

2009:

Comparison of eukaryotic phylogenetic profiling approaches using species tree aware methods.

Ruano-Rubio V, Poch O, Thompson JD.
BMC Bioinformatics. 2009 Nov 24;10:383.PMID: 19930674 [PubMed - in process]Related articlesFree article

TBP2 is essential for germ cell development by regulating transcription and chromatin condensation in the oocyte.

Gazdag E, Santenard A, Ziegler-Birling C, Altobelli G, Poch O, Tora L, Torres-Padilla ME.
Genes Dev. 2009 Sep 15;23(18):2210-23.PMID: 19759265 [PubMed - indexed for MEDLINE]Related articles

Time-resolved analysis of transcriptional events during SNAI1-triggered epithelial to mesenchymal transition.

Vetter G, Le Béhec A, Muller J, Muller A, Moes M, Yatskou M, Al Tanoury Z, Poch O, Vallar L, Friederich E.
Biochem Biophys Res Commun. 2009 Aug 7;385(4):485-91. Epub 2009 May 12.PMID: 19442650 [PubMed - indexed for MEDLINE]Related articles

The thioredoxin-like protein rod-derived cone viability factor (RdCVFL) interacts with TAU and inhibits its phosphorylation in the retina.

Fridlich R, Delalande F, Jaillard C, Lu J, Poidevin L, Cronin T, Perrocheau L, Millet-Puel G, Niepon ML, Poch O, Holmgren A, Van Dorsselaer A, Sahel JA, Léveillard T. Mol Cell Proteomics. 2009 Jun;8(6):1206-18. Epub 2009 Mar 11. PMID: 19279044 [PubMed - indexed for MEDLINE]Related articles

Structure of the archaeal pab87 peptidase reveals a novel self-compartmentalizing protease family.

Delfosse V, Girard E, Birck C, Delmarcelle M, Delarue M, Poch O, Schultz P, Mayer C. PLoS One. 2009;4(3):e4712. Epub 2009 Mar 5. PMID: 19266066 [PubMed - indexed for MEDLINE]Related articlesFree article

Strategies for reliable exploitation of evolutionary concepts in high throughput biology.

Levasseur A, Pontarotti P, Poch O, Thompson JD. Evol Bioinform Online. 2008;4:121-37. Epub 2008 May 8. PMID: 19204813 [PubMed - in process]Related articlesFree article

Defining and characterizing protein surface using alpha shapes.

Albou LP, Schwarz B, Poch O, Wurtz JM, Moras D. Proteins. 2009 Jul;76(1):1-12. PMID: 19089982 [PubMed - indexed for MEDLINE]Related articles

Knowledge-based expert systems and a proof-of-concept case study for multiple sequence alignment construction and analysis.

Aniba MR, Siguenza S, Friedrich A, Plewniak F, Poch O, Marchler-Bauer A, Thompson JD. Brief Bioinform. 2009 Jan;10(1):11-23. Epub 2008 Oct 29. PMID: 18971242 [PubMed - indexed for MEDLINE]

[Ortho-proteogenomics: multiple proteomes investigation through orthology and a new MS-based protocol.](#)

Gallien S, Perrodou E, Carapito C, Deshayes C, Reyrat JM, Van Dorsselaer A, Poch O, Schaeffer C, Lecompte O.

Genome Res. 2009 Jan;19(1):128-35.

2008:

Levasseur A, Pontarotti P, Poch O, Thompson JD. (2008) *Strategies for reliable exploitation of evolutionary concepts in high throughput biology.*

Evol Bioinform Online, 4:121-37.

Lecompte O, Poch O, Laporte J. (2008) *PtdIns5P regulation through evolution: roles in membrane trafficking?*

Trends Biochem. Sci., 33(10):453-60

Befort K, Filliol D, Darcq E, Ghate A, Matifas A, Lardenois A, Muller J, Thibault C, Dembele D, Poch O, Kieffer BL. (2008) *Gene expression is altered in the lateral hypothalamus upon activation of the mu opioid receptor.*

Ann N Y Acad Sci., 1129:175-84.

