239. Iwasaki Y, Ikemura T, Kurokawa k, Okada N. 
Implication of a new function of human tDNAs in chromatin organization.
Scientific Reports 10, 17440 (2020)

238. Vu TD, Iwasaki Y, Oshima K, Nikaido M, Chiu MT, Okada N. 
A unique neurogenomic state emerges after aggressive confrontations in males of the fish Betta splendens. 
bioRxiv 10.237586 (2020)

Behavioral and brain-transcriptomic synchronization between the two opponents of a fighting pair of the fish *Betta splendens*. 
PLOS Genetics 16(6), June (2020)

Intron retention as a new marker of the pre-disease state and its recovery to the normal state by a traditional Japanese multi-herbal medicine. 
bioRxiv 2020.02.10.941435 (2020)

Patterns of genomic differentiation between two Lake Victoria cichlid species, *Haplochromis pyrrhocephalus* and *H. sp. ‘macula’*. 
BMC Evolutionary Biology 19(68), March (2019)

Evolution of Shh endoderm enhancers during morphological transition from ventral lungs to dorsal gas bladder. 
Nature Communications 8 (14300), Feb (2017)

Visual adaptation in Lake Victoria cichlid fishes: depth-related
variation of color and scotopic opsins in species from sand/mud bottoms.
BMC Evolutionary Biology 17, Article number:200 (2017)


Okada N.
A microsatellite-based genetic linkage map and putative sex-determining genomic regions in Lake Victoria cichlids.

Distinct functions of two olfactory marker protein genes derived from teleost-specific whole genome duplication.
BMC Evolutionary Biology 15, Article number:245 (2015)

223. Yamaguchi K, Kajikawa M, Okada N.
Integrated mechanism for the generation of the 5’ junctions of LINE inserts
Nucleic Acids Research 42(21) 13269 -13279 (2014)

High prevalence of non-synonymous substitutions in mtDNA of cichlid fishes from Lake Victoria.

221. Brawand D, (45 coauthors), Nikaido M, Nishihara H, (18 coauthors), Okada N, (10coauthors) and Palma F.
The genomic substrate for adaptive radiation in African cichlid fish.

220. Hayashi Y, Kajikawa M, Matsumoto T, Okada N.
Mechanism by which a LINE protein recognizes its 3 tail RNA.

Multiple episodic evolution events in V1R receptor genes of East-African cichlids.

Sensory drive speciation and patterns of variation at selectively neutral genes.
Evolutionary Ecology 28, 591-609 (2014)

Evolutionary Changes in Vertebrate Genome Signatures with Special
Focus on Coelacanth.
DNA Research, Volume 21, Issue 5, October 2014,
Pages 459-467(2014)

Construction of Chromosome Markers from the Lake Victoria Cichlid Paralabidochromis chilotes and Their Application to Comparative Mapping.
Cytogenetic and Genome Research 2014; 142:112-120 (2014)

The complete mitochondrial genomes of deep-sea squid (Bathyteuthis abyssicola), bob-tail squid (Semirossia patagonica) and four giant cuttlefish (Sepia apama, S. latimanus, S. lycidas and S. pharaonis), and their application to the phylogenetic analysis of Decapodiformes.

Genetic Structure of Pelagic and Littoral Cichlid Fishes from Lake Victoria.
PLOS ONE| Volume 8 | Issue 9 | e74088 (2013)

In Vitro Screening for Compounds That Enhance Human L1 Mobilization.
PLOS ONE| Volume 8 | Issue 9 | e74629 (2013)

Lineage-Specific Expansion of Vomeronasal Type 2 Receptor-like (OlfC) Genes in Cichlids May Contribute to Diversification of Amino Acid Detection Systems.

211. Nikaido M (27 coauthors) Okada,N.
Coelacanth genomes reveal signatures for evolutionary transition from water to land.
Genome Res. 1, October (2013)

Mechanisms of T-DNA transfer and integration into plant chromosomes: role of vir B, vir D4 and vir E2 and a short interspersed repetitive element (SINE) from tobacco. Molecular Mechanisms of Bacterial Virulence (2012)

209. Kajikawa M, Yamaguchi K, Okada N.
A new mechanism to ensure integration during LINE retrotransposition: A suggestion from analyses of the 5’ extra nucleotides.

208. Kajikawa M, Sugano T, Sakurai R, Okada N.
Low dependency of retrotransposition on the ORF1 protein of the zebrafish LINE, ZfL2-1.

