biological Chemistry</i> , 2006 , 281, 8296-304	5.4	12
1241	Solution structure of human peptidyl prolyl isomerase-like protein 1 and insights into its interaction with SKIP. <i>Journal of Biological Chemistry</i> , 2006 , 281, 15900-8	5.4	31
1240	Staphylococcus aureus Sortase A transpeptidase. Calcium promotes sorting signal binding by altering the mobility and structure of an active site loop. <i>Journal of Biological Chemistry</i> , 2006 , 281, 181	7 ⁵ 26	73
1239	Keap1 recruits Neh2 through binding to ETGE and DLG motifs: characterization of the two-site molecular recognition model. 2006 , 26, 2887-900		489
1238	Solution structures and backbone dynamics of a flavodoxin MioC from Escherichia coli in both Apo- and Holo-forms: implications for cofactor binding and electron transfer. <i>Journal of Biological</i> <i>Chemistry</i> , 2006 , 281, 35454-66	5.4	14
1237	Identification of the substrate interaction region of the chitin-binding domain of Streptomyces griseus chitinase C. 2006 , 139, 483-93		44
1236	Structure and carboxyl-terminal domain (CTD) binding of the Set2 SRI domain that couples histone H3 Lys36 methylation to transcription. <i>Journal of Biological Chemistry</i> , 2006 , 281, 13-5	5.4	67
1235	Structural study of the H/ACA snoRNP components Nop10p and the 3Lhairpin of U65 snoRNA. 2006 , 12, 40-52		31
1234	Intrinsic inhibition of the Hsp90 ATPase activity. <i>Journal of Biological Chemistry</i> , 2006 , 281, 11301-11	5.4	61

1233	Peptidoglycan recognition by Pal, an outer membrane lipoprotein. <i>Biochemistry</i> , 2006 , 45, 2122-8	3.2	138	
1232	HIV-1 Tat is a natively unfolded protein: the solution conformation and dynamics of reduced HIV-1 Tat-(1-72) by NMR spectroscopy. <i>Journal of Biological Chemistry</i> , 2006 , 281, 8347-56	5.4	99	
1231	The delivery of copper for thylakoid import observed by NMR. 2006, 103, 8320-5		55	
1230	The structure of Prp40 FF1 domain and its interaction with the crn-TPR1 motif of Clf1 gives a new insight into the binding mode of FF domains. <i>Journal of Biological Chemistry</i> , 2006 , 281, 356-64	5.4	31	
1229	Structure of the cadherin-related neuronal receptor/protocadherin-alpha first extracellular cadherin domain reveals diversity across cadherin families. <i>Journal of Biological Chemistry</i> , 2006 , 281, 33650-63	5.4	62	
1228	The interaction between calcium- and integrin-binding protein 1 and the alphallb integrin cytoplasmic domain involves a novel C-terminal displacement mechanism. <i>Journal of Biological Chemistry</i> , 2006 , 281, 26455-64	5.4	30	
1227	Solution structure of the conserved hypothetical protein Rv2302 from Mycobacterium tuberculosis. 2006 , 188, 5993-6001		7	
1226	NMR solution structure of the tandem Src homology 3 domains of p47phox complexed with a p22phox-derived proline-rich peptide. <i>Journal of Biological Chemistry</i> , 2006 , 281, 3660-8	5.4	55	
1225	Beads-on-a-string, characterization of ETS-1 sumoylated within its flexible N-terminal sequence. Journal of Biological Chemistry, 2006 , 281, 4164-72	5.4	31	
1224	Solution structure and intermolecular interactions of the third metal-binding domain of ATP7A, the Menkes disease protein. <i>Journal of Biological Chemistry</i> , 2006 , 281, 29141-7	5.4	36	
1223	Direct demonstration of the flexibility of the glycosylated proline-threonine linker in the Cellulomonas fimi Xylanase Cex through NMR spectroscopic analysis. <i>Journal of Biological Chemistry</i> , 2007 , 282, 2091-100	5.4	50	
1222	Solution structure of selenoprotein W and NMR analysis of its interaction with 14-3-3 proteins. Journal of Biological Chemistry, 2007 , 282, 37036-44	5.4	75	
1221	Curculin exhibits sweet-tasting and taste-modifying activities through its distinct molecular surfaces. <i>Journal of Biological Chemistry</i> , 2007 , 282, 33252-33256	5.4	27	
1220	The existence of multiple conformers of interleukin-21 directs engineering of a superpotent analogue. <i>Journal of Biological Chemistry</i> , 2007 , 282, 23326-36	5.4	29	
1219	A model for agonism and antagonism in an ancient and ubiquitous cAMP-binding domain. <i>Journal of Biological Chemistry</i> , 2007 , 282, 581-93	5.4	40	
1218	Crystallographic and NMR analyses of UvsW and UvsW.1 from bacteriophage T4. <i>Journal of Biological Chemistry</i> , 2007 , 282, 34392-400	5.4	19	
1217	Structural insights into activation of phosphatidylinositol 4-kinase (Pik1) by yeast frequenin (Frq1). Journal of Biological Chemistry, 2007 , 282, 30949-59	5.4	52	
1216	NMR investigation of Tyr105 mutants in TEM-1 beta-lactamase: dynamics are correlated with function. <i>Journal of Biological Chemistry</i> , 2007 , 282, 21448-59	5.4	27	

1215	NMR structural analysis of cadmium sensing by winged helix repressor CmtR. <i>Journal of Biological Chemistry</i> , 2007 , 282, 30181-8	5.4	36
1214	L11 domain rearrangement upon binding to RNA and thiostrepton studied by NMR spectroscopy. <i>Nucleic Acids Research</i> , 2007 , 35, 441-54	20.1	50
1213	Structural characterization of the ribosome maturation protein, RimM. 2007, 189, 6397-406		15
1212	Functional dynamics of response regulators using NMR relaxation techniques. 2007 , 423, 149-65		37
1211	The "jaws" of the tau-microtubule interaction. <i>Journal of Biological Chemistry</i> , 2007 , 282, 12230-9	5.4	131
1210	Solution structure and backbone dynamics of an endopeptidase HycI from Escherichia coli: implications for mechanism of the [NiFe] hydrogenase maturation. <i>Journal of Biological Chemistry</i> , 2007 , 282, 3856-63	5.4	21
1209	Structures of the thermophilic F1-ATPase epsilon subunit suggesting ATP-regulated arm motion of its C-terminal domain in F1. 2007 , 104, 11233-8		94
1208	Solution structure of Domains IVa and V of the tau subunit of Escherichia coli DNA polymerase III and interaction with the alpha subunit. <i>Nucleic Acids Research</i> , 2007 , 35, 2825-32	20.1	30
1207	NMR Studies of Encapsulated Macromolecules. 2007 , 179-219		6
1206	Structural insight into dimeric interaction of the SARAH domains from Mst1 and RASSF family proteins in the apoptosis pathway. 2007 , 104, 9236-41		109
1205	Controlling the inhibition of the sarcoplasmic Ca2+-ATPase by tuning phospholamban structural dynamics. <i>Journal of Biological Chemistry</i> , 2007 , 282, 37205-14	5.4	50
1204	NMR characterization of the pH 4 beta-intermediate of the prion protein: the N-terminal half of the protein remains unstructured and retains a high degree of flexibility. 2007 , 401, 533-40		34
1203	Insight into the binding properties of MEKK3 PB1 to MEK5 PB1 from its solution structure. <i>Biochemistry</i> , 2007 , 46, 13478-89	3.2	17
1202	Dynamics of backbone conformational heterogeneity in Bacillus subtilis ribonuclease P protein. <i>Biochemistry</i> , 2007 , 46, 15062-75	3.2	5
1201	NMR methods for studying quadruplex nucleic acids. 2007 , 43, 264-77		97
1200	Solution structure of the bacterial chemotaxis adaptor protein CheW from Escherichia coli. 2007 , 360, 863-7		23
1199	Solution structure of the cryptic mannitol-specific phosphotransferase enzyme IIA CmtB from Escherichia coli. 2007 , 362, 1001-6		1
	Structural basis of integrin activation by talin. 2007 , 128, 171-82		519

1197	Equilibrium unfolding of DLC8 monomer by urea and guanidine hydrochloride: Distinctive global and residue level features. 2007 , 89, 117-34		22	
1196	Structural characterization of the ribosomal P1A-P2B protein dimer by small-angle X-ray scattering and NMR spectroscopy. <i>Biochemistry</i> , 2007 , 46, 1988-98	3.2	23	
1195	Solution structure of NOD1 CARD and mutational analysis of its interaction with the CARD of downstream kinase RICK. <i>Journal of Molecular Biology</i> , 2007 , 365, 160-74	6.5	62	
1194	The mechanism of discrimination between cognate and non-specific DNA by dimeric b/HLH/LZ transcription factors. <i>Journal of Molecular Biology</i> , 2007 , 365, 1163-75	6.5	30	
1193	The folding pathway of T4 lysozyme: the high-resolution structure and folding of a hidden intermediate. <i>Journal of Molecular Biology</i> , 2007 , 365, 870-80	6.5	33	
1192	NMR analysis of the conformational properties of the trapped on-pathway folding intermediate of the bacterial immunity protein Im7. <i>Journal of Molecular Biology</i> , 2007 , 366, 1001-15	6.5	47	
1191	Three-dimensional structure determined for a subunit of human tRNA splicing endonuclease (Sen15) reveals a novel dimeric fold. <i>Journal of Molecular Biology</i> , 2007 , 366, 155-64	6.5	13	
1190	Solution structure and backbone dynamics of the reduced form and an oxidized form of E. coli methionine sulfoxide reductase A (MsrA): structural insight of the MsrA catalytic cycle. <i>Journal of Molecular Biology</i> , 2007 , 366, 193-206	6.5	22	
1189	Improved structural characterizations of the drkN SH3 domain unfolded state suggest a compact ensemble with native-like and non-native structure. <i>Journal of Molecular Biology</i> , 2007 , 367, 1494-510	6.5	99	
1188	Structure and dynamics of pin1 during catalysis by NMR. <i>Journal of Molecular Biology</i> , 2007 , 367, 1370-8	B 1 6.5	69	
1187	Propagation of dynamic changes in barnase upon binding of barstar: an NMR and computational study. <i>Journal of Molecular Biology</i> , 2007 , 367, 1079-92	6.5	48	
1186	NMR dynamics distinguish between hard and soft hydrophobic cores in the DNA-binding domain of PhoB and demonstrate different roles of the cores in binding to DNA. <i>Journal of Molecular Biology</i> , 2007 , 367, 1093-117	6.5	8	
1185	Dynamic requirements for a functional protein hinge. <i>Journal of Molecular Biology</i> , 2007 , 368, 131-49	6.5	71	
1184	Structure and interactions of the first three RNA recognition motifs of splicing factor prp24. Journal of Molecular Biology, 2007 , 367, 1447-58	6.5	34	
1183	Global changes in local protein dynamics reduce the entropic cost of carbohydrate binding in the arabinose-binding protein. <i>Journal of Molecular Biology</i> , 2007 , 368, 822-32	6.5	64	
1182	The solution and crystal structures of a module pair from the Staphylococcus aureus-binding site of human fibronectina tale with a twist. <i>Journal of Molecular Biology</i> , 2007 , 368, 833-44	6.5	32	
1181	Plasticity of the TSG-6 HA-binding loop and mobility in the TSG-6-HA complex revealed by NMR and X-ray crystallography. <i>Journal of Molecular Biology</i> , 2007 , 371, 669-84	6.5	20	
1180	Embryonic neural inducing factor churchill is not a DNA-binding zinc finger protein: solution structure reveals a solvent-exposed beta-sheet and zinc binuclear cluster. <i>Journal of Molecular Biology</i> 2007 371 1274-89	6.5	20	

1179	The box H/ACA RNP assembly factor Naf1p contains a domain homologous to Gar1p mediating its interaction with Cbf5p. <i>Journal of Molecular Biology</i> , 2007 , 371, 1338-53	6.5	34
1178	Investigating the substrate specificity and oligomerisation of the leader protease of foot and mouth disease virus using NMR. <i>Journal of Molecular Biology</i> , 2007 , 373, 1071-87	6.5	16
1177	Backbone dynamics in an intramolecular prolylpeptide-SH3 complex from the diphtheria toxin repressor, DtxR. <i>Journal of Molecular Biology</i> , 2007 , 374, 977-92	6.5	10
1176	Identification of the WW domain-interaction sites in the unstructured N-terminal domain of EBV LMP 2A. 2007 , 581, 65-70		3
1175	The high-resolution NMR structure of a single-chain chimeric protein mimicking a SH3-peptide complex. 2007 , 581, 687-92		16
1174	Catalytic domain of MMP20 (Enamelysin) - the NMR structure of a new matrix metalloproteinase. 2007 , 581, 4723-6		15
1173	Protein Interactions. 2007,		5
1172	A new mutant of bovine seminal ribonuclease with a reversed swapping propensity. <i>Biochemistry</i> , 2007 , 46, 2227-32	3.2	20
1171	Backbone dynamics of the monomeric lambda repressor denatured state ensemble under nondenaturing conditions. <i>Biochemistry</i> , 2007 , 46, 1141-51	3.2	12
1170	EXPERIMENTAL NMR RELAXATION METHODS. 2007 , 679-724		5
1169	An engineered second disulfide bond restricts lymphotactin/XCL1 to a chemokine-like conformation with XCR1 agonist activity. <i>Biochemistry</i> , 2007 , 46, 2564-73	3.2	42
1168	The isolated sixth gelsolin repeat and headpiece domain of villin bundle F-actin in the presence of calcium and are linked by a 40-residue unstructured sequence. <i>Biochemistry</i> , 2007 , 46, 7488-96	3.2	12
1167	Functional implications for a prototypical K-turn binding protein from structural and dynamical studies of 15.5K. <i>Biochemistry</i> , 2007 , 46, 14979-86	3.2	6
1166	Peptide binding by a fragment of calmodulin composed of EF-hands 2 and 3. <i>Biochemistry</i> , 2007 , 46, 852	2 <u>5.3</u> 6	4
1165	Domain 2 of nonstructural protein 5A (NS5A) of hepatitis C virus is natively unfolded. <i>Biochemistry</i> , 2007 , 46, 11550-8	3.2	78
1164	Structure and dynamics of surfactin studied by NMR in micellar media. 2007 , 129, 1968-77		40
1163	Solution structure of polymerase muls BRCT Domain reveals an element essential for its role in nonhomologous end joining. <i>Biochemistry</i> , 2007 , 46, 12100-10	3.2	22
1162	Solution structure of the PABC domain from wheat poly (A)-binding protein: an insight into RNA metabolic and translational control in plants. <i>Biochemistry</i> , 2007 , 46, 4221-31	3.2	14

1161	Kinetics and mechanism of the acid transition of the active site in plastocyanin. <i>Biochemistry</i> , 2007 , 46, 14619-28	3.2	8
1160	An exchange-free measure of 15N transverse relaxation: an NMR spectroscopy application to the study of a folding intermediate with pervasive chemical exchange. 2007 , 129, 11468-79		52
1159	Conformational plasticity of the lipid transfer protein SCP2. <i>Biochemistry</i> , 2007 , 46, 7980-91	3.2	20
1158	Methyl rotation barriers in proteins from 2H relaxation data. Implications for protein structure. 2007 , 129, 6827-38		66
1157	Using Molecular Dynamics Simulations To Provide New Insights into Protein Structure on the Nanosecond Timescale: Comparison with Experimental Data and Biological Inferences for the Hyaluronan-Binding Link Module of TSG-6. 2007 , 3, 1-16		16
1156	Effects of zinc binding on the structure and dynamics of the intrinsically disordered protein prothymosin alpha: evidence for metalation as an entropic switch. <i>Biochemistry</i> , 2007 , 46, 13120-30	3.2	47
1155	Interesting structural and dynamical behaviors exhibited by the AF-6 PDZ domain upon Bcr peptide binding. <i>Biochemistry</i> , 2007 , 46, 15042-53	3.2	15
1154	Combined analysis of (15)N relaxation data from solid- and solution-state NMR spectroscopy. 2007 , 129, 12594-5		56
1153	Effects of heme pocket structure and mobility on cytochrome c stability. <i>Biochemistry</i> , 2007 , 46, 2537-4	443.2	17
1152	Restricted backbone conformational and motional flexibilities of loops containing peptidyl-proline bonds dominate the enzyme activity of staphylococcal nuclease. <i>Biochemistry</i> , 2007 , 46, 11504-13	3.2	7
1151	Solution NMR studies of the maturation intermediates of a 13 MDa viral capsid. 2007 , 129, 7867-76		14
1150	Folding stability and cooperativity of the three forms of 1-110 residues fragment of staphylococcal nuclease. <i>Biophysical Journal</i> , 2007 , 92, 2090-107	2.9	9
1149	Structure of the first transmembrane domain of the neuronal acetylcholine receptor beta2 subunit. <i>Biophysical Journal</i> , 2007 , 92, 1616-22	2.9	9
1148	Conformational dynamics in loop swap mutants of homologous fibronectin type III domains. <i>Biophysical Journal</i> , 2007 , 93, 2447-56	2.9	13
1147	Temperature dependence of fast dynamics in proteins. <i>Biophysical Journal</i> , 2007 , 92, L43-5	2.9	35
1146	Structure and plasticity of the human immunodeficiency virus gp41 fusion domain in lipid micelles and bilayers. <i>Biophysical Journal</i> , 2007 , 93, 876-85	2.9	84
1145	Intrinsic dynamics of the partly unstructured PX domain from the Sendai virus RNA polymerase cofactor P. <i>Biophysical Journal</i> , 2007 , 93, 2830-44	2.9	33
1144	Elucidation of Protein B rotein and Protein L igand Interactions by NMR Spectroscopy. 2007 , 189-229		

1143	NMR spectroscopic characterization of a beta-(1,4)-glycosidase along its reaction pathway: stabilization upon formation of the glycosyl-enzyme intermediate. <i>Biochemistry</i> , 2007 , 46, 1759-70	16
1142	The novel CXCL12gamma isoform encodes an unstructured cationic domain which regulates bioactivity and interaction with both glycosaminoglycans and CXCR4. 2007 , 2, e1110	80
1141	Structure and Dynamics of Disordered Proteins. 2007,	
1140	Conformational analyses of a partially-folded bioactive prodomain of human furin. 2007 , 86, 329-44	9
1139	Merozoite surface protein 2 of Plasmodium falciparum: expression, structure, dynamics, and fibril formation of the conserved N-terminal domain. 2007 , 87, 12-22	40
1138	Simultaneous definition of high resolution protein structure and backbone conformational dynamics using NMR residual dipolar couplings. 2007 , 8, 1901-9	43
1137	Solution structure of ApaG from Xanthomonas axonopodis pv. citri reveals a fibronectin-3 fold. 2007 , 67, 490-500	9
1136	Probing nascent structures in peptides using natural abundance 13C NMR relaxation and reduced spectral density mapping. 2007 , 67, 18-30	7
1135	Solution structures, dynamics, and lipid-binding of the sterile alpha-motif domain of the deleted in liver cancer 2. 2007 , 67, 1154-66	29
1134	Solution NMR structure of Escherichia coli ytfP expands the structural coverage of the UPF0131 protein domain family. 2007 , 68, 789-95	4
1133	NMR-based modeling and binding studies of a ternary complex between chicken liver bile acid binding protein and bile acids. 2007 , 69, 177-91	25
1132	Complex assembly mechanism and an RNA-binding mode of the human p14-SF3b155 spliceosomal protein complex identified by NMR solution structure and functional analyses. 2008 , 71, 1617-36	13
1131	Tom20 recognizes mitochondrial presequences through dynamic equilibrium among multiple bound states. 2007 , 26, 4777-87	118
1130	Sequence-specific dynamics modulate recognition specificity in WW domains. 2007, 14, 325-31	52
1129	CFTR regulatory region interacts with NBD1 predominantly via multiple transient helices. 2007 , 14, 738-45	233
1128	Conformational entropy in molecular recognition by proteins. <i>Nature</i> , 2007 , 448, 325-9 50.4	526
1127	Eukaryotic class 1 translation termination factor eRF1the NMR structure and dynamics of the middle domain involved in triggering ribosome-dependent peptidyl-tRNA hydrolysis. 2007 , 274, 4223-37	18
1126	Structural insights into the interaction of insulin-like growth factor 2 with IGF2R domain 11. Structure, 2007 , 15, 1065-78	33

1125	Structure, interactions, and dynamics of the RING domain from human TRAF6. <i>Protein Science</i> , 2007 , 16, 602-14	6.3	22
1124	Solution structure and backbone dynamics of the AF-6 PDZ domain/Bcr peptide complex. <i>Protein Science</i> , 2007 , 16, 1053-62	6.3	14
1123	NMR structure of the pseudo-receiver domain of CikA. <i>Protein Science</i> , 2007 , 16, 465-75	6.3	26
1122	Solution structure of human sorting nexin 22. <i>Protein Science</i> , 2007 , 16, 807-14	6.3	13
1121	Calcium-induced folding of a fragment of calmodulin composed of EF-hands 2 and 3. <i>Protein Science</i> , 2007 , 16, 1119-32	6.3	27
1120	NMR structure of a KlbA intein precursor from Methanococcus jannaschii. <i>Protein Science</i> , 2007 , 16, 131	66238	40
1119	Solution structure of HI1506, a novel two-domain protein from Haemophilus influenzae. <i>Protein Science</i> , 2007 , 16, 977-82	6.3	
1118	A high-resolution solution structure of a trypanosomatid FYVE domain. <i>Protein Science</i> , 2007 , 16, 2552-	9 6.3	7
1117	Solution structure of the region 51-160 of human KIN17 reveals an atypical winged helix domain. <i>Protein Science</i> , 2007 , 16, 2750-5	6.3	17
1116	An investigation of the dynamics of spermine bound to duplex and quadruplex DNA by (13)C NMR spectroscopy. 2007 , 36, 637-46		11
1115	Measurement of dissociation constants of high-molecular weight protein-protein complexes by transferred 15N-relaxation. 2007 , 38, 65-72		13
1114	Maximum entropy reconstruction of joint phi, psi-distribution with a coil-library prior: the backbone conformation of the peptide hormone motilin in aqueous solution from phi and psi-dependent J-couplings. 2007 , 38, 107-23		7
1113	Model-free analysis for large proteins at high magnetic field strengths. 2007, 38, 315-24		4
1112	Hadamard NMR spectroscopy for relaxation measurements of large (>35 kDa) proteins. 2007 , 39, 239-4	5	2
1111	The high resolution NMR structure of the third SH3 domain of CD2AP. 2007 , 39, 331-6		14
1110	1H, 13C and 15N resonance assignments for the small G protein RalB in its active conformation. <i>Biomolecular NMR Assignments</i> , 2007 , 1, 147-9	0.7	7
1109	TROSY-based NMR experiments for NMR studies of large biomolecules. 2008 , 52, 49-68		15
1108	Structure discrimination for the C-terminal domain of Escherichia coli trigger factor in solution. 2008 , 40, 23-30		14

1107	Comparison of the backbone dynamics of a natural and a consensus designed 3-TPR domain. 2008 , 41, 169-78		7
1106	Direct methods and residue type specific isotope labeling in NMR structure determination and model-driven sequential assignment. 2008 , 42, 111-27		4
1105	Model-independent interpretation of NMR relaxation data for unfolded proteins: the acid-denatured state of ACBP. 2008 , 42, 163-77		26
1104	The structural plasticity of heparan sulfate NA-domains and hence their role in mediating multivalent interactions is confirmed by high-accuracy (15)N-NMR relaxation studies. 2008 , 25, 401-14		35
1103	Phosphorylation on histidine is accompanied by localized structural changes in the phosphocarrier protein, HPr from Bacillus subtilis. <i>Protein Science</i> , 1997 , 6, 2107-19	6.3	29
1102	Conformation and dynamics of the three-helix bundle UBA domain of p62 from experiment and simulation. 2008 , 71, 227-40		7
1101	Biotinoyl domain of human acetyl-CoA carboxylase: Structural insights into the carboxyl transfer mechanism. 2008 , 72, 613-24		17
1100	NMR structure and dynamics of human ephrin-B2 ectodomain: the functionally critical C-D and G-H loops are highly dynamic in solution. 2008 , 72, 1019-29		17
1099	Description of the low-affinity interaction between nociceptin and the second extracellular loop of its receptor by fluorescence and NMR spectroscopies. 2008 , 14, 1183-94		6
1098	The complex inter-relationships between protein flexibility and stability. 2008, 97, 3494-517		86
1097	Functional role of polyhydroxy compounds on protein structure and thermal stability studied by circular dichroism spectroscopy. 2008 , 46, 428-34		15
1096	Protein conformational flexibility prediction using machine learning. 2008 , 192, 37-47		10
1095	pH dependent unfolding characteristics of DLC8 dimer: Residue level details from NMR. 2008 , 1784, 1795-803		8
1094	Analysis of the C12A-p8MTCP1 protein internal motions using fast spectral density mapping at multiple magnetic fields. 2008 , 11, 530-540		
1093	Protein effective rotational correlation times from translational self-diffusion coefficients measured by PFG-NMR. 2008 , 136, 145-51		33
1092	Effect of a single point mutation on the stability, residual structure and dynamics in the denatured state of GED: relevance to self-assembly. 2008 , 137, 13-8		2
1091	Folding kinetics and thermodynamics of Pseudomonas syringae effector protein AvrPto provide insight into translocation via the type III secretion system. <i>Protein Science</i> , 2008 , 17, 1109-19	6.3	4
1090	Structural basis for controlling the dimerization and stability of the WW domains of an atypical subfamily. <i>Protein Science</i> , 2008 , 17, 1531-41	6.3	6