Befort K, Filliol D, Ghate A, Darcq E, Matifas A, Muller J, Lardenois A, Thibault C, Dembele D, Le Merrer J, Becker JA, Poch O, Kieffer BL. (2008) *Mu-opioid receptor activation induces transcriptional plasticity in the central extended amygdala.*

Eur J Neurosci., 27(11):2973-84.

Kalathur RK, Gagniere N, Berthommier G, Poidevin L, Raffelsberger W, Ripp R, Léveillard T, Poch O. (2008) *RETINOBASE: a web database, data mining and analysis platform for gene expression data on retina.*

BMC Genomics, 9:208.

Perrodou E, Chica C, Poch O, Gibson TJ, Thompson JD. (2008) *A new protein linear motif benchmark for multiple sequence alignment software.*

BMC Bioinformatics, 9:213.

Deshayes C, Perrodou E, Euphrasie D, Frapy E, Poch O, Bifani P, Lecompte O, Reyrat JM. (2008) *Detecting the molecular scars of evolution in the Mycobacterium tuberculosis complex by analyzing interrupted coding sequences* .

BMC Evol Biol., 6(8):78

Lagier-Tourenne C, Tazir M, López LC, Quinzii CM, Assoum M, Drouot N, Busso C, Makri S, Ali-Pacha L, Benhassine T, Anheim M, Lynch DR, Thibault C, Plewniak F, Bianchetti L, Tranchant C, Poch O, DiMauro S, Mandel JL, Barros MH, Hirano M, Koenig M. (2008) *ADCK3, an ancestral kinase, is mutated in a form of recessive ataxia associated with coenzyme Q10 deficiency* .

Am J Hum Genet., 82(3):661-72.

Thiersch M, Raffelsberger W, Frigg R, Samardzija M, Wenzel A, Poch O, Grimm C. (2008) *Analysis of the retinal gene expression profile after hypoxic preconditioning identifies candidate genes for neuroprotection*

BMC Genomics, 9:73.

Thiersch M, Raffelsberger W, Frigg E, Samardzija M, Blank P, Poch O, Grimm C. (2008) *The hypoxic transcriptome of the retina: identification of factors with potential neuroprotective activity*

Adv Exp Med Biol., 613:75-85.

Raffelsberger W, Krause Y, Moulinier L, Kieffer D, Morand AL, Brino L, Poch O. (2008) *RReportGenerator: automatic reports from routine statistical analysis using R*

Bioinformatics, 24(2):276-8.

Bianchetti L, Wu Y, Guerin E, Plewniak F, Poch O. (2007) *SAGETTARIUS: a program to reduce the number of tags mapped to multiple transcripts and to plan SAGE sequencing stages.*

Nucleic Acids Res., 35(18):e122

2007:

Schluter A, Fourcade S, Domenech-Estevéz E, Gabaldon T, Huerta-Cepas J, Berthommier G, Ripp R, Wanders RJ, Poch O, Pujol A. (2007) *PeroxisomeDB: a database for the peroxisomal proteome, functional genomics and disease.*

Nucleic Acids Res., 35(Database issue):D815-22.

Stoetzel C, Muller J, Laurier V, Davis EE, Zaghoul NA, Vicaire S, Jacquelin C, Plewniak F, Leitch CC, Sarda P, Hamel C, de Ravel TJ, Lewis RA, Friederich E, Thibault C, Danse JM, Verloes A, Bonneau D, Katsanis N, Poch O, Mandel JL, Dollfus H. (2007) *Identification of a novel BBS gene (BBS12) highlights the major role of a vertebrate-specific branch of*

chaperonin-related proteins in Bardet-Biedl syndrome.

Am J Hum Genet., 80(1):1-11.

