

BII – Gene Function Prediction Publications

***(Publications sorted: Newest – Oldest)*

1.	Sirota FL, Maurer-Stroh S, Li Z, Eisenhaber F, Eisenhaber B. Functional Classification of Super-Large Families of Enzymes Based on Substrate Binding Pocket Residues for Biocatalysis and Enzyme Engineering Applications. <i>Frontiers in Bioengineering and Biotechnology</i> , 2 Aug 2021, doi: 10.3389/fbioe.2021.701120, PMID: 34409021
2.	Eisenhaber B, Sinha S, Jadalanki CK, Shitov VA, Tan QW, Sirota FL, Eisenhaber F. Conserved sequence motifs in human TMTC1, TMTC2, TMTC3, and TMTC4, new Omannosyltransferases from the GT-C/PMT clan, are rationalized as ligand binding sites. <i>Biology Direct</i> 16, Article no 4, 2021, doi: 10.1186/s13062-021-00291-w
3.	Su TTC, Sinha S, Eisenhaber B, Eisenhaber F. Structural modelling of the luminal domain of human GPAA1, the metallo-peptide synthetase subunit of the transamidase complex, reveals zinc-binding mode and two flaps surrounding the active site. <i>Biology Direct</i> , 15, Article number: 14 (2020), doi: 10.1186/s13062-020-00266-3
4.	Goh F, Zhang MM, Lim TR, Low KN, Nge CE, Heng E, Yeo WL, Sirota FL, Crasta S, Tan Z, Ng V, Leong CY, Zhang H, Lezhava A, Chen SL, Hoon SS, Eisenhaber F, Eisenhaber B, Kanagasundaram Y, Wong FT, Ng SB (2020). Identification and engineering of 32 membered antifungal macrolactone notonesomycins. <i>Microbial Cell Factories</i> , 2020 Mar 19;19(1):71. doi: 10.1186/s12934-020-01328-x
5.	Zhang Z, Yu J, Eisenhaber F, Gao X, Gojobori T. (2019). In Memory of Vladimir B. Bajic (1952–2019). <i>Genomics Proteomics Bioinformatics</i> . 2019 Dec 12, doi: 10.1016/j.gpb.2019.12.001
6.	Toh YK, Shin J, Balakrishna AM, Kamariah N, Gruber A, Eisenhaber F, Eisenhaber B, Gruber G. (2019). Effect of the additional cysteine 503 of vancomycin-resistant Enterococcus faecalis (V583) alkylhydroperoxide reductase subunit F (AhpF) and the mechanism of AhpF and subunit C assembling. <i>Free Radical Biology and Medicine</i> , Vol. 138, July 2019, Pg 10-12, doi:10.1016/j.freeradbiomed.2019.04.036
7.	Tantoso E, Wong WC, Tay WH, Lee J, Sinha S, Eisenhaber B, Eisenhaber F (2019). Hypocrisy Around Medical Patient Data: Issues of Access for Biomedical Research, Data Quality, Usefulness for the Purpose and Omics Data as Game Changer. <i>Asian Bioethics Review</i> , Jun 2019, Vol. 11, Issue 2, pg 189-207, doi: 10.1007/s41649-019-00085-3
8.	Tay WH, Tantoso E, Eisenhaber F, Wong WC (2019). Translational Informatics Management System (TIMS): Towards OMICS based clinical data management for long term curation of clinical studies. <i>Journal of Open Source Software</i> , 2019, 4(40), 1533, DOI: 10.21105/joss.01533
9.	Niska-Blakie J, Gopinathan L, Low KN, Yang LK, Goh CMF, Caldez MJ, Pfeiffenberger E, Jones OS, Ong CB, Kurochkin IV, Coppola V, Tessarollo L, Choi H, Kanagasundaram Y, Eisenhaber F, Maurer-Stroh S, Kaldis P (2019). Knockout of the non-essential gene SUGCT creates diet-linked, age-related microbiome disbalance with a diabetes-like metabolic syndrome phenotype. <i>Cellular and Molecular Life Sciences</i> , 2019 Nov 13, doi: 10.1007/s00018-019-03359-z

10.	Sinha S, Nge CE, Leong CY, Ng V, Crasta S, Alfatah M, Goh F, Low KN, Zhang H, Arumugam P, Lezhava A, Chen SL, Yoganathan K, Ng SB, Eisenhaber F, Eisenhaber B. (2019). Genomics-driven discovery of a biosynthetic gene cluster required for the synthesis of BII-Rafflesfungin from the fungus <i>Phoma</i> sp. F3723. BMC Genomics 2019, 20:374, doi: 10.1186/s12864-019-5762-6
11.	Maurer-Stroh S, Krutz NL, Kern PS, Gunalan V, Nguyen MN, Limviphuvadh V, Eisenhaber F, Gerberick GF. (2018). AllerCatPro – Prediction of protein allergenicity potential from the protein sequence. Bioinformatics. 2019 Jan 18. doi: 10.1093/bioinformatics/btz029. [Epub ahead of print]
12.	Berger KA, Pigott DM, Tomlinson F, Godding D, Maurer-Stroh S, Taye B, Sirota FL, Han A, Lee RTC, Gunalan V, Eisenhaber F, Hay SI, Russell CA. (2018). The Geographic Variation of Surveillance and Zoonotic Spillover Potential of Influenza Viruses in Domestic Poultry and Swine. Open Forum Infect Dis. 2018 Nov 27;5(12):ofy318. doi: 10.1093/ofid/ofy318. eCollection 2018 Dec.
13.	Sinha S, Eisenhaber B, Jensen LJ, Kalbuaji B, Eisenhaber F. (2018). Darkness in the Human Gene and Protein Function Space: Widely Modest or Absent Illumination by the Life Science Literature and the Trend for Fewer Protein Function Discoveries Since 2000. Proteomics. 2018 Nov;18(21-22):e1800093. doi: 10.1002/pmic.201800093. Epub 2018 Oct 30.
14.	Kamariah N, Eisenhaber B, Eisenhaber F, Grüber G. (2018). Molecular mechanism of the <i>Escherichia coli</i> AhpC in the function of a chaperone under heat-shock conditions. Sci Rep. 2018 Sep 20;8(1):14151. doi: 10.1038/s41598-018-32527-7.
15.	Amit M, Na'ara S, Francis D, Matanis W, Zolotov S, Eisenhaber B, Eisenhaber F, Weiler Sagie M, Malkin L, Billan S, Charas T, Gil Z. (2018). Post-translational Regulation of Radioactive Iodine Therapy Response in Papillary Thyroid Carcinoma. J Natl Cancer Inst. 2017 Dec 1;109(12). doi: 10.1093/jnci/djx092.
16.	Ng SB, Kanagasundaram Y, Fan H, Arumugam P, Eisenhaber B, Eisenhaber F. (2018). The 160K Natural Organism Library, a unique resource for natural products research. Nat Biotechnol. 2018 Jul 6;36(7):570-573. doi: 10.1038/nbt.4187.
17.	Sirota FL, Goh F, Low KN, Yang LK, Crasta SC, Eisenhaber B, Eisenhaber F, Kanagasundaram Y, Ng SB. (2018). Isolation and Identification of an Anthracimycin Analogue from <i>Nocardiosis kunsanensis</i>, a Halophile from a Saltern, by Genomic Mining Strategy. J Genomics. 2018 May 21;6:63-73. doi: 10.7150/jgen.24368. eCollection 2018.
18.	Eisenhaber B, Sinha S, Wong WC, Eisenhaber F. (2018). Function of a membrane-embedded domain evolutionarily multiplied in the GPI lipid anchor pathway proteins PIG-B, PIG-M, PIG-U, PIG-W, PIG-V, and PIG-Z. Cell Cycle. 2018;17(7):874-880. doi: 10.1080/15384101.2018.1456294. Epub 2018 May 15.
19.	Limviphuvadh V, Tan CS, Konishi F, Jenjaroenpun P, Xiang JS, Kremenska Y, Mu YS, Syn N, Lee SC, Soo RA, Eisenhaber F, Maurer-Stroh S, Yong WP. (2018). Discovering novel SNPs that are correlated with patient outcome in a Singaporean cancer patient cohort treated with gemcitabine-based chemotherapy. BMC Cancer. 2018 May 11;18(1):555. doi: 10.1186/s12885-018-4471-x.
20.	Kamariah N, Eisenhaber B, Eisenhaber F, Grüber G. (2018). Active site Cp-loop dynamics

