## **Bo-Feng Zhu**

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Comprehensive analyses for genetic diversities of 19 autosomal STRs in Chinese Kazak group and its phylogenetic relationships with other continental populations. Forensic Sciences Research, 2022, 7, 163-171.	0.9	3
2	Genetic polymorphisms and phylogenetic analyses of the Ü-Tsang Tibetan from Lhasa based on 30 slowly and moderately mutated Y-STR loci. Forensic Sciences Research, 2022, 7, 181-188.	0.9	5
3	Dual origins of the Northwest Chinese Kyrgyz: the admixture of Bronze age Siberian and Medieval Niru'un Mongolian Y chromosomes. Journal of Human Genetics, 2022, 67, 175-180.	1.1	4
4	Genetic characterization evaluation of a novel multiple system containing 57 deletion/insertion polymorphic loci with short amplicons in Hunan Han population and its intercontinental populations analyses. Gene, 2022, 809, 146006.	1.0	5
5	Establishing an integrated pipeline for automatic and efficient detection of trace DNA encountered in forensic applications. Science and Justice - Journal of the Forensic Science Society, 2022, 62, 50-59.	1.3	0
6	Evaluations and comparisons of microbial diversities in four types of body fluids based on two 16S rRNA gene sequencing methods. Forensic Science International, 2022, 331, 111128.	1.3	5
7	Development a multiplex panel of AISNPs, multiâ€allelic InDels, microhaplotypes, and Yâ€&NP/InDel loci for multiple forensic purposes via the NGS. Electrophoresis, 2022, 43, 632-644.	1.3	6
8	Forensic features and genetic structure revealed by 47 Individual Identification InDels in the Shaanxi Han population. Legal Medicine, 2022, 56, 102030.	0.6	0
9	Genetic insights and evaluation of forensic features in Mongolian and Ewenki groups using the InDel variations. Frontiers in Bioscience, 2022, 27, 067.	0.8	2
10	Genetic Background of Kirgiz Ethnic Group From Northwest China Revealed by Mitochondrial DNA Control Region Sequences on Massively Parallel Sequencing. Frontiers in Genetics, 2022, 13, 729514.	1.1	2
11	Genetic diversity analysis of forty-three insertion/deletion loci for forensic individual identification in Han Chinese from Beijing based on a novel panel. Journal of Zhejiang University: Science B, 2022, 23, 241-248.	1.3	3
12	Multiple genetic analyses for Chinese Hunan Han population via 46 A-STRs. Annals of Human Biology, 2022, , 1-26.	0.4	0
13	Forensic Feature Exploration and Comprehensive Genetic Insights Into Yugu Ethnic Minority and Northern Han Population via a Novel NGS-Based Marker Set. Frontiers in Genetics, 2022, 13, .	1.1	1
14	Independent development and validation of a novel sixâ€color fluorescence multiplex panel including 61 diallelic DIPs and 2 miniSTRs for forensic degradation sample. Electrophoresis, 2022, 43, 1423-1437.	1.3	7
15	Forensic and genetic landscape explorations of Chinese Kyrgyz group based on autosomal SNPs, Y-chromosomal SNPs and STRs. Gene, 2022, 832, 146552.	1.0	1
16	Insights into AIM-InDel diversities in Yunnan Miao and Hani ethnic groups of China for forensic and population genetic purposes. Hereditas, 2022, 159, 22.	0.5	1
17	Exploration of the microbiome community for saliva, skin, and a mixture of both from a population living in Guangdong. International Journal of Legal Medicine, 2021, 135, 53-62.	1.2	14
18	The Polymorphism Analyses of Short Tandem Repeats as a Basis for Understanding the Genetic Characteristics of the Guanzhong Han Population. BioMed Research International, 2021, 2021, 1-13.	0.9	3

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19	A Novel Panel of 43 Insertion/Deletion Loci for Human Identifications of Forensic Degraded DNA Samples: Development and Validation. Frontiers in Genetics, 2021, 12, 610540.	1.1	24
