Piotr Neumann’s Publications from 2001 – 2021 (in APA referencing style)

# Total	**# Per Year**	**Title**
2021		
81	3	Blersch, KF., Burchert, JP., August, SC., Welp, L., Neumann, P., Köster, S., Urlaub, H. and Ficner R. **(2021)** Structural model of the M7G46 Methyltransferase TrmB in complex with tRNA. *RNA Biol. 2021 May 19:1-14.*
80	2	Valpadashi, A., Callegari, S., Linden, A., Neumann, P., Ficner, R., Urlaub, H., Deckers, M., & Rehling, P. (2021). Defining the architecture of the human TIM22 complex by chemical crosslinking. *FEBS letters*, *595*(2), 157–168. https://doi.org/10.1002/1873-3468.13978
79	1	Hamann, F., Zimmerningkat, L. C., Becker, R. A., Garbers, T. B., Neumann, P., Hub, J. S., & Ficner, R. (2021). The structure of Prp2 bound to RNA and ADP-BeF3− reveals structural features important for RNA unwinding by DEAH-box ATPases. *Acta crystallographica. Section D, Structural biology*, *77*(Pt 4), 496–509. https://doi.org/10.1107/S2059798321001194
2020		
78	5	Linden, A., Deckers, M., Parfentev, I., Pflanz, R., Homberg, B., Neumann, P., Ficner, R., Rehling, P., & Urlaub, H. (2020). A Cross-linking Mass Spectrometry Approach Defines Protein Interactions in Yeast Mitochondria. *Molecular & cellular proteomics : MCP*, *19*(7), 1161–1178. https://doi.org/10.1074/mcp.RA120.002028
77	4	Munzel, L., Neumann, P., Otto, F. B., Krick, R., Metje-Sprink, J., Kroppen, B., Karedla, N., Enderlein, J., Meinecke, M., Ficner, R., & Thumm, M. (2020). Atg21 organizes Atg8 lipidation at the contact of the vacuole with the phagophore. *Autophagy*, 1–21. https://doi.org/10.1080/15548627.2020.1766332
76	3	Shaikhqasem, A., Dickmanns, A., Neumann, P., & Ficner, R. (2020). Characterization of Inhibition Reveals Distinctive Properties for Human and Saccharomyces cerevisiae CRM1. *Journal of medicinal chemistry*, *63*(14), 7545–7558. https://doi.org/10.1021/acs.jmedchem.0c00143
75	2	Metje-Sprink, J., Groffmann, J., Neumann, P., Barg-Kues, B., Ficner, R., Kühnel, K., Schalk, A. M., & Binotti, B. (2020). Crystal structure of the Rab33B/Atg16L1 effector complex. *Scientific reports*, *10*(1), 12956. https://doi.org/10.1038/s41598-020-69637-0
74	1	Hamann, F., Schmitt, A., Favretto, F., Hofele, R., Neumann, P., Xiang, S., Urlaub, H., Zweckstetter, M., & Ficner, R. (2020). Structural analysis of the intrinsically disordered splicing factor Spp2 and its binding to the DEAH-box ATPase Prp2. *Proceedings of the National Academy of Sciences of the United States of America*, *117*(6), 2948–2956. https://doi.org/10.1073/pnas.1907960117
2019		