Characterization of V1R receptor (ora) genes in Lake Victoria cichlids.

206. Nakamura M, Kajikawa M, Okada N.
Self-interaction, nucleic acid binding, and nucleic acid chaperone activities are unexpectedly retained in the unique ORF1p of zebrafish.

A SINE-derived element constitutes a unique modular enhancer for mammalian diencephalic Fgf8.
PLOS One 2012; 7(8)e43785 (2012)

Extremely slow rate of evolution in the HOX cluster revealed by comparison between Tanzanian and Indonesian coelacanths.

Correlation between nuptial colors and visual sensitivities tuned by opsins leads to species richness in sympatric Lake Victoria cichlid fishes.


194. Sugawara T, Imai H, Nikaido M, Imamoto Y, Okada N


190. Okada N.
Special issue on phylogenomics and its future

189. Kojima K.K, and Okada N.

188. Nishihara H, Maruyama S, Okada N.
Retroposon analysis and recent geological data suggest near-simultaneous divergence of the three superorders of mammals. Proc Natl Acad Sci USA. Mar 31;106(13):5235-40 (2009) [Abstract] [OPEN ACCESS]

186. Hirakawa M, Nishihara H, Kanehisa M, Okada N.
Characterization and evolutionary landscape of AmnSINE1 in Amniota genomes.

Population structure of two closely related pelagic cichlids in Lake Victoria, Haplochromis pyrrhocephalus and H. laparogramma.

Chronology of the extant African elephant species and case study of the species identification of the small African elephant with the molecular phylogenetic method.

183. Piskurek O, Nishihara H, Okada N.
The evolution of two partner LINE/SINE families and a full-length chromodomain-containing Ty3/Gypsy LTR element in the first reptilian genome of Anolis carolinensis.

182. Matveev V, Okada N.
Retroposons of salmonoid fishes (Actinopterygii: Salmonoidei) and their evolution.

Speciation through sensory drive in cichlid fish.

180. Fujimura K, Okada N
Shaping of the lower jaw bone during growth of Nile tilapia Oreochromis niloticus and a Lake Victoria cichlid Haplochromis chilotes: A geometric morphometric approach.

179. Nishihara H, Okada N.
Retroposons: Genetic Footprints on the Evolutionary Paths of Life.
Phylogenomics (Methods in Molecular Biology, vol. 422)
Chapter 13, Pages 201-225, Ed. Murphy, W. J., Humana Press. (2008)


169. Ichiyanagi K, Nishihara H, Duvernell D.D, Okada N.
Acquisition of Endonuclease Specificity During Evolution of L1 Retrotransposon.

168. Watanabe M, Hiraide K, Okada N.
Functional diversification of kir7.1 in cichlids accelerated by gene duplication.

167. Piskurek O, Okada N.
Poxviruses as possible vectors for horizontal transfer of retroposons from reptiles to mammals.

166. Matveev V, Nishihara H, Okada N.
Novel SINE Families from Salmons Validate Parahucho (Salmonidae) as a Distinct Genus and Evidence that SINEs Can Incorporate LINE-related 3'-Tails of Other SINEs.

165. Onami J, Nikaido M, Mannen H, Okada N.
Genomic expansion of the Bov-A2 retroposon relating to phylogeny and breed management.

164. Yonezawa T, Nikaido M, Kohno N, Fukumoto Y, Okada N, Hasegawa M.
Molecular phylogenetic study on the origin and evolution of Mustelidae.

163. Xue B, Rooney AP, Kajikawa M, Okada N, Roelofs WL.
Novel sex pheromone desaturases in the genomes of corn borers generated through gene duplication and retroposon fusion.

162. Fujimura K, Okada N.
Development of the embryo, larva and early juvenile of Nile tilapia Oreochromis niloticus (Pisces: Cichlidae).
Developmental staging system
161. Nikaido M, Piskurek O, Okada N.
Toothed whale monophyly reassessed by SINE insertion analysis: The absence of lineage sorting effects suggests a small population of a common ancestral species.

A new system for analyzing LINE retrotransposition in the chicken DT40 cell line widely used for reverse genetics.

159. Sasaki T, Sato T, Miura S, Bwathondi PO, Ngatunga BP, Okada N.
Mitogenomic analysis for coelacanths (Latimeria chalumnae) caught in Tanzania.