	modulate substrate binding, catalysis, oligomerization, stability, over-oxidation and recycling of 2-Cys Peroxiredoxins . Free Radic Biol Med. 2018 Apr;118:59-70. doi: 10.1016/j.freeradbiomed.2018.02.027. Epub 2018 Feb 21.
21.	Wong WC, Ng HK, Tantoso E, Soong R, Eisenhaber F. (2018). Finite-size effects in transcript sequencing count distribution: its power-law correction necessarily precedes downstream normalization and comparative analysis . Biol Direct. 2018 Feb 12;13(1):2. doi: 10.1186/s13062-018-0204-y.
22.	Toh YK, Balakrishna AM, Manimekalai MSS, Chionh BB, Seetharaman RRC, Eisenhaber F, Eisenhaber B, Grüber G. (2017). Novel insights into the vancomycin-resistant Enterococcus faecalis (V583) alkylhydroperoxide reductase subunit F . Biochim Biophys Acta Gen Subj. 2017 Dec;1861(12):3201-3214. doi: 10.1016/j.bbagen.2017.09.011. Epub 2017 Sep 19.
23.	Marakasova ES, Eisenhaber B, Maurer-Stroh S, Eisenhaber F, Baranova A. (2017). Prenylation of viral proteins by enzymes of the host: Virus-driven rationale for therapy with statins and FT/GGT1 inhibitors . Bioessays. 2017 Oct;39(10). doi: 10.1002/bies.201700014. Epub 2017 Sep 8. Review.
24.	Baker JA, Wong WC, Eisenhaber B, Warwicker J, Eisenhaber F. (2017). Erratum to: Charged residues next to transmembrane regions revisited: "Positive-inside rule" is complemented by the "negative inside depletion/outside enrichment rule" . BMC Biol. 2017 Aug 18;15(1):72. doi: 10.1186/s12915-017-0410-6. No abstract available.
25.	Baker JA, Wong WC, Eisenhaber B, Warwicker J, Eisenhaber F. (2017). Charged residues next to transmembrane regions revisited: "Positive-inside rule" is complemented by the "negative inside depletion/outside enrichment rule" . BMC Biol. 2017 Jul 24;15(1):66. doi: 10.1186/s12915-017-0404-4. Erratum in: BMC Biol. 2017 Aug 18;15(1):72.
26.	Taye B, Vaz C, Tanavde V, Kuznetsov VA, Eisenhaber F, Sugrue RJ, Maurer-Stroh S. (2017). Benchmarking selected computational gene network growing tools in context of virus-host interactions . Sci Rep. 2017 Jul 19;7(1):5805. doi: 10.1038/s41598-017-06020-6.
27.	Kamariah N, Eisenhaber B, Eisenhaber F, Grüber G. (2017). Essential role of the flexible linker on the conformational equilibrium of bacterial peroxiredoxin reductase for effective regeneration of peroxiredoxin . J Biol Chem. 2017 Apr 21;292(16):6667-6679. doi: 10.1074/jbc.M117.775858. Epub 2017 Mar 7.
28.	Lua WH, Ling WL, Su CT, Yeo JY, Verma CS, Eisenhaber B, Eisenhaber F, Gan SK. (2017). Discovery of a novel splice variant of Fcar (CD89) unravels sequence segments necessary for efficient secretion: A story of bad signal peptides and good ones that nevertheless do not make it . Cell Cycle. 2017 Mar 4;16(5):457-467. doi: 10.1080/15384101.2017.1281480. Epub 2017 Jan 19.
29.	Kurochkin IV, Guarnera E, Wong JH, Eisenhaber F, Berezovsky IN. (2017). Toward Allosterically Increased Catalytic Activity of Insulin-Degrading Enzyme against Amyloid Peptides . Biochemistry. 2017 Jan 10;56(1):228-239. doi: 10.1021/acs.biochem.6b00783. Epub 2016 Dec 16.
30.	Yap CK, Eisenhaber B, Eisenhaber F, Wong WC. (2016). xHMMER3x2: Utilizing HMMER3's speed and HMMER2's sensitivity and specificity in the glocal alignment mode

