

## Patrick Cramer – Medline-listed publications

### **2020**

227. Lykke-Andersen S, Žumer K, Molska EŠ, Rouvière JO, Wu G, Demel C, Schwalb B, Schmid M, **Cramer P**, Jensen TH.  
Integrator is a genome-wide attenuator of non-productive transcription.  
*Mol Cell*. 2020 Dec 23;S1097-2765(20)30906-0. doi: 10.1016/j.molcel.2020.12.014.
226. Bonekamp NA, Peter B, Hillen HS, Felser A, Bergbrede T, Choidas A, Horn M, Unger A, Di Lucrezia R, Atanassov I, Li X, Koch U, Menninger S, Boros J, Habenberger P, Giavalisco P, **Cramer P**, Denzel MS, Nussbaumer P, Klebl B, Falkenberg M, Gustafsson CM, Larsson NG.  
Small-molecule inhibitors of human mitochondrial DNA transcription.  
*Nature*. 2020 Dec;588(7839):712-716. doi: 10.1038/s41586-020-03048-z.
225. Maier KC, Gressel S, **Cramer P**, Schwalb B.  
Native molecule sequencing by nano-ID reveals synthesis and stability of RNA isoforms.  
*Genome Res*. 2020 Sep;30(9):1332-1344. doi: 10.1101/gr.257857.119. Epub 2020 Sep 4. PMID: 32887688
224. Osman S, **Cramer P**.  
Structural Biology of RNA Polymerase II Transcription: 20 Years On.  
*Annu Rev Cell Dev Biol*. 2020 Oct 6;36:1-34. doi: 10.1146/annurev-cellbio-042020-021954. Epub 2020 Aug 21. PMID: 32822539
223. Kim KP, Choi J, Yoon J, Bruder JM, Shin B, Kim J, Arauzo-Bravo MJ, Han D, Wu G, Han DW, Kim J, **Cramer P**, Schöler HR.  
Permissive epigenomes endow reprogramming competence to transcriptional regulators.  
*Nat Chem Biol*. 2020 Aug 17. doi: 10.1038/s41589-020-0618-6. Online ahead of print. PMID: 32807969
222. Tellier M, Zaborowska J, Caizzi L, Mohammad E, Velychko T, Schwalb B, Ferrer-Vicens I, Blears D, Nojima T, **Cramer P**, Murphy S.  
CDK12 globally stimulates RNA polymerase II transcription elongation and carboxyl-terminal domain phosphorylation.  
*Nucleic Acids Res*. 2020 Aug 20;48(14):7712-7727. doi: 10.1093/nar/gkaa514. PMID: 32805052
221. O'Reilly FJ, Xue L, Graziadei A, Sinn L, Lenz S, Tegunov D, Blötz C, Singh N, Hagen WJH, **Cramer P**, Stülke J, Mahamid J, Rappsilber J.  
In-cell architecture of an actively transcribing-translating expressome.  
*Science*. 2020 Jul 31;369(6503):554-557. doi: 10.1126/science.abb3758. PMID: 32732422
220. **Cramer P**.  
Rosalind Franklin and the Advent of Molecular Biology.  
*Cell*. 2020 Aug 20;182(4):787-789. doi: 10.1016/j.cell.2020.07.028. Epub 2020 Jul 29. PMID: 32730810
219. Farnung L, Ochmann M, **Cramer P**.  
Nucleosome-CHD4 chromatin remodeller structure maps human disease mutations.  
*Elife*. 2020 Jun 16;9:e56178. doi: 10.7554/eLife.56178. Online ahead of print. PMID: 32543371 Free article.
218. Vos SM, Farnung L, Linden A, Urlaub H, **Cramer P**.  
Structure of complete Pol II-DSIF-PAF-SPT6 transcription complex reveals RTF1 allosteric activation.  
*Nat Struct Mol Biol*. 2020 Jun 15. doi: 10.1038/s41594-020-0437-1. Online ahead of print. PMID: 32541898
217. Stik G, Vidal E, Barrero M, Cuartero S, Vila-Casadesús M, Mendieta-Esteban J, Tian TV, Choi J, Berenguer C, Abad A, Borsari B, le Dily F, **Cramer P**, Marti-Renom MA, Stadhouders R, Graf T.  
CTCF is dispensable for immune cell transdifferentiation but facilitates an acute inflammatory response.  
*Nat Genet*. 2020 Jun 8. doi: 10.1038/s41588-020-0643-0. Online ahead of print. PMID: 32514124

216. Jaeger MG, Schwalb B, Mackowiak SD, Velychko T, Hanzl A, Imrichova H, Brand M, Agerer B, Chorn S, Nabet B, Ferguson F, Müller AC, Bergthaler A, Gray NS, Bradner JE, Bock C, Hnisz D, **Cramer P**, Winter GE. Selective Mediator dependence of cell-type-specifying transcription. *Nat Genet.* 2020 Jun 1. doi: 10.1038/s41588-020-0635-0.

215. Hillen HS, Kokic G, Farnung L, Dienemann C, Tegunov D, **Cramer P**. Structure of replicating SARS-CoV-2 polymerase. *Nature.* 2020 May 21. doi: 10.1038/s41586-020-2368-8.

214. Dodonova SO, Zhu F, Dienemann C, Taipale J, **Cramer P**. Nucleosome-bound SOX2 and SOX11 structures elucidate pioneer factor function. *Nature.* 2020 Apr;580(7805):669-672. doi: 10.1038/s41586-020-2195-y.

213. Parfentev I, Schilbach S, **Cramer P**, Urlaub H. An experimentally generated peptide database increases the sensitivity of XL-MS with complex samples. *J Proteomics.* 2020 May 30;220:103754. doi: 10.1016/j.jprot.2020.103754.

212. Wagner FR, Dienemann C, Wang H, Stützer A, Tegunov D, Urlaub H, **Cramer P**. Structure of SWI/SNF chromatin remodeller RSC bound to a nucleosome. *Nature.* 2020 Mar;579(7799):448-451. doi: 10.1038/s41586-020-2088-0.

211. Wang H, Dienemann C, Stützer A, Urlaub H, Cheung AM, **Cramer P**. Structure of transcription coactivator SAGA. *Nature.* 2020, Jan 22. doi: 10.1038/s41586-020-1933-5.

210. **Cramer P**. 500 years after the first circumnavigation of the world: the efforts, rewards and drawbacks of exploration. *FEBS Lett.* 2020 Jan;594(2):207-208.

## **2019**

209. Hillen HS, Bartuli J, Grimm C, Dienemann C, Bedenk K, Szalay AA, Fischer U, **Cramer P**. Structural basis of Poxvirus transcription: transcribing and capping Vaccinia complexes. *Cell.* 2019 Dec 12;179(7):1525-1536.

208. Grimm C, Hillen HS, Bedenk K, Bartuli J, Neyer S, Zhang Q, Hüttenhofer A, Erlacher M, Dienemann C, Schlosser A, Urlaub H, Böttcher B, Szalay AA, **Cramer P**, Fischer U. Structural basis of Poxvirus transcription: Vaccinia RNA polymerase complexes. *Cell.* 2019 Dec 12;179(7):1537-1550.

207. Wang H, Farnung L, Dienemann C, **Cramer P**. Structure of H3K36-methylated nucleosome–PWWP complex reveals multivalent cross-gyre binding. *Nature Struct Mol Biol.* 2019 doi:10.1038/s41594-019-0345-4

206. **Cramer P**. Eukaryotic transcription turns 50. *Cell.* 2019 Oct 31;179(4):808-812.

205. Tegunov D, **Cramer P**. Real-time cryo-electron microscopy data preprocessing with Warp. *Nat Methods.* 2019 Oct 7. doi: 10.1038/s41592-019-0580-y.

204. **Cramer P**. Organization and regulation of gene transcription. *Nature.* 2019 Sep;573(7772):45-54.

203. Gressel S, Schwalb B, **Cramer P**.

The pause-initiation limit restricts transcription activation in human cells.  
*Nat Commun.* 2019 Aug 9;10(1):3603.

202. Hendriks GJ, Jung LA, Larsson AJM, Lidschreiber M, Andersson Forsman O, Lidschreiber K, **Cramer P**, Sandberg R.  
NASC-seq monitors RNA synthesis in single cells.  
*Nat Commun.* 2019 Jul 17;10(1):3138.

201. Kokic G, Chernev A, Tegunov D, Dienemann C, Urlaub H, **Cramer P**.  
Structural basis of TFIIH activation for nucleotide excision repair.  
*Nat Commun.* 2019 Jun 28;10(1):2885.

200. Chen Y, **Cramer P**.  
Structure of the super-elongation complex subunit AFF4 C-terminal homology domain reveals requirements for AFF homo- and heterodimerization.  
*J Biol Chem.* 2019 May 30. pii: jbc.RA119.008577.

199. Sohrabi-Jahromi S, Hofmann K, Boltendahl A, Roth C, Gressel S, Baejen C, Soeding J, **Cramer P**.  
Transcriptome maps of general eukaryotic RNA degradation factors.  
*Elife.* 2019 May 28;8. pii: e47040.