A novel testis ubiquitin-binding protein gene arose by exon shuffling in hominoids.
Genome Research 17(8) 1129 - 1138 (2007)

Novel retrotransposon analysis reveals multiple mobility pathways dictated by hosts.

156. Sasaki T, Yasukawa Y, Takahashi K, Miura S, Shedlock AM, Okada N.
Extensive morphological convergence and rapid radiation in the evolutionary history of the family Geoemydidae (old world pond turtles) revealed by SINE insertion analysis.

155. Tamura M, Kajikawa M, Okada N.
Functional splice sites in a zebrafish LINE and their influence on zebrafish gene expression.

Divergent Selection on Opsins Drives Incipient Speciation in Lake Victoria Cichlids.


137. Watanabe M, Nikaido M, Tsuda TT, Inoko H, Mindell DP, Murata K, Okada N. The rise and fall of the CR1 subfamily in the lineage leading to
penguins.

136.Ohshima K, and Okada N.
SINEs and LINEs: symbionts of eukaryotic genomes with a common tail.
Cytogenet Genome Res. 110, 475-90. (2005)

A Retroposon Analysis of Afrotherian Phylogeny.
Mol Biol Evol. 22(9), 1823-33. (2005)

cimp1, A Novel Astacin Family Metalloproteinase Gene from East African Cichlids, Is Differentially Expressed Between Species During Growth.
Mol Biol Evol. 22(8), 1649-60. (2005)

Parallelism of amino acid changes at the RH1 affecting spectral sensitivity among deep-water cichlids from Lakes Tanganyika and Malawi.

Mitochondrial phylogenetics and evolution of mysticete whales.
Syst Biol. 54, 77-90 (2005)

131.Kajikawa M, Ichiyanagi K, Tanaka N, and Okada N.
Isolation and characterization of active LINE and SINEs from the eel.

130.Segawa T, Miyamoto K, Ushida K, Agata K, Okada N, and Kohshima S.
Seasonal Change in Bacterial Flora and Biomass in Mountain Snow from the Tateyama Mountains, Japan, Analyzed by 16S rRNA Gene Sequencing and Real-Time PCR.
Applied and Environmental Microbiology 71(1), 123-30 (2005)

129.Sugie A, Terai Y, Ota R, and Okada N.
The evolution of genes for pigmentation in African cichlid fishes.
128. Watanabe M, Kobayashi N, Shin’i T, Tateno Y, Kohara Y, and Okada N.
   Extensive analysis of ORF sequences from two different cichlid species in Lake Victoria provides molecular evidence for a recent radiation event of the Victoria species flock.

   Solution structure of an RNA stem-loop derived from the 3' conserved region of eel LINE UnaL2.
   RNA 10(9), 1380-7 (2004)

126. Shedlock A M, Takahashi K, and Okada N.
   SINEs of speciation: tracking lineages with retroposons.

125. Imanishi T, et al.
   Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones.
   Plos Biology 2(6), 856-75 (2004)

124. Okada N, Shedlock A M, and Nikaido M.
   Retroposon mapping in molecular systematics.

123. Sasaki T, Takahashi K, Nikaido M, Miura S, Yasukawa Y, and Okada N.
   First Application of the SINE (Short Interspersed Repetitive Element) Method to Infer Phylogenetic Relationships in Reptiles: An Example from the Turtle Superfamily Testudinoidea.

122. Terai Y, Takezaki N, Mayer W E, Tichy H, Takahata N, Klein J, and Okada N.
   Phylogenetic relationships among East African haplochromine fishes as revealed by short interspersed elements (SINEs).

   Molecular Phylogenetics and Evolution. 30(1)259(2004)


112. Watanabe M, Kobayashi N, Fujiyama A, and Okada N.
Construction of a BAC library for Haplochromis chilotes, a cichlid fish from Lake Victoria.

111. Nikaido M, Cao Y, Okada N, and Hasegawa M.
The phylogenetic relationships of insectivores with special reference to the lesser hedgehog tenrec as inferred from the complete sequence of their mitochondrial genome.

110. Ishitani R, Nureki O, Nameki N, Okada N, Nishimura S, and Yokoyama S.
Alternative Tertiary Structure of tRNA for Recognition by a Posttranscriptional Modification Enzyme.

109. D Huchon, Nikaido M, Okada N.
Use of SINE retroposon in phylogeny.

108. Pupko T, Huchon D, Cao Y, Okada N, and Hasegawa M.
Combining multiple data sets in a likelihood analysis: which models are the best?