73	1	Heidemann, J. L., Neumann, P., Dickmanns, A., & Ficner, R. (2019). Crystal structures of the c-di-AMP-synthesizing enzyme CdaA. *The Journal of biological chemistry*, *294*(27), 10463–10470. https://doi.org/10.1074/jbc.RA119.009246
2018		
72	6	Johannsson, S., Neumann, P., & Ficner, R. (2018). Crystal Structure of the Human tRNA Guanine Transglycosylase Catalytic Subunit QTRT1. *Biomolecules*, *8*(3). https://doi.org/10.3390/biom8030081
71	5	Schmitt, A., Hamann, F., Neumann, P., & Ficner, R. (2018). Crystal structure of the spliceosomal DEAH-box ATPase Prp2. *Acta crystallographica. Section D, Structural biology*, *74*(Pt 7), 643–654. https://doi.org/10.1107/S2059798318006356
70	4	Kolog Gulko, M., Heinrich, G., Gross, C., Popova, B., Valerius, O., Neumann, P., Ficner, R., & Braus, G. H. (2018). Sem1 links proteasome stability and specificity to multicellular development. *PLoS genetics*, *14*(2), e1007141. https://doi.org/10.1371/journal.pgen.1007141
69	3	Dickmanns, A., Zschiedrich, C. P., Arens, J., Parfentev, I., Gundlach, J., Hofele, R., Neumann, P., Urlaub, H., Görke, B., Ficner, R., & Stülke, J. (2018). Structural basis for the regulatory interaction of the methylglyoxal synthase MgsA with the carbon flux regulator Crh in Bacillus subtilis. *The Journal of biological chemistry*, *293*(16), 5781–5792. https://doi.org/10.1074/jbc.RA117.001289
68	2	Johannsson, S., Neumann, P., Wulf, A., Welp, L. M., Gerber, H.-D., Krull, M., Diederichsen, U., Urlaub, H., & Ficner, R. (2018). Structural insights into the stimulation of S. pombe Dnmt2 catalytic efficiency by the tRNA nucleoside queuosine. *Scientific reports*, *8*(1), 8880. https://doi.org/10.1038/s41598-018-27118-5
67	1	Neumann, P., Dickmanns, A., & Ficner, R. (2018). Validating Resolution Revolution. *Structure (London, England : 1993)*, *26*(5), 785–795. https://doi.org/10.1016/j.str.2018.03.004
2017		
66	5	Schmitt, K., Smolinski, N., Neumann, P., Schmaul, S., Hofer-Pretz, V., Braus, G. H., & Valerius, O. (2017). Asc1p/RACK1 Connects Ribosomes to Eukaryotic Phosphosignaling. *Molecular and cellular biology*, *37*(3). https://doi.org/10.1128/MCB.00279-16
65	4	Bujacz, A., Talaj, J. A., Zielinski, K., Pietrzyk-Brzezinska, A. J., & Neumann, P. (2017). Crystal structures of serum albumins from domesticated ruminants and their complexes with 3,5-diiodosalicylic acid. *Acta crystallographica. Section D, Structural biology*, *73*(Pt 11), 896–909. https://doi.org/10.1107/S205979831701470X
64	3	Newie, J., Neumann, P., Werner, M., Mata, R. A., Ficner, R., & Feussner, I. (2017). Lipoxygenase 2 from Cyanothece sp. controls dioxygen insertion by steric shielding and substrate fixation. *Scientific reports*, *7*(1), 2069.

