Mapping the intrinsically disordered properties of the flexible loop domain of Bcl-2: a molecular dynamics simulation study

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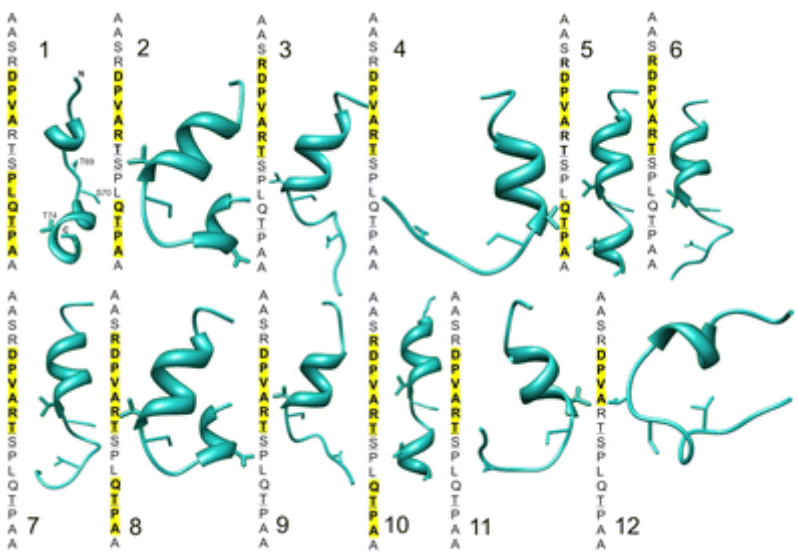
Abstract

Most of the B-cell lymphoma-2 (Bcl-2) protein structure has been elucidated; however, the conformation of its flexible loop domain (FLD) has not yet been experimentally predicted. Its high flexibility under physiological conditions is the reason. FLD behaves as an intrinsically disordered region (IDR) and can adopt regular structures in particular conditions associated with the control of Bcl-2's anti-apoptotic functions. In a previous contribution, we analyzed an engineered Bcl-2 construct (Bcl-2-Δ22Σ3) submitted to 25-ns MD and reported a disordered-to-helix transitions in a region of FLD (rFLD, residues 60–77). However, the conformational preferences in solution of rFLD in the nanosecond to microsecond scale were not analyzed. Herein, an average model was obtained for the native Bcl-2 protein by homology modeling and MD simulation techniques. From this, only the atomic coordinates corresponding to the rFLD were simulated for 1 μs by MD at 310 K. In concordance with previous studies, a disordered-to-helix transitions were exhibited, implying that this "interconversion of folding" in the rFLD suggest a possible set of conformations encoded in its sequence. Principal component analysis (PCA) showed that most of the conformational fluctuation of Bcl-2 is provided by rFLD. Dihedral PCA (dPCA) offered information about all the conformations of rFLD in the μs of the simulation, characterizing a dPCA-based free energy landscape of rFLD, and a conformational ensemble of fast interconverting conformations as other IDRs. Furthermore, despite the conformational heterogeneity of rFLD, the analysis of the dihedral angles (Φ, Ψ) showed that this region does not randomly explore the conformational space in solution.



Graphical Abstract

Emergence of the Bcl-2-rFLD's structural heterogeneity in solution, evidenced by molecular dynamics simulation.

Keywords

Bcl-2 Molecular dynamics Intrinsic disorder Flexible loop domain

Notes

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References

1. Beck DAC, Alonso DOV, Inoyama D, Daggett V (2008) The intrinsic conformational propensities of the 20 naturally occurring amino acids and reflection of these propensities in proteins. Proc Natl Acad Sci U S A 105:12259–12264. doi: 10.1073/pnas.0706527105 (https://doi.org/10.1073/pnas.0706527105)
CrossRef (https://doi.org/10.1073/pnas.0706527105)
Google Scholar (http://scholar.google.com/scholar_lookup?title=The%20intrinsic%20conformational%20propensities%20of%20the%2020%20naturally%20occurring%20amino%20acids%20and%20reflection%20of%20these%20propensities%20in%20proteins&author=DAC.%20Beck&author=DOV.%20Alonso&author=D.%20Inoyama&author=V.%20Daggett&journal=Proc%20Natl%20Acad%20Sci%20U%20S%20A&volume=105&pages=12259-12264&publication_year=2008&doi=10.1073%2Fpnas.0706527105)

2. Sali A, Shakhnovich E, Karplus M (1994) How does a protein fold? Nature 369:248–251. doi: 10.1038/369248a0 (https://doi.org/10.1038/369248a0)
CrossRef (https://doi.org/10.1038/369248a0)
Google Scholar (http://scholar.google.com/scholar_lookup?title=How%20does%20a%20protein%20fold%3F&author=A.%20Sali&author=E.%20Shakhnovich&author=M.%20Karplus&journal=Nature&volume=369&pages=248-251&publication_year=1994&doi=10.1038%2F369248a0)

3. Dill KA, Ozkan SB, Shell MS, Weikl TR (2008) The protein folding problem. Annu Rev Biophys 37:289–316. doi: 10.1146/annurev.biophys.37.092707.153558 (https://doi.org/10.1146/annurev.biophys.37.092707.153558)
CrossRef (https://doi.org/10.1146/annurev.biophys.37.092707.153558)
Google Scholar (http://scholar.google.com/scholar_lookup?title=The%20protein%20folding%20problem&author=KA.%20Dill&author=SB.%20Ozkan&author=MS.%20Shell&author=TR.%20Weikl&journal=Annu%20Rev%20Biophys&volume=37&pages=289-316&publication_year=2008&doi=10.1146%2Fannurev.biophys.37.092707.153558)

4. Pentony MM, Ward J, Jones DT (2010) Computational resources for the prediction and analysis of native disorder in proteins. Methods Mol Biol 604:369–393. doi: 10.1007/978-1-60761-444-9 (https://doi.org/10.1007/978-1-60761-444-9)
CrossRef (https://doi.org/10.1007/978-1-60761-444-9_25)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Computational%20resources%20for%20the%20prediction%20and%20analysis%20of%20native%20disorder%20in%20proteins&author=MM.%20Pentony&author=J.%20Ward&author=DT.%20Jones&journal=Methods%20Mol%20Biol&volume=604&pages=369-393&publication_year=2010&doi=10.1007%2F978-1-60761-444-9)