	for improved large-scale protein domain annotation . Biol Direct. 2016 Nov 29;11(1):63.
31.	Kamariah N, Sek MF, Eisenhaber B, Eisenhaber F, Grüber G. (2016). Transition steps in peroxide reduction and a molecular switch for peroxide robustness of prokaryotic peroxiredoxins . Sci Rep. 2016 Nov 28;6:37610. doi: 10.1038/srep37610.
32.	Berezovsky IN, Guarnera E, Zheng Z, Eisenhaber B, Eisenhaber F. (2016). Protein function machinery: from basic structural units to modulation of activity . Curr Opin Struct Biol. 2017 Feb;42:67-74. doi: 10.1016/j.sbi.2016.10.021. Epub 2016 Nov 16. Review.
33.	Prabha R, Singh DP, Sinha S, Ahmad K, Rai A. (2016). Genome-wide comparative analysis of codon usage bias and codon context patterns among cyanobacterial genomes . Mar Genomics. 2017 Apr;32:31-39. doi: 10.1016/j.margen.2016.10.001. Epub 2016 Oct 10.
34.	Kulemzina I, Ang K, Zhao X, Teh JT, Verma V, Suranthran S, Chavda AP, Huber RG, Eisenhaber B, Eisenhaber F, Yan J, Ivanov D. (2016). A Reversible Association between Smc Coiled Coils Is Regulated by Lysine Acetylation and Is Required for Cohesin Association with the DNA . Mol Cell. 2016 Sep 15;63(6):1044-54. doi: 10.1016/j.molcel.2016.08.008. Epub 2016 Sep 8.
35.	Eisenhaber B, Kuchibhatla D, Sherman W, Sirota FL, Berezovsky IN, Wong WC, Eisenhaber F. (2016). The Recipe for Protein Sequence-Based Function Prediction and Its Implementation in the ANNOTATOR Software Environment . Methods Mol Biol. 2016;1415:477-506. doi: 10.1007/978-1-4939-3572-7_25.
36.	Kamariah N, Nartey W, Eisenhaber B, Eisenhaber F, Grüber G. (2015). Low resolution solution structure of an enzymatic active AhpC10:AhpF2 ensemble of the Escherichia coli Alkyl hydroperoxide Reductase . J Struct Biol. 2016 Jan;193(1):13-22. doi: 10.1016/j.jsb.2015.11.004. Epub 2015 Nov 14.
37.	Sherman WA, Kuchibhatla DB, Limviphuvadh V, Maurer-Stroh S, Eisenhaber B, Eisenhaber F. (2015). HPMV: human protein mutation viewer - relating sequence mutations to protein sequence architecture and function changes . J Bioinform Comput Biol. 2015 Oct;13(5):1550028. doi: 10.1142/S0219720015500286. Epub 2015 Oct 27.
38.	Nartey W, Basak S, Kamariah N, Manimekalai MS, Robson S, Wagner G, Eisenhaber B, Eisenhaber F, Grüber G. (2015). NMR studies reveal a novel grab and release mechanism for efficient catalysis of the bacterial 2-Cys peroxiredoxin machinery . FEBS J. 2015 Dec;282(23):4620-38. doi: 10.1111/febs.13522. Epub 2015 Oct 16.
39.	Wong WC, Yap CK, Eisenhaber B, Eisenhaber F. (2015). dissectHMMER: a HMMER-based score dissection framework that statistically evaluates fold-critical sequence segments for domain fold similarity . Biol Direct. 2015 Aug 1;10:39. doi: 10.1186/s13062-015-0068-3.
40.	Kamariah N, Manimekalai MS, Nartey W, Eisenhaber F, Eisenhaber B, Grüber G. (2015). Crystallographic and solution studies of NAD(+)- and NADH-bound alkylhydroperoxide reductase subunit F (AhpF) from Escherichia coli provide insight into sequential enzymatic steps . Biochim Biophys Acta. 2015 Oct;1847(10):1139-52. doi: 10.1016/j.bbabi.2015.06.011. Epub 2015 Jun 17.
41.	Sirota FL, Maurer-Stroh S, Eisenhaber B, Eisenhaber F. (2015). Single-residue posttranslational modification sites at the N-terminus, C-terminus or in-between: To be

	or not to be exposed for enzyme access . Proteomics. 2015 Jul;15(14):2525-46. doi: 10.1002/pmic.201400633.
42.	Mah TL, Yap XN, Limviphuvadh V, Li N, Sridharan S, Kuralmani V, Feng M, Liem N, Adhikari S, Yong WP, Soo RA, Maurer-Stroh S, Eisenhaber F, Tong JC. (2014). Novel SNP improves differential survivability and mortality in non-small cell lung cancer patients . BMC Genomics. 2014;15 Suppl 9:S20. doi: 10.1186/1471-2164-15-S9-S20. Epub 2014 Dec 8.
43.	Dip PV, Kamariah N, Subramanian Manimekalai MS, Nartey W, Balakrishna AM, Eisenhaber F, Eisenhaber B, Grüber G. (2014). Structure, mechanism and ensemble formation of the alkylhydroperoxide reductase subunits AhpC and AhpF from Escherichia coli . Acta Crystallogr D Biol Crystallogr. 2014 Nov;70(Pt 11):2848-62. doi: 10.1107/S1399004714019233. Epub 2014 Oct 16.
44.	Dip PV, Kamariah N, Nartey W, Beushausen C, Kostyuchenko VA, Ng TS, Lok SM, Saw WG, Eisenhaber F, Eisenhaber B, Grüber G. (2014). Key roles of the Escherichia coli AhpC C-terminus in assembly and catalysis of alkylhydroperoxide reductase, an enzyme essential for the alleviation of oxidative stress . Biochim Biophys Acta. 2014 Dec;1837(12):1932-1943. doi: 10.1016/j.bbabi.2014.08.007.
45.	Maurer-Stroh S, Li Y, Bastien N, Gunalan V, Lee RT, Eisenhaber F, Booth TF. (2014). Potential human adaptation mutation of influenza A(H5N1) virus, Canada . Emerg Infect Dis. 2014 Sep;20(9):1580-2. doi: 10.3201/eid2009.140240
46.	Eisenhaber F. (2014). Unix interfaces, Kleisli, bucardin structure, etc. -- the heroic beginning of bioinformatics in Singapore . J Bioinform Comput Biol. 2014 Jun;12(3):1471002. doi: 10.1142/S0219720014710024. Epub 2014 Jun 5.
47.	Eisenhaber F, Sherman WA. (2014). 10 years for the Journal of Bioinformatics and Computational Biology (2003-2013) -- a retrospective . J Bioinform Comput Biol. 2014 Jun;12(3):1471001. doi: 10.1142/S0219720014710012. Epub 2014 May 21.
48.	Wong WC, Maurer-Stroh S, Eisenhaber B, Eisenhaber F. (2014). On the necessity of dissecting sequence similarity scores into segment-specific contributions for inferring protein homology, function prediction and annotation . BMC Bioinformatics. 2014 Jun 2;15:166. doi: 10.1186/1471-2105-15-166.
49.	Eisenhaber B, Eisenhaber S, Kwang TY, Grüber G, Eisenhaber F. (2014). Transamidase subunit GAA1/GPAA1 is a M28 family metallo-peptide-synthetase that catalyzes the peptide bond formation between the substrate protein's omega-site and the GPI lipid anchor's phosphoethanolamine . Cell Cycle. 2014;13(12):1912-7. doi: 10.4161/cc.28761. Epub 2014 Apr 17.
50.	Eisenhaber F, Sung WK, Wong L. (2013). International Conference on Genome Informatics (GIW 2013) in Singapore: Introduction to the systems biology contributions . BMC Syst Biol. 2013;7 Suppl 6:I1. doi: 10.1186/1752-0509-7-S6-I1. Epub 2013 Dec 13.
51.	Ma J, Eisenhaber F, Maurer-Stroh S. (2013). Automatic phylogenetic classification of bacterial beta-lactamase sequences including structural and antibiotic substrate preference information . J Bioinform Comput Biol. 2013 Dec;11(6):1343011. doi: 10.1142/S0219720013430117. Epub 2013 Dec 11.
52.	Maurer-Stroh S, Gunalan V, Wong WC, Eisenhaber F. (2013). A simple shortcut to