20	Development of the decision tree model for distinguishing individuals of Chinese four surnames from Zhanjiang Han population based on Y-STR haplotypes. Legal Medicine, 2021, 49, 101848.	0.6	1
21	The forensic landscape and the population genetic analyses of Hainan Li based on massively parallel sequencing DNA profiling. International Journal of Legal Medicine, 2021, 135, 1295-1317.	1.2	16
22	Diversities of HLA-A, -B, -C, -DRB1 and -DQB1 loci in Chinese Kazak population and its genetic relatedness dissection with multiple populations: a comparative study. Human Immunology, 2021, 82, 215-225.	1.2	1
23	Developmental validations of a self-developed 39 AIM-InDel panel and its forensic efficiency evaluations in the Shaanxi Han population. International Journal of Legal Medicine, 2021, 135, 1359-1367.	1.2	16
24	Haplotype diversity and phylogenetic relationship analysis of Chinese Yulin Han population using 59 Y-STR loci of two novel Y-STR typing systems. Legal Medicine, 2021, 50, 101871.	0.6	3
25	Genetic structure analyses and ancestral information inference of Chinese Kyrgyz group via a panel of 39 AIM-DIPs. Genomics, 2021, 113, 2056-2064.	1.3	3
26	Fine-Scale Genetic Structure and Natural Selection Signatures of Southwestern Hans Inferred From Patterns of Genome-Wide Allele, Haplotype, and Haplogroup Lineages. Frontiers in Genetics, 2021, 12, 727821.	1.1	15
27	Aptamerâ€mediated synthesis of multifunctional nanoâ€hydroxyapatite for active tumour bioimaging and treatment. Cell Proliferation, 2021, 54, e13105.	2.4	21
28	Validation of a 6-Dye Short Tandem Repeat System: A Dry Kit With Lyophilized Amplification Reagent. Frontiers in Genetics, 2021, 12, 705819.	1.1	1
29	Comprehensive Insights Into Forensic Features and Genetic Background of Chinese Northwest Hui Group Using Six Distinct Categories of 231 Molecular Markers. Frontiers in Genetics, 2021, 12, 705753.	1.1	5
30	Polymorphic investigation and interpopulation genetic differentiation analyses of 20 STR loci in Inner Mongolia Han population. Gene Reports, 2021, 25, 101373.	0.4	0
31	Forensic Application Evaluation of a Novel Canine STR System in Pembroke Welsh Corgi and Shiba Inu Groups. BioMed Research International, 2021, 2021, 1-7.	0.9	1
32	Systematic Evaluation of a Novel 6-dye Direct and Multiplex PCR-CE-Based InDel Typing System for Forensic Purposes. Frontiers in Genetics, 2021, 12, 744645.	1.1	9
33	Development and Performance Evaluation of a Novel Ancestry Informative DIP Panel for Continental Origin Inference. Frontiers in Genetics, 2021, 12, 801275.	1.1	4
34	The validation study of a novel assay with 30 slow and moderate mutation Y-STR markers for criminal investigation and database applications. International Journal of Legal Medicine, 2020, 134, 491-499.	1.2	9
35	Detection and analysis of the cause of false-tetra-allelic patterns of locus D10S1435 at the sequence level. International Journal of Legal Medicine, 2020, 134, 833-843.	1.2	1
36	MicroRNAâ€214â€3p modified tetrahedral framework nucleic acids target survivin to induce tumour cell apoptosis. Cell Proliferation, 2020, 53, e12708.	2.4	25

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37	Haplogroup Structure and Genetic Variation Analyses of 60 Mitochondrial DNA Markers in Southern Shaanxi Han Population. Biochemical Genetics, 2020, 58, 279-293.	0.8	3
38	AS1411 aptamer modified carbon dots via polyethylenimineâ€assisted strategy for efficient targeted cancer cell imaging. Cell Proliferation, 2020, 53, e12713.	2.4	45
39	Ancestry informative DIP loci for dissecting genetic structure and ancestry proportions of Qinghai Tibetan and Tibet Tibetan groups. Molecular Biology Reports, 2020, 47, 1079-1087.	1.0	5