5. Uversky VN, Dunker AK (2010) Understanding protein non-folding. Biochim Biophys Acta Proteins Proteomics 1804:1231–1264. doi: 10.1016/j.bbapap.2010.01.017 (https://doi.org/10.1016/j.bbapap.2010.01.017)
CrossRef (https://doi.org/10.1016/j.bbapap.2010.01.017)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Understanding%20protein%20non-folding&author=VN.%20Uversky&author=AK.%20Dunker&journal=Biochim%20Biophys%20Acta%20Proteins%20Proteomics&volume=1804&pages=1231-1264&publication_year=2010&doi=10.1016%2Fj.bbapap.2010.01.017)

6. Rezaei-Ghaleh N, Blackledge M, Zweckstetter M (2012) Intrinsically disordered proteins: from sequence and conformational properties toward drug discovery. ChemBioChem 13:930–950. doi: 10.1002/cbic.201200093 (https://doi.org/10.1002/cbic.201200093)
CrossRef (https://doi.org/10.1002/cbic.201200093)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Intrinsically%20disordered%20proteins%3A%20from%20sequence%20and%20conformational%20properties%20toward%20drug%20discovery&author=N.%20Rezaei-Ghaleh&author=M.%20Blackledge&author=M.%20Zweckstetter&journal=ChemBioChem&volume=13&pages=930-950&publication_year=2012&doi=10.1002%2Fcbic.201200093)

7. Xie H, Vucetic S, Iakoucheva LM et al (2007) Functional anthology of intrinsic disorder. 1. Biological processes and functions of proteins with long disordered regions. J Proteome Res 6:1882–1898. doi: 10.1021/pr060392u (https://doi.org/10.1021/pr060392u)
CrossRef (https://doi.org/10.1021/pr060392u)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Functional%20anthology%20of%20intrinsic%20disorder.%201.%20Biological%20processes%20and%20functions%20of%20proteins%20with%20long%20disordered%20regions&author=H.%20Xie&author=S.%20Vucetic&author=LM.%20Iakoucheva&journal=J%20Proteome%20Res&volume=6&pages=1882-1898&publication_year=2007&doi=10.1021%2Fpr060392u)

8. Vucetic S, Xie H, Iakoucheva LM et al (2007) Functional anthology of intrinsic disorder. 2. cellular components, domains, technical terms, developmental processes, and coding sequence diversities correlated with long disordered regions. J Proteome Res 6:1899–1916. doi: 10.1021/pr060393m (https://doi.org/10.1021/pr060393m)
CrossRef (https://doi.org/10.1021/pr060393m)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Functional%20anthology%20of%20intrinsic%20disorder.%202.%20cellular%20components%2C%20domains%2C%20technical%20terms%2C%20developmental%20processes%2C%20and%20coding%20sequence%20diversities%20correlated%20with%20long%20disordered%20regions&author=S.%20Vucetic&author=H.%20Xie&author=L

M.%20Iakoucheva&journal=J%20Proteome%20Res&volume=6&pages=1899-1916&publication_year=2007&doi=10.1021%2Fpr060393m)

9. Galea CA, Wang Y, Sivakolundu SG, Kriwacki RW (2008) Regulation of cell division by intrinsically unstructured proteins: intrinsic flexibility, modularity, and signaling conduits. Biochemistry 47:7598–7609. doi: 10.1021/bi8006803 (https://doi.org/10.1021/bi8006803)
CrossRef (https://doi.org/10.1021/bi8006803)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Regulation%20of%20cell%20division%20by%20intrinsically%20unstructured%20proteins%3A%20intrinsic%20flexibility%2C%20modularity%2C%20and%20signaling%20conduits&author=CA.%20Galea&author=Y.%20Wang&author=SG.%20Sivakolundu&author=RW.%20Kriwacki&journal=Biochemistry&volume=47&pages=7598-7609&publication_year=2008&doi=10.1021%2Fbi8006803)

10. Garza AS, Ahmad N, Kumar R (2009) Role of intrinsically disordered protein regions/domains in transcriptional regulation. Life Sci 84:189–193. doi: 10.1016/j.lfs.2008.12.002 (https://doi.org/10.1016/j.lfs.2008.12.002)
CrossRef (https://doi.org/10.1016/j.lfs.2008.12.002)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Role%20of%20intrinsically%20disordered%20protein%20regions%2Fdomains%20in%20transcriptional%20regulation&author=AS.%20Garza&author=N.%20Ahmad&author=R.%20Kumar&journal=Life%20Sci&volume=84&pages=189-193&publication_year=2009&doi=10.1016%2Fj.lfs.2008.12.002)

11. Mittag T, Orlicky S, Choy W-Y et al (2008) Dynamic equilibrium engagement of a polyvalent ligand with a single-site receptor. Proc Natl Acad Sci U S A 105:17772–17777. doi: 10.1073/pnas.0809222105 (https://doi.org/10.1073/pnas.0809222105)
CrossRef (https://doi.org/10.1073/pnas.0809222105)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Dynamic%20equilibrium%20engagement%20of%20a%20polyvalent%20ligand%20with%20a%20single-site%20receptor&author=T.%20Mittag&author=S.%20Orlicky&author=W-Y.%20Choy&journal=Proc%20Natl%20Acad%20Sci%20U%20S%20A&volume=105&pages=17772-17777&publication_year=2008&doi=10.1073%2Fpnas.0809222105)

12. Vuzman D, Levy Y (2010) DNA search efficiency is modulated by charge composition and distribution in the intrinsically disordered tail. Proc Natl Acad Sci U S A 107:21004–21009. doi: 10.1073/pnas.1011775107 (https://doi.org/10.1073/pnas.1011775107)
CrossRef (https://doi.org/10.1073/pnas.1011775107)
Google Scholar (http://scholar.google.com/scholar_lookup?title=DNA%20search%20efficiency%20is%20modulated%20by%20charge%20composition%20and%20distribution%20in%20the%20intrinsically%20disordered%20tail&author=D.%20Vuzman&author=Y.%20Levy&journal=Proc%20Natl%20Acad%20Sci%20U%20S%20A&volume=107&pages=21004-21009&publication_year=2010&doi=10.1073%2Fpnas.1011775107)

13. Sugase K, Dyson HJ, Wright PE (2007) Mechanism of coupled folding and binding of an intrinsically disordered protein. Nature 447:1021–1025. doi: 10.1038/nature05858 (https://doi.org/10.1038/nature05858)
CrossRef (https://doi.org/10.1038/nature05858)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Mechanism%20of%20coupled%20folding%20and%20binding%20of%20an%20intrinsically%20disordered%20protein&author=K.%20Sugase&author=HJ.%20Dyson&author=PE.%20Wright&journal=Nature&volume=447&pages=1021-1025&publication_year=2007&doi=10.1038%2Fnature05858)