	unsupervised alignment-free phylogenetic genome groupings, even from unassembled sequencing reads . J Bioinform Comput Biol. 2013 Dec;11(6):1343005. doi: 10.1142/S0219720013430051. Epub 2013
53.	Eisenhaber F, Sung WK, Wong L. (2014). Guest Editorial for the International Conference on Genome Informatics (GIW 2013) . IEEE/ACM Trans Comput Biol Bioinform. 2014 Jan-Feb;11(1):5-6. No abstract available.
54.	Van TD, Tran N, Le L, Eisenhaber F. (2016). A Perspective on Rational Designs of a Hemagglutinin Based Universal Influenza Vaccine . Curr Pharm Des. 2016 Apr 19. [Epub ahead of print].
55.	Lee RT, Gunalan V, Van TD, Le LT, Eisenhaber F, Maurer-Stroh S. (2013). A new piece in the puzzle of the novel avian-origin influenza A (H7N9) virus . Biol Direct. 2013 Oct 26;8:26. doi: 10.1186/1745-6150-8-26.
56.	Kuchibhatla DB, Sherman WA, Chung BY, Cook S, Schneider G, Eisenhaber B, Karlin DG. (2013). Powerful sequence similarity search methods and in-depth manual analyses can identify remote homologs in many apparently "orphan" viral proteins . J Virol. 2014 Jan;88(1):10-20. doi: 10.1128/JVI.02595-13. Epub 2013 Oct 23.
57.	Marakasova ES, Akhmatova NK, Amaya M, Eisenhaber B, Eisenhaber F, van Hoek ML, Baranova AV. (2013). [Prenylation: from bacteria to eukaryotes] . Mol Biol (Mosk). 2013 Sep-Oct;47(5):717-30. Review. Russian.
58.	Plasman K, Maurer-Stroh S, Ahmad J, Hao H, Kaiserman D, Sirota FL, Jonckheere V, Bird PI, Gevaert K, Van Damme P. (2013). Conservation of the extended substrate specificity profiles among homologous granzymes across species . Mol Cell Proteomics. 2013 Oct;12(10):2921-34. doi: 10.1074/mcp.M113.028670. Epub 2013 Jun 20.
59.	Goncearenco A, Mitternacht S, Yong T, Eisenhaber B, Eisenhaber F, Berezovsky IN. (2013). SPACER: Server for predicting allosteric communication and effects of regulation . Nucleic Acids Res. 2013 Jul;41(Web Server issue):W266-72. doi: 10.1093/nar/gkt460. Epub 2013 Jun 3.
60.	Maurer-Stroh S, Lee RT, Gunalan V, Eisenhaber F. (2013). The highly pathogenic H7N3 avian influenza strain from July 2012 in Mexico acquired an extended cleavage site through recombination with host 28S rRNA . Virol J. 2013 May 1;10:139. doi: 10.1186/1743-422X-10-139.
61.	Saw WG, Eisenhaber B, Eisenhaber F, Grüber G. (2013). Low-resolution structure of the soluble domain GPAA1 (yGPAA170-247) of the glycosylphosphatidylinositol transamidase subunit GPAA1 from Saccharomyces cerevisiae . Biosci Rep. 2013 Mar 28;33(2):e00033. doi: 10.1042/BSR20120107.
62.	Maurer-Stroh S, Gao H, Han H, Baeten L, Schymkowitz J, Rousseau F, Zhang L, Eisenhaber F. (2013). Motif discovery with data mining in 3D protein structure databases: discovery, validation and prediction of the U-shape zinc binding ("Huf-Zinc") motif . J Bioinform Comput Biol. 2013 Feb;11(1):1340008. doi: 10.1142/S0219720013400088. Epub 2013 Jan 16.
63.	Kuznetsov V, Lee HK, Maurer-Stroh S, Molnár MJ, Pongor S, Eisenhaber B, Eisenhaber F. (2013). How bioinformatics influences health informatics: usage of biomolecular sequences, expression profiles and automated microscopic image analyses for clinical

	needs and public health . Health Inf Sci Syst. 2013 Jan 10;1:2. doi: 10.1186/2047-2501-1-2. eCollection 2013. Review.
64.	Sirota FL, Batagov A, Schneider G, Eisenhaber B, Eisenhaber F, Maurer-Stroh S. (2012). Beware of moving targets: reference proteome content fluctuates substantially over the years . J Bioinform Comput Biol. 2012 Dec;10(6):1250020. doi: 10.1142/S0219720012500205. Epub 2012 Aug 7.
65.	Eisenhaber F. (2012). A decade after the first full human genome sequencing: when will we understand our own genome? J Bioinform Comput Biol. 2012 Oct;10(5):1271001. doi: 10.1142/S0219720012710011. Epub 2012 Jun 22.
66.	Wong WC, Maurer-Stroh S, Schneider G, Eisenhaber F. (2012). Transmembrane helix: simple or complex . Nucleic Acids Res. 2012 Jul;40(Web Server issue):W370-5. doi: 10.1093/nar/gks379. Epub 2012 May 7.
67.	Tan J, Kuchibhatla D, Sirota FL, Sherman WA, Gattermayer T, Kwoh CY, Eisenhaber F, Schneider G, Maurer-Stroh S. (2012). Tachyon search speeds up retrieval of similar sequences by several orders of magnitude . Bioinformatics. 2012 Jun 15;28(12):1645-6. doi: 10.1093/bioinformatics/bts197. Epub 2012 Apr 23.
68.	Romeo A, Sonnleitner E, Sorger-Domenigg T, Nakano M, Eisenhaber B, Bläsi U. (2012). Transcriptional regulation of nitrate assimilation in Pseudomonas aeruginosa occurs via transcriptional antitermination within the nirBD-PA1779-cobA operon . Microbiology. 2012 Jun;158(Pt 6):1543-52. doi: 10.1099/mic.0.053850-0. Epub 2012 Apr 5.
69.	Eisenhaber B, Sammer M, Lua WH, Benetka W, Liew LL, Yu W, Lee HK, Koranda M, Eisenhaber F, Adhikari S. (2011). Nuclear import of a lipid-modified transcription factor: mobilization of NFAT5 isoform a by osmotic stress . Cell Cycle. 2011 Nov 15;10(22):3897-911. doi: 10.4161/cc.10.22.18043. Epub 2011 Nov 15.
70.	Kunze M, Neuberger G, Maurer-Stroh S, Ma J, Eck T, Braverman N, Schmid JA, Eisenhaber F, Berger J. (2011). Structural requirements for interaction of peroxisomal targeting signal 2 and its receptor PEX7 . J Biol Chem. 2011 Dec 30;286(52):45048-62. doi: 10.1074/jbc.M111.301853. Epub 2011 Nov 5.
71.	Wong WC, Maurer-Stroh S, Eisenhaber F. (2011). Not all transmembrane helices are born equal: Towards the extension of the sequence homology concept to membrane proteins . Biol Direct. 2011 Oct 25;6:57. doi: 10.1186/1745-6150-6-57.
72.	Kamariah N, Eisenhaber F, Adhikari S, Eisenhaber B, Grüber G. (2011). Purification and crystallization of yeast glycosylphosphatidylinositol transamidase subunit PIG-S (PIG-S(71-467)) . B Acta Crystallogr Sect F Struct Biol Cryst Commun. 2011 Aug 1;67(Pt 8):896-9. doi: 10.1107/S1744309111024080. Epub 2011 Jul 19.
73.	Dellago H, Löscher M, Ajuh P, Ryder U, Kaisermayer C, Grillari-Voglauer R, Fortschegger K, Gross S, Gstraunthaler A, Borth N, Eisenhaber F, Lamond AI, Grillari J. (2011). Exo70, a subunit of the exocyst complex, interacts with SNEV(hPrp19/hPso4) and is involved in pre-mRNA splicing . Biochem J. 2011 Aug 15;438(1):81-91. doi: 10.1042/BJ20110183.
74.	Wong WC, Maurer-Stroh S, Eisenhaber F. (2011). The Janus-faced E-values of HMMER2: extreme value distribution or logistic function? J Bioinform Comput Biol. 2011 Feb;9(1):179-206.