		https://doi.org/10.1038/s41598-017-02153-w
63	2	Gonzalez, G. M., Durica-Mitic, S., Hardwick, S. W., Moncrieffe, M. C., Resch, M., Neumann, P., Ficner, R., Görke, B., & Luisi, B. F. (2017). Structural insights into RapZ-mediated regulation of bacterial amino-sugar metabolism. *Nucleic acids research*, *45*(18), 10845–10860. https://doi.org/10.1093/nar/gkx732
62	1	Ficner, R., Dickmanns, A., & Neumann, P. (2017). Studying structure and function of spliceosomal helicases. *Methods (San Diego, Calif.)*, *125*, 63–69. https://doi.org/10.1016/j.ymeth.2017.06.028
2016		
61	4	Koch, C., Neumann, P., Valerius, O., Feussner, I., & Ficner, R. (2016). Crystal Structure of Alcohol Oxidase from Pichia pastoris. *PloS one*, *11*(2), e0149846. https://doi.org/10.1371/journal.pone.0149846
60	3	Newie, J., Andreou, A., Neumann, P., Einsle, O., Feussner, I., & Ficner, R. (2016). Crystal structure of a lipoxygenase from Cyanothece sp. may reveal novel features for substrate acquisition. *Journal of lipid research*, *57*(2), 276–287. https://doi.org/10.1194/jlr.M064980
59	2	Tauchert, M. J., Hémonnot, C., Neumann, P., Köster, S., Ficner, R., & Dickmanns, A. (2016). Impact of the crystallization condition on importin-β conformation. *Acta crystallographica. Section D, Structural biology*, *72*(Pt 6), 705–717. https://doi.org/10.1107/S2059798316004940
58	1	Fischer, N., Neumann, P., Bock, L. V., Maracci, C., Wang, Z., Paleskava, A., Konevega, A. L., Schröder, G. F., Grubmüller, H., Ficner, R., Rodnina, M. V., & Stark, H. (2016). The pathway to GTPase activation of elongation factor SelB on the ribosome. *Nature*, *540*(7631), 80–85. https://doi.org/10.1038/nature20560
2015		
57	6	Melin, J., Kilisch, M., Neumann, P., Lytovchenko, O., Gomkale, R., Schendzielorz, A., Schmidt, B., Liepold, T., Ficner, R., Jahn, O., Rehling, P., & Schulz, C. (2015). A presequence-binding groove in Tom70 supports import of Mdl1 into mitochondria. *Biochimica et biophysica acta*, *1853*(8), 1850–1859. https://doi.org/10.1016/j.bbamcr.2015.04.021
56	5	Zimmermann, S., Pfennig, S., Neumann, P., Yonus, H., Weininger, U., Kovermann, M., Balbach, J., & Stubbs, M. T. (2015). High-resolution structures of the D-alanyl carrier protein (Dcp) DltC from Bacillus subtilis reveal equivalent conformations of apo- and holo-forms. *FEBS letters*, *589*(18), 2283–2289. https://doi.org/10.1016/j.febslet.2015.07.008
55	4	Gundlach, J., Dickmanns, A., Schröder-Tittmann, K., Neumann, P., Kaesler, J., Kampf, J., Herzberg, C., Hammer, E., Schwede, F., Kaever, V., Tittmann, K., Stülke, J., & Ficner, R. (2015). Identification, characterization, and structure analysis of the cyclic di-AMP-binding PII-like signal transduction protein DarA. *The Journal of biological chemistry*, *290*(5), 3069–3080.

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54	3	Rosenberg, J., Dickmanns, A., Neumann, P., Gunka, K., Arens, J., Kaever, V., Stülke, J., Ficner, R., & Commichau, F. M. (2015). Structural and biochemical analysis of the essential diadenylate cyclase CdaA from Listeria monocytogenes. *The Journal of biological chemistry*, *290*(10), 6596–6606. https://doi.org/10.1074/jbc.M114.630418
53	2	Fischer, N., Neumann, P., Konevega, A. L., Bock, L. V., Ficner, R., Rodnina, M. V., & Stark, H. (2015). Structure of the E. coli ribosome–EF-Tu complex at< 3 Å resolution by C s-corrected cryo-EM. *Nature*, *520*(7548), 567–570. https://doi.org/10.1038/nature14275
52	1	Wechsler, C., Meyer, D., Loschonsky, S., Funk, L.-M., Neumann, P., Ficner, R., Brodhun, F., Müller, M., & Tittmann, K. (2015). Tuning and switching enantioselectivity of asymmetric carboligation in an enzyme through mutational analysis of a single hot spot. *ChemBioChem*, *16*(18), 2580–2584. https://doi.org/10.1002/cbic.201500529