14. Wright PE, Dyson HJ (2009) Linking folding and binding. Curr Opin Struct Biol 19:31–38. doi: 10.1016/j.sbi.2008.12.003 (https://doi.org/10.1016/j.sbi.2008.12.003)
CrossRef (https://doi.org/10.1016/j.sbi.2008.12.003)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Linking%20folding%20and%20binding&author=PE.%20Wright&author=HJ.%20Dyson&journal=Curr%20Opin%20Struct%20Biol&volume=19&pages=31-38&publication_year=2009&doi=10.1016%2Fj.sbi.2008.12.003)

15. Knott M, Best RB (2012) A preformed binding interface in the unbound ensemble of an intrinsically disordered protein: evidence from molecular simulations. PLoS Comput Biol. doi: 10.1371/journal.pcbi.1002605 (https://doi.org/10.1371/journal.pcbi.1002605)
Google Scholar (http://scholar.google.com/scholar_lookup?title=A%20preformed%20binding%20interface%20in%20the%20unbound%20ensemble%20of%20an%20intrinsically%20disordered%20protein%3A%20evidence%20from%20molecular%20simulations&author=M.%20Knott&author=RB.%20Best&journal=PLoS%20Comput%20Biol&publication_year=2012&doi=10.1371%2Fjournal.pcbi.1002605)

16. Oldfield CJ, Cheng Y, Cortese MS et al (2005) Coupled folding and binding with alpha-helix-forming molecular recognition elements. Biochemistry 44:12454–12470. doi: 10.1021/bi050736e (https://doi.org/10.1021/bi050736e)
CrossRef (https://doi.org/10.1021/bi050736e)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Coupled%20folding%20and%20binding%20with%20alpha-helix-forming%20molecular%20recognition%20elements&author=CJ.%20Oldfield&author=Y.%20Cheng&author=MS.%20Cortese&journal=Biochemistry&volume=44&pages=12454-12470&publication_year=2005&doi=10.1021%2Fbi050736e)

17. Csizmók V, Bokor M, Bánki P et al (2005) Primary contact sites in intrinsically unstructured proteins: the case of calpastatin and microtubule-associated protein 2. Biochemistry 44:3955–3964. doi: 10.1021/bi047817f (https://doi.org/10.1021/bi047817f)
CrossRef (https://doi.org/10.1021/bi047817f)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Primary%20contact%20sites%20in%20intrinsically%20unstructured%20proteins%3A%20the%20case%20of%20calpastatin%20and%20microtubule-associated%20protein%202&author=V.%20Csizm%C3%B3k&author=M.%20Bokor&author=P.%20B%C3%A1nki&journal=Biochemistry&volume=44&pages=3955-3964&publication_year=2005&doi=10.1021%2Fbi047817f)

18. Fuxreiter M, Simon I, Friedrich P, Tompa P (2004) Preformed structural elements feature in partner recognition by intrinsically unstructured proteins. J Mol Biol 338:1015–1026. doi: 10.1016/j.jmb.2004.03.017 (https://doi.org/10.1016/j.jmb.2004.03.017)

CrossRef (https://doi.org/10.1016/j.jmb.2004.03.017)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Preformed%20structural%20elements%20feature%20in%20partner%20recognition%20by%20intrinsically%20unstructured%20proteins&author=M.%20Fuxreiter&author=I.%20Simon&author=P.%20Friedrich&author=P.%20Tompa&journal=J%20Mol%20Biol&volume=338&pages=1015-1026&publication_year=2004&doi=10.1016%2Fj.jmb.2004.03.017)

19. Hua QX, Jia WH, Bullock BP et al (1998) Transcriptional activator-coactivator recognition: nascent folding of a kinase-inducible transactivation domain predicts its structure on coactivator binding. Biochemistry 37:5858–5866. doi: 10.1021/bi9800808 (https://doi.org/10.1021/bi9800808)
CrossRef (https://doi.org/10.1021/bi9800808)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Transcriptional%20activator-coactivator%20recognition%3A%20nascent%20folding%20of%20a%20kinase-inducible%20transactivation%20domain%20predicts%20its%20structure%20on%20coactivator%20binding&author=QX.%20Hua&author=WH.%20Jia&author=BP.%20Bullock&journal=Biochemistry&volume=37&pages=5858-5866&publication_year=1998&doi=10.1021%2Fbi9800808)

20. Michel Espinoza-Fonseca L, Ilizaliturri-Flores I, Correa-Basurto J (2012) Backbone conformational preferences of an intrinsically disordered protein in solution. Mol Biosyst 8:1798. doi: 10.1039/c2mb00004k (https://doi.org/10.1039/c2mb00004k)
CrossRef (https://doi.org/10.1039/c2mb00004k)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Backbone%20conformational%20preferences%20of%20an%20intrinsically%20disordered%20protein%20in%20solution&author=L.%20Michel%20Espinoza-Fonseca&author=I.%20Ilizaliturri-Flores&author=J.%20Correa-Basurto&journal=Mol%20Biosyst&volume=8&pages=1798&publication_year=2012&doi=10.1039%2Fc2mb00004k)

21. Reed JC, Zha H, Aime-Sempe C et al (1996) Structure-function analysis of Bcl-2 family proteins. Regulators of programmed cell death. Adv Exp Med Biol 406:99–112
CrossRef (https://doi.org/10.1007/978-1-4899-0274-0_10)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Structure-function%20analysis%20of%20Bcl-2%20family%20proteins.%20Regulators%20of%20programmed%20cell%20death&author=JC.%20Reed&author=H.%20Zha&author=C.%20Aime-Sempe&journal=Adv%20Exp%20Med%20Biol&volume=406&pages=99-112&publication_year=1996)

22. Huang DC, Adams JM, Cory S (1998) The conserved N-terminal BH4 domain of Bcl-2 homologues is essential for inhibition of apoptosis and interaction with CED-4. EMBO J 17:1029–39. doi: 10.1093/emboj/17.4.1029 (https://doi.org/10.1093/emboj/17.4.1029)
CrossRef (https://doi.org/10.1093/emboj/17.4.1029)
Google Scholar (http://scholar.google.com/scholar_lookup?title=The%20conserved%20N-terminal%20BH4%20domain%20of%20Bcl-2%20homologues%20is%20essential%20for%20inhibition%20of%20apoptosis%20and%20interaction%20with%20CED-4&author=DC.%20Huang&author=JM.%20Adams&author=S.%20Cory&journal=EMBO%20J&volume=17&pages=1029-39&publication_year=1998&doi=10.1093%2Femboj%2F17.4.1029)