75.	Prokesch A, Bogner-Strauss JG, Hackl H, Rieder D, Neuhold C, Walenta E, Krogsdam A, Scheideler M, Papak C, Wong WC, Vinson C, Eisenhaber F, Trajanoski Z. (2010). Arxes: retrotransposed genes required for adipogenesis . Nucleic Acids Res. 2011 Apr;39(8):3224-39. doi: 10.1093/nar/gkq1289. Epub 2010 Dec 21.
76.	Toh YK, Kamariah N, Maurer-Stroh S, Roessle M, Eisenhaber F, Adhikari S, Eisenhaber B, Grüber G. (2010). Structural insight into the glycosylphosphatidylinositol transamidase subunits PIG-K and PIG-S from yeast . J Struct Biol. 2011 Feb;173(2):271-81. doi: 10.1016/j.jsb.2010.11.026. Epub 2010 Dec 4.
77.	Lee VJ, Yap J, Maurer-Stroh S, Lee RT, Eisenhaber F, Tay JK, Ting PJ, Loh JP, Wong CW, Tan BH, Koay ES, Kelly PM, Hibberd ML. (2010). Investigation of causes of oseltamivir chemoprophylaxis failures during influenza A (H1N1-2009) outbreaks . J Clin Virol. 2011 Feb;50(2):104-8. doi: 10.1016/j.jcv.2010.10.004. Epub 2010 Nov 19.
78.	Lee RT, Santos CL, de Paiva TM, Cui L, Sirota FL, Eisenhaber F, Maurer-Stroh S. (2010). All that glitters is not gold--founder effects complicate associations of flu mutations to disease severity . Virol J. 2010 Nov 1;7:297. doi: 10.1186/1743-422X-7-297.
79.	Maurer-Stroh S, Paing SS, Lee RT, Eisenhaber F. (2010). Sporadic human cases of swine-origin influenza before 2009 share the Sa epitope . Cell Cycle. 2010 Sep 15;9(18):3826-8. doi: 10.4161/cc.9.18.13166. Epub 2010 Sep 26
80.	Dhir S, Pacurar M, Franklin D, Gáspári Z, Kertész-Farkas A, Kocsor A, Eisenhaber F, Pongor S. (2010). Detecting atypical examples of known domain types by sequence similarity searching: the SBASE domain library approach . Curr Protein Pept Sci. 2010 Nov;11(7):538-49. Review.
81.	Limviphuvadh V, Chua LL, Rahim RA, Eisenhaber F, Maurer-Stroh S, Adhikari S. (2010). Similarity of molecular phenotype between known epilepsy gene LGI1 and disease candidate gene LGI2 . BMC Biochem. 2010 Sep 24;11:39. doi: 10.1186/1471-2091-11-39.
82.	Wong WC, Maurer-Stroh S, Eisenhaber F. (2010). More than 1,001 problems with protein domain databases: transmembrane regions, signal peptides and the issue of sequence homology . PLoS Comput Biol. 2010 Jul 29;6(7):e1000867. doi: 10.1371/journal.pcbi.1000867.
83.	Bogner-Strauss JG, Prokesch A, Sanchez-Cabo F, Rieder D, Hackl H, Duszka K, Krogsdam A, Di Camillo B, Walenta E, Klatzer A, Lass A, Pinent M, Wong WC, Eisenhaber F, Trajanoski Z. (2010). Reconstruction of gene association network reveals a transmembrane protein required for adipogenesis and targeted by PPARγ . Cell Mol Life Sci. 2010 Dec;67(23):4049-64. doi: 10.1007/s00018-010-0424-5. Epub 2010 Jun 15.
84.	Van Damme P, Maurer-Stroh S, Hao H, Colaert N, Timmerman E, Eisenhaber F, Vandekerckhove J, Gevaert K. (2010). The substrate specificity profile of human granzyme A . Biol Chem. 2010 Aug;391(8):983-97. doi: 10.1515/BC.2010.096.
85.	Maurer-Stroh S, Lee RT, Eisenhaber F, Cui L, Phuah SP, Lin RT. (2010). A new common mutation in the hemagglutinin of the 2009 (H1N1) influenza A virus . PLoS Curr. 2010 Jun 1;2:RRN1162.
86.	Eisenhaber B, Eisenhaber F. (2010). Prediction of posttranslational modification of proteins from their amino acid sequence . Methods Mol Biol. 2010;609:365-84. doi:

	10.1007/978-1-60327-241-4_21. Review.
87.	Schneider G, Wildpaner M, Sirota FL, Maurer-Stroh S, Eisenhaber B, Eisenhaber F. (2010). Integrated tools for biomolecular sequence-based function prediction as exemplified by the ANNOTATOR software environment. <i>Methods Mol Biol.</i> 2010;609:257-67. doi: 10.1007/978-1-60327-241-4_15.
88.	Ooi HS, Schneider G, Chan YL, Lim TT, Eisenhaber B, Eisenhaber F. (2010). Databases of protein-protein interactions and complexes. <i>Methods Mol Biol.</i> 2010;609:145-59. doi: 10.1007/978-1-60327-241-4_9. Review.
89.	Ooi HS, Schneider G, Lim TT, Chan YL, Eisenhaber B, Eisenhaber F. (2010). Biomolecular pathway databases. <i>Methods Mol Biol.</i> 2010;609:129-44. doi: 10.1007/978-1-60327-241-4_8. Review.
90.	Sirota FL, Ooi HS, Gattermayer T, Schneider G, Eisenhaber F, Maurer-Stroh S. (2010). Parameterization of disorder predictors for large-scale applications requiring high specificity by using an extended benchmark dataset. <i>BMC Genomics.</i> 2010 Feb 10;11 Suppl 1:S15. doi: 10.1186/1471-2164-11-S1-S15.
91.	Mujezinovic N, Schneider G, Wildpaner M, Mechtler K, Eisenhaber F. (2010). Reducing the haystack to find the needle: improved protein identification after fast elimination of non-interpretable peptide MS/MS spectra and noise reduction. <i>BMC Genomics.</i> 2010 Feb 10;11 Suppl 1:S13. doi: 10.1186/1471-2164-11-S1-S13.
92.	Limviphuvadh V, Chua LL, Eisenhaber F, Adhikari S, Maurer-Stroh S. (2010). Is LGI2 the candidate gene for partial epilepsy with pericentral spikes? <i>J Bioinform Comput Biol.</i> 2010 Feb;8(1):117-27.
93.	Kawase-Koga Y, Low R, Otaegi G, Pollock A, Deng H, Eisenhaber F, Maurer-Stroh S, Sun T. (2010). RNAase-III enzyme Dicer maintains signaling pathways for differentiation and survival in mouse cortical neural stem cells. <i>J Cell Sci.</i> 2010 Feb 15;123(Pt 4):586-94. doi: 10.1242/jcs.059659. Epub 2010 Jan 26.
94.	Kawase-Koga Y, Low R, Otaegi G, Pollock A, Deng H, Eisenhaber F, Maurer-Stroh S, Sun T, Ranganathan S, Eisenhaber F, Tong JC, Tan TW. (2009). Extending Asia Pacific bioinformatics into new realms in the "-omics" era. <i>BMC Genomics.</i> 2009 Dec 3;10 Suppl 3:S1. doi: 10.1186/1471-2164-10-S3-S1.
95.	Tse WK, Eisenhaber B, Ho SH, Ng Q, Eisenhaber F, Jiang YJ. (2009). Genome-wide loss-of-function analysis of deubiquitylating enzymes for zebrafish development. <i>BMC Genomics.</i> 2009 Dec 30;10:637. doi: 10.1186/1471-2164-10-637.
96.	Eisenhaber F, Kwoh CK, Ng SK, Sung WK, Wong L. (2009). Brief overview of bioinformatics activities in Singapore. <i>PLoS Comput Biol.</i> 2009 Sep;5(9):e1000508. doi: 10.1371/journal.pcbi.1000508. Epub 2009 Sep 25. No abstract available. Erratum in: <i>PLoS Comput Biol.</i> 2009 Nov;5(11). doi: 10.1371/annotation/5d07cf0b-75f8-4452-a932-46574f5faf3f. Sung, Wing-King [corrected to Sung, Wing-Kin].
97.	Grillari J, Löscher M, Denegri M, Lee K, Fortschegger K, Eisenhaber F, Ajuh P, Lamond AI, Katinger H, Grillari-Voglauer R. (2009). Blom7alpha is a novel heterogeneous nuclear ribonucleoprotein K homology domain protein involved in pre-mRNA splicing that interacts with SNEVPrp19-Pso4. <i>J Biol Chem.</i> 2009 Oct 16;284(42):29193-204. doi: 10.1074/jbc.M109.036632. Epub 2009 Jul 29.

98.	Maurer-Stroh S, Ma J, Lee RT, Sirota FL, Eisenhaber F. (2009). Mapping the sequence mutations of the 2009 H1N1 influenza A virus neuraminidase relative to drug and antibody binding sites. Biol Direct. 2009 May 20;4:18; discussion 18. doi: 10.1186/1745-6150-4-18.
99.	Ooi HS, Kwo CY, Wildpaner M, Sirota FL, Eisenhaber B, Maurer-Stroh S, Wong WC, Schleiffer A, Eisenhaber F, Schneider G. (2009). ANNIE: integrated de novo protein sequence annotation. Nucleic Acids Res. 2009 Jul;37(Web Server issue):W435-40. doi: 10.1093/nar/gkp254. Epub 2009 Apr 23.
100.	Roser M, Eibl N, Eisenhaber B, Seringer J, Nagel M, Nagorka S, Luft FC, Frei U, Gollasch M. (2009). Gitelman syndrome. Hypertension. 2009 Jun;53(6):893-7. doi: 10.1161/HYPERTENSIONAHA.108.127993. Epub 2009 Apr.
101.	Dhar PK, Thwin CS, Tun K, Tsumoto Y, Maurer-Stroh S, Eisenhaber F, Surana U. (2009). Synthesizing non-natural parts from natural genomic template. J Biol Eng. 2009 Feb 3;3:2. doi: 10.1186/1754-1611-3-2.
102.	Benetka W, Mehlmer N, Maurer-Stroh S, Sammer M, Koranda M, Neumüller R, Betschinger J, Knoblich JA, Teige M, Eisenhaber F. (2008). Experimental testing of predicted myristoylation targets involved in asymmetric cell division and calcium-dependent signalling. Cell Cycle. 2008 Dec;7(23):3709-19. Epub 2008 Dec 13. Erratum in: Cell Cycle. 2009 Feb 1;8(3):508-9.
103.	Malevanets A, Sirota FL, Wodak SJ. (2008). Mechanism and energy landscape of domain swapping in the B1 domain of protein G. J Mol Biol. 2008 Sep 26;382(1):223-35. doi: 10.1016/j.jmb.2008.06.025. Epub 2008 Jun 17.
104.	Wong WC, Loh M, Eisenhaber F. (2008). On the necessity of different statistical treatment for Illumina BeadChip and Affymetrix GeneChip data and its significance for biological interpretation. Biol Direct. 2008 Jun 3;3:23. doi: 10.1186/1745-6150-3-23.
105.	Sirota FL, Héry-Huynh S, Maurer-Stroh S, Wodak SJ. (2008). Role of the amino acid sequence in domain swapping of the B1 domain of protein G. Proteins. 2008 Jul;72(1):88-104. doi: 10.1002/prot.21901.
106.	Eisenhaber B, Eisenhaber F. (2007). Posttranslational modifications and subcellular localization signals: indicators of sequence regions without inherent 3D structure? Curr Protein Pept Sci. 2007 Apr;8(2):197-203. Review.
107.	Maurer-Stroh S, Koranda M, Benetka W, Schneider G, Sirota FL, Eisenhaber F. (2007). Towards complete sets of farnesylated and geranylgeranylated proteins. PLoS Comput Biol. 2007 Apr 6;3(4):e66. Epub 2007 Feb 23.
108.	Eisenhaber B, Chumak N, Eisenhaber F, Hauser MT. (2007). The ring between ring fingers (RBR) protein family. Genome Biol. 2007;8(3):209. Review.
109.	Neuberger G, Schneider G, Eisenhaber F. (2006). pkaPS: prediction of protein kinase A phosphorylation sites with the simplified kinase-substrate binding model. Biol Direct. 2007 Jan 12;2:1.
110.	Mujezinovic N, Raidl G, Hutchins JR, Peters JM, Mechtler K, Eisenhaber F. (2006). Cleaning of raw peptide MS/MS spectra: improved protein identification following deconvolution of multiply charged peaks, isotope clusters, and removal of background noise. Proteomics. 2006 Oct;6(19):5117-31.