1089	Conformational change upon ligand binding and dynamics of the PDZ domain from leukemia-associated Rho guanine nucleotide exchange factor. <i>Protein Science</i> , 2008 , 17, 1003-14	6.3	18
1088	Key interactions in the immunoglobulin-like structure of apo-neocarzinostatin: evidence from nuclear magnetic resonance relaxation data and molecular dynamics simulations. <i>Protein Science</i> , 2001 , 10, 2228-40	6.3	14
1087	Distance mapping of protein-binding sites using spin-labeled oligosaccharide ligands. <i>Protein Science</i> , 2001 , 10, 2393-400	6.3	46
1086	Structure and dynamics of translation initiation factor aIF-1A from the archaeon Methanococcus jannaschii determined by NMR spectroscopy. <i>Protein Science</i> , 2001 , 10, 2426-38	6.3	9
1085	Reconstitution of a native-like SH2 domain from disordered peptide fragments examined by multidimensional heteronuclear NMR. <i>Protein Science</i> , 2001 , 10, 2162-75	6.3	5
1084	Backbone dynamics of the regulatory domain of calcium vector protein, studied by (15)N relaxation at four fields, reveals unique mobility characteristics of the intermotif linker. <i>Protein Science</i> , 2001 , 10, 1393-402	6.3	3
1083	The solution structure of the anti-HIV chemokine vMIP-II. <i>Protein Science</i> , 1999 , 8, 2270-80	6.3	27
1082	Solution structure and dynamics of bovine beta-lactoglobulin A. <i>Protein Science</i> , 1999 , 8, 2541-5	6.3	134
1081	Comparison of the backbone dynamics of the apo- and holo-carboxy-terminal domain of the biotin carboxyl carrier subunit of Escherichia coli acetyl-CoA carboxylase. <i>Protein Science</i> , 1999 , 8, 307-17	6.3	23
1080	Topology and dynamics of the 10 kDa C-terminal domain of DnaK in solution. <i>Protein Science</i> , 1999 , 8, 343-54	6.3	31
1079	Structure and dynamics in solution of the complex of Lactobacillus casei dihydrofolate reductase with the new lipophilic antifolate drug trimetrexate. <i>Protein Science</i> , 1999 , 8, 467-81	6.3	25
1078	Dynamics of the Hck-SH3 domain: comparison of experiment with multiple molecular dynamics simulations. <i>Protein Science</i> , 2000 , 9, 95-103	6.3	20
1077	Analysis of the dynamic properties of Bacillus circulans xylanase upon formation of a covalent glycosyl-enzyme intermediate. <i>Protein Science</i> , 2000 , 9, 512-24	6.3	21
1076	NMR solution structure of the theta subunit of DNA polymerase III from Escherichia coli. <i>Protein Science</i> , 2000 , 9, 721-33	6.3	17
1075	[Study of the structure and dynamics of a chimeric variant of the SH3 domain (SHA-Bergerac) by NMR spectroscopy]. 2008 , 34, 645-53		4
1074	Structural mobility of the monomeric C-terminal domain of the HIV-1 capsid protein. 2008, 275, 3299-3	11	22
1073	Soluble recombinant CD69 receptors optimized to have an exceptional physical and chemical stability display prolonged circulation and remain intact in the blood of mice. 2008 , 275, 5589-606		24
1072	A comparison of BRCT domains involved in nonhomologous end-joining: introducing the solution structure of the BRCT domain of polymerase lambda. 2008 , 7, 1340-51		28

1071	Crystal structures of beta-neurexin 1 and beta-neurexin 2 ectodomains and dynamics of splice insertion sequence 4. <i>Structure</i> , 2008 , 16, 410-21	5.2	33
1070	Equilibrium refolding transitions driven by trifluoroethanol and by guanidine hydrochloride dilution are similar in GTPase effector domain: implications to sequence-self-association paradigm. <i>Biochemistry</i> , 2008 , 47, 12945-53	3.2	2
1069	NMR study of general anesthetic interaction with nAChR beta2 subunit. <i>Biophysical Journal</i> , 2008 , 94, 1681-8	2.9	22
1068	Four-alpha-helix bundle with designed anesthetic binding pockets. Part I: structural and dynamical analyses. <i>Biophysical Journal</i> , 2008 , 94, 4454-63	2.9	18
1067	NMR evidence for forming highly populated helical conformations in the partially folded hNck2 SH3 domain. <i>Biophysical Journal</i> , 2008 , 95, 4803-12	2.9	17
1066	Biophysical characterization of the unstructured cytoplasmic domain of the human neuronal adhesion protein neuroligin 3. <i>Biophysical Journal</i> , 2008 , 95, 1928-44	2.9	34
1065	Thioredoxin as a fusion tag for carrier-driven crystallization. <i>Protein Science</i> , 2008 , 17, 2070-9	6.3	29
1064	Multiple conformations of the metal-bound pyoverdine PvdI, a siderophore of Pseudomonas aeruginosa: a nuclear magnetic resonance study. <i>Biochemistry</i> , 2008 , 47, 3397-406	3.2	15
1063	Crystal structure of the FK506 binding domain of Plasmodium falciparum FKBP35 in complex with FK506. <i>Biochemistry</i> , 2008 , 47, 5951-61	3.2	28
1062	Dynamic characterisation of the netrin-like domain of human type 1 procollagen C-proteinase enhancer and comparison to the N-terminal domain of tissue inhibitor of metalloproteinases (TIMP). 2008 , 4, 417-25		7
1061	Structure of the yeast SR protein Npl3 and Interaction with mRNA 3Lend processing signals. Journal of Molecular Biology, 2008 , 375, 136-50	6.5	21
1060	Modulation of cardiac troponin C function by the cardiac-specific N-terminus of troponin I: influence of PKA phosphorylation and involvement in cardiomyopathies. <i>Journal of Molecular Biology</i> , 2008 , 375, 735-51	6.5	41
1059	Analysis of the thermodynamics of binding of an SH3 domain to proline-rich peptides using a chimeric fusion protein. <i>Journal of Molecular Biology</i> , 2008 , 377, 117-35	6.5	15
1058	A ligand-induced switch in the periplasmic domain of sensor histidine kinase CitA. <i>Journal of Molecular Biology</i> , 2008 , 377, 512-23	6.5	99
1057	Compensatory and long-range changes in picosecond-nanosecond main-chain dynamics upon complex formation: 15N relaxation analysis of the free and bound states of the ubiquitin-like domain of human plexin-B1 and the small GTPase Rac1. <i>Journal of Molecular Biology</i> , 2008 , 377, 1474-83	6.5 7	43
1056	Characterization of conformational and dynamic properties of natively unfolded human and mouse alpha-synuclein ensembles by NMR: implication for aggregation. <i>Journal of Molecular Biology</i> , 2008 , 378, 1104-15	6.5	96
1055	Novel structural and functional mode of a knot essential for RNA binding activity of the Esa1 presumed chromodomain. <i>Journal of Molecular Biology</i> , 2008 , 378, 987-1001	6.5	32
1054	The solution structure and dynamics of human pancreatic ribonuclease determined by NMR spectroscopy provide insight into its remarkable biological activities and inhibition. <i>Journal of Molecular Biology</i> , 2008 , 379, 953-65	6.5	24

1053	Molecular structure and metal-binding properties of the periplasmic CopK protein expressed in Cupriavidus metallidurans CH34 during copper challenge. <i>Journal of Molecular Biology</i> , 2008 , 380, 386-	463 ⁵	26	
1052	Transfer of flexibility between ankyrin repeats in IkappaB* upon formation of the NF-kappaB complex. <i>Journal of Molecular Biology</i> , 2008 , 380, 917-31	6.5	56	
1051	Assembly of chloroplast signal recognition particle involves structural rearrangement in cpSRP43. Journal of Molecular Biology, 2008 , 381, 49-60	6.5	15	
1050	Solution structure of the C-terminal nucleoprotein-RNA binding domain of the vesicular stomatitis virus phosphoprotein. <i>Journal of Molecular Biology</i> , 2008 , 382, 525-38	6.5	57	
1049	The affinity of Ets-1 for DNA is modulated by phosphorylation through transient interactions of an unstructured region. <i>Journal of Molecular Biology</i> , 2008 , 382, 1014-30	6.5	51	
1048	The NMR structure and dynamics of the two-domain tick carboxypeptidase inhibitor reveal flexibility in its free form and stiffness upon binding to human carboxypeptidase B. <i>Biochemistry</i> , 2008 , 47, 7066-78	3.2	15	
1047	Residual ligand entropy in the binding of p-substituted benzenesulfonamide ligands to bovine carbonic anhydrase II. 2008 , 130, 12420-6		31	
1046	Solution structure of stem-loop alpha of the hepatitis B virus post-transcriptional regulatory element. <i>Nucleic Acids Research</i> , 2008 , 36, 1681-9	20.1	27	
1045	Solution structure of the iron-sulfur cluster cochaperone HscB and its binding surface for the iron-sulfur assembly scaffold protein IscU. <i>Biochemistry</i> , 2008 , 47, 9394-404	3.2	38	
1044	Solution structures and backbone dynamics of Escherichia coli rhodanese PspE in its sulfur-free and persulfide-intermediate forms: implications for the catalytic mechanism of rhodanese. <i>Biochemistry</i> , 2008 , 47, 4377-85	3.2	9	
1043	Remote changes in the dynamics of the phosphotyrosine-binding domain of insulin receptor substrate-1 induced by phosphopeptide binding. <i>Biochemistry</i> , 2008 , 47, 13371-82	3.2	13	
1042	Dynamics of the RING domain from human TRAF6 by 15N NMR spectroscopy: implications for biological function. <i>Biochemistry</i> , 2008 , 47, 10010-7	3.2	7	
1041	Solution structure and dynamics of the reduced and oxidized forms of the N-terminal domain of PilB from Neisseria meningitidis. <i>Biochemistry</i> , 2008 , 47, 8577-89	3.2	4	
1040	The periplasmic domain of TolR from Haemophilus influenzae forms a dimer with a large hydrophobic groove: NMR solution structure and comparison to SAXS data. <i>Biochemistry</i> , 2008 , 47, 313	31 ³ 4 ² 2	34	
1039	15N relaxation studies of Apo-Mts1: a dynamic S100 protein. <i>Biochemistry</i> , 2008 , 47, 7637-47	3.2	11	
1038	NMR relaxation study of the complex formed between CBP and the activation domain of the nuclear hormone receptor coactivator ACTR. <i>Biochemistry</i> , 2008 , 47, 1299-308	3.2	71	
1037	Nop10 is a conserved H/ACA snoRNP molecular adaptor. <i>Biochemistry</i> , 2008 , 47, 6148-56	3.2	9	
1036	Protein side-chain dynamics as observed by solution- and solid-state NMR spectroscopy: a similarity revealed. 2008 , 130, 16611-21		87	

1035	Extensive formation of off-pathway species during folding of an alpha-beta parallel protein is due to docking of (non)native structure elements in unfolded molecules. 2008 , 130, 16914-20		31
1034	Structural basis and binding properties of the second bromodomain of Brd4 with acetylated histone tails. <i>Biochemistry</i> , 2008 , 47, 6403-17	3.2	45
1033	Structure, dynamics, and selectivity of the sodium channel blocker mu-conotoxin SIIIA. <i>Biochemistry</i> , 2008 , 47, 10940-9	3.2	59
1032	NMR studies of a heterotypic Sam-Sam domain association: the interaction between the lipid phosphatase Ship2 and the EphA2 receptor. <i>Biochemistry</i> , 2008 , 47, 12721-8	3.2	52
1031	Integrin binding immunoglobulin type filamin domains have variable stability. <i>Biochemistry</i> , 2008 , 47, 11055-61	3.2	9
1030	A stabilizing alpha/beta-hydrophobic core greatly contributes to hyperthermostability of archaeal [P62A]Ssh10b. <i>Biochemistry</i> , 2008 , 47, 11212-21	3.2	11
1029	Rational design of protein-based MRI contrast agents. 2008 , 130, 9260-7		100
1028	Dependence of the size of a protein-SDS complex on detergent and Na+ concentrations. 2008 , 112, 42	42-5	13
1027	Structural and motional changes induced in apo-S100A1 protein by the disulfide formation between its Cys 85 residue and beta-mercaptoethanol. <i>Biochemistry</i> , 2008 , 47, 640-50	3.2	16
1026	Monitoring aromatic picosecond to nanosecond dynamics in proteins via 13C relaxation: expanding perturbation mapping of the rigidifying core mutation, V54A, in eglin c. <i>Biochemistry</i> , 2008 , 47, 4876-86	5 ^{3.2}	33
1025	Anesthetic modulation of protein dynamics: insight from an NMR study. 2008, 112, 14312-8		20
1024	NMR structure of DREAM: Implications for Ca(2+)-dependent DNA binding and protein dimerization. <i>Biochemistry</i> , 2008 , 47, 2252-64	3.2	40
1023	Metal binding domains 3 and 4 of the Wilson disease protein: solution structure and interaction with the copper(I) chaperone HAH1. <i>Biochemistry</i> , 2008 , 47, 7423-9	3.2	85
1022	NMR characterization of structural and dynamics perturbations due to a single point mutation in Drosophila DLC8 dimer: functional implications. <i>Biochemistry</i> , 2008 , 47, 6251-9	3.2	11
1021	The low-pH unfolded state of the C-terminal domain of the ribosomal protein L9 contains significant secondary structure in the absence of denaturant but is no more compact than the low-pH urea unfolded state. <i>Biochemistry</i> , 2008 , 47, 9565-73	3.2	20
1020	Hydrophobic core mutations in CI2 globally perturb fast side-chain dynamics similarly without regard to position. <i>Biochemistry</i> , 2008 , 47, 8566-76	3.2	14
1019	Solution structure and backbone dynamics of the cysteine 103 to serine mutant of the N-terminal domain of DsbD from Neisseria meningitidis. <i>Biochemistry</i> , 2008 , 47, 12710-20	3.2	6
1018	13C relaxation studies of the DNA target sequence for hhai methyltransferase reveal unique motional properties. <i>Biochemistry</i> , 2008 , 47, 7617-25	3.2	19

1017	Solution structure of the second RNA recognition motif (RRM) domain of murine T cell intracellular antigen-1 (TIA-1) and its RNA recognition mode. <i>Biochemistry</i> , 2008 , 47, 6437-50	3.2	15
1016	Re-evaluation of the model-free analysis of fast internal motion in proteins using NMR relaxation. 2008 , 112, 12095-103		20
1015	Insight into disulfide bond catalysis in Chlamydia from the structure and function of DsbH, a novel oxidoreductase. <i>Journal of Biological Chemistry</i> , 2008 , 283, 824-32	5.4	17
1014	Structure and dynamics of human apolipoprotein CIII. Journal of Biological Chemistry, 2008, 283, 17416-	2 7 .4	57
1013	Structural basis of the migfilin-filamin interaction and competition with integrin beta tails. <i>Journal of Biological Chemistry</i> , 2008 , 283, 35154-63	5.4	89
1012	Structural insights into membrane targeting by the flagellar calcium-binding protein (FCaBP), a myristoylated and palmitoylated calcium sensor in Trypanosoma cruzi. <i>Journal of Biological Chemistry</i> , 2008 , 283, 23388-96	5.4	23
1011	The RRM domain of poly(A)-specific ribonuclease has a noncanonical binding site for mRNA cap analog recognition. <i>Nucleic Acids Research</i> , 2008 , 36, 4754-67	20.1	39
1010	Structural determinants of calmodulin binding to the intracellular C-terminal domain of the metabotropic glutamate receptor 7A. <i>Journal of Biological Chemistry</i> , 2008 , 283, 5577-88	5.4	10
1009	Probing the mechanism of recognition of ssDNA by the Cdc13-DBD. <i>Nucleic Acids Research</i> , 2008 , 36, 1624-33	20.1	15
1008	NMR and MD studies of the temperature-dependent dynamics of RNA YNMG-tetraloops. <i>Nucleic Acids Research</i> , 2008 , 36, 1928-40	20.1	50
1007	Entropy-driven cAMP-dependent allosteric control of inhibitory interactions in exchange proteins directly activated by cAMP. <i>Journal of Biological Chemistry</i> , 2008 , 283, 19691-703	5.4	58
1006	Effects of redox potential and Ca2+ on the inositol 1,4,5-trisphosphate receptor L3-1 loop region: implications for receptor regulation. <i>Journal of Biological Chemistry</i> , 2008 , 283, 25567-25575	5.4	35
1005	Structural mechanism of signal transduction between the RNA-binding domain and the phosphotransferase system regulation domain of the LicT antiterminator. <i>Journal of Biological Chemistry</i> , 2008 , 283, 30838-49	5.4	15
1004	Solution structure of the calponin homology (CH) domain from the smoothelin-like 1 protein: a unique apocalmodulin-binding mode and the possible role of the C-terminal type-2 CH-domain in smooth muscle relaxation. <i>Journal of Biological Chemistry</i> , 2008 , 283, 20569-78	5.4	23
1003	NMR-detected conformational exchange observed in a computationally designed variant of protein Gbeta1. 2008 , 21, 577-87		5
1002	The solution structures of two soybean calmodulin isoforms provide a structural basis for their selective target activation properties. <i>Journal of Biological Chemistry</i> , 2008 , 283, 14619-28	5.4	22
1001	Intrinsically disordered gamma-subunit of cGMP phosphodiesterase encodes functionally relevant transient secondary and tertiary structure. 2008 , 105, 1505-10		82
1000	Molecular basis of histone H3K4me3 recognition by ING4. <i>Journal of Biological Chemistry</i> , 2008 , 283, 15956-64	5.4	66

999	The structure of the GAF A domain from phosphodiesterase 6C reveals determinants of cGMP binding, a conserved binding surface, and a large cGMP-dependent conformational change. <i>Journal of Biological Chemistry</i> , 2008 , 283, 25913-9	5.4	40
998	The IsdC protein from Staphylococcus aureus uses a flexible binding pocket to capture heme. Journal of Biological Chemistry, 2008 , 283, 31591-600	5.4	55
997	Dynamic equilibrium engagement of a polyvalent ligand with a single-site receptor. 2008, 105, 17772-7		257
996	Measurement of 15N-T1 relaxation rates in a perdeuterated protein by magic angle spinning solid-state nuclear magnetic resonance spectroscopy. <i>Journal of Chemical Physics</i> , 2008 , 128, 052316	3.9	57
995	Nuclear Magnetic Resonance (NMR) Spectroscopy of Metallobiomolecules. 2008,		O
994	Conformational transition associated with E1-E2 interaction in small ubiquitin-like modifications. Journal of Biological Chemistry, 2009 , 284, 20340-8	5.4	19
993	Raf kinase inhibitory protein function is regulated via a flexible pocket and novel phosphorylation-dependent mechanism. 2009 , 29, 1306-20		37
992	Hidden dynamic allostery in a PDZ domain. 2009 , 106, 18249-54		243
991	Structural basis for the multiple interactions of the MyD88 TIR domain in TLR4 signaling. 2009 , 106, 102	260-5	160
990	The cavity-chaperone Skp protects its substrate from aggregation but allows independent folding of substrate domains. 2009 , 106, 1772-7		96
989	Regulation of Class IA PI 3-kinases: C2 domain-iSH2 domain contacts inhibit p85/p110alpha and are disrupted in oncogenic p85 mutants. 2009 , 106, 20258-63		64
988	The HD-exchange motions of ribosomal protein S6 are insensitive to reversal of the protein-folding pathway. 2009 , 106, 21619-24		13
987	Dynamically driven ligand selectivity in cyclic nucleotide binding domains. <i>Journal of Biological Chemistry</i> , 2009 , 284, 23682-96	5.4	64
986	Structure and function of the two tandem WW domains of the pre-mRNA splicing factor FBP21 (formin-binding protein 21). <i>Journal of Biological Chemistry</i> , 2009 , 284, 25375-87	5.4	33
985	Structure, function, and targets of the transcriptional regulator SvtR from the hyperthermophilic archaeal virus SIRV1. <i>Journal of Biological Chemistry</i> , 2009 , 284, 22222-22237	5.4	30
984	Dimerization and protein binding specificity of the U2AF homology motif of the splicing factor Puf60. <i>Journal of Biological Chemistry</i> , 2009 , 284, 630-639	5.4	49
983	Structural basis for the sequence-specific RNA-recognition mechanism of human CUG-BP1 RRM3. <i>Nucleic Acids Research</i> , 2009 , 37, 5151-66	20.1	62
982	Cross-reactivity of pollen and food allergens: soybean Gly m 4 is a member of the Bet v 1 superfamily and closely resembles yellow lupine proteins. 2009 , 29, 183-92		35

(2009-2009)

981	NMR analysis of the dynamic exchange of the NS2B cofactor between open and closed conformations of the West Nile virus NS2B-NS3 protease. 2009 , 3, e561	64
980	Solution structure of the factor H-binding protein, a survival factor and protective antigen of Neisseria meningitidis. <i>Journal of Biological Chemistry</i> , 2009 , 284, 9022-6	52
979	Analysis of the varicella-zoster virus IE62 N-terminal acidic transactivating domain and its interaction with the human mediator complex. 2009 , 83, 6300-5	23
978	Dynamic dysfunction in dihydrofolate reductase results from antifolate drug binding: modulation of dynamics within a structural state. <i>Structure</i> , 2009 , 17, 386-94	63
977	Synergy of NMR, computation, and X-ray crystallography for structural biology. <i>Structure</i> , 2009 , 17, 499-502	7 48
976	A surface loop directs conformational switching of a lipoyl domain between a folded and a novel misfolded structure. <i>Structure</i> , 2009 , 17, 1117-27	11
975	Intrinsic domain and loop dynamics commensurate with catalytic turnover in an induced-fit enzyme. <i>Structure</i> , 2009 , 17, 1356-67	24
974	Solution structure of DnaE intein from Nostoc punctiforme: structural basis for the design of a new split intein suitable for site-specific chemical modification. 2009 , 583, 1451-6	74
973	The high resolution NMR structure of parvulustat (Z-2685) from Streptomyces parvulus FH-1641: comparison with tendamistat from Streptomyces tendae 4158. 2009 , 10, 119-27	13
972	The cadmium binding domains in the metallothionein isoform Cd(7)-MT10 from Mytilus galloprovincialis revealed by NMR spectroscopy. 2009 , 14, 167-78	17
971	Phosphorylation-induced changes in backbone dynamics of the dematin headpiece C-terminal domain. 2009 , 43, 39-50	7
970	Detection of nanosecond time scale side-chain jumps in a protein dissolved in water/glycerol solvent. 2009 , 45, 57-72	7
969	Mesodynamics in the SARS nucleocapsid measured by NMR field cycling. 2009 , 45, 217-25	24
968	Hydration dependent dynamics in RNA. 2009 , 45, 133-42	30
967	Conformational entropy changes upon lactose binding to the carbohydrate recognition domain of galectin-3. 2009 , 45, 157-69	67
966	Backbone and side-chain (1)H, (13)C and (15)N resonance assignments of LEN, a human immunoglobulin kappaIV light-chain variable domain. <i>Biomolecular NMR Assignments</i> , 2009 , 3, 255-9	3
965	NMR structural studies of the Ste11 SAM domain in the dodecyl phosphocholine micelle. 2009 , 74, 328-43	22
964	Substrate induced structural and dynamics changes in human phosphomevalonate kinase and implications for mechanism. 2009 , 75, 127-38	6

963	Conserved structural and dynamics features in the denatured states of drosophila SUMO, human SUMO and ubiquitin proteins: Implications to sequence-folding paradigm. 2009 , 76, 387-402		8
962	Construct optimization for protein NMR structure analysis using amide hydrogen/deuterium exchange mass spectrometry. 2009 , 76, 882-94		33
961	Solution structure of the AT-rich interaction domain of Jumonji/JARID2. 2009, 76, 1023-8		5
960	Temperature-induced partially unfolded state of hUBF HMG Box-5: conformational and dynamic investigations of the Box-5 thermal intermediate ensemble. 2009 , 77, 432-47		3
959	Solution structure of the fourth FF domain of yeast Prp40 splicing factor. 2009 , 77, 1000-3		7
958	Backbone dynamics of TFE-induced native-like fold of region 4 of Escherichia coli RNA polymerase sigma70 subunit. 2010 , 78, 754-68		3
957	Native like structure in the unfolded state of the villin headpiece helical subdomain, an ultrafast folding protein. <i>Protein Science</i> , 2009 , 18, 1692-701	6.3	24
956	Solution structures and backbone dynamics of the ribosomal protein S6 and its permutant P(54-55). <i>Protein Science</i> , 2010 , 19, 183-9	6.3	11
955	Dynamics of a truncated prion protein, PrP(113-231), from (15)N NMR relaxation: order parameters calculated and slow conformational fluctuations localized to a distinct region. <i>Protein Science</i> , 2009 , 18, 410-23	6.3	26
954	Fast structural dynamics in reduced and oxidized cytochrome c. <i>Protein Science</i> , 2009 , 18, 670-4	6.3	14
953	Solution structure of the parvulin-type PPIase domain of Staphylococcus aureus PrsAimplications for the catalytic mechanism of parvulins. 2009 , 9, 17		36
952	Unusual bipartite mode of interaction between the nonsense-mediated decay factors, UPF1 and UPF2. 2009 , 28, 2293-306		105
951	Solution structure of the Mesorhizobium loti K1 channel cyclic nucleotide-binding domain in complex with cAMP. 2009 , 10, 729-35		35
950	Haematopoietic malignancies caused by dysregulation of a chromatin-binding PHD finger. <i>Nature</i> , 2009 , 459, 847-51	50.4	330
949	MIA40 is an oxidoreductase that catalyzes oxidative protein folding in mitochondria. 2009 , 16, 198-206		206
948	Functional aspects of the solution structure and dynamics of PAFa highly-stable antifungal protein from Penicillium chrysogenum. 2009 , 276, 2875-90		72
947	Recent Advances in the Application of Solution NMR Spectroscopy to Multi-Span Integral Membrane Proteins. 2009 , 55, 335-360		132
946	Solution structure and dynamics of the chimeric SH3 domains, SHH- and SHA-"Bergeracs". 2009 , 1794, 1813-22		13