23. Petros AM, Medek A, Nettesheim DG et al (2001) Solution structure of the antiapoptotic protein bcl-2. Proc Natl Acad Sci U S A 98:3012–3017. doi: 10.1073/pnas.041619798 (https://doi.org/10.1073/pnas.041619798)
CrossRef (https://doi.org/10.1073/pnas.041619798)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Solution%20structure%20of%20the%20antiapoptotic%20protein%20bcl-2&author=AM.%20Petros&author=A.%20Medek&author=DG.%20Nettesheim&journal=Proc%20Natl%20Acad%20Sci%20U%20S%20A&volume=98&pages=3012-3017&publication_year=2001&doi=10.1073%2Fpnas.041619798)

24. Petros AM, Olejniczak ET, Fesik SW (2004) Structural biology of the Bcl-2 family of proteins. Biochim Biophys Acta 1644:83–94. doi: 10.1016/j.bbamcr.2003.08.012 (https://doi.org/10.1016/j.bbamcr.2003.08.012)
CrossRef (https://doi.org/10.1016/j.bbamcr.2003.08.012)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Structural%20biology%20of%20the%20Bcl-2%20family%20of%20proteins&author=AM.%20Petros&author=ET.%20Olejniczak&author=SW.%20Fesik&journal=Biochim%20Biophys%20Acta&volume=1644&pages=83-94&publication_year=2004&doi=10.1016%2Fj.bbamcr.2003.08.012)

25. Rautureau GJP, Day CL, Hinds MG (2010) Intrinsically disordered proteins in Bcl-2 regulated apoptosis. Int J Mol Sci 11:1808–1824. doi: 10.3390/ijms11041808 (https://doi.org/10.3390/ijms11041808)
CrossRef (https://doi.org/10.3390/ijms11041808)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Intrinsically%20disordered%20proteins%20in%20Bcl-2%20regulated%20apoptosis&author=GJP.%20Rautureau&author=CL.%20Day&author=MG.%20Hinds&journal=Int%20J%20Mol%20Sci&volume=11&pages=1808-1824&publication_year=2010&doi=10.3390%2Fijms11041808)

26. Kutuk O, Letai A (2008) Regulation of Bcl-2 family proteins by posttranslational modifications. Curr Mol Med 8:102–118. doi: 10.2174/156652408783769599 (https://doi.org/10.2174/156652408783769599)
CrossRef (https://doi.org/10.2174/156652408783769599)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Regulation%20of%20Bcl-2%20family%20proteins%20by%20posttranslational%20modifications&author=O.%20Kutuk&author=A.%20Letai&journal=Curr%20Mol%20Med&volume=8&pages=102-118&publication_year=2008&doi=10.2174%2F156652408783769599)

27. Blagosklonny MV (2001) Unwinding the loop of Bcl-2 phosphorylation. Leuk Off J Leuk Soc Am Leuk Res Fund UK 15:869–874. doi: 10.1038/sj.leu.2402134 (https://doi.org/10.1038/sj.leu.2402134)
CrossRef (https://doi.org/10.1038/sj.leu.2402134)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Unwinding%20the%20loop%20of%20Bcl-2%20phosphorylation&author=MV.%20Blagosklonny&journal=Leuk%20Off%20J%20Leuk%20Soc%20Am%20Leuk%20Res%20Fund%20UK&volume=15&pages=869-874&publication_year=2001&doi=10.1038%2Fsj.leu.2402134)

28. Haldar S, Basu A, Croce CM (1998) Serine-70 is one of the critical sites for drug-induced Bcl2 phosphorylation in cancer cells. Cancer Res 58:1609–1615

Google Scholar (http://scholar.google.com/scholar_lookup?title=Serine-70%20is%20one%20of%20the%20critical%20sites%20for%20drug-induced%20Bcl2%20phosphorylation%20in%20cancer%20cells&author=S.%20Haldar&author=A.%20Basu&author=CM.%20Croce&journal=Cancer%20Res&volume=58&pages=1609-1615&publication_year=1998)

29. Kirsch DG, Doseff A, Chau BN et al (1999) Caspase-3-dependent cleavage of Bcl-2 promotes release of cytochrome c. J Biol Chem 274:21155–21161. doi: 10.1074/jbc.274.30.21155 (https://doi.org/10.1074/jbc.274.30.21155)
CrossRef (https://doi.org/10.1074/jbc.274.30.21155)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Caspase-3-dependent%20cleavage%20of%20Bcl-2%20promotes%20release%20of%20cytochrome%20c&author=DG.%20Kirsch&author=A.%20Doseff&author=BN.%20Chau&journal=J%20Biol%20Chem&volume=274&pages=21155-21161&publication_year=1999&doi=10.1074%2Fjbc.274.30.21155)

30. Blagosklonny MV, Schulte T, Nguyen P et al (1996) Taxol-induced apoptosis and phosphorylation of Bcl-2 protein involves c- Raf-1 and represents a novel c-Raf-1 signal transduction pathway. Cancer Res 56:1851–1854
Google Scholar (http://scholar.google.com/scholar_lookup?title=Taxol-induced%20apoptosis%20and%20phosphorylation%20of%20Bcl-2%20protein%20involves%20c-%20Raf-1%20and%20represents%20a%20novel%20c-Raf-1%20signal%20transduction%20pathway&author=MV.%20Blagosklonny&author=T.%20Schulte&author=P.%20Nguyen&journal=Cancer%20Res&volume=56&pages=1851-1854&publication_year=1996)

31. Ito T, Deng X, Carr B, May WS (1997) Bcl-2 phosphorylation required for anti-apoptosis function. J Biol Chem 272:11671–11673. doi: 10.1074/jbc.272.18.11671 (https://doi.org/10.1074/jbc.272.18.11671)
CrossRef (https://doi.org/10.1074/jbc.272.18.11671)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Bcl-2%20phosphorylation%20required%20for%20anti-apoptosis%20function&author=T.%20Ito&author=X.%20Deng&author=B.%20Carr&author=WS.%20May&journal=J%20Biol%20Chem&volume=272&pages=11671-11673&publication_year=1997&doi=10.1074%2Fjbc.272.18.11671)