107. Terai Y, Mayer W E, Klein J, Tichy H, and Okada N.

106. Kajikawa M, and Okada N.
LINEs Mobilize SINEs in the Eel through a Shared 3’ Sequence.

105. Nishihara H, Terai Y, and Okada N.
Characterization of Novel Alu- and tRNA-Related SINEs from the Tree Shrew and Evolutionary Implications of Their Origins.

104. Sugawara T, Terai Y, and Okada N.
Natural selection of the rhodopsin gene during the adaptive radiation of East african great lakes cichlid fishes.
103. Terai Y, Morikawa N, and Okada N.  
The evolution of the pro-domain of bone morphogenetic protein 4 (bmp4) in an explosively speciated lineage of East african cichlid fishes.  

Hasegawa M, and Okada N.  
Intra- and Interfamily Relationships of Vespertilionidae Inferred by Various Molecular Markers Including SINE Insertion Data.  

101. Takahashi K, and Okada N.  
Mosaic structure and retropositional dynamics during evolution of subfamilies of short interspersed elements in african cichlids.  

100. Terai Y, Morikawa N, Kawakami K, and Okada N.  
Accelerated Evolution of the Surface Amino Acids in the WD-Repeat Domain Encoded by the hagoromo Gene in an Explosively Speciated Lineage of East African Cichlid Fishes.  

99. Ishitani R, Nureki O, Fukai S, Kijimoto T, Nameki N, Watanabe M,  
Kondo H, Sekine M, Okada N, Nishimura S, and Yokoyama S.  
Crystal structure of archaeosine tRNA-guanine transglycosylase.  

98. Ogiwara I, Miya M, Ohshima K, and Okada N.  
V-SINEs: a new superfamily of vertebrate SINEs that are widespread in vertebrate genomes and retain a strongly conserved segment within each repetitive unit.  
Genome Res. 12, 316-24 (2002)

97. Ishitani R, Nureki O, Kijimoto T, Watanabe M, Kondo H, Nameki N,  
Okada N, Nishimura S, and Yokoyama S.  
Crystallization and preliminary X-ray analysis of the archaeosine tRNA-guanine transglycosylase from Pyrococcus horikoshii.  

96. Nikaido M, Matsuno F, Abe H, Shimamura M, Hamilton H,  
Matsubayashi H, and Okada N.  
Evolution of CHR-2 SINEs in cetartiodactyl genomes: possible evidence for the monophyletic origin of toothed whales.  
Mamm. Genome. 12, 909-15 (2001)
95. Takahashi K, Terai Y, Nishida M, and Okada N.
Phylogenetic relationships and ancient incomplete lineage sorting among cichlid fishes in Lake Tanganyika as revealed by analysis of the insertion of retroposons.

94. Nikaido M, Kawai K, Cao Y, Harada M, Tomita S, Okada N, and Hasegawa M.
Maximum likelihood analysis of the complete mitochondrial genomes of eutherians and a reevaluation of the phylogeny of bats and insectivores.

93. Takahashi K, Nishida M, Yuma M, and Okada N.
Retroposition of the AFC family of SINEs (short interspersed repetitive elements) before and during the adaptive radiation of cichlid fishes in Lake Malawi and related inferences about phylogeny.

Retroposon analysis of major cetacean lineages: the monophyly of toothed whales and the paraphyly of river dolphins.

91. Watanabe M, Nameki N, Matsuo-Takasaki M, Nishimura S, and Okada N.
tRNA recognition of tRNA-guanine transglycosylase from a hyperthermophilic archaean, Pyrococcus horikoshii.

90. Cao Y, Fujiwara M, Nikaido M, Okada N, and Hasegawa M.
Interordinal relationships and timescale of eutherian evolution as inferred from mitochondrial genome data.
GENE 259, 149-58 (2000)

89. Nikaido M, and Okada N.
CetSINEs and AREs are not SINEs but are parts of cetartiodactyl L1.
Mamm. Genome. 11 (12), 1123-6 (2000)

88. Nikaido M, Harada M, Cao Y, Hasegawa M, and Okada N.
Monophyletic origin of the order chiroptera and its phylogenetic position among mammalia, as inferred from the complete sequence of the mitochondrial DNA of a Japanese megabat, the Ryukyu flying fox (Pteropus dasymallus).