945	15N nuclear magnetic resonance relaxation studies on rat beta-parvalbumin and the pentacarboxylate variants, S55D and G98D. <i>Protein Science</i> , 2002 , 11, 158-73	6.3	4
944	Selective characterization of microsecond motions in proteins by NMR relaxation. 2009 , 131, 16257-65		45
943	Domain mobility in proteins from NMR/SRLS. 2009 , 113, 12050-60		19
942	Dynamics of the conformational transitions in the assembling of the Michaelis complex of a bisubstrate enzyme: a (15)N relaxation study of Escherichia coli 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase. <i>Biochemistry</i> , 2009 , 48, 302-12	3.2	11
941	The solution structure of Bacillus anthracis dihydrofolate reductase yields insight into the analysis of structure-activity relationships for novel inhibitors. <i>Biochemistry</i> , 2009 , 48, 4100-8	3.2	11
940	Structural basis for differential binding of the interleukin-8 monomer and dimer to the CXCR1 N-domain: role of coupled interactions and dynamics. <i>Biochemistry</i> , 2009 , 48, 8795-805	3.2	46
939	Deuterium spin probes of backbone order in proteins: 2H NMR relaxation study of deuterated carbon alpha sites. 2009 , 131, 15853-65		34
938	The unfolded state of the C-terminal domain of the ribosomal protein L9 contains both native and non-native structure. <i>Biochemistry</i> , 2009 , 48, 4707-19	3.2	27
937	Bruno protein contains an expanded RNA recognition motif. <i>Biochemistry</i> , 2009 , 48, 12202-12	3.2	6
936	Accurate sampling of high-frequency motions in proteins by steady-state (15)N-{(1)H} nuclear Overhauser effect measurements in the presence of cross-correlated relaxation. 2009 , 131, 6048-9		53
935	Structure of a nickel chaperone, HypA, from Helicobacter pylori reveals two distinct metal binding sites. 2009 , 131, 10031-40		83
934	Solution structures of the actuator domain of ATP7A and ATP7B, the Menkes and Wilson disease proteins. <i>Biochemistry</i> , 2009 , 48, 7849-55	3.2	31
933	Structural basis of the broad specificity of a general odorant-binding protein from honeybee. <i>Biochemistry</i> , 2009 , 48, 2431-41	3.2	45
932	The structure of the cataract-causing P23T mutant of human gammaD-crystallin exhibits distinctive local conformational and dynamic changes. <i>Biochemistry</i> , 2009 , 48, 2597-609	3.2	51
931	Conformational exchange in pseudoazurin: different kinds of microsecond to millisecond dynamics characterized by their pH and buffer dependence using 15N NMR relaxation. <i>Biochemistry</i> , 2009 , 48, 50-8	3.2	8
930	NMR structure and dynamics of the engineered fluorescein-binding lipocalin FluA reveal rigidification of beta-barrel and variable loops upon enthalpy-driven ligand binding. <i>Biochemistry</i> , 2009 , 48, 7411-9	3.2	10
929	Prion proteins with pathogenic and protective mutations show similar structure and dynamics. <i>Biochemistry</i> , 2009 , 48, 8120-8	3.2	49
928	Evidence for domain motion in proteins affecting global diffusion properties: a nuclear magnetic resonance study. 2009 , 113, 7003-11		12

927	Ternary protein complex of ferredoxin, ferredoxin:thioredoxin reductase, and thioredoxin studied by paramagnetic NMR spectroscopy. 2009 , 131, 17576-82		13
926	Noncooperative folding of subdomains in adenylate kinase. <i>Biochemistry</i> , 2009 , 48, 1911-27	3.2	47
925	Structure, stability, and flexibility of ribosomal protein L14e from Sulfolobus solfataricus. <i>Biochemistry</i> , 2009 , 48, 5553-62	3.2	4
924	A dihydropyridine receptor alpha1s loop region critical for skeletal muscle contraction is intrinsically unstructured and binds to a SPRY domain of the type 1 ryanodine receptor. 2009 , 41, 677-8	6	41
923	Hierarchy in guanidine unfolding of DLC8 dimer: regulatory functional implications. 2009 , 91, 401-7		6
922	Transient non-native hydrogen bonds promote activation of a signaling protein. 2009 , 139, 1109-18		98
921	alphaB-crystallin: a hybrid solid-state/solution-state NMR investigation reveals structural aspects of the heterogeneous oligomer. <i>Journal of Molecular Biology</i> , 2009 , 385, 1481-97	6.5	97
920	Structural and motional contributions of the Bacillus subtilis ClpC N-domain to adaptor protein interactions. <i>Journal of Molecular Biology</i> , 2009 , 387, 639-52	6.5	13
919	Insights into the dynamics of specific telomeric single-stranded DNA recognition by Pot1pN. Journal of Molecular Biology, 2009 , 387, 935-48	6.5	8
918	Structure and ligand binding of the extended Tudor domain of D. melanogaster Tudor-SN. <i>Journal of Molecular Biology</i> , 2009 , 387, 921-34	6.5	48
917	Structure, dynamics and folding of an immunoglobulin domain of the gelation factor (ABP-120) from Dictyostelium discoideum. <i>Journal of Molecular Biology</i> , 2009 , 388, 865-79	6.5	27
916	Configurational entropy in protein-peptide binding: computational study of Tsg101 ubiquitin E2 variant domain with an HIV-derived PTAP nonapeptide. <i>Journal of Molecular Biology</i> , 2009 , 389, 315-35	6.5	70
915	NMR structure of the N-terminal domain of capsid protein from the mason-pfizer monkey virus. Journal of Molecular Biology, 2009 , 392, 100-14	6.5	28
914	Structural studies of FF domains of the transcription factor CA150 provide insights into the organization of FF domain tandem arrays. <i>Journal of Molecular Biology</i> , 2009 , 393, 409-24	6.5	9
913	Comparison of NMR structural and dynamics features of the urea and guanidine-denatured states of GED. 2009 , 481, 169-76		6
912	Structure-function correlation of human programmed cell death 5 protein. 2009 , 486, 141-9		9
911	NMR dynamics of PSE-4 beta-lactamase: an interplay of ps-ns order and mus-ms motions in the active site. <i>Biophysical Journal</i> , 2009 , 96, 4681-91	2.9	25
910	The role of disulfide bond in the amyloidogenic state of beta(2)-microglobulin studied by heteronuclear NMR. <i>Protein Science</i> , 2002 , 11, 2218-29	6.3	80

(2010-2005)

909	Backbone nuclear relaxation characteristics and calorimetric investigation of the human Grb7-SH2/erbB2 peptide complex. <i>Protein Science</i> , 2005 , 14, 1556-69	6.3	13
908	Methods in molecular biology. Therapeutic antibodies. Methods and protocols. Preface. 2009 , 525, vii-viii, xiii		9
907	The copper-responsive repressor CopR of Lactococcus lactis is a lwinged helixLprotein. 2009, 417, 493-	9	18
906	Chimeric SHA-D domain BH3-Bergeract[3D structure and dynamics studies. 2010 , 36, 468-476		
905	Mechanism of phosphorylation-induced activation of phospholipase C-gamma isozymes. <i>Journal of Biological Chemistry</i> , 2010 , 285, 35836-47	5.4	83
904	NMR structural analysis of the soluble domain of ZiaA-ATPase and the basis of selective interactions with copper metallochaperone Atx1. 2010 , 15, 87-98		16
903	A microscale protein NMR sample screening pipeline. 2010 , 46, 11-22		85
902	Tunable paramagnetic relaxation enhancements by [Gd(DPA)(3)] (3-) for protein structure analysis. 2010 , 47, 143-53		20
901	Comparison of fast backbone dynamics at amide nitrogen and carbonyl sites in dematin headpiece C-terminal domain and its S74E mutant. 2010 , 47, 155-62		2
900	Protein alignment using cellulose nanocrystals: practical considerations and range of application. 2010 , 47, 195-204		27
899	Molecular basis of photochromism of a fluorescent protein revealed by direct 13C detection under laser illumination. 2010 , 48, 237-46		12
898	High yield expression and purification of HIV-1 Tat1-72 for structural studies. 2010 , 164, 35-42		8
897	Structure of the GLD-1 homodimerization domain: insights into STAR protein-mediated translational regulation. <i>Structure</i> , 2010 , 18, 377-89	5.2	23
896	Two-state conformations in the hyaluronan-binding domain regulate CD44 adhesiveness under flow condition. <i>Structure</i> , 2010 , 18, 649-56	5.2	48
895	Mapping the interactions between a major pollen allergen and human IgE antibodies. <i>Structure</i> , 2010 , 18, 1011-21	5.2	44
894	Structural insight into the zinc finger CW domain as a histone modification reader. <i>Structure</i> , 2010 , 18, 1127-39	5.2	93
893	Structural characterization of the DAXX N-terminal helical bundle domain and its complex with Rassf1C. <i>Structure</i> , 2010 , 18, 1642-53	5.2	22
892	Solution structure of Rv2377c-founding member of the MbtH-like protein family. 2010 , 90, 245-51		27

891	Solution structure of a Plasmodium falciparum AMA-1/MSP 1 chimeric protein vaccine candidate (PfCP-2.9) for malaria. 2010 , 9, 76		11
890	Interaction between separated consecutive complement control modules of human C1r: implications for dimerization of the full-length protease. 2010 , 584, 4565-9		3
889	Solution structure of the C-terminal X domain of the measles virus phosphoprotein and interaction with the intrinsically disordered C-terminal domain of the nucleoprotein. 2010 , 23, 435-47		70
888	Restricted domain mobility in the Candida albicans Ess1 prolyl isomerase. 2010 , 1804, 1537-41		5
887	Experimental approaches for NMR studies of side-chain dynamics in high-molecular-weight proteins. 2010 , 56, 1-45		52
886	NMR and crystallographic structures of the FK506 binding domain of human malarial parasite Plasmodium vivax FKBP35. <i>Protein Science</i> , 2010 , 19, 1577-86	6.3	22
885	Structure of an atypical Tudor domain in the Drosophila Polycomblike protein. <i>Protein Science</i> , 2010 , 19, 1906-16	6.3	16
884	Two-state conformational equilibrium in the Par-4 leucine zipper domain. 2010 , 78, 2433-49		8
883	X-ray crystallographic and NMR studies of pantothenate synthetase provide insights into the mechanism of homotropic inhibition by pantoate. 2010 , 277, 697-712		3
882	NMR solution structure and function of the C-terminal domain of eukaryotic class 1 polypeptide chain release factor. 2010 , 277, 2611-27		17
881	NMR backbone dynamics studies of human PED/PEA-15 outline protein functional sites. 2010 , 277, 4229	9-40	9
880	Cooperative interaction of transcription termination factors with the RNA polymerase II C-terminal domain. 2010 , 17, 1195-201		106
879	NMR structure and dynamics of the chimeric protein SH3-F2. 2010 , 44, 948-957		4
878	Dynamics connect substrate recognition to catalysis in protein kinase A. 2010 , 6, 821-8		155
877	Structural transformation of the tandem ubiquitin-interacting motifs in ataxin-3 and their cooperative interactions with ubiquitin chains. 2010 , 5, e13202		34
876	NMR characterizations of the ice binding surface of an antifreeze protein. 2010 , 5, e15682		9
875	A low affinity ground state conformation for the Dynein microtubule binding domain. <i>Journal of Biological Chemistry</i> , 2010 , 285, 15994-6002	5.4	11
874	Structure and function of the regulatory HRDC domain from human Bloom syndrome protein. <i>Nucleic Acids Research</i> , 2010 , 38, 7764-77	20.1	33

(2010-2010)

873	Structural basis for homodimerization of the Src-associated during mitosis, 68-kDa protein (Sam68) Qua1 domain. <i>Journal of Biological Chemistry</i> , 2010 , 285, 28893-901	5.4	32
872	Differences in the structure and dynamics of the apo- and palmitate-ligated forms of Aedes aegypti sterol carrier protein 2 (AeSCP-2). <i>Journal of Biological Chemistry</i> , 2010 , 285, 17046-53	5.4	9
871	Local conformation and dynamics of isoleucine in the collagenase cleavage site provide a recognition signal for matrix metalloproteinases. <i>Journal of Biological Chemistry</i> , 2010 , 285, 34181-90	5.4	28
870	When simple sequence comparison fails: the cryptic case of the shared domains of the bacterial replication initiation proteins DnaB and DnaD. <i>Nucleic Acids Research</i> , 2010 , 38, 6930-42	20.1	18
869	Analysis of the specific interactions between the lectin domain of malectin and diglucosides. 2010 , 20, 1010-20		46
868	Structural basis of O6-alkylguanine recognition by a bacterial alkyltransferase-like DNA repair protein. <i>Journal of Biological Chemistry</i> , 2010 , 285, 13736-41	5.4	19
867	Unique structural characteristics of the rabbit prion protein. <i>Journal of Biological Chemistry</i> , 2010 , 285, 31682-93	5.4	75
866	The binding mode of ATP revealed by the solution structure of the N-domain of human ATP7A. <i>Journal of Biological Chemistry</i> , 2010 , 285, 2537-44	5.4	20
865	Phosphorylation at S87 is enhanced in synucleinopathies, inhibits alpha-synuclein oligomerization, and influences synuclein-membrane interactions. 2010 , 30, 3184-98		207
864	Insights into function, catalytic mechanism, and fold evolution of selenoprotein methionine sulfoxide reductase B1 through structural analysis. <i>Journal of Biological Chemistry</i> , 2010 , 285, 33315-33	3 23	20
863	A large intrinsically disordered region in SKIP and its disorder-order transition induced by PPIL1 binding revealed by NMR. <i>Journal of Biological Chemistry</i> , 2010 , 285, 4951-63	5.4	24
862	Crystal and solution structures of an odorant-binding protein from the southern house mosquito complexed with an oviposition pheromone. 2010 , 107, 19102-7		96
861	Three arginine residues within the RGG box are crucial for ICP27 binding to herpes simplex virus 1 GC-rich sequences and for efficient viral RNA export. 2010 , 84, 6367-76		19
860	Structure and RNA recognition by the snRNA and snoRNA transport factor PHAX. 2010 , 16, 1205-16		13
859	The regulation of class IA PI 3-kinases by inter-subunit interactions. 2010 , 346, 87-114		63
858	Protein flexibility and conformational entropy in ligand design targeting the carbohydrate recognition domain of galectin-3. 2010 , 132, 14577-89		181
857	Millisecond timescale dynamics of human liver fatty acid binding protein: testing of its relevance to the ligand entry process. <i>Biophysical Journal</i> , 2010 , 98, 3054-61	2.9	26
856	Apparent tradeoff of higher activity in MMP-12 for enhanced stability and flexibility in MMP-3. <i>Biophysical Journal</i> , 2010 , 99, 273-83	2.9	15

855	NMR backbone dynamics of VEK-30 bound to the human plasminogen kringle 2 domain. <i>Biophysical Journal</i> , 2010 , 99, 302-12	2.9	11
854	Interpretation of biomolecular NMR spin relaxation parameters. 2010 , 88, 131-42		17
853	Structure-independent analysis of the breadth of the positional distribution of disordered groups in macromolecules from order parameters for long, variable-length vectors using NMR paramagnetic relaxation enhancement. 2010 , 132, 13346-56		31
852	NMR relaxation studies of an RNA-binding segment of the rous sarcoma virus gag polyprotein in free and bound states: a model for autoinhibition of assembly. <i>Biochemistry</i> , 2010 , 49, 4006-17	3.2	13
851	NMR characterization of copper-binding domains 4-6 of ATP7B. <i>Biochemistry</i> , 2010 , 49, 8468-77	3.2	33
850	The length of the bound fatty acid influences the dynamics of the acyl carrier protein and the stability of the thioester bond. <i>Biochemistry</i> , 2010 , 49, 470-7	3.2	25
849	Direct determination of the insulin-insulin receptor interface using transferred cross-saturation experiments. 2010 , 53, 1917-22		10
848	NMR structure of navel orangeworm moth pheromone-binding protein (AtraPBP1): implications for pH-sensitive pheromone detection. <i>Biochemistry</i> , 2010 , 49, 1469-76	3.2	44
847	Backbone amide dynamics studies of Apo-L75F-TrpR, a temperature-sensitive mutant of the tryptophan repressor protein (TrpR): comparison with the (15)N NMR relaxation profiles of wild-type and A77V mutant Apo-TrpR repressors. <i>Biochemistry</i> , 2010 , 49, 8006-19	3.2	3
846	Constraining binding hot spots: NMR and molecular dynamics simulations provide a structural explanation for enthalpy-entropy compensation in SH2-ligand binding. 2010 , 132, 11058-70		37
845	Long-range interaction networks in the function and fidelity of poliovirus RNA-dependent RNA polymerase studied by nuclear magnetic resonance. <i>Biochemistry</i> , 2010 , 49, 9361-71	3.2	45
844	Circular permutation of Bacillus circulans xylanase: a kinetic and structural study. <i>Biochemistry</i> , 2010 , 49, 2464-74	3.2	36
843	Importance of the C-terminal loop L137-S141 for the folding and folding stability of staphylococcal nuclease. <i>Biochemistry</i> , 2010 , 49, 4318-26	3.2	8
842	Mechanism for recognition of polyubiquitin chains: balancing affinity through interplay between multivalent binding and dynamics. 2010 , 132, 11247-58		27
841	Intrinsically disordered PEP-19 confers unique dynamic properties to apo and calcium calmodulin. <i>Biochemistry</i> , 2010 , 49, 10287-97	3.2	15
840	Detecting the "afterglow" of 13C NMR in proteins using multiple receivers. 2010 , 132, 18008-11		42
839	Comparison of entropic contributions to binding in a "hydrophilic" versus "hydrophobic" ligand-protein interaction. 2010 , 132, 8682-9		41
838	Monitoring real-time metabolism of living cells by fast two-dimensional NMR spectroscopy. 2010 , 82, 2405-11		36

(2010-2010)

837	Carbon-13 NMR relaxation study of the internal dynamics in cyclodextrins in isotropic solution. 2010 , 114, 59-65		11
836	Catalytic proficiency of ubiquitin conjugation enzymes: balancing pK(a) suppression, entropy, and electrostatics. 2010 , 132, 17775-86		20
835	Probing slow protein dynamics by adiabatic R(1rho) and R(2rho) NMR experiments. 2010 , 132, 9979-81		31
834	Structure, dynamics and thermodynamics of the human centrin 2/hSfi1 complex. <i>Journal of Molecular Biology</i> , 2010 , 395, 191-204	6.5	24
833	Increase in backbone mobility of the VTS1p-SAM domain on binding to SRE-RNA. <i>Journal of Molecular Biology</i> , 2010 , 396, 732-46	6.5	18
832	Conformational dynamics and structural plasticity play critical roles in the ubiquitin recognition of a UIM domain. <i>Journal of Molecular Biology</i> , 2010 , 396, 1128-44	6.5	19
831	Spatial structure of the transmembrane domain heterodimer of ErbB1 and ErbB2 receptor tyrosine kinases. <i>Journal of Molecular Biology</i> , 2010 , 400, 231-43	6.5	99
830	Backbone dynamics and global effects of an activating mutation in minimized Mtu RecA inteins. Journal of Molecular Biology, 2010 , 400, 755-67	6.5	22
829	Solution structure of histone chaperone ANP32B: interaction with core histones H3-H4 through its acidic concave domain. <i>Journal of Molecular Biology</i> , 2010 , 401, 97-114	6.5	23
828	The unfolded state of the murine prion protein and properties of single-point mutants related to human prion diseases. <i>Journal of Molecular Biology</i> , 2010 , 401, 7-12	6.5	16
827	Tail-mediated collapse of HMGB1 is dynamic and occurs via differential binding of the acidic tail to the A and B domains. <i>Journal of Molecular Biology</i> , 2010 , 403, 706-22	6.5	68
826	Using NMR to study fast dynamics in proteins: methods and applications. 2010 , 10, 723-30		60
825	Correlating structure, dynamics, and function in transmembrane segment VII of the Na+/H+ exchanger isoform 1. 2010 , 1798, 94-104		8
824	Backbone dynamics of the antifungal Psd1 pea defensin and its correlation with membrane interaction by NMR spectroscopy. 2010 , 1798, 105-13		72
823	Fast-time scale dynamics of outer membrane protein A by extended model-free analysis of NMR relaxation data. 2010 , 1798, 68-76		33
822	A method for solution NMR structural studies of large integral membrane proteins: reverse micelle encapsulation. 2010 , 1798, 150-60		26
821	The impact of window functions on NMR-based paramagnetic relaxation enhancement measurements in membrane proteins. 2010 , 1798, 140-9		13
820	NMR dynamics and antibody recognition of the meningococcal lipidated outer membrane protein LP2086 in micellar solution. 2010 , 1798, 87-93		19

819	Solution structure of Atg8 reveals conformational polymorphism of the N-terminal domain. 2010 , 395, 426-31		18
818	A quantitative NMR spectroscopic examination of the flexibility of the C-terminal extensions of the molecular chaperones, A - and B -crystallin. 2010 , 91, 691-9		50
817	Allostery and intrinsic disorder mediate transcription regulation by conditional cooperativity. 2010 , 142, 101-11		199
816	Elucidation of the structure of the membrane anchor of penicillin-binding protein 5 of Escherichia coli. 2010 , 132, 4110-8		6
815	Hierarchy of local structural and dynamics perturbations due to subdenaturing urea in the native state ensemble of DLC8 dimer. 2010 , 153, 17-26		8
814	Protein Dynamics as Reported by NMR. 2010 , 35-75		13
813	Free energy, entropy, and enthalpy of a water molecule in various protein environments. 2010 , 114, 115	552-60	33
812	Multi-domain conformational selection underlies pre-mRNA splicing regulation by U2AF. <i>Nature</i> , 2011 , 475, 408-11	50.4	156
811	Blue flickers of hope: secondary structure, dynamics, and putative dimerization interface of the blue-light receptor YtvA from Bacillus subtilis. <i>Biochemistry</i> , 2011 , 50, 8163-71	3.2	20
810	Structural characterization of Escherichia coli BamE, a lipoprotein component of the #barrel assembly machinery complex. <i>Biochemistry</i> , 2011 , 50, 1081-90	3.2	43
809	Structural and metal binding characterization of the C-terminal metallochaperone domain of membrane fusion protein SilB from Cupriavidus metallidurans CH34. <i>Biochemistry</i> , 2011 , 50, 2194-204	3.2	25
808	NSAID-based ⊡secretase modulators do not bind to the amyloid-#polypeptide. <i>Biochemistry</i> , 2011 , 50, 10328-42	3.2	20
807	1H-Detected 13C photo-CIDNP as a sensitivity enhancement tool in solution NMR. 2011 , 133, 8062-5		28
806	Boosting protein dynamics studies using quantitative nonuniform sampling NMR spectroscopy. 2011 , 115, 13740-5		25
805	Osteogenesis imperfecta missense mutations in collagen: structural consequences of a glycine to alanine replacement at a highly charged site. <i>Biochemistry</i> , 2011 , 50, 10771-80	3.2	22
804	NMR Structure of the C-terminal domain of a tyrosyl-tRNA synthetase that functions in group I intron splicing. <i>Biochemistry</i> , 2011 , 50, 3816-26	3.2	5
803	Structural signature of the MYPT1-PP1 interaction. 2011 , 133, 73-80		37
802	Solution structure of 4Lphosphopantetheine - GmACP3 from Geobacter metallireducens: a specialized acyl carrier protein with atypical structural features and a putative role in lipopolysaccharide biosynthesis. <i>Biochemistry</i> , 2011 , 50, 1442-53	3.2	6

801	Gramicidin A backbone and side chain dynamics evaluated by molecular dynamics simulations and nuclear magnetic resonance experiments. II: nuclear magnetic resonance experiments. 2011, 115, 7427-	32	5	
800	The metastasis-associated extracellular matrix protein osteopontin forms transient structure in ligand interaction sites. <i>Biochemistry</i> , 2011 , 50, 6113-24	3.2	56	
799	Structural characterization of partially disordered human Chibby: insights into its function in the Wnt-signaling pathway. <i>Biochemistry</i> , 2011 , 50, 715-26	3.2	18	
798	Determination of the rotational diffusion tensor of porphycene by 13C and 1H spin relaxation methods. 2011 , 115, 8604-7		3	
797	Structure and dynamics of Mycobacterium tuberculosis truncated hemoglobin N: insights from NMR spectroscopy and molecular dynamics simulations. <i>Biochemistry</i> , 2011 , 50, 11121-30	3.2	21	
796	Murine interleukin-3: structure, dynamics, and conformational heterogeneity in solution. Biochemistry, 2011 , 50, 2464-77	3.2	16	
795	High-resolution conformation and backbone dynamics of a soluble aggregate of apomyoglobin119. <i>Biophysical Journal</i> , 2011 , 100, 747-755	2.9	3	
794	Protein Dynamics. 2011 ,			
793	Motion of a disordered polypeptide chain as studied by paramagnetic relaxation enhancements, 15N relaxation, and molecular dynamics simulations: how fast is segmental diffusion in denatured ubiquitin?. 2011 , 133, 14614-28		45	
792	Characterization of intrinsically disordered prostate associated gene (PAGE5) at single residue resolution by NMR spectroscopy. 2011 , 6, e26633		18	
791	Conformational flexibility of a human immunoglobulin light chain variable domain by relaxation dispersion nuclear magnetic resonance spectroscopy: implications for protein misfolding and amyloid assembly. <i>Biochemistry</i> , 2011 , 50, 5845-57	3.2	19	
790	Solution structure of LCI, a novel antimicrobial peptide from Bacillus subtilis. <i>Biochemistry</i> , 2011 , 50, 3621-7	3.2	35	
7 ⁸ 9	Inaugural structure from the DUF3349 superfamily of proteins, Mycobacterium tuberculosis Rv0543c. 2011 , 506, 150-6		6	
788	Structural and functional characterization of the N-terminal domain of human Rad51D. 2011 , 43, 416-22	2	5	
787	Secondary structure, dynamics, and architecture of the p7 membrane protein from hepatitis C virus by NMR spectroscopy. 2011 , 1808, 1448-53		53	
786	Comparative NMR analysis of an 80-residue G protein-coupled receptor fragment in two membrane mimetic environments. 2011 , 1808, 2674-84		11	
7 ⁸ 5	Extraordinary 🛭 ms backbone dynamics in Arabidopsis thaliana peroxiredoxin Q. 2011 , 1814, 1880-90		18	
7 ⁸ 4	Conformational conversion during amyloid formation at atomic resolution. 2011 , 41, 161-72		142	