2014		
51	9	Tziridis, A., Rauh, D., Neumann, P., Kolenko, P., Menzel, A., Bräuer, U., Ursel, C., Steinmetzer, P., Stürzebecher, J., Schweinitz, A., Steinmetzer, T., & Stubbs, M. T. (2014). Correlating structure and ligand affinity in drug discovery: a cautionary tale involving second shell residues. *Biological chemistry*, *395*(7-8), 891–903. https://doi.org/10.1515/hsz-2014-0158
50	8	Neumann, P., Lakomek, K., Naumann, P.-T., Erwin, W. M., Lauhon, C. T., & Ficner, R. (2014). Crystal structure of a 4-thiouridine synthetase-RNA complex reveals specificity of tRNA U8 modification. *Nucleic acids research*, *42*(10), 6673–6685. https://doi.org/10.1093/nar/gku249
49	7	Monecke, T., Buschmann, J., Neumann, P., Wahle, E., & Ficner, R. (2014). Crystal Structures of the Novel Cytosolic 5′-Nucleotidase IIIB Explain Its Preference for m 7 GMP. *PLoS One*, *9*(3), e90915. https://doi.org/10.1371/journal.pone.0090915
48	6	Lehneck, R., Neumann, P., Vullo, D., Elleuche, S., Supuran, C. T., Ficner, R., & Pöggeler, S. (2014). Crystal structures of two tetrameric β-carbonic anhydrases from the filamentous ascomycete Sordaria macrospora. *The FEBS journal*, *281*(7), 1759–1772. https://doi.org/10.1111/febs.12738
47	5	Neumann, P., & Tittmann, K. (2014). Marvels of enzyme catalysis at true atomic resolution: distortions, bond elongations, hidden flips, protonation states and atom identities. *Current opinion in structural biology*, *29*, 122–133. https://doi.org/10.1016/j.sbi.2014.11.001
46	4	Möhlmann, S., Mathew, R., Neumann, P., Schmitt, A., Lührmann, R., & Ficner, R. (2014). Structural and functional analysis of the human spliceosomal DEAD-box helicase Prp28. *Acta crystallographica. Section D, Biological crystallography*,

		70(Pt 6), 1622–1630. https://doi.org/10.1107/S1399004714006439
45	3	Khoshnevis, S., Gunišová, S., Vlčková, V., Kouba, T., Neumann, P., Beznosková, P., Ficner, R., & Valášek, L. S. (2014). Structural integrity of the PCI domain of eIF3a/TIF32 is required for mRNA recruitment to the 43S pre-initiation complexes. *Nucleic acids research*, *42*(6), 4123–4139. https://doi.org/10.1093/nar/gkt1369
44	2	Menzel, A., Neumann, P., Schwieger, C., & Stubbs, M. T. (2014). Thermodynamic signatures in macromolecular interactions involving conformational flexibility. *Biological chemistry*, *395*(7-8), 905–911. https://doi.org/10.1515/hsz-2014-0177
43	1	Liu, Y., Neumann, P., Kuhle, B., Monecke, T., Schell, S., Chari, A., & Ficner, R. (2014). Translation initiation factor eIF3b contains a nine-bladed β-propeller and interacts with the 40S ribosomal subunit. *Structure (London, England : 1993)*, *22*(6), 923–930. https://doi.org/10.1016/j.str.2014.03.010
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42	6	Volkov, A., Khoshnevis, S., Neumann, P., Herrfurth, C., Wohlwend, D., Ficner, R., & Feussner, I. (2013). Crystal structure analysis of a fatty acid double-bond hydratase from Lactobacillus acidophilus. *Acta crystallographica. Section D, Biological crystallography*, *69*(Pt 4), 648–657. https://doi.org/10.1107/S0907444913000991
41	5	Meyer, D., Neumann, P., Ficner, R., & Tittmann, K. (2013). Observation of a stable carbene at the active site of a thiamin enzyme. *Nature chemical biology*, *9*(8), 488–490. https://doi.org/10.1038/nchembio.1275
40	4	Monecke, T., Haselbach, D., Voß, B., Russek, A., Neumann, P., Thomson, E., Hurt, E., Zachariae, U., Stark, H., Grubmüller, H., Dickmanns, A., & Ficner, R. (2013). Structural basis for cooperativity of CRM1 export complex formation. *Proceedings of the National Academy of Sciences of the United States of America*, *110*(3), 960–965. https://doi.org/10.1073/pnas.1215214110