32. Poommipanit PB, Chen B, Oltvai ZN (1999) Interleukin-3 induces the phosphorylation of a distinct fraction of Bcl- 2. J Biol Chem 274:1033–1039. doi: 10.1074/jbc.274.2.1033 (https://doi.org/10.1074/jbc.274.2.1033)
CrossRef (https://doi.org/10.1074/jbc.274.2.1033)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Interleukin-3%20induces%20the%20phosphorylation%20of%20a%20distinct%20fraction%20of%20Bcl-%202&author=PB.%20Poommipanit&author=B.%20Chen&author=ZN.%20Oltvai&journal=J%20Biol%20Chem&volume=274&pages=1033-1039&publication_year=1999&doi=10.1074%2Fjbc.274.2.1033)

33. Scatena CD, Stewart ZA, Mays D et al (1998) Mitotic phosphorylation of Bcl-2 during normal cell cycle progression and taxol-induced growth arrest. J Biol Chem 273:30777–30784. doi: 10.1074/jbc.273.46.30777 (https://doi.org/10.1074/jbc.273.46.30777)
CrossRef (https://doi.org/10.1074/jbc.273.46.30777)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Mitotic%20phosphorylation%20of%20Bcl-2%20during%20normal%20cell%20cycle%20progression%20and%20taxol-induced%20growth%20arrest&author=CD.%20Scatena&author=ZA.%20Stewart&author=D.%20Mays&journal=J%20Biol%20Chem&volume=273&pages=30777-30784&publication_year=1998&doi=10.1074%2Fjbc.273.46.30777)

34. Chang BS, Minn AJ, Muchmore SW et al (1997) Identification of a novel regulatory domain in Bcl-X(L) and Bcl-2. EMBO J 16:968–977. doi: 10.1093/emboj/16.5.968 (https://doi.org/10.1093/emboj/16.5.968)
CrossRef (https://doi.org/10.1093/emboj/16.5.968)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Identification%20of%20a%20novel%20regulatory%20domain%20in%20Bcl-X%28L%29%20and%20Bcl-2&author=BS.%20Chang&author=AJ.%20Minn&author=SW.%20Muchmore&journal=EMBO%20J&volume=16&pages=968-977&publication_year=1997&doi=10.1093%2Femboj%2F16.5.968)

35. Fang G, Chang BS, Kim CN et al (1998) “Loop” domain is necessary for taxol-induced mobility shift and phosphorylation of Bcl-2 as well as for inhibiting taxol-induced cytosolic accumulation of cytochrome c and apoptosis. Cancer Res 58:3202–3208
Google Scholar (http://scholar.google.com/scholar_lookup?title=%E2%80%9CLoop%E2%80%9D%20domain%20is%20necessary%20for%20taxol-induced%20mobility%20shift%20and%20phosphorylation%20of%20Bcl-2%20as%20well%20as%20for%20inhibiting%20taxol-induced%20cytosolic%20accumulation%20of%20cytochrome%20c%20and%20apoptosis&author=G.%20Fang&author=BS.%20Chang&author=CN.%20Kim&journal=Cancer%20Res&volume=58&pages=3202-3208&publication_year=1998)

36. Yamamoto K, Ichijo H, Korsmeyer SJ (1999) BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal protein kinase pathway normally activated at G(2)/M. Mol Cell Biol 19:8469–8478
CrossRef (https://doi.org/10.1128/MCB.19.12.8469)
Google Scholar (http://scholar.google.com/scholar_lookup?title=BCL-2%20is%20phosphorylated%20and%20inactivated%20by%20an%20ASK1%2FJun%20N-terminal%20protein%20kinase%20pathway%20normally%20activated%20at%20G%282%29%2FM&author=K.%20Yamamoto&author=H.%20Ichijo&author=SJ.%20Korsmeyer&journal=Mol%20Cell%20Biol&volume=19&pages=8469-8478&publication_year=1999)

37. Srivastava RK, Mi QS, Hardwick JM, Longo DL (1999) Deletion of the loop region of Bcl-2 completely blocks paclitaxel-induced apoptosis. Proc Natl Acad Sci U S A 96:3775–3780. doi: 10.1073/pnas.96.7.3775 (https://doi.org/10.1073/pnas.96.7.3775)
CrossRef (https://doi.org/10.1073/pnas.96.7.3775)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Deletion%20of%20the%20loop%20region%20of%20Bcl-2%20completely%20blocks%20paclitaxel-induced%20apoptosis&author=RK.%20Srivastava&author=QS.%20Mi&author=JM.%20Hardwick&author=DL.%20Longo&journal=Proc%20Natl%20Acad%20Sci%20U%20S%20A&volume=96&pages=3775-3780&publication_year=1999&doi=10.1073%2Fpnas.96.7.3775)

38. Deng X, Gao F, Flagg T et al (2006) Bcl2’s flexible loop domain regulates p53 binding and survival. Mol Cell Biol 26:4421–4434. doi: 10.1128/MCB.01647-05 (https://doi.org/10.1128/MCB.01647-05)

CrossRef (https://doi.org/10.1128/MCB.01647-05)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Bcl2%E2%80%99s%20flexible%20loop%20domain%20regulates%20p53%20binding%20and%20survival&author=X.%20Deng&author=F.%20Gao&author=T.%20Flagg&journal=Mol%20Cell%20Biol&volume=26&pages=4421-4434&publication_year=2006&doi=10.1128%2FMCB.01647-05)

39. Lin B, Kolluri SK, Lin F et al (2004) Conversion of Bcl-2 from Protector to killer by interaction with nuclear orphan receptor Nur77/TR3. Cell 116:527–540. doi: 10.1016/S0092-8674(04)00162-X (https://doi.org/10.1016/S0092-8674(04)00162-X)

40. Ruvolo PP, Deng X, May WS (2001) Phosphorylation of Bcl2 and regulation of apoptosis. Leuk Off J Leuk Soc Am Leuk Res Fund UK 15:515–522. doi: 10.1038/sj.leu.2402090 (https://doi.org/10.1038/sj.leu.2402090)
CrossRef (https://doi.org/10.1038/sj.leu.2402090)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Phosphorylation%20of%20Bcl2%20and%20regulation%20of%20apoptosis&author=PP.%20Ruvolo&author=X.%20Deng&author=WS.%20May&journal=Leuk%20Off%20J%20Leuk%20Soc%20Am%20Leuk%20Res%20Fund%20UK&volume=15&pages=515-522&publication_year=2001&doi=10.1038%2Fsj.leu.2402090)