40	Biogeographic origin prediction of three continental populations through 42 ancestry informative SNPs. Electrophoresis, 2020, 41, 235-245.	1.3	8
41	Developmental validation study of a 24-plex Y-STR direct amplification system for forensic application. International Journal of Legal Medicine, 2020, 134, 945-951.	1.2	8
42	Forensic applicability of autosomal insertion/deletion loci in Chinese Daur ethnic group and genetic affinity evaluations between Daur group and reference populations. Legal Medicine, 2020, 47, 101741.	0.6	2
43	The Genetic Structure of Chinese Hui Ethnic Group Revealed by Complete Mitochondrial Genome Analyses Using Massively Parallel Sequencing. Genes, 2020, 11, 1352.	1.0	13
44	Development and Validation of a Novel Five-Dye Short Tandem Repeat Panel for Forensic Identification of 11 Species. Frontiers in Genetics, 2020, 11, 1005.	1.1	5
45	A set of novel multiâ€allelic SNPs for forensic application developed through massively parallel sequencing and its examples of population genetic studies. Electrophoresis, 2020, 41, 2036-2046.	1.3	2
46	Genetic Structural Differentiation Analyses of Intercontinental Populations and Ancestry Inference of the Chinese Hui Group Based on a Novel Developed Autosomal AIM-InDel Genotyping System. BioMed Research International, 2020, 2020, 1-12.	0.9	5
47	Cloning, expression and enzyme activity delineation of two novel CANT1 mutations: the disappearance of dimerization may indicate the change of protein conformation and even function. Orphanet Journal of Rare Diseases, 2020, 15, 240.	1.2	4
48	A Highly Polymorphic Panel Consisting of Microhaplotypes and Compound Markers with the NGS and Its Forensic Efficiency Evaluations in Chinese Two Groups. Genes, 2020, 11, 1027.	1.0	11
49	Ancestry Prediction Comparisons of Different AISNPs for Five Continental Populations and Population Structure Dissection of the Xinjiang Hui Group via a Self-Developed Panel. Genes, 2020, 11, 505.	1.0	9
50	Next generation sequencing of a set of ancestry-informative SNPs: ancestry assignment of three continental populations and estimating ancestry composition for Mongolians. Molecular Genetics and Genomics, 2020, 295, 1027-1038.	1.0	5
51	Forensic characteristic and population structure dissection of Shaanxi Han population in the light of diallelic deletion/insertion polymorphism data. Genomics, 2020, 112, 3837-3845.	1.3	5
52	Pegylated carbon nitride nanosheets for enhanced reactive oxygen species generation and photodynamic therapy under hypoxic conditions. Nanomedicine: Nanotechnology, Biology, and Medicine, 2020, 25, 102167.	1.7	10
53	Ancestry inference and admixture component estimations of Chinese Kazak group based on 165 AIM-SNPs via NGS platform. Journal of Human Genetics, 2020, 65, 461-468.	1.1	12
54	A small NGS–SNP panel of ancestry inference designed to distinguish African, European, East, and South Asian populations. Electrophoresis, 2020, 41, 649-656.	1.3	13

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55	Genetic Polymorphisms and Forensic Efficiencies of a Set of Novel Autosomal InDel Markers in a Chinese Mongolian Group. BioMed Research International, 2020, 2020, 1-9.	0.9	4
56	Developing and population analysis of a new multiplex panel of 18 microhaplotypes and compound markers using next generation sequencing and its application in the Shaanxi Han population. Electrophoresis, 2020, 41, 1230-1237.	1.3	11
57	Insights into the genetic characteristics and population structures of Chinese two Tibetan groups using 35 insertion/deletion polymorphic loci. Molecular Genetics and Genomics, 2020, 295, 957-968.	1.0	7