198. Wachutka L, Caizzi L, Gagneur J, **Cramer P**.  
Global donor and acceptor splicing site kinetics in human cells.  
*Elife.* 2019 Apr 26;8. pii: e45056. doi: 10.7554/eLife.45056.

197. Baluapuri A, Hofstetter J, Dudvarski Stankovic N, Endres T, Bhandare P, Vos SM, Adhikari B, Schwarz JD, Narain A, Vogt M, Wang SY, Düster R, Jung LA, Vanselow JT, Wiegeling A, Geyer M, Maric HM, Gallant P, Walz S, Schlosser A, **Cramer P**, Eilers M, Wolf E.  
MYC Recruits SPT5 to RNA Polymerase II to Promote Processive Transcription Elongation.  
*Mol Cell.* 2019 May 16;74(4):674-687.e11.

196. Jones JL, Hofmann KB, Cowan AT, Temiakov D, **Cramer P**, Anikin M.  
Yeast mitochondrial protein Pet111p binds directly to two distinct targets in COX2 mRNA, suggesting a mechanism of translational activation.  
*J Biol Chem.* 2019 May 3;294(18):7528-7536.

195. Žylicz JJ, Bousard A, Žumer K, Dossin F, Mohammad E, da Rocha ST, Schwalb B, Syx L, Dingli F, Loew D, **Cramer P**, Heard E.  
The Implication of Early Chromatin Changes in X Chromosome Inactivation.  
*Cell.* 2019 Jan 10;176(1-2):182-197.e23.

194. Farnung L, Vos SM, **Cramer P**.  
Structure of transcribing RNA polymerase II-nucleosome complex.  
*Nat Commun.* 2018 Dec 21;9(1):5432.

193. Dienemann C, Schwalb B, Schilbach S, **Cramer P**.  
Promoter Distortion and Opening in the RNA Polymerase II Cleft.  
*Mol Cell.* 2019 Jan 3;73(1):97-106.e4.

## **2018**

192. Zhu F, Farnung L, Kaasinen E, Sahu B, Yin Y, Wei B, Dodonova SO, Nitta KR, Morgunova E, Taipale M, **Cramer P**, Taipale J.  
The interaction landscape between transcription factors and the nucleosome.  
*Nature.* 2018 Oct; 562(7725):76-81. doi: 10.1038/s41586-018-0549-5.

191. Lidschreiber M, Easter AD, Battaglia S, Rodríguez-Molina JB, Casañal A, Carminati M, Baejen C, Grzechnik P, Maier KC, **Cramer P**, Passmore LA.  
The APT complex is involved in non-coding RNA transcription and is distinct from CPF.  
*Nucleic Acids Res.* 2018 Sep 21. doi: 10.1093/nar/gky845.
190. Hillen HS, Temiakov D, **Cramer P**.  
Structural basis of mitochondrial transcription.  
*Nat Struct Mol Biol.* 2018 Sep;25(9):754-765. doi: 10.1038/s41594-018-0122-9. Epub 2018 Sep 6.
189. Vos SM, Farnung L, Urlaub H, **Cramer P**.  
Structure of paused transcription complex Pol II-DSIF-NELF.  
*Nature.* 2018 Aug;560(7720):601-606. doi: 10.1038/s41586-018-0442-2. Epub 2018 Aug 22.
188. Vos SM, Farnung L, Boehning M, Wigge C, Linden A, Urlaub H, **Cramer P**.  
Structure of activated transcription complex Pol II-DSIF-PAF-SPT6.  
*Nature.* 2018 Aug;560(7720):607-612. doi: 10.1038/s41586-018-0440-4. Epub 2018 Aug 22.
187. Boehning M, Dugast-Darzacq C, Rankovic M, Hansen AS, Yu T, Marie-Nelly H, McSwiggen DT, Kocic G, Dailey GM, **Cramer P**\*, Darzacq X\*, Zweckstetter M\*.  
RNA polymerase II clustering through carboxy-terminal domain phase separation.  
*Nat Struct Mol Biol.* 2018 Sep;25(9):833-840. doi: 10.1038/s41594-018-0112-y. Epub 2018 Aug 20.
186. La Manno G, Soldatov R, Zeisel A, Braun E, Hochgerner H, Petukhov V, Lidschreiber K, Kastri ME, Lönnerberg P, Furlan A, Fan J, Borm LE, Liu Z, van Bruggen D, Guo J, He X, Barker R, Sundström E, Castelo-Branco G, **Cramer P**, Adameyko I, Linnarsson S, Kharchenko PV.  
RNA velocity of single cells.  
*Nature.* 2018 Aug 8; doi: 10.1038/s41586-018-0414-6. Epub ahead of print.
185. Engel C, Neyer S, **Cramer P**.  
Distinct Mechanisms of Transcription initiation by RNA Polymerases I and II.  
*Annu Rev Biophys.* 2018 May 20; 47:425-446. doi: 10.1146/annurev-biophys-070317-033058.
184. Liu X, Farnung L, Wigge C, **Cramer P**.  
Cryo-EM structure of a mammalian RNA polymerase II elongation complex inhibited by  $\alpha$ -amanitin.  
*J Biol Chem.* 2018 May 11; 293(19):7189-7194. doi: 10.1074/jbc.RA118.002545.
- 2017**
183. Hillen HS, Morozov YI, Sarfallah A, Temiakov D, **Cramer P**.  
Structural Basis of Mitochondrial Transcription Initiation.  
*Cell.* 2017 Nov 16; 171(5):1072-1081. doi: 10.1016/j.cell.2017.10.036.
182. Schilbach S, Hantsche M, Tegenov D, Dienemann C, Wigge C, Urlaub H, Cramer P.  
Structures of transcription pre-initiation complex with TFIIF and Mediator.  
*Nature.* 2017 Nov 9; 551(7679):204-209. doi: 10.1038/nature24282. Epub Nov 1.
181. Malvezzi S, Farnung L, Aloisi CMN, Angelov T, **Cramer P**, Sturla SJ.  
Mechanism of RNA polymerase II stalling by DNA alkylation.  
*Proc Natl Acad Sci U S A.* 2017 Oct 30; 114(46):12172-12177. doi: 10.1073/pnas.1706592114.
180. Hillen HS, Parshin AV, Agaronyan K, Morozov YI, Graber JJ, Chernev A, Schwinghammer K, Urlaub H, Anikin M, **Cramer P**, Temiakov D.  
Mechanism of Transcription Ant-termination in Human Mitochondria.  
*Cell.* 2017 Nov 16; 171(5):1082-1093. doi: 10.1016/j.cell.2017.09.035. Epub 2017 Oct 12.
179. Farnung L, Vos SM, Wigge C, **Cramer P**.  
Nucleosome-Chd 1 structure and implications for chromatin remodelling.

*Nature*. 2017 Oct 26; 550(7677):539-542. doi: 10.1038/nature24046. Epub 2017 Oct 11.

178. Gressel S, Schwalb B, Decker TM, Qin W, Leonhardt H, Eick D, **Cramer P**.  
CDK9-dependent RNA polymerase II pausing controls transcription initiation.  
*Elife*. 2017 Oct 10. doi: 10.7554/eLife.29736.

177. Bernecky C, Plitzko JM, **Cramer P**.  
Structure of a transcribing RNA polymerase II-DSIF complex reveals a multidentate DNA-RNA clamp.  
*Nat Struct Mol Biol*. 2017 Oct; 24(10):809-815. doi: 10.1038/nsmb.3465. Epub 2017 Sep 11.

176. Xu Y, Bernecky C, Lee CT, Maier KC, Schwalb B, Tegunov D, Plitzko JM, Urlaub H, **Cramer P**.  
Architecture of the RNA polymerase II-Paf1C-TFIIS transcription elongation complex.  
*Nat Commun*. 2017 Jun 6; 8:15741. doi: 10.1038/ncomms15741.

175. Battaglia S, Lidschreiber M, Baejen C, Torkler P, Vos SM, **Cramer P**.  
RNA-dependent chromatin association of transcription elongation factors and Pol II CTD kinases.  
*Elife*. 2017 May 24;6. doi: 10.7554/eLife.25637.

174. **Cramer P**.  
Structural molecular biology – a personal reflection on the occasion of John Kendrew's 100<sup>th</sup> birthday.  
*J Mol Biol*. 2017 Aug 18; 429(17):2603-2610. doi: 10.1016/j.jmb.2017.05.007. Epub 2017 May 10.

173. Nozawa K, Schneider TR, **Cramer P**.  
Core Mediator structure at 3.4 Å extends model of transcription initiation complex.  
*Nature*. 2017 May 11;656(7653):248-251. doi: 10.1038/nature22328. Epub 2017 May 3.

172. Hantsche M, **Cramer P**.  
Conserved RNA polymerase II initiation complex structure.  
*Curr Opin Struct Biol*. 2017 Apr 21;47:17-22. doi: 10.1016/j.sbi.2017.03.013.

171. Kohler R, Mooney RA, Mills DJ, Landick R, **Cramer P**.  
Architecture of a transcribing-translating expressome.  
*Science*. 2017 Apr 14;356(6334):194-197. doi: 10.1126/science.aal.3059.