Deshayes C, Perrodou E, Gallien S, Euphrasie D, Schaeffer C, Van-Dorsselaer A, Poch O, Lecompte O, Reyrat JM. (2007) *Interrupted coding sequences in Mycobacterium smegmatis: authentic mutations or sequencing errors?*

Genome Biol., 8(2):R20

Friedrich A, Ripp R, Garnier N, Bettler E, Deleage G, Poch O, Moulinier L. (2007) *Blast sampling for structural and functional analyses.*

BMC Bioinformatics, 8:62.

Wicker N, Carles A, Mills IG, Wolf M, Veerakumarasivam A, Edgren H, Boileau F, Wasyluk B, Schalken JA, Neal DE, Kallioniemi O, Poch O. (2007) *A new look towards BAC-based array CGH through a comprehensive comparison with oligo-based array CGH.*

BMC Genomics, 8(1):84

Brulliard M, Lorphelin D, Collignon O, Lorphelin W, Thouvenot B, Gothie E, Jacquenet S, Ogier V, Roitel O, Monnez JM, Vallois P, Yen FT, Poch O, Guenneugues M, Karcher G, Oudet P, Bihain BE. (2007) *Nonrandom variations in human cancer ESTs indicate that RNA heterogeneity increases during carcinogenesis.*

Proc Natl Acad Sci U S A, 104(18):7522-7.

Muller J, Mehlen A, Vetter G, Yatskou M, Muller A, Chalmel F, Poch O, Friederich E, Vallar L. (2007) *Design and evaluation of Actichip, a thematic microarray for the study of the actin cytoskeleton* .

BMC Genomics., 8(1):294

Chalmel F, Leveillard T, Jaillard C, Lardenois A, Berdugo N, Morel E, Koehl P, Lambrou G, Holmgren A, Sahel JA, Poch O. (2007) *Rod-derived Cone Viability Factor-2 is a novel bifunctional-thioredoxin-like protein with therapeutic potential.*

BMC Mol Biol., 8(1):74

2006:

Stoetzel C, Laurier V, Davis EE, Muller J, Rix S, Badano JL, Leitch CC, Salem N, Chouery E, Corbani S, Jalk N, Vicaire S, Sarda P, Hamel C, Lacombe D, Holder M, Odent S, Holder S, Brooks AS, Elcioglu NH, Silva ED, Rossillion B, Sigaudy S, de Ravel TJ, Lewis RA, Leheup B, Verloes A, Amati-Bonneau P, Megarbane A, Poch O, Bonneau D, Beales PL, Mandel JL, Katsanis N, Dollfus H. (2006) *BBS10 encodes a vertebrate-specific chaperonin-like protein and is a major BBS locus.*

Nat Genet., 38(5):521-4. Erratum in: Nat Genet. 2006 Jun;38(6):727.

Gaillard E, Bruck N, Brelivet Y, Bour G, Lalevee S, Bauer A, Poch O, Moras D, Rochette-Egly C. (2006) *Phosphorylation by PKA potentiates retinoic acid receptor alpha activity by means of increasing interaction with and phosphorylation by cyclin H/cdk7.*

Proc Natl Acad Sci U S A., 103(25):9548-53.

Thompson JD, Muller A, Waterhouse A, Procter J, Barton GJ, Plewniak F, Poch O. (2006) *MA CSIMS: multiple alignment of complete sequences information management system.*

BMC Bioinformatics, 7:318.

Garnier N, Friedrich A, Bolze R, Bettler E, Moulinier L, Geourjon C, Thompson JD, Deleage G, Poch O. (2006) *MAGOS: multiple alignment and modelling server.*

Bioinformatics, 22(17):2164-5.

