

**Supplementary Table 3 Metadata for PDB reference structures.** Extracted from PDB entries.

<b>Protein number</b>	1
<b>PDB code</b>	6SVC, doi:10.2210/pdb6SVC/pdb
<b>BMRB code</b>	34432, doi:10.13018/BMR34432
<b>PDB Header</b>	PEPTIDE BINDING PROTEIN
<b>Protein name</b>	PROTEIN ALLOSTERY OF WW DOMAIN AT ATOMIC RESOLUTION: APO STRUCTURE
<b>Deposition date</b>	18.09.2019
<b>PDB title</b>	PROTEIN ALLOSTERY OF THE WW DOMAIN AT ATOMIC RESOLUTION: APO STRUCTURE
<b>PDB authors</b>	D.STROTZ, J.ORTS, M.FRIEDMANN, P.GUNTERT, B.VOGELI, R.RIEK
<b>Last author</b>	RIEK
<b>Reference</b>	ANGEW.CHEM.INT.ED.ENGL. 59, 22132 (2020), doi:10.1002/ANIE.202008734
<b>Reference authors</b>	D.STROTZ, J.ORTS, H.KADAVATH, M.FRIEDMANN, D.GHOSH, S.OLSSON, C.N.CHI, A.POKHARNA, P.GUNTERT, B.VOGELI, R.RIEK
<b>Reference title</b>	PROTEIN ALLOSTERY AT ATOMIC RESOLUTION
<b>Software listed</b>	CCPNMR, CYANA, NMRDRAW, NMRPIPE
<b>Spectrometer</b>	BRUKER (700 MHZ)

  

<b>Protein number</b>	2
<b>PDB code</b>	2JVD, doi:10.2210/pdb2JVD/pdb
<b>BMRB code</b>	15476, doi:10.13018/BMR15476
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	FOLDED N-TERMINAL FRAGMENT OF UPF0291 PROTEIN YNZC FROM BACILLUS SUBTILIS
<b>Deposition date</b>	18.09.2007
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE FOLDED N-TERMINAL FRAGMENT OF UPF0291 PROTEIN YNZC FROM BACILLUS SUBTILIS. NORTHEAST STRUCTURAL GENOMICS TARGET SR384-1-46
<b>PDB authors</b>	J.M.ARAMINI, S.SHARMA, Y.J.HUANG, L.ZHAO, L.A.OWENS, K.STOKES, M.JIANG, R.XIAO, M.C.BARAN, G.V.T.SWAPNA, T.B.ACTON, G.T.MONTELLIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELLIONE
<b>Reference</b>	PROTEINS 72, 526 (2008), doi:10.1002/PROT.22064
<b>Reference authors</b>	J.M.ARAMINI, S.SHARMA, Y.J.HUANG, G.V.SWAPNA, C.K.HO, K.SHETTY, K.CUNNINGHAM, L.C.MA, L.ZHAO, L.A.OWENS, M.JIANG, R.XIAO, J.LIU, M.C.BARAN, T.B.ACTON, B.ROST, G.T.MONTELLIONE
<b>Reference title</b>	SOLUTION NMR STRUCTURE OF THE SOS RESPONSE PROTEIN YNZC FROM BACILLUS SUBTILIS
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CYANA, MOLPROBITY, NMRPIPE, PDBSTAT, PROCHECK, PSVS, SPARKY, TOPSPIN, VNMR
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

  

<b>Protein number</b>	3
<b>PDB code</b>	2K57, doi:10.2210/pdb2K57/pdb
<b>BMRB code</b>	15825, doi:10.13018/BMR15825
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	PUTATIVE LIPOPROTEIN FROM PSEUDOMONAS SYRINGAE GENE LOCUS PSPT02350
<b>Deposition date</b>	25.06.2008
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF PUTATIVE LIPOPROTEIN FROM PSEUDOMONAS SYRINGAE GENE LOCUS PSPT02350. NORTHEAST STRUCTURAL GENOMICS TARGET PSR76A
<b>PDB authors</b>	D.HANG, J.A.ARAMINI, P.ROSSI, D.WANG, M.JIANG, M.MAGLAQUI, R.XIAO, J.LIU, M.C.BARAN, T.B.ACTON, B.ROST, G.T.MONTELLIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELLIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, CNS, CYANA, MOLMOL, MOLPROBITY, NMRPIPE, PDBSTAT, PROCHECK, PSVS, RPF(AUTOSTRUCTURE), SPARKY, TALOS, TOPSPIN
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

  

<b>Protein number</b>	4
<b>PDB code</b>	6SOW, doi:10.2210/pdb6SOW/pdb
<b>BMRB code</b>	34430, doi:10.13018/BMR34430
<b>PDB Header</b>	PROTEIN BINDING
<b>Protein name</b>	STAPHYLOCOCCAL PROTEIN A, C DOMAIN
<b>Deposition date</b>	30.08.2019
<b>PDB title</b>	NMR SOLUTION STRUCTURE OF STAPHYLOCOCCAL PROTEIN A, C DOMAIN
<b>PDB authors</b>	S.M.BACKLUND, H.IWAI
<b>Last author</b>	IWAI
<b>Reference</b>	MOLECULES 2, 6 (2021), doi:10.3390/MOLECULES26030747
<b>Reference authors</b>	H.A.HEIKKINEN, S.M.BACKLUND, H.IWAI
<b>Reference title</b>	NMR STRUCTURE DETERMINATIONS OF SMALL PROTEINS USING ONLY ONE FRACTIONALLY 20% 13 C- AND UNIFORMLY 100% 15 N-LABELED SAMPLE
<b>Software listed</b>	AMBER, CCPNMR, CYANA, PSVS, TALOS
<b>Spectrometer</b>	BRUKER (850 MHZ)

  

<b>Protein number</b>	5
<b>PDB code</b>	2LX7, doi:10.2210/pdb2LX7/pdb

<b>BMRB code</b>	18662, doi:10.13018/BMR18662
<b>PDB Header</b>	PROTEIN BINDING
<b>Protein name</b>	SH3 DOMAIN OF GROWTH ARREST-SPECIFIC PROTEIN 7 (GAS7) (FRAGMENT 1-60) FROM HOMO SAPIENS
<b>Deposition date</b>	15.08.2012
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF SH3 DOMAIN OF GROWTH ARREST-SPECIFIC PROTEIN 7 (GAS7) (FRAGMENT 1-60) FROM HOMO SAPIENS, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG) TARGET HR8574A
<b>PDB authors</b>	Y.YANG, T.A.RAMELOT, L.DAN, E.KOHAN, H.JANJUA, R.XIAO, T.ACTON, J.K.EVERETT, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PINE, PSVS, SPARKY, TALOS+, TOPSPIN, VNMRJ
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	6
<b>PDB code</b>	2MA6, doi:10.2210/pdb2MA6/pdb
<b>BMRB code</b>	19329, doi:10.13018/BMR19329
<b>PDB Header</b>	LIGASE
<b>Protein name</b>	RING FINGER DOMAIN FROM KIP1 UBIQUITINATION-PROMOTING E3 COMPLEX PROTEIN 1 (KPC1/RNF123) FROM HOMO SAPIENS
<b>Deposition date</b>	28.06.2013
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE RING FINGER DOMAIN FROM THE KIP1 UBIQUITINATION-PROMOTING E3 COMPLEX PROTEIN 1 (KPC1/RNF123) FROM HOMO SAPIENS, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG) TARGET HR8700A
<b>PDB authors</b>	T.A.RAMELOT, Y.YANG, H.JANJUA, E.KOHAN, H.WANG, R.XIAO, T.B.ACTON, J.K.EVERETT, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOSTRUCTURE, CNS, CYANA, FMCGUI, NMRPIPE, PINE, PSVS, SPARKY, TALOS+, TOPSPIN, VNMRJ
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	7
<b>PDB code</b>	2JRM, doi:10.2210/pdb2JRM/pdb
<b>BMRB code</b>	15339, doi:10.13018/BMR15339
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	RIBOSOME MODULATION FACTOR VP1593 FROM VIBRIO PARAHAEOLYTICUS
<b>Deposition date</b>	27.06.2007
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF RIBOSOME MODULATION FACTOR VP1593 FROM VIBRIO PARAHAEOLYTICUS. NORTHEAST STRUCTURAL GENOMICS TARGET VPR55
<b>PDB authors</b>	Y.TANG, P.ROSSI, G.SWAPNA, H.WANG, M.JIANG, K.CUNNINGHAM, L.OWENS, L.MA, R.XIAO, J.LIU, M.C.BARAN, T.B.ACTON, B.ROST, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PDBSTAT, PSVS, SPARKY, TOPSPIN, X-PLOR
<b>Spectrometer</b>	BRUKER (800 MHZ, 600 MHZ)

<b>Protein number</b>	8
<b>PDB code</b>	1YEZ, doi:10.2210/pdb1YEZ/pdb
<b>BMRB code</b>	6505, doi:10.13018/BMR6505
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	CONSERVED PROTEIN FROM GENE LOCUS MM1357 OF METHANOSARCINA MAZEI
<b>Deposition date</b>	29.12.2004
<b>PDB title</b>	SOLUTION STRUCTURE OF THE CONSERVED PROTEIN FROM THE GENE LOCUS MM1357 OF METHANOSARCINA MAZEI. NORTHEAST STRUCTURAL GENOMICS TARGET MAR30
<b>PDB authors</b>	P.ROSSI, J.M.ARAMINI, G.V.T.SWAPNA, Y.P.HUANG, R.XIAO, C.K.HO, L.C.MA, T.B.ACTON, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, NMRPIPE, SPARKY, VNMR, XWINNMR
<b>Spectrometer</b>	BRUKER, VARIAN (600 MHZ, 500 MHZ)

<b>Protein number</b>	9
<b>PDB code</b>	2L9R, doi:10.2210/pdb2L9R/pdb
<b>BMRB code</b>	17484, doi:10.13018/BMR17484
<b>PDB Header</b>	TRANSCRIPTION
<b>Protein name</b>	HOMEBOX DOMAIN OF HOMEBOX PROTEIN NKX-3.1 FROM HOMO SAPIENS

<b>Deposition date</b>	22.02.2011
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF HOMEBOX DOMAIN OF HOMEBOX PROTEIN NKX-3.1 FROM HOMO SAPIENS, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET HR6470A
<b>PDB authors</b>	G.LIU, R.XIAO, H.-W.LEE, K.HAMILTON, C.CICCOSANTI, H.B.WANG, T.B.ACTON, J.K.EVERETT, Y.J.HUANG, G.T.MONTELLIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELLIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, TALOS+, TOPSPIN, VNMRJ, XEASY
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

<b>Protein number</b>	10
<b>PDB code</b>	2K52, doi:10.2210/pdb2K52/pdb
<b>BMRB code</b>	15821, doi:10.13018/BMR15821
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	UNCHARACTERIZED PROTEIN MJ1198 FROM METHANOCALDOCOCUS JANNASCHII
<b>Deposition date</b>	24.06.2008
<b>PDB title</b>	STRUCTURE OF UNCHARACTERIZED PROTEIN MJ1198 FROM METHANOCALDOCOCUS JANNASCHII. NORTHEAST STRUCTURAL GENOMICS TARGET MJR117B
<b>PDB authors</b>	P.ROSSI, M.MAGLAQUI, E.L.FOOTE, K.HAMILTON, C.CICCOSANTI, R.XIAO, R.NAIR, G.SWAPNA, J.K.EVERETT, T.B.ACTON, B.ROST, G.T.MONTELLIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELLIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, CNS, CYANA, MOLMOL, MOLPROBITY, NMRPIPE, PROCHECK, PSVS, RPF(AUTOSTRUCTURE), SPARKY, TALOS, TOPSPIN
<b>Spectrometer</b>	BRUKER (800 MHZ, 600 MHZ)

<b>Protein number</b>	11
<b>PDB code</b>	2KRS, doi:10.2210/pdb2KRS/pdb
<b>BMRB code</b>	16647, doi:10.13018/BMR16647
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	SH3 DOMAIN FROM CPF_0587 (FRAGMENT 415-479) FROM CLOSTRIDIUM PERFRINGENS
<b>Deposition date</b>	22.12.2009
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF SH3 DOMAIN FROM CPF_0587 (FRAGMENT 415-479) FROM CLOSTRIDIUM PERFRINGENS. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG) TARGET CPR74A
<b>PDB authors</b>	T.A.RAMELOT, J.R.CORT, M.MAGLAQUI, C.CICCOSANTI, H.JANJUA, R.NAIR, B.ROST, T.B.ACTON, R.XIAO, J.K.EVERETT, G.T.MONTELLIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, NMRPIPE, PDBSTAT, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	12
<b>PDB code</b>	2K53, doi:10.2210/pdb2K53/pdb
<b>BMRB code</b>	15822, doi:10.13018/BMR15822
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	A3DK08 PROTEIN FROM CLOSTRIDIUM THERMOCELLUM
<b>Deposition date</b>	24.06.2008
<b>PDB title</b>	NMR SOLUTION STRUCTURE OF A3DK08 PROTEIN FROM CLOSTRIDIUM THERMOCELLUM: NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET CMR9
<b>PDB authors</b>	G.V.T.SWAPNA, W.HUANG, M.JIANG, E.L.FOOTE, R.XIAO, R.NAIR, J.EVERETT, T.B.ACTON, B.ROST, G.T.MONTELLIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELLIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

<b>Protein number</b>	13
<b>PDB code</b>	2JT1, doi:10.2210/pdb2JT1/pdb
<b>BMRB code</b>	15386, doi:10.13018/BMR15386
<b>PDB Header</b>	TRANSCRIPTION
<b>Protein name</b>	PEFI (PLASMID-ENCODED FIMBRIAE REGULATORY) PROTEIN FROM SALMONELLA TYPHIMURIUM
<b>Deposition date</b>	17.07.2007
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF PEFI (PLASMID-ENCODED FIMBRIAE REGULATORY) PROTEIN FROM SALMONELLA TYPHIMURIUM. NORTHEAST STRUCTURAL GENOMICS TARGET STR82