783	Solution NMR structure and dynamics of human apo-S100A1 protein. 2011, 174, 391-9		14
782	Multi-timescale dynamics study of FKBP12 along the rapamycin-mTOR binding coordinate. <i>Journal of Molecular Biology</i> , 2011 , 405, 378-94	6.5	27
781	NMR insights into the core of GED assembly by H/D exchange coupled with DMSO dissociation and analysis of the denatured state. <i>Journal of Molecular Biology</i> , 2011 , 405, 1202-14	6.5	10
7 ⁸ 0	The structural and dynamic response of MAGI-1 PDZ1 with noncanonical domain boundaries to the binding of human papillomavirus E6. <i>Journal of Molecular Biology</i> , 2011 , 406, 745-63	6.5	39
779	Association of the disordered C-terminus of CDC34 with a catalytically bound ubiquitin. <i>Journal of Molecular Biology</i> , 2011 , 407, 425-38	6.5	18
778	Lipid-mediated folding/unfolding of phospholamban as a regulatory mechanism for the sarcoplasmic reticulum Ca2+-ATPase. <i>Journal of Molecular Biology</i> , 2011 , 408, 755-65	6.5	45
777	Probing the determinants of diacylglycerol binding affinity in the C1B domain of protein kinase C\(\textit{Journal of Molecular Biology}\), 2011 , 408, 949-70	6.5	25
776	The NMR structure of FliK, the trigger for the switch of substrate specificity in the flagellar type III secretion apparatus. <i>Journal of Molecular Biology</i> , 2011 , 409, 558-73	6.5	26
775	Increased hydrophobicity and decreased backbone flexibility explain the lower solubility of a cataract-linked mutant of ID-crystallin. <i>Journal of Molecular Biology</i> , 2011 , 412, 647-59	6.5	17
774	Structural characterization of the interactions between palladin and 🗟 ctinin. <i>Journal of Molecular Biology</i> , 2011 , 413, 712-25	6.5	17
773	NMR characterisation of the relationship between frustration and the excited state of Im7. <i>Journal of Molecular Biology</i> , 2011 , 414, 511-29	6.5	16
772	VPS29 is not an active metallo-phosphatase but is a rigid scaffold required for retromer interaction with accessory proteins. 2011 , 6, e20420		46
771	In-cell NMR in E. coli to monitor maturation steps of hSOD1. 2011 , 6, e23561		49
770	Predicting protein-ligand binding sites based on an improved geometric algorithm. 2011 , 18, 997-1001		2
769	Hexameric architecture of CstF supported by CstF-50 homodimerization domain structure. 2011 , 17, 412-8		17
768	Solution NMR studies of A∄monomer dynamics. 2011 , 18, 354-61		7
767	Probing protein dynamics by nuclear magnetic resonance. 2011 , 18, 373-9		3
766	Membrane proteins structure and dynamics by nuclear magnetic resonance. 2011 , 1, 2175-87		1

765	Pilotin-secretin recognition in the type II secretion system of Klebsiella oxytoca. 2011 , 82, 1422-32	33
764	Intrinsic local disorder and a network of charge-charge interactions are key to actinoporin membrane disruption and cytotoxicity. 2011 , 278, 2080-9	20
763	Plasmodium falciparum apicoplast transit peptides are unstructured in vitro and during apicoplast import. 2011 , 12, 1124-38	22
762	Site-resolved measurement of water-protein interactions by solution NMR. 2011 , 18, 245-9	178
761	Structure and VP16 binding of the Mediator Med25 activator interaction domain. 2011 , 18, 404-9	74
760	The structure of MESD45-184 brings light into the mechanism of LDLR family folding. <i>Structure</i> , 2011 , 19, 337-48	7
759	Locked tether formation by cooperative folding of Rna14p monkeytail and Rna15p hinge domains in the yeast CF IA complex. <i>Structure</i> , 2011 , 19, 534-45	24
758	Structural basis for the Trembler-J phenotype of Charcot-Marie-Tooth disease. <i>Structure</i> , 2011 , 19, 1160-92	30
757	Parallel receivers and sparse sampling in multidimensional NMR. 2011 , 213, 1-13	24
756	Water proton spin saturation affects measured protein backbone 15N spin relaxation rates. 2011 , 213, 151-7	19
755	Protein dynamics and allostery: an NMR view. 2011 , 21, 62-7	190
754	A practical guide to protein dynamics from 15N spin relaxation in solution. 2011 , 59, 245-62	36
753	Intrinsic disorder in the common N-terminus of human adenovirus 5 E1B-55K and its related E1BN proteins indicated by studies on E1B-93R. 2011 , 418, 133-43	12
752	Two closely spaced tyrosines regulate NFAT signaling in B cells via Syk association with Vav. 2011 , 31, 2984-96	18
751	HMGB1-carbenoxolone interactions: dynamics insights from combined nuclear magnetic resonance and molecular dynamics. 2011 , 6, 1171-80	6
750	Temperature dependence of fast carbonyl backbone dynamics in chicken villin headpiece subdomain. 2011 , 50, 119-27	10
749	Solution structure, dynamics and thermodynamics of the three SH3 domains of CD2AP. 2011 , 50, 103-17	13
748	Active site dynamics in NADH oxidase from Thermus thermophilus studied by NMR spin relaxation. 2011 , 51, 71-82	4

747	Backbone assignment and dynamics of human Bynuclein in viscous 2 M glucose solution. <i>Biomolecular NMR Assignments</i> , 2011 , 5, 43-6	0.7	11
746	Solution structure of an arsenate reductase-related protein, YffB, from Brucella melitensis, the etiological agent responsible for brucellosis. 2011 , 67, 1129-36		5
745	Solution-state NMR structure and biophysical characterization of zinc-substituted rubredoxin B (Rv3250c) from Mycobacterium tuberculosis. 2011 , 67, 1148-53		8
744	Temperature-dependent oligomerization in M-crystallin: lead or lag toward cataract, an NMR perspective. 2011 , 79, 569-80		5
743	Structure, dynamics, and Hck interaction of full-length HIV-1 Nef. 2011 , 79, 1609-22		13
742	Tat peptide-calmodulin binding studies and bioinformatics of HIV-1 protein-calmodulin interactions. 2011 , 79, 2233-46		6
741	NMR structure and dynamics of recombinant wild type and mutated jerdostatin, a selective inhibitor of integrin 日日. 2011 , 79, 2530-42		10
740	Structural and biochemical analysis of mammalian methionine sulfoxide reductase B2. 2011 , 79, 3123-3	1	11
739	Solution structure of the human HSPC280 protein. <i>Protein Science</i> , 2011 , 20, 216-23	6.3	6
738	The N(0)-binding region of the vesicular stomatitis virus phosphoprotein is globally disordered but contains transient Helices. <i>Protein Science</i> , 2011 , 20, 542-56	6.3	46
737	Solution structure and backbone dynamics of the DNA-binding domain of FOXP1: insight into its domain swapping and DNA binding. <i>Protein Science</i> , 2011 , 20, 908-24	6.3	26
736	Nuclear magnetic resonance structure of calcium-binding protein 1 in a Ca(2+) -bound closed state: implications for target recognition. <i>Protein Science</i> , 2011 , 20, 1356-66	6.3	9
735	Expression and purification of the membrane protein p7 from hepatitis C virus. 2011, 96, 32-40		23
734	Peptide inhibitors of the malaria surface protein, apical membrane antigen 1: identification of key binding residues. 2011 , 95, 354-64		12
733	Binding energetics of ferredoxin-NADP+ reductase with ferredoxin and its relation to function. 2011 , 12, 2062-70		22
732	Structure determination and dynamics of protein-RNA complexes by NMR spectroscopy. 2011 , 58, 1-61		74
731	Recognition of unmodified histone H3 by the first PHD finger of bromodomain-PHD finger protein 2 provides insights into the regulation of histone acetyltransferases monocytic leukemic zinc-finger protein (MOZ) and MOZ-related factor (MORF). <i>Journal of Biological Chemistry</i> , 2011 , 286, 36944-55	5.4	49
730	Structural and mutational studies of a hyperthermophilic intein from DNA polymerase II of Pyrococcus abyssi. <i>Journal of Biological Chemistry</i> , 2011 , 286, 38638-38648	5.4	23

729	Structural insights into the dynamics and function of the C-terminus of the E. coli RNA chaperone Hfq. <i>Nucleic Acids Research</i> , 2011 , 39, 4900-15	20.1	65
728	Structural basis for the dual RNA-recognition modes of human Tra2-#RRM. <i>Nucleic Acids Research</i> , 2011 , 39, 1538-53	20.1	54
727	Reluctance to membrane binding enables accessibility of the synaptobrevin SNARE motif for SNARE complex formation. 2011 , 108, 12723-8		36
726	Solution structure of the state 1 conformer of GTP-bound H-Ras protein and distinct dynamic properties between the state 1 and state 2 conformers. <i>Journal of Biological Chemistry</i> , 2011 , 286, 3964	. 4-9 3	75
7 ² 5	Multivalent binding of formin-binding protein 21 (FBP21)-tandem-WW domains fosters protein recognition in the pre-spliceosome. <i>Journal of Biological Chemistry</i> , 2011 , 286, 38478-38487	5.4	18
724	Solution structure of tandem SH2 domains from Spt6 protein and their binding to the phosphorylated RNA polymerase II C-terminal domain. <i>Journal of Biological Chemistry</i> , 2011 , 286, 29218	- 29 220	6 ²⁷
723	Structural and biochemical characterization of NarE, an iron-containing ADP-ribosyltransferase from Neisseria meningitidis. <i>Journal of Biological Chemistry</i> , 2011 , 286, 14842-51	5.4	16
722	Structural and functional characterization of the Streptococcus pneumoniae RrgB pilus backbone D1 domain. <i>Journal of Biological Chemistry</i> , 2011 , 286, 14588-97	5.4	17
721	Interaction with polyglutamine-expanded huntingtin alters cellular distribution and RNA processing of huntingtin yeast two-hybrid protein A (HYPA). <i>Journal of Biological Chemistry</i> , 2011 , 286, 25236-45	5.4	21
720	Structural characterization of the Crimean-Congo hemorrhagic fever virus Gn tail provides insight into virus assembly. <i>Journal of Biological Chemistry</i> , 2011 , 286, 21678-86	5.4	32
719	Structures of Anabaena calcium-binding protein CcbP: insights into Ca2+ signaling during heterocyst differentiation. <i>Journal of Biological Chemistry</i> , 2011 , 286, 12381-8	5.4	17
718	Cisplatin binds human copper chaperone Atox1 and promotes unfolding in vitro. 2011 , 108, 6951-6		85
717	Structural dynamics and multiregion interactions in dynein-dynactin recognition. <i>Journal of Biological Chemistry</i> , 2011 , 286, 39349-59	5.4	27
716	Dynamically committed, uncommitted, and quenched states encoded in protein kinase A revealed by NMR spectroscopy. 2011 , 108, 6969-74		117
715	Dimer interface of the effector domain of non-structural protein 1 from influenza A virus: an interface with multiple functions. <i>Journal of Biological Chemistry</i> , 2011 , 286, 26050-60	5.4	45
714	Nuclear Magnetic Resonance (NMR) Spectroscopy of Metallobiomolecules. 2011 ,		4
713	Intrinsic disorder in measles virus nucleocapsids. 2011 , 108, 9839-44		151
712	Structure of the vesicular stomatitis virus NEP complex. 2011 , 7, e1002248		89

711	A component of the Xanthomonadaceae type IV secretion system combines a VirB7 motif with a N0 domain found in outer membrane transport proteins. 2011 , 7, e1002031		49
710	Structural elucidation and functional characterization of the Hyaloperonospora arabidopsidis effector protein ATR13. 2011 , 7, e1002428		45
709	Solution structure of the Pdp1 PWWP domain reveals its unique binding sites for methylated H4K20 and DNA. 2012 , 442, 527-38		43
708	Solution structure of IseA, an inhibitor protein of DL-endopeptidases from Bacillus subtilis, reveals a novel fold with a characteristic inhibitory loop. <i>Journal of Biological Chemistry</i> , 2012 , 287, 44736-48	5.4	10
707	CD2AP regulates SUMOylation of CIN85 in podocytes. 2012 , 32, 1068-79		15
706	Allostery. 2012,		4
705	Selective recruitment of an E2~ubiquitin complex by an E3 ubiquitin ligase. <i>Journal of Biological Chemistry</i> , 2012 , 287, 17374-17385	5.4	36
704	The zinc regulated antivirulence pathway of Salmonella is a multiprotein immunoglobulin adhesion system. <i>Journal of Biological Chemistry</i> , 2012 , 287, 32324-37	5.4	10
703	Structure of nucleophosmin DNA-binding domain and analysis of its complex with a G-quadruplex sequence from the c-MYC promoter. <i>Journal of Biological Chemistry</i> , 2012 , 287, 26539-48	5.4	43
702	The FF4 and FF5 domains of transcription elongation regulator 1 (TCERG1) target proteins to the periphery of speckles. <i>Journal of Biological Chemistry</i> , 2012 , 287, 17789-17800	5.4	12
701	Microneme protein 5 regulates the activity of Toxoplasma subtilisin 1 by mimicking a subtilisin prodomain. <i>Journal of Biological Chemistry</i> , 2012 , 287, 36029-40	5.4	15
700	The apo-structure of the low molecular weight protein-tyrosine phosphatase A (MptpA) from Mycobacterium tuberculosis allows for better target-specific drug development. <i>Journal of Biological Chemistry</i> , 2012 , 287, 34569-82	5.4	30
699	AIRE-PHD fingers are structural hubs to maintain the integrity of chromatin-associated interactome. <i>Nucleic Acids Research</i> , 2012 , 40, 11756-68	20.1	30
698	Structural and functional analysis of the archaeal endonuclease Nob1. <i>Nucleic Acids Research</i> , 2012 , 40, 3259-74	20.1	54
697	Determination of solution structures of proteins up to 40 kDa using CS-Rosetta with sparse NMR data from deuterated samples. 2012 , 109, 10873-8		151
696	Transient structure and dynamics in the disordered c-Myc transactivation domain affect Bin1 binding. <i>Nucleic Acids Research</i> , 2012 , 40, 6353-66	20.1	75
695	Structural flexibility of RNA as molecular basis for Hfq chaperone function. <i>Nucleic Acids Research</i> , 2012 , 40, 8072-84	20.1	27
694	Is a malleable protein necessarily highly dynamic? The hydrophobic core of the nuclear coactivator binding domain is well ordered. <i>Biophysical Journal</i> , 2012 , 102, 1627-35	2.9	17

693	Transiently populated intermediate functions as a branching point of the FF domain folding pathway. 2012 , 109, 17777-82		13
692	Internal motions and exchange processes in human ileal bile acid binding protein as studied by backbone (15)N nuclear magnetic resonance spectroscopy. <i>Biochemistry</i> , 2012 , 51, 1848-61	3.2	22
691	Carbohydrate affinity for the glucose-galactose binding protein is regulated by allosteric domain motions. 2012 , 134, 19869-76		30
690	The First structure of a lantibiotic immunity protein, SpaI from Bacillus subtilis, reveals a novel fold. Journal of Biological Chemistry, 2012 , 287, 35286-35298	5.4	19
689	The PNT domain from Drosophila pointed-P2 contains a dynamic N-terminal helix preceded by a disordered phosphoacceptor sequence. <i>Protein Science</i> , 2012 , 21, 1716-25	6.3	6
688	Solution NMR structure of a sheddase inhibitor prodomain from the malarial parasite Plasmodium falciparum. 2012 , 80, 2810-7		3
687	Measurement of ФN relaxation rates in perdeuterated proteins by TROSY-based methods. 2012 , 53, 209-21		127
686	A study on the influence of fast amide exchange on the accuracy of (15)N relaxation rate constants. 2012 , 54, 389-400		10
685	Solution NMR structure of Alr2454 from Nostoc sp. PCC 7120, the first structural representative of Pfam domain family PF11267. 2012 , 13, 171-6		3
684	Tuning the structural coupling between the transmembrane and cytoplasmic domains of phospholamban to control sarcoplasmic reticulum Ca(2+)-ATPase (SERCA) function. 2012 , 33, 485-92		16
683	The C-terminal domain of human Rev1 contains independent binding sites for DNA polymerase and Rev7 subunit of polymerase 2012 , 586, 3051-6		35
682	Solution structure of an atypical PHD finger in BRPF2 and its interaction with DNA. 2012 , 180, 165-73		38
681	Structural characterization of CHCHD5 and CHCHD7: two atypical human twin CX9C proteins. 2012 , 180, 190-200		23
680	The C-terminal sterile alpha motif (SAM) domain of human p73 is a highly dynamic protein, which acquires high thermal stability through a decrease in backbone flexibility. 2012 , 14, 10308-23		9
679	Denaturation of HIV-1 protease (PR) monomer by acetic acid: mechanistic and trajectory insights from molecular dynamics simulations and NMR. 2012 , 29, 893-903		4
678	Solution NMR structure, backbone dynamics, and heme-binding properties of a novel cytochrome c maturation protein CcmE from Desulfovibrio vulgaris. <i>Biochemistry</i> , 2012 , 51, 3705-7	3.2	8
677	SRLS analysis of 15N relaxation from bacteriophage T4 lysozyme: a tensorial perspective that features domain motion. 2012 , 116, 6118-27		7
676	Influence of heme post-translational modification and distal ligation on the backbone dynamics of a monomeric hemoglobin. <i>Biochemistry</i> , 2012 , 51, 5733-47	3.2	16

675	Local folding and misfolding in the PBX homeodomain from a three-state analysis of CPMG relaxation dispersion NMR data. 2012 , 116, 10317-29		13
674	Structural basis for matrix metalloproteinase 1-catalyzed collagenolysis. 2012 , 134, 2100-10		88
673	In vitro phosphorylation of the focal adhesion targeting domain of focal adhesion kinase by Src kinase. <i>Biochemistry</i> , 2012 , 51, 2213-23	3.2	7
672	Structural and biophysical insights into the ligand-free Pitx2 homeodomain and a ring dermoid of the cornea inducing homeodomain mutant. <i>Biochemistry</i> , 2012 , 51, 665-76	3.2	7
671	NMR structure and dynamics of the C-terminal domain from human Rev1 and its complex with Rev1 interacting region of DNA polymerase []Biochemistry, 2012 , 51, 5506-20	3.2	60
670	Identification of a hydrophobic cleft in the LytTR domain of AgrA as a locus for small molecule interactions that inhibit DNA binding. <i>Biochemistry</i> , 2012 , 51, 10035-43	3.2	33
669	Conformational and dynamic changes at the interface contribute to ligand binding by ubiquitin. <i>Biochemistry</i> , 2012 , 51, 8111-24	3.2	6
668	Transient structure and SH3 interaction sites in an intrinsically disordered fragment of the hepatitis C virus protein NS5A. <i>Journal of Molecular Biology</i> , 2012 , 420, 310-23	6.5	48
667	NMR and crystal structures of the Pyrococcus horikoshii RadA intein guide a strategy for engineering a highly efficient and promiscuous intein. <i>Journal of Molecular Biology</i> , 2012 , 421, 85-99	6.5	50
666	Structural and thermodynamic insight into the process of "weak" dimerization of the ErbB4 transmembrane domain by solution NMR. 2012 , 1818, 2158-70		50
665	The transiently ordered regions in intrinsically disordered ExsE are correlated with structural elements involved in chaperone binding. 2012 , 417, 129-34		7
664	Residual structure and dynamics in DMSO-d6 denatured dynein light chain protein. 2012 , 94, 231-41		6
663	The solution structure of the prototype foamy virus RNase H domain indicates an important role of the basic loop in substrate binding. 2012 , 9, 73		7
662	5.7 Solution NMR Spectroscopy of Integral Membrane Proteins. 2012 , 120-138		1
661	1.13 NMR Spectroscopy: NMR Relaxation Methods. 2012 , 216-244		1
660	Alpha proton detection based backbone assignment of intrinsically disordered proteins. 2012 , 895, 211-2	26	5
659	Isotope labeling methods for relaxation measurements. 2012 , 992, 63-82		3
658	Structure, dynamics and domain organization of the repeat protein Cin1 from the apple scab fungus. 2012 , 1824, 1118-28		8

(2012-2012)

657	AMP-activated protein kinase #subunit requires internal motion for optimal carbohydrate binding. <i>Biophysical Journal</i> , 2012 , 102, 305-14	2.9	18	
656	Solution structure and backbone dynamics of human liver fatty acid binding protein: fatty acid binding revisited. <i>Biophysical Journal</i> , 2012 , 102, 2585-94	2.9	40	
655	Structure, dynamics, and antimicrobial and immune modulatory activities of human LL-23 and its single-residue variants mutated on the basis of homologous primate cathelicidins. <i>Biochemistry</i> , 2012 , 51, 653-64	3.2	44	
654	Allostery and binding cooperativity of the catalytic subunit of protein kinase A by NMR spectroscopy and molecular dynamics simulations. 2012 , 87, 363-89		33	
653	NMR and fluorescence studies of drug binding to the first nucleotide binding domain of SUR2A. <i>Biochemistry</i> , 2012 , 51, 9211-22	3.2	7	
652	NMR studies on structure and dynamics of the monomeric derivative of BS-RNase: new insights for 3D domain swapping. 2012 , 7, e29076		13	
651	Structure of S. aureus HPPK and the discovery of a new substrate site inhibitor. 2012 , 7, e29444		19	
650	Structure and dynamics of the G121V dihydrofolate reductase mutant: lessons from a transition-state inhibitor complex. 2012 , 7, e33252		24	
649	Guanidine-HCl dependent structural unfolding of M-crystallin: fluctuating native state like topologies and intermolecular association. 2012 , 7, e42948		4	
648	Proliferating cell nuclear antigen (PCNA) interactions in solution studied by NMR. 2012 , 7, e48390		21	
647	The dynamical response of hen egg white lysozyme to the binding of a carbohydrate ligand. <i>Protein Science</i> , 2012 , 21, 1066-73	6.3	24	
646	Coupled motion in proteins revealed by pressure perturbation. 2012 , 134, 8543-50		83	
645	Signal transduction in receptor for advanced glycation end products (RAGE): solution structure of C-terminal rage (ctRAGE) and its binding to mDia1. <i>Journal of Biological Chemistry</i> , 2012 , 287, 5133-44	5.4	71	
644	Model of a six immunoglobulin-like domain fragment of filamin A (16-21) built using residual dipolar couplings. 2012 , 134, 6660-72		16	
643	Studying "invisible" excited protein states in slow exchange with a major state conformation. 2012 , 134, 8148-61		321	
642	Guanine nucleotides differentially modulate backbone dynamics of the STAS domain of the SulP/SLC26 transport protein Rv1739c of Mycobacterium tuberculosis. 2012 , 279, 420-36		2	
641	The alternatively spliced acid box region plays a key role in FGF receptor autoinhibition. <i>Structure</i> , 2012 , 20, 77-88	5.2	50	
640	The WSXWS motif in cytokine receptors is a molecular switch involved in receptor activation: insight from structures of the prolactin receptor. <i>Structure</i> , 2012 , 20, 270-82	5.2	54	

639	Solution structure analysis of the HPV16 E6 oncoprotein reveals a self-association mechanism required for E6-mediated degradation of p53. <i>Structure</i> , 2012 , 20, 604-17	5.2	90
638	Dynamics induced by \mathbb{H}lactam antibiotics in the active site of Bacillus subtilis L,D-transpeptidase. <i>Structure</i> , 2012 , 20, 850-61	5.2	25
637	NMR determines transient structure and dynamics in the disordered C-terminal domain of WASp interacting protein. <i>Biophysical Journal</i> , 2013 , 105, 481-93	2.9	21
636	Cooperative unfolding of compact conformations of the intrinsically disordered protein osteopontin. <i>Biochemistry</i> , 2013 , 52, 5167-75	3.2	61
635	Fast hydrogen exchange affects [I]N relaxation measurements in intrinsically disordered proteins. 2013 , 55, 249-56		13
634	Interaction of nonstructural protein 5A of the hepatitis C virus with Src homology 3 domains using noncanonical binding sites. <i>Biochemistry</i> , 2013 , 52, 6160-8	3.2	21
633	Backbone resonance assignments of the micro-RNA precursor binding region of human TRBP. <i>Biomolecular NMR Assignments</i> , 2013 , 7, 229-33	0.7	8
632	[H, [IC] and [I]N resonance assignments and peptide binding site chemical shift perturbation mapping for the Escherichia coli redox enzyme chaperone DmsD. <i>Biomolecular NMR Assignments</i> , 2013 , 7, 193-7	0.7	4
631	Nuclear Magnetic Resonance Methods for Studying Soluble, Fibrous, and Membrane-Embedded Proteins. 2013 , 23-48		2
630	The heterogeneous structural behavior of E7 from HPV16 revealed by NMR spectroscopy. 2013 , 14, 1	876-82	12
630 629	The heterogeneous structural behavior of E7 from HPV16 revealed by NMR spectroscopy. 2013 , 14, 1 A solution NMR investigation into the impaired self-assembly properties of two murine amelogenins containing the point mutations T21->I or P41->T. 2013 , 537, 217-24	876-82	12
	A solution NMR investigation into the impaired self-assembly properties of two murine		
629	A solution NMR investigation into the impaired self-assembly properties of two murine amelogenins containing the point mutations T21->I or P41->T. 2013 , 537, 217-24		12
629 628	A solution NMR investigation into the impaired self-assembly properties of two murine amelogenins containing the point mutations T21->I or P41->T. 2013 , 537, 217-24 Structure and dynamics of human Nedd4-1 WW3 in complex with the ENaC PY motif. 2013 , 1834, 163 Modeling of the [E43S]SNase-ssDNA-Cd(2+) complex: structural insight into the action of nuclease		12
629 628 627	A solution NMR investigation into the impaired self-assembly properties of two murine amelogenins containing the point mutations T21->I or P41->T. 2013 , 537, 217-24 Structure and dynamics of human Nedd4-1 WW3 in complex with the ENaC PY motif. 2013 , 1834, 163 Modeling of the [E43S]SNase-ssDNA-Cd(2+) complex: structural insight into the action of nuclease on ssDNA. 2013 , 532, 103-13 Conformational dynamics is more important than helical propensity for the folding of the all	2-41	12
629 628 627	A solution NMR investigation into the impaired self-assembly properties of two murine amelogenins containing the point mutations T21->I or P41->T. 2013, 537, 217-24 Structure and dynamics of human Nedd4-1 WW3 in complex with the ENaC PY motif. 2013, 1834, 163 Modeling of the [E43S]SNase-ssDNA-Cd(2+) complex: structural insight into the action of nuclease on ssDNA. 2013, 532, 103-13 Conformational dynamics is more important than helical propensity for the folding of the all thelical protein Im7. <i>Protein Science</i> , 2013, 22, 1722-38 Structural dynamics and topology of phosphorylated phospholamban homopentamer reveal its	2-41 6.3	12 25 4
629 628 627 626	A solution NMR investigation into the impaired self-assembly properties of two murine amelogenins containing the point mutations T21->I or P41->T. 2013, 537, 217-24 Structure and dynamics of human Nedd4-1 WW3 in complex with the ENaC PY motif. 2013, 1834, 163 Modeling of the [E43S]SNase-ssDNA-Cd(2+) complex: structural insight into the action of nuclease on ssDNA. 2013, 532, 103-13 Conformational dynamics is more important than helical propensity for the folding of the all Ehelical protein Im7. <i>Protein Science</i> , 2013, 22, 1722-38 Structural dynamics and topology of phosphorylated phospholamban homopentamer reveal its role in the regulation of calcium transport. <i>Structure</i> , 2013, 21, 2119-30 The arginine-rich RNA-binding motif of HIV-1 Rev is intrinsically disordered and folds upon RRE	6.3 5.2	12 25 4 36

