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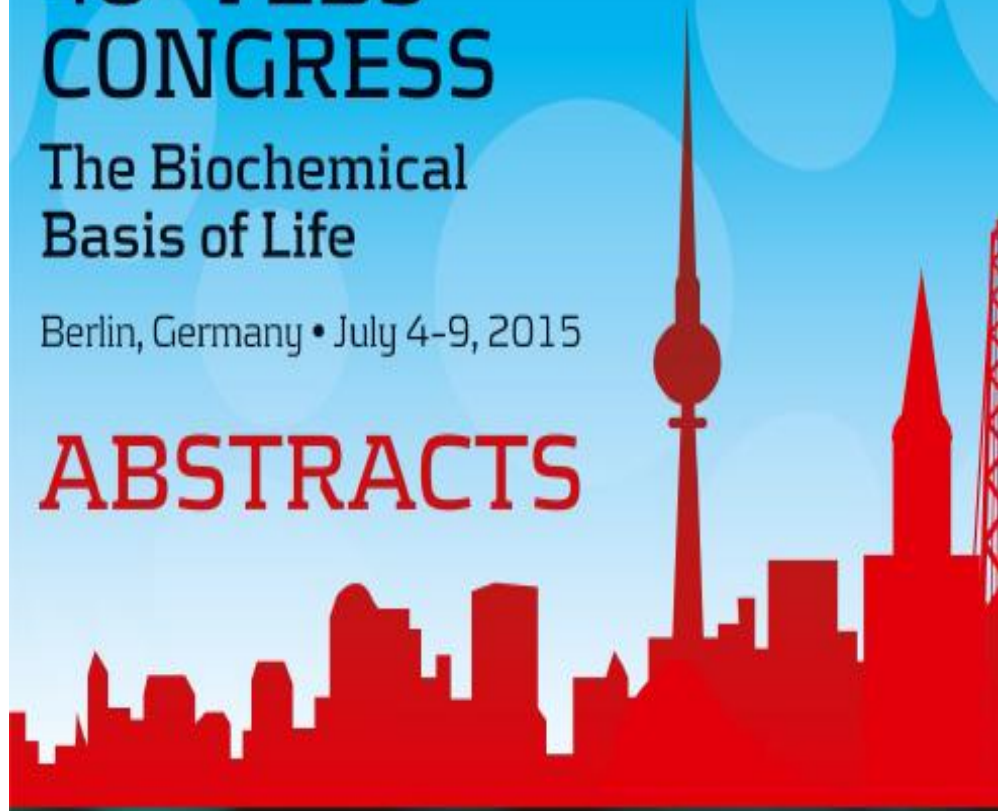
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## 40<sup>th</sup> FEBS CONGRESS

### The Biochemical Basis of Life

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# ABSTRACTS



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# the FEBS Journal

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#### Poster Sessions

##### Table of Contents

##### Poster Session 1

###### Sunday 5 July & Monday 6 July

08:30-19:30, Foyer Convention Center

- 56 Gen EX S1, Chromatin Structure and Epigenetic Modifications and Maintenance of the Genome
- 70 Gen EX S2, Turning Signals into Messages – the Complexity of Gene Regulation
- 89 Gen EX S3, Translational Control and Protein Turnover
- 98 Mem Biol S1, Organelle Dynamics and Communication
- 107 Mem Biol S2, Autophagy and Degradation
- 110 Mem Biol S3, Redox-Regulation of Biological Activities
- 129 Chem Biol S1, Probing Cellular Function with Small Molecules
- 158 Chem Biol S2, Targeted Cancer Therapy
- 160 Chem Biol S4, RNA-Based Disease Mechanism and Therapy
- 166 Mol Neu S1, Neuronal Ion Channels and their Role in Disease
- 168 Mol Neu S2, Mechanisms of Nervous System Development and Regeneration
- 172 Mol Neu S3, Degeneration and Ageing of the Nervous System
- 184 Sys Biol S2, Molecular Clocks
- 187 Sys Biol S3, Comprehensive Models of Metabolism and Signaling
- 198 Struct Biol S1, Mechanisms of Membrane Transport
- 205 Struct Biol S2, Channels and Transporters
- 206 Struct Biol S3, Protein-Mediated Membrane Deformation and Penetration