170. Wittmann S, Renner M, Watts BR, Adams O, Huseyin M, Baejen C, El Omari K, Kilchert C, Heo DH, Kecman T, **Cramer P**, Grimes JM, Vasiljeva L.  
The conserved protein Seb1 drives transcription termination by binding RNA polymerase II and nascent RNA.  
*Nat Commun*. 2017 Apr 3;8:14861. doi: 10.1038/ncomms14861.

169. Shetty A, Kallgren SP, Demel C, Maier KC, Spatt D, Alver BH, **Cramer P**, Park PJ, Winston F.  
Spt5 Plays Vital Roles in the Control of Sense and Antisense Transcription Elongation.  
*Mol Cell*. 2017 Apr 6;66(1):77-88.e5. doi: 10.1016/j.molcel.2017.02.023. Epub 2017 Mar 30.

168. Engel C, Gubbey T, Neyer S, Sainsbury S, Oberthuer C, Baejen C, Bernecky C, **Cramer P**.  
Structural Basis of RNA Polymerase I Transcription Initiation.  
*Cell*. 2017 Mar 23;169(1):120-131.e22. doi: 10.1016/j.cell.2017.03.003.

167. Baejen C, Andreani J, Torkler P, Battaglia S, Schwalb B, Lidschreiber M, Maier KC, Boltendahl A, Rus P, Esslinger S, Söding J, **Cramer P**.  
Genome-wide Analysis of RNA Polymerase II Termination at Protein-Coding Genes.  
*Mol Cell*. 2017 Apr 6;66(1):38-49.e6. doi: 10.1016/j.molcel.2017.02.009. Epub 2017 Mar 16.

166. Michel M, Demel C, Zacher B, Schwalb B, Krebs S, Blum H, Gagneur J, **Cramer P**.  
TT-seq captures enhancer landscapes immediately after T-cell stimulation.  
*Mol Syst Biol*. 2017 Mar 7;13(3):920. doi: 10.15252/msb.20167507.

165. Zacher B, Michel M, Schwalb B, **Cramer P**, Tresch A, Gagneur J.

Accurate Promoter and Enhancer Identification in 127 ENCODE and Roadmap Epigenomics Cell Types and Tissues by GenoSTAN.

*PLoS One*. 2017 Jan 5;12(1):e0169249. doi: 10.1371/journal.pone.0169249. eCollection 2017.

## **2016**

164. Neyer S, Kunz M, Geiss C, Hantsche M, Hodirnau VV, Seybert A, Engel C, Scheffer MP, **Cramer P**, Frangakis AS.

Structure of RNA polymerase I transcribing ribosomal DNA genes.

*Nature*. 2016 Nov 14; 540(7634):607-10. doi: 10.1038/nature20561.

163. Fitz V, Shin J, Ehrlich C, Farnung L, **Cramer P**, Ziburdaev V, Grill SW.

Nucleosomal arrangement affects single-molecule transcription dynamics.

*Proc Natl Acad Sci USA*. 2016 Oct 24; 113(45):12733-8. doi: 10.1073/pnas.1602764113.

162. Hillenbrand P, Maier KC, **Cramer P**, Gerland U.

Inference of gene regulation functions from dynamic transcriptome data.

*Elife*. 2016 Sep 21; 5. doi: 10.7554/eLife.12188.

161. Hantsche M, **Cramer P**.

The Structural Basis of Transcription: 10 Years After the Nobel Prize in Chemistry.

*Angew Chem Int Ed Engl*. 2016 Dec 23;55(52):15972-81. doi: 10.1002/anie.201608066. Epub 2016 Nov 11.

160. **Cramer P**.

Structure determination of transient transcription complexes.

*Biochem Soc Trans*. 2016 Aug 15; 44(4):1177-82. doi: 10.1042/BST20160079. (Review)

159. Engel C, Plitzko J, **Cramer P**.

RNA polymerase I-Rrn3 complex at 4.8 Å resolution.

*Nat Commun*. 2016 Jul 05; 7:12129. doi: 10.1038/ncomms12129.

158. Vos SM, Pöllmann D, Caizzi L, Hofmann KB, Rombaut P, Zimniak T, Herzog F, **Cramer P**.

Architecture and RNA binding of the human negative elongation factor.

*Elife*. 2016 Jun 10;5. doi: 10.7554/eLife.14981.

157. Schwalb B, Michel M, Zacher B, Frühauf K, Demel C, Tresch A, Gagneur J, **Cramer P**.

TT-seq maps the human transient genome.

*Science*. 2016 Jun 3; 352(6290):1225-8. doi: 10.1126/science.aad9841.

156. Plaschka C, Hantsche M, Dienemann C, Burzinski C, Plitzko J, **Cramer P**.

Transcription initiation complex structures elucidate DNA opening.

*Nature*. 2016 May 19; 533(7603):353-8. doi: 10.1038/nature17990. Epub 2016 May 11.

155. Lisica A, Engel C, Jahnel M, Roldán É, Galburt EA, **Cramer P**, Grill SW.

Mechanisms of backtrack recovery by RNA polymerases I and II.

*Proc Natl Acad Sci USA*. 2016 Mar 15;113(11):2946-51. doi: 10.1073/pnas.1517011113.

154. Eser P, Wachutka L, Maier KC, Demel C, Boroni M, Iyer S, **Cramer P**, Gagneur J.

Determinants of RNA metabolism in the *Schizosaccharomyces pombe* genome.

*Mol Syst Biol*. 2016 Feb 16; 12(2):857. doi: 10.15252/msb.20156526.

153. Plaschka C, Nozawa K, **Cramer P**.

Mediator Architecture and RNA Polymerase II Interaction.

*J Mol Biol*. 2016 Jun 19;428(12):2569-74. doi: 10.1016/j.jmb.2016.01.028. Epub 2016 Feb 3.

152. Bernecky C, Herzog F, Baumeister W, Plitzko JM, **Cramer P**.

Structure of transcribing mammalian RNA polymerase II.

*Nature*. 2016 Jan 28; 529(7587):551-4. doi: 10.1038/nature16482. Epub 2016 Jan 20.

## **2015**

151. Niesser J, Wagner FR, Kostrewa D, Mühlbacher W, **Cramer P**.

Structure of GPN-loop GTPase Npa3 and implications for RNA polymerase II assembly.

*Mol Cell Biol*. 2015 Dec 28; 36(5):820-31. doi: 0.1128/MCB.01009-15.

150. Kostrewa D, Kuhn CD, Engel C, **Cramer P**.

An alternative RNA polymerase I structure reveals a dimer hinge.

*Acta Crystallogr D Biol Crystallogr*. 2015 Sep; 71(Pt 9):1850-5. doi: 10.1107/S1399004715012651. Epub 2015 Aug 25.

149. Mühlbacher W, Mayer A, Sun M, Remmert M, Cheung AC, Niesser J, Soeding J, **Cramer P**.

Structure of Ctk3, a subunit of the RNA polymerase II CTD kinase complex, reveals a non-canonical CTD-interacting domain fold.

*Proteins*. 2015 Oct; 83(10):1849-58. doi: 10.1002/prot.24869. Epub 2015 Aug 24.

148. Martinez-Rucobo FW, Kohler R, van de Waterbeemd M, Heck AJ, Henemann M, Herzog F, Stark H, **Cramer P**.

Molecular Basis of Transcription-Coupled Preo-mRNA Capping.

*Mol Cell*. 2015 Jun 18; 58(6):1079-89. doi: 10.1016/j.molcel.2015.04.004. Epub 2015 May 7.

147. Morozov YI, Parshin AV, Agaronyan K, Cheung AC, Anikin M, **Cramer P**, Temiakov D.

A model for transcription initiation in human mitochondria.

*Nucleic Acids Res*. 2015 Apr 20; 43(7):3726-35. doi: 10.1093/nar/gkv235. Epub 2015 Mar 23.

146. Sainsbury S, Bernecky C, **Cramer P**.

Structural basis of transcription initiation by RNA polymerase II.

*Nat Rev Mol Cell Biol*. 2015 Mar; 16(3):129-43. doi: 10.1038/nrm3952, Epub 2015 Feb 18.

145. Plaschka C, Larivière L, Wenzek L, Seizl M, Hermann M, Tegunov D, Petrotchenko EV, Borchers CH, Baumeister W, Herzog F, Villa E, **Cramer P**.

Architecture of the RNA polymerase II-Mediator core initiation complex.

*Nature*. 2015 Feb 19; 518(7539):376-80. doi: 10.1038/nature14229. Epub 2015 Feb 4.

144. Borck G, Hög F, Dentici ML, Tan PL, Sowada N, Medeira A, Gueneau L, Thiele H, Kousi M, Lepri F, Wenzek L, Blumenthal I, Radicioni A, Schwarzenberg TL, Mandriani B, Fischetto R, Morris-Rosendahl DJ, Altmüller J, Reymond A, Nürnberg P, Merla G, Dallapiccola B, Katsanis N, **Cramer P**, Kubisch C. BRF1 mutations alter RNA polymerase III-dependent transcription and cause neurodevelopmental anomalies.

*Genome Res*. 2015 Feb; 25(2):155-66. doi: 10.1101/gr.176925.114. Epub 2015 Jan 05.