<b>PDB authors</b>	J.M.ARAMINI, P.ROSSI, H.WANG, C.NWOSU, K.CUNNINGHAM, L.-C.MA, R.XIAO, J.LIU, M.C.BARAN, G.V.T.SWAPNA, T.B.ACTON, B.ROST, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	PROTEINS 79, 335 (2011), doi:10.1002/PROT.22869
<b>Reference authors</b>	J.M.ARAMINI, P.ROSSI, J.R.CORT, L.C.MA, R.XIAO, T.B.ACTON, G.T.MONTELIONE
<b>Reference title</b>	SOLUTION NMR STRUCTURE OF THE PLASMID-ENCODED FIMBRIAE REGULATORY PROTEIN PEFI FROM SALMONELLA ENTERICA SEROVAR TYPHIMURIUM
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, MOLMOL, MOLPROBITY, NMRPIPE, PDBSTAT, PROCHECK, PSVS, SPARKY, TOPSPIN
<b>Spectrometer</b>	BRUKER (800 MHZ, 600 MHZ)

<b>Protein number</b>	14
<b>PDB code</b>	2JVO, doi:10.2210/pdb2JVO/pdb
<b>BMRB code</b>	15485, doi:10.13018/BMR15485
<b>PDB Header</b>	RNA BINDING PROTEIN
<b>Protein name</b>	SEGMENTAL ISOTOPE LABELING OF NPL3
<b>Deposition date</b>	24.09.2007
<b>PDB title</b>	SEGMENTAL ISOTOPE LABELING OF NPL3
<b>PDB authors</b>	L.SKRIISOVSKA, F.H.-T.ALLAIN
<b>Last author</b>	ALLAIN
<b>Reference</b>	J.MOL.BIOL. 375, 151 (2008), doi:10.1016/J.JMB.2007.09.030
<b>Reference authors</b>	L.SKRIISOVSKA, F.H.ALLAIN
<b>Reference title</b>	IMPROVED SEGMENTAL ISOTOPE LABELING METHODS FOR THE NMR STUDY OF MULTIDOMAIN OR LARGE PROTEINS: APPLICATION TO THE RRMS OF NPL3P AND HNRNP L
<b>Software listed</b>	ATNOS/CANDID, SPARKY, XWINNMR
<b>Spectrometer</b>	BRUKER (900 MHZ, 600 MHZ, 500 MHZ)

<b>Protein number</b>	15
<b>PDB code</b>	2ERR, doi:10.2210/pdb2ERR/pdb
<b>BMRB code</b>	6895, doi:10.13018/BMR6895
<b>PDB Header</b>	RNA BINDING PROTEIN
<b>Protein name</b>	RNA BINDING DOMAIN OF HUMAN FOX-1 IN COMPLEX WITH UGCAUGU
<b>Deposition date</b>	25.10.2005
<b>PDB title</b>	NMR STRUCTURE OF THE RNA BINDING DOMAIN OF HUMAN FOX-1 IN COMPLEX WITH UGCAUGU
<b>PDB authors</b>	F.H.ALLAIN, S.D.AUWETER
<b>Last author</b>	AUWETER
<b>Reference</b>	EMBO J. 25, 163 (2006), doi:10.1038/SJ.EMBOJ.7600918
<b>Reference authors</b>	S.D.AUWETER, R.FASAN, L.REYMOND, J.G.UNDERWOOD, D.L.BLACK, S.PITSCH, F.H.ALLAIN
<b>Reference title</b>	MOLECULAR BASIS OF RNA RECOGNITION BY THE HUMAN ALTERNATIVE SPLICING FACTOR FOX-1
<b>Software listed</b>	AMBER, CYANA
<b>Spectrometer</b>	BRUKER (900 MHZ, 600 MHZ, 500 MHZ)

<b>Protein number</b>	16
<b>PDB code</b>	2L1P, doi:10.2210/pdb2L1P/pdb
<b>BMRB code</b>	17092, doi:10.13018/BMR17092
<b>PDB Header</b>	DNA BINDING PROTEIN
<b>Protein name</b>	N-TERMINAL DOMAIN OF DNA-BINDING PROTEIN SATB1 FROM HOMO SAPIENS
<b>Deposition date</b>	02.08.2010
<b>PDB title</b>	NMR SOLUTION STRUCTURE OF THE N-TERMINAL DOMAIN OF DNA-BINDING PROTEIN SATB1 FROM HOMO SAPIENS: NORTHEAST STRUCTURAL GENOMICS TARGET HR4435B(179-250)
<b>PDB authors</b>	G.V.T.SWAPNA, A.F.MONTELIONE, R.SHASTRY, C.CICCOSANTI, H.JANJUA, R.XIAO, T.B.ACTON, J.K.EVERETT, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA
<b>Spectrometer</b>	BRUKER (800 MHZ, 600 MHZ)

<b>Protein number</b>	17
<b>PDB code</b>	2LN3, doi:10.2210/pdb2LN3/pdb
<b>BMRB code</b>	18145, doi:10.13018/BMR18145
<b>PDB Header</b>	DE NOVO PROTEIN
<b>Protein name</b>	DE NOVO DESIGNED PROTEIN, IF3-LIKE FOLD
<b>Deposition date</b>	15.12.2011
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF DE NOVO DESIGNED PROTEIN, IF3-LIKE FOLD, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET OR135 (CASD TARGET)
<b>PDB authors</b>	G.LIU, R.KOGA, N.KOGA, R.XIAO, H.LEE, H.JANJUA, E.KOHAN, T.B.ACTON, J.K.EVERETT, D.BAKER, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	NATURE 491, 222 (2012), doi:10.1038/NATURE11600
<b>Reference authors</b>	N.KOGA, R.TATSUMI-KOGA, G.LIU, R.XIAO, T.B.ACTON, G.T.MONTELIONE, D.BAKER
<b>Reference title</b>	PRINCIPLES FOR DESIGNING IDEAL PROTEIN STRUCTURES

<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, REDCAT, SPARKY, TALOS+, TOPSPIN, VNMRJ, XEASY
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

<b>Protein number</b>	18
<b>PDB code</b>	2HEQ, doi:10.2210/pdb2HEQ/pdb
<b>BMRB code</b>	7175, doi:10.13018/BMR7175
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	BACILLUS SUBTILIS PROTEIN YORP
<b>Deposition date</b>	21.06.2006
<b>PDB title</b>	NMR STRUCTURE OF BACILLUS SUBTILIS PROTEIN YORP, NORTHEAST STRUCTURAL GENOMICS TARGET SR399
<b>PDB authors</b>	T.A.RAMELOT, J.R.CORT, D.WANG, H.JANJUA, K.CUNNINGHAM, L.-C.MA, R.XIAO, J.LIU, M.BARAN, G.V.T.SWAPNA, T.B.ACTON, B.ROST, G.M.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOSTRUCTURE, CNS, NMRPIPE, SPARKY, VNMR, X-PLOR_NIH
<b>Spectrometer</b>	VARIAN (750 MHZ, 600 MHZ)

<b>Protein number</b>	19
<b>PDB code</b>	2KK8, doi:10.2210/pdb2KK8/pdb
<b>BMRB code</b>	16355, doi:10.13018/BMR16355
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	A PUTATIVE UNCHARACTERIZED PROTEIN OBTAINED FROM ARABIDOPSIS THALIANA
<b>Deposition date</b>	16.06.2009
<b>PDB title</b>	NMR SOLUTION STRUCTURE OF A PUTATIVE UNCHARACTERIZED PROTEIN OBTAINED FROM ARABIDOPSIS THALIANA: NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET AR3449A
<b>PDB authors</b>	R.MANI, S.V.T.GURLA, R.SHASTRY, C.CICCOSANTI, E.FOOTE, M.JIANG, R.XIAO, R.NAIR, J.EVERETT, Y.HUANG, T.ACTON, B.ROST, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ, 500 MHZ)

<b>Protein number</b>	20
<b>PDB code</b>	2KD0, doi:10.2210/pdb2KD0/pdb
<b>BMRB code</b>	16101, doi:10.13018/BMR16101
<b>PDB Header</b>	SIGNALING PROTEIN
<b>Protein name</b>	O64736 PROTEIN FROM ARABIDOPSIS THALIANA
<b>Deposition date</b>	31.12.2008
<b>PDB title</b>	NMR SOLUTION STRUCTURE OF O64736 PROTEIN FROM ARABIDOPSIS THALIANA. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM MEGA TARGET AR3445A
<b>PDB authors</b>	G.V.T.SWAPNA, R.SHASTRY, E.FOOTE, C.CICCOSANTI, M.JIANG, R.XIAO, R.NAIR, J.EVERETT, Y.HUANG, T.B.ACTON, B.ROST, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, SPARKY
<b>Spectrometer</b>	BRUKER (800 MHZ, 600 MHZ)

<b>Protein number</b>	21
<b>PDB code</b>	2LML, doi:10.2210/pdb2LML/pdb
<b>BMRB code</b>	16860, doi:10.13018/BMR16860
<b>PDB Header</b>	TRANSPORT PROTEIN
<b>Protein name</b>	HOLO ACYL CARRIER PROTEIN FROM GEOBACTER METALLIREDCENS REFINED WITH NH RDCS
<b>Deposition date</b>	05.12.2011
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF HOLO ACYL CARRIER PROTEIN FROM GEOBACTER METALLIREDCENS REFINED WITH NH RDCS, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET GMR141
<b>PDB authors</b>	T.A.RAMELOT, M.J.SMOLA, H.LEE, L.ZHAO, C.CICCOSANTI, E.L.FOOTE, K.HAMILTON, R.NAIR, B.ROST, G.SWAPNA, T.B.ACTON, R.XIAO, J.K.EVERETT, J.H.PRESTEGARD, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	BIOCHEMISTRY 50, 1442 (2011), doi:10.1021/BI101932S
<b>Reference authors</b>	T.A.RAMELOT, M.J.SMOLA, H.W.LEE, C.CICCOSANTI, K.HAMILTON, T.B.ACTON, R.XIAO, J.K.EVERETT, J.H.PRESTEGARD, G.T.MONTELIONE, M.A.KENNEDY
<b>Reference title</b>	SOLUTION STRUCTURE OF 4'-PHOSPHOPANTETHEINE - GMACP3 FROM GEOBACTER METALLIREDCENS: A SPECIALIZED ACYL CARRIER PROTEIN WITH ATYPICAL STRUCTURAL FEATURES AND A PUTATIVE ROLE IN LIPOPOLYSACCHARIDE BIOSYNTHESIS
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, FMCGUI, NMRPIPE, PDBSTAT, PINE_SERVER, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR_NIH
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	22
<b>PDB code</b>	2K3D, doi:10.2210/pdb2K3D/pdb
<b>BMRB code</b>	15750, doi:10.13018/BMR15750
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	FOLDED 79 RESIDUE FRAGMENT OF LIN0334 FROM LISTERIA INNOCUA
<b>Deposition date</b>	02.05.2008
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE FOLDED 79 RESIDUE FRAGMENT OF LIN0334 FROM LISTERIA INNOCUA. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET LKR15
<b>PDB authors</b>	T.A.RAMELOT, L.ZHAO, M.JIANG, E.L.FOOTE, R.XIAO, J.LIU, M.C.BARAN, G.V.T.SWAPNA, T.B.ACTON, B.ROST, G.T.MONTELLIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, NMRPIPE, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	23
<b>PDB code</b>	2LK2, doi:10.2210/pdb2LK2/pdb
<b>BMRB code</b>	17971, doi:10.13018/BMR17971
<b>PDB Header</b>	TRANSCRIPTION
<b>Protein name</b>	HOMEODOMAIN (171-248) OF HUMAN HOMEODOMAIN PROTEIN TGIF1
<b>Deposition date</b>	30.09.2011
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF HOMEODOMAIN (171-248) OF HUMAN HOMEODOMAIN PROTEIN TGIF1, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET HR4411B
<b>PDB authors</b>	Y.YANG, T.A.RAMELOT, J.R.CORT, R.SHAstry, C.CICCOSANTI, K.HAMILTON, T.B.ACTON, R.XIAO, J.K.EVERETT, G.T.MONTELLIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	ASDP, AUTOASSIGN, CNS, CYANA, NMRPIPE, PDBSTAT, PINE_SERVER, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR NIH
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	24
<b>PDB code</b>	(MH04)
<b>BMRB code</b>	
<b>PDB Header</b>	
<b>Protein name</b>	
<b>Deposition date</b>	
<b>PDB title</b>	
<b>PDB authors</b>	
<b>Last author</b>	
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	
<b>Spectrometer</b>	

<b>Protein number</b>	25
<b>PDB code</b>	1PQX, doi:10.2210/pdb1PQX/pdb
<b>BMRB code</b>	5844, doi:10.13018/BMR5844
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	STAPHYLOCOCCUS AUREUS PROTEIN SAV1430
<b>Deposition date</b>	19.06.2003
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF STAPHYLOCOCCUS AUREUS PROTEIN SAV1430. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET ZR18
<b>PDB authors</b>	M.C.BARAN, J.M.ARAMINI, R.XIAO, Y.J.HUANG, T.B.ACTON, L.SHIH, G.T.MONTELLIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELLIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOPROC, AUTOSTRUCTURE, NMRPIPE, SPARKY, VNMR, X-PLOR
<b>Spectrometer</b>	VARIAN (600 MHZ, 500 MHZ)

<b>Protein number</b>	26
<b>PDB code</b>	2L33, doi:10.2210/pdb2L33/pdb
<b>BMRB code</b>	17169, doi:10.13018/BMR17169
<b>PDB Header</b>	TRANSCRIPTION REGULATOR
<b>Protein name</b>	DRBM 2 DOMAIN OF INTERLEUKIN ENHANCER- BINDING FACTOR 3 FROM HOMO SAPIENS
<b>Deposition date</b>	03.09.2010
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF DRBM 2 DOMAIN OF INTERLEUKIN ENHANCER- BINDING FACTOR 3 FROM HOMO SAPIENS, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET HR4527E