39	3	Monecke, T., Haselbach, D., Voß, B., Russek, A., Neumann, P., Thomson, E., Hurt, E., Zachariae, U., Stark, H., Grubmüller, H., & others. (2013). Structural Determinants of Conformational Flexibility and Long-Range Allostery of the CRM1 Export Complex. *Biophysical Journal*, *104*(2), 68a. https://doi.org/10.1016/j.bpj.2012.11.411
38	2	Lüdtke, S., Neumann, P., Erixon, K. M., Leeper, F., Kluger, R., Ficner, R., & Tittmann, K. (2013). Sub-ångström-resolution crystallography reveals physical distortions that enhance reactivity of a covalent enzymatic intermediate. *Nature chemistry*, *5*(9), 762–767. https://doi.org/10.1038/nchem.1728
37	1	Ahmed, Y. L., Gerke, J., Park, H.-S., Bayram, Ö., Neumann, P., Ni, M., Dickmanns, A., Kim, S. C., Yu, J.-H., Braus, G. H., & Ficner, R. (2013). The velvet family of fungal regulators

		contains a DNA-binding domain structurally similar to NF-κB. *PLoS biology*, *11*(12), e1001750. https://doi.org/10.1371/journal.pbio.1001750
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36	2	Neumann, P., Brodhun, F., Sauer, K., Herrfurth, C., Hamberg, M., Brinkmann, J., Scholz, J., Dickmanns, A., Feussner, I., & Ficner, R. (2012). Crystal structures of Physcomitrella patens AOC1 and AOC2: insights into the enzyme mechanism and differences in substrate specificity. *Plant physiology*, *160*(3), 1251–1266. https://doi.org/10.1104/pp.112.205138
35	1	Meyer, D., Neumann, P., Koers, E., Sjuts, H., Lüdtke, S., Sheldrick, G. M., Ficner, R., & Tittmann, K. (2012). Unexpected tautomeric equilibria of the carbanion-enamine intermediate in pyruvate oxidase highlight unrecognized chemical versatility of thiamin. *Proceedings of the National Academy of Sciences of the United States of America*, *109*(27), 10867–10872. https://doi.org/10.1073/pnas.1201280109
2011		
34	8	Maestre-Martínez, M., Haupt, K., Edlich, F., Neumann, P., Parthier, C., Stubbs, M. T., Fischer, G., & Lücke, C. (2011). A charge-sensitive loop in the FKBP38 catalytic domain modulates Bcl-2 binding. *Journal of molecular recognition : JMR*, *24*(1), 23–34. https://doi.org/10.1002/jmr.1020
33	7	Lehwess-Litzmann, A., Neumann, P., Golbik, R., Parthier, C., & Tittmann, K. (2011). Crystallization and preliminary X-ray diffraction analysis of transaldolase from Thermoplasma acidophilum. *Acta crystallographica. Section F, Structural biology and crystallization communications*, *67*(Pt 5), 584–586. https://doi.org/10.1107/S1744309111009274
32	6	Arnold, U., Leich, F., Neumann, P., Lilie, H., & Ulbrich-Hofmann, R. (2011). Crystal structure of RNase A tandem enzymes and their interaction with the cytosolic ribonuclease inhibitor. *The FEBS journal*, *278*(2), 331–340. https://doi.org/10.1111/j.1742-4658.2010.07957.x
31	5	Stolte, S., Steudte, S., Markowska, A., Arning, J., Neumann, J., & Stepnowski, P. (2011). Ion chromatographic determination of structurally varied ionic liquid cations and anions—a reliable analytical methodology applicable to technical and natural matrices. *Analytical Methods*, *3*(4), 919–926. https://doi.org/10.1039/C1AY05029J
30	4	Dickmanns, A., Damerow, S., Neumann, P., Schulz, E.-C., Lamerz, A.-C., Routier, F. H., & Ficner, R. (2011). Structural basis for the broad substrate range of the UDP-sugar pyrophosphorylase from Leishmania major. *Journal of molecular biology*, *405*(2), 461–478. https://doi.org/10.1016/j.jmb.2010.10.057
29	3	Helfmann, S., Neumann, P., Tittmann, K., Moser, T., Ficner, R., & Reisinger, E. (2011). The crystal structure of the C2A domain of otoferlin reveals an unconventional top loop region. *Journal of molecular biology*, *406*(3), 479–490.