41. Raghav PK, Verma YK, Gangenahalli GU (2012) Molecular dynamics simulations of the Bcl-2 protein to predict the structure of its unordered flexible loop domain. J Mol Model 18:1885–1906. doi: 10.1007/s00894-011-1201-6 (https://doi.org/10.1007/s00894-011-1201-6)
CrossRef (https://doi.org/10.1007/s00894-011-1201-6)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Molecular%20dynamics%20simulations%20of%20the%20Bcl-2%20protein%20to%20predict%20the%20structure%20of%20its%20unordered%20flexible%20loop%20domain&author=PK.%20Raghav&author=YK.%20Verma&author=GU.%20Gangenahalli&journal=J%20Mol%20Model&volume=18&pages=1885-1906&publication_year=2012&doi=10.1007%2Fs00894-011-1201-6)

42. Ilizaliturri-Flores I, Correa-Basurto J, Benítez-Cardoza CG, Zamorano-Carrillo A (2013) A study of the structural properties and thermal stability of human Bcl-2 by molecular dynamics simulations. J Biomol Struct Dyn 32:1707–1719. doi: 10.1080/07391102.2013.833858 (https://doi.org/10.1080/07391102.2013.833858)
CrossRef (https://doi.org/10.1080/07391102.2013.833858)
Google Scholar (http://scholar.google.com/scholar_lookup?title=A%20study%20of%20the%20structural%20properties%20and%20thermal%20stability%20of%20human%20Bcl-2%20by%20molecular%20dynamics%20simulations&author=I.%20Ilizaliturri-Flores&author=J.%20Correa-Basurto&author=CG.%20Ben%C3%ADtez-Cardoza&author=A.%20Zamorano-Carrillo&journal=J%20Biomol%20Struct%20Dyn&volume=32&pages=1707-1719&publication_year=2013&doi=10.1080%2F07391102.2013.833858)

43. Zhang Y (2008) I-TASSER server for protein 3D structure prediction. BMC Bioinformatics 9:40. doi: 10.1186/1471-2105-9-40 (https://doi.org/10.1186/1471-2105-9-40)
CrossRef (https://doi.org/10.1186/1471-2105-9-40)
Google Scholar (http://scholar.google.com/scholar_lookup?title=I-TASSER%20server%20for%20protein%203D%20structure%20prediction&author=Y.%20Zhang&journal=BMC%20Bioinformatics&volume=9&pages=40&publication_year=2008&doi=10.1186%2F1471-2105-9-40)

44. Laskowski RA, MacArthur MW, Moss DS, Thornton JM (1993) PROCHECK: a program to check the stereochemical quality of protein structures. J Appl Crystallogr 26:283–291. doi: 10.1107/S0021889892009944 (https://doi.org/10.1107/S0021889892009944)
CrossRef (https://doi.org/10.1107/S0021889892009944)
Google Scholar (http://scholar.google.com/scholar_lookup?title=PROCHECK%3A%20a%20program%20to%20check%20the%20stereochemical%20quality%20of%20protein%20structures&author=RA.%20Laskowski&author=MW.%20MacArthur&author=DS.%20Moss&author=JM.%20Thornton&journal=J%20Appl%20Crystallogr&volume=26&pages=283-291&publication_year=1993&doi=10.1107%2FS0021889892009944)

45. Colovos C, Yeates TO (1993) Verification of protein structures: patterns of nonbonded atomic interactions. Protein Sci 2:1511–1519. doi: 10.1002/pro.5560020916 (https://doi.org/10.1002/pro.5560020916)
CrossRef (https://doi.org/10.1002/pro.5560020916)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Verification%20of%20protein%20structures%3A%20patterns%20of%20nonbonded%20atomic%20interactions&author=C.%20Colovos&author=TO.%20Yeates&journal=Protein%20Sci&volume=2&pages=1511-1519&publication_year=1993&doi=10.1002%2Fpro.5560020916)

46. Eisenberg D, Lüthy R, Bowie JU (1997) VERIFY3D: Assessment of protein models with three-dimensional profiles. Methods Enzymol 277:396–406. doi: 10.1016/S0076-6879(97)77022-8 (https://doi.org/10.1016/S0076-6879(97)77022-8)
CrossRef (https://doi.org/10.1016/S0076-6879(97)77022-8)
Google Scholar (http://scholar.google.com/scholar_lookup?title=VERIFY3D%3A%20Assessment%20of%20protein%20models%20with%20three-dimensional%20profiles&author=D.%20Eisenberg&author=R.%20L%C3%BCthy&author=JU.%20Bowie&journal=Methods%20Enzymol&volume=277&pages=396-406&publication_year=1997&doi=10.1016%2FS0076-6879%2897%2977022-8)

47. Wiederstein M, Sippl MJ (2007) ProSA-web: Interactive web service for the recognition of errors in three-dimensional structures of proteins. Nucleic Acids Res. doi: 10.1093/nar/gkm290 (https://doi.org/10.1093/nar/gkm290)
Google Scholar (http://scholar.google.com/scholar_lookup?title=ProSA-web%3A%20Interactive%20web%20service%20for%20the%20recognition%20of%20errors%20in%20three-dimensional%20structures%20of%20proteins&author=M.%20Wiederstein&author=MJ.%20Sippl&journal=Nucleic%20Acids%20Res&publication_year=2007&doi=10.1093%2Fnar%2Fgkm290)

48. Humphrey W, Dalke A, Schulten K (1996) VMD: Visual molecular dynamics. J Mol Graph 14:33–38. doi: 10.1016/0263-7855(96)00018-5 (https://doi.org/10.1016/0263-7855(96)00018-5)
CrossRef (https://doi.org/10.1016/0263-7855(96)00018-5)

Google Scholar (http://scholar.google.com/scholar_lookup?title=VMD%3A%20Visual%20molecular%20dynamics&author=W.%20Humphrey&author=A.%20Dalke&author=K.%20Schulten&journal=J%20Mol%20Graph&volume=14&pages=33-38&publication_year=1996&doi=10.1016%2F0263-7855%2896%2900018-5)

49. Phillips JC, Braun R, Wang W et al (2005) Scalable molecular dynamics with NAMD. J Comput Chem 26:1781–1802. doi: 10.1002/jcc.20289 (https://doi.org/10.1002/jcc.20289)
CrossRef (https://doi.org/10.1002/jcc.20289)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Scalable%20molecular%20dynamics%20with%20NAMD&author=JC.%20Phillips&author=R.%20Braun&author=W.%20Wang&journal=J%20Comput%20Chem&volume=26&pages=1781-1802&publication_year=2005&doi=10.1002%2Fjcc.20289)