79. Terai Y, Takahashi K, and Okada N. SINE cousins: The 3' end tails of the two oldest and distantly related families of SINEs are descended from the 3' ends of LINEs with the
same genealogical origin.

78. Shimamura M, Nikaido M, Ohshima K, and Okada N.
A SINE that acquired a role in signal transduction during evolution.

77. Hamada M, Takasaki N, Reist J D, DeCicco A L, Goto A, and Okada N.
Detection of the on-going sorting of ancestrally polymorphic SINEs
wards fixation or loss in populations of two species of charr during
speciation.
Genetics 150(1), 301-11 (1998)

76. Takahasi I, Nobukuni T, Ohmori H, Kobayashi M, Tanaka S, Ohshima
K, Okada N, Masui T, Hashimoto K, and Iwashita S.
Existence of a bovine LINE repetitive insert that appears in the cDNA of
bovine protein BCNT in ruminant, but not in human, genomes.

75. Takahashi K, Terai Y, Nishida M, and Okada N.
A novel family of short interspersed repetitive elements (SINEs) from
cichlids: the patterns of insertion of SINEs at orthologous loci support
the proposed monophyly of four major groups of cichlid fishes in Lake
Tanganyika.

74. Hamada M, Himberg M, Bodalu R A, Reist J D, and Okada N.
Monophyletic origin of the genera stenodus and coregonus as inferred
from an analysis of the insertion of SINEs (short interspersed repetitive
elements).

73. Cao Y, Waddell P J, Okada N, and Hasegawa M.
The complete mitochondrial DNA sequence of the shark Mustelus
manazo: evaluating rooting contradictions to living bony vertebrates.

72. Cao Y, Janke A., Waddell P J., Westerman M, Takenaka O, Murata S,
Okada N, Paabo S, and Hasegawa M.
Conflict among individual mitochondrial proteins in resolving the
phylogeny of eutherian orders.

71. Watanabe M, Matsuo M, Tanaka S, Akimoto H, Asahi S, Nishimura S,
Katze J R, Hashizume T, Crain P F, McCloskey J A, and Okada N.
Biosynthesis of archaeosine, a novel derivative of 7-deazaguanosine specific to archaeal tRNA, proceeds via a pathway involving base replacement on the tRNA polynucleotide chain.
J. Biol. Chem. 272, 20146-51 (1997)

70. Okada N, Hamada M, Ogiwara I, and Ohshima K.
SINEs and LINEs share common 3' sequences: a review.
GENE 205(1-2), 229-43 (1997)

Molecular evidence that whales form a clade within even-toed ungulates.
Nature 388 (6643), 666-70 (1997)

68. Ishida K, Cao Y, Hasegawa M, Okada N, and Hara Y.
The origin of chlorarachniophyte plastids, as inferred from phylogenetic comparisons of amino acid sequences of EF-Tu.

A newly isolated family of short interspersed repetitive elements (SINEs) in coregonid fishes (whitefishes) with sequences that are almost identical to those of the Sma I family of repeats: possible evidence for the horizontal transfer of SINEs.
Genetics 146(1), 355-67 (1997)

66. Takasaki N, Yamaki T, Hamada M, Park L, and Okada N.
The salmon Sma I family of SINEs: interspecific and intraspecific polymorphism of the insertion of SINEs in the genomes of chum and pink salmon.
Genetics 146(1), 369-80 (1997)

65. Kajikawa M, Ohshima K, and Okada N.
Determination of the entire sequence of turtle CR1: the first open reading frame of the turtle CR1 element encodes a protein with a novel zinc finger motif.

64. Okada N, and Hamada M.
The 3' ends of tRNA-derived SINEs originated from the 3" ends of LINEs: A new example from the bovine genome.

63. Ohshima K, Hamada M, Terai Y, and Okada N.
The 3' ends of tRNA-derived short interspersed repetitive elements are
derived from the 3' ends of long interspersed repetitive elements.


61. Murata S, Takasaki N, Saitoh M, Tachida H, and Okada N. Details of retropositional genome dynamics that provide a rational for a generic division: The distinct branching of all the Pacific salmon and trout (Oncorhynchus) from the Atlantic salmon and trout (Salmo). Genetics 142(3), 915-26 (1996)


49. Sakagami M, Ohshima K, Mukoyama H, Yasue H, and Okada N. A novel tRNA species as an origin of short interspersed repetitive elements (SINEs); Equine SINEs may have originated from tRNA(Ser). J. Mol. Biol. 239(5), 731-5 (1994)


47. Ozawa Y, Uchida K, Uchida M, Ami Y, Kushida S, Okada N, and Miwa M.
Isolation of cDNAs encoding the catalytic domain of poly(ADP-ribose) polymerase from Xenopus laevis and cherry salmon using heterologous oligonucleotide consensus sequences.