58	Joint Genetic Analyses of Mitochondrial and Y-Chromosome Molecular Markers for a Population from Northwest China. Genes, 2020, 11, 564.	1.0	2
59	Potent antiâ€angiogenesis and antiâ€ŧumour activity of pegaptanibâ€loaded tetrahedral DNA nanostructure. Cell Proliferation, 2019, 52, e12662.	2.4	17
60	Multiple genetic analyses to investigate the polymorphisms of Chinese Mongolian population with an efficient short tandem repeat panel. Croatian Medical Journal, 2019, 60, 191-200.	0.2	5
61	Polymorphism analyses of 19 STRs in Labrador Retriever population from China and its heterozygosity comparisons with other retriever breeds. Molecular Biology Reports, 2019, 46, 1577-1584.	1.0	12
62	The endocytic pathways of carbon dots in human adenoid cystic carcinoma cells. Cell Proliferation, 2019, 52, e12586.	2.4	21
63	P34HB electrospun fibres promote bone regeneration in vivo. Cell Proliferation, 2019, 52, e12601.	2.4	23
64	The massive assimilation of indigenous East Asian populations in the origin of Muslim Hui people inferred from paternal Y chromosome. American Journal of Physical Anthropology, 2019, 169, 341-347.	2.1	16
65	Genetic distribution and forensic evaluation of multiplex autosomal short tandem repeats in the Chinese Xinjiang Mongolian group. Journal of Zhejiang University: Science B, 2019, 20, 287-290.	1.3	2
66	Development of a novel multiplex polymerase chain reaction system for forensic individual identification using insertion/deletion polymorphisms. Electrophoresis, 2019, 40, 1691-1698.	1.3	25
67	Genetic distribution analyses and population background explorations of Gansu Yugur and Guizhou Miao groups via InDel markers. Journal of Human Genetics, 2019, 64, 535-543.	1.1	9
68	Distinguishing three distinct biogeographic regions with an inâ€house developed 39â€AIMâ€InDel panel and further admixture proportion estimation for Uyghurs. Electrophoresis, 2019, 40, 1525-1534.	1.3	46
69	Internal validation study of a newly developed 24-plex Y-STRs genotyping system for forensic application. International Journal of Legal Medicine, 2019, 133, 733-743.	1.2	13
70	KIR gene presence/absence polymorphisms and global diversity in the Kirgiz ethnic minority and populations distributed worldwide. Molecular Biology Reports, 2019, 46, 1043-1055.	1.0	2
71	Genetic polymorphism analysis of mitochondrial DNA from Chinese XinjiangÂKazakÂethnic group by a novel mitochondrial DNA genotyping panel. Molecular Biology Reports, 2019, 46, 17-25.	1.0	10
72	A set of novel SNP loci for differentiating continental populations and three Chinese populations. PeerJ, 2019, 7, e6508.	0.9	9

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73	Forensic characteristics and population genetics of Chinese Kazakh ethnic minority with an efficient STR panel. PeerJ, 2019, 7, e6802.	0.9	1
74	Forensic molecular genetic diversity analysis of Chinese Hui ethnic group based on a novel STR panel. International Journal of Legal Medicine, 2018, 132, 1297-1299.	1.2	22
75	Genetic structure and polymorphism analysis of Xinjiang Hui ethnic minority based on 21 STRs. Molecular Biology Reports, 2018, 45, 99-108.	1.0	12
76	CDK5-mediated tau accumulation triggers methamphetamine-induced neuronal apoptosis via endoplasmic reticulum-associated degradation pathway. Toxicology Letters, 2018, 292, 97-107.	0.4	31
77	Mutation analysis of 19 commonly used short tandem repeat loci in a Guangdong Han population. Legal Medicine, 2018, 32, 92-97.	0.6	8
78	A set of autosomal multiple InDel markers for forensic application and population genetic analysis in the Chinese Xinjiang Hui group. Forensic Science International: Genetics, 2018, 35, 1-8.	1.6	43
79	CRB3 regulates contact inhibition by activating the Hippo pathway in mammary epithelial cells. Cell Death and Disease, 2018, 8, e2546-e2546.	2.7	34