## **2014**

143. Zacher B, Lidschreiber M, **Cramer P**, Gagneur J, Tresch A.

Annotation of genomics data using bidirectional hidden Markov models unveils variations in Pol II transcription cycle.

*Mol Syst Biol*. 2014 Dec 19; 10(12):768. doi: 10.15252/msb.20145654.

142. **Cramer P**.

A tale of chromatin and transcription in 100 structures.

*Cell*. 2014 Nov 20; 159(5):985-94. doi: 10.1016/j.cell.2014.10.047.

141. Bäjén C, Torkler P, Gressel S, Essig K, Söding J, **Cramer P**.

Transcriptome maps of mRNP biogenesis factors define pre-mRNA recognition.

*Mol Cell*. 2014 Sep 4; 55 (5), 745-757. doi: 10.1016/j.molcel.2014.08.005

140. Tudek A, Porrua O, Kabzinski T, Lidschreiber M, Kubicek K, Fortova A, Lacroute F, Vanakova S, **Cramer P**, Stefl R, Libri D.

Molecular basis for coordination transcription termination with noncoding RNA degradation.  
*Mol Cell*. 2014 Aug 7; 55 (3), 467-481. doi: 10.1016/j.molcel.2014.05.031. Epub 2014 Jul 24.

139. Muehlbacher W, Sainsbury S, Hemann M, Hantsche M, Neyer S, Herzog F, **Cramer P**. Conserved architecture of the core RNA polymerase II initiation complex.

*Nat Commun*. 2014 Jul 10; 5:4310. doi: 10.1038/ncomms5310.

138. Sydow JF, Lipsmeier F, Larraillet V, Hilger M, Mautz B, Mølhø M, Kuentzer J, Klostermann S, Schoch J, Voelger HR, Regula JT, **Cramer P**, Papadimitriou A, Kettenberger H.

Structure-based prediction of asparagine and aspartate degradation sites in antibody variable regions.  
*PLoS One*. 2014 Jun 24; 9 (6):e100736. doi: 10.1371/journal.pone.0100736. eCollection 2014.

137. Schulz D, Pirkl N, Lehmann E, **Cramer P**.

Rbp4 functions mainly in mRNA synthesis by RNA polymerase II.

*J Biol Chem*. 2014 Jun 20. 289 (25), 17446-17452. doi: 10.1074/jbc.M114.568014. Epub 2014 May 5.

136. Eser P, Demel C, Maier KC., Schwalb B, Pirkl N, Martin DE., **Cramer P**, Tresch A.

Periodic mRNA synthesis and degradation co-operate during cell cycle gene expression.

*Mol Syst Biol*. 2014 Jan 30. 10:717. doi: 10.1002/msb.134886. Prin2014. Erratum in: *Mol Syst Biol*. 2014; 10:726.

135. Hirschmann WD, Westendorf H, Mayer A, Cannarozzi G, **Cramer P**, Jansen RP.

Scp160p is required for translational efficiency of codon-optimized mRNAs in yeast.

*Nucleic Acids Res*. 2014 Apr; 42 (6), 4043-3055. doi: 10.1093/nar/gkt1392. Epub 2014 Jan 20.

134. Schrieck A, Easter AD, Etzold S, Wiederhold K, Lidschreiber M, **Cramer P**, Passmore LA. RNA polymerase II termination involves C-terminal-domain tyrosine dephosphorylation by CPF subunit Glc7.

*Nat Struct Mol Biol*. 2014 Feb; 21 (2), 175-179. doi: 10.1038/nsmb.2753. Epub 2014 Jan 12.

133. Morozov YI, Agaronyan K, Cheung AC, Anikin M, **Cramer P**, Temiakov D.

A novel intermediate in transcription initiation by human mitochondrial RNA polymerase.

*Nucleic Acids Res*. 2014 Apr; 42(6):3884-93. doi: 10.1093/nar/gkt1356. Epub 2014 Jan 6.

## **2013**

132. Meinel DM, Burkert-Kautzsch C, Kieser A, O'Duibhir E, Siebert M, Mayer A, **Cramer P**, Söding J, Holstege FC, Strässer K.

Recruitment of TREX to the transcription machinery by its direct binding to the phospho-CTD of RNA polymerase II.

*PLoS Genet*. 2013 Nov;9(11):e1003914. doi: 10.1371/journal.pgen.1003914.

131. Schulz D, Schwalb B, Kiesel A, Baejen C, Torkler P, Gagneur J, Soeding J, **Cramer P**.

*Transcriptome Surveillance by Selective Termination of Noncoding RNA Synthesis*.

*Cell*. 2013 Nov 21; 155(5):1075-87. doi: 10.1016/j.cell.2013.10.024. Epub 2013 Nov 07.

130. Heo DH, Yoo I, Kong J, Lidschreiber M, Mayer A, Choi BY, Hahn Y, **Cramer P**, Buratowski S, Kim M. The RNA Polymerase II C-terminal Domain-Interacting Domain of Yeast Nrd1 Contributes to the Choice of Termination Pathway and Couples to RNA Processing by the Nuclear Exosome.

*J. Biol. Chem*. 2013 Dec 20; 288(51):36676-90. doi: 10.1074/jbc.M113.508267. Epub 2013 Nov 06.

129. Engel C, Sainsbury S, Cheung AC, Kostrewa D, **Cramer P**.

RNA polymerase I structure and transcription regulation.

*Nature*. 2013 Oct 31; 502(7473):650-5. doi: 10.1038/nature12712. Epub 2013 Oct 23.



128. Sun M, Schwalb B, Pirkl N, Maier KC, Schenk A, Failmezger H, Tresch A, **Cramer P**.  
Global analysis of eukaryotic mRNA degradation reveals xrn1-dependent buffering of transcript levels.  
*Mol Cell*. 2013, 52(1):52-62. Doi:10.1016/j.molcel.2013.09.010.
127. Schwinghammer K, Cheung AC, Morozov YI, Agaronyan K, Temiakov D, **Cramer P**.  
Structure of human mitochondrial RNA polymerase elongation complex.  
*Nat Struct Mol Biol*. 2013 Nov; 20(11):1298-303. doi: 10.1038/nsmb.2683. Epub 2013 Oct 6.
126. Kinkelin K, Wozniak GG, Rothbart SB, Lidschreiber M, Strahl BD, **Cramer P**.  
Structures of RNA polymerase II complexes with Bye1, a chromatin-binding PHF3/DIDO homologue.  
*Proc Natl Acad Sci U S A*. 2013, 110, 15277-15282. doi: 10.1073/pnas.1311010110.
125. Larivière L, Plaschka C, Seizl M, Petrotchenko EV, Wenzek L, Borchers CH, **Cramer P**.  
Model of the Mediator middle module based on protein cross-linking.  
*Nucleic Acids Res*. 2013 Nov 1; 41(20):9266-73. doi: 10.1093/nar/gkt704. Epub 2013 Aug 11.
124. Lidschreiber M, Leike K, **Cramer P**.  
Cap completion and C-terminal repeat domain kinase recruitment underlie the initiation-elongation transition of RNA polymerase II.  
*Mol Cell Biol*. 2013 Oct; 33(19):3805-3816. doi: 10.1128/MCB.00361-13.
123. Fouqueau T, Zeller ME, Cheung AC, **Cramer P**, Thomm M.  
The RNA polymerase trigger loop functions in all three phases of the transcription cycle.  
*Nucleic Acids Res*. 2013 Aug; 41(14):7048-7059. doi: 10.1093/nar/gkt433. Epub 2013 Jun 3.
122. Michel M, **Cramer P**.  
Transitions for regulating early transcription.  
*Cell*. 2013 May 23;153(5):943-4. doi: 10.1016/j.cell.2013.04.050.
121. Esslinger SM, Schwalb B, Helfer S, Michalik KM, Witte H, Maier KC, Martin D, Michalke B, Tresch A, **Cramer P**, Förstemann K.  
Drosophila miR-277 controls branched-chain amino acid catabolism and affects lifespan.  
*RNA Biol*. 2013 Jun; 10(6):1042-1056. doi: 10.4161/rna.24810. Epub 2013 Apr 30.
120. Bernecky C, **Cramer P**.  
Struggling to let go: a non-coding RNA directs its own extension and destruction.  
*EMBO J*. 2013 Mar 20; 32(6):771-772. doi: 10.1038/emboj.2013.36. Epub 2013 Feb 22.
119. Sainsbury S, Niesser J, **Cramer P**.  
Structure and function of the initially transcribing RNA polymerase II-TFIIB complex.  
*Nature* 2013 Jan 17;493(7432):437-440. doi: 10.1038/nature11715. Epub 2012 Nov 14.
- 2012**
118. Miller C, Matic I, Maier K, Schwalb B, Roether S, Straesser K, Tresch A, Mann M, **Cramer P**.  
Mediator phosphorylation prevents stress response transcription during non-stress conditions.  
*J Biol Chem* 2012 Dec 28; 287(53):44017-26. doi: 10.1074/jbc.M112.430140. Epub 2012 Nov 7.
117. Wu CC, Herzog F, Jennebach S, Lin YC, Pai CY, Aebersold R, **Cramer P**, Chen HT.  
RNA polymerase III subunit architecture and implications for open promoter complex formation.  
*Proc Natl Acad Sci USA*. 2012 Nov 20; 109(47):19232-7. doi: 10.1073/pnas.1211665109. Epub 2012 Nov 6.
116. Larivière L, Plaschka C, Seizl M, Wenzek L, Kurth F, **Cramer P**.  
Structure of the Mediator head module.  
*Nature*. 2012 Dec 20; 492(7429):448-51. doi: 10.1038/nature11670. Epub Oct 31.