<b>PDB authors</b>	G.LIU, H.JANJUA, R.XIAO, T.B.ACTON, A.CICCOSANTI, R.B.SHAstry, J.EVERETT, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, TALOS+, TOPSPIN, VNMRJ, XEASY
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

<b>Protein number</b>	27
<b>PDB code</b>	2KZV, doi:10.2210/pdb2KZV/pdb
<b>BMRB code</b>	17020, doi:10.13018/BMR17020
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	CV_0373(175-257) PROTEIN FROM CHROMOBACTERIUM VIOLACEUM
<b>Deposition date</b>	25.06.2010
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF CV_0373(175-257) PROTEIN FROM CHROMOBACTERIUM VIOLACEUM, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET CVR118A
<b>PDB authors</b>	Y.YANG, T.A.RAMELOT, D.WANG, C.CICCOSANTI, L.MAO, H.JANJUA, T.B.ACTON, R.XIAO, J.K.EVERETT, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PDBSTAT, PINE, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	28
<b>PDB code</b>	2KCT, doi:10.2210/pdb2KCT/pdb
<b>BMRB code</b>	16096, doi:10.13018/BMR16096
<b>PDB Header</b>	CHAPERONE
<b>Protein name</b>	OB-FOLD DOMAIN OF HEME CHAPERONE CCME FROM DESULFOVIBRIO VULGARIS
<b>Deposition date</b>	29.12.2008
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE OB-FOLD DOMAIN OF HEME CHAPERONE CCME FROM DESULFOVIBRIO VULGARIS. NORTHEAST STRUCTURAL GENOMICS TARGET DVR115G
<b>PDB authors</b>	J.M.ARAMINI, P.ROSSI, H.LEE, A.LEMAK, H.WANG, E.L.FOOTE, M.JIANG, R.XIAO, R.NAIR, G.V.T.SWAPNA, T.B.ACTON, B.ROST, J.K.EVERETT, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PALES, PDBSTAT, PINE, PSVS, SPARKY, TOPSPIN, VNMRJ
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

<b>Protein number</b>	29
<b>PDB code</b>	2MDR, doi:10.2210/pdb2MDR/pdb
<b>BMRB code</b>	19502, doi:10.13018/BMR19502
<b>PDB Header</b>	HYDROLASE
<b>Protein name</b>	THIRD DOUBLE-STRANDED RNA-BINDING DOMAIN (DSRBD3) OF HUMAN ADENOSINE-DEAMINASE ADAR1
<b>Deposition date</b>	17.09.2013
<b>PDB title</b>	SOLUTION STRUCTURE OF THE THIRD DOUBLE-STRANDED RNA-BINDING DOMAIN (DSRBD3) OF HUMAN ADENOSINE-DEAMINASE ADAR1
<b>PDB authors</b>	P.BARRAUD, S.BANERJEE, W.I.MOHAMED, M.F.JANTSCH, F.H.ALLAIN
<b>Last author</b>	ALLAIN
<b>Reference</b>	PROC.NATL.ACAD.SCI.USA 111, E1852 (2014), doi:10.1073/PNAS.1323698111
<b>Reference authors</b>	P.BARRAUD, S.BANERJEE, W.I.MOHAMED, M.F.JANTSCH, F.H.ALLAIN
<b>Reference title</b>	A BIMODULAR NUCLEAR LOCALIZATION SIGNAL ASSEMBLED VIA AN EXTENDED DOUBLE-STRANDED RNA-BINDING DOMAIN ACTS AS AN RNA-SENSING SIGNAL FOR TRANSPORTIN 1
<b>Software listed</b>	ATNOS, CING, CNS, CYANA, PROCHECKNMR, SPARKY, TOPSPIN
<b>Spectrometer</b>	BRUKER (900 MHZ, 750 MHZ, 700 MHZ, 600 MHZ, 500 MHZ)

<b>Protein number</b>	30
<b>PDB code</b>	2FB7, doi:10.2210/pdb2FB7/pdb
<b>BMRB code</b>	7084, doi:10.13018/BMR7084
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	PROTEIN FROM ZEBRA FISH DR.13312
<b>Deposition date</b>	08.12.2005
<b>PDB title</b>	NMR SOLUTION STRUCTURE OF PROTEIN FROM ZEBRA FISH DR.13312
<b>PDB authors</b>	R.C.TYLER, J.SONG, J.L.MARKLEY, CENTER FOR EUKARYOTIC STRUCTURAL GENOMICS (CESG)
<b>Last author</b>	MARKLEY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	ARIA, CNS, NMRPIPE, NMRVIEW

<b>Spectrometer</b>	VARIAN (600 MHZ)
<b>Protein number</b>	31
<b>PDB code</b>	2MB0, doi:10.2210/pdb2MB0/pdb
<b>BMRB code</b>	19382, doi:10.13018/BMR19382
<b>PDB Header</b>	SPLICING/RNA
<b>Protein name</b>	HNRNP G RRM IN COMPLEX WITH RNA 5'-AUCAAA-3'
<b>Deposition date</b>	22.07.2013
<b>PDB title</b>	SOLUTION STRUCTURE OF HNRNP G RRM IN COMPLEX WITH THE RNA 5'-AUCAAA-3'
<b>PDB authors</b>	A.MOURS, F.H.-T.ALLAIN, A.CLERY
<b>Last author</b>	CLERY
<b>Reference</b>	NUCLEIC ACIDS RES. 42, 6659 (2014), doi:10.1093/NAR/GKU244
<b>Reference authors</b>	A.MOURS, F.H.ALLAIN, A.CLERY
<b>Reference title</b>	CHARACTERIZATION OF THE RNA RECOGNITION MODE OF HNRNP G EXTENDS ITS ROLE IN SMN2 SPLICING REGULATION
<b>Software listed</b>	AMBER
<b>Spectrometer</b>	BRUKER (900 MHZ, 700 MHZ, 600 MHZ, 500 MHZ)

<b>Protein number</b>	32
<b>PDB code</b>	2L05, doi:10.2210/pdb2L05/pdb
<b>BMRB code</b>	17030, doi:10.13018/BMR17030
<b>PDB Header</b>	TRANSFERASE
<b>Protein name</b>	RAS-BINDING DOMAIN OF SERINE/THREONINE- PROTEIN KINASE B-RAF FROM HOMO SAPIENS
<b>Deposition date</b>	30.06.2010
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE RAS-BINDING DOMAIN OF SERINE/THREONINE- PROTEIN KINASE B-RAF FROM HOMO SAPIENS, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET HR4694F
<b>PDB authors</b>	J.M.ARAMINI, H.JANJUA, C.CICCOSANTI, R.SHASTRY, Y.J.HUANG, T.B.ACTON, R.XIAO, J.K.EVERETT, G.T.MONTELLIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELLIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOSTRUCTURE, CNS, CYANA, MOLPROBITY, NMRPIPE, PDBSTAT, PINE, PSVS, SPARKY, TALOS+, TOPSPIN
<b>Spectrometer</b>	BRUKER (800 MHZ, 600 MHZ)

<b>Protein number</b>	33
<b>PDB code</b>	2KJR, doi:10.2210/pdb2KJR/pdb
<b>BMRB code</b>	16338, doi:10.13018/BMR16338
<b>PDB Header</b>	CHAPERONE
<b>Protein name</b>	N-TERMINAL UBIQUITIN-LIKE DOMAIN FROM TUBULIN-BINDING COFACTOR B, CG11242, FROM DROSOPHILA MELANOGASTER
<b>Deposition date</b>	08.06.2009
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE N-TERMINAL UBIQUITIN-LIKE DOMAIN FROM TUBULIN-BINDING COFACTOR B, CG11242, FROM DROSOPHILA MELANOGASTER. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET FR629A (RESIDUES 8- 92)
<b>PDB authors</b>	T.A.RAMELOT, J.R.CORT, R.SHASTRY, C.CICCOSANTI, M.JIANG, R.NAIR, B.ROST, G.SWAPNA, T.B.ACTON, R.XIAO, J.K.EVERETT, G.T.MONTELLIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, NMRPIPE, PDBSTAT, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 500 MHZ)

<b>Protein number</b>	34
<b>PDB code</b>	2M50, doi:10.2210/pdb2M50/pdb
<b>BMRB code</b>	19068, doi:10.13018/BMR19068
<b>PDB Header</b>	BIOSYNTHETIC PROTEIN
<b>Protein name</b>	SOLUTION NMR STRUCTURE CTD DOMAIN OF NFU1 IRON-SULFUR CLUSTER SCAFFOLD HOMOLOG FROM HOMO SAPIENS
<b>Deposition date</b>	01.03.2013
<b>PDB title</b>	SOLUTION NMR STRUCTURE CTD DOMAIN OF NFU1 IRON-SULFUR CLUSTER SCAFFOLD HOMOLOG FROM HOMO SAPIENS, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG) TARGET HR2876C
<b>PDB authors</b>	G.LIU, R.XIAO, H.JANJUA, K.HAMILTON, R.SHASTRY, E.KOHAN, T.B.ACTON, J.K.EVERETT, K.PEDERSON, Y.J.HUANG, G.T.MONTELLIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG), MITOCHONDRIAL PROTEIN PARTNERSHIP (MPP)
<b>Last author</b>	MONTELLIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PSVS, REDCAT, SPARKY, TALOS+, TOPSPIN, VNMRJ, XEASY
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)



<b>Protein number</b>	35
<b>PDB code</b>	(MDM2)
<b>BMRB code</b>	
<b>PDB Header</b>	
<b>Protein name</b>	
<b>Deposition date</b>	
<b>PDB title</b>	
<b>PDB authors</b>	
<b>Last author</b>	
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	
<b>Spectrometer</b>	

<b>Protein number</b>	36
<b>PDB code</b>	2LNA, doi:10.2210/pdb2LNA/pdb
<b>BMRB code</b>	18156, doi:10.13018/BMR18156
<b>PDB Header</b>	HYDROLASE
<b>Protein name</b>	MITOCHONDRIAL INNER MEMBRANE DOMAIN (RESIDUES 164-251), FTSH_EXT, FROM PARAPLEGIN-LIKE PROTEIN AFG3L2 FROM HOMO SAPIENS
<b>Deposition date</b>	20.12.2011
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE MITOCHONDRIAL INNER MEMBRANE DOMAIN (RESIDUES 164-251), FTSH_EXT, FROM THE PARAPLEGIN-LIKE PROTEIN AFG3L2 FROM HOMO SAPIENS, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET HR6741A
<b>PDB authors</b>	T.A.RAMELOT, Y.YANG, H.LEE, H.JANUA, E.KOHAN, R.SHASTRY, T.B.ACTON, R.XIAO, J.K.EVERETT, J.H.PRESTEGARD, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG), MITOCHONDRIAL PROTEIN PARTNERSHIP (MPP)
<b>Last author</b>	KENNEDY
<b>Reference</b>	FEBS LETT. 587, 3522 (2013), doi:10.1016/J.FEBSLET.2013.09.009
<b>Reference authors</b>	T.A.RAMELOT, Y.YANG, I.D.SAHU, H.W.LEE, R.XIAO, G.A.LORIGAN, G.T.MONTELIONE, M.A.KENNEDY
<b>Reference title</b>	NMR STRUCTURE AND MD SIMULATIONS OF THE AAA PROTEASE INTERMEMBRANE SPACE DOMAIN INDICATES PERIPHERAL MEMBRANE LOCALIZATION WITHIN THE HEXAOLIGOMER
<b>Software listed</b>	AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PALES, PINE, PSVS, SPARKY, TALOS+, TOPSPIN, VNMRJ, X-PLOR NIH
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	37
<b>PDB code</b>	2LA6, doi:10.2210/pdb2LA6/pdb
<b>BMRB code</b>	17508, doi:10.13018/BMR17508
<b>PDB Header</b>	RNA BINDING PROTEIN
<b>Protein name</b>	RRM DOMAIN OF RNA-BINDING PROTEIN FUS FROM HOMO SAPIENS
<b>Deposition date</b>	04.03.2011
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF RRM DOMAIN OF RNA-BINDING PROTEIN FUS FROM HOMO SAPIENS, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET HR6430A
<b>PDB authors</b>	G.LIU, R.XIAO, H.JANJUA, C.CICCOSANTI, H.WANG, H.LEE, T.B.ACTON, J.K.EVERETT, Y.J.HUANG, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, SPARKY, TALOS+, TOPSPIN, VNMRJ, XEASY
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

<b>Protein number</b>	38
<b>PDB code</b>	6FIP, doi:10.2210/pdb6FIP/pdb
<b>BMRB code</b>	34235, doi:10.13018/BMR34235
<b>PDB Header</b>	TRANSPORT PROTEIN
<b>Protein name</b>	PSEUDOMONAS AERUGINOSA TONB CTD
<b>Deposition date</b>	19.01.2018
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF PSEUDOMONAS AERUGINOSA TONB CTD
<b>PDB authors</b>	J.S.OEEMIG, O.H.SAMULI OLLILA, H.A.HEIKKINEN, H.IWAI
<b>Last author</b>	IWAI
<b>Reference</b>	PEERJ 6, E5412 (2018), doi:10.7717/PEERJ.5412
<b>Reference authors</b>	J.S.OEEMIG, O.H.S.OLLILA, H.IWAI
<b>Reference title</b>	NMR STRUCTURE OF THE C-TERMINAL DOMAIN OF TONB PROTEIN FROM PSEUDOMONAS AERUGINOSA
<b>Software listed</b>	AMBER, CCPNMR, CYANA, NMRPIPE
<b>Spectrometer</b>	VARIAN (800 MHZ)

<b>Protein number</b>	39
<b>PDB code</b>	2LEA, doi:10.2210/pdb2LEA/pdb
<b>BMRB code</b>	17705, doi:10.13018/BMR17705
<b>PDB Header</b>	RNA BINDING PROTEIN
<b>Protein name</b>	HUMAN SRSF2 (SC35) RRM
<b>Deposition date</b>	15.06.2011
<b>PDB title</b>	SOLUTION STRUCTURE OF HUMAN SRSF2 (SC35) RRM