Laurier V, Stoetzel C, Muller J, Thibault C, Corbani S, Jalkh N, Salem N, Chouery E, Poch O, Licaire S, Danse JM, Amati-Bonneau P, Bonneau D, Megarbane A, Mandel JL, Dollfus H. (2006) *Pitfalls of homozygosity mapping: an extended consanguineous Bardet-Biedl syndrome family with two mutant genes (BBS2, BBS10), three mutations, but no triallelism.*

Eur J Hum Genet., 14(11):1195-203.

Lardenois A, Chalmel F, Bianchetti L, Sahel JA, Leveillard T, Poch O. (2006) *PromAn: an integrated knowledge-based web server dedicated to promoter analysis.*

Nucleic Acids Res., 34(Web Server issue):W578-83.

Dollfus H, Muller J, Stoetzel C, Laurier V, Bonneau D, Megarbane A, Poch O, Mandel JL. (2006) *ardet-Biedl syndrome: a unique family for a major gene (BBS10)* [B]

Med Sci (Paris). 22(11):901-4.

Carles A., Millon R., Cromer A., Ganguli G., Lemaire F., Young J., Wasylyk C., Muller D., Schultz I., Rabouel Y., Dembélé D., Zhao C., Marchal P., Ducray C., Bracco L., Abecassis J., Poch O. and Wasylyk B. (2006) *Head and neck squamous cell carcinoma (HNSCC) transcriptome analysis by comprehensive validated differential display.*

Oncogene, 25 (12):1821-1831.

Perrodou E, Deshayes C, Muller J, Schaeffer C, Van Dorsselaer A, Ripp R, Poch O, Reyrat

JM, Lecompte O. (2006) *ICDS database: interrupted CoDing sequences in prokaryotic genomes.*

Nucleic Acids Res., 34(Database issue):D338-43.

Abou-Sleymane G, Chalmel F, Helmlinger D, Lardenois A, Thibault C, Weber C, Merienne K, Mandel JL, Poch O, Devys D, Trottier Y. (2006)
Polyglutamine expansion causes neurodegeneration by altering the neuronal differentiation program

Hum Mol Genet., 15(5):691-703.

Schluter A, Fourcade S, Ripp R, Mandel JL, Poch O, Pujol A. (2006) *The evolutionary origin of peroxisomes: an ER-peroxisome connection.*

Mol Biol Evol., 23(4):838-45.

2005:

Leveillard T., Mohand-Said S., Poch O. and Sahel J.A.. (2005) [*Rod-derived cone viability factor : a clue for therapy of retinitis pigmentosa?*]
French.

Med. Sci. (Paris), 21(1):22-24.

Chalmel F., Lardenois A., Thompson J.D., Muller J., Sahel J.A., Leveillard T. and Poch O. (2005) *GOAnno: GO annotation based on multiple alignment.*

Bioinformatics, 21(9):2095-6.

Thompson J.D., Holbrook S.R., Katoh K., Koehl P., Moras D., Westhof E. and Poch O. (2005) *MAO: a Multiple Alignment Ontology for nucleic acid and protein sequences.*

Nucleic Acids Res., 33(13):4164-71.

Thompson J.D., Koehl P., Ripp R. and Poch O. (2005) *BAlIiBASE 3.0: Latest developments of the multiple sequence alignment benchmark.*

Proteins, 61(1):127-136.

Bianchetti L., Thompson J.D., Lecompte O., Plewniak F. and Poch O. (2005) *vALId: validation of protein sequence quality based on multiple alignment data.*

Bioinform Comput Biol., 3(4):929-947.

Muller J., Oma Y., Vallar L., Friederich E., Poch O. and Winsor, B. (2005). *Sequence and comparative genomic analysis of Actin Related Proteins.*

Mol. Biol. Cell., 16(12):5736-5748.

Uhring M, Bey G, Lecompte O, Cavarelli J, Moras D, Poch O. (2005) *Cloning, purification and crystallization of a Walker-type Pyrococcus abyssi ATPase family member.*

Acta Crystallograph Sect F Struct Biol Cryst Commun., 61(Pt 10):925-7.