115. Martinez-Rucobo FW, **Cramer P**.  
Structural basis of transcription elongation.  
*Biochim Biophys Acta* 2013 Jan; 1829(1):9-19. doi: 10.1016/j.bbagr.2012.09.002.  
Epub 2012 Sep 13.
114. Dümcke S, Seizl M, Etzold S, Pirkl N, Martin DE, **Cramer P**, Tresch A.  
One hand clapping: detection of condition-specific transcription factor interactions from genome-wide gene activity data.  
*Nucleic Acids Res.* 2012 Oct; 40(18):8883-8892. doi: 10.1093/nar/gks695. Epub 2012 Jul 25.
113. Mayer A, Heidemann M, Lidschreiber M, Schrieck A, Sun M, Hintermair C, Kremmer E, Eick D, **Cramer P**.  
CTD tyrosine phosphorylation impairs termination factor recruitment to RNA polymerase II.  
*Science.* 2012 Jun 29; 336(6089):1723-1725. Doi: 10.1126/science.1219651.
112. Niederberger T, Etzold S, Lidschreiber M, Maier KC, Martin DE, Fröhlich H, **Cramer P**, Tresch A.  
MC EMINEM Maps the Interaction Landscape of the Mediator.  
*PLoS Comput Biol.* 2012 Jun 21; 8(6): e1002568. doi: 10.1371/journal.pcbi.1002568.
111. Cheung AC, **Cramer P**.  
A Movie of RNA Polymerase II Transcription.  
*Cell.* 2012 Jun 22; 149(7):1431-1437. doi: 10.1016/j.cell.2012.06.006.
110. Sun M, Schwalb B, Schulz D, Pirkl N, Etzold S, Larivière L, Maier KC, Seizl M, Tresch A, **Cramer P**.  
Comparative dynamic transcriptome analysis (cDTA) reveals mutual feedback between mRNA synthesis and degradation.  
*Genome Res.* 2012 Jul; 22(7):1350-9. doi: 10.1101/gr.130161.111. Epub 2012 Mar 30.
109. Treutlein B, Muschielok A, Andrecka J, Jawhari A, Buchen C, Kostrewa D, Hög F, **Cramer P**, Michaelis J.  
Dynamic architecture of a minimal RNA polymerase II open promoter complex.  
*Mol Cell.* 2012 Apr 27; 46(2):136-46. doi: 10.1016/j.molcel.2012.02.008. Epub 2012 Mar 15.
108. Walmacq C, Cheung AC, Kireeva ML, Lubkowska L, Ye C, Gotte D, Strathern JN, Carell T, **Cramer P**, Kashlev M.  
Mechanism of translesion transcription by RNA polymerase II and its role in cellular resistance to DNA damage.  
*Mol Cell.* 2012 Apr 13; 46(1):18-29. doi: 10.1016/j.molcel.2012.02.006. Epub 2012 Mar 8.
107. Jennebach S, Herzog F, Aebersold R, **Cramer P**.  
Crosslinking-MS analysis reveals RNA polymerase I domain architecture and basis of rRNA cleavage.  
*Nucleic Acids Res.* 2012 Jul; 40(12):5591-5601. doi: 10.1093/nar.gks220. Epub 2012 Mar 6.
106. Vannini A, **Cramer P**.  
Conservation between the RNA Polymerase I, II, and III transcription initiation machineries.  
*Molecular Cell.* 2012 Feb 24; 45(4):439-46. doi: 10.1016/j.molcel.2012.01.023.
105. Larivière L, Seizl M, **Cramer P**.  
A structural perspective on Mediator function.  
*Curr Opin Cell Biol.* 2012 Jun; 24(3):305-13. doi: 10.1016/j.ceb.2012.01.007. Epub 2012 Feb 15.
104. Mayer A, Schrieck A, Lidschreiber M, Leike K, Martin DE, **Cramer P**.  
The Spt5 C-terminal region recruits yeast 3' RNA cleavage factor I.  
*Mol Cell Biol.* 2012 Apr; 32(7):1321-31. doi: 10.1128/MCB.06310-11. Epub 2012 Jan 30.
103. Schwalb B, Schulz D, Sun M, Zacher B, Dümcke S, Martin DE, **Cramer P**, Tresch A.

Measurement of genome-wide RNA synthesis and decay rates with Dynamic Transcriptome Analysis (DTA). *Bioinformatics* 2012 Mar 15; 28(6):884-5. doi: 10.1093/bioinformatics/bts052. Epub Jan 28.

102. Wild T, **Cramer P**.

Biogenesis of multisubunit RNA polymerases.

*Trends Biochem Sci.* 2012 Mar; 37(3):99-105. doi: 10.1016/j.tibs.2011.12.001. Epub 2012 Jan 17.

## 2011

101. Koschubs T, Dengl S, Dürr H, Kaluza K, Georges G, Hartl C, Jennewein S, Lanzendörfer M, Auer J, Stern A, Huang KS, Packman K, Gubler U, Kostrewa D, Ries S, Hansen S, Kohnert U, **Cramer P**, Mundigl O. Allosteric antibody inhibition of human hepsin protease.

*Biochem J.* 2011 Mar 15; 442(3):483-94. doi: 10.1042/BJ20111317.

100. Seizl M, Hartmann H, Hoeg F, Kurth F, Martin DE, Söding J, **Cramer P**.

A conserved GA element in TATA-less RNA polymerase II promoters.

*PLoS One.* 2011; 6(11): e27595. doi: 10.1371/journal.pone.0027595. Epub 2011 Nov 16.

99. **Cramer P**, Wolberger C.

Proteins: histones and chromatin.

*Curr Opin Struct Biol.* 2011 Dec; 21(6):695-7. Epub 2011 Nov 11.

98. Cheung AC, Sainsbury S, **Cramer P**.

Structural basis of initial RNA polymerase II transcription.

*EMBO J.* 2011 Nov 4; 30(23):4755-4763. doi: 10.1038/emboj.2011.396.

97. Ringel R, Sologub M, Morozov YI, Litonin D, **Cramer P**, Temiakov D.

Structure of human mitochondrial RNA polymerase.

*Nature.* 2011 Sep 25; 478(7368):269-73. doi: 10.1038/nature10435.

96. Blattner C, Jennebach S, Herzog F, Mayer A, Cheung AC, Witte G, Lorenzen K, Hopfner KP, Heck AJ, Aebersold R, **Cramer P**.

Molecular basis of Rrn3-regulated RNA polymerase I initiation and cell growth.

*Genes Dev.* 2011 Oct 1; 25(19):2093-105. doi: 10.1101/gad.17363311. Epub 2011 Sep 22.

95. Geiger SR, Böttcher T, Sieber SA, **Cramer P**.

A conformational switch underlies ClpP protease function.

*Angew Chem Int Ed Engl.* 2011 Jun 14; 50(25):5749-5752. doi: 10.1002/anie,201100666.

94. Müller M, Heym RG, Mayer A, Kramer K, Schmid M, **Cramer P**, Urlaub H, Jansen RP, Niessing D.

A cytoplasmic complex mediates specific mRNA recognition and localization in yeast.

*PLoS Biology* 2011 Apr; 9(4): e1000611. doi: 10.1371/journal.pbio.1000611. Epub 2011 Apr 19.

93. Czeko E, Seizl M, Augsberger C, Mielke T, **Cramer P**.

Iwr1 directs RNA polymerase II nuclear import.

*Mol Cell.* 2011 Apr 22; 42(2):261-6. doi: 10.1016/j.molcel.2011.02.033.

92. Seizl M, Larivière L, Pfaffeneder T, Wenzek L, **Cramer P**.

Mediator head subcomplex Med11/22 contains a common helix bundle building block with a specific function in transcription initiation complex stabilization.

*Nucleic Acids Res.* 2011 Aug; 39(14):6291-304. Doi: 10.1093/nar/gkr229. Epub 2011 Apr 15.

91. Ruan W, Lehmann E, Thomm M, Kostrewa D, **Cramer P**.

Evolution of two modes of intrinsic RNA polymerase transcript cleavage.

*J Biol Chem.* 2011 May 27; 286(21):18701-7. doi: 10.1074/jbc.M111.222273. Epub 2011 Mar 23.