##### Poster Session 2

###### Tuesday 7 July & Wednesday 8 July

08:30-19:30, Foyer Convention Center

- 209 Gen EX S4, RNA Processing and Modifications
- 215 Gen EX S5, Non-Coding RNAs in Gene Regulation
- 220 Mem Biol S4, Extrinsic and intrinsic regulation of cellular growth control
- 228 Mem Biol S5, Lipid Signaling & Dynamics
- 240 Chem Biol S2, Targeted Cancer Therapy
- 274 Chem Biol S3, Functional Glycobiology – from Mechanism to Disease
- 281 Chem Biol S5, Signal Transduction in Tumor Development, Differentiation and Immune Escape
- 293 Mol Neu S4, Molecular Architecture and Assembly of the Synapse
- 297 Mol Neu S5, Control of Neuronal Function by Regulating Protein Homeostasis
- 302 Sys Biol S1, Interspecies Communications
- 304 Sys Biol S4, Functional Networks Regulating Cellular Stress Response and Ageing
- 315 Sys Biol S5, Systems Biology in Stem Cells
- 316 Struct Biol S2, Channels and Transporters
- 324 Struct Biol S4, Monitoring Protein Conformational Dynamics and Movement
- 329 Struct Biol S5, Advances in Structural Biology – from Subcellular to Molecular Resolution
- 353 FEBS Education Session
- 380 Late-breaking abstracts

Each poster has been given a unique number and the first part of the poster number relates to the session in which the poster was presented. Gen EX S1-S5, Mem Biol S1-S5, Chem Biol S1-S5, Mol Neu S1-S5, Sys Biol S1-S5, Struct Biol S1-S5.

tional mechanisms which underlying these responses. This is due to the capacity of sugar to act as nutrients, osmotic regulators and signalling molecules. Cis-acting sugar regulatory elements are important molecular switches involved in the temporal and spatial expression of a dynamic network of gene activities. This network controls hormone and abiotic stress responses, and developmental events such as juvenility and floral induction. In this study, we have examined expression levels and promoter features of different genes encoding proteins that have been implicated as targets of glucose signal transduction pathways, and might participate in juvenility and floral induction. Identifying the functionally active sugar response elements in the proximal promoter regions of genes that undergo glucose induced transcriptional regulation will lead us closer to understanding these signal transduction mechanisms.

## P28-026

### Study of *Brachypodium distachyon* and local breed soft wheat varieties tolerance to adverse environmental factor

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The Republic of Kazakhstan is one of the world leading countries in production of trade wheat grain, and the problem of lands salinity here is quite acute. Proline is one of the most widely distributed natural osmolytes, which is accumulated in plants during their protection against various abiotic factors. *Brachypodium distachyon* is a widely recognized model plant, closely related to wheat. The aim of our study was to evaluate the content of proline and soluble protein in *Brachypodium* and local breed soft wheat varieties (Shagala and Kazakhstanskaya 3) under standard 2% NaCl salinity. Experimental data on Shagala variety have shown 3 times increase in proline content under salinity for seedlings (namely, 126.53±0.01 mg/g from 45.21±0.02), and 5 times increase in such for roots; thus leading to a conclusion that under salinity proline is mostly accumulated in seedlings, rather than in roots. However, we got an opposite picture for Kazakhstanskaya 3: 9 times proline increase in seedlings (169.00±0.03 mg/g), with only 3 times increase in roots (16.65±0.05 mg/g). In *Brachypodium* proline content under salinity in seedlings raised up to 101.00±0.03 mg/g, in roots 16.50±0.05 mg/g; absence of change in proline content in seedlings and roots has been observed. Content of soluble protein in *Brachypodium* is higher (0.460±0.002 mg/ml) in comparison with such of Kazakhstanskaya 3 and Shagala (0.179±0.01 and 0.188±0.01 mg/ml, correspondingly), using microbioassay method by Bailey. Experimental data allowed to place them in the following order of salt tolerance *Brachypodium* < Shagala < Kazakhstanskaya 3.