2004:

Thompson J., Prigent V and Poch O. (2004) LEON: multiple aLignment Evaluation Of Neighbours.

Nucleic Acids Res., 32(4): 1298-1307.

Cromer A., Carles A., Millon R., Ganguli G., Chalmel F., Lemaire F., Young J., Dembélé D., Thibault C., Diemunsch F., Poch O., Abecassis J. and Wasyluk B. (2004) *Identification of genes associated with hypopharyngeal cancer and metastatic potential by microarray analysis.*

Oncogene, 23(14):2484-2498.

Léveillard T., Mohand-Saïd S., Lorentz O., Hicks D., Fintz A.C., Clerin E., Simonutti M., Forster V., Cavusoglu N., Chalmel F., Dolle P., Poch O., Lambrou G. and Sahel J.A. (2004) *Identification and characterization of rod-derived cone viability factor*

Nature Genetics, 36(7):755-759

Brelivet Y., Kammerer S., Rochel N., Poch O. and Moras D. (2004) *Signature of the oligomeric behaviour of nuclear receptors at the sequence and structural level.*

EMBO reports, 5(4):423-429

Jawhari A., Boussert S., Lamour V., Atkinson R.A., Kieffer B., Poch O., Potier N., van Dorselaer A., Moras D. and Poterszman A. (2004) *Domain architecture of the p62 subunit from the human transcription/repair factor TFIIH deduced by limited proteolysis and mass spectrometry analysis.*

Biochemistry, 43(45):14420-14430.

Prigent V., Thierry J.C., Poch O. and Plewniak F. (2004) *DbW: automatic update of a functional family-specific multiple alignment.*

Bioinformatics, 21(8):1437-42.

2003:

Cohen G., Barbe V., Flament D., Galperin M., Heilig R., Ripp R., Lecompte O., Prieur D., Poch O, Quérellou J., Thierry J.C., Van der Oost J., Weissenbach J., Zivanovic Y and Forterre P. (2003) *An integrated analysis of the genome of the hyperthermophilic archaeon Pyrococcus abyssi.*

Mol. Microbiol. 47(6):1495-1512.

Gozuacik D., Chami M., Murakami Y., Faivre J., Lagorce D., Poch O., Biermann E., Knippers R., Bréchet C. and Paterlini-Bréchet P. (2003) *Identification and functional characterization of a new member of the human Mcm protein family: hMcm8.*

Nucleic Acids Res., 31(2): 570-579.

Plewniak F., Bianchetti L., Brelivet Y., Carles A., Chalmel F., Lecompte O., Mochel T., Moulinier L., Muller A., Muller J. Prigent V., Ripp R., Thierry J.C., Thompson J., Wicker N. and Poch O. (2003) *PipeAlign : a new toolkit for protein family analysis.*

Nucleic Acids Res., 31(13): 3829-3832.

Thompson J.D., Thierry J.C. and Poch O. (2003) ***RASCAL: Rapid scanning and correction of multiple sequence alignment programs.***

Bioinformatics, 19(9):1155-1161.

Cavusoglu N., Thierse D., Mohand-Said S., Chalmel F., Poch O., Van Dorsselaer A., Sahel J.A. and Leveillard T. (2003) *Differential proteomic analysis of the mouse retina: The induction of crystallin proteins by retinal degeneration in the rd1 mouse.*

Mol. Cell Proteomics, 2(8): 494-505.

Duval D., Duval G., Keding C., Poch O. and Boeuf H. (2003) *The "PINIT" motif, of a newly identified conserved domain of the PIAS protein family, is essential for nuclear retention of PIAS3L*

FEBS Lett., 554(1-2): 111-118.

Bianchetti L., Oudet C. and Poch O. (2002) *M13 Endopeptidases : New Conserved Motifs correlated with Structure, and Simultaneous Phylogenetic Occurrence of PHEX and the Bony Fish*

Proteins, 47 (4): 481-8.