111.	Novatchkova M, Schneider G, Fritz R, Eisenhaber F, Schleiffer A. (2006). DOUfinder-- identification of distant domain outliers using subsignificant sequence similarity . Nucleic Acids Res. 2006 Jul 1;34(Web Server issue):W214-8.
112.	Watrin E, Schleiffer A, Tanaka K, Eisenhaber F, Nasmyth K, Peters JM. (2006). Human Scc4 is required for cohesin binding to chromatin, sister-chromatid cohesion, and mitotic progression . Curr Biol. 2006 May 9;16(9):863-74.
113.	Schneider G, Neuberger G, Wildpaner M, Tian S, Berezovsky I, Eisenhaber F. (2006). Application of a sensitive collection heuristic for very large protein families: evolutionary relationship between adipose triglyceride lipase (ATGL) and classic mammalian lipases . BMC Bioinformatics. 2006 Mar 21;7:164.
114.	Benetka W, Koranda M, Maurer-Stroh S, Pittner F, Eisenhaber F. (2006). Farnesylation or geranylgeranylation? Efficient assays for testing protein prenylation in vitro and in vivo . BMC Biochem. 2006 Feb 28;7:6.
115.	Hackl H, Burkard TR, Sturn A, Rubio R, Schleiffer A, Tian S, Quackenbush J, Eisenhaber F, Trajanoski Z. (2005). Molecular processes during fat cell development revealed by gene expression profiling and functional annotation . Genome Biol. 2005;6(13):R108. Epub 2005 Dec 19.
116.	Grillari J, Ajuh P, Stadler G, Löscher M, Voglauer R, Ernst W, Chusainow J, Eisenhaber F, Pokar M, Fortschegger K, Grey M, Lamond AI, Katinger H. (2005). SNEV is an evolutionarily conserved splicing factor whose oligomerization is necessary for spliceosome assembly . Nucleic Acids Res. 2005 Dec 6;33(21):6868-83. Print 2005.
117.	Novatchkova M, Wildpaner M, Schweizer D, Eisenhaber F. (2005). PhyloDome-- visualization of taxonomic distributions of domains occurring in eukaryote protein sequence sets . Nucleic Acids Res. 2005 Jul 1;33(Web Server issue):W121-5.
118.	Maurer-Stroh S, Eisenhaber F. (2005). Refinement and prediction of protein prenylation motifs . Genome Biol. 2005;6(6):R55. Epub 2005 May 27.
119.	Kraft C, Vodermaier HC, Maurer-Stroh S, Eisenhaber F, Peters JM. (2005). The WD40 propeller domain of Cdh1 functions as a destruction box receptor for APC/C substrates . Mol Cell. 2005 May 27;18(5):543-53.
120.	O'Connor E, Eisenhaber B, Dalley J, Wang T, Missen C, Bulleid N, Bishop PN, Trump D. (2005). Species specific membrane anchoring of nyctalopin, a small leucine-rich repeat protein . Hum Mol Genet. 2005 Jul 1;14(13):1877-87. Epub 2005 May 19.
121.	Novatchkova M, Bachmair A, Eisenhaber B, Eisenhaber F. (2005). Proteins with two SUMO-like domains in chromatin-associated complexes: the RENi (Rad60-Esc2-NIP45) family . BMC Bioinformatics. 2005 Feb 7;6:22.
122.	Betschinger J, Eisenhaber F, Knoblich JA. (2005). Phosphorylation-induced autoinhibition regulates the cytoskeletal protein Lethal (2) giant larvae . Curr Biol. 2005 Feb 8;15(3):276-82.
123.	Neuberger G, Kunze M, Eisenhaber F, Berger J, Hartig A, Brocard C. (2004). Hidden localization motifs: naturally occurring peroxisomal targeting signals in non-peroxisomal proteins . Genome Biol. 2004;5(12):R97. Epub 2004 Nov 30.
124.	Zimmermann R, Strauss JG, Haemmerle G, Schoiswohl G, Birner-Gruenberger R, Riederer M, Lass A, Neuberger G, Eisenhaber F, Hermetter A, Zechner R. (2004). Fat

	mobilization in adipose tissue is promoted by adipose triglyceride lipase . Science. 2004 Nov 19;306(5700):1383-6.
125.	Novatchkova M, Budhiraja R, Coupland G, Eisenhaber F, Bachmair A. (2004). SUMO conjugation in plants . Planta. 2004 Nov;220(1):1-8. Epub 2004 Sep 23. Review.
126.	Silverman J, Takai H, Buonomo SB, Eisenhaber F, de Lange T. (2004). Human Rif1, ortholog of a yeast telomeric protein, is regulated by ATM and 53BP1 and functions in the S-phase checkpoint . Genes Dev. 2004 Sep 1;18(17):2108-19.
127.	Kurzbauer R, Teis D, de Araujo ME, Maurer-Stroh S, Eisenhaber F, Bourenkov GP, Bartunik HD, Hekman M, Rapp UR, Huber LA, Clausen T. (2004). Crystal structure of the p14/MP1 scaffolding complex: how a twin couple attaches mitogen-activated protein kinase signaling to late endosomes . Proc Natl Acad Sci U S A. 2004 Jul 27;101(30):10984-9. Epub 2004 Jul 19.
128.	Lorenz A, Wells JL, Pryce DW, Novatchkova M, Eisenhaber F, McFarlane RJ, Loidl J. (2004). S. pombe meiotic linear elements contain proteins related to synaptonemal complex components . J Cell Sci. 2004 Jul 1;117(Pt 15):3343-51.
129.	Eisenhaber B, Eisenhaber F, Maurer-Stroh S, Neuberger G. (2004). Prediction of sequence signals for lipid post-translational modifications: insights from case studies . Proteomics. 2004 Jun;4(6):1614-25.
130.	Maurer-Stroh S, Eisenhaber F. (2004). Myristoylation of viral and bacterial proteins . Trends Microbiol. 2004 Apr;12(4):178-85. Review.
131.	Maurer-Stroh S, Gouda M, Novatchkova M, Schleiffer A, Schneider G, Sirota FL, Wildpaner M, Hayashi N, Eisenhaber F. (2004). A sensitive predictor for potential GPI lipid modification sites in fungal protein sequences and its application to genome-wide studies for Aspergillus nidulans, Candida albicans, Neurospora crassa, Saccharomyces cerevisiae and Schizosaccharomyces pombe . J Mol Biol. 2004 Mar 19;337(2):243-53.
132.	Maurer-Stroh S, Gouda M, Novatchkova M, Schleiffer A, Schneider G, Sirota FL, Wildpaner M, Hayashi N, Eisenhaber F. (2004). MYRbase: analysis of genome-wide glycine myristoylation enlarges the functional spectrum of eukaryotic myristoylated proteins . Genome Biol. 2004;5(3):R21. Epub 2004 Feb 13.
133.	Rabitsch KP, Gregan J, Schleiffer A, Javerzat JP, Eisenhaber F, Nasmyth K. (2004). Two fission yeast homologs of Drosophila Mei-S332 are required for chromosome segregation during meiosis I and II . Curr Biol. 2004 Feb 17;14(4):287-301.
134.	Novatchkova M, Eisenhaber F. (2004). Linking transcriptional mediators via the GACKIX domain super family . Curr Biol. 2004 Jan 20;14(2):R54-5.
135.	Cserzo M, Eisenhaber F, Eisenhaber B, Simon I. (2004). TM or not TM: transmembrane protein prediction with low false positive rate using DAS-TMfilter . Bioinformatics. 2004 Jan 1;20(1):136-7.
136.	Eisenhaber B, Wildpaner M, Schultz CJ, Borner GH, Dupree P, Eisenhaber F. (2003). Glycosylphosphatidylinositol lipid anchoring of plant proteins. Sensitive prediction from sequence- and genome-wide studies for Arabidopsis and rice . Plant Physiol. 2003 Dec;133(4):1691-701.
137.	Washietl S, Eisenhaber F. (2003). Reannotation of the CELO genome characterizes a set of previously unassigned open reading frames and points to novel modes of host