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28	2	Schulz, C., Lytovchenko, O., Melin, J., Chacinska, A., Guiard, B., Neumann, P., Ficner, R., Jahn, O., Schmidt, B., & Rehling, P. (2011). Tim50’s presequence receptor domain is essential for signal driven transport across the TIM23 complex. *The Journal of cell biology*, *195*(4), 643–656. https://doi.org/10.1083/jcb.201105098
27	1	Lehwess-Litzmann, A., Neumann, P., Parthier, C., Lüdtke, S., Golbik, R., Ficner, R., & Tittmann, K. (2011). Twisted Schiff base intermediates and substrate locale revise transaldolase mechanism. *Nature chemical biology*, *7*(10), 678–684. https://doi.org/10.1038/nchembio.633
2010		
26	7	Löw, C., Neumann, P., Tidow, H., Weininger, U., Haupt, C., Friedrich-Epler, B., Scholz, C., Stubbs, M. T., & Balbach, J. (2010). Crystal structure determination and functional characterization of the metallochaperone SlyD from Thermus thermophilus. *Journal of molecular biology*, *398*(3), 375–390. https://doi.org/10.1016/j.jmb.2010.03.014
25	6	Khoshnevis, S., Neumann, P., & Ficner, R. (2010). Crystal structure of the RNA recognition motif of yeast translation initiation factor eIF3b reveals differences to human eIF3b. *PloS one*, *5*(9). https://doi.org/10.1371/journal.pone.0012784
24	5	Meyer, D., Neumann, P., Parthier, C., Friedemann, R., Nemeria, N., Jordan, F., & Tittmann, K. (2010). Double duty for a conserved glutamate in pyruvate decarboxylase: evidence of the participation in stereoelectronically controlled decarboxylation and in protonation of the nascent carbanion/enamine intermediate . *Biochemistry*, *49*(37), 8197–8212. https://doi.org/10.1021/bi100828r
23	4	Schulenburg, C., Weininger, U., Neumann, P., Meiselbach, H., Stubbs, M. T., Sticht, H., Balbach, J., Ulbrich-Hofmann, R., & Arnold, U. (2010). Impact of the C-terminal disulfide bond on the folding and stability of onconase. *Chembiochem : a European journal of chemical biology*, *11*(7), 978–986. https://doi.org/10.1002/cbic.200900773
22	3	Carrillo, D. R., Parthier, C., Jänckel, N., Grandke, J., Stelter, M., Schilling, S., Boehme, M., Neumann, P., Wolf, R., Demuth, H.-U., Stubbs, M. T., & Rahfeld, J.-U. (2010). Kinetic and structural characterization of bacterial glutaminyl cyclases from Zymomonas mobilis and Myxococcus xanthus. *Biological chemistry*, *391*(12), 1419–1428. https://doi.org/10.1515/BC.2010.130
21	2	Güttler, T., Madl, T., Neumann, P., Deichsel, D., Corsini, L., Monecke, T., Ficner, R., Sattler, M., & Görlich, D. (2010). NES consensus redefined by structures of PKI-type and Rev-type nuclear export signals bound to CRM1. *Nature structural & molecular biology*, *17*(11), 1367–1376. https://doi.org/10.1038/nsmb.1931
20	1	Schulz, E. C., Neumann, P., Gerardy-Schahn, R., Sheldrick, G.