## P28-027

### Collagen I induces TNF- $\alpha$ production and down-regulation of dendritic cells

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The activation of dendritic cells (DCs) plays a role to regulate the immune response. Inflammatory modulators such as tumour necrosis factor (TNF)- $\alpha$ , interleukin (IL)-1 $\beta$  and lipopolysaccharide (LPS) are also known to activate DCs. We have previously

shown that collagen I enhances the maturation and function of DCs. Here we investigated the involvement of TNF- $\alpha$  on the collagen I-induced DCs activation. The of neutralization of TNF- $\alpha$  inhibited collagen I-induced IL-12 secretion by DCs. Additionally, we observed suppression of collagen I-induced co-stimulatory molecules expression along with down-regulation of genes involved in DCs activation pathway. Furthermore, TNF- $\alpha$  inhibition upon collagen I stimulation up-regulated the expression of interferon regulatory transcription factor IRF4, when compared to collagen I only treated cells. Collectively, our data demonstrate that collagen I induce TNF- $\alpha$  production, which is crucial for the activation and function of DCs, through down-regulation of IRF4, and implicates the importance in development of anti-TNF- $\alpha$  therapeutics for several inflammatory diseases.

## P28-028

### Luteolin attenuates adipocyte-derived inflammatory responses via suppression of NF- $\kappa$ B/MAPK pathway

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Inflammation of adipocytes has been a therapeutic target for treatment of obesity and metabolic disorders which cause insulin resistance and hence lead to type II diabetes. Luteolin is a bioflavonoid with many beneficial properties like antioxidant, anti-proliferative and anti-cancer. To elucidate the potential anti-inflammatory response and the underlying mechanism of luteolin in 3T3-L1 adipocytes we stimulated 3T3-L1 adipocytes with the mixture of TNF- $\alpha$ , LPS and IFN- $\gamma$  (TLI) in the presence or absence of luteolin. Luteolin opposed the stimulation of inducible nitric oxide synthase (iNOS) mRNA and protein expression and NO production by simultaneous treatment of adipocytes with TLI. Also, it reduced the mRNA expression of pro-inflammatory genes like COX-2, IL-6, and matrix metalloproteinase (MMP-1). This inhibition was associated with suppression of I $\kappa$ B- $\alpha$  degradation and subsequent inhibition of NF- $\kappa$ B p65 translocation to the nucleus. In addition, luteolin blocked the phosphorylation of ERK1/2, JNK and also p38 MAPKs. These results illustrate that luteolin attenuates inflammatory responses in the adipocytes through suppression of NF- $\kappa$ B and MAPKs activation, suggesting that luteolin may represent a therapeutic agent to prevent obesity-associated inflammation and insulin resistance.