(2013-2013)

621	Analysis of 15N-1H NMR relaxation in proteins by a combined experimental and molecular dynamics simulation approach: picosecond-nanosecond dynamics of the Rho GTPase binding domain of plexin-B1 in the dimeric state indicates allosteric pathways. 2013 , 117, 174-84	21
620	Microscopic insights into the NMR relaxation-based protein conformational entropy meter. 2013 , 135, 15092-100	105
619	Divergent evolution of protein conformational dynamics in dihydrofolate reductase. 2013 , 20, 1243-9	104
618	The dynamics of dendrimers by NMR relaxation: interpretation pitfalls. 2013, 135, 1972-7	42
617	Solution structure of Escherichia coli FeoA and its potential role in bacterial ferrous iron transport. 2013 , 195, 46-55	35
616	Iron-sulfur cluster binding by mitochondrial monothiol glutaredoxin-1 of Trypanosoma brucei: molecular basis of iron-sulfur cluster coordination and relevance for parasite infectivity. 2013 , 19, 665-82	33
615	Impact of calcium binding and thionylation of S100A1 protein on its nuclear magnetic resonance-derived structure and backbone dynamics. <i>Biochemistry</i> , 2013 , 52, 1149-59	17
614	Unraveling the mechanism of protein disaggregation through a ClpB-DnaK interaction. 2013 , 339, 1080-3	193
613	Heterotypic Sam-Sam association between Odin-Sam1 and Arap3-Sam: binding affinity and structural insights. 2013 , 14, 100-6	13
612	NMR investigations of structural and dynamics features of natively unstructured drug peptide - salmon calcitonin: implication to rational design of potent sCT analogs. 2013 , 19, 33-45	9
611	Interaction of the eukaryotic initiation factor 4E with 4E-BP2 at a dynamic bipartite interface. Structure, 2013, 21, 2186-96 5.2	64
610	Colocalization of fast and slow timescale dynamics in the allosteric signaling protein CheY. <i>Journal of Molecular Biology</i> , 2013 , 425, 2372-81	26
609	Solution structure and dynamics of C-terminal regulatory domain of Vibrio vulnificus extracellular metalloprotease. 2013 , 430, 541-6	10
608	Structural and dynamics characterization of norovirus protease. <i>Protein Science</i> , 2013 , 22, 347-57 6.3	16
607	Structural insights into the Trp-cage folding intermediate formation. 2013 , 19, 2628-40	45
606	Interactions of Anopheles gambiae odorant-binding proteins with a human-derived repellent: implications for the mode of action of n,n-diethyl-3-methylbenzamide (DEET). <i>Journal of Biological</i> 5.4 <i>Chemistry</i> , 2013 , 288, 4475-85	33
605	A surprising role for conformational entropy in protein function. 2013 , 337, 69-94	26
604	Solution structure, dynamics and binding studies of a family 11 carbohydrate-binding module from Clostridium thermocellum (CtCBM11). 2013 , 451, 289-300	15

603 Protein Dynamics. **2013**, 289-310

602	BEST-TROSY experiments for time-efficient sequential resonance assignment of large disordered proteins. 2013 , 55, 311-21		141
601	Three-dimensional structure of the actinoporin sticholysin I. Influence of long-distance effects on protein function. 2013 , 532, 39-45		41
600	Probing arginine side-chains and their dynamics with carbon-detected NMR spectroscopy: application to the 42 kDa human histone deacetylase 8 at high pH. 2013 , 52, 3145-7		30
599	Structure and dynamics of the fish eye lens protein, IM7-crystallin. <i>Biochemistry</i> , 2013 , 52, 3579-87	3.2	14
598	Ligand-induced dynamic changes in extended PDZ domains from NHERF1. <i>Journal of Molecular Biology</i> , 2013 , 425, 2509-28	6.5	25
597	Structural basis for protein trans-splicing by a bacterial intein-like domainprotein ligation without nucleophilic side chains. 2013 , 280, 3256-69		10
596	Solution nuclear magnetic resonance structure of the GATase subunit and structural basis of the interaction between GATase and ATPPase subunits in a two-subunit-type GMPS from Methanocaldococcus jannaschii. <i>Biochemistry</i> , 2013 , 52, 4308-23	3.2	5
595	Solution structure of the Q41N variant of ubiquitin as a model for the alternatively folded N2 state of ubiquitin. <i>Biochemistry</i> , 2013 , 52, 1874-85	3.2	23
594	NMR studies of the dynamics of nitrophorin 2 bound to nitric oxide. <i>Biochemistry</i> , 2013 , 52, 7910-25	3.2	4
593	Nuclear magnetic resonance solution structure of the peptidoglycan-binding SPOR domain from Escherichia coli DamX: insights into septal localization. <i>Biochemistry</i> , 2013 , 52, 627-39	3.2	11
592	The denatured state ensemble contains significant local and long-range structure under native conditions: analysis of the N-terminal domain of ribosomal protein L9. <i>Biochemistry</i> , 2013 , 52, 2662-71	3.2	23
591	The structure of integrin &I domain in complex with a collagen-mimetic peptide. <i>Journal of Biological Chemistry</i> , 2013 , 288, 36796-809	5.4	19
590	Enhanced accuracy of kinetic information from CT-CPMG experiments by transverse rotating-frame spectroscopy. 2013 , 57, 73-82		18
589	Probing Arginine Side-Chains and Their Dynamics with Carbon-Detected NMR Spectroscopy: Application to the 42 kDa Human Histone Deacetylase 8 at High pH. 2013 , 125, 3227-3229		6
588	Regulatory R region of the CFTR chloride channel is a dynamic integrator of phospho-dependent intra- and intermolecular interactions. 2013 , 110, E4427-36		110
587	Hydramacin-1 in action: scrutinizing the barnacle model. 2013 , 57, 2955-66		8
586	The methyltransferase NSD3 has chromatin-binding motifs, PHD5-C5HCH, that are distinct from other NSD (nuclear receptor SET domain) family members in their histone H3 recognition. <i>Journal of Biological Chemistry</i> , 2013 , 288, 4692-703	5.4	41

585	Atomic resolution description of the interaction between the nucleoprotein and phosphoprotein of Hendra virus. 2013 , 9, e1003631		56
584	Analysing the visible conformational substates of the FK506-binding protein FKBP12. 2013 , 453, 371-80		17
583	Solution NMR analyses of the C-type carbohydrate recognition domain of DC-SIGNR protein reveal different binding modes for HIV-derived oligosaccharides and smaller glycan fragments. <i>Journal of Biological Chemistry</i> , 2013 , 288, 22745-57	5.4	13
582	Structural features of Argonaute-GW182 protein interactions. 2013 , 110, E3770-9		78
581	Structure, phosphorylation and U2AF65 binding of the N-terminal domain of splicing factor 1 during 3Lsplice site recognition. <i>Nucleic Acids Research</i> , 2013 , 41, 1343-54	20.1	38
580	Structures of apo- and ssDNA-bound YdbC from Lactococcus lactis uncover the function of protein domain family DUF2128 and expand the single-stranded DNA-binding domain proteome. <i>Nucleic Acids Research</i> , 2013 , 41, 2756-68	20.1	8
579	Structural basis for complement evasion by Lyme disease pathogen Borrelia burgdorferi. <i>Journal of Biological Chemistry</i> , 2013 , 288, 18685-95	5.4	40
578	Crystal and NMR structures give insights into the role and dynamics of subunit F of the eukaryotic V-ATPase from Saccharomyces cerevisiae. <i>Journal of Biological Chemistry</i> , 2013 , 288, 11930-9	5.4	8
577	Solution structure of mouse hepatitis virus (MHV) nsp3a and determinants of the interaction with MHV nucleocapsid (N) protein. 2013 , 87, 3502-15		26
576	Long-lived states in an intrinsically disordered protein domain. 2013 , 51, 729-33		9
576 575	Long-lived states in an intrinsically disordered protein domain. 2013, 51, 729-33 Role of the two structural domains from the periplasmic Escherichia coli histidine-binding protein HisJ. <i>Journal of Biological Chemistry</i> , 2013, 288, 31409-22	5.4	9
	Role of the two structural domains from the periplasmic Escherichia coli histidine-binding protein	- /	
575	Role of the two structural domains from the periplasmic Escherichia coli histidine-binding protein HisJ. <i>Journal of Biological Chemistry</i> , 2013 , 288, 31409-22 Structure of the mouse sex peptide pheromone ESP1 reveals a molecular basis for specific binding	- /	18
575 574	Role of the two structural domains from the periplasmic Escherichia coli histidine-binding protein HisJ. <i>Journal of Biological Chemistry</i> , 2013 , 288, 31409-22 Structure of the mouse sex peptide pheromone ESP1 reveals a molecular basis for specific binding to the class C G-protein-coupled vomeronasal receptor. <i>Journal of Biological Chemistry</i> , 2013 , 288, 16064 Structural insights into the role of the cyclic backbone in a squash trypsin inhibitor. <i>Journal of</i>	1 ⁵ 72	18
575 574 573	Role of the two structural domains from the periplasmic Escherichia coli histidine-binding protein HisJ. <i>Journal of Biological Chemistry</i> , 2013 , 288, 31409-22 Structure of the mouse sex peptide pheromone ESP1 reveals a molecular basis for specific binding to the class C G-protein-coupled vomeronasal receptor. <i>Journal of Biological Chemistry</i> , 2013 , 288, 16064 Structural insights into the role of the cyclic backbone in a squash trypsin inhibitor. <i>Journal of Biological Chemistry</i> , 2013 , 288, 36141-8 Structure of RNA-interacting cyclophilin A-like protein from Piriformospora indica that provides	1 ⁵ 72 5·4	18 15 34
575 574 573	Role of the two structural domains from the periplasmic Escherichia coli histidine-binding protein HisJ. <i>Journal of Biological Chemistry</i> , 2013 , 288, 31409-22 Structure of the mouse sex peptide pheromone ESP1 reveals a molecular basis for specific binding to the class C G-protein-coupled vomeronasal receptor. <i>Journal of Biological Chemistry</i> , 2013 , 288, 1606. Structural insights into the role of the cyclic backbone in a squash trypsin inhibitor. <i>Journal of Biological Chemistry</i> , 2013 , 288, 36141-8 Structure of RNA-interacting cyclophilin A-like protein from Piriformospora indica that provides salinity-stress tolerance in plants. <i>Scientific Reports</i> , 2013 , 3, 3001	1 ⁵ 72 5·4	18 15 34 29
575 574 573 572 571	Role of the two structural domains from the periplasmic Escherichia coli histidine-binding protein HisJ. <i>Journal of Biological Chemistry</i> , 2013 , 288, 31409-22 Structure of the mouse sex peptide pheromone ESP1 reveals a molecular basis for specific binding to the class C G-protein-coupled vomeronasal receptor. <i>Journal of Biological Chemistry</i> , 2013 , 288, 1606. Structural insights into the role of the cyclic backbone in a squash trypsin inhibitor. <i>Journal of Biological Chemistry</i> , 2013 , 288, 36141-8 Structure of RNA-interacting cyclophilin A-like protein from Piriformospora indica that provides salinity-stress tolerance in plants. <i>Scientific Reports</i> , 2013 , 3, 3001 Electron self-exchange of cytochrome c measured via13C detected protonless NMR. 2013 , 17, 142-149 Molecular basis of glycosaminoglycan heparin binding to the chemokine CXCL1 dimer. <i>Journal of</i>	1 ⁵ √2 5·4 4·9	18 15 34 29 3

567	Cluster and fold stability of E. coli ISC-type ferredoxin. 2013 , 8, e78948		8
566	Solution structure and Rpn1 interaction of the UBL domain of human RNA polymerase II C-terminal domain phosphatase. 2013 , 8, e62981		6
565	The C-terminal V5 domain of Protein Kinase Clas intrinsically disordered, with propensity to associate with a membrane mimetic. 2013 , 8, e65699		13
564	Measuring dynamic and kinetic information in the previously inaccessible supra-(c) window of nanoseconds to microseconds by solution NMR spectroscopy. 2013 , 18, 11904-37		31
563	Dynamics of linker residues modulate the nucleic acid binding properties of the HIV-1 nucleocapsid protein zinc fingers. 2014 , 9, e102150		13
562	Molecular basis for impaired DNA damage response function associated with the RAP80 E 81 defect. <i>Journal of Biological Chemistry</i> , 2014 , 289, 12852-62	5.4	8
561	Backbone-independent nucleic acid binding by splicing factor SUP-12 reveals key aspects of molecular recognition. <i>Nature Communications</i> , 2014 , 5, 4595	17.4	16
560	The TFE-induced transient native-like structure of the intrinsically disordered domain of Escherichia coli RNA polymerase. 2014 , 43, 581-94		7
559	Structural insights into the mechanism of negative regulation of single-box high mobility group proteins by the acidic tail domain. <i>Journal of Biological Chemistry</i> , 2014 , 289, 29817-26	5.4	13
558	Structure of transmembrane domain of lysosome-associated membrane protein type 2a (LAMP-2A) reveals key features for substrate specificity in chaperone-mediated autophagy. <i>Journal of Biological Chemistry</i> , 2014 , 289, 35111-23	5.4	48
557	NMR characterization of the near native and unfolded states of the PTB domain of Dok1: alternate conformations and residual clusters. 2014 , 9, e90557		7
556	Role of electrostatic interactions in binding of peptides and intrinsically disordered proteins to their folded targets. 1. NMR and MD characterization of the complex between the c-Crk N-SH3 domain and the peptide Sos. <i>Biochemistry</i> , 2014 , 53, 6473-95	3.2	29
555	Outer-membrane lipoprotein LpoB spans the periplasm to stimulate the peptidoglycan synthase PBP1B. 2014 , 111, 8197-202		77
554	Structure of the membrane anchor of pestivirus glycoprotein E(rns), a long tilted amphipathic helix. 2014 , 10, e1003973		23
553	RNA recognition and self-association of CPEB4 is mediated by its tandem RRM domains. <i>Nucleic Acids Research</i> , 2014 , 42, 10185-95	20.1	6
552	Conformational flexibility in the binding surface of the potassium channel blocker ShK. 2014 , 15, 2402-1	0	11
551	Structure of bacterial transcription factor SpoIIID and evidence for a novel mode of DNA binding. 2014 , 196, 2131-42		4
550	Collapse of the native structure caused by a single amino acid exchange in human NAD(P)H:quinone oxidoreductase(1.). 2014 , 281, 4691-4704		45

549	Novel RNA recognition motif domain in the cytoplasmic polyadenylation element binding protein 3. 2014 , 82, 2879-86		2
548	Structural and mechanistic insights into the interaction between Pyk2 and paxillin LD motifs. <i>Journal of Molecular Biology</i> , 2014 , 426, 3985-4001	6.5	11
547	Structural insights into activation of the retinal L-type Ca†+ channel (Cav1.4) by Ca†+-binding protein 4 (CaBP4). <i>Journal of Biological Chemistry</i> , 2014 , 289, 31262-73	5.4	10
546	Stochastic gate dynamics regulate the catalytic activity of ubiquitination enzymes. 2014 , 136, 17446-58		14
545	Structural characterization of a flexible two-domain protein in solution using small angle X-ray scattering and NMR data. <i>Structure</i> , 2014 , 22, 1862-1874	5.2	6
544	Characterization of the interaction between HMGB1 and H3-a possible means of positioning HMGB1 in chromatin. <i>Nucleic Acids Research</i> , 2014 , 42, 848-59	20.1	28
543	Long-chain flavodoxin FldB from Escherichia coli. 2014 , 60, 283-8		
542	Retinoblastoma-binding protein 1 has an interdigitated double Tudor domain with DNA binding activity. <i>Journal of Biological Chemistry</i> , 2014 , 289, 4882-95	5.4	14
541	Intramolecular binding mode of the C-terminus of Escherichia coli single-stranded DNA binding protein determined by nuclear magnetic resonance spectroscopy. <i>Nucleic Acids Research</i> , 2014 , 42, 2750) 2 0.1	34
540	Structural and biophysical characterization of Staphylococcus aureus SaMazF shows conservation of functional dynamics. <i>Nucleic Acids Research</i> , 2014 , 42, 6709-25	20.1	27
539	A novel non-canonical forkhead-associated (FHA) domain-binding interface mediates the interaction between Rad53 and Dbf4 proteins. <i>Journal of Biological Chemistry</i> , 2014 , 289, 2589-99	5.4	13
538	Dimeric switch of Hakai-truncated monomers during substrate recognition: insights from solution studies and NMR structure. <i>Journal of Biological Chemistry</i> , 2014 , 289, 25611-23	5.4	11
537	Multiple functional roles of the accessory I-domain of bacteriophage P22 coat protein revealed by NMR structure and CryoEM modeling. <i>Structure</i> , 2014 , 22, 830-41	5.2	35
536	Identification of an actin binding surface on vinculin that mediates mechanical cell and focal adhesion properties. <i>Structure</i> , 2014 , 22, 697-706	5.2	38
535	p15PAF is an intrinsically disordered protein with nonrandom structural preferences at sites of interaction with other proteins. <i>Biophysical Journal</i> , 2014 , 106, 865-74	2.9	42
534	Evidence against the "Y-T coupling" mechanism of activation in the response regulator NtrC. <i>Journal of Molecular Biology</i> , 2014 , 426, 1554-67	6.5	23
533	Solution structure of CEH-37 homeodomain of the nematode Caenorhabditis elegans. 2014 , 443, 370-5		О
532	A probe to monitor performance of IIIN longitudinal relaxation experiments for proteins in solution. 2014 , 58, 113-22		2

531	NMR-monitored titration of acid-stress bacterial chaperone HdeA reveals that Asp and Glu charge neutralization produces a loosened dimer structure in preparation for protein unfolding and chaperone activation. <i>Protein Science</i> , 2014 , 23, 167-78	6.3	19
530	Structure of the mitochondrial translocator protein in complex with a diagnostic ligand. 2014 , 343, 136	3-6	182
529	NMR studies of interactions between Bax and BH3 domain-containing peptides in the absence and presence of CHAPS. 2014 , 545, 33-43		10
528	The sea anemone actinoporin (Arg-Gly-Asp) conserved motif is involved in maintaining the competent oligomerization state of these pore-forming toxins. 2014 , 281, 1465-78		27
527	Optimized reverse micelle surfactant system for high-resolution NMR spectroscopy of encapsulated proteins and nucleic acids dissolved in low viscosity fluids. 2014 , 136, 3465-74		45
526	Thermodynamic and structural investigation of the specific SDS binding of Humicola insolens cutinase. <i>Protein Science</i> , 2014 , 23, 1023-35	6.3	26
525	Flexible and rigid structures in HIV-1 p17 matrix protein monitored by relaxation and amide proton exchange with NMR. 2014 , 1844, 520-6		5
524	Structure of human Sp140 PHD finger: an atypical fold interacting with Pin1. 2014 , 281, 216-31		15
523	The structure of TAX1BP1 UBZ1+2 provides insight into target specificity and adaptability. <i>Journal of Molecular Biology</i> , 2014 , 426, 674-90	6.5	9
522	Functional implications of large backbone amplitude motions of the glycoprotein 130-binding epitope of interleukin-6. 2014 , 281, 2471-83		5
521	Insight into the allosteric mechanism of Scapharca dimeric hemoglobin. <i>Biochemistry</i> , 2014 , 53, 7199-27	103.2	20
520	Photoconversion changes bilin chromophore conjugation and protein secondary structure in the violet/orange cyanobacteriochrome NpF2164g3L[corrected]. 2014 , 13, 951-62		30
519	NMR structure of the human Rad18 zinc finger in complex with ubiquitin defines a class of UBZ domains in proteins linked to the DNA damage response. <i>Biochemistry</i> , 2014 , 53, 5895-906	3.2	20
518	Temperature dependence of backbone dynamics in human ileal bile acid-binding protein: implications for the mechanism of ligand binding. <i>Biochemistry</i> , 2014 , 53, 5186-98	3.2	6
517	Structural basis for RNA recognition in roquin-mediated post-transcriptional gene regulation. 2014 , 21, 671-8		63
516	NMR characterization of the conformational fluctuations of the human lymphocyte function-associated antigen-1 I-domain. <i>Protein Science</i> , 2014 , 23, 1596-606	6.3	7
515	Probing the non-native H helix translocation in apomyoglobin folding intermediates. <i>Biochemistry</i> , 2014 , 53, 3767-80	3.2	10
514	Structural basis of the activation and degradation mechanisms of the E3 ubiquitin ligase Nedd4L. <i>Structure</i> , 2014 , 22, 1446-57	5.2	42

513	A compare-and-contrast NMR dynamics study of two related RRMs: U1A and SNF. <i>Biophysical Journal</i> , 2014 , 107, 208-19	2.9	4
512	Long-range effects of tag sequence on marginally stabilized structure in HIV-1 p24 capsid protein monitored using NMR. 2014 , 1844, 1638-47		
511	Conformational propensities and dynamics of a 即crystallin, an intrinsically disordered protein. 2014 , 16, 12703-18		5
510	Dynamic Pictures of Proteins by NMR. 2014 , 1-66		5
509	Structural characterization of the C3 domain of cardiac myosin binding protein C and its hypertrophic cardiomyopathy-related R502W mutant. <i>Biochemistry</i> , 2014 , 53, 5332-42	3.2	10
508	Exploring the backbone dynamics of native spider silk proteins in Black Widow silk glands with solution-state NMR spectroscopy. 2014 , 55, 3879-3885		19
507	Dynamic and thermodynamic response of the Ras protein Cdc42Hs upon association with the effector domain of PAK3. <i>Journal of Molecular Biology</i> , 2014 , 426, 3520-38	6.5	7
506	Intrinsic disorder within the erythrocyte binding-like proteins from Plasmodium falciparum. 2014 , 1844, 2306-14		8
505	Ligand-dependent dynamics of the active-site lid in bacterial dimethylarginine dimethylaminohydrolase. <i>Biochemistry</i> , 2014 , 53, 1092-104	3.2	4
504	Study of the structural and dynamic effects in the FimH adhesin upon ⊞-heptyl mannose binding. 2014 , 57, 1416-27		38
503	Structure of the small Dictyostelium discoideum myosin light chain MlcB provides insights into MyoB IQ motif recognition. <i>Journal of Biological Chemistry</i> , 2014 , 289, 17030-42	5.4	3
502	Solution NMR structure and functional analysis of the integral membrane protein YgaP from Escherichia coli. <i>Journal of Biological Chemistry</i> , 2014 , 289, 23482-503	5.4	13
501	Bound or free: interaction of the C-terminal domain of Escherichia coli single-stranded DNA-binding protein (SSB) with the tetrameric core of SSB. <i>Biochemistry</i> , 2014 , 53, 1925-34	3.2	32
500	Elements and modulation of functional dynamics. 2014 , 57, 7819-37		14
499	Steric mechanism of auto-inhibitory regulation of specific and non-specific DNA binding by the ETS transcriptional repressor ETV6. <i>Journal of Molecular Biology</i> , 2014 , 426, 1390-406	6.5	34
498	Proton-decoupled CPMG: a better experiment for measuring (15)N R2 relaxation in disordered proteins. 2014 , 241, 155-69		17
497	Solution structure of the TatB component of the twin-arginine translocation system. 2014 , 1838, 1881-8		35
496	Solution structure of Rv0569, potent hypoxic signal transduction protein, from Mycobacterium tuberculosis. 2014 , 94, 43-50		О

495	Ebolavirus entry requires a compact hydrophobic fist at the tip of the fusion loop. 2014 , 88, 6636-49		33
494	Capping of the N-terminus of PSD-95 by calmodulin triggers its postsynaptic release. 2014 , 33, 1341-53		49
493	DNA binding by Sgf11 protein affects histone H2B deubiquitination by Spt-Ada-Gcn5-acetyltransferase (SAGA). <i>Journal of Biological Chemistry</i> , 2014 , 289, 8989-99	5.4	19
492	Molecular basis for the wide range of affinity found in Csr/Rsm protein-RNA recognition. <i>Nucleic Acids Research</i> , 2014 , 42, 5332-46	20.1	60
491	Structure determination of archaea-specific ribosomal protein L46a reveals a novel protein fold. 2014 , 450, 67-72		1
490	Asymmetric perturbations of signalling oligomers. 2014 , 114, 153-69		11
489	Characterization of the near native conformational states of the SAM domain of Ste11 protein by NMR spectroscopy. 2014 , 82, 2957-69		1
488	Solution structure of an avirulence protein, AVR-Pia, from Magnaporthe oryzae. 2015 , 63, 229-35		12
487	Structural Analysis of the Pin1-CPEB1 interaction and its potential role in CPEB1 degradation. <i>Scientific Reports</i> , 2015 , 5, 14990	4.9	11
486	Disruption of the autoinhibited state primes the E3 ligase parkin for activation and catalysis. 2015 , 34, 2506-21		119
486 485		'-778	119
	34, 2506-21		
485	34, 2506-21 Conditional Membrane Proteins: Solution NMR Studies of Structure, Dynamics, and Function. 2015, 767		1
485 484	34, 2506-21 Conditional Membrane Proteins: Solution NMR Studies of Structure, Dynamics, and Function. 2015, 767 HdeB chaperone activity is coupled to its intrinsic dynamic properties. <i>Scientific Reports</i> , 2015, 5, 16856 Structural determination of virus protein U from HIV-1 by NMR in membrane environments. 2015,		1
485 484 483	Conditional Membrane Proteins: Solution NMR Studies of Structure, Dynamics, and Function. 2015, 767 HdeB chaperone activity is coupled to its intrinsic dynamic properties. <i>Scientific Reports</i> , 2015, 5, 16856 Structural determination of virus protein U from HIV-1 by NMR in membrane environments. 2015, 1848, 3007-3018 Structure-Free Validation of Residual Dipolar Coupling and Paramagnetic Relaxation Enhancement	4.9	1 13 11
485 484 483 482	Conditional Membrane Proteins: Solution NMR Studies of Structure, Dynamics, and Function. 2015, 767 HdeB chaperone activity is coupled to its intrinsic dynamic properties. <i>Scientific Reports</i> , 2015, 5, 16856 Structural determination of virus protein U from HIV-1 by NMR in membrane environments. 2015, 1848, 3007-3018 Structure-Free Validation of Residual Dipolar Coupling and Paramagnetic Relaxation Enhancement Measurements of Disordered Proteins. <i>Biochemistry</i> , 2015, 54, 6876-86	4.9	1 13 11 15
485 484 483 482 481	Conditional Membrane Proteins: Solution NMR Studies of Structure, Dynamics, and Function. 2015, 767 HdeB chaperone activity is coupled to its intrinsic dynamic properties. <i>Scientific Reports</i> , 2015, 5, 16856 Structural determination of virus protein U from HIV-1 by NMR in membrane environments. 2015, 1848, 3007-3018 Structure-Free Validation of Residual Dipolar Coupling and Paramagnetic Relaxation Enhancement Measurements of Disordered Proteins. <i>Biochemistry</i> , 2015, 54, 6876-86 Conformational Flexibility in the Transmembrane Protein TSPO. 2015, 21, 16555-63 Functional conformer of c-Myb DNA-binding domain revealed by variable temperature studies.	4.9	1 13 11 15 15