46. Murata S, Takasaki N, Saitoh M, and Okada N.
Determination of the phylogenetic relationships among Pacific salmonids using short interspersed elements (SINEs) as temporal landmarks of evolution.

Molecular characterization of a short interspersed repetitive element from tobacco that exhibits sequence homology to specific tRNAs.

44. Ohshima K, Koishi R, Matsuo M, and Okada N.
Several short interspersed repetitive elements (SINEs) in distant species may have originated from a common ancestral retrovirus: characterization of a squid SINE and a possible mechanism for generation of tRNA-derived retroposons.

43. Kojima S, Hashimoto T, Hasegawa M, Murata S, Ohta S, Seki F, and Okada N.
Close phylogenetic relationship between Vestimentifera (tube worms) and Annelida revealed by the amino acid sequence of elongation factor-1a.

42. Okada N, and Ohshima K.
A model for the mechanism of initial generation of short interspersed elements (SINEs).

41. Kido Y, Aono M, Matsumoto K, Yamaki T, Saneyoshi M, and Okada N.
Shaping and reshaping of salmonid genomes by amplification of tRNA-derived retroposons during evolution.

40. Okada N.
Transfer RNA-derived retroposons.
New Aspect of the Genetics of Molecular Evolution
JSpringer-Verlag pp.175-86(1991)

38. Okada N.
SINEs: Short interspersed repeated elements of the eukaryotic genome.
Trends in Ecology & Evolution. 6(11), 358-61 (1991)

37. Okada N.
SINEs.

36. Koishi R, and Okada N.
Distribution of the salmonid HPA-1 family in the salmonid species demonstrated by In vitro run-off transcription assay of total genomic DNA : A procedure to estimate repetitive frequency and sequence divergence of a certain repetitive family with a few known sequences.

35. Nagahashi S, Endoh H, Suzuki Y, and Okada N.
Characterization of a tandemly repeated DNA sequence family originally derived by retroposition of tRNAGlu in the newt.

34. Endoh H, Nagahashi S, and Okada N.
Highly repetitive and transcribable sequence in the tortoise genome is probably a retroposon.

33. Okada N.
Transfer RNA-like structure of the human Alu family: Implications of its generation mechanism and possible functions.
J. Mol. Evol. 31(6), 500-10 (1990)

32. Matsumoto K, Takii T, and Okada N.
Characterization of a new termination signal for RNA polymerase III responsible for generation of a discrete-sized RNA transcribed from salmon genomic total DNA in a HeLa cell extract.
J. Biol. Chem. 264(2),1124-31 (1989)
31. Endoh H, Nagahashi S, and Okada N.
Tetrahymena pyriformis DNA fragment with a gene cluster for 3 putative serine tRNAs and an asparagine tRNA.
Nucleic Acids Res. 17, 10122 (1989)

Shaping and reshaping of the genomes of salmonid species during evolution. Biology of Charrs and Masu Salmon .
(eds. Kawanabe, Yamazaki and Noakes)

Several aspects of total genomic DNA transcription in a HeLa cell extract.

Tetrahymena actin, cloning and sequencing of the Tetrahymena actin gene and identification of its gene product.

27. Okada N, Mimori T, Mukai R, Kashiwagi H, and Hardin J A.
Characterization of human autoantibodies that selectively precipitate the 7SL RNA component of the signal recognition particle.
J. Immunology 138, 3219-23 (1987)

26. Endoh H, and Okada N.
Total DNA transcription in vitro: A procedure to detect highly repetitive and transcribable sequences with tRNA-like structures.

25. Matsumoto K, Murakami K, and Okada N.
Gene for lysine tRNA1 as a progenitor of the highly repetitive and transcribable sequences present in the salmon genome.

24. Sakamoto K, and Okada N.
Rodent type 2 Alu family, rat identifier sequence, rabbit C family, and bovine or goat 73-bp repeat may have evolved from tRNA genes.

Many highly repetitive and transcribable sequences are derived from
tRNA genes.