<b>PDB authors</b>	G.M.DAUBNER, A.CLERY, S.JAYNE, J.STEVENIN, F.H.-T.ALLAIN
<b>Last author</b>	ALLAIN
<b>Reference</b>	EMBO J. 31, 162 (2012), doi:10.1038/EMBOJ.2011.367
<b>Reference authors</b>	G.M.DAUBNER, A.CLERY, S.JAYNE, J.STEVENIN, F.H.ALLAIN
<b>Reference title</b>	A SYN-ANTI CONFORMATIONAL DIFFERENCE ALLOWS SRSF2 TO RECOGNIZE GUANINES AND CYTOSINES EQUALLY WELL
<b>Software listed</b>	AMBER, CYANA, SPARKY
<b>Spectrometer</b>	BRUKER (900 MHZ, 700 MHZ, 600 MHZ, 500 MHZ)

<b>Protein number</b>	40
<b>PDB code</b>	2LL8, doi:10.2210/pdb2LL8/pdb
<b>BMRB code</b>	18032, doi:10.13018/BMR18032
<b>PDB Header</b>	TRANSFERASE
<b>Protein name</b>	SPECIALIZED HOLO-ACYL CARRIER PROTEIN RPA2022 FROM RHODOPSEUDOMONAS PALUSTRIS REFINED WITH NH RDCS
<b>Deposition date</b>	31.10.2011
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE SPECIALIZED HOLO-ACYL CARRIER PROTEIN RPA2022 FROM RHODOPSEUDOMONAS PALUSTRIS REFINED WITH NH RDCS, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET RPR324
<b>PDB authors</b>	T.A.RAMELOT, S.NI, P.ROSSI, Y.YANG, H.WANG, C.CICCOSANTI, M.MAGLAQUI, H.JANJUA, R.NAIR, B.ROSET, T.B.ACTON, R.XIAO, J.K.EVERETT, J.H.PRESTEGARD, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	BIOCHEMISTRY 51, 7239 (2012), doi:10.1021/BI300546B
<b>Reference authors</b>	T.A.RAMELOT, P.ROSSI, F.FOROUHAR, H.W.LEE, Y.YANG, S.NI, S.UNSER, S.LEW, J.SEETHARAMAN, R.XIAO, T.B.ACTON, J.K.EVERETT, J.H.PRESTEGARD, J.F.HUNT, G.T.MONTELIONE, M.A.KENNEDY
<b>Reference title</b>	STRUCTURE OF A SPECIALIZED ACYL CARRIER PROTEIN ESSENTIAL FOR LIPID A BIOSYNTHESIS WITH VERY LONG-CHAIN FATTY ACIDS IN OPEN AND CLOSED CONFORMATIONS
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, FMCGUI, NMRPIPE, PDBSTAT, PINE_SERVER, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR NIH
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	41
<b>PDB code</b>	2KPN, doi:10.2210/pdb2KPN/pdb
<b>BMRB code</b>	16561, doi:10.13018/BMR16561
<b>PDB Header</b>	HYDROLASE
<b>Protein name</b>	A BACTERIAL IG-LIKE (BIG_3) DOMAIN FROM BACILLUS CEREUS
<b>Deposition date</b>	16.10.2009
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF A BACTERIAL IG-LIKE (BIG_3) DOMAIN FROM BACILLUS CEREUS. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET BCR147A
<b>PDB authors</b>	J.M.ARAMINI, D.WANG, C.T.CICCOSANTI, H.JANJUA, B.ROST, T.B.ACTON, R.XIAO, G.V.T.SWAPNA, J.K.EVERETT, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, CNS, CYANA, MOLPROBITY, NMRPIPE, PDBSTAT, PINE, PSVS, SPARKY, TALOS, TOPSPIN
<b>Spectrometer</b>	BRUKER (800 MHZ, 600 MHZ)

<b>Protein number</b>	42
<b>PDB code</b>	2K0M, doi:10.2210/pdb2K0M/pdb
<b>BMRB code</b>	15652, doi:10.13018/BMR15652
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	UNCHARACTERIZED PROTEIN FROM RHODOSPIRILLUM RUBRUM GENE LOCUS RRU_A0810
<b>Deposition date</b>	04.02.2008
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE UNCHARACTERIZED PROTEIN FROM RHODOSPIRILLUM RUBRUM GENE LOCUS RRU_A0810. NORTHEAST STRUCTURAL GENOMICS TARGET RRR43
<b>PDB authors</b>	P.ROSSI, H.WANG, M.JIANG, E.L.FOOTE, R.XIAO, J.LIU, G.SWAPNA, T.B.ACTON, M.C.BARAN, B.ROST, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, CNS, CYANA, MOLMOL, MOLPROBITY, NMRPIPE, PROCHECKNMR, PSVS, SPARKY, TALOS, TOPSPIN
<b>Spectrometer</b>	BRUKER (800 MHZ)

<b>Protein number</b>	43
<b>PDB code</b>	2K5V, doi:10.2210/pdb2K5V/pdb
<b>BMRB code</b>	15849, doi:10.13018/BMR15849
<b>PDB Header</b>	DNA BINDING PROTEIN
<b>Protein name</b>	SECOND OB-FOLD DOMAIN OF REPLICATION PROTEIN A FROM METHANOCOCCUS MARIPALUDIS
<b>Deposition date</b>	30.06.2008
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE SECOND OB-FOLD DOMAIN OF REPLICATION PROTEIN A FROM METHANOCOCCUS MARIPALUDIS. NORTHEAST STRUCTURAL GENOMICS TARGET MRR110B

<b>PDB authors</b>	J.M.ARAMINI, M.MAGLAQUI, M.JIANG, C.CICCOSANTI, R.XIAO, R.NAIR, J.K.EVERETT, G.VT.SWAPNA, T.B.ACTON, B.ROST, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
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<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PDBSTAT, PSVS, SPARKY, TOPSPIN
<b>Spectrometer</b>	BRUKER (800 MHZ, 600 MHZ)

<b>Protein number</b>	44
<b>PDB code</b>	2MQL, doi:10.2210/pdb2MQL/pdb
<b>BMRB code</b>	25038, doi:10.13018/BMR25038
<b>PDB Header</b>	RNA BINDING PROTEIN
<b>Protein name</b>	STRUCTURAL INVESTIGATION OF HNRNP L
<b>Deposition date</b>	24.06.2014
<b>PDB title</b>	STRUCTURAL INVESTIGATION OF HNRNP L
<b>PDB authors</b>	M.BLATTER, F.ALLAIN
<b>Last author</b>	ALLAIN
<b>Reference</b>	J.MOL.BIOL. 427, 3001 (2015), doi:10.1016/J.JMB.2015.05.020
<b>Reference authors</b>	M.BLATTER, S.DUNIN-HORKAWICZ, I.GRISHINA, C.MARIS, S.THORE, T.MAIER, A.BINDEREIF, J.M.BUJNICKI, F.H.ALLAIN
<b>Reference title</b>	THE SIGNATURE OF THE FIVE-STRANDED VRRM FOLD DEFINED BY FUNCTIONAL, STRUCTURAL AND COMPUTATIONAL ANALYSIS OF THE HNRNP L PROTEIN
<b>Software listed</b>	AMBER, CYANA, SPARKY, TOPSPIN
<b>Spectrometer</b>	BRUKER (900 MHZ, 700 MHZ)

<b>Protein number</b>	45
<b>PDB code</b>	2K75, doi:10.2210/pdb2K75/pdb
<b>BMRB code</b>	15902, doi:10.13018/BMR15902
<b>PDB Header</b>	DNA BINDING PROTEIN
<b>Protein name</b>	OB DOMAIN OF TA0387 FROM THERMOPLASMA ACIDOPHILUM
<b>Deposition date</b>	01.08.2008
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE OB DOMAIN OF TA0387 FROM THERMOPLASMA ACIDOPHILUM. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET TAR80B
<b>PDB authors</b>	T.A.RAMELOT, K.DING, D.LEE, M.JIANG, C.CICCOSANTI, R.XIAO, R.NAIR, J.K.EVERETT, G.SWAPNA, T.B.ACTON, B.ROST, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, NMRPIPE, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	46
<b>PDB code</b>	2LTM, doi:10.2210/pdb2LTM/pdb
<b>BMRB code</b>	18489, doi:10.13018/BMR18489
<b>PDB Header</b>	ELECTRON TRANSPORT
<b>Protein name</b>	NFU1 IRON-SULFUR CLUSTER SCAFFOLD HOMOLOG FROM HOMO SAPIENS
<b>Deposition date</b>	29.05.2012
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF NFU1 IRON-SULFUR CLUSTER SCAFFOLD HOMOLOG FROM HOMO SAPIENS, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG) TARGET HR2876B
<b>PDB authors</b>	G.LIU, R.XIAO, H.JANJUA, K.HAMILTON, R.SHASTRY, E.KOHAN, T.B.ACTON, J.K.EVERETT, H.LEE, Y.J.HUANG, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG), MITOCHONDRIAL PROTEIN PARTNERSHIP (MPP)
<b>Last author</b>	MONTELIONE
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<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PALES, PSVS, REDCAT, SPARKY, TALOS+, TOPSPIN, VNMRJ, XEASY
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

<b>Protein number</b>	47
<b>PDB code</b>	2KOB, doi:10.2210/pdb2KOB/pdb
<b>BMRB code</b>	16498, doi:10.13018/BMR16498
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	CLOLEP_01837 (FRAGMENT 61-160) FROM CLOSTRIDIUM LEPTUM
<b>Deposition date</b>	15.09.2009
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF CLOLEP_01837 (FRAGMENT 61-160) FROM CLOSTRIDIUM LEPTUM. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET QLR8A
<b>PDB authors</b>	T.A.RAMELOT, D.LEE, C.CICCOSANTI, M.JIANG, R.NAIR, B.ROST, T.B.ACTON, R.XIAO, J.K.EVERETT, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	

<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, NMRPIPE, PDBSTAT, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	48
<b>PDB code</b>	2KHD, doi:10.2210/pdb2KHD/pdb
<b>BMRB code</b>	16238, doi:10.13018/BMR16238
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	VC A0919 FROM VIBRIO CHOLERAE
<b>Deposition date</b>	02.04.2009
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF VC A0919 FROM VIBRIO CHOLERAE. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET VCR52
<b>PDB authors</b>	T.A.RAMELOT, J.R.CORT, H.WANG, C.CICCOSANTI, M.JIANG, J.LIU, B.ROST, G.V.T.SWAPNA, T.B.ACTON, R.XIAO, J.K.EVERETT, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, NMRPIPE, PDBSTAT, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 750 MHZ, 600 MHZ)

<b>Protein number</b>	49
<b>PDB code</b>	2RN7, doi:10.2210/pdb2RN7/pdb
<b>BMRB code</b>	11017, doi:10.13018/BMR11017
<b>PDB Header</b>	UNKNOWN FUNCTION
<b>Protein name</b>	TNPE PROTEIN FROM SHIGELLA FLEXNERI
<b>Deposition date</b>	08.12.2007
<b>PDB title</b>	NMR SOLUTION STRUCTURE OF TNPE PROTEIN FROM SHIGELLA FLEXNERI. NORTHEAST STRUCTURAL GENOMICS TARGET SFR125
<b>PDB authors</b>	T.A.RAMELOT, J.R.CORT, A.SEMESI, M.GARCIA, A.A.YEE, C.H.ARROWSMITH, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOSTRUCTURE, CNS, NMRPIPE, SPARKY, VNMR, X-PLOR
<b>Spectrometer</b>	VARIAN (750 MHZ, 600 MHZ)

<b>Protein number</b>	50
<b>PDB code</b>	2LXU, doi:10.2210/pdb2LXU/pdb
<b>BMRB code</b>	18698, doi:10.13018/BMR18698
<b>PDB Header</b>	RNA BINDING PROTEIN
<b>Protein name</b>	EUKARYOTIC RNA RECOGNITION MOTIF, RRM1, FROM HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H FROM HOMO SAPIENS
<b>Deposition date</b>	31.08.2012
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE EUKARYOTIC RNA RECOGNITION MOTIF, RRM1, FROM THE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H FROM HOMO SAPIENS, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG) TARGET HR8614A
<b>PDB authors</b>	T.A.RAMELOT, Y.YANG, K.PEDERSON, R.SHASTRY, E.KOHAN, H.JANJUA, R.XIAO, T.B.ACTON, J.K.EVERETT, J.H.PRESTEGARD, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOSTRUCTURE, CNS, CYANA, FMCGUI, NMRPIPE, PALES, PINE, PSVS, SPARKY, TALOS+, TOPSPIN, VNMRJ
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

<b>Protein number</b>	51
<b>PDB code</b>	2KIF, doi:10.2210/pdb2KIF/pdb
<b>BMRB code</b>	16272, doi:10.13018/BMR16272
<b>PDB Header</b>	TRANSFERASE
<b>Protein name</b>	AN O6-METHYLGUANINE DNA METHYLTRANSFERASE FAMILY PROTEIN FROM VIBRIO PARAHAEVOLYTICUS
<b>Deposition date</b>	03.05.2009
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF AN O6-METHYLGUANINE DNA METHYLTRANSFERASE FAMILY PROTEIN FROM VIBRIO PARAHAEVOLYTICUS. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET VPR247
<b>PDB authors</b>	J.M.ARAMINI, R.L.BELOTE, C.T.CICCOSANTI, M.JIANG, B.ROST, R.NAIR, G.V.T.SWAPNA, T.B.ACTON, R.XIAO, J.K.EVERETT, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	J.BIOL.CHEM. 285, 13736 (2010), doi:10.1074/JBC.M109.093591
<b>Reference authors</b>	J.M.ARAMINI, J.L.TUBBS, S.KANUGULA, P.ROSSI, A.ERTEKIN, M.MAGLAQUI, K.HAMILTON, C.T.CICCOSANTI, M.JIANG, R.XIAO, T.T.SOONG, B.ROST, T.B.ACTON, J.K.EVERETT, A.E.PEGG, J.A.TAINER, G.T.MONTELIONE