## P28-029

### CrossHub: cross-analysis of TCGA RNA-Seq, miRNA-Seq, methylation and mutation data

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The Cancer Genome Atlas Project (TCGA) is the largest resource in the field of molecular oncology. It accumulates genomic, transcriptomic and methylomic data for more than 15 cancers. We developed the CrossHub software (available at [Montefano, G., 234  
Moon, E.-K., 63  
Moon, E.Y., 302  
Morawczuk, J., 333  
de Moraes, E.C., 72  
Moran, T., 386  
Morales Hernández, A., 69  
Morales-Montor, J., 134  
Mori, S.V., 390, 390  
Moroni, C., 317  
Moroni, C.J., 319  
Moroni, A.C., 336  
Moroni, S., 182  
Moroni, C., 363  
Moroni, M.C., 373  
Moroni, X., 134  
Moroni, E., 285, 288  
Moroni, S., 189  
Morjan, B., 127  
Morjan, H., 326  
Morjan, M., 406  
Mori, S., 114  
Morris, C., 121  
Morton, H., 229  
Mortrud, D., 173  
Moussallem, D., 367  
Mouchon, N.K., 214  
Moukalev, A.A., 311, 312  
Moukalev-Dimitrova, V., 254, 319  
Mouton, J., 122, 373  
Mouton, A., 151  
Mouton-Riad, N., 380  
Motta, C., 96, 223, 237, 290  
Motta, V., 269  
Moura-Alves, P., 287  
Mourier, A., 408  
Mouragiar, B., 62  
Mršak, H., 341  
Mucillo Castillo, E., 382  
Mudera, V., 317, 319  
Muehler, J.W., 236  
Müller, A., 166  
Mullerbach, M., 270  
Munoz, J., 129  
Munoz, J.M., 80  
Mukai, Y., 202, 225, 225  
Mukherjee, D., 251  
Muller, M.P.C., 337  
Muller, P., 329  
Miller, A.J., 374, 375  
Miller, G., 274  
Miller, G.A., 71  
Miller, H.L., 203  
Miller, M., 74  
Miller, O.J., 91  
Miller, P., 204  
Miller, R., 239  
Mitsch, D., 330  
Mitsch, J., 330  
Mittelbach, S., 74  
Mizler Garcia-Martinez, S., 211  
Mizler, C., 155, 227  
Mizler-Monroe, J., 261  
Mizutani, A., 237  
Mizutani, A.-C., 315  
Mizutani, Y., 309  
Mizuta, G.M.M., 233  
Mizutani, S., 147  
Mizutani, A., 375  
Mizutani, T., 338  
Mizutani, T., 118, 146, 208  
Mizutani-Chalovitz, H., 288  
Mizutani, Y., 231  
Mizutani, R., 258  
Mizutani, V., 341  
Mizutani, G., 388  
Mizutani, T.N., 235  
Mizutani, D., 56  
Mizutani, O., 138  
Mizutani, J., 138  
Mizutani, M., 60  
Mizutani, M.Y., 235  
Mizutani, H., 235  
Miyasawa, N.R., 171, 300  
Miyahara, V.V., 137  
Miyahara, V.V., 329  
Miyahara, H., 336  
Miyata, L., 76, 88, 287  
Miyata, H., 183](https://</a></p>
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Nack, M., 317  
Nader, M.S., 387  
Nagahara, M., 165  
Nagata, G., 331  
Nagai, L., 79  
Naka, T., 238, 369  
Nakada, C., 327  
Nakamura, M., 59  
Nakano, M., 58  
Nakata, N., 395  
Nakoto, I., 90  
Nam, M.-K., 302, 178  
Nam, T.-J., 308  
Nanajiyay, S., 283  
Nance, J., 227  
Napolitano, V., 308  
Narita, K., 362  
Narita, N., 216  
Nao, K., 361  
Nasikava, G.L., 133  
Nasiri-Banizadeh, M., 219  
Nathan, I., 308  
Nativ, D., 115  
Natsch-Bak, M., 207, 208  
Nawroth, P., 264  
Nawroth, N., 146  
Nawroth, T., 402  
Nawroth, A.A., 116  
Nawroth, A., 76, 285, 305  
Nawroth-Torad, R., 260  
Navarro Bernal, G., 208  
Navarro, P., 210  
Navarro, G., 265  
Navarro, N.J., 136  
Navarro, R., 138  
Navarro, A.M., 153  
Navarro, V., 170  
Navarro, A., 181  
Nave, T., 379  
Navon, P., 197  
Nayag, G., 151  
Nayag, M., 151  
Nayag, S.A., 238  
Nayag, Y., 407  
Nayindorj, L.J., 188  
Nayindorj, V.V., 137  
Nayindorj-Walton, C., 312  
Nayindorj, O., 166  
Nayindorj, O.V., 167  
Nayindorj, W., 69  
Nomi-Gargani, M., 173  
Nepal, S., 183  
Nepowski, K., 127  
Nesher, E., 174  
Nesher, N., 241  
Nesher, P., 271, 273  
Nesher, N., 89  
Nesher, K.M., 212  
Nesher, H., 70  
Nesher, S., 173  
Nesher, U., 408  
Nesher, A., 251  
Nesher, G., 408  
Nesher, G.A., 131, 132, 134  
Nesher, I., 381  
Nesher, G., 205  
Nesher, W., 377  
Nesher, M., 87  
Nesher, L.S., 147  
Nesher, I., 383  
Nesher, K., 175  
Nesher, G., 338  
Nesher, O.S., 280  
Nesher, L.S., 147  
Nesher, I., 383  
Nesher, A.C., 206  
Nesher, P., 188, 198, 386  
Nesher, A., 387  
Nesher, M., 96, 225, 227  
Nesher, A.M., 383  
Nesher, S., 200  
Nesher, I., 383  
Nesher, A., 127  
Nesher, N., 84  
Nesher, N.A., 145  
Nesher, N.A., 134, 139  
Nesher, T., 142  
Nesher, M.Y., 235  
Nesher, A., 388  
Nesher, M., 134  
Nesher, G., 341  
Nesher, S., 341  
Nesher, E., 341  
Nesher, A., 341  
Nesher, A.D., 178, 180