90. Martinez-Rucobo FW, Sainsbury S, Cheung AC, **Cramer P**.  
Architecture of the RNA polymerase-Spt4/5 complex and basis of universal transcription processivity.  
*EMBO J*. 2011 Apr 6; 30(7):1302-10. doi: 10.1038/emboj.2011.64. Epub 2011 Mar 8.
89. Vojnic E, Mourão A, Seizl M, Simon B, Wenzek L, Larivière L, Baumli S, Baumgart K, Meisterernst M, Sattler M, **Cramer P**.  
Structure and VP16 binding of the Mediator Med25 activator interaction domain.  
*Nat Struct Mol Biol*. 2011 Apr; 18(4):404-9. doi: 10.1038/nsmb.1997. Epub 2011 Mar 6.
88. Cheung AC, **Cramer P**.  
Structural basis of RNA polymerase II backtracking, arrest and reactivation.  
*Nature*. 2011 Mar 10; 471(7337):249-53. doi: 10.1038/emboj.2011.64. Epub 2011 Mar 8.
87. Miller C, Schwalb B, Maier K, Schulz D, Dümcke S, Zacher B, Mayer A, Sydow J, Marcinowski L, Dölken L, Martin DE, Tresch A, **Cramer P**.  
Dynamic transcriptome analysis measures rates of mRNA synthesis and decay in yeast.  
*Mol Syst Biol*. 2011 Jan 4, 7:458. doi: 10.1038/msb.2010.112.
- 2010**
86. Clausing E, Mayer A, Chanarat S, Müller B, Germann SM, **Cramer P**, Lisby M, Strässer K.  
The transcription elongation factor Bur1-Bur2 interacts with replication protein A and maintains genome stability during replication stress.  
*J Biol Chem*. 2010 Dec 31; 285(53):41665-74. doi: 10.1074/jbc.M110.193292. Epub 2010 Nov 12.
85. Sun M, Larivière L, Dengl S, Mayer A, **Cramer P**.  
A tandem SH2 domain in transcription elongation factor Spt6 binds the phosphorylated RNA polymerase II C-terminal repeat domain (CTD).  
*J Biol Chem*. 2010 Dec 31, 285(53):41597-603. doi: 10.1074/jbc.M110.144568. Epub 2010 Oct 6.
84. Vannini A, Ringel R, Kusser AG, Berninghausen O, Kassavetis GA, **Cramer P**.  
Molecular basis for RNA polymerase III transcription repression by Maf1.  
*Cell*. 2010 Oct 1; 143(1):59-70. doi: 10.1016/j.cell.2010.09.002.
83. Mayer A, Lidschreiber M, Siebert M, Leike K, Söding J, **Cramer P**.  
Uniform transitions of the general RNA polymerase II transcription complex.  
*Nat Struct Mol Biol*. 2010 Oct; 17(10):1272-1278. doi: 10.1038/nsmb.1903. Epub 2010 Sep 5.
82. Geiger SR, Lorenzen K, Schreieck A, Hanecker P, Kostrewa D, Heck AJ, **Cramer P**.  
RNA polymerase I contains a TFIIF-related DNA-binding subcomplex.  
*Mol Cell*. 2010 Aug 27; 39(4):583-94. doi: 10.1016/j.molcel.2010.07.028.
81. Beck K, Vannini A, **Cramer P**, Lipps G.  
The archaeo-eukaryotic primase of plasmid pRN1 requires a helix bundle domain for faithful primer synthesis.  
*Nucleic Acids Res*. 2010 Oct; 38(19):6707-18. Doi: 10.1093/nar/gkq447. Epub 2010 May 28.
80. **Cramer P**.  
Towards molecular systems biology of gene transcription and regulation.  
*Biol Chem*. 2010 Jul; 391(7):731-5. Doi: 10.1515/BC.2010.094.
79. Hirtreiter A, Damsma GE, Cheung AC, Klose D, Grohmann D, Vojnic E, Martin AC, **Cramer P**, Werner F.  
Spt4/5 stimulates transcription elongation through the RNA polymerase clamp coiled-coil motif.  
*Nucleic Acids Res*. 2010 Jul; 38(12):4040-51. doi: 10.1093/nar/gkq135. Epub 2010 Mar 2.
78. Koschubs T, Lorenzen K, Baumli S, Sandström S, Heck AJ, **Cramer P**.  
Preparation and topology of the Mediator middle module.

*Nucleic Acids Res.* 2010 Jun; 38(10):3186-95. doi: 10.1093/nar/gkq029. Epub 2010 Jan 31.

77. Chen ZA, Jawhari A, Fischer L, Buchen C, Tahir S, Kamenski T, Rasmussen M, Lariviere L, Bukowski-Wills JC, Nilges M, **Cramer P**, Rappsilber J.

Architecture of the RNA polymerase II-TFIIF complex revealed by cross-linking and mass spectrometry. *EMBO J.* 2010 Feb 17; 29(4):717-26. doi: 10.1038/emboj.2009.401. Epub 2010 Jan 21.

## **2009**

76. Sydow JF, **Cramer P**.

RNA polymerase fidelity and transcriptional proofreading.

*Curr Opin Struct Biol.* 2009 Dec; 19(6):732-9. Doi: 10.1016/j.sbi.2009.10.009. Epub 2009 Nov 13.

75. **Cramer P**, Arnold E.

Proteins: how RNA polymerases work.

*Curr Opin Struct Biol.* 2009 Dec; 19(6):680-2. doi: 10.1016/j.sbi.2009.10.013. Epub 2009 Nov 10.

74. Kostrewa D, Zeller ME, Armache KJ, Seizl M, Leike K, Thomm M, **Cramer P**.

RNA polymerase II-TFIIB structure and mechanism of transcription initiation.

*Nature.* 2009 Nov 19; 462(7271):323-30. doi: 10.1038/nature08548.

73. Damsma GE, **Cramer P**.

Molecular basis of transcriptional mutagenesis at 8-oxoguanine.

*J Biol Chem.* 2009 Nov 13; 284(46):31658-63. doi: 10.1074/jbc.M109.022764. Epub 2009 Sep 16.

72. Andrecka J, Treutlein B, Arcusa MA, Muschielok A, Lewis R, Cheung AC, **Cramer P**, Michaelis J.

Nano positioning system reveals the course of upstream and nontemplate DNA within the RNA polymerase II elongation complex.

*Nucleic Acids Res.* 2009 Sep; 37(17):5803-9. Doi: 10.1093/nar/gkp601. Epub 2009 Jul 20.

71. Sydow JF, Brueckner F, Cheung AC, Damsma GE, Dengl S, Lehmann E, Vassilyev D, **Cramer P**.

Structural basis of transcription: mismatch-specific fidelity mechanisms and paused RNA polymerase II with frayed RNA.

*Mol Cell.* 2009 Jun 26; 34(6):710-21. doi: 10.1016/j.molcel.2009.06.002.

70. Dengl S, **Cramer P**.

Torpedo nuclease Rat1 is insufficient to terminate RNA polymerase II in vitro.

*J Biol Chem.* 2009 Aug 7; 284(32):21270-9. doi: 10.1074/jbc.M109.013847. Epub 2009 Jun 17.

69. Brueckner F, Ortiz J, **Cramer P**.

A movie of the RNA polymerase nucleotide addition cycle.

*Curr Opin Struct Biol.* 2009 Jun; 19(3):294-9. doi: 10.1016/j.sbi.2009.04.005. Epub 2009 May 27.

68. Dengl S, Mayer A, Sun M, **Cramer P**.

Structure and in vivo requirement of the yeast Spt6 SH2 domain.

*J Mol Biol.* 2009 May 29; 389(1):211-5. doi: 10.1016/j.jmb.2009.04.016. Epub 2009 Apr 14.

67. Reich C, Zeller M, Milkereit P, Hausner W, **Cramer P**, Tschochner H, Thomm M.

The archaeal RNA polymerase subunit P and the eukaryotic polymerase subunit Rpb12 are interchangeable in vivo and in vitro.

*Mol. Microbiol.* 2009 Feb 7; 71(4):989-1002. doi: 10.1111/j.1365-2958.2008.06577.x.

Epub 2008 Dec 18.

66. Brueckner F, Armache KJ, Cheung A, Damsma GE, Kettenberger H, Lehmann E, Sydow J, **Cramer P**.

Structure-function studies of the RNA polymerase II elongation complex.

*Acta Crystallogr D Biol Crystallogr.* 2009 Feb; 65(2):112-20. doi: 10.1107/S09074444908039875.

Epub 2009 Jan 20.

65. Koschubs T, Seizl M, Larivière L, Kurth F, Baumli S, Martin DE, **Cramer P**. Identification, structure, and functional requirement of the Mediator submodule Med7N/31. *EMBO J*. 2009 Jan 7; 28(1):69-80. doi: 10.1038/emboj.2008.254. Epub 2008 Dec 4.

## **2008**

64. Muschielok A, Andrecka J, Jawhari A, Brückner F, **Cramer P**, Michaelis J. A nano-positioning system for macromolecular structural analysis. *Nat Methods*. 2008 Nov; 5(11):965-71. doi: 10.1038/nmeth.1259. Epub 2008 Oct 12.

63. Jasiak AJ, Hartmann H, Karakasili E, Kalocsay M, Flatley A, Kremmer E, Strässer K, Martin DE, Söding J, **Cramer P**. Genome-associated RNA polymerase II includes the dissociable Rpb4/7 subcomplex. *J Biol Chem*. 2008 Sep 26; 283(39):26423-7. doi: 10.1074/jbc.M803237200. Epub 2008 Jul 30.