80	Regulating osteogenesis and adipogenesis in adiposeâ€derived stem cells by controlling underlying substrate stiffness. Journal of Cellular Physiology, 2018, 233, 3418-3428.	2.0	55
81	Genetic characteristics of 19 STRs in Chinese Uzbek ethnic and its phylogenetic relationships with other 24 populations. International Journal of Legal Medicine, 2018, 132, 729-731.	1.2	3
82	Population Genetic Diversity and Clustering Analysis for Chinese Dongxiang Group With 30 Autosomal InDel Loci Simultaneously Analyzed. Frontiers in Genetics, 2018, 9, 279.	1.1	16
83	Research Progress of the Types and Preparation Techniques of Scaffold Materials in Cartilage Tissue Engineering. Current Stem Cell Research and Therapy, 2018, 13, 583-590.	0.6	16
84	Genetic and structural characterization of 20 autosomal short tandem repeats in the Chinese Qinghai Han population and its genetic relationships and interpopulation differentiations with other reference populations. Forensic Sciences Research, 2018, 3, 145-152.	0.9	7
85	Forensic efficiency estimate and phylogenetic analysis for Chinese Kyrgyz ethnic group revealed by a panel of 21 short tandem repeats. Royal Society Open Science, 2018, 5, 172089.	1.1	13
86	SUMOylation of Alpha-Synuclein Influences on Alpha-Synuclein Aggregation Induced by Methamphetamine. Frontiers in Cellular Neuroscience, 2018, 12, 262.	1.8	19
87	Effect of substrate stiffness on proliferation and differentiation of periodontal ligament stem cells. Cell Proliferation, 2018, 51, e12478.	2.4	37
88	Doxorubicin conjugated carbon dots as a drug delivery system for human breast cancer therapy. Cell Proliferation, 2018, 51, e12488.	2.4	115
89	Autosomal DIPs for population genetic structure and differentiation analyses of Chinese Xinjiang Kyrgyz ethnic group. Scientific Reports, 2018, 8, 11054.	1.6	21
90	Mutability analysis towards 21 STR loci included in the AGCU 21 + 1 kit in Chinese Han population. International Journal of Legal Medicine, 2018, 132, 1287-1291.	1.2	8

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91	Electrospun Fibers for Cartilage Tissue Regeneration. Current Stem Cell Research and Therapy, 2018, 13, 591-599.	0.6	13
92	Genetic polymorphisms and forensic efficiency of 19 X-chromosomal STR loci for Xinjiang Mongolian population. PeerJ, 2018, 6, e5117.	0.9	15
93	Forensic effectiveness and population differentiations study of AGCU 21 + 1 fluorescence multiplex in Chinese Henan Han population. Forensic Science International: Genetics, 2017, 28, e18-e21.	1.6	5
94	Effect of matrix stiffness on osteoblast functionalization. Cell Proliferation, 2017, 50, .	2.4	67
95	Genetic polymorphism and evolutionary differentiation of Eastern Chinese Han: a comprehensive and comparative analysis on KIRs. Scientific Reports, 2017, 7, 42486.	1.6	8
96	Hypoxia triggers angiogenesis by increasing expression of LOX genes in 3-D culture of ASCs and ECs. Experimental Cell Research, 2017, 352, 157-163.	1.2	16
97	Chinese Xibe population genetic composition according to linkage groups of X-chromosomal STRs: population genetic variability and interpopulation comparisons. Annals of Human Biology, 2017, 44, 546-553.	0.4	12
98	Detection of fetal epigenetic biomarkers through genome-wide DNA methylation study for non-invasive prenatal diagnosis. Molecular Medicine Reports, 2017, 15, 3989-3998.	1.1	12
99	Genetic polymorphisms of 54 mitochondrial DNA SNP loci in Chinese Xibe ethnic minority group. Scientific Reports, 2017, 7, 44407.	1.6	14
100	<i>MMPâ€2</i> and Notch signal pathway regulate migration of adiposeâ€derived stem cells and chondrocytes in coâ€culture systems. Cell Proliferation, 2017, 50, .	2.4	16