Nikolaev Marić, T., 202  
Nikol, D., 387  
Ning, J., 335  
Nishino, T., 247  
Nishino, M., 284, 285, 286  
Nita, R., 277  
Nishitani, A., 338  
Nishitani, W., 407  
Nishitani, M., 58  
Noda, T., 38  
Noguchi, C.R., 72, 313  
Noguchi, G.R., 313  
Noh, E.K., 147  
Noh, I., 351  
Noguchi, S., 373  
Noh, S., 243  
Noh, G.A., 286  
Noh, A., 281, 281  
Noh, K., 351  
Novák, P., 331, 341  
Novák, M.S., 145  
Novikova, I., 92, 135  
Novikova, J., 276  
Novikova, G., 138  
Novotny, N., 117  
Novotny, E., 204, 323  
Nole Kang, P., 197  
Nokar, M., 189  
Noro, M.J., 182  
Noro, S., 98  
Norgulova, A., 118  
Norgulova, S., 321  
Norkov, I.K., 299  
Nori-Tok, A., 289  
O'Donnell, J.P., 338  
O'Keefe, R., 401  
O'Shea, M., 80  
Oshin, P., 110, 227, 273, 383  
Oshin, T., 328  
Oshin, V., 328  
Oshin, M.A.H., 144  
Oshin, P., 388  
Oshin, P., 328  
Oshin, L.J., 188  
Oshin, N., 286  
Oshin-Zarova, A., 153  
Oshin, P., 346  
Oshin, M.M., 57  
Oshin, D., 374  
Oshin, E.S., 132  
Oshin, W., 390  
Oshin, T., 405  
Oshin, L., 174  
Oshin, A., 263  
Oshin, M., 238  
Oshin, T., 235  
Oshin, D., 230  
Oshin, H., 257, 301  
Oshin, I., 381  
Oshin, K.S., 314  
Oshin, N., 238  
Oshin, N., 38  
Oshin, S., 173  
Oshin, T., 264  
Oshin, K., 75  
Oshin, G., 338  
Oshin, O.S., 280  
Oshin, L.S., 147  
Oshin, N., 230  
Oshin, A.C., 206  
Oshin, P., 188, 198, 386  
Oshin, A., 387  
Oshin, M., 96, 225, 227  
Oshin, A.M., 383  
Oshin, S., 200  
Oshin, I., 383  
Oshin, A., 127  
Oshin, N., 84  
Oshin, N.A., 145  
Oshin, N.A., 134, 139  
Oshin, T., 142  
Oshin, M.Y., 235  
Oshin, A., 388  
Oshin, N.R., 171, 300  
Oshin, V.V., 137  
Oshin, V.V., 329  
Oshin, H., 336  
Oshin, L., 76, 88, 287  
Oshin, H., 183