<b>Reference title</b>	STRUCTURAL BASIS OF O6-ALKYLGUANINE RECOGNITION BY A BACTERIAL ALKYLTRANSFERASE-LIKE DNA REPAIR PROTEIN
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, MOLPROBITY, NMRPIPE, PDBSTAT, PINE, PSVS, SPARKY, TOPSPIN
<b>Spectrometer</b>	BRUKER (800 MHZ, 600 MHZ)

<b>Protein number</b>	52
<b>PDB code</b>	2KBN, doi:10.2210/pdb2KBN/pdb
<b>BMRB code</b>	16051, doi:10.13018/BMR16051
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	OB DOMAIN (RESIDUES 67-166) OF MM0293 FROM METHANOSARCINA MAZEI
<b>Deposition date</b>	03.12.2008
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE OB DOMAIN (RESIDUES 67-166) OF MM0293 FROM METHANOSARCINA MAZEI. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET MAR214A
<b>PDB authors</b>	T.A.RAMELOT, K.DING, M.MAGLIQUI, M.JIANG, C.CICCOSANTI, R.XIAO, J.LUI, J.K.EVERETT, G.SWAPNA, T.B.ACTON, B.ROST, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, PSVS, SPARKY, TOPSPIN, X-PLOR
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	53
<b>PDB code</b>	2MK2, doi:10.2210/pdb2MK2/pdb
<b>BMRB code</b>	19749, doi:10.13018/BMR19749
<b>PDB Header</b>	HYDROLASE
<b>Protein name</b>	N-TERMINAL DOMAIN (SH2 DOMAIN) OF HUMAN INOSITOL POLYPHOSPHATE PHOSPHATASE-LIKE PROTEIN 1 (INPPL1) (FRAGMENT 20-117)
<b>Deposition date</b>	23.01.2014
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF N-TERMINAL DOMAIN (SH2 DOMAIN) OF HUMAN INOSITOL POLYPHOSPHATE PHOSPHATASE-LIKE PROTEIN 1 (INPPL1) (FRAGMENT 20-117), NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET HR9134A
<b>PDB authors</b>	Y.YANG, T.A.RAMELOT, H.JANJUA, R.XIAO, J.K.EVERETT, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PALES, PINE, PSVS, REDCAT, SPARKY, TALOS+, TOPSPIN, VNMRJ, XEASY
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	54
<b>PDB code</b>	2K50, doi:10.2210/pdb2K50/pdb
<b>BMRB code</b>	15819, doi:10.13018/BMR15819
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	REPLICATION FACTOR A RELATED PROTEIN FROM METHANOBACTERIUM THERMOAUTOTROPHICUM
<b>Deposition date</b>	23.06.2008
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE REPLICATION FACTOR A RELATED PROTEIN FROM METHANOBACTERIUM THERMOAUTOTROPHICUM. NORTHEAST STRUCTURAL GENOMICS TARGET TR91A
<b>PDB authors</b>	P.ROSSI, R.XIAO, M.MAGLAQUI, E.L.FOOTE, C.CICCOSANTI, G.SWAPNA, T.B.ACTON, B.ROST, J.K.EVERETT, M.JIANG, R.NAIR, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, CNS, CYANA, MOLMOL, MOLPROBITY, NMRPIPE, PROCHECK, PSVS, RPF(AUTOSTRUCTURE), SPARKY, TALOS, TOPSPIN
<b>Spectrometer</b>	BRUKER (800 MHZ, 600 MHZ)

<b>Protein number</b>	55
<b>PDB code</b>	2KL5, doi:10.2210/pdb2KL5/pdb
<b>BMRB code</b>	16384, doi:10.13018/BMR16384
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	PROTEIN YUTD FROM B.SUBTILIS
<b>Deposition date</b>	30.06.2009
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF PROTEIN YUTD FROM B.SUBTILIS, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET SR232
<b>PDB authors</b>	G.LIU, K.HAMILTON, R.XIAO, C.CICCOSANTI, C.J.HO, J.EVERETT, R.NAIR, T.ACTON, B.ROST, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, TOPSPIN, VNMRJ, XEASY

<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)
<b>Protein number</b>	56
<b>PDB code</b>	2LTA, doi:10.2210/pdb2LTA/pdb
<b>BMRB code</b>	18465, doi:10.13018/BMR18465
<b>PDB Header</b>	DE NOVO PROTEIN
<b>Protein name</b>	DE NOVO DESIGNED PROTEIN, ROSSMANN 3X1 FOLD
<b>Deposition date</b>	15.05.2012
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF DE NOVO DESIGNED PROTEIN, ROSSMANN 3X1 FOLD, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET OR157
<b>PDB authors</b>	G.LIU, R.KOGA, N.KOGA, R.XIAO, K.PEDERSON, K.HAMILTON, E.KOHAN, T.B.ACTON, G.KORNHABER, J.K.EVERETT, D.BAKER, G.T.MONTELLONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELLONE
<b>Reference</b>	NATURE 491, 222 (2012), doi:10.1038/NATURE11600
<b>Reference authors</b>	N.KOGA, R.TATSUMI-KOGA, G.LIU, R.XIAO, T.B.ACTON, G.T.MONTELLONE, D.BAKER
<b>Reference title</b>	PRINCIPLES FOR DESIGNING IDEAL PROTEIN STRUCTURES
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PSVS, REDCAT, SPARKY, TALOS+, TOPSPIN, VNMRJ, XEASY
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

<b>Protein number</b>	57
<b>PDB code</b>	2KIW, doi:10.2210/pdb2KIW/pdb
<b>BMRB code</b>	16298, doi:10.13018/BMR16298
<b>PDB Header</b>	DNA BINDING PROTEIN
<b>Protein name</b>	DOMAIN N-TERMINAL TO INTEGRASE DOMAIN OF SH1003 FROM STAPHYLOCOCCUS HAEMOLYTICUS
<b>Deposition date</b>	12.05.2009
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE DOMAIN N-TERMINAL TO THE INTEGRASE DOMAIN OF SH1003 FROM STAPHYLOCOCCUS HAEMOLYTICUS. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET SHR105F (64-166)
<b>PDB authors</b>	Y.YANG, T.A.RAMELOT, R.L.BELOTE, E.L.FOOTE, H.JANJUA, R.NAIR, B.ROST, G.SWAPNA, T.B.ACTON, R.XIAO, J.K.EVERETT, G.T.MONTELLONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, NMRPIPE, PDBSTAT, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	58
<b>PDB code</b>	2LVB, doi:10.2210/pdb2LVB/pdb
<b>BMRB code</b>	18561, doi:10.13018/BMR18561
<b>PDB Header</b>	DE NOVO PROTEIN
<b>Protein name</b>	SOLUTION NMR STRUCTURE DE NOVO DESIGNED PFK FOLD PROTEIN
<b>Deposition date</b>	30.06.2012
<b>PDB title</b>	SOLUTION NMR STRUCTURE DE NOVO DESIGNED PFK FOLD PROTEIN, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG) TARGET OR250
<b>PDB authors</b>	G.LIU, N.KOGA, R.KOGA, R.XIAO, K.HAMILTON, E.KOHAN, T.B.ACTON, G.KORNHABER, J.K.EVERETT, D.BAKER, G.T.MONTELLONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELLONE
<b>Reference</b>	NATURE 491, 222 (2012), doi:10.1038/NATURE11600
<b>Reference authors</b>	N.KOGA, R.TATSUMI-KOGA, G.LIU, R.XIAO, T.B.ACTON, G.T.MONTELLONE, D.BAKER
<b>Reference title</b>	PRINCIPLES FOR DESIGNING IDEAL PROTEIN STRUCTURES
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PSVS, SPARKY, TALOS+, TOPSPIN, VNMRJ, XEASY
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

<b>Protein number</b>	59
<b>PDB code</b>	2LND, doi:10.2210/pdb2LND/pdb
<b>BMRB code</b>	18161, doi:10.13018/BMR18161
<b>PDB Header</b>	DE NOVO PROTEIN
<b>Protein name</b>	DE NOVO DESIGNED PROTEIN, PFK FOLD
<b>Deposition date</b>	23.12.2011
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF DE NOVO DESIGNED PROTEIN, PFK FOLD, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET OR134
<b>PDB authors</b>	G.LIU, N.KOGA, R.KOGA, R.XIAO, H.LEE, H.JANJUA, E.KOHAN, T.B.ACTON, J.K.EVERETT, D.BAKER, G.T.MONTELLONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELLONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PSVS, SPARKY, TALOS+, TOPSPIN, VNMRJ, XEASY
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

<b>Protein number</b>	60
<b>PDB code</b>	1WQU, doi:10.2210/pdb1WQU/pdb
<b>BMRB code</b>	6331, doi:10.13018/BMR6331
<b>PDB Header</b>	TRANSFERASE
<b>Protein name</b>	HUMAN FES SH2 DOMAIN
<b>Deposition date</b>	02.10.2004
<b>PDB title</b>	SOLUTION STRUCTURE OF THE HUMAN FES SH2 DOMAIN
<b>PDB authors</b>	A.SCOTT, D.PANTOJA-UCEDA, S.KOSHIBA, M.INOUE, T.KIGAWA, T.TERADA, M.SHIROUZU, A.TANAKA, S.SUGANO, S.YOKOYAMA, P.GUNTERT, RIKEN STRUCTURAL GENOMICS/PROTEOMICS INITIATIVE (RSGI)
<b>Last author</b>	GUNTERT
<b>Reference</b>	J.BIOMOL.NMR 31, 357 (2005), doi:10.1007/S10858-005-0946-6
<b>Reference authors</b>	A.SCOTT, D.PANTOJA-UCEDA, S.KOSHIBA, M.INOUE, T.KIGAWA, T.TERADA, M.SHIROUZU, A.TANAKA, S.SUGANO, S.YOKOYAMA, P.GUNTERT
<b>Reference title</b>	SOLUTION STRUCTURE OF THE SRC HOMOLOGY 2 DOMAIN FROM THE HUMAN FELINE SARCOMA ONCOGENE FES
<b>Software listed</b>	CYANA, NMRPIPE, NMRVIEW, OPALP
<b>Spectrometer</b>	BRUKER (800 MHZ, 600 MHZ)

<b>Protein number</b>	61
<b>PDB code</b>	2KL6, doi:10.2210/pdb2KL6/pdb
<b>BMRB code</b>	16385, doi:10.13018/BMR16385
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	CARDB DOMAIN OF PF1109 FROM PYROCOCCLUS FURIOSUS
<b>Deposition date</b>	30.06.2009
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE CARDB DOMAIN OF PF1109 FROM PYROCOCCLUS FURIOSUS. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET PFR193A
<b>PDB authors</b>	J.M.ARAMINI, D.LEE, C.CICCOSANTI, K.HAMILTON, R.NAIR, B.ROST, T.B.ACTON, R.XIAO, G.V.T.SWAPNA, J.K.EVERETT, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOSTRUCTURE, CNS, CYANA, MOLPROBITY, NMRPIPE, PDBSTAT, PINE, PSVS, SPARKY, TALOS, TOPSPIN
<b>Spectrometer</b>	BRUKER (800 MHZ, 600 MHZ)

<b>Protein number</b>	62
<b>PDB code</b>	6GT7, doi:10.2210/pdb6GT7/pdb
<b>BMRB code</b>	34287, doi:10.13018/BMR34287
<b>PDB Header</b>	TRANSFERASE
<b>Protein name</b>	FREE HELIX BUNDLE DOMAIN FROM FUNCTIONAL PRN1 PRIMASE
<b>Deposition date</b>	15.06.2018
<b>PDB title</b>	NMR STRUCTURE OF THE FREE HELIX BUNDLE DOMAIN FROM THE FUNCTIONAL PRN1 PRIMASE
<b>PDB authors</b>	J.BOUDET, G.LIPPS, F.ALLAIN
<b>Last author</b>	ALLAIN
<b>Reference</b>	CELL 176, 154 (2019), doi:10.1016/J.CELL.2018.11.031
<b>Reference authors</b>	J.BOUDET, J.C.DEVILLIER, T.WIEGAND, L.SALMON, B.H.MEIER, G.LIPPS, F.H.ALLAIN
<b>Reference title</b>	A SMALL HELICAL BUNDLE PREPARES PRIMER SYNTHESIS BY BINDING TWO NUCLEOTIDES THAT ENHANCE SEQUENCE-SPECIFIC RECOGNITION OF THE DNA TEMPLATE
<b>Software listed</b>	AMBER, CANDID, CYANA, SPARKY
<b>Spectrometer</b>	BRUKER (900 MHZ, 700 MHZ, 600 MHZ)

<b>Protein number</b>	63
<b>PDB code</b>	2JN8, doi:10.2210/pdb2JN8/pdb
<b>BMRB code</b>	15089, doi:10.13018/BMR15089
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	Q8ZRJ2 FROM SALMONELLA TYPHIMURIUM
<b>Deposition date</b>	29.12.2006
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF Q8ZRJ2 FROM SALMONELLA TYPHIMURIUM. NORTHEAST STRUCTURAL GENOMICS TARGET STR65
<b>PDB authors</b>	J.M.ARAMINI, J.R.CORT, C.K.HO, K.CUNNINGHAM, L.-C.MA, R.XIAO, J.LIU, M.C.BARAN, G.V.T.SWAPNA, T.B.ACTON, B.ROST, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, BRUKER, NMRPIPE, PDBSTAT, PSVS, SPARKY, VNMR, X-PLOR
<b>Spectrometer</b>	BRUKER, VARIAN (750 MHZ, 600 MHZ, 500 MHZ)

<b>Protein number</b>	64
<b>PDB code</b>	2K5D, doi:10.2210/pdb2K5D/pdb
<b>BMRB code</b>	15829, doi:10.13018/BMR15829
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	SAG0934 FROM STREPTOCOCCUS AGALACTIAE
<b>Deposition date</b>	26.06.2008