50. MacKerell ADJ, Bashford D, Bellott M et al (1998) All-atom empirical potential for molecular modeling and dynamics studies of proteins. J Phys Chem B 102:3586–616. doi: 10.1021/jp973084f (https://doi.org/10.1021/jp973084f)
CrossRef (https://doi.org/10.1021/jp973084f)
Google Scholar (http://scholar.google.com/scholar_lookup?title=All-atom%20empirical%20potential%20for%20molecular%20modeling%20and%20dynamics%20studies%20of%20proteins&author=ADJ.%20MacKerell&author=D.%20Bashford&author=M.%20Bellott&journal=J%20Phys%20Chem%20B&volume=102&pages=3586-616&publication_year=1998&doi=10.1021%2Fjp973084f)

51. Batcho PA, Case DA, Schlick T (2001) Optimized particle-mesh Ewald/multiple time step integration for molecular dynamics simulation. J Chem Phys 115:4003–4018
CrossRef (https://doi.org/10.1063/1.1389854)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Optimized%20particle-mesh%20Ewald%2Fmultiple%20time%20step%20integration%20for%20molecular%20dynamics%20simulation&author=PA.%20Batcho&author=DA.%20Case&author=T.%20Schlick&journal=J%20Chem%20Phys&volume=115&pages=4003-4018&publication_year=2001)

52. Ryckaert J-P, Ciccotti G, Berendsen HJ (1977) Numerical integration of the Cartesian equations of motion of a system with constraints: molecular dynamics of *n*-alkanes. J Comput Phys 23:327–341. doi: 10.1016/0021-9991(77)90098-5 (https://doi.org/10.1016/0021-9991(77)90098-5)
CrossRef (https://doi.org/10.1016/0021-9991(77)90098-5)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Numerical%20integration%20of%20the%20Cartesian%20equations%20of%20motion%20of%20a%20system%20with%20constraints%3A%20molecular%20dynamics%20of%20n-alkanes&author=J-P.%20Ryckaert&author=G.%20Ciccotti&author=HJ.%20Berendsen&journal=J%20Comput%20Phys&volume=23&pages=327-341&publication_year=1977&doi=10.1016%2F0021-9991%2877%2990098-5)

53. Olson MA, Chaudhury S, Lee MS (2011) Comparison between self-guided Langevin dynamics and molecular dynamics simulations for structure refinement of protein loop conformations. J Comput Chem 32:3014–3022. doi: 10.1002/jcc.21883 (https://doi.org/10.1002/jcc.21883)
CrossRef (https://doi.org/10.1002/jcc.21883)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Comparison%20between%20self-guided%20Langevin%20dynamics%20and%20molecular%20dynamics%20simulations%20for%20structure%20refinement%20of%20protein%20loop%20conformations&author=MA.%20Olson&author=S.%20Chaudhury&author=MS.%20Lee&journal=J%20Comput%20Chem&volume=32&pages=3014-3022&publication_year=2011&doi=10.1002%2Fjcc.21883)

54. Glykos NM (2006) Software news and updates. Carma: a molecular dynamics analysis program. J Comput Chem 27:1765–1768. doi: 10.1002/jcc.20482 (https://doi.org/10.1002/jcc.20482)
CrossRef (https://doi.org/10.1002/jcc.20482)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Software%20news%20and%20updates.%20Carma%3A%20a%20molecular%20dynamics%20analysis%20program&author=NM.%20Glykos&journal=J%20Comput%20Chem&volume=27&pages=1765-1768&publication_year=2006&doi=10.1002%2Fjcc.20482)

55. Berendsen HJ, Hayward S (2000) Collective protein dynamics in relation to function. Curr Opin Struct Biol 10:165–169. doi: 10.1016/S0959-440X(00)00061-0 (https://doi.org/10.1016/S0959-440X(00)00061-0)
CrossRef (https://doi.org/10.1016/S0959-440X(00)00061-0)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Collective%20protein%20dynamics%20in%20relation%20to%20function&author=HJ.%20Berendsen&author=S.%20Hayward&journal=Curr%20Opin%20Struct%20Biol&volume=10&pages=165-169&publication_year=2000&doi=10.1016%2FS0959-440X%2800%2900061-0)

56. Osterhout JJ (2005) Understanding protein folding through peptide models. Protein Pept Lett 12:159–164. doi: 10.2174/0929866053005890 (https://doi.org/10.2174/0929866053005890)
CrossRef (https://doi.org/10.2174/0929866053005890)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Understanding%20protein%20folding%20through%20peptide%20models&author=JJ.%20Osterhout&journal=Protein%20Pept%20Lett&volume=12&pages=159-164&publication_year=2005&doi=10.2174%2F0929866053005890)

57. De Mori GMS, Meli M, Monticelli L, Colombo G (2005) Folding and mis-folding of peptides and proteins: insights from molecular simulations. Mini Rev Med Chem 5:353–359. doi: 10.2174/1389557053544038 (https://doi.org/10.2174/1389557053544038)
CrossRef (https://doi.org/10.2174/1389557053544038)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Folding%20and%20mis-folding%20of%20peptides%20and%20proteins%3A%20insights%20from%20molecular%20simulations&author=GMS.%20Mori&author=M.%20Meli&author=L.%20Monticelli&author=G.%20Colombo&journal=Mini%20Rev%20Med%20Chem&volume=5&pages=353-359&publication_year=2005&doi=10.2174%2F1389557053544038)

58. Gnanakaran S, Nymeyer H, Portman J et al (2003) Peptide folding simulations. Curr Opin Struct Biol 13:168–174. doi: 10.1016/S0959-440X(03)00040-X (https://doi.org/10.1016/S0959-440X(03)00040-X)
CrossRef (https://doi.org/10.1016/S0959-440X(03)00040-X)

Google Scholar (http://scholar.google.com/scholar_lookup?title=Peptide%20folding%20simulations&author=S.%20Gnanakaran&author=H.%20Nymeyer&author=J.%20Portman&journal=Curr%20Opin%20Struct%20Biol&volume=13&pages=168-174&publication_year=2003&doi=10.1016%2FS0959-440X%2803%2900040-X)

59. Patapati KK, Glykos NM (2010) Order through disorder: hyper-mobile C-terminal residues stabilize the folded state of a helical peptide. A molecular dynamics study. PLoS ONE. doi: 10.1371/journal.pone.0015290 (https://doi.org/10.1371/journal.pone.0015290)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Order%20through%20disorder%3A%20hyper-mobile%20C-terminal%20residues%20stabilize%20the%20folded%20state%20of%20a%20helical%20peptide.%20A%20molecular%20dynamics%20study&author=KK.%20Patapati&author=NM.%20Glykos&journal=PLoS%20ONE&publication_year=2010&doi=10.1371%2Fjournal.pone.0015290)