(2015-2015)

477	2015, 28, 316-24		1	
476	NMR and MD Studies Reveal That the Isolated Dengue NS3 Protease Is an Intrinsically Disordered Chymotrypsin Fold Which Absolutely Requests NS2B for Correct Folding and Functional Dynamics. 2015 , 10, e0134823		30	
475	Biophysical Studies on BEX3, the p75NTR-Associated Cell Death Executor, Reveal a High-Order Oligomer with Partially Folded Regions. 2015 , 10, e0137916		6	
474	Local destabilization of the metal-binding region in human copper-zinc superoxide dismutase by remote mutations is a possible determinant for progression of ALS. <i>Biochemistry</i> , 2015 , 54, 323-33	3.2	7	
473	An optimized method for (15)N R(1) relaxation rate measurements in non-deuterated proteins. 2015 , 62, 209-20		10	
472	Structural and Functional Analysis of the Signal-Transducing Linker in the pH-Responsive One-Component System CadC of Escherichia coli. <i>Journal of Molecular Biology</i> , 2015 , 427, 2548-2561	6.5	20	
471	Halophilic Protein Adaptation Results from Synergistic Residue-Ion Interactions in the Folded and Unfolded States. 2015 , 22, 1597-607		29	
470	NMR-based Structural Analysis of Threonylcarbamoyl-AMP Synthase and Its Substrate Interactions. Journal of Biological Chemistry, 2015 , 290, 20032-43	5.4	9	
469	Interactions of Yeast Dynein with Dynein Light Chain and Dynactin: GENERAL IMPLICATIONS FOR INTRINSICALLY DISORDERED DUPLEX SCAFFOLDS IN MULTIPROTEIN ASSEMBLIES. <i>Journal of Biological Chemistry</i> , 2015 , 290, 23863-74	5.4	12	
468	A Crystallin Fold in the Interleukin-4-inducing Principle of Schistosoma mansoni Eggs (IPSE/日1) Mediates IgE Binding for Antigen-independent Basophil Activation. <i>Journal of Biological Chemistry</i> , 2015 , 290, 22111-26	5.4	22	
467	NMR Dynamics of Transmembrane and Intracellular Domains of p75NTR in Lipid-Protein Nanodiscs. <i>Biophysical Journal</i> , 2015 , 109, 772-82	2.9	21	
466	The influenza hemagglutinin fusion domain is an amphipathic helical hairpin that functions by inducing membrane curvature. <i>Journal of Biological Chemistry</i> , 2015 , 290, 228-38	5.4	30	
465	Structural basis of dynamic membrane recognition by trans-Golgi network specific FAPP proteins. <i>Journal of Molecular Biology</i> , 2015 , 427, 966-981	6.5	27	
464	NMR studies of the dynamics of high-spin nitrophorins: comparative studies of NP4 and NP2 at close to physiological pH. <i>Biochemistry</i> , 2015 , 54, 221-39	3.2	1	
463	Disorder-to-order transition of MAGI-1 PDZ1 C-terminal extension upon peptide binding: thermodynamic and dynamic insights. <i>Biochemistry</i> , 2015 , 54, 1327-37	3.2	9	
462	Dengue virus NS4A cytoplasmic domain binding to liposomes is sensitive to membrane curvature. 2015 , 1848, 1119-26		16	
461	The RAS-Binding Domain of Human BRAF Protein Serine/Threonine Kinase Exhibits Allosteric Conformational Changes upon Binding HRAS. <i>Structure</i> , 2015 , 23, 1382-1393	5.2	24	
460	Structure and Functional Characterization of the Conserved JAK Interaction Region in the Intrinsically Disordered N-Terminus of SOCS5. <i>Biochemistry</i> , 2015 , 54, 4672-82	3.2	11	

459	On the interaction of Helicobacter pylori NikR, a Ni(II)-responsive transcription factor, with the urease operator: in solution and in silico studies. 2015 , 20, 1021-37	1.	4
458	X-ray, spectroscopic and normal-mode dynamics of calexcitin: structure-function studies of a neuronal calcium-signalling protein. 2015 , 71, 615-31	7	
457	The EBNA-2 N-Terminal Transactivation Domain Folds into a Dimeric Structure Required for Target Gene Activation. 2015 , 11, e1004910	5	
456	Unraveling the folding mechanism of the smallest knotted protein, MJ0366. 2015 , 119, 4359-70	3.	5
455	High-resolution NMR structure of a Zn2+-containing form of the bacteriophage T5 L-alanyl-D-glutamate peptidase. 2015 , 5, 41041-41049	9	
454	Utilization of paramagnetic relaxation enhancements for high-resolution NMR structure determination of a soluble loop-rich protein with sparse NOE distance restraints. 2015 , 61, 55-64	1	5
453	NMR resonance assignments of the lantibiotic immunity protein NisI from Lactococcus lactis. Biomolecular NMR Assignments, 2015 , 9, 293-7	3	
452	Insight into conformational modification of alpha-synuclein in the presence of neuronal whole cells and of their isolated membranes. 2015 , 589, 798-804	5	
451	A Disulfide Stabilized #Sandwich Defines the Structure of a New Cysteine Framework M-Superfamily Conotoxin. <i>ACS Chemical Biology</i> , 2015 , 10, 1847-60	4	
450	Pliable natural biocide: Jaburetox is an intrinsically disordered insecticidal and fungicidal polypeptide derived from jack bean urease. 2015 , 282, 1043-64	2	3
449	Protecting Gram-negative bacterial cell envelopes from human lysozyme: Interactions with Ivy inhibitor proteins from Escherichia coli and Pseudomonas aeruginosa. 2015 , 1848, 3032-46	1	0
448	A Natural Interruption Displays Higher Global Stability and Local Conformational Flexibility than a Similar Gly Mutation Sequence in Collagen Mimic Peptides. <i>Biochemistry</i> , 2015 , 54, 6106-13	1	1
447	The Solution Structure of the Lantibiotic Immunity Protein Nisl and Its Interactions with Nisin. Journal of Biological Chemistry, 2015, 290, 28869-86 5-4	2	5
446	The C-terminal domain of human Cdc37 studied by solution NMR. 2015 , 63, 315-21	5	
445	Nuclear Magnetic Resonance Characterization of the Type III Secretion System Tip Chaperone Protein PcrG of Pseudomonas aeruginosa. <i>Biochemistry</i> , 2015 , 54, 6576-85	3	
444	The C-terminal domains of two homologous Oleaceae #1,3-glucanases recognise carbohydrates differently: Laminarin binding by NMR. 2015 , 580, 93-101	6	
443	Allosteric Breakage of the Hydrogen Bond within the Dual-Histidine Motif in the Active Site of Human Pin1 PPlase. <i>Biochemistry</i> , 2015 , 54, 5242-53	1	2
442	Structural Characterization of Interaction between Human Ubiquitin-specific Protease 7 and Immediate-Early Protein ICP0 of Herpes Simplex Virus-1. <i>Journal of Biological Chemistry</i> , 2015 , 290, 2290 7^4 1	8 ²	6

441	Effects of Linker Length and Transient Secondary Structure Elements in the Intrinsically Disordered Notch RAM Region on Notch Signaling. <i>Journal of Molecular Biology</i> , 2015 , 427, 3587-3597	6.5	16
440	Determination of the Full Catalytic Cycle among Multiple Cyclophilin Family Members and Limitations on the Application of CPMG-RD in Reversible Catalytic Systems. <i>Biochemistry</i> , 2015 , 54, 581.	5 ³ 2 ² 7	9
439	A novel RNA binding surface of the TAM domain of TIP5/BAZ2A mediates epigenetic regulation of rRNA genes. <i>Nucleic Acids Research</i> , 2015 , 43, 5208-20	20.1	20
438	NMR structure and dynamics of the agonist dynorphin peptide bound to the human kappa opioid receptor. 2015 , 112, 11852-7		60
437	Conformational ensembles of neuromedin C reveal a progressive coil-helix transition within a binding-induced folding mechanism. 2015 , 5, 83074-83088		6
436	The LcrG Tip Chaperone Protein of the Yersinia pestis Type III Secretion System Is Partially Folded. Journal of Molecular Biology, 2015 , 427, 3096-109	6.5	9
435	Phosphorylation-induced Conformational Ensemble Switching in an Intrinsically Disordered Cancer/Testis Antigen. <i>Journal of Biological Chemistry</i> , 2015 , 290, 25090-102	5.4	45
434	Deletion of Phenylalanine 508 in the First Nucleotide-binding Domain of the Cystic Fibrosis Transmembrane Conductance Regulator Increases Conformational Exchange and Inhibits Dimerization. <i>Journal of Biological Chemistry</i> , 2015 , 290, 22862-78	5.4	15
433	NMR studies demonstrate a unique AAB composition and chain register for a heterotrimeric type IV collagen model peptide containing a natural interruption site. <i>Journal of Biological Chemistry</i> , 2015 , 290, 24201-9	5.4	15
432	Low stability of the reduced state of Mycobacterium tuberculosis NrdH redoxin. 2016 , 590, 387-95		
431	CD and NMR investigation of collagen peptides mimicking a pathological Gly-Ser mutation and a natural interruption in a similar highly charged sequence context. <i>Protein Science</i> , 2016 , 25, 383-92	6.3	5
430	Protein stabilizer, NDSB-195, enhances the dynamics of the 🗗 -🗗 loop of ubiquitin. 2016 , 22, 174-80		1
429	Solution Observation of Dimerization and Helix Handedness Induction in a Human Carbonic Anhydrase-Helical Aromatic Amide Foldamer Complex. 2016 , 17, 727-36		18
428	Accurate determination of rates from non-uniformly sampled relaxation data. 2016 , 65, 157-170		13
427	Structural basis for KCNE3 modulation of potassium recycling in epithelia. 2016 , 2, e1501228		32
426	Dimerization of the fungal defense lectin CCL2 is essential for its toxicity against nematodes. 2017 , 27, 486-500		12
425	Structural and dynamics studies of a truncated variant of CI repressor from bacteriophage TP901-1. <i>Scientific Reports</i> , 2016 , 6, 29574	4.9	9
424	Structural and Dynamics Studies of Pax5 Reveal Asymmetry in Stability and DNA Binding by the Paired Domain. <i>Journal of Molecular Biology</i> , 2016 , 428, 2372-2391	6.5	8

423	Protein dynamics and function from solution state NMR spectroscopy. 2016, 49, e6		88
422	Structural basis of nucleic acid recognition by FK506-binding protein 25 (FKBP25), a nuclear immunophilin. <i>Nucleic Acids Research</i> , 2016 , 44, 2909-25	20.1	17
421	1H, 13C, and 15N resonance assignments of an enzymatically active domain from the catalytic component (CDTa, residues 216-420) of a binary toxin from Clostridium difficile. <i>Biomolecular NMR Assignments</i> , 2016 , 10, 213-7	0.7	3
420	Protein dynamics from nuclear magnetic relaxation. 2016 , 45, 2410-22		31
419	Interactions of a fungal lytic polysaccharide monooxygenase with ⊕glucan substrates and cellobiose dehydrogenase. 2016 , 113, 5922-7		100
418	Structural and Functional Investigation of the Ag(+)/Cu(+) Binding Domains of the Periplasmic Adaptor Protein SilB from Cupriavidus metallidurans CH34. <i>Biochemistry</i> , 2016 , 55, 2883-97	3.2	4
417	NMR structure and conformational dynamics of AtPDFL2.1, a defensin-like peptide from Arabidopsis thaliana. 2016 , 1864, 1739-1747		8
416	High sensitivity high-resolution full range relaxometry using a fast mechanical sample shuttling device and a cryo-probe. 2016 , 66, 187-194		5
415	Molecular Basis of Chemokine CXCL5-Glycosaminoglycan Interactions. <i>Journal of Biological Chemistry</i> , 2016 , 291, 20539-50	5.4	37
414	Influence of pH on the structure and stability of the sweet protein MNEI. 2016, 590, 3681-3689		16
413	S-Nitrosylation Induces Structural and Dynamical Changes in a Rhodanese Family Protein. <i>Journal of Molecular Biology</i> , 2016 , 428, 3737-51	6.5	9
412	Elucidating the pH-Dependent Structural Transition of T7 Bacteriophage Endolysin. <i>Biochemistry</i> , 2016 , 55, 4614-25	3.2	22
411	Solution Nuclear Magnetic Resonance Studies of Sterol Carrier Protein 2 Like 2 (SCP2L2) Reveal the Insecticide Specific Structural Characteristics of SCP2 Proteins in Aedes aegypti Mosquitoes. <i>Biochemistry</i> , 2016 , 55, 4919-27	3.2	6
410	Solution NMR structures of the C-domain of Tetrahymena cytoskeletal protein Tcb2 reveal distinct calcium-induced structural rearrangements. 2016 , 84, 1748-1756		1
409	PEP-19 modulates calcium binding to calmodulin by electrostatic steering. <i>Nature Communications</i> , 2016 , 7, 13583	17.4	10
408	An SRLS Study of H Methyl-Moiety Relaxation and Related Conformational Entropy in Free and Peptide-Bound PLC1C SH2. 2016 , 120, 10695-10705		7
407	Signaling States of a Short Blue-Light Photoreceptor Protein PpSB1-LOV Revealed from Crystal Structures and Solution NMR Spectroscopy. <i>Journal of Molecular Biology</i> , 2016 , 428, 3721-36	6.5	21
406	Multilevel Changes in Protein Dynamics upon Complex Formation of the Calcium-Loaded S100A4 with a Nonmuscle Myosin IIA Tail Fragment. 2016 , 17, 1829-1838		8

(2016-2016)

405	PSCD Domains of Pleuralin-1 from the Diatom Cylindrotheca fusiformis: NMR Structures and Interactions with Other Biosilica-Associated Proteins. <i>Structure</i> , 2016 , 24, 1178-91	5.2	8
404	Capturing a Dynamic Chaperone-Substrate Interaction Using NMR-Informed Molecular Modeling. 2016 , 138, 9826-39		23
403	Conformational Dynamics and the Binding of Specific and Nonspecific DNA by the Autoinhibited Transcription Factor Ets-1. <i>Biochemistry</i> , 2016 , 55, 4105-18	3.2	11
402	Ligand Binding Enhances Millisecond Conformational Exchange in Xylanase B2 from Streptomyces lividans. <i>Biochemistry</i> , 2016 , 55, 4184-96	3.2	16
401	Dynamically Coupled Residues within the SH2 Domain of FYN Are Key to Unlocking Its Activity. <i>Structure</i> , 2016 , 24, 1947-1959	5.2	6
400	The complex binding mode of the peptide hormone H2 relaxin to its receptor RXFP1. <i>Nature Communications</i> , 2016 , 7, 11344	17.4	28
399	Recent excitements in protein NMR: Large proteins and biologically relevant dynamics. 2016 , 41, 787-86	03	7
398	Antibiotic binding of STY3178, a yfdX protein from Salmonella Typhi. <i>Scientific Reports</i> , 2016 , 6, 21305	4.9	11
397	VirB8-like protein TraH is crucial for DNA transfer in Enterococcus faecalis. <i>Scientific Reports</i> , 2016 , 6, 24643	4.9	21
396	STARD6 on steroids: solution structure, multiple timescale backbone dynamics and ligand binding mechanism. <i>Scientific Reports</i> , 2016 , 6, 28486	4.9	16
395	A new mode of SAM domain mediated oligomerization observed in the CASKIN2 neuronal scaffolding protein. 2016 , 14, 17		5
394	Structural Basis of the High Affinity Interaction between the Alphavirus Nonstructural Protein-3 (nsP3) and the SH3 Domain of Amphiphysin-2. <i>Journal of Biological Chemistry</i> , 2016 , 291, 16307-17	5.4	22
393	Flexibility of KorA, a plasmid-encoded, global transcription regulator, in the presence and the absence of its operator. <i>Nucleic Acids Research</i> , 2016 , 44, 4947-56	20.1	3
392	(1)H, (13)C and (15)N resonance assignments and secondary structure analysis of translation initiation factor 1 from Pseudomonas aeruginosa. <i>Biomolecular NMR Assignments</i> , 2016 , 10, 249-52	0.7	3
391	Nuclear Magnetic Resonance Structure of a Major Lens Protein, Human IC-Crystallin: Role of the Dipole Moment in Protein Solubility. <i>Biochemistry</i> , 2016 , 55, 3136-49	3.2	9
390	Characterisation of the conformational preference and dynamics of the intrinsically disordered N-terminal region of Beclin 1 by NMR spectroscopy. 2016 , 1864, 1128-1137		5
389	Just a Flexible Linker? The Structural and Dynamic Properties of CBP-ID4 Revealed by NMR Spectroscopy. <i>Biophysical Journal</i> , 2016 , 110, 372-381	2.9	18
388	Gbp2 interacts with THO/TREX through a novel type of RRM domain. <i>Nucleic Acids Research</i> , 2016 , 44, 437-48	20.1	17

387	Novel Structural Components Contribute to the High Thermal Stability of Acyl Carrier Protein from Enterococcus faecalis. <i>Journal of Biological Chemistry</i> , 2016 , 291, 1692-1702	5.4	12
386	Antibody Binding Modulates Conformational Exchange in Domain III of Dengue Virus E Protein. 2016 , 90, 1802-11		11
385	Molecular Mechanism of Pin1-Tau Recognition and Catalysis. <i>Journal of Molecular Biology</i> , 2016 , 428, 1760-75	6.5	17
384	CXCL1/MGSA Is a Novel Glycosaminoglycan (GAG)-binding Chemokine: STRUCTURAL EVIDENCE FOR TWO DISTINCT NON-OVERLAPPING BINDING DOMAINS. <i>Journal of Biological Chemistry</i> , 2016 , 291, 4247-55	5.4	37
383	Anomer-Specific Recognition and Dynamics in a Fucose-Binding Lectin. <i>Biochemistry</i> , 2016 , 55, 1195-20.	33.2	16
382	Non-uniform sampling of NMR relaxation data. 2016 , 64, 165-73		25
381	Improved Accuracy from Joint X-ray and NMR Refinement of a Protein-RNA Complex Structure. 2016 , 138, 1601-10		18
3 80	Structural basis for PHDVC5HCHNSD1-C2HRNizp1 interaction: implications for Sotos syndrome. <i>Nucleic Acids Research</i> , 2016 , 44, 3448-63	20.1	4
379	The Nedd4-1 WW Domain Recognizes the PY Motif Peptide through Coupled Folding and Binding Equilibria. <i>Biochemistry</i> , 2016 , 55, 659-74	3.2	18
378	The S2 Cu(i) site in CupA from Streptococcus pneumoniae is required for cellular copper resistance. <i>Metallomics</i> , 2016 , 8, 61-70	4.5	15
377	Structural biology of supramolecular assemblies by magic-angle spinning NMR spectroscopy. 2017 , 50, e1		54
376	Insights into the mechanism of ApoptinIs exquisitely selective anti-tumor action from atomic level characterization of its conformation and dynamics. 2017 , 614, 53-64		3
375	Structural Characterization of Monomeric/Dimeric State of p59 SH2 Domain. 2017, 1555, 257-267		1
374	Conformational Entropy from NMR Relaxation in Proteins: The SRLS Perspective. 2017 , 121, 758-768		6
373	Identification of a Ligand-Binding Site on the Staphylococcus aureus DnaG Primase C-Terminal Domain. <i>Biochemistry</i> , 2017 , 56, 932-943	3.2	1
372	Chemical Synthesis of Glycoproteins with the Specific Installation of Gradient-Enriched N-Labeled Amino Acids for Getting Insights into Glycoprotein Behavior. 2017 , 23, 6579-6585		6
371	Backbone assignments for the SPOUT methyltransferase MTT , a knotted protein from Thermotoga maritima. <i>Biomolecular NMR Assignments</i> , 2017 , 11, 151-154	0.7	
370	Structural and Dynamic Insights into a Glycine-Mediated Short Analogue of a Designed Peptide in Lipopolysaccharide Micelles: Correlation Between Compact Structure and Anti-Endotoxin Activity. <i>Biochemistry</i> , 2017 , 56, 1348-1362	3.2	11

369	Dynein Binding of Competitive Regulators Dynactin and NudE Involves Novel Interplay between Phosphorylation Site and Disordered Spliced Linkers. <i>Structure</i> , 2017 , 25, 421-433	5.2	13
368	Mitochondrial Ca Uniporter Is a Mitochondrial Luminal Redox Sensor that Augments MCU Channel Activity. 2017 , 65, 1014-1028.e7		132
367	Structural Characterization of the Early Events in the Nucleation-Condensation Mechanism in a Protein Folding Process. 2017 , 139, 6899-6910		15
366	Fragment-Based NMR Study of the Conformational Dynamics in the bHLH Transcription Factor Ascl1. <i>Biophysical Journal</i> , 2017 , 112, 1366-1373	2.9	6
365	Structure-function analysis of the DNA-binding domain of a transmembrane transcriptional activator. <i>Scientific Reports</i> , 2017 , 7, 1051	4.9	25
364	Elevated B-ms timescale backbone dynamics in the transition state analog form of arginine kinase. 2017 , 200, 258-266		1
363	Direct observation of structure and dynamics during phase separation of an elastomeric protein. 2017 , 114, E4408-E4415		124
362	RRM domain of ALS/FTD-causing FUS characteristic of irreversible unfolding spontaneously self-assembles into amyloid fibrils. <i>Scientific Reports</i> , 2017 , 7, 1043	4.9	23
361	Ligand-Mediated Folding of the OmpA Periplasmic Domain from Acinetobacter baumannii. <i>Biophysical Journal</i> , 2017 , 112, 2089-2098	2.9	5
360	Structure and Dimerization of IreB, a Negative Regulator of Cephalosporin Resistance in Enterococcus faecalis. <i>Journal of Molecular Biology</i> , 2017 , 429, 2324-2336	6.5	8
359	Point mutations in the N-terminal domain of transactive response DNA-binding protein 43 kDa (TDP-43) compromise its stability, dimerization, and functions. <i>Journal of Biological Chemistry</i> , 2017 , 292, 11992-12006	5.4	43
358	Allosteric modulation of peroxisomal membrane protein recognition by farnesylation of the peroxisomal import receptor PEX19. <i>Nature Communications</i> , 2017 , 8, 14635	17.4	26
357	Hyperinsulinism-Causing Mutations Cause Multiple Molecular Defects in SUR1 NBD1. <i>Biochemistry</i> , 2017 , 56, 2400-2416	3.2	5
356	Probing conformational dynamics in biomolecules via chemical exchange saturation transfer: a primer. 2017 , 67, 243-271		78
355	Structure of phosphorylated UBL domain and insights into PINK1-orchestrated parkin activation. 2017 , 114, 298-303		52
354	Structural Insights into c-Myc-interacting Zinc Finger Protein-1 (Miz-1) Delineate Domains Required for DNA Scanning and Sequence-specific Binding. <i>Journal of Biological Chemistry</i> , 2017 , 292, 3323-3340	5.4	3
353	Structural perturbations induced by Asn131 and Asn171 glycosylation converge within the EFSAM core and enhance stromal interaction molecule-1 mediated store operated calcium entry. 2017 , 1864, 1054-1063		16
352	Unraveling the stereochemical and dynamic aspects of the catalytic site of bacterial peptidyl-tRNA hydrolase. 2017 , 23, 202-216		6