<b>PDB title</b>	SOLUTION NMR STRUCTURE OF SAG0934 FROM STREPTOCOCCUS AGALACTIAE. NORTHEAST STRUCTURAL GENOMICS TARGET SAR32[1-108]
<b>PDB authors</b>	J.M.ARAMINI, P.ROSSI, L.ZHAO, E.L.FOOTE, M.JIANG, R.XIAO, S.SHARMA, G.VT.SWAPNA, R.NAIR, J.K.EVERETT, T.B.ACTON, B.ROST, G.T.MONTELLIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELLIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PDBSTAT, PSVS, SPARKY, TOPSPIN
<b>Spectrometer</b>	BRUKER (800 MHZ, 600 MHZ)

<b>Protein number</b>	65
<b>PDB code</b>	2KD1, doi:10.2210/pdb2KD1/pdb
<b>BMRB code</b>	16102, doi:10.13018/BMR16102
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	INTEGRASE-LIKE DOMAIN FROM BACILLUS CEREUS ORDERED LOCUS BC_1272
<b>Deposition date</b>	31.12.2008
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE INTEGRASE-LIKE DOMAIN FROM BACILLUS CEREUS ORDERED LOCUS BC_1272. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET BCR268F
<b>PDB authors</b>	P.ROSSI, H.LEE, M.MAGLAQUI, E.L.FOOTE, W.A.BUCHWALD, M.JIANG, G.V.T.SWAPNA, R.NAIR, R.XIAO, T.B.ACTON, B.ROST, J.H.PRESTEGARD, G.T.MONTELLIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELLIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	CNS, CYANA, MOLMOL, MOLPROBITY, NMRPIPE, PDBSTAT, PINE, PROCHECK, PSVS, SPARKY, TALOS, TOPSPIN
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

<b>Protein number</b>	66
<b>PDB code</b>	2LTL, doi:10.2210/pdb2LTL/pdb
<b>BMRB code</b>	18487, doi:10.13018/BMR18487
<b>PDB Header</b>	ELECTRON TRANSPORT
<b>Protein name</b>	NIFU-LIKE PROTEIN FROM SACCHAROMYCES CEREVISIAE
<b>Deposition date</b>	29.05.2012
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF NIFU-LIKE PROTEIN FROM SACCHAROMYCES CEREVISIAE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG) TARGET YR313A
<b>PDB authors</b>	G.LIU, R.XIAO, K.HAMILTON, H.JANJUA, R.SHASTRY, E.KOHAN, T.B.ACTON, J.K.EVERETT, H.LEE, Y.J.HUANG, G.T.MONTELLIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG), MITOCHONDRIAL PROTEIN PARTNERSHIP (MPP)
<b>Last author</b>	MONTELLIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PALES, PINE, PSVS, REDCAT, SPARKY, TALOS+, TOPSPIN, VNMRJ, XEASY
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

<b>Protein number</b>	67
<b>PDB code</b>	2KVO, doi:10.2210/pdb2KVO/pdb
<b>BMRB code</b>	16782, doi:10.13018/BMR16782
<b>PDB Header</b>	PHOTOSYNTHESIS
<b>Protein name</b>	PHOTOSYSTEM II REACTION CENTER PSB28 PROTEIN FROM SYNECHOCYSTIS SP.(STRAIN PCC 6803)
<b>Deposition date</b>	22.03.2010
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF PHOTOSYSTEM II REACTION CENTER PSB28 PROTEIN FROM SYNECHOCYSTIS SP.(STRAIN PCC 6803), NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET SGR171
<b>PDB authors</b>	Y.YANG, T.A.RAMELOT, J.R.CORT, D.WANG, C.CICCOSANTI, K.HAMILTON, R.NAIR, B.ROST, T.B.ACTON, R.XIAO, J.K.EVERETT, G.T.MONTELLIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	PROTEINS 79, 340 (2011), doi:10.1002/PROT.22876
<b>Reference authors</b>	Y.YANG, T.A.RAMELOT, J.R.CORT, D.WANG, C.CICCOSANTI, K.HAMILTON, R.NAIR, B.ROST, T.B.ACTON, R.XIAO, J.K.EVERETT, G.T.MONTELLIONE, M.A.KENNEDY
<b>Reference title</b>	SOLUTION NMR STRUCTURE OF PHOTOSYSTEM II REACTION CENTER PROTEIN PSB28 FROM SYNECHOCYSTIS SP. STRAIN PCC 6803
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, NMRPIPE, PDBSTAT, PINE_SERVER, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR NIH
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	68
<b>PDB code</b>	1T0Y, doi:10.2210/pdb1T0Y/pdb
<b>BMRB code</b>	6176, doi:10.13018/BMR6176
<b>PDB Header</b>	CHAPERONE
<b>Protein name</b>	A UBIQUITIN-LIKE DOMAIN FROM TUBULIN-BINDING COFACTOR B



<b>Deposition date</b>	13.04.2004
<b>PDB title</b>	SOLUTION STRUCTURE OF A UBIQUITIN-LIKE DOMAIN FROM TUBULIN-BINDING COFACTOR B
<b>PDB authors</b>	B.L.LYTTLE, F.C.PETERSON, S.H.QIU, M.LUO, B.F.VOLKMAN, J.L.MARKLEY, CENTER FOR EUKARYOTIC STRUCTURAL GENOMICS (CESG)
<b>Last author</b>	MARKLEY
<b>Reference</b>	J.BIOL.CHEM. 279, 46787 (2004), doi:10.1074/JBC.M409422200
<b>Reference authors</b>	B.L.LYTTLE, F.C.PETERSON, S.H.QIU, M.LUO, Q.ZHAO, J.L.MARKLEY, B.F.VOLKMAN
<b>Reference title</b>	SOLUTION STRUCTURE OF A UBIQUITIN-LIKE DOMAIN FROM TUBULIN-BINDING COFACTOR B
<b>Software listed</b>	CYANA, NMRPIPE, SPSCAN, X-PLOR NIH, XEASY, XWINNMR
<b>Spectrometer</b>	BRUKER (600 MHZ)

<b>Protein number</b>	69
<b>PDB code</b>	2KCD, doi:10.2210/pdb2KCD/pdb
<b>BMRB code</b>	16072, doi:10.13018/BMR16072
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	SSP0047 FROM STAPHYLOCOCCUS SAPROPHYTICUS
<b>Deposition date</b>	19.12.2008
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF SSP0047 FROM STAPHYLOCOCCUS SAPROPHYTICUS. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET SYR6
<b>PDB authors</b>	T.A.RAMELOT, K.DING, C.X.CHEN, M.JIANG, C.CICCOSANTI, R.XIAO, J.LIU, M.C.BARAN, G.SWAPNA, T.B.ACTON, B.ROST, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, NMRPIPE, PDBSTAT, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 750 MHZ, 600 MHZ)

<b>Protein number</b>	70
<b>PDB code</b>	2KRT, doi:10.2210/pdb2KRT/pdb
<b>BMRB code</b>	16648, doi:10.13018/BMR16648
<b>PDB Header</b>	LIPID BINDING PROTEIN
<b>Protein name</b>	A CONSERVED HYPOTHETICAL MEMBRANE LIPOPROTEIN OBTAINED FROM UREAPLASMA PARVUM
<b>Deposition date</b>	22.12.2009
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF A CONSERVED HYPOTHETICAL MEMBRANE LIPOPROTEIN OBTAINED FROM UREAPLASMA PARVUM: NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET UUR17A (139-239)
<b>PDB authors</b>	R.MANI, G.SWAPNA, H.JANJUA, C.CICCOSANTI, Y.HUANG, D.PATEL, R.XIAO, T.ACTON, J.EVERETT, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, PINE
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ, 500 MHZ)

<b>Protein number</b>	71
<b>PDB code</b>	2LFI, doi:10.2210/pdb2LFI/pdb
<b>BMRB code</b>	17754, doi:10.13018/BMR17754
<b>PDB Header</b>	METAL BINDING PROTEIN
<b>Protein name</b>	A MUCBP DOMAIN (FRAGMENT 187-294) OF PROTEIN LBA1460 FROM LACTOBACILLUS ACIDOPHILUS
<b>Deposition date</b>	30.06.2011
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF A MUCBP DOMAIN (FRAGMENT 187-294) OF THE PROTEIN LBA1460 FROM LACTOBACILLUS ACIDOPHILUS, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET LAR80A
<b>PDB authors</b>	E.A.FELDMANN, T.A.RAMELOT, Y.YANG, H.LEE, C.CICCOSANTI, H.JANJUA, R.NAIR, T.B.ACTON, R.XIAO, J.K.EVERETT, J.H.PRESTEGARD, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PDBSTAT, PINE_SERVER, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR NIH
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	72
<b>PDB code</b>	2JQN, doi:10.2210/pdb2JQN/pdb
<b>BMRB code</b>	15281, doi:10.13018/BMR15281
<b>PDB Header</b>	STRUCTURAL GENOMICS
<b>Protein name</b>	CC0527 FROM CAULOBACTER CRESCENTUS
<b>Deposition date</b>	05.06.2007
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF CC0527 FROM CAULOBACTER CRESCENTUS. NORTHEAST STRUCTURAL GENOMICS TARGET CCR55
<b>PDB authors</b>	J.M.ARAMINI, P.ROSSI, H.N.B.MOSELEY, D.WANG, C.NWOSU, K.CUNNINGHAM, L.MA, R.XIAO, J.LIU, M.C.BARAN, G.V.T.SWAPNA, T.B.ACTON, B.ROST, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)

<b>Last author</b>	MONTELIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, NMRPIPE, PDBSTAT, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

<b>Protein number</b>	73
<b>PDB code</b>	2L7Q, doi:10.2210/pdb2L7Q/pdb
<b>BMRB code</b>	17370, doi:10.13018/BMR17370
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	CONJUGATE TRANSPOSON PROTEIN BVU 1572(27- 141) FROM BACTEROIDES VULGATUS
<b>Deposition date</b>	20.12.2010
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF CONJUGATE TRANSPOSON PROTEIN BVU_1572(27- 141) FROM BACTEROIDES VULGATUS, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET BVR155
<b>PDB authors</b>	Y.YANG, T.A.RAMELOT, J.R.CORT, D.WANG, C.CICCOSANTI, H.JANJUA, T.B.ACTON, R.XIAO, J.K.EVERETT, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	PROTEINS 80, 667 (2012), doi:10.1002/PROT.23235
<b>Reference authors</b>	T.A.RAMELOT, Y.YANG, R.XIAO, T.B.ACTON, J.K.EVERETT, G.T.MONTELIONE, M.A.KENNEDY
<b>Reference title</b>	SOLUTION NMR STRUCTURE OF BT_0084, A CONJUGATIVE TRANSPOSON LIPOPROTEIN FROM BACTEROIDES THETA10TAMICRON
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PDBSTAT, PINE_SERVER, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR NIH
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	74
<b>PDB code</b>	2KFP, doi:10.2210/pdb2KFP/pdb
<b>BMRB code</b>	16186, doi:10.13018/BMR16186
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	PSPTO 3016 FROM PSEUDOMONAS SYRINGAE
<b>Deposition date</b>	24.02.2009
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF PSPTO 3016 FROM PSEUDOMONAS SYRINGAE. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET PSR293
<b>PDB authors</b>	E.A.FELDMANN, T.A.RAMELOT, L.ZHAO, K.HAMILTON, C.CICCOSANTI, R.XIAO, R.NAIR, J.K.EVERETT, G.SWAPNA, T.B.ACTON, B.ROST, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	J.STRUCT.FUNCT.GENOM. 13, 155 (2012), doi:10.1007/S10969-012-9140-8
<b>Reference authors</b>	E.A.FELDMANN, J.SEETHARAMAN, T.A.RAMELOT, S.LEW, L.ZHAO, K.HAMILTON, C.CICCOSANTI, R.XIAO, T.B.ACTON, J.K.EVERETT, L.TONG, G.T.MONTELIONE, M.A.KENNEDY
<b>Reference title</b>	SOLUTION NMR AND X-RAY CRYSTAL STRUCTURES OF PSEUDOMONAS SYRINGAE PSPTO 3016 FROM PROTEIN DOMAIN FAMILY PF04237 (DUF419) ADOPT A "DOUBLE WING" DNA BINDING MOTIF
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, NMRPIPE, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	75
<b>PDB code</b>	1SE9, doi:10.2210/pdb1SE9/pdb
<b>BMRB code</b>	6128, doi:10.13018/BMR6128
<b>PDB Header</b>	PLANT PROTEIN
<b>Protein name</b>	AT3G01050, A UBIQUITIN-FOLD PROTEIN FROM ARABIDOPSIS THALIANA
<b>Deposition date</b>	16.02.2004
<b>PDB title</b>	STRUCTURE OF AT3G01050, A UBIQUITIN-FOLD PROTEIN FROM ARABIDOPSIS THALIANA
<b>PDB authors</b>	B.F.VOLKMAN, B.L.LYTLE, F.C.PETERSON, CENTER FOR EUKARYOTIC STRUCTURAL GENOMICS (CESG)
<b>Last author</b>	PETERSON
<b>Reference</b>	NAT.METHODS 1, 149 (2004), doi:10.1038/NMETH716
<b>Reference authors</b>	D.A.VINAROV, B.L.LYTLE, F.C.PETERSON, E.M.TYLER, B.F.VOLKMAN, J.L.MARKLEY
<b>Reference title</b>	CELL-FREE PROTEIN PRODUCTION AND LABELING PROTOCOL FOR NMR-BASED STRUCTURAL PROTEOMICS
<b>Software listed</b>	CYANA, NMRPIPE, SPSCAN, X-PLOR_NIH, XEASY, XWINNMR
<b>Spectrometer</b>	BRUKER (600 MHZ)

<b>Protein number</b>	76
<b>PDB code</b>	2L3G, doi:10.2210/pdb2L3G/pdb
<b>BMRB code</b>	17192, doi:10.13018/BMR17192
<b>PDB Header</b>	SIGNALING PROTEIN
<b>Protein name</b>	CH DOMAIN OF RHO GUANINE NUCLEOTIDE EXCHANGE FACTOR 7 FROM HOMO SAPIENS
<b>Deposition date</b>	13.09.2010
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF CH DOMAIN OF RHO GUANINE NUCLEOTIDE EXCHANGE FACTOR 7 FROM HOMO SAPIENS, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET HR4495E
<b>PDB authors</b>	G.LIU, R.XIAO, H.JANJUA, T.B.ACTON, A.CICCOSANTI, R.SHASTRY, J.EVERETT, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	