2002:

Wicker N., Dembele D., Raffelsberger W. and Poch O. (2002) *Density of points clustering, application to transcriptomic data analysis.*

Nucleic Acids Res., 30(18):3992-4000.

Lecompte O., Ripp R., Thierry J.C., Moras D. and Poch O. (2002) *Comparative analysis of ribosomal proteins in complete genomes: an example of reductive evolution at the domain-scale.*

Nucleic Acids Res., 30(24): 5382-5390.

2001:

Bahr A., Thompson J.D., Thierry J.C., Poch O. (2001) *BAlIiBASE (Benchmark alignment dataBASE): enhancements for repeats, transmembrane sequences and circular permutations.*

Nucleic Acids Res., 29 (1): 323-326.

Mayer C., Suck D. and Poch O. (2001) *A new component of the U3 snoRNP in Archaea: the U3 specific Imp4-related protein.*

Trends Biochem. Sci., 26 (3):143-4.

Lecompte O., Thompson J.D., Plewniak F., Thierry J.C. and Poch O. (2001) *Multiple alignment of complete sequences (MACS) in the post-genomic era.*

Gene, 270:17-30.

Lecompte O., Ripp R., Puzos-Barbe V., Duprat S., Heilig R., Dietrich J., Thierry J.C. and Poch O. (2001) *Genome evolution at the genus level : comparison of three complete genomes of hyperthermophilic Archaea.*

Genome Research, 11 (6): 981-993.

Wicker N., Perrin G.R., Thierry J.C. and Poch O. (2001) *Secator: a program for inferring*

protein subfamilies from phylogenetic trees.

Mol. Biol. Evol., 18 (8): 1435-41.

Thompson J.D., Plewniak F., Ripp R., J-C Thierry J.C. and Poch O. (2001) *Towards A Reliable Measure for Multiple Sequence Alignments*

J. Mol. Biol., 314 (4): 937-951

2000:

Gangloff Y.-G., Werten S., Romier C., Carré L., Poch O., Moras D. and Davidson I. (2000) *The human TFIID components TAFII135-TAFII20 and the yeast SAGA components ADA1-TAFII68 heterodimerise to form histone-like pairs*

Mol. Cell. Biol., 20(1): 340-351.

Plewniak F, Thompson JD, Poch O. (2000) *Ballast : blast post-processing based on locally conserved segments.*

Bioinformatics, 16(9): 750-759.

Thompson J.D., Plewniak F. and Poch O. (2000) *DbClustal : rapid and reliable global multiple alignments of protein sequences detected by database searches.*

Nucleic Acids Res., 28(15): 2919-2926.

1999:

Thompson J.D., Plewniak F. and Poch O. (1999) *BAlIiBASE: A benchmark alignment database for the evaluation of multiple sequence alignment programs.*

Bioinformatics, 15(1): 87-88.

Thompson J.D., Plewniak F. and Poch O. (1999) *A comprehensive comparison of protein sequence alignment programs.*

Nucleic Acids Res., 27(13): 2682-2690.

Lavigne A.C., Gangloff Y.-G., Carré L., Mengus G., Birck C., Poch O., Romier C., Moras D. and Davidson I. (1999) *Asynergistic transcriptional activation by TATA-binding protein and hTAFII28 requires specific amino acids of the hTAFII28 histone fold.*

Mol. Cell. Biol., 19(7): 5050-5060.

Dantonel J.C., Wurtz J.M., Poch O., Moras D. and Tora L. (1999) *The TBP-like factor τ : an alternative transcription factor in metazoa ?*

Trends Biochem. Sci., 24(9): 335-9.

1998:

Birck C., Poch O., Romier C., Ruff M., Mengus G., Lavigne A.C., Davidson I. and Moras D. (1998) *Human TAFII28 and TAFII18 interact through a canonical histone fold encoded by atypical evolutionary conserved sequence motifs also found in the SPT3 TAFII family.*

Cell, 94(2): 239-249.