22. Sakamoto K, and Okada N.
5-Methylcytidylic modification of in vitro transcript from the rat identifier sequence: evidence that the transcript forms a tRNA-like structure.
Nucleic Acids Res. 13, 7195-206 (1985)

Nucleotide sequences homologous to human T-cell leukemia virus are present in pig and wild bore cells.
Gann. 75, 849-52 (1984)

Isolation of a novel antibody which precipitates ribonucleoprotein complex containing threonine tRNA from a patient with polymyositis.

The 6S RNA transcribed from rodent total DNA in vitro is the transcript of the type 2 Alu family.

18. Matsumoto K, Murakami K, and Okada N.
Pseudouridylic modification of a 6S RNA transcribed in vitro from highly repetitive and transcribable (Hirt) sequences of salmon total DNA.

Total DNA transcription reveals the existence of highly repetitive transcribable sequences in higher animals.
J. Biochem. 93, 723-31 (1983)

Structural analysis of gene loci for rat U1 small nuclear RNA.
Nucleic Acids Research. 11, 1791-801 (1983)

15. Tani T., Watanabe-Nagasu N., Okada N. and Ohshima Y.
Molecular cloning and characterization of a gene for rat U2 small nuclear RNA.
   Sequence determination of rat U5 RNA using a chemical modification procedure for counteracting sequence compression.
   J. Biochem. 91, 1281-91 (1982)

13. Nakao Y., Mukai R., Kabashima T., Ohshima Y., Hamaguchi H.,
   Kashiwagi H. and Okada N.
   A novel antibody which precipitates 7.5S RNA is isolated from a patient with autoimmune disease.

12. Shindo-Okada N., Kuchino Y., Harada F., Okada N. and Nishimura S.
   Biological and structural differences between tRNAVal species isolated from rat ascites hepatoma cells and normal rat liver.

11. Ohshima Y., Itoh M., Okada N. and Miyata T.
   Novel models for RNA splicing that involve a small nuclear RNA.

10. Ohshima Y., Okada N., Tani T., Itoh Y. and Itoh M.
   Nucleotide sequences of mouse genomic loci including a gene or pseudogene for U6(4.8S) nuclear RNA.
   Nucleic Acids Res. 9, 5145-58 (1981)

9. Shindo-Okada N., Okada N., Ohgi T., Goto T. and Nishimura S.
   Transfer ribonucleic acid guanine transglycosylase isolated from rat liver.
   Biochemistry 19, 395-400 (1980)

8. Okada N. and Nishimura S.
   Isolation and characterization of a guanine insertion enzyme, a specific tRNA transglycosylase, from Escherichia coli.
   J. Biol. Chem. 254, 3061-6 (1979)

7. Okada N., Noguchi S., Kasai H., Shindo-Okada N., Ohgi T., Goto T. and Nishimura S.
   Novel mechanism of posttranscriptional modification of tRNA. - insertion of bases of Q-precursors into transfer-RNA by a specific transfer-RNA transglycosylase reaction.
   J. Biol. Chem. 254, 3067-73 (1979)

6. Okada N., Noguchi S., Nishimura S., Ohgi T., Goto T., Crain P.F. and MacCloskey J.A.
   Structure determination of a nucleoside Q precursor isolated from E. coli
tRNA: 7-(aminomethyl)-7-deazaguanosine.
Nucleic Acids Res. 5, 2289-96 (1978)

Detection of unique tRNA species in tumor tissues by Escherichia coli
guanine insertion enzyme.

4. Okada N. Shindo-Okada N. and Nishimura S.
Isolation of mammalian tRNAAsp and tRNATyr by lectin-Sepharose
affinity column chromatography.
Nucleic Acids Res. 4, 415-23 (1977)

3. Okada N. and Nishimura S.
Enzymatic synthesis of Q* nucleoside containing mannose in the
anticodon of tRNA: Isolation of a novel mannosyltransferase from a cell-
free extract of rat liver.
Nucleic Acids Res. 4, 2931-7 (1977)

2. Okada N., Yasuda T. and Nishimura S.
Detection of nucleoside Q precursor in methyl-deficient E. coli tRNA.
Nucleic Acids Res. 4, 4063-75 (1977)

1. Okada N., Harada F. and Nishimura S.
Specific replacement of Q base in the anticodon of tRNA by guanine
catalyzed by a cell-free extract of rabbit reticulocytes.
Nucleic Acids Res. 3, 2593-603 (1976)