62. **Cramer P**, Armache KJ, Baumli S, Benkert S, Brueckner F, Buchen C, Damsma GE, Dengl S, Geiger SR, Jasiak AJ, Jawhari A, Jennebach S, Kamenski T, Kettenberger H, Kuhn CD, Lehmann E, Leike K, Sydow JF, Vannini A. Structure of eukaryotic RNA polymerases. *Annu Rev Biophys*. 2008; 37:337-52. doi: 10.1146/annurev.biophys.37.032807.130008.

61. Brueckner F, **Cramer P**. Structural basis of transcription inhibition by  $\alpha$ -amanitin and implications for RNA polymerase II translocation. *Nat Struct Mol Biol*. 2008 Aug; 15(8):811-8. doi: 10.038/nsmb.1458. Epub 2008 Jun 13.

60. Geiger SR, Kuhn CD, Leidig C, Renkawitz J, **Cramer P**. Crystallization of RNA polymerase I subcomplex A14/A43 by iterative prediction, probing and removal of flexible regions. *Acta Crystallogr Sect F Struct Biol Cryst Commun*. 2008 May 1; 64(5):413-8. doi: 10.1107/S174430910800972X. Epub 2008 Apr 24.

59. Mohammed S, Lorenzen K, Kerkhoven R, van Breukelen B, Vannini A, **Cramer P**, Heck AJ. Multiplexed proteomics mapping of yeast RNA polymerase II and III allows near-complete sequence coverage and reveals several novel phosphorylation sites. *Anal Chem*. 2008 May 15; 80(10):3584-92. doi: 10.1107/S174430910800972X. Epub 2008 Apr 24.

58. Larivière L, Seizl M, van Wageningen S, Röther S, van de Pasch L, Feldmann H, Strässer K, Hahn S, Holstege FC, **Cramer P**. Structure-system correlation identifies a gene regulatory Mediator submodule. *Genes Dev*. 2008 Apr 1; 22(7):872-7. doi: 10.1101/gad.465108.

57. Wendt KU, Weiss MS, **Cramer P**, Heinz DW. Structures and diseases. *Nat Struct Mol Biol*. 2008 Feb; 15(2):117-20. doi: 10.1038/nsmb0208-117.

56. Kusser AG, Bertero MG, Naji S, Becker T, Thomm M, Beckmann R, **Cramer P**. Structure of an archaeal RNA polymerase. *J Mol Biol*. 2008 Feb 15; 376(2):303-7. doi: 10.1016/j.jmb.2007.08.066. Epub 2007 Sep 5.

## **2007**

55. Andrecka J, Lewis R, Brückner F, Lehmann E, **Cramer P**, Michaelis J. Single-molecule tracking of mRNA exiting from RNA polymerase II. *Proc Natl Acad Sci U S A*. 2008 Jan 8; 105(1):135-40. doi: 10.1073/pnas.0703815105. Epub Dec 27.

54. Kuhn CD, Geiger SR, Baumli S, Gartmann M, Gerber J, Jennebach S, Mielke T, Tschochner H, Beckmann R, **Cramer P**.  
Functional architecture of RNA Polymerase I.  
*Cell*. 2007, 131, 1260-1272.
53. Gerber J, Reiter A, Steinbauer R, Jakob S, Kuhn CD, **Cramer P**, Griesenbeck J, Milkereit P, Tschochner H.  
Site specific phosphorylation of yeast RNA polymerase I.  
*Nucleic Acids Res*. 2008, 36, 793-802.
52. Naji S, Bertero MG, Spitalny P, **Cramer P**, Thomm M.  
Structure-function analysis of the RNA polymerase cleft loops elucidates initial transcription, DNA unwinding, and RNA displacement.  
*Nucleic Acids Res*. 2008, 36, 676-687.
51. Carell T, **Cramer P**, Hopfner KP.  
The chemistry of transcription through damaged DNA and of translesion synthesis at atomic resolution.  
*Nucleic Acids Symp Ser (Oxf)*. 2007, 51, 103.
50. Lehmann E, Brueckner F, **Cramer P**.  
Molecular basis of RNA-dependent RNA polymerase II activity.  
*Nature*. 2007, 450, 445-449.
49. Damsma GE, Alt A, Brueckner F, Carell T, **Cramer P**.  
Mechanism of transcriptional stalling at cisplatin-damaged DNA.  
*Nat Struct Mol Biol*. 2007, 14, 1127-1133.
48. Micorescu M, Grünberg S, Franke A, **Cramer P**, Thomm M, Bartlett M.  
Archaeal transcription: function of an alternative transcription factor B from *Pyrococcus furiosus*.  
*J Bacteriol*. 2008, 190, 157-167.
47. Lorenzen K, Vannini A, **Cramer P**, Heck AJ.  
Structural biology of RNA polymerase III: mass spectrometry elucidates subcomplex architecture.  
*Structure*. 2007, 15, 1237-1245.
46. **Cramer P**.  
Finding the right spot to start transcription.  
*Nat Struct Mol Biol*. 2007, 14, 686-687.
45. **Cramer P**.  
Gene transcription: extending the message.  
*Nature*. 2007, 448, 142-143.
44. Kashkina E, Anikin M, Brueckner F, Lehmann E, Kochetkov SN, McAllister WT, **Cramer P**, Temiakov D.  
Multisubunit RNA polymerases melt only a single DNA base pair downstream of the active site.  
*J Biol Chem*. 2007, 282, 21578-21582.
43. Brueckner F, **Cramer P**.  
DNA photodamage recognition by RNA polymerase II.  
*FEBS Lett*. 2007, 581, 2757-2760.
42. Brueckner F, Hennecke U, Carell T, **Cramer P**.  
CPD damage recognition by transcribing RNA polymerase II.  
*Science*. 2007, 315, 859-862.

**2006**

41. **Cramer P.**

Deciphering the RNA polymerase II structure: a personal perspective.  
*Nat Struct Mol Biol.* 2006, 13, 1042-1044.

40. **Cramer P.**

Recent structural studies of RNA polymerases II and III.  
*Biochem Soc Trans.* 2006, 34, 1058-1061.

39. Kashkina E, Anikin M, Brueckner F, Pomerantz RT, McAllister WT, **Cramer P**, Temiakov D.  
Template misalignment in multisubunit RNA polymerases and transcription fidelity.  
*Mol Cell.* 2006, 24, 257-266.

38. Larivière L, Geiger S, Hoepfner S, Röther S, Strässer K, **Cramer P.**  
Structure and TBP binding of the Mediator head subcomplex Med8-Med18-Med20.  
*Nat Struct Mol Biol.* 2006, 13, 895-901.

37. **Cramer P.**

Molecular biology. Self-correcting messages.  
*Science.* 2006, 313, 447-448.

36. Jasiak AJ, Armache KJ, Martens B, Jansen RP, **Cramer P.**  
Structural biology of RNA Polymerase III: subcomplex C17/25 X-ray structure and 11 subunit enzyme model.  
*Mol. Cell* 2006, 23, 71-81.

35. **Cramer P.**

Mechanistic studies of the mRNA transcription cycle.  
*Biochem Soc Symp.* 2006, 73, 41-47.

34. Kettenberger H, **Cramer P.**

Fluorescence detection of nucleic acids and proteins in multi-component crystals.  
*Acta Crystallogr D Biol Crystallogr.* 2006, 62, 146–150.

33. Kettenberger H, Eisenführ A, Brueckner F, Theis M, Famulok M, **Cramer P.**  
Structure of an RNA polymerase II-RNA inhibitor complex elucidates transcription regulation by noncoding RNAs.  
*Nat Struct Mol Biol.* 2006, 13, 44-48.

32. Vojnic E, Simon B, Strahl BD, Sattler M, **Cramer P.**

Structure and carboxyl-terminal domain (CTD) binding of the Set2 SRI domain that couples histone H3 Lys36 methylation to transcription.  
*J Biol Chem.* 2006, 281, 13–15.

**2005**

31. Hoepfner S, Baumli S, **Cramer P.**

Structure of the mediator subunit cyclin C and its implications for CDK8 function.  
*J Mol Biol.* 2005, 350, 833-842.

30. Meinhart A, Kamenski T, Hoepfner S, Baumli S, **Cramer P.**

A structural perspective of CTD function.  
*Genes Dev.* 2005, 19, 1401-1415.

29. Armache KJ, Kettenberger H, **Cramer P.**

The dynamic machinery of mRNA elongation.  
*Curr Opin Struct Biol.* 2005, 15, 197-203.



28. **Cramer P.** and Baumeister W.

Macromolecular assemblages – from molecules to functional modules.  
*Curr Opin Struct Biol.* 2005, 15, 185-187.

27. Baumli S, Hoepfner S, **Cramer P.**

A conserved mediator hinge revealed in the structure of the MED7.MED21  
(Med7.Srb7) heterodimer.  
*J Biol Chem.* 2005, 280, 18171-18178.

26. Kettenberger H, Armache KJ, **Cramer P.**

Complete RNA Polymerase II Elongation Complex Structure and Its Interactions with NTP and TFIIS.  
*Mol Cell.* 2004, 16, 955-965.