<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, TALOS+, TOPSPIN, VNMRJ, XEASY
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

<b>Protein number</b>	77
<b>PDB code</b>	2L3B, doi:10.2210/pdb2L3B/pdb
<b>BMRB code</b>	17176, doi:10.13018/BMR17176
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	BT_0084 LIPOPROTEIN FROM BACTEROIDES THETAOTAOOMICRON
<b>Deposition date</b>	10.09.2010
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE BT_0084 LIPOPROTEIN FROM BACTEROIDES THETAOTAOOMICRON, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET BTR376
<b>PDB authors</b>	T.A.RAMELOT, Y.YANG, D.WANG, C.CICCOSANTI, H.JANJUA, T.B.ACTON, R.XIAO, J.K.EVERETT, G.T.MONTELLIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	PROTEINS 867 2012, doi:10.1002/PROT.23235
<b>Reference authors</b>	T.A.RAMELOT, Y.YANG, R.XIAO, T.B.ACTON, J.K.EVERETT, G.T.MONTELLIONE, M.A.KENNEDY
<b>Reference title</b>	SOLUTION NMR STRUCTURE OF BT_0084, A CONJUGATIVE TRANSPOSON LIPOPROTEIN FROM BACTEROIDES THETAOTAOOMICRON
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CYANA, NMRPIPE, PDBSTAT, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	78
<b>PDB code</b>	2LRH, doi:10.2210/pdb2LRH/pdb
<b>BMRB code</b>	18372, doi:10.13018/BMR18372
<b>PDB Header</b>	DE NOVO PROTEIN
<b>Protein name</b>	DE NOVO DESIGNED PROTEIN, P-LOOP NTPASE FOLD
<b>Deposition date</b>	30.03.2012
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF DE NOVO DESIGNED PROTEIN, P-LOOP NTPASE FOLD, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET OR137
<b>PDB authors</b>	G.LIU, N.KOGA, R.KOGA, R.XIAO, H.LEE, H.JANJUA, E.KOHAN, T.B.ACTON, J.K.EVERETT, D.BAKER, G.T.MONTELLIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELLIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PALES, PSVS, REDCAT, SPARKY, TALOS+, TOPSPIN, VNMRJ, XEASY
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

<b>Protein number</b>	79
<b>PDB code</b>	1VEE, doi:10.2210/pdb1VEE/pdb
<b>BMRB code</b>	5929, doi:10.13018/BMR5929
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	HYPOTHETICAL RHODANESE DOMAIN AT4G01050 FROM ARABIDOPSIS THALIANA
<b>Deposition date</b>	30.03.2004
<b>PDB title</b>	NMR STRUCTURE OF THE HYPOTHETICAL RHODANESE DOMAIN AT4G01050 FROM ARABIDOPSIS THALIANA
<b>PDB authors</b>	D.PANTOJA-UCEDA, B.LOPEZ-MENDEZ, S.KOSHIBA, M.INOUE, T.KIGAWA, T.TERADA, M.SHIROUZU, A.TANAKA, M.SEKI, K.SHINOZAKI, S.YOKOYAMA, P.GUNTERT, RIKEN STRUCTURAL GENOMICS/PROTEOMICS INITIATIVE (RSGI)
<b>Last author</b>	GUNTERT
<b>Reference</b>	PROTEIN SCI. 14, 224 (2005), doi:10.1110/PS.041138705
<b>Reference authors</b>	D.PANTOJA-UCEDA, B.LOPEZ-MENDEZ, S.KOSHIBA, M.INOUE, T.KIGAWA, T.TERADA, M.SHIROUZU, A.TANAKA, M.SEKI, K.SHINOZAKI, S.YOKOYAMA, P.GUNTERT
<b>Reference title</b>	SOLUTION STRUCTURE OF THE RHODANESE HOMOLOG DOMAIN AT4G01050(175-295) FROM ARABIDOPSIS THALIANA
<b>Software listed</b>	CYANA, OPALP
<b>Spectrometer</b>	BRUKER (800 MHZ, 600 MHZ)

<b>Protein number</b>	80
<b>PDB code</b>	2K1G, doi:10.2210/pdb2K1G/pdb
<b>BMRB code</b>	15603, doi:10.13018/BMR15603
<b>PDB Header</b>	LIPOPROTEIN
<b>Protein name</b>	LIPOPROTEIN SPR FROM ESCHERICHIA COLI K12
<b>Deposition date</b>	03.03.2008
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF LIPOPROTEIN SPR FROM ESCHERICHIA COLI K12. NORTHEAST STRUCTURAL GENOMICS TARGET ER541-37-162
<b>PDB authors</b>	J.M.ARAMINI, P.ROSSI, L.ZHAO, M.JIANG, M.MAGLAQUI, R.XIAO, J.LIU, M.C.BARAN, G.V.T.SWAPNA, Y.J.HUANG, T.B.ACTON, B.ROST, G.T.MONTELLIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELLIONE
<b>Reference</b>	BIOCHEMISTRY 47, 9715 (2008), doi:10.1021/BI8010779
<b>Reference authors</b>	J.M.ARAMINI, P.ROSSI, Y.J.HUANG, L.ZHAO, M.JIANG, M.MAGLAQUI, R.XIAO, J.LOCKE, R.NAIR, B.ROST, T.B.ACTON, M.INOUE, G.T.MONTELLIONE

<b>Reference title</b>	SOLUTION NMR STRUCTURE OF THE NLPC/P60 DOMAIN OF LIPOPROTEIN SPR FROM ESCHERICHIA COLI: STRUCTURAL EVIDENCE FOR A NOVEL CYSTEINE PEPTIDASE CATALYTIC TRIAD
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PDBSTAT, PSVS, SPARKY, TOPSPIN, VNMR
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

<b>Protein number</b>	81
<b>PDB code</b>	2KKZ, doi:10.2210/pdb2KKZ/pdb
<b>BMRB code</b>	16376, doi:10.13018/BMR16376
<b>PDB Header</b>	ANTIVIRAL PROTEIN
<b>Protein name</b>	MONOMERIC W187R MUTANT OF A/UDORN NS1 EFFECTOR DOMAIN
<b>Deposition date</b>	29.06.2009
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE MONOMERIC W187R MUTANT OF A/UDORN NS1 EFFECTOR DOMAIN. NORTHEAST STRUCTURAL GENOMICS TARGET OR8C[W187R]
<b>PDB authors</b>	J.M.ARAMINI, L.MA, H.LEE, L.ZHAO, K.CUNNINGHAM, C.CICCOSANTI, H.JANJUA, Y.FANG, R.XIAO, R.M.KRUG, G.T.MONTELLIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELLIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, MOLPROBITY, NMRPIPE, PDBSTAT, PSVS, SPARKY, TALOS, TOPSPIN
<b>Spectrometer</b>	BRUKER (800 MHZ, 600 MHZ)

<b>Protein number</b>	82
<b>PDB code</b>	1VDY, doi:10.2210/pdb1VDY/pdb
<b>BMRB code</b>	5928, doi:10.13018/BMR5928
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	HYPOTHETICAL ENTH-VHS DOMAIN AT3G16270 FROM ARABIDOPSIS THALIANA
<b>Deposition date</b>	25.03.2004
<b>PDB title</b>	NMR STRUCTURE OF THE HYPOTHETICAL ENTH-VHS DOMAIN AT3G16270 FROM ARABIDOPSIS THALIANA
<b>PDB authors</b>	B.LOPEZ-MENDEZ, D.PANTOJA-UCEDA, T.TOMIZAWA, S.KOSHIBA, T.KIGAWA, M.SHIROUZU, T.TERADA, M.INOUE, T.YABUKI, M.AOKI, E.SEKI, T.MATSUDA, H.HIROTA, M.YOSHIDA, A.TANAKA, T.OSANAI, M.SEKI, K.SHINOZAKI, S.YOKOYAMA, P.GUNTERT, RIKEN STRUCTURAL GENOMICS/PROTEOMICS INITIATIVE (RSGI)
<b>Last author</b>	GUNTERT
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	CYANA, OPALP
<b>Spectrometer</b>	BRUKER (800 MHZ, 600 MHZ)

<b>Protein number</b>	83
<b>PDB code</b>	2KKL, doi:10.2210/pdb2KKL/pdb
<b>BMRB code</b>	16364, doi:10.13018/BMR16364
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	FHA DOMAIN OF MB1858 FROM MYCOBACTERIUM BOVIS
<b>Deposition date</b>	25.06.2009
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF FHA DOMAIN OF MB1858 FROM MYCOBACTERIUM BOVIS. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET MBR243C (24- 155)
<b>PDB authors</b>	Y.YANG, T.A.RAMELOT, D.WANG, E.L.FOOTE, M.JIANG, R.NAIR, B.ROST, G.SWAPNA, T.B.ACTON, R.XIAO, J.K.EVERETT, G.T.MONTELLIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, NMRPIPE, PDBSTAT, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	84
<b>PDB code</b>	2N4B, doi:10.2210/pdb2N4B/pdb
<b>BMRB code</b>	17611, doi:10.13018/BMR17611
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	RALSTONIA METALLIDURANS RMET_5065 DETERMINED BY COMBINING EVOLUTIONARY COUPLINGS (EC) AND SPARSE NMR DATA
<b>Deposition date</b>	17.06.2015
<b>PDB title</b>	EC-NMR STRUCTURE OF RALSTONIA METALLIDURANS RMET_5065 DETERMINED BY COMBINING EVOLUTIONARY COUPLINGS (EC) AND SPARSE NMR DATA. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET CRR115
<b>PDB authors</b>	Y.TANG, Y.J.HUANG, T.A.HOPF, C.SANDER, D.MARKS, G.T.MONTELLIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELLIONE
<b>Reference</b>	NAT.METHODS 12, 751 (2015), doi:10.1038/NMETH.3455
<b>Reference authors</b>	Y.TANG, Y.J.HUANG, T.A.HOPF, C.SANDER, D.S.MARKS, G.T.MONTELLIONE

<b>Reference title</b>	PROTEIN STRUCTURE DETERMINATION BY COMBINING SPARSE NMR DATA WITH EVOLUTIONARY COUPLINGS
<b>Software listed</b>	ASDP, CYANA, EC-NMR, EVFOLD-PLM, REDUCE, ROSETTA, TALOS+
<b>Spectrometer</b>	

<b>Protein number</b>	85
<b>PDB code</b>	2L8V, doi:10.2210/pdb2L8V/pdb
<b>BMRB code</b>	17429, doi:10.13018/BMR17429
<b>PDB Header</b>	PHOTOSYNTHESIS
<b>Protein name</b>	PHYCOBILISOME LINKER POLYPEPTIDE DOMAIN OF CPCC (20-153) FROM THERMOSYNECHOCOCCUS ELONGATUS
<b>Deposition date</b>	26.01.2011
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE PHYCOBILISOME LINKER POLYPEPTIDE DOMAIN OF CPCC (20-153) FROM THERMOSYNECHOCOCCUS ELONGATUS, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET TER219A
<b>PDB authors</b>	T.A.RAMELOT, Y.YANG, J.R.CORT, D.LEE, C.CICCOSANTI, K.HAMILTON, T.B.ACTON, R.XIAO, J.K.EVERETT, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PDBSTAT, PINE_SERVER, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR NIH
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	86
<b>PDB code</b>	2LGH, doi:10.2210/pdb2LGH/pdb
<b>BMRB code</b>	17809, doi:10.13018/BMR17809
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	AHSA1-LIKE PROTEIN AHA_2358 FROM AEROMONAS HYDROPHILA REFINED WITH NH RDCS
<b>Deposition date</b>	26.07.2011
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE AHSA1-LIKE PROTEIN AHA_2358 FROM AEROMONAS HYDROPHILA REFINED WITH NH RDCS, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET AHR99
<b>PDB authors</b>	T.A.RAMELOT, Y.YANG, H.LEE, D.WANG, C.CICCOSANTI, H.JANJUA, R.NAIR, T.B.ACTON, R.XIAO, J.K.EVERETT, J.H.PRESTEGARD, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PDBSTAT, PINE_SERVER, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR NIH
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	87
<b>PDB code</b>	2K1S, doi:10.2210/pdb2K1S/pdb
<b>BMRB code</b>	15683, doi:10.13018/BMR15683
<b>PDB Header</b>	LIPOPROTEIN
<b>Protein name</b>	FOLDED C-TERMINAL FRAGMENT OF YIAD FROM ESCHERICHIA COLI
<b>Deposition date</b>	14.03.2008
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE FOLDED C-TERMINAL FRAGMENT OF YIAD FROM ESCHERICHIA COLI. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET ER553
<b>PDB authors</b>	T.A.RAMELOT, L.ZHAO, K.HAMILTON, M.MAGLAQUI, R.XIAO, J.LIU, M.C.BARAN, G.SWAPNA, T.B.ACTON, B.ROST, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, NMRPIPE, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	88
<b>PDB code</b>	2M4F, doi:10.2210/pdb2M4F/pdb
<b>BMRB code</b>	19001, doi:10.13018/BMR19001
<b>PDB Header</b>	IMMUNE SYSTEM
<b>Protein name</b>	OUTER SURFACE PROTEIN E
<b>Deposition date</b>	05.02.2013
<b>PDB title</b>	SOLUTION STRUCTURE OF OUTER SURFACE PROTEIN E
<b>PDB authors</b>	A.BHATTACHARJEE, J.S.OEEMIG, R.KOŁODZIEJCZYK, T.MERI, T.KAJANDER, H.IWAI, T.JOKIRANTA, A.GOLDMAN
<b>Last author</b>	GOLDMAN
<b>Reference</b>	J.BIOL.CHEM. 288, 18685 (2013), doi:10.1074/JBC.M113.459040
<b>Reference authors</b>	A.BHATTACHARJEE, J.S.OEEMIG, R.KOŁODZIEJCZYK, T.MERI, T.KAJANDER, M.J.LEHTINEN, H.IWAI, T.S.JOKIRANTA, A.GOLDMAN
<b>Reference title</b>	STRUCTURAL BASIS FOR COMPLEMENT EVASION BY LYME DISEASE PATHOGEN BORRELIA BURGDORFERI
<b>Software listed</b>	AMBER, CCPNMR ANALYSIS, CING, CYANA, NMRPIPE, VNMRJ