		M., & Ficner, R. (2010). Structure analysis of endosialidase NF at 0.98 A resolution. *Acta crystallographica. Section D, Biological crystallography*, *66*(Pt 2), 176–180. https://doi.org/10.1107/S0907444909048720
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19	5	Barak, N. N., Neumann, P., Sevvana, M., Schutkowski, M., Naumann, K., Malesević, M., Reichardt, H., Fischer, G., Stubbs, M. T., & Ferrari, D. M. (2009). Crystal structure and functional analysis of the protein disulfide isomerase-related protein ERp29. *Journal of molecular biology*, *385*(5), 1630–1642. https://doi.org/10.1016/j.jmb.2008.11.052
18	4	Neumann, P., Lieber, D., Meyer, S., Dautel, P., Kerth, A., Kraus, I., Garten, W., & Stubbs, M. T. (2009). Crystal structure of the Borna disease virus matrix protein (BDV-M) reveals ssRNA binding properties. *Proceedings of the National Academy of Sciences of the United States of America*, *106*(10), 3710–3715. https://doi.org/10.1073/pnas.0808101106
17	3	Monecke, T., Güttler, T., Neumann, P., Dickmanns, A., Görlich, D., & Ficner, R. (2009). Crystal structure of the nuclear export receptor CRM1 in complex with Snurportin1 and RanGTP. *Science (New York, N.Y.)*, *324*(5930), 1087–1091. https://doi.org/10.1126/science.1173388
16	2	Weidner, A., Neumann, P., Pech, A., Stubbs, M. T., & Tittmann, K. (2009). New insights into the membrane-binding and activation mechanism of pyruvate oxidase from Escherichia coli. *Journal of Molecular Catalysis B: Enzymatic*, *61*(1-2), 88–92. https://doi.org/10.1016/j.molcatb.2009.02.020
15	1	Weininger, U., Zeeb, M., Neumann, P., Löw, C., Stubbs, M. T., Lipps, G., & Balbach, J. (2009). Structure-based stability analysis of an extremely stable dimeric DNA binding protein from Sulfolobus islandicus. *Biochemistry*, *48*(42), 10030–10037. https://doi.org/10.1021/bi900760n
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14	8	Kopycki, J. G., Rauh, D., Chumanevich, A. A., Neumann, P., Vogt, T., & Stubbs, M. T. (2008). Biochemical and structural analysis of substrate promiscuity in plant Mg2+-dependent O-methyltransferases. *Journal of molecular biology*, *378*(1), 154–164. https://doi.org/10.1016/j.jmb.2008.02.019
13	7	Hoffmann, A., Funkner, A., Neumann, P., Juhnke, S., Walther, M., Schierhorn, A., Weininger, U., Balbach, J., Reuter, G., & Stubbs, M. T. (2008). Biophysical characterization of refolded Drosophila Spätzle, a cystine knot protein, reveals distinct properties of three isoforms. *The Journal of biological chemistry*, *283*(47), 32598–32609. https://doi.org/10.1074/jbc.M801815200
12	6	Weidner, A., Neumann, P., Wille, G., Stubbs, M. T., & Tittmann, K. (2008). Crystallization and preliminary X-ray diffraction analysis of full-length and proteolytically activated pyruvate oxidase from Escherichia coli. *Acta crystallographica. Section*

		F, Structural biology and crystallization communications, *64*(Pt 3), 179–181. https://doi.org/10.1107/S1744309108003473
11	5	Hoffmann, A., Neumann, P., Schierhorn, A., & Stubbs, M. T. (2008). Crystallization of Spätzle, a cystine-knot protein involved in embryonic development and innate immunity in Drosophila melanogaster. *Acta crystallographica. Section F, Structural biology and crystallization communications*, *64*(Pt 8), 707–710. https://doi.org/10.1107/S1744309108018812
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