	interaction in avian adenoviruses . BMC Bioinformatics. 2003 Nov 7;4:55.
138.	Vodermaier HC, Gieffers C, Maurer-Stroh S, Eisenhaber F, Peters JM. (2003). TPR subunits of the anaphase-promoting complex mediate binding to the activator protein CDH1 . Curr Biol. 2003 Sep 2;13(17):1459-68.
139.	Maurer-Stroh S, Washietl S, Eisenhaber F. (2003). Protein prenyltransferases: anchor size, pseudogenes and parasites . Biol Chem. 2003 Jul;384(7):977-89. Review.
140.	Eisenhaber F, Eisenhaber B, Kubina W, Maurer-Stroh S, Neuberger G, Schneider G, Wildpaner M. (2003). Prediction of lipid posttranslational modifications and localization signals from protein sequences: big-Pi, NMT and PTS1 . Nucleic Acids Res. 2003 Jul 1;31(13):3631-4.
141.	Novatchkova M, Leibbrandt A, Werzowa J, Neubüser A, Eisenhaber F. (2003). The STIR-domain superfamily in signal transduction, development and immunity . Trends Biochem Sci. 2003 May;28(5):226-9. Review.
142.	Wick N, Luedemann S, Vietor I, Cotten M, Wildpaner M, Schneider G, Eisenhaber F, Huber LA. (2003). Induction of short interspersed nuclear repeat-containing transcripts in epithelial cells upon infection with a chicken adenovirus . J Mol Biol. 2003 May 9;328(4):779-90.
143.	Neuberger G, Maurer-Stroh S, Eisenhaber B, Hartig A, Eisenhaber F. (2003). Prediction of peroxisomal targeting signal 1 containing proteins from amino acid sequence . J Mol Biol. 2003 May 2;328(3):581-92.
144.	Neuberger G, Maurer-Stroh S, Eisenhaber B, Hartig A, Eisenhaber F. (2003). Motif refinement of the peroxisomal targeting signal 1 and evaluation of taxon-specific differences . J Mol Biol. 2003 May 2;328(3):567-79.
145.	Maurer-Stroh S, Washietl S, Eisenhaber F. (2003). Protein prenyltransferases . Genome Biol. 2003;4(4):212. Epub 2003 Apr 1. Review.
146.	Schleiffer A, Kaitna S, Maurer-Stroh S, Glotzer M, Nasmyth K, Eisenhaber F. (2003). Kleisins: a superfamily of bacterial and eukaryotic SMC protein partners . Mol Cell. 2003 Mar;11(3):571-5.
147.	Eisenhaber B, Maurer-Stroh S, Novatchkova M, Schneider G, Eisenhaber F. (2003). Enzymes and auxiliary factors for GPI lipid anchor biosynthesis and post-translational transfer to proteins . Bioessays. 2003 Apr;25(4):367-85. Review.
148.	Maurer-Stroh S, Dickens NJ, Hughes-Davies L, Kouzarides T, Eisenhaber F, Ponting CP. (2003). The Tudor domain 'Royal Family': Tudor, plant Agenet, Chromo, PWWP and MBT domains . Trends Biochem Sci. 2003 Feb;28(2):69-74.
149.	N Cserző M, Eisenhaber F, Eisenhaber B, Simon I. (2002). On filtering false positive transmembrane protein predictions . Protein Eng. 2002 Sep;15(9):745-52.
150.	Novatchkova M, Eisenhaber F. (2002). A CH domain-containing N terminus in NuMA? Protein Sci. 2002 Oct;11(10):2281-4.
151.	Maurer-Stroh S, Eisenhaber B, Eisenhaber F. (2002). N-terminal N-myristoylation of proteins: prediction of substrate proteins from amino acid sequence . J Mol Biol. 2002 Apr 5;317(4):541-57.
152.	Sirota FL, Pascutti PG, Anteneodo C. (2002). Molecular modeling and dynamics of the sodium channel inactivation gate . Biophys J. 2002 Mar;82(3):1207-15.

153.	Ivanov D, Schleiffer A, Eisenhaber F, Mechtler K, Haering CH, Nasmyth K. (2002). Eco1 is a novel acetyltransferase that can acetylate proteins involved in cohesion. Curr Biol. 2002 Feb 19;12(4):323-8.
154.	Wildpaner M, Schneider G, Schleiffer A, Eisenhaber F. (2001). Taxonomy workbench. Bioinformatics. 2001 Dec;17(12):1179-82.
155.	Novatchkova M, Eisenhaber F. (2001). Can molecular mechanisms of biological processes be extracted from expression profiles? Case study: endothelial contribution to tumor-induced angiogenesis. Bioessays. 2001 Dec;23(12):1159-75. Review.
156.	Bachmair A, Novatchkova M, Potuschak T, Eisenhaber F. (2001). Ubiquitylation in plants: a post-genomic look at a post-translational modification. Trends Plant Sci. 2001 Oct;6(10):463-70. Review.
157.	Christian S, Ahorn H, Novatchkova M, Garin-Chesa P, Park JE, Weber G, Eisenhaber F, Rettig WJ, Lenter MC. (2001). Molecular cloning and characterization of EndoGlyx-1, an EMILIN-like multisubunit glycoprotein of vascular endothelium. J Biol Chem. 2001 Dec 21;276(51):48588-95. Epub 2001 Sep 14.
158.	Eisenhaber F, Wechselberger C, Kreil G. (2001). The Brix domain protein family -- a key to the ribosomal biogenesis pathway? Trends Biochem Sci. 2001 Jun;26(6):345-7.
159.	Eisenhaber B, Bork P, Eisenhaber F. (2001). Post-translational GPI lipid anchor modification of proteins in kingdoms of life: analysis of protein sequence data from complete genomes. Protein Eng. 2001 Jan;14(1):17-25.