101	Curved microstructures promote osteogenesis of mesenchymal stem cells via the RhoA/ <scp>ROCK</scp> pathway. Cell Proliferation, 2017, 50, .	2.4	40
102	Substrate stiffness regulates arterial-venous differentiation of endothelial progenitor cells via the Ras/Mek pathway. Biochimica Et Biophysica Acta - Molecular Cell Research, 2017, 1864, 1799-1808.	1.9	29
103	Angiogenesis in a 3D model containing adipose tissue stem cells and endothelial cells is mediated by canonical Wnt signaling. Bone Research, 2017, 5, 17048.	5.4	52
104	Genetic diversity and haplotypic structure of Chinese Kazak ethnic group revealed by 19 STRs on the X chromosome. Gene, 2017, 600, 64-69.	1.0	27
105	The <scp>JAK</scp> / <scp>STAT</scp> 3 signalling pathway regulated angiogenesis in an endothelial cell/adiposeâ€derived stromal cell coâ€culture, 3D gel model. Cell Proliferation, 2017, 50, .	2.4	60
106	Forensic efficiency and genetic variation of 30 InDels in Vietnamese and Nigerian populations. Oncotarget, 2017, 8, 88934-88940.	0.8	17
107	Genetic variation and forensic efficiency of autosomal insertion/deletion polymorphisms in Chinese Bai ethnic group: phylogenetic analysis to other populations. Oncotarget, 2017, 8, 39582-39591.	0.8	11
108	Autosomal InDel polymorphisms for population genetic structure and differentiation analysis of Chinese Kazak ethnic group. Oncotarget, 2017, 8, 56651-56658.	0.8	23

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109	Phylogenic analysis and forensic genetic characterization of Chinese Uyghur group via autosomal multi STR markers. Oncotarget, 2017, 8, 73837-73845.	0.8	25
110	Genetic variation and forensic characteristic analysis of 25 STRs of a novel fluorescence co-amplification system in Chinese Southern Shaanxi Han population. Oncotarget, 2017, 8, 55443-55452.	0.8	8
111	Allele and haplotype diversity of new multiplex of 19 ChrXâ€STR loci in Han population from Guanzhong region (China). Electrophoresis, 2016, 37, 1669-1675.	1.3	23
112	Population Differentiations and Phylogenetic Analysis of Tibet and Qinghai Tibetan Groups Based on 30 InDel Loci. DNA and Cell Biology, 2016, 35, 787-794.	0.9	37
113	Genetic evidence for an East Asian origin of Chinese Muslim populations Dongxiang and Hui. Scientific Reports, 2016, 6, 38656.	1.6	46
114	24 Y-chromosomal STR haplotypic structure for Chinese Kazak ethnic group and its genetic relationships with other groups. International Journal of Legal Medicine, 2016, 130, 1199-1201.	1.2	8
115	Genetic structure and differentiation analysis of a Eurasian Uyghur population by use of 27 continental ancestry-informative SNPs. International Journal of Legal Medicine, 2016, 130, 897-903.	1.2	4
116	Study of genetic diversity of killer cell immunoglobulin-like receptor loci in the Tujia ethnic minority. Human Immunology, 2016, 77, 869-875.	1.2	4
117	Genetic polymorphism analyses of a novel panel of 19 X-STR loci in the Chinese Uygur ethnic minority. Journal of Zhejiang University: Science B, 2016, 17, 367-374.	1.3	13
118	A 30-InDel Assay for Genetic Variation and Population Structure Analysis of Chinese Tujia Group. Scientific Reports, 2016, 6, 36842.	1.6	32
119	Population genetic structure analysis and forensic evaluation of Xinjiang Uigur ethnic group on genomic deletion and insertion polymorphisms. SpringerPlus, 2016, 5, 1087.	1.2	27
120	<scp>PCL</scp> â€ <scp>PEG</scp> â€ <scp>PCL</scp> film promotes cartilage regeneration in vivo. Cell Proliferation, 2016, 49, 729-739.	2.4	44
121	Autosomal-STR based genetic structure of Chinese Xibe ethnic group and its relationships to various groups. International Journal of Legal Medicine, 2016, 130, 1501-1503.	1.2	22