351	Insights on the conformational dynamics of human frataxin through modifications of loop-1. 2017 , 636, 123-137		6
350	Conformational dynamics of the TTD-PHD histone reader module of the UHRF1 epigenetic regulator reveals multiple histone-binding states, allosteric regulation, and druggability. <i>Journal of Biological Chemistry</i> , 2017 , 292, 20947-20959	5.4	23
349	Targeting Cysteine Thiols for in Vitro Site-specific Glycosylation of Recombinant Proteins. 2017,		1
348	Intrinsic Differences in Backbone Dynamics between Wild Type and DNA-Contact Mutants of the p53 DNA Binding Domain Revealed by Nuclear Magnetic Resonance Spectroscopy. <i>Biochemistry</i> , 2017 , 56, 4962-4971	3.2	7
347	Structural and hydrodynamic properties of an intrinsically disordered region of a germ cell-specific protein on phase separation. 2017 , 114, E8194-E8203		227
346	Structural and functional insights into the periplasmic detector domain of the GacS histidine kinase controlling biofilm formation in Pseudomonas aeruginosa. <i>Scientific Reports</i> , 2017 , 7, 11262	4.9	9
345	The intrinsically disordered N-terminal domain of galectin-3 dynamically mediates multisite self-association of the protein through fuzzy interactions. <i>Journal of Biological Chemistry</i> , 2017 , 292, 17845-17856	5.4	32
344	Homeodomain-like DNA binding proteins control the haploid-to-diploid transition in. 2017 , 3, e1602937		14
343	Effect of amino acid mutations on the conformational dynamics of amyloidogenic immunoglobulin light-chains: A combined NMR and in silico study. <i>Scientific Reports</i> , 2017 , 7, 10339	4.9	2
342	Engineering Aromatic-Aromatic Interactions To Nucleate Folding in Intrinsically Disordered Regions of Proteins. <i>Biochemistry</i> , 2017 , 56, 4346-4359	3.2	11
341	The LC8 Recognition Motif Preferentially Samples Polyproline II Structure in Its Free State. <i>Biochemistry</i> , 2017 , 56, 4656-4666	3.2	6
340	Secondary structure and dynamics study of the intrinsically disordered silica-mineralizing peptide P S during silicic acid condensation and silica decondensation. 2017 , 85, 2111-2126		2
339	Solution structure and interaction with copper in vitro and in living cells of the first BIR domain of XIAP. <i>Scientific Reports</i> , 2017 , 7, 16630	4.9	12
338	Disulfide driven folding for a conditionally disordered protein. <i>Scientific Reports</i> , 2017 , 7, 16994	4.9	9
337	Joint non-uniform sampling of all incremented time delays for quicker acquisition in protein relaxation studies. 2017 , 68, 155-161		11
336	Structural and Biophysical Characterization of the Mycobacterium tuberculosis Protein Rv0577, a Protein Associated with Neutral Red Staining of Virulent Tuberculosis Strains and Homologue of the Streptomyces coelicolor Protein KbpA. <i>Biochemistry</i> , 2017 , 56, 4015-4027	3.2	4
335	Structure of the competence pilus major pilin ComGC in. <i>Journal of Biological Chemistry</i> , 2017 , 292, 1413	8 4. 4141	4261
334	Structure and dynamics study of translation initiation factor 1 from Staphylococcus aureus suggests its RNA binding mode. 2017 , 1865, 65-75		2

333	Large-scale synthesis and structural analysis of a synthetic glycopeptide dendrimer as an anti-cancer vaccine candidate. 2016 , 15, 114-123		15
332	The C terminus of Pcf11 forms a novel zinc-finger structure that plays an essential role in mRNA 3Lend processing. 2017 , 23, 98-107		13
331	Structural Insight into the Recognition of r(UAG) by Musashi-1 RBD2, and Construction of a Model of Musashi-1 RBD1-2 Bound to the Minimum Target RNA. 2017 , 22,		16
330	Interactions Controlling the Slow Dynamic Conformational Motions of Ubiquitin. 2017, 22,		3
329	Solution Nuclear Magnetic Resonance Spectroscopy of Integral Membrane Proteins?. 2017,		1
328	Solution NMR structure of the TRIM21 B-box2 and identification of residues involved in its interaction with the RING domain. 2017 , 12, e0181551		5
327	The metastasis suppressor KISS1 is an intrinsically disordered protein slightly more extended than a random coil. 2017 , 12, e0172507		4
326	Alternative data processing techniques for serial NMR experiments. 2017 , 46A, e21429		8
325	Extreme disorder in an ultrahigh-affinity protein complex. <i>Nature</i> , 2018 , 555, 61-66	50.4	343
324	Effects of the Arg9Cys and Arg25Cys mutations on phospholambanls conformational equilibrium in membrane bilayers. 2018 , 1860, 1335-1341		9
323	Plant Villin Headpiece Domain Demonstrates a Novel Surface Charge Pattern and High Affinity for F-Actin. <i>Biochemistry</i> , 2018 , 57, 1690-1701	3.2	4
322	Effects of maturation on the conformational free-energy landscape of SOD1. 2018 , 115, E2546-E2555		34
321	The cytochrome P450 24A1 interaction with adrenodoxin relies on multiple recognition sites that vary among species. <i>Journal of Biological Chemistry</i> , 2018 , 293, 4167-4179	5.4	6
320	Evolution of chalcone isomerase from a noncatalytic ancestor. 2018 , 14, 548-555		78
319	A charge-sensing region in the stromal interaction molecule 1 luminal domain confers stabilization-mediated inhibition of SOCE in response to -nitrosylation. <i>Journal of Biological Chemistry</i> , 2018 , 293, 8900-8911	5.4	11
318	Lysine Side-Chain Dynamics in the Binding Site of Homeodomain/DNA Complexes As Observed by NMR Relaxation Experiments and Molecular Dynamics Simulations. <i>Biochemistry</i> , 2018 , 57, 2796-2813	3.2	10
317	Nuclear Magnetic Resonance-Based Structural Characterization and Backbone Dynamics of Recombinant Bee Venom Melittin. <i>Biochemistry</i> , 2018 , 57, 2775-2785	3.2	9
316	NMR Structure, Dynamics and Interactions of the Integrin む Cytoplasmic Tail with Filamin Domain IgFLNa21. <i>Scientific Reports</i> , 2018 , 8, 5490	4.9	5

315	Backbone resonance assignment of the response regulator protein PhoB from Escherichia coli. <i>Biomolecular NMR Assignments</i> , 2018 , 12, 133-137	0.7	2
314	Measuring Entropy in Molecular Recognition by Proteins. 2018 , 47, 41-61		45
313	Dynamics of dehaloperoxidase-hemoglobin A derived from NMR relaxation spectroscopy and molecular dynamics simulation. 2018 , 181, 65-73		3
312	Phosphorylation induced cochaperone unfolding promotes kinase recruitment and client class-specific Hsp90 phosphorylation. <i>Nature Communications</i> , 2018 , 9, 265	17.4	25
311	Conformational Entropy of FK506 Binding to FKBP12 Determined by Nuclear Magnetic Resonance Relaxation and Molecular Dynamics Simulations. <i>Biochemistry</i> , 2018 , 57, 1451-1461	3.2	9
310	The NMR solution structure of Mycobacterium tuberculosis F-ATP synthase subunit $\bar{\mu}$ provides new insight into energy coupling inside the rotary engine. 2018 , 285, 1111-1128		29
309	Solution structure and dynamics of Xanthomonas albilineans Cas2 provide mechanistic insight on nuclease activity. 2018 , 592, 147-155		1
308	Unraveling the differential structural stability and dynamics features of T7 endolysin partially folded conformations. 2018 , 1862, 924-935		10
307	A structurally dynamic N-terminal region drives function of the staphylococcal peroxidase inhibitor (SPIN). <i>Journal of Biological Chemistry</i> , 2018 , 293, 2260-2271	5.4	6
306	Solution NMR Structure and Backbone Dynamics of Partially Disordered Arabidopsis thaliana Phloem Protein 16-1, a Putative mRNA Transporter. <i>Biochemistry</i> , 2018 , 57, 912-924	3.2	3
305	Structure and function of the N-terminal domain of the yeast telomerase reverse transcriptase. <i>Nucleic Acids Research</i> , 2018 , 46, 1525-1540	20.1	15
304	Dimerization and Conformational Exchanges of the Receiver Domain of Response Regulator PhoB from Escherichia coli. 2018 , 122, 5749-5757		3
303	Proline Restricts Loop I Conformation of the High Affinity WW Domain from Human Nedd4-1 to a Ligand Binding-Competent Type I ₱Turn. 2018 , 122, 4219-4230		
302	H, C and N chemical shift assignment of lissencephaly-1 homology (LisH) domain homodimer of human two-hybrid-associated protein 1 with RanBPM (Twa1). <i>Biomolecular NMR Assignments</i> , 2018 , 12, 99-102	0.7	2
301	Backbone and Ile-II, Leu, Val methyl H, N, and C, chemical shift assignments for Rhizopus chinensis lipase. <i>Biomolecular NMR Assignments</i> , 2018 , 12, 63-68	0.7	3
300	NMR elucidation of monomer-dimer transition and conformational heterogeneity in histone-like DNA binding protein of Helicobacter pylori. 2018 , 56, 285-299		13
299	Biophysical characterization of the basic cluster in the transcription repression domain of human MeCP2 with AT-rich DNA. 2018 , 495, 145-150		4
298	Spatial attributes of the four-helix bundle group of bacteriocins - The high-resolution structure of BacSp222 in solution. 2018 , 107, 2715-2724		8

297	What Drives N Spin Relaxation in Disordered Proteins? Combined NMR/MD Study of the H4 Histone Tail. <i>Biophysical Journal</i> , 2018 , 115, 2348-2367	2.9	13
296	Oligomeric transition and dynamics of RNA binding by the HuR RRM1 domain in solution. 2018 , 72, 179	9-192	8
295	Effects of N-Glycans on Glycoprotein Folding and Protein Dynamics. 2018, 1104, 1-19		2
294	Structural Basis of TRPV4´N Terminus Interaction with Syndapin/PACSIN1-3 and PIP. <i>Structure</i> , 2018 , 26, 1583-1593.e5	5.2	18
293	Dynamics of the Proline-Rich C-Terminus of Huntingtin Exon-1 Fibrils. 2018 , 122, 9507-9515		11
292	The lantibiotic nukacin ISK-1 exists in an equilibrium between active and inactive lipid-II binding states. <i>Communications Biology</i> , 2018 , 1, 150	6.7	15
291	N transverse relaxation measurements for the characterization of µ́s-ms dynamics are deteriorated by the deuterium isotope effect on N resulting from solvent exchange. 2018 , 72, 125-137		5
290	Dynamics-Derived Insights into Complex Formation between the CXCL8 Monomer and CXCR1 N-Terminal Domain: An NMR Study. 2018 , 23,		4
289	Protein Dynamics revealed by NMR Relaxation Methods. 2020 , 2, 93-105		10
288	Conformational Entropy as a Determinant of the Thermodynamic Stability of the p53 Core Domain. <i>Biochemistry</i> , 2018 , 57, 6265-6269	3.2	3
287	Skeletal Muscle Dystrophy mutant of lamin A alters the structure and dynamics of the Ig fold domain. <i>Scientific Reports</i> , 2018 , 8, 13793	4.9	6
286	Narrowing the gap between experimental and computational determination of methyl group dynamics in proteins. 2018 , 20, 24577-24590		21
285	The C-terminal GGAP motif of Hsp70 mediates substrate recognition and stress response in yeast. Journal of Biological Chemistry, 2018 , 293, 17663-17675	5.4	16
284	The Structure of Melanoregulin Reveals a Role for Cholesterol Recognition in the Proteinls Ability to Promote Dynein Function. <i>Structure</i> , 2018 , 26, 1373-1383.e4	5.2	4
283	Rotational Dynamics of Proteins from Spin Relaxation Times and Molecular Dynamics Simulations. 2018 , 122, 6559-6569		15
282	Conformation and dynamics of soluble repetitive domain elucidates the initial #sheet formation of spider silk. <i>Nature Communications</i> , 2018 , 9, 2121	17.4	35
281	Tadpole-like Conformations of Huntingtin Exon 1 Are Characterized by Conformational Heterogeneity that Persists regardless of Polyglutamine Length. <i>Journal of Molecular Biology</i> , 2018 , 430, 1442-1458	6.5	35
280	NMR resonance assignments for a ProQ homolog from Legionella pneumophila. <i>Biomolecular NMR Assignments</i> , 2018 , 12, 319-322	0.7	5

279	Structural basis for cross-reactivity and conformation fluctuation of the major beech pollen allergen Fag s 1. <i>Scientific Reports</i> , 2018 , 8, 10512	4.9	9
278	Active Site Gate Dynamics Modulate the Catalytic Activity of the Ubiquitination Enzyme E2-25K. <i>Scientific Reports</i> , 2018 , 8, 7002	4.9	8
277	Structure dissection of zebrafish progranulins identifies a well-folded granulin/epithelin module protein with pro-cell survival activities. <i>Protein Science</i> , 2018 , 27, 1476-1490	6.3	2
276	Characterization of the two conformations adopted by the T3SS inner-membrane protein PrgK. <i>Protein Science</i> , 2018 , 27, 1680-1691	6.3	2
275	The structure of the ubiquitin-like modifier FAT10 reveals an alternative targeting mechanism for proteasomal degradation. <i>Nature Communications</i> , 2018 , 9, 3321	17.4	14
274	Structures of REV1 UBM2 Domain Complex with Ubiquitin and with a Small-Molecule that Inhibits the REV1 UBM2-Ubiquitin Interaction. <i>Journal of Molecular Biology</i> , 2018 , 430, 2857-2872	6.5	7
273	Minute Additions of DMSO Affect Protein Dynamics Measurements by NMR Relaxation Experiments through Significant Changes in Solvent Viscosity. 2019 , 20, 326-332		6
272	NMR resonance assignments for the GSPII-C domain of the PilF ATPase from Thermus thermophilus in complex with c-di-GMP. <i>Biomolecular NMR Assignments</i> , 2019 , 13, 361-366	0.7	2
271	Structure, amphipathy, and topology of the membrane-proximal helix 8 influence apelin receptor plasma membrane localization. 2019 , 1861, 183036		2
270	Diflunisal targets the HMGB1/CXCL12 heterocomplex and blocks immune cell recruitment. 2019 , 20, e47788		14
269	The MTR4 helicase recruits nuclear adaptors of the human RNA exosome using distinct arch-interacting motifs. <i>Nature Communications</i> , 2019 , 10, 3393	17.4	16
268	Dynamics of the intrinsically disordered protein NUPR1 in isolation and in its fuzzy complexes with DNA and prothymosin 2019 , 1867, 140252		6
267	Structural Basis for Cell-Wall Recognition by Bacteriophage PBC5 Endolysin. Structure, 2019, 27, 1355-	13⁄6∕ 5 .e	4 12
266	Comparison of backbone dynamics of the p50 dimerization domain of NF B in the homodimeric transcription factor NF B 1 and in its heterodimeric complex with RelA (p65). <i>Protein Science</i> , 2019 , 28, 2064-2072	6.3	4
265	Solution structure of the autophagy-related protein LC3C reveals a polyproline II motif on a mobile tether with phosphorylation site. <i>Scientific Reports</i> , 2019 , 9, 14167	4.9	8
264	Switching the Post-translational Modification of Translation Elongation Factor EF-P. 2019 , 10, 1148		10
263	Conformational flexibility of adenine riboswitch aptamer in apo and bound states using NMR and an X-ray free electron laser. 2019 , 73, 509-518		2
262	Intrinsic disorder and amino acid specificity modulate binding of the WW2 domain in kidney and brain protein (KIBRA) to synaptopodin. <i>Journal of Biological Chemistry</i> , 2019 , 294, 17383-17394	5.4	3

261	NMR Reveals Light-Induced Changes in the Dynamics of a Photoswitchable Fluorescent Protein. <i>Biophysical Journal</i> , 2019 , 117, 2087-2100	2.9	5
260	The LC8-RavP ensemble Structure Evinces A Role for LC8 in Regulating Lyssavirus Polymerase Functionality. <i>Journal of Molecular Biology</i> , 2019 , 431, 4959-4977	6.5	10
259	Structural Basis by Which the N-Terminal Polypeptide Segment of Lipase Regulates Its Substrate Binding Affinity. <i>Biochemistry</i> , 2019 , 58, 3943-3954	3.2	9
258	Structural Analysis and Dynamic Processes of the Transmembrane Segment Inside Different Micellar Environments-Implications for the TM4 Fragment of the Bilitranslocase Protein. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	1
257	Double Monoubiquitination Modifies the Molecular Recognition Properties of p15 Promoting Binding to the Reader Module of Dnmt1. <i>ACS Chemical Biology</i> , 2019 , 14, 2315-2326	4.9	9
256	Altered Protein Dynamics and Increased Aggregation of Human IS-Crystallin Due to Cataract-Associated Deamidations. <i>Biochemistry</i> , 2019 , 58, 4112-4124	3.2	20
255	Development of a Fragment-Based Screening Assay for the Focal Adhesion Targeting Domain Using SPR and NMR. 2019 , 24,		8
254	Retinoic Acid Binding Leads to CRABP2 Rigidification and Dimerization. <i>Biochemistry</i> , 2019 , 58, 4183-47	19;42	2
253	The structure of a highly-conserved picocyanobacterial protein reveals a Tudor domain with an RNA-binding function. <i>Journal of Biological Chemistry</i> , 2019 , 294, 14333-14344	5.4	2
252	Structural insights into the tyrosine phosphorylation-mediated inhibition of SH3 domain-ligand interactions. <i>Journal of Biological Chemistry</i> , 2019 , 294, 4608-4620	5.4	5
251	Enhanced dynamics of conformationally heterogeneous T7 bacteriophage lysozyme native state attenuates its stability and activity. 2019 , 476, 613-628		6
250	Selective Inhibitors of FKBP51 Employ Conformational Selection of Dynamic Invisible States. 2019 , 131, 9529-9533		3
249	Rapid NMR Relaxation Measurements Using Optimal Nonuniform Sampling of Multidimensional Accordion Data Analyzed by a Sparse Reconstruction Method. 2019 , 123, 5718-5723		4
248	Increased Aggregation Tendency of Alpha-Synuclein in a Fully Disordered Protein Complex. <i>Journal of Molecular Biology</i> , 2019 , 431, 2581-2598	6.5	8
247	Non-Cryogenic Structure and Dynamics of HIV-1 Integrase Catalytic Core Domain by X-ray Free-Electron Lasers. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	6
246	Selective Inhibitors of FKBP51 Employ Conformational Selection of Dynamic Invisible States. 2019 , 58, 9429-9433		7
245	Super resolution NOESY spectra of proteins. 2019 , 73, 105-116		О
244	An NMR View of Protein Dynamics in Health and Disease. 2019 , 48, 297-319		60

243	The Co-chaperone Cns1 and the Recruiter Protein Hgh1 Link Hsp90 to Translation Elongation via Chaperoning Elongation Factor 2. 2019 , 74, 73-87.e8		13
242	Artificially Linked Ubiquitin Dimers Characterised Structurally and Dynamically by NMR Spectroscopy. 2019 , 20, 1772-1777		5
241	Structure of G57W mutant of human 🗈-crystallin and its involvement in cataract formation. 2019 , 205, 72-78		15
240	Solution structure and novel insights into phylogeny and mode of action of the Neosartorya (Aspergillus) fischeri antifungal protein (NFAP). 2019 , 129, 511-522		10
239	Fast NMR method to probe solvent accessibility and disordered regions in proteins. <i>Scientific Reports</i> , 2019 , 9, 1647	4.9	8
238	Concomitant disorder and high-affinity zinc binding in the human zinc- and iron-regulated transport protein 4 intracellular loop. <i>Protein Science</i> , 2019 , 28, 868-880	6.3	5
237	Structure, dynamics and roX2-lncRNA binding of tandem double-stranded RNA binding domains dsRBD1,2 of Drosophila helicase Maleless. <i>Nucleic Acids Research</i> , 2019 , 47, 4319-4333	20.1	7
236	Role of Backbone Dynamics in Modulating the Interactions of Disordered Ligands with the TAZ1 Domain of the CREB-Binding Protein. <i>Biochemistry</i> , 2019 , 58, 1354-1362	3.2	20
235	Lipid-targeting pleckstrin homology domain turns its autoinhibitory face toward the TEC kinases. 2019 , 116, 21539-21544		10
234	Rotational and Translational Diffusion of Proteins as a Function of Concentration. <i>ACS Omega</i> , 2019 , 4, 20654-20664	3.9	7
233	Conformational and functional characterization of artificially conjugated non-canonical ubiquitin dimers. <i>Scientific Reports</i> , 2019 , 9, 19991	4.9	5
232	The intrinsically disordered C terminus of troponin T binds to troponin C to modulate myocardial force generation. <i>Journal of Biological Chemistry</i> , 2019 , 294, 20054-20069	5.4	13
231	Structure of the PUB Domain from Ubiquitin Regulatory X Domain Protein 1 (UBXD1) and Its Interaction with the p97 AAA+ ATPase. 2019 , 9,		1
230	Integrated NMR, Fluorescence, and Molecular Dynamics Benchmark Study of Protein Mechanics and Hydrodynamics. 2019 , 123, 1453-1480		16
229	Conformational Properties Relevant to the Amyloidogenicity of 卧Microglobulin Analyzed Using Pressure- and Salt-Dependent Chemical Shift Data. 2019 , 123, 836-844		5
228	Cell-Penetrating Peptides as Theranostics Against Impaired Blood-Brain Barrier Permeability: Implications for Pathogenesis and Therapeutic Treatment of Neurodegenerative Disease. 2019 , 115-1.	36	
227	Isotopic Labeling of Eukaryotic Membrane Proteins for NMR Studies of Interactions and Dynamics. 2019 , 614, 37-65		6
226	The Structure of the Pro-domain of Mouse proNGF in Contact with the NGF Domain. <i>Structure</i> , 2019 , 27, 78-89.e3	5.2	7

225	Molecular interaction between human SUMO-I and histone like DNA binding protein of Helicobacter pylori (Hup) investigated by NMR and other biophysical tools. 2019 , 123, 446-456		13
224	Structural and functional characterization of a frataxin from a thermophilic organism. 2019 , 286, 495-50)6	1
223	H, C and N resonance assignments and structure prediction of translation initiation factor 1 from Clostridium difficile. <i>Biomolecular NMR Assignments</i> , 2019 , 13, 91-95	0.7	
222	Characterization of Internal Protein Dynamics and Conformational Entropy by NMR Relaxation. 2019 , 615, 237-284		13
221	Structure and dynamics of the platelet integrin-binding C4 domain of von Willebrand factor. 2019 , 133, 366-376		9
220	Solution Structure and Dynamics of the Small Protein HVO_2922 from Haloferax volcanii. 2020 , 21, 149-	-156	6
219	NMR and crystallographic structural studies of the extremely stable monomeric variant of human cystatin C with single amino acid substitution. 2020 , 287, 361-376		4
218	Structural Fuzziness of the RNA-Organizing Protein SERF Determines a Toxic Gain-of-interaction. <i>Journal of Molecular Biology</i> , 2020 , 432, 930-951	6.5	5
217	Dimerization regulates the human APC/C-associated ubiquitin-conjugating enzyme UBE2S. 2020 , 13,		3
216	C-Terminal Tail Polyglycylation and Polyglutamylation Alter Microtubule Mechanical Properties. <i>Biophysical Journal</i> , 2020 , 119, 2219-2230	2.9	3
215	HACS1 signaling adaptor protein recognizes a motif in the paired immunoglobulin receptor B cytoplasmic domain. <i>Communications Biology</i> , 2020 , 3, 672	6.7	1
214	HSP40 proteins use class-specific regulation to drive HSP70 functional diversity. <i>Nature</i> , 2020 , 587, 489-	494 4	47
213	Backbone resonance assignment and dynamics of 110 kDa hexameric inorganic pyrophosphatase from Mycobacterium tuberculosis. <i>Biomolecular NMR Assignments</i> , 2020 , 14, 281-287	0.7	0
212	Solution structure and RNA-binding of a minimal ProQ-homolog from (Lpp1663). 2020 , 26, 2031-2043		7
211	Biophysical and Dynamic Characterization of Fine-Tuned Binding of the Human Respiratory Syncytial Virus M2-1 Core Domain to Long RNAs. 2020 , 94,		3
2 10	Molecular insights into the differential structure-dynamics-stability features of interleukin-8 orthologs: Implications to functional specificity. 2020 , 164, 3221-3234		3
209	RNA Binding by the KTS Splice Variants of WilmsLTumor Suppressor Protein WT1. <i>Biochemistry</i> , 2020 , 59, 3889-3901	3.2	1
208	The dynamics of free and phosphopeptide-bound Grb2-SH2 reveals two dynamically independent subdomains and an encounter complex with fuzzy interactions. <i>Scientific Reports</i> , 2020 , 10, 13040	4.9	4

207	Structural Analysis of the SANT/Myb Domain of FLASH and YARP Proteins and Their Complex with the C-Terminal Fragment of NPAT by NMR Spectroscopy and Computer Simulations. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	1
206	Ligand- and pH-Induced Structural Transition of Gypsy Moth Pheromone-Binding Protein 1 (LdisPBP1). <i>Biochemistry</i> , 2020 , 59, 3411-3426	3.2	4
205	Dynamic N{H} NOE measurements: a tool for studying protein dynamics. 2020 , 74, 707-716		5
204	Heterogeneous dynamics in partially disordered proteins. 2020 , 22, 21185-21196		3
203	Structural and mechanistic insights into the CRISPR inhibition of AcrIF7. <i>Nucleic Acids Research</i> , 2020 , 48, 9959-9968	20.1	7
202	Taf14 recognizes a common motif in transcriptional machineries and facilitates their clustering by phase separation. <i>Nature Communications</i> , 2020 , 11, 4206	17.4	6
201	Met125 is essential for maintaining the structural integrity of calmodulinls C-terminal domain. <i>Scientific Reports</i> , 2020 , 10, 21320	4.9	1
200	The arrhythmogenic N53I variant subtly changes the structure and dynamics in the calmodulin N-terminal domain, altering its interaction with the cardiac ryanodine receptor. <i>Journal of Biological Chemistry</i> , 2020 , 295, 7620-7634	5.4	12
199	HK97 gp74 Possesses an Helical Insertion in the Fold That Affects Its Metal Binding, Site Digestion, and Activities. 2020 , 202,		3
198	Resolving overlapped signals with automated FitNMR analytical peak modeling. 2020 , 318, 106773		2
197	Intrinsic disorder is essential for Cas9 inhibition of anti-CRISPR AcrIIA5. <i>Nucleic Acids Research</i> , 2020 , 48, 7584-7594	20.1	5
196	Conformational dynamics modulate the catalytic activity of the molecular chaperone Hsp90. <i>Nature Communications</i> , 2020 , 11, 1410	17.4	24
195	HPF1 completes the PARP active site for DNA damage-induced ADP-ribosylation. <i>Nature</i> , 2020 , 579, 598-602	50.4	90
194	NMR Structure and Dynamics of TonB Investigated by Scar-Less Segmental Isotopic Labeling Using a Salt-Inducible Split Intein. 2020 , 8, 136		11
193	Computational Design of an Allosteric Antibody Switch by Deletion and Rescue of a Complex Structural Constellation. 2020 , 6, 390-403		3
192	Different regions of synaptic vesicle membrane regulate VAMP2 conformation for the SNARE assembly. <i>Nature Communications</i> , 2020 , 11, 1531	17.4	10
191	Liquid-liquid phase separation and extracellular multivalent interactions in the tale of galectin-3. <i>Nature Communications</i> , 2020 , 11, 1229	17.4	33
190	Specificity and regulation of phosphotyrosine signaling through SH2 domains. 2020 , 4, 100026		6