## **2004**

25. Armache KJ, Mitterweger S, Meinhart A, **Cramer P.**

Structures of complete RNA polymerase II and its subcomplex, Rpb4/7.  
*J Biol Chem.* 2005, 280, 7131-7134.

24. Kamenski T, Heilmeyer S, Meinhart A, **Cramer P.**

Structure and mechanism of RNA polymerase II CTD phosphatases.  
*Mol Cell.* 2004, 15, 399-407.

23. Meinhart A, **Cramer P.**

Recognition of RNA polymerase II carboxy-terminal domain by 3'-RNA processing factors.  
*Nature.* 2004, 430, 223-226.

22. **Cramer P.**

RNA polymerase II structure: from core to functional complexes.  
*Curr Opin Genet Dev.* 2004, 14, 218-226.

21. Cikala M, Alexandrova O, David CN, Pröschel M, Stiening B, **Cramer P.**, Böttger A.

The phosphatidylserine receptor from Hydra is a nuclear protein with potential Fe(II) dependent oxygenase activity.  
*BMC Cell Biol.* 2004, 5, 26.

20. **Cramer P.**

Structure and function of RNA polymerase II.  
*Adv Protein Chem.* 2004, 67, 1-42.

19. Lipps G, Weinzierl AO, von Scheven G, Buchen C, **Cramer P.**

Structure of a bifunctional DNA primase-polymerase.  
*Nat Struct Mol Biol.* 2004, 11, 157-162.

## **2003**

18. Meinhart A, Blobel J, **Cramer P.**

An extended winged helix domain in general transcription factor E/II $\alpha$ .  
*J Biol Chem.* 2003, 278, 48267-48274.

17. Kettenberger H, Armache KJ, **Cramer P.**

Architecture of the RNA polymerase II-TFIIS complex and implications for mRNA cleavage.  
*Cell.* 2003, 114, 347-357.

16. Armache KJ, Kettenberger H, **Cramer P.**

Architecture of initiation-competent 12-subunit RNA polymerase II.  
*Proc Natl Acad Sci U S A.* 2003, 100, 6964-6968.

15. Meinhart A, Silberzahn T, **Cramer P**.  
The mRNA transcription/processing factor Ssu72 is a potential tyrosine phosphatase.  
*J Biol Chem.* 2003, 278, 15917-15921.

## **2002**

14. **Cramer P**.  
Common structural features of nucleic acid polymerases.  
*Bioessays.* 2002, 24, 724-729.

13. **Cramer P**.  
Multisubunit RNA polymerases.  
*Curr Opin Struct Biol.* 2002, 12, 89-97.

12. Bushnell DA, **Cramer P**, Kornberg RD.  
Structural basis of transcription: alpha-amanitin RNA polymerase II cocystal at 2.8 Å resolution.  
*Proc Natl Acad Sci U S A.* 2002, 99, 1218-1222.

## **2001**

11. Michel F, Soler-Lopez M, Petosa C, **Cramer P**, Siebenlist U, Müller CW.  
Crystal structure of the ankyrin repeat domain of Bcl-3: a unique member of the IkappaB protein family.  
*EMBO J.* 2001, 20, 6180-6190.

10. Bushnell DA, **Cramer P**, Kornberg RD.  
Selenomethionine incorporation in *Saccharomyces cerevisiae* RNA polymerase II.  
*Structure.* 2001, 9, R11-14.

10. Gnatt AL, **Cramer P**, Fu J, Bushnell DA, Kornberg RD.  
Structural basis of transcription: an RNA polymerase II elongation complex at 3.3 Å resolution.  
*Science.* 2001, 292, 1876-82.

9. **Cramer P**, Bushnell DA, Kornberg RD.  
Structural basis of transcription: RNA polymerase II at 2.8 angstrom resolution.  
*Science.* 2001, 292, 1863-76.

## **2000 and earlier**

7. **Cramer P**, Bushnell DA, Fu J, Gnatt AL, Maier-Davis B, Thompson NE, Burgess RR, Edwards AM, David PR, Kornberg RD.  
Architecture of RNA polymerase II and implications for the transcription mechanism.  
*Science.* 2000, 288, 640-9.

6. **Cramer P**, Varrot A, Barillas-Mury C, Kafatos FC, Müller CW.  
Structure of the specificity domain of the Dorsal homologue Gambif1 bound to DNA.  
*Structure.* 1999, 7, 841-52.

5. **Cramer P**, Müller CW.  
A firm hand on NFkappaB: structures of the IkappaBalpha-NFkappaB complex.  
*Structure.* 1999, 7, R1-6.

4. **Cramer P**, Larson CJ, Verdine GL, Müller CW.  
Structure of the human NF-kappaB p52 homodimer-DNA complex at 2.1 Å resolution.  
*EMBO J.* 1997, 16, 7078-90.

3. **Cramer P**, Müller CW.

Engineering of diffraction-quality crystals of the NF-kappaB P52 homodimer-DNA complex.  
*FEBS Lett.* 1997, 405, 373-7.

2. Buckle AM, **Cramer P**, Fersht AR.

Structural and energetic responses to cavity-creating mutations in hydrophobic cores: observation of a buried water molecule and the hydrophilic nature of such hydrophobic cavities.  
*Biochemistry.* 1996, 35, 4298-305.

1. Bergamini P, Costa E, **Cramer P**, Hogg JK, Orpen AG, Pringle PG.

Diastereoselective C-C bond formation by carbene insertions into Pt-CH<sub>3</sub> bonds.  
*Organometallics.* 1994, 13, 1058-60.

## Patrick Cramer – Other publications

P. Cramer. Ein Schalter für menschliche Gene. Jahrbuch der Max-Planck-Gesellschaft 2018/2019.

N. Nozawa, Thomas R. Schneider and Patrick Cramer. Crystal structure of the 15-subunit core Mediator at 3.4 Å extends the structural understanding of transcription. Photon Science Report 2017, DESY Hamburg.

P. Cramer. Wie Gene aktiv werden. Jahrbuch der Max-Planck-Gesellschaft 2015/2016.

P. Cramer: "Pioniere auf einem neuen Forschungsfeld – Genzentrum und Department Biochemie" in U. Löhns, W. Neupert, K. Peter, S. Sattler, G. Sittner (Hrsg.): Forschen, heilen, lehren. Deutsche Verlagsanstalt. ISBN 978-3-421-04672-7 (2014).

P. Cramer: "Aufbruch in die molekulare Systembiologie" – Essay für die Jubiläumsausgabe "20 Jahre Laborjournal", Laborjournal vom 11.7.2014 (2014)

P. Cramer: "Wie betreibe ich gute Wissenschaft?" Vorwort des Schirmherrn in M. Spieker (Hrsg.): Gute Lebenswissenschaft für das 21. Jahrhundert. Akademie Tutzing. ISBN 978-3-9814111-1-9 (2013).

P. Cramer: "Gaining the future in biomedicine" – Vorwort in der Broschüre "Das bayerische Forschungsnetzwerk für Molekulare Biosysteme" (2012)

P. Cramer: "Entwicklungen in der Biomedizin: Genom-Sequenzierung in Diagnose, Prävention und Therapie; Systembiologie und Medizin" in T. Rendtorff (Hrsg.): Zukunft der biomedizinischen Wissenschaften. Nomos, ISBN 978-3-8487-0849-9 (2013).

O. Primavesi, P. Cramer, R. Hickel, T. O. Höllmann, W. Schön. Lob der Promotion. Frankfurter Allgemeine Zeitung (19. Juli 2013).

P. Cramer: Director's Report. Bericht anlässlich des Forschungsberichts des Genzentrums der LMU München 2009-2012 (März 2013).

P. Cramer. Der Systemwechsel in den Lebenswissenschaften. Bayer Research, 24 (2012).

J.F. Sydow, D. Kostrewa, D.E. Martin, P. Cramer. 10 Jahre RNA-Polymerase-Struktur: von Transkription zu Genregulation. Biospektrum 01, 24-27 (2010).

P. Cramer. Gentranskription im Film. Der mathematische und naturwissenschaftliche Unterricht (Dezember 2009).

J. Hacker, T. Rendtorff, P. Cramer, M. Hallek, K. Hilpert, C. Kupatt, M. Lohse, A. Müller, U. Schroth, F. Voigt, M. Zichy. Biomedizinische Eingriffe am Menschen - Ein Stufenmodell zur ethischen Bewertung von Gen- und Zelltherapie. Water de Gruyter, Berlin. ISBN 978-3-11-021306-5. (2009).

P. Cramer. Report of the managing director. Bericht anlässlich des 5-Jahres-Berichts des Genzentrums der LMU München 2004-2008 (April 2009).

P. Cramer, K. Straesser, D. Niessing, G. Meister, R.-P. Jansen. RNA als Koordinator und Regulator der Genexpression. Biospektrum 23, 525 (2005).

P. Cramer. Gene expression in eukaryotes: RNA polymerase II structure. Encyclopedia of Biological Chemistry 3, 770-774 (2004).

K. Armache, H. Kettenberger, P. Cramer. Transiente RNA-Polymerase-Komplexe. Biospektrum 04, 378-380 (2004).

P. Cramer. Strukturbiologie der Transkription. Nachrichten aus der Chemie 50, 312-315 (2002).