Oshin, M., 232, 285  
Oshin, M., 144  
Oshin, T., 369  
Oshin, L., 235  
Oshin, M., 86  
Oshin, S.N., 234  
Oshin, Y., 94  
Oshin, N., 84  
Oshin, M., 58  
Oshin, L., 215  
Oshin, J.M., 202  
Oshin, S., 284, 285, 286  
Oshin, S.I., 353  
Oshin, V.C., 197  
Oshin, S., 126  
Oshin, R., 98, 139  
Oshin, V., 98, 132  
Oshin, L., 131  
Oshin, L., 136, 140, 143  
Oshin, L., 146  
Oshin, L., 371  
Oshin, C., 343  
Oshin, O.S., 199  
Oshin, M., 386  
Oshin, A.A., 80, 82, 83, 84, 85, 86, 183  
Oshin, A., 247  
Oshin, M.S., 377  
Oshin, S., 89  
Oshin, C., 200  
van Oshin, A., 216  
Oshin, H., 337  
Oshin, L., 408  
Oshin, E., 153  
Oshin, S., 177, 309  
Oshin, Y., 136  
Oshin, S., 110  
Oshin, U., 227  
Oshin, M., 265  
Oshin, D., 123, 279  
Oshin, H., 384  
Oshin, A.K., 322  
Oshin, N.K., 111  
Oshin, M., 349  
Oshin, P., 126  
Oshin, T., 83  
Oshin, A., 340  
Oshin, N., 286  
Oshin-Zarova, A., 153  
Oshin, P., 346  
Oshin, M.M., 57  
Oshin, D., 374  
Oshin, E.S., 132  
Oshin, W., 390  
Oshin, T., 405  
Oshin, L., 174  
Oshin, A., 263  
Oshin, M., 238  
Oshin, T., 235  
Oshin, D., 230  
Oshin, H., 257, 301  
Oshin, I., 381  
Oshin, K.S., 314  
Oshin, N., 238  
Oshin, N., 38  
Oshin, S., 173  
Oshin, T., 264  
Oshin, K., 75  
Oshin, G., 338  
Oshin, O.S., 280  
Oshin, L.S., 147  
Oshin, N., 230  
Oshin, A.C., 206  
Oshin, P., 188, 198, 386  
Oshin, A., 387  
Oshin, M., 96, 225, 227  
Oshin, A.M., 383  
Oshin, S., 200  
Oshin, I., 383  
Oshin, A., 127  
Oshin, N., 84  
Oshin, N.A., 145  
Oshin, N.A., 134, 139  
Oshin, T., 142  
Oshin, M.Y., 235  
Oshin, A., 388  
Oshin, N.R., 171, 300  
Oshin, V.V., 137  
Oshin, V.V., 329  
Oshin, H., 336  
Oshin, L., 76, 88, 287  
Oshin, H., 183

Oshin, M., 232, 285  
Oshin, M., 144  
Oshin, T., 369  
Oshin, L., 235  
Oshin, M., 86  
Oshin, S.N., 234  
Oshin, Y., 94  
Oshin, N., 84  
Oshin, M., 58  
Oshin, L., 215  
Oshin, J.M., 202  
Oshin, S., 284, 285, 286  
Oshin, S.I., 353  
Oshin, V.C., 197  
Oshin, S., 126  
Oshin, R., 98, 139  
Oshin, V., 98, 132  
Oshin, L., 131  
Oshin, L., 136, 140, 143  
Oshin, L., 146  
Oshin, L., 371  
Oshin, C., 343  
Oshin, O.S., 199  
Oshin, M., 386  
Oshin, A.A., 80, 82, 83, 84, 85, 86, 183  
Oshin, A., 247  
Oshin, M.S., 377  
Oshin, S., 89  
Oshin, C., 200  
van Oshin, A., 216  
Oshin, H., 337  
Oshin, L., 408  
Oshin, E., 153  
Oshin, S., 177, 309  
Oshin, Y., 136  
Oshin, S., 110  
Oshin, U., 227  
Oshin, M., 265  
Oshin, D., 123, 279  
Oshin, H., 384  
Oshin, A.K., 322  
Oshin, N.K., 111  
Oshin, M., 349  
Oshin, P., 126  
Oshin, T., 83  
Oshin, A., 340  
Oshin, N., 286  
Oshin-Zarova, A., 153  
Oshin, P., 346  
Oshin, M.M., 57  
Oshin, D., 374  
Oshin, E.S., 132  
Oshin, W., 390  
Oshin, T., 405  
Oshin, L., 174  
Oshin, A., 263  
Oshin, M., 238  
Oshin, T., 235  
Oshin, D., 230  
Oshin, H., 257, 301  
Oshin, I., 381  
Oshin, K.S., 314  
Oshin, N., 238  
Oshin, N., 38  
Oshin, S., 173  
Oshin, T., 264  
Oshin, K., 75  
Oshin, G., 338  
Oshin, O.S., 280  
Oshin, L.S., 147  
Oshin, N., 230  
Oshin, A.C., 206  
Oshin, P., 188, 198, 386  
Oshin, A., 387  
Oshin, M., 96, 225, 227  
Oshin, A.M., 383  
Oshin, S., 200  
Oshin, I., 383  
Oshin, A., 127  
Oshin, N., 84  
Oshin, N.A., 145  
Oshin, N.A., 134, 139  
Oshin, T., 142  
Oshin, M.Y., 235  
Oshin, A., 388  
Oshin, N.R., 171, 300  
Oshin, V.V., 137  
Oshin, V.V., 329  
Oshin, H., 336  
Oshin, L., 76, 88, 287  
Oshin, H., 183