1997:

Bordonne R., Camasses A., Madania A., Poch O., Tarassov I., Winsor B. and Martin R. (1997) *Analysis of a 35.6 kb region on the right arm of Saccharomyces cerevisiae chromosome XV.*

Yeast, 13(1): 73-83.

Dujon B, Albermann K, Aldea M, Alexandraki D, Ansorge W, Arino J, Benes V, Bohn C, Bolotin-Fukuhara M, Bordonne R, Boyer J, Camasses A, Casamayor A, Casas C, Cheret G, Cziepluch C, Daignan-Fornier B, Dang DV, de Haan M, Delius H, Durand P, Fairhead C, Feldmann H, Gaillon L, ...Poch O., ...and Kleine K, (1997) *The nucleotide sequence of Saccharomyces cerevisiae chromosome XV.*

Nature, 387(6632 Suppl): 98-102.

Friant S., Heyman T., Poch O., Wilhelm M. and Wilhelm F.X. (1997) *Sequence comparison of the Ty1 and Ty2 elements of the yeast genome supports the structural model of the tRNAⁱMet-Ty1 RNA reverse transcription initiation complex.*

Yeast, 13(7): 639-645.

Poch O. and Winsor B. (1997) *Who's who among the Saccharomyces cerevisiae actin-related proteins? A classification and nomenclature proposal for a large family.*

Yeast, 13(11): 1053-1058.

Poch O. (1997) *Conservation of a putative inhibitory domain in the GAL4 family members.*

Gene, 184(2): 229-235.

Poterszman A., Lamour V., Egly J.M., Moras D., Thierry J.C. and Poch O. (1997) *A eukaryotic XPB/ERCC3-like helicase in Mycobacterium leprae?*

Trends Biochem. Sci., 22(11): 418-419.

Before 1997:

Madania A., Poch O., Tarassov I., Winsor B. and Martin R. (1996) *Analysis of a 22,956 bp region on the right arm of Saccharomyces cerevisiae chromosome XV.*

Yeast, 12(15): 1563-1573.

Muller R., Poch O., Delarue M., Bishop D.H. and Bouloy M. (1994) *Rift Valley fever virus L segment: correction of the sequence and possible functional role of newly identified regions conserved in RNA-dependent polymerases.*

J. Gen. Virol., 75(6): 1345-1352.

De Murcia G., Schreiber V., Molinete M., Saulier B., Poch O., Masson M., Niedergang C. and Menissier-de Murcia J. (1994) *Structure and function of poly(ADP-ribose) polymerase.*

Mol. Cell. Biochem., 138(1-2): 15-24.

Poch O., Schwob E., de Fraipont F., Camasses A., Bordonne R. and Martin R.P. (1994) *RPK1, an essential yeast protein kinase involved in the regulation of the onset of mitosis, shows homology to mammalian dual-specificity kinases.*

Mol. Gen. Genet., 243(6): 641-653.

Simonin F., Poch O., Delarue M. and de Murcia G. (1993) *Identification of potential active-site*

residues in the human poly(ADP-ribose) polymerase.

J. Biol. Chem., 268(12): 8529-8535.

Poch O., L'Hote H., Dallery V., Debeaux F., Fleer R. and Sodoyer R. (1992) *Sequence of the Kluyveromyces lactis beta-galactosidase: comparison with prokaryotic enzymes and secondary structure analysis.*

Gene, 118(1): 55-63.

Poch O., Blumberg B.M., Bougueleret L. and Tordo N. (1990) *Sequence comparison of five polymerases (L proteins) of unsegmented negative-strand RNA viruses: theoretical assignment of functional domains.*

J. Gen. Virol., 71(5): 1153-1162.

Delarue M., Poch O., Tordo N., Moras D. and Argos P. (1990) *An attempt to unify the structure of polymerases.*

Protein Eng., 3(6): 461-467.