189	Insights into the structure and function of Est3 from the Hansenula polymorpha telomerase. <i>Scientific Reports</i> , 2020 , 10, 11109	4.9	Ο
188	A Role of Cholesterol in Modulating the Binding of Esynuclein to Synaptic-Like Vesicles. 2020 , 14, 18		10
187	Dynamics of the intrinsically disordered inhibitor IF7 of glutamine synthetase in isolation and in complex with its partner. 2020 , 683, 108303		1
186	Pro-islet amyloid polypeptide in micelles contains a helical prohormone segment. 2020 , 287, 4440-4457		1
185	Conformational Priming of RepA-WH1 for Functional Amyloid Conversion Detected by NMR Spectroscopy. <i>Structure</i> , 2020 , 28, 336-347.e4	5.2	4
184	Partial Metal Ion Saturation of C2 Domains Primes Synaptotagmin 1-Membrane Interactions. <i>Biophysical Journal</i> , 2020 , 118, 1409-1423	2.9	3
183	Dissecting the differential structural and dynamics features of CCL2 chemokine orthologs. 2020 , 156, 239-251		6
182	Structure and Molecular Recognition Mechanism of IMP-13 Metallo-⊕Lactamase. 2020 , 64,		5
181	The Charged Linker Modulates the Conformations and Molecular Interactions of Hsp90. 2021 , 22, 1084-	1092	9
180	H, C and N resonance assignment of the YTH domain of YTHDC2. <i>Biomolecular NMR Assignments</i> , 2021 , 15, 1-7	0.7	O
179	NMR resonance assignment and backbone dynamics of a C-terminal domain homolog of orange carotenoid protein. <i>Biomolecular NMR Assignments</i> , 2021 , 15, 17-23	0.7	O
178	The muscle-relaxing C-terminal peptide from troponin I populates a nascent helix, facilitating binding to tropomyosin with a potent therapeutic effect. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100	252B	1
177	Phosphotyrosine couples peptide binding and SHP2 activation via a dynamic allosteric network. 2021 , 19, 2398-2415		7
176	Dynamics of the HD regulatory subdomain of PARP-1; substrate access and allostery in PARP activation and inhibition. <i>Nucleic Acids Research</i> , 2021 , 49, 2266-2288	20.1	7
175	Solution NMR Structure of the SH3 Domain of Human Caskin1 Validates the Lack of a Typical Peptide Binding Groove and Supports a Role in Lipid Mediator Binding. 2021 , 10,		0
174	NMR-Based Methods for Protein Analysis. 2021 , 93, 1866-1879		5
173	NMR Characterization of Angiogenin Variants and tRNA Products Impacting Aberrant Protein Oligomerization. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	О
172	The docking of synaptic vesicles on the presynaptic membrane induced by	17.4	20

171	NMR Structure Determinations of Small Proteins Using only One Fractionally 20% C- and Uniformly 100% N-Labeled Sample. 2021 , 26,		2
170	Structural elements in the flexible tail of the co-chaperone p23 coordinate client binding and progression of the Hsp90 chaperone cycle. <i>Nature Communications</i> , 2021 , 12, 828	17.4	10
169	Structures of the germline-specific Deadhead and thioredoxin T proteins from reveal unique features among thioredoxins. 2021 , 8, 281-294		1
168	The Interaction Mechanism of Intrinsically Disordered PP2A Inhibitor Proteins ARPP-16 and ARPP-19 With PP2A. 2021 , 8, 650881		2
167	Membrane Interactions of the Peroxisomal Proteins PEX5 and PEX14. 2021 , 9, 651449		6
166	Structural Insights into the Interaction of the Intrinsically Disordered Co-activator TIF2 with Retinoic Acid Receptor Heterodimer (RXR/RAR). <i>Journal of Molecular Biology</i> , 2021 , 433, 166899	6.5	6
165	Insights into the NF- B -DNA Interaction through NMR Spectroscopy. <i>ACS Omega</i> , 2021 , 6, 12877-12886	3.9	1
164	Structure and antimicrobial activity of NCR169, a nodule-specific cysteine-rich peptide of Medicago truncatula. <i>Scientific Reports</i> , 2021 , 11, 9923	4.9	3
163	Anchored and labile pools of Calcineurin are enabled by a disordered AKAP scaffold.		O
162	Conformational Dynamics of Histone H3 Tails in Chromatin. 2021 , 12, 6174-6181		3
161	Structural insights into the modes of relaxin-binding and tethered-agonist activation of RXFP1 and RXFP2.		
160	Solution Structure of the C-terminal Domain of A20, the Missing Brick for the Characterization of the Interface between Vaccinia Virus DNA Polymerase and its Processivity Factor. <i>Journal of Molecular Biology</i> , 2021 , 433, 167009	6.5	3
159	Solution structure of the Myb domain of Terfa derived from Zebrafish interacting with both human and plant telomeric DNA. 2021 , 559, 252-258		
158	H, C, and N backbone resonance assignments of the SET/TAF-1#/I2PP2A oncoprotein (residues 23-225). <i>Biomolecular NMR Assignments</i> , 2021 , 15, 383-387	0.7	O
157	Dynamics in natural and designed elastins and their relation to elastic fiber structure and recoil. <i>Biophysical Journal</i> , 2021 , 120, 4623-4634	2.9	2
156	Dynamic Connection between Enzymatic Catalysis and Collective Protein Motions. <i>Biochemistry</i> , 2021 , 60, 2246-2258	3.2	5
155	Modulation of Toll-like receptor 1 intracellular domain structure and activity by Zn ions. <i>Communications Biology</i> , 2021 , 4, 1003	6.7	О
154	Interaction mechanism of endogenous PP2A inhibitor protein ENSA with PP2A. 2021,		O

153	PD-L1 degradation is regulated by electrostatic membrane association of its cytoplasmic domain. <i>Nature Communications</i> , 2021 , 12, 5106	17.4	0
152	Zinc-chelating postsynaptic density-95 N-terminus impairs its palmitoyl modification. <i>Protein Science</i> , 2021 , 30, 2246-2257	6.3	1
151	Electrostatic Drivers of GPx4 Interactions with Membrane, Lipids, and DNA. <i>Biochemistry</i> , 2021 , 60, 27	61 3 23772	2 2
150	Changes in dynamic and static structures of the HIV-1 p24 capsid protein N-domain caused by amino-acid substitution are associated with its viral viability. <i>Protein Science</i> , 2021 , 30, 2233-2245	6.3	1
149	Conformational dynamics of Tetracenomycin aromatase/cyclase regulate polyketide binding and enzyme aggregation propensity. 2021 , 1865, 129949		1
148	pH-dependent polymorphism of the structure of SARS-CoV-2 nsp7.		
147	Conformational exchange of fatty acid binding protein induced by protein-nanodisc interactions. <i>Biophysical Journal</i> , 2021 , 120, 4672-4681	2.9	0
146	Structural Insights into the Unique Modes of Relaxin-Binding and Tethered-Agonist Mediated Activation of RXFP1 and RXFP2. <i>Journal of Molecular Biology</i> , 2021 , 433, 167217	6.5	O
145	Solution Structure, Dynamics, and New Antifungal Aspects of the Cysteine-Rich Miniprotein PAFC. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	1
144	Bacterial Cell Wall Analogue Peptides Control the Oligomeric States and Activity of the Glycopeptide Antibiotic Eremomycin: Solution NMR and Antimicrobial Studies. 2021 , 14,		2
143	The evolutionary background and functional consequences of the rs2071307 polymorphism in human tropoelastin. 2021 , 112, e23414		2
142	NMR Studies of Protein Sidechain Dynamics. 1998 , 147-162		1
141	Dynamics of antibody domains studied by solution NMR. 2009 , 525, 533-43, xv		2
140	Combining NMR and molecular dynamics studies for insights into the allostery of small GTPase-protein interactions. 2012 , 796, 235-59		23
139	Monitoring side-chain dynamics of proteins using (2)H relaxation. 2014 , 1084, 3-27		1
138	Protein Dynamics Revealed by CPMG Dispersion. 2018 , 435-452		3
137	Protein Mobility from Multiple 15N Relaxation Parameters. 1994 , 373-454		7
136	Spin Relaxation Methods for Characterizing Picosecond-Nanosecond and Microsecond-Millisecond Motions in Proteins. 1999 , 171-190		5

135	Dynamic Response of the C2 Domain of Protein Kinase Ct Ca Binding. <i>Biophysical Journal</i> , 2016 , 111, 1655-1667		8
134	Continuous Interdomain Orientation Distributions Reveal Components of Binding Thermodynamics. <i>Journal of Molecular Biology</i> , 2018 , 430, 3412-3426		5
133	Conformational Dynamics from Ambiguous Zinc Coordination in the RanBP2-Type Zinc Finger of RBM5. <i>Journal of Molecular Biology</i> , 2020 , 432, 4127-4138	į	1
132	The PipX Protein, When Not Bound to Its Targets, Has Its Signaling C-Terminal Helix in a Flexed Conformation. <i>Biochemistry</i> , 2017 , 56, 3211-3224		5
131	Comparative structure, dynamics and evolution of acyl-carrier proteins from Borrelia burgdorferi, Brucella melitensis and Rickettsia prowazekii. 2020 , 477, 491-508		3
130	Evolution of chalcone isomerase from a non-catalytic ancestor.	·	1
129	Tadpole-like conformations of huntingtin exon 1 with expanded polyglutamine engenders novel interactions in cells.		1
128	ATP induces protein folding, inhibits aggregation and antagonizes destabilization by effectively mediating water-protein-ion interactions, the heart of protein folding and aggregation.		1
127	Structural fuzziness of the RNA-organizing protein SERF1a determines a toxic gain-of-interaction.		1
126	Insights into protein aggregation by NMR characterization of insoluble SH3 mutants solubilized in salt-free water. 2009 , 4, e7805		19
125	Structural basis for sequence specific DNA binding and protein dimerization of HOXA13. 2011 , 6, e23069	:	23
124	Solution structure, copper binding and backbone dynamics of recombinant Ber e 1-the major allergen from Brazil nut. 2012 , 7, e46435		27
123	Chimeric ⊪lactamases: global conservation of parental function and fast time-scale dynamics with increased slow motions. 2012 , 7, e52283		11
122	Solution structure of an archaeal DNA binding protein with an eukaryotic zinc finger fold. 2013 , 8, e52908		10
121	Ligand-induced protein mobility in complexes of carbonic anhydrase II and benzenesulfonamides with oligoglycine chains. 2013 , 8, e57629	:	2
120	Unique structure and dynamics of the EphA5 ligand binding domain mediate its binding specificity as revealed by X-ray crystallography, NMR and MD simulations. 2013 , 8, e74040		13
119	High-resolution NMR reveals secondary structure and folding of amino acid transporter from outer chloroplast membrane. 2013 , 8, e78116		2
118	New insights into histidine triad proteins: solution structure of a Streptococcus pneumoniae PhtD domain and zinc transfer to AdcAII. 2013 , 8, e81168		35

117	Atypical response regulator ChxR from Chlamydia trachomatis is structurally poised for DNA binding. 2014 , 9, e91760	8
116	Solution structure of CXCL5a novel chemokine and adipokine implicated in inflammation and obesity. 2014 , 9, e93228	24
115	Conformational dynamics of Escherichia coli flavodoxins in apo- and holo-states by solution NMR spectroscopy. 2014 , 9, e103936	8
114	Structural basis for inhibition of the MDM2:p53 interaction by an optimized MDM2-binding peptide selected with mRNA display. 2014 , 9, e109163	13
113	The lifestyle switch protein Bd0108 of Bdellovibrio bacteriovorus is an intrinsically disordered protein. 2014 , 9, e115390	5
112	The Neurite Outgrowth Inhibitory Nogo-A-20 Region Is an Intrinsically Disordered Segment Harbouring Three Stretches with Helical Propensity. 2016 , 11, e0161813	2
111	Effect of Glu12-His89 Interaction on Dynamic Structures in HIV-1 p17 Matrix Protein Elucidated by NMR. 2016 , 11, e0167176	2
110	Biophysical characterization of the calmodulin-like domain of Plasmodium falciparum calcium dependent protein kinase 3. 2017 , 12, e0181721	1
109	Calcium-dependent binding of Myc to calmodulin. 2017 , 8, 3327-3343	12
108	Characterisation of class VI TRIM RING domains: linking RING activity to C-terminal domain identity. 2019 , 2,	14
107	Solution Structure and Backbone Dynamics of the Biotinylation Domain of Helicobacter pylori Biotin-carboxyl Carrier Protein. 2008 , 29, 347-351	1
106	NMR spectroscopic assessment of the structure and dynamic properties of an amphibian antimicrobial peptide (Gaegurin 4) bound to SDS micelles. 2007 , 40, 261-9	8
105	Thermal fluctuations of immature SOD1 lead to separate folding and misfolding pathways. 2015 , 4, e07296	67
104	A Dynamic molecular basis for malfunction in disease mutants of p97/VCP. 2016 , 5,	54
103	Cooperative interactions facilitate stimulation of Rad51 by the Swi5-Sfr1 auxiliary factor complex. 2020 , 9,	4
102	Multi-state recognition pathway of the intrinsically disordered protein kinase inhibitor by protein kinase A. 2020 , 9,	11
101	Protein Labeling and Structure Determination by NMR Spectroscopy. 2021 , 65-131	
100	Molecular Insights into Conformational Heterogeneity and Enhanced Structural Integrity of DNA Binding Protein Hup at Low pH. <i>Biochemistry</i> , 2021 , 60, 3236-3252	1

99	Molecular Basis of Ca(II)-Induced Tetramerization and Transition-Metal Sequestration in Human Calprotectin. 2021 , 143, 18073-18090		O
98	Native state fluctuations in a peroxiredoxin active site match motions needed for catalysis. <i>Structure</i> , 2021 ,	5.2	
97	Biotinoyl Domain of Human Acetyl-CoA Carboxylase;Structural Insights into the Carboxyl Transfer Mechanism. 2008 , 12, 1-13		1
96	NMR derived model of GTPase effector domain (GED) self association: relevance to dynamin assembly. 2012 , 7, e30109		
95	Multidimensional NMR of macromolecules. 1996 , 85-157		
94	Structural, Dynamic, and Folding Studies of SH2 and SH3 Domains. 1996 , 35-47		
93	Protein Dynamics Revealed by CPMG Dispersion. 2016 , 1-19		
92	Direct and Indirect Models for Protein Chemical Denaturation are Characteristic of Opposite Dynamic Properties.		
91	Dynamic Profile of the Copper Chaperone CopP from Helicobacter Pylori Depending on the Bound Metals. 2016 , 20, 76-81		
90	Continuous interdomain orientation distributions reveal components of binding thermodynamics.		
89	Solution NMR structures of oxidized and reduced Ehrlichia chaffeensis thioredoxin: NMR-invisible structure owing to backbone dynamics. 2018 , 74, 46-56		1
88	Switching the Post-Translational Modification of Elongation Factor P. SSRN Electronic Journal,	1	
87	The structure of the Pro-domain of mouse proNGF in contact with the NGF domain.		
86	Phosphorylation of HspB1 regulates its mechanosensitive molecular chaperone interaction with native filamin C.		
85	Misfolded proteins share a common capacity in disrupting LLPS organizing membrane-less organelles.		
84	Structure, dynamics and roX2-lncRNA binding of tandem double-stranded RNA binding domains dsRBD1,2 of Drosophila helicase Maleless.		
83	Diflunisal targets the HMGB1/CXCL12 heterocomplex and blocks immune cell recruitment.		
82	Conformational Priming of RepA-WH1 for Functional Amyloid Conversion Detected by NMR Spectroscopy.		

81	Cataract-associated deamidations on the surface of IB-crystallin increase protein unfolding and flexibility at distant regions.		
80	Rad51 Interaction Analysis Reveals a Functional Interplay Among Recombination Auxiliary Factors.		
79	ATP emerged to induce protein folding, inhibit aggregation and increase stability.		
78	C-terminal tail polyglycylation and polyglutamylation alter microtubule mechanical properties.		
77	Partial metal ion saturation of C2 domains primes Syt1-membrane interactions.		О
76	An original structural fold underlies the multitask P1, a silencing suppressor encoded by the Rice yellow mottle virus.		
75	Dynamics of the HD regulatory subdomain of PARP-1; substrate access and allostery in PARP activation and inhibition.		
74	DMPC Phospholipid Bilayer as a Potential Interface for Human Cystatin C Oligomerization: Analysis of Protein-Liposome Interactions Using NMR Spectroscopy. <i>Membranes</i> , 2020 , 11,	3.8	1
73	Zn(II) binding causes interdomain changes in the structure and flexibility of the human prion protein. <i>Scientific Reports</i> , 2021 , 11, 21703	4.9	1
72	Biophysical and dynamic characterization of a fine-tuned binding of the human Respiratory Syncytial Virus M2-1 core domain to long RNAs.		
71	Dynamics in Natural and Designed Elastins and Their Relation to Elastic Fiber Structure and Recoil.		
70	Structures of the germline-specific Deadhead and Thioredoxin T proteins from Drosophila melanogaster reveal unique features among Thioredoxins.		
69	Structural insights into the cooperative interaction of the intrinsically disordered co-activator TIF2 with retinoic acid receptor heterodimer (RXR/RAR).		
68	Structural basis for variable IgE reactivities of Cor a 1 hazelnut allergens.		
67	An engineered construct of cFLIP provides insight into DED1 structure and interactions. <i>Structure</i> , 2021 ,	5.2	O
66	Structure, dynamics, and function of SrnR, a transcription factor for nickel-dependent gene expression. <i>Metallomics</i> , 2021 ,	4.5	1
65	Double Mutant of Chymotrypsin Inhibitor 2 Stabilized through Increased Conformational Entropy <i>Biochemistry</i> , 2022 ,	3.2	1
64	Engineering of a T7 Bacteriophage Endolysin Variant with Enhanced Amidase Activity <i>Biochemistry</i> , 2022 ,	3.2	О

63	The structure of AcrIE4-F7 reveals a common strategy for dual CRISPR inhibition by targeting PAM recognition sites <i>Nucleic Acids Research</i> , 2022 ,	20.1	O
62	The importance of the compact disordered state in the fuzzy interactions between intrinsically disordered proteins <i>Chemical Science</i> , 2022 , 13, 2363-2377	9.4	2
61	Backbone chemical shift assignment and dynamics of the N-terminal domain of ClpB from Francisella tularensis type VI secretion system <i>Biomolecular NMR Assignments</i> , 2022 , 1	0.7	
60	Resonance assignment of the Shank1 PDZ domain <i>Biomolecular NMR Assignments</i> , 2022 , 1	0.7	
59	Structures of highly flexible intracellular domain of human ∄ nicotinic acetylcholine receptor <i>Nature Communications</i> , 2022 , 13, 793	17.4	2
58	Pre-B cell receptor acts as a selectivity switch for Galectin-1 at the pre-B cell surface.		
57	The Residual Structure of Acid-Denatured <code>Q-Microglobulin</code> is Relevant to an Ordered Fibril Morphology. <i>SSRN Electronic Journal</i> ,	1	
56	RNA-Binding Specificity of the SARS-CoV-2 Nucleocapsid Protein is Determined by Binding Kinetics of the N-Terminal Domain to ssRNA. <i>SSRN Electronic Journal</i> ,	1	
55	Visualizing protein breathing motions associated with aromatic ring flipping Nature, 2022,	50.4	2
54	Structural Analysis of the Black-Legged Tick Saliva Protein Salp15 <i>International Journal of Molecular Sciences</i> , 2022 , 23,	6.3	O
53	Architecture of the Two Metal Binding Sites in Prolactin Biophysical Journal, 2022,	2.9	
52	The dimerization mechanism of the N-terminal domain of spider silk proteins is conserved despite extensive sequence divergence <i>Journal of Biological Chemistry</i> , 2022 , 101913	5.4	1
51	Dissecting the stability determinants of a challenging de novo protein fold using massively parallel design and experimentation.		О
50	Solution Structure of the BPSL1445 Protein of Reveals the SYLF Domain Three-Dimensional Fold ACS Chemical Biology, 2021 ,	4.9	O
49	Structural and dynamic studies of the peptidase domain from Clostridium thermocellum PCAT1. <i>Protein Science</i> , 2021 ,	6.3	1
48	Conserved Apical Proline Regulating the Structure and DNA Binding Properties of Histone-like DNA Binding Protein (Hup) <i>ACS Omega</i> , 2022 , 7, 15231-15246	3.9	
47	Super-Resolution NMR Spectroscopy using the Intersection of Non-Redundant Information on Resonance Groups.		
46	Isotope Labels Combined with Solution NMR Spectroscopy Make Visible the Invisible Conformations of Small-to-Large RNAs <i>Chemical Reviews</i> , 2022 ,	68.1	4

45	Data_Sheet_1.pdf. 2020 ,		
44	Data_Sheet_1.xlsx. 2019 ,		
43	Data_Sheet_2.pdf. 2019 ,		
42	Data_Sheet_3.fasta. 2019 ,		
41	Data_Sheet_4.pdf. 2019 ,		
40	Data_Sheet_1.PDF. 2020 ,		
39	A Flexible and Original Architecture of Two Unrelated Zinc Fingers Underlies the Role of the Multitask P1 in Rymv Spread. <i>SSRN Electronic Journal</i> ,	1	
38	Intrinsically disordered regions couple the ligand binding and kinase activation of Trk neurotrophin receptors. <i>IScience</i> , 2022 , 104348	6.1	O
37	Nanobody Paratope Ensembles in Solution Characterized by MD Simulations and NMR. <i>International Journal of Molecular Sciences</i> , 2022 , 23, 5419	6.3	2
36	Negative thermal expansion of a disordered native protein. <i>Chemical Physics</i> , 2022 , 560, 111569	2.3	O
35	1H, 13C, and 15N resonance assignments of human glutathione peroxidase 4. <i>Biomolecular NMR Assignments</i> ,	0.7	
34	A topological refactoring design strategy yields highly stable granulopoietic proteins. <i>Nature Communications</i> , 2022 , 13,	17.4	O
33	Glycation of Bynuclein hampers its binding to synaptic-like vesicles and its driving effect on their fusion. <i>Cellular and Molecular Life Sciences</i> , 2022 , 79,	10.3	0
32	Hidden multivalency in phosphatase recruitment by a disordered AKAP scaffold. <i>Journal of Molecular Biology</i> , 2022 , 167682	6.5	О
31	Structure-based rational design of an enhanced fluorogen-activating protein for fluorogens based on GFP chromophore. <i>Communications Biology</i> , 2022 , 5,	6.7	0
30	A Flexible and Original Architecture of Two Unrelated Zinc Fingers Underlies the Role of the Multitask P1 in RYMV Spread. <i>Journal of Molecular Biology</i> , 2022 , 434, 167715	6.5	1
29	Npl3 functions in mRNP assembly by recruitment of mRNP components to the transcription site and their transfer onto the mRNA.		
28	Explicit models of motions to analyze NMR relaxation data in proteins. Journal of Chemical Physics,	3.9	О

27	ATP-competitive inhibitors modulate the substrate binding cooperativity of a kinase by altering its conformational entropy. 2022 , 8,	1
26	Dynamics and structural changes of calmodulin upon interaction with the antagonist calmidazolium. 2022 , 20,	1
25	Structural and mutational analysis of MazE6-operator DNA complex provide insights into autoregulation of toxin-antitoxin systems. 2022 , 5,	0
24	Multiple Timescale Dynamic Analysis of Functionally-Impairing Mutations in Human Ileal Bile Acid-Binding Protein. 2022 , 23, 11346	O
23	Spatial Structure of nanoFAST in the Apo State and in Complex with its Fluorogen HBR-DOM2. 2022 , 23, 11361	0
22	The Role of Disordered Regions in Orchestrating the Properties of Multidomain Proteins: The SARS-CoV-2 Nucleocapsid Protein and Its Interaction with Enoxaparin. 2022 , 12, 1302	1
21	An Arg/Ala-Rich Helix in the N-Terminal Region of M. tuberculosis FtsQ Anchors FtsZ to Membranes.	0
20	Effects of ligand binding on dynamics of fatty acid binding protein and interactions with membranes. 2022 ,	1
19	1H, 15N and 13C backbone resonance assignments of the acidic domain of the human MDM2 protein.	0
18	The residual structure of acid-denatured $\#2$ -microglobulin is relevant to an ordered fibril morphology.	O
17	Multivalent binding of the hub protein LC8 at a newly discovered site in 53BP1. 2022,	1
16	A redox switch regulates the assembly and anti-CRISPR activity of AcrIIC1. 2022, 13,	O
15	A glutamine-based single Helix scaffold to target globular proteins. 2022 , 13,	0
14	Exploration of the cysteine reactivity of human inducible Hsp70 and cognate Hsc70. 2022 , 102723	O
13	Relaxation-based NMR assignment: Spotlights on ligand binding sites in human CISD3. 2023 , 239, 112089	1
12	Next-generation sequencing of a combinatorial peptide phage library screened against ubiquitin identifies peptide aptamers that can inhibit the in vitro ubiquitin transfer cascade. 13,	O
11	The plasma membrane-associated cation-binding protein PCaP1 of Arabidopsis thaliana is a uranyl-binding protein. 2022 , 130668	0
10	Intramolecular autoinhibition of human PEX13 modulates peroxisomal import.	О

CITATION REPORT

9	Structural basis for the ligand promiscuity of the neofunctionalized, carotenoid-binding fasciclin domain protein AstaP.	0
8	DMSO-Induced Unfolding of the Antifungal Disulfide Protein PAF and Its Inactive Variant: A Combined NMR and DSC Study. 2023 , 24, 1208	O
7	Structural insights into the activity regulation of full-length non-structural protein 1 from SARS-CoV-2. 2023 ,	0
6	On the effect of methionine oxidation on the interplay between Bynuclein and synaptic-like vesicles. 2023 , 229, 92-104	0
5	Pressure, motion, and conformational entropy in molecular recognition by proteins. 2023, 3, 100098	0
4	Npl3 functions in mRNP assembly by recruitment of mRNP components to the transcription site and their transfer onto the mRNA.	O
3	Structural features, intrinsic disorder, and modularity of a pyriform spidroin 1 core repetitive domain.	0
2	Backbone NMR assignment of the yeast expressed Fab fragment of the NISTmAb reference antibody.	O
1	An Arg/Ala-rich helix in the N-terminal region of M. tuberculosis FtsQ is a potential membrane anchor of the Z-ring. 2023 , 6,	O