60. Schuler B, Eaton WA (2008) Protein folding studied by single-molecule FRET. Curr Opin Struct Biol 18:16–26. doi: 10.1016/j.sbi.2007.12.003 (https://doi.org/10.1016/j.sbi.2007.12.003)
CrossRef (https://doi.org/10.1016/j.sbi.2007.12.003)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Protein%20folding%20studied%20by%20single-molecule%20FRET&author=B.%20Schuler&author=WA.%20Eaton&journal=Curr%20Opin%20Struct%20Biol&volume=18&pages=16-26&publication_year=2008&doi=10.1016%2Fj.sbi.2007.12.003)

61. Colletier J-P, Bourgeois D, Sanson B et al (2008) Shoot-and-Trap: use of specific X-ray damage to study structural protein dynamics by temperature-controlled cryo-crystallography. Proc Natl Acad Sci U S A 105:11742–11747. doi: 10.1073/pnas.0804828105 (https://doi.org/10.1073/pnas.0804828105)
CrossRef (https://doi.org/10.1073/pnas.0804828105)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Shoot-and-Trap%3A%20use%20of%20specific%20X-ray%20damage%20to%20study%20structural%20protein%20dynamics%20by%20temperature-controlled%20cryo-crystallography&author=J-P.%20Colletier&author=D.%20Bourgeois&author=B.%20Sanson&journal=Proc%20Natl%20Acad%20Sci%20U%20S%20A&volume=105&pages=11742-11747&publication_year=2008&doi=10.1073%2Fpnas.0804828105)

62. Boehr DD, McElheny D, Dyson HJ, Wright PE (2006) The dynamic energy landscape of dihydrofolate reductase catalysis. Science 313:1638–1642. doi: 10.1126/science.1130258 (https://doi.org/10.1126/science.1130258)
CrossRef (https://doi.org/10.1126/science.1130258)
Google Scholar (http://scholar.google.com/scholar_lookup?title=The%20dynamic%20energy%20landscape%20of%20dihydrofolate%20reductase%20catalysis&author=DD.%20Boehr&author=D.%20McElheny&author=HJ.%20Dyson&author=PE.%20Wright&journal=Science&volume=313&pages=1638-1642&publication_year=2006&doi=10.1126%2Fscience.1130258)

63. Rao F, Karplus M (2010) Protein dynamics investigated by inherent structure analysis. Proc Natl Acad Sci U S A 107:9152–9157. doi: 10.1073/pnas.0915087107 (https://doi.org/10.1073/pnas.0915087107)
CrossRef (https://doi.org/10.1073/pnas.0915087107)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Protein%20dynamics%20investigated%20by%20inherent%20structure%20analysis&author=F.%20Rao&author=M.%20Karplus&journal=Proc%20Natl%20Acad%20Sci%20U%20S%20A&volume=107&pages=9152-9157&publication_year=2010&doi=10.1073%2Fpnas.0915087107)

64. Bystroff C, Garde S (2003) Helix propensities of short peptides: molecular dynamics versus bioinformatics. Proteins Struct Funct Genet 50:552–562. doi: 10.1002/prot.10252 (https://doi.org/10.1002/prot.10252)
CrossRef (https://doi.org/10.1002/prot.10252)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Helix%20propensities%20of%20short%20peptides%3A%20molecular%20dynamics%20versus%20bioinformatics&author=C.%20Bystroff&author=S.%20Garde&journal=Proteins%20Struct%20Funct%20Genet&volume=50&pages=552-562&publication_year=2003&doi=10.1002%2Fprot.10252)

65. Das RK, Pappu RV (2013) Conformations of intrinsically disordered proteins are influenced by linear sequence distributions of oppositely charged residues. Proc Natl Acad Sci U S A 110:13392–7. doi: 10.1073/pnas.1304749110 (https://doi.org/10.1073/pnas.1304749110)
CrossRef (https://doi.org/10.1073/pnas.1304749110)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Conformations%20of%20intrinsically%20disordered%20proteins%20are%20influenced%20by%20linear%20sequence%20distributions%20of%20oppositely%20charged%20residues&author=RK.%20Das&author=RV.%20Pappu&journal=Proc%20Natl%20Acad%20Sci%20U%20S%20A&volume=110&pages=13392-7&publication_year=2013&doi=10.1073%2Fpnas.1304749110)

66. Fisher CK, Stultz CM (2011) Constructing ensembles for intrinsically disordered proteins. Curr Opin Struct Biol 21:426–431. doi: 10.1016/j.sbi.2011.04.001 (https://doi.org/10.1016/j.sbi.2011.04.001)
CrossRef (https://doi.org/10.1016/j.sbi.2011.04.001)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Constructing%20ensembles%20for%20intrinsically%20disordered%20proteins&author=CK.%20Fisher&author=CM.%20Stultz&journal=Curr%20Opin%20Struct%20Biol&volume=21&pages=426-431&publication_year=2011&doi=10.1016%2Fj.sbi.2011.04.001)

67. Espinoza-Fonseca LM (2009) Leucine-rich hydrophobic clusters promote folding of the N-terminus of the intrinsically disordered transactivation domain of p53. FEBS Lett 583:556–560. doi: 10.1016/j.febslet.2008.12.060 (https://doi.org/10.1016/j.febslet.2008.12.060)
CrossRef (https://doi.org/10.1016/j.febslet.2008.12.060)
Google Scholar (http://scholar.google.com/scholar_lookup?title=Leucine-rich%20hydrophobic%20clusters%20promote%20folding%20of%20the%20N-terminus%20of%20the%20intrinsically%20disordered%20transactivation%20domain%20of%20p53&author=LM.%20Espinoza-Fonseca&journal=FEBS%20Lett&volume=583&pages=556-560&publication_year=2009&doi=10.1016%2Fj.febslet.2008.12.060)

68. Shapovalov MV, Dunbrack RL Jr (2011) A smoothed backbone-dependent rotamer library for proteins derived from adaptive kernel density estimates and regressions. Structure 6:844–58. doi: 10.1016/j.str.2011.03.019

(https://doi.org/10.1016/j.str.2011.03.019)
CrossRef (https://doi.org/10.1016/j.str.2011.03.019)
Google Scholar (http://scholar.google.com/scholar_lookup?title=A%20smoothed%20backbone-dependent%20rotamer%20library%20for%20proteins%20derived%20from%20adaptive%20kernel%20density%20estimates%20and%20regressions&author=MV.%20Shapovalov&author=RL.%20Dunbrack&journal=Structure&volume=6&pages=844-58&publication_year=2011&doi=10.1016%2Fj.str.2011.03.019)

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