<b>Spectrometer</b>	VARIAN (800 MHZ, 600 MHZ)
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<b>Protein number</b>	89
<b>PDB code</b>	2JXP, doi:10.2210/pdb2JXP/pdb
<b>BMRB code</b>	15568, doi:10.13018/BMR15568
<b>PDB Header</b>	LIPOPROTEIN
<b>Protein name</b>	UNCHARACTERIZED LIPOPROTEIN B FROM NITROSOMONAS EUROPAEA
<b>Deposition date</b>	27.11.2007
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF UNCHARACTERIZED LIPOPROTEIN B FROM NITROSOMONAS EUROPAEA. NORTHEAST STRUCTURAL GENOMICS TARGET NER45A
<b>PDB authors</b>	P.ROSSI, D.WANG, H.JANJUA, L.OWENS, R.XIAO, M.C.BARAN, G.SWAPNA, T.B.ACTON, B.ROST, G.T.MONTELLIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELLIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, CNS, CYANA, MOLMOL, MOLPROBITY, NMRPIPE, PROCHECK, PSVS, RPF, SPARKY, TOPSPIN, XEASY
<b>Spectrometer</b>	BRUKER (800 MHZ)

  

<b>Protein number</b>	90
<b>PDB code</b>	2L06, doi:10.2210/pdb2L06/pdb
<b>BMRB code</b>	17031, doi:10.13018/BMR17031
<b>PDB Header</b>	PROTEIN BINDING
<b>Protein name</b>	PBS LINKER POLYPEPTIDE DOMAIN (FRAGMENT 254-400) OF PHYCOBILISOME LINKER PROTEIN APCE FROM SYNECHOCYSTIS SP. PCC 6803
<b>Deposition date</b>	30.06.2010
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE PBS LINKER POLYPEPTIDE DOMAIN (FRAGMENT 254-400) OF PHYCOBILISOME LINKER PROTEIN APCE FROM SYNECHOCYSTIS SP. PCC 6803. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET SGR209C
<b>PDB authors</b>	T.A.RAMELOT, Y.YANG, J.R.CORT, K.HAMILTON, C.CICCOSANTI, D.LEE, T.B.ACTON, R.XIAO, J.K.EVERETT, G.T.MONTELLIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CYANA, NMRPIPE, PDBSTAT, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 750 MHZ, 600 MHZ, 500 MHZ)

  

<b>Protein number</b>	91
<b>PDB code</b>	2LAH, doi:10.2210/pdb2LAH/pdb
<b>BMRB code</b>	17524, doi:10.13018/BMR17524
<b>PDB Header</b>	CELL CYCLE, APOPTOSIS
<b>Protein name</b>	MITOTIC CHECKPOINT SERINE/THREONINE-PROTEIN KINASE BUB1 N-TERMINAL DOMAIN FROM HOMO SAPIENS
<b>Deposition date</b>	14.03.2011
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF MITOTIC CHECKPOINT SERINE/THREONINE-PROTEIN KINASE BUB1 N-TERMINAL DOMAIN FROM HOMO SAPIENS, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET HR5460A (METHODS DEVELOPMENT)
<b>PDB authors</b>	G.LIU, R.XIAO, H.LEE, K.HAMILTON, T.B.ACTON, C.CICCOSANTI, J.K.EVERETT, R.T.SHASTRY, Y.J.HUANG, G.T.MONTELLIONE, N.NORTHEAST STRUCTURAL GENOMICS CONSORTIUM, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELLIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, SPARKY, TALOS+, TOPSPIN, VNMRJ, XEASY
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

  

<b>Protein number</b>	92
<b>PDB code</b>	2LAK, doi:10.2210/pdb2LAK/pdb
<b>BMRB code</b>	17530, doi:10.13018/BMR17530
<b>PDB Header</b>	STRUCTURE GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	AHSA1-LIKE PROTEIN RHE_CH02687 (1-152) FROM RHIZOBIUM ETLI
<b>Deposition date</b>	16.03.2011
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE AHSA1-LIKE PROTEIN RHE_CH02687 (1-152) FROM RHIZOBIUM ETLI, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET RER242
<b>PDB authors</b>	Y.YANG, T.A.RAMELOT, J.R.CORT, D.WANG, C.CICCOSANTI, H.JANJUA, R.NAIR, B.ROST, T.B.ACTON, R.XIAO, J.K.EVERETT, G.T.MONTELLIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PDBSTAT, PINE_SERVER, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR NIH
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	93
<b>PDB code</b>	2L82, doi:10.2210/pdb2L82/pdb
<b>BMRB code</b>	17390, doi:10.13018/BMR17390
<b>PDB Header</b>	DE NOVO PROTEIN
<b>Protein name</b>	DE NOVO DESIGNED PROTEIN, P-LOOP NTPASE FOLD
<b>Deposition date</b>	31.12.2010
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF DE NOVO DESIGNED PROTEIN, P-LOOP NTPASE FOLD, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET OR32
<b>PDB authors</b>	G.LIU, N.KOGA, R.KOGA, R.XIAO, K.HAMILTON, H.JANJUA, S.TONG, T.B.ACTON, J.EVERETT, D.BAKER, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PALES, PINE, REDCAT, SPARKY, TALOS+, TOPSPIN, VNMRJ, XEASY
<b>Spectrometer</b>	BRUKER, VARIAN (800 MHZ, 600 MHZ)

<b>Protein number</b>	94
<b>PDB code</b>	2M47, doi:10.2210/pdb2M47/pdb
<b>BMRB code</b>	18989, doi:10.13018/BMR18989
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	POLYKETIDE CYC-LIKE PROTEIN CGL2372 FROM CORYNEBACTERIUM GLUTAMICUM
<b>Deposition date</b>	30.01.2013
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE POLYKETIDE CYC-LIKE PROTEIN CGL2372 FROM CORYNEBACTERIUM GLUTAMICUM, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET CGR160
<b>PDB authors</b>	Y.YANG, T.A.RAMELOT, D.LEE, C.CICCOSANTI, A.SAPIN, H.JANJUA, R.NAIR, B.ROST, T.B.ACTON, R.XIAO, J.K.EVERETT, G.T.MONTELIONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PINE, PSVS, SPARKY, TALOS+, TOPSPIN, VNMRJ, XEASY
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)

<b>Protein number</b>	95
<b>PDB code</b>	2K3A, doi:10.2210/pdb2K3A/pdb
<b>BMRB code</b>	15335, doi:10.13018/BMR15335
<b>PDB Header</b>	HYDROLASE
<b>Protein name</b>	STAPHYLOCOCCUS SAPROPHYTICUS CHAP (CYSTEINE, HISTIDINE-DEPENDENT AMIDOHYDROLASES/PEPTIDASES) DOMAIN PROTEIN
<b>Deposition date</b>	29.04.2008
<b>PDB title</b>	NMR SOLUTION STRUCTURE OF STAPHYLOCOCCUS SAPROPHYTICUS CHAP (CYSTEINE, HISTIDINE-DEPENDENT AMIDOHYDROLASES/PEPTIDASES) DOMAIN PROTEIN. NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET SYR11
<b>PDB authors</b>	P.ROSSI, J.M.ARAMINI, C.X.CHEN, C.NWOSU, K.C.CUNNINGHAM, L.A.OWENS, R.XIAO, J.LIU, M.C.BARAN, G.SWAPNA, T.B.ACTON, B.ROST, G.T.MONTELIONE, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	MONTELIONE
<b>Reference</b>	PROTEINS 74, 515 (2008), doi:10.1002/PROT.22267
<b>Reference authors</b>	P.ROSSI, J.M.ARAMINI, R.XIAO, C.X.CHEN, C.NWOSU, L.A.OWENS, M.MAGLAQUI, R.NAIR, M.FISCHER, T.B.ACTON, B.HONIG, B.ROST, G.T.MONTELIONE
<b>Reference title</b>	STRUCTURAL ELUCIDATION OF THE CYS-HIS-GLU-ASN PROTEOLYTIC RELAY IN THE SECRETED CHAP DOMAIN ENZYME FROM THE HUMAN PATHOGEN STAPHYLOCOCCUS SAPROPHYTICUS
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, MOLMOL, MOLPROBITY, NMRPIPE, PDBSTAT, PROCHECK, PROSA, PSVS, SPARKY, TOPSPIN, VERIFY3D, X-PLOR
<b>Spectrometer</b>	BRUKER (800 MHZ, 600 MHZ)

<b>Protein number</b>	96
<b>PDB code</b>	2M7U, doi:10.2210/pdb2M7U/pdb
<b>BMRB code</b>	19213, doi:10.13018/BMR19213
<b>PDB Header</b>	SIGNALING PROTEIN
<b>Protein name</b>	BLUE LIGHT-ABSORBING STATE OF TEPIXJ, AN ACTIVE CYANOBACTERIOCHROME DOMAIN
<b>Deposition date</b>	01.05.2013
<b>PDB title</b>	BLUE LIGHT-ABSORBING STATE OF TEPIXJ, AN ACTIVE CYANOBACTERIOCHROME DOMAIN
<b>PDB authors</b>	G.CORNILESCU, C.C.CORNILESCU, S.E.BURGIE, J.M.WALKER, J.L.MARKLEY, A.T.ULIJASZ, R.D.VIERSTRA
<b>Last author</b>	VIERSTRA
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	NMRPIPE, PIPP, X-PLOR NIH
<b>Spectrometer</b>	BRUKER, VARIAN (900 MHZ, 800 MHZ, 700 MHZ, 600 MHZ)

<b>Protein number</b>	97
<b>PDB code</b>	2B3W, doi:10.2210/pdb2B3W/pdb
<b>BMRB code</b>	6782, doi:10.13018/BMR6782
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	E.COLI PROTEIN YBIA
<b>Deposition date</b>	21.09.2005
<b>PDB title</b>	NMR STRUCTURE OF THE E.COLI PROTEIN YBIA, NORTHEAST STRUCTURAL GENOMICS TARGET ET24
<b>PDB authors</b>	T.A.RAMELOT, J.R.CORT, R.XIAO, L.Y.SHIH, T.B.ACTON, G.T.MONTELLONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOSTRUCTURE, CNS, NMRPIPE, SPARKY, VNMR, X-PLOR
<b>Spectrometer</b>	VARIAN (800 MHZ, 750 MHZ, 600 MHZ)

<b>Protein number</b>	98
<b>PDB code</b>	(KRAS4B)
<b>BMRB code</b>	
<b>PDB Header</b>	
<b>Protein name</b>	
<b>Deposition date</b>	
<b>PDB title</b>	
<b>PDB authors</b>	
<b>Last author</b>	
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	
<b>Spectrometer</b>	

<b>Protein number</b>	99
<b>PDB code</b>	2G0Q, doi:10.2210/pdb2G0Q/pdb
<b>BMRB code</b>	7007, doi:10.13018/BMR7007
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	AT5G39720.1 FROM ARABIDOPSIS THALIANA
<b>Deposition date</b>	13.02.2006
<b>PDB title</b>	SOLUTION STRUCTURE OF AT5G39720.1 FROM ARABIDOPSIS THALIANA
<b>PDB authors</b>	B.F.VOLKMAN, F.C.PETERSON, B.L.LYTLE, CENTER FOR EUKARYOTIC STRUCTURAL GENOMICS (CESG)
<b>Last author</b>	LYTLE
<b>Reference</b>	ACTA CRYSTALLOGR.,SECT.F 62, 490 (2006), doi:10.1107/S1744309106015946
<b>Reference authors</b>	B.L.LYTLE, F.C.PETERSON, E.M.TYLER, C.L.NEWMAN, D.A.VINAROV, J.L.MARKLEY, B.F.VOLKMAN
<b>Reference title</b>	SOLUTION STRUCTURE OF ARABIDOPSIS THALIANA PROTEIN AT5G39720.1, A MEMBER OF THE AIG2-LIKE PROTEIN FAMILY
<b>Software listed</b>	GARANT, NMRPIPE, SPSCAN, X-PLOR_NIH, XEASY, XWINNMR
<b>Spectrometer</b>	BRUKER (600 MHZ)

<b>Protein number</b>	100
<b>PDB code</b>	2LF2, doi:10.2210/pdb2LF2/pdb
<b>BMRB code</b>	17736, doi:10.13018/BMR17736
<b>PDB Header</b>	STRUCTURAL GENOMICS, UNKNOWN FUNCTION
<b>Protein name</b>	AHSA1-LIKE PROTEIN CHU 1110 FROM CYTOPHAGA HUTCHINSONII
<b>Deposition date</b>	28.06.2011
<b>PDB title</b>	SOLUTION NMR STRUCTURE OF THE AHSA1-LIKE PROTEIN CHU 1110 FROM CYTOPHAGA HUTCHINSONII, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM TARGET CHR152
<b>PDB authors</b>	Y.YANG, T.A.RAMELOT, D.LEE, C.CICCOSANTI, T.B.ACTON, R.XIAO, J.K.EVERETT, G.T.MONTELLONE, M.A.KENNEDY, NORTHEAST STRUCTURAL GENOMICS CONSORTIUM (NESG)
<b>Last author</b>	KENNEDY
<b>Reference</b>	
<b>Reference authors</b>	
<b>Reference title</b>	
<b>Software listed</b>	AUTOASSIGN, AUTOSTRUCTURE, CNS, CYANA, NMRPIPE, PDBSTAT, PINE_SERVER, PSVS, SPARKY, TOPSPIN, VNMR, X-PLOR_NIH
<b>Spectrometer</b>	BRUKER, VARIAN (850 MHZ, 600 MHZ)