Schmitter D., Poch O., Zeder G., Heinrich G.F., Kocher H.P., Quesniaux V.F. and Van Regenmortel M.H. (1990) *Analysis of the structural diversity of monoclonal antibodies to cyclosporine.*

Mol. Immunol., 27(10): 1029-1038.

Simonin F., Menissier-de Murcia J., Poch O., Muller S., Gradwohl G., Molinete M., Penning C., Keith G. and de Murcia G. (1990) *Expression and site-directed mutagenesis of the catalytic domain of human poly(ADP-ribose)polymerase in Escherichia coli. Lysine 893 is critical for activity.*

J. Biol. Chem., 265(31): 19249-19256.

Eriani G., Delarue M., Poch O., Gangloff J. and Moras D. (1990) *Partition of tRNA synthetases into two classes based on mutually exclusive sets of sequence motifs.*

Nature, 347(6289): 203-206.

Poch O., Sauvaget I., Delarue M. and Tordo N. (1989) *Identification of four conserved motifs among the RNA-dependent polymerase encoding elements.*

EMBO J., 8(12): 3867-3874.

Poch O., Tordo N. and Keith G. (1988) *Sequence of the 3386 3' nucleotides of the genome of the AVO1 strain rabies virus: structural similarities in the protein regions involved in transcription.*

Biochimie, 70(8): 1019-1029.

Tordo N., Poch O., Ermine A., Keith G. and Rougeon F. (1988) *Completion of the rabies virus genome sequence determination: highly conserved domains among the L (polymerase) proteins of unsegmented negative-strand RNA viruses.*

Virology, 165(2): 565-576.

Tordo N., Poch O., Ermine A. and Keith G. (1986) *Primary structure of leader RNA and nucleoprotein genes of the rabies genome: segmented homology with VSV.*

Nucleic Acids Res., 14(6): 2671-2683.

Tordo N., Poch O., Ermine A., Keith G. and Rougeon F. (1986) *Walking along the rabies genome: is the large G-L intergenic region a remnant gene?*

Proc. Natl. Acad. Sci. U S A., 83(11): 3914-3918.

Tibayrenc M., Hoffmann A., Poch O., Echalar L., Le pont F., Lemesre J.L., Desjeux P. and Ayala F.J. (1986) *Additional data on Trypanosoma cruzi isozymic strains encountered in Bolivian domestic transmission cycles.*

Trans. R. Soc. Trop. Med. Hyg., 80(3): 442-447.

Tordo, N; Poch, O; Keith, G, Ermine A. (1985) *Primary structure of the rabies Pasteur virus genome*

Biological ChemistryHoppe-Seyler; 366 (9): 860-861.

Carrasco R.L., Breniere S.F., Poch O., Miguez H.V., Selaes H., Antezana G., Desjeux P., Carlier Y. (1985) *Chagas serology and its problems.*

Ann. Soc. Belg. Med. Trop., 65(1): 79-84.

Tibayrenc M., Cariou M.L., Solignac M., Delet J.P., Poch O. and Desjeux P. (1985) *New electrophoretic evidence of genetic variation and diploidy in Trypanosoma cruzi, the causative agent of Chagas' disease.*

Genetica, 67(3): 223-230.

Breniere S.F., Poch O., Selaes H., Tibayrenc M., Lemesre J.L., Antezana G. and Desjeux P.

(1984) *Specific humoral depression in chronic patients infected by Trypanosoma cruzi.*

Rev. Inst. Med. Trop. Sao Paulo, 26(5): 254-258.

Tibayrenc M., Echalar L., Dujardin J.P., Poch O. and Desjeux P. (1984) *The microdistribution of isoenzymic strains of Trypanosoma cruzi in southern Bolivia; new isoenzyme profiles and further arguments against Mendelian sexuality.*

Trans. R. Soc. Trop. Med. Hyg., 78(4): 519-525.