122	Genetic analysis of 15 mtDNA SNP loci in Chinese Yi ethnic group using SNaPshot minisequencing. Gene, 2016, 576, 105-108.	1.0	8
123	Genetic Variability and Phylogenetic Analysis of Han Population from Guanzhong Region of China based on 21 non-CODIS STR Loci. Scientific Reports, 2015, 5, 8872.	1.6	26
124	Developmental validation of the AGCU 21+1 STR kit: A novel multiplex assay for forensic application. Electrophoresis, 2015, 36, 271-276.	1.3	48
125	Forensic evaluation and population genetic study of 30 insertion/deletion polymorphisms in a Chinese Yi group. Electrophoresis, 2015, 36, 1196-1201.	1.3	30
126	Genetic diversities of 20 novel autosomal STRs in Chinese Xibe ethnic group and its genetic relationships with neighboring populations. Gene, 2015, 557, 222-228.	1.0	20

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127	Allelic diversity of KIR3DL1/3DS1 in a southern Chinese population. Human Immunology, 2015, 76, 663-666.	1.2	9
128	Genetic polymorphism analyses of 30 InDels in Chinese Xibe ethnic group and its population genetic differentiations with other groups. Scientific Reports, 2015, 5, 8260.	1.6	43
129	24 Y hromosomal STR haplotypic polymorphisms for Chinese Uygur ethnic group and its phylogenic analysis with other Chinese groups. Electrophoresis, 2015, 36, 626-632.	1.3	9
130	Analysis of 19 STR loci reveals genetic characteristic of eastern Chinese Han population. Forensic Science International: Genetics, 2015, 14, 108-109.	1.6	38
131	Genetic diversity and haplotype structure of 24 <scp>Y</scp> â€chromosomal <scp>STR</scp> in <scp>C</scp> hinese <scp>H</scp> ui ethnic group and its genetic relationships with other populations. Electrophoresis, 2014, 35, 1993-2000.	1.3	22
132	Genetic polymorphisms of 20 short tandem repeat loci from the Han population in Henan, China. Electrophoresis, 2014, 35, 1509-1514.	1.3	26
133	Diversity study of 12 <scp>X</scp> â€chromosomal <scp>STR</scp> loci in <scp>H</scp> ui ethnic from <scp>C</scp> hina. Electrophoresis, 2014, 35, 2001-2007.	1.3	15
134	Genetic profile characterization and population study of 21 autosomal <scp>STR</scp> in <scp>C</scp> hinese <scp>K</scp> azak ethnic minority group. Electrophoresis, 2014, 35, 503-510.	1.3	31
135	Allelic frequency distributions of 21 non-combined DNA index system STR loci in a Russian ethnic minority group from Inner Mongolia, China. Journal of Zhejiang University: Science B, 2013, 14, 533-540.	1.3	23
136	Allelic polymorphic investigation of 21 autosomal short tandem repeat loci in a Chinese Bai ethnic group. Legal Medicine, 2013, 15, 109-113.	0.6	27
137	Polymorphic analysis of 21 new STR loci in Chinese Uigur group. Forensic Science International: Genetics, 2013, 7, e97-e98.	1.6	11
138	Population genetics and forensic efficiency of twentyâ€one novel microsatellite loci of Chinese Yi ethnic group. Electrophoresis, 2013, 34, 3345-3351.	1.3	18
139	The distribution of genetic diversity of KIR genes in the Chinese Mongolian population. Human Immunology, 2012, 73, 1031-1038.	1.2	10
140	Genetic data provided by 21 autosomal STR loci from Chinese Tujia ethnic group. Molecular Biology Reports, 2012, 39, 10265-10271.	1.0	28
141	Genetic polymorphism analysis of killer cell immunoglobulin-like receptor genes in the Chinese Uygur population. Molecular Biology Reports, 2012, 39, 3017-3028.	1.0	8
142	Diversity distributions of killer cell immunoglobulin-like receptor genes and their ligands in the Chinese Shaanxi Han population. Human Immunology, 2011, 72, 733-740.	1.2	13
143	Genetic polymorphism analysis of 15 STR loci in Chinese Hui ethnic group residing in Qinghai province of China. Molecular Biology Reports, 2011, 38, 2315-2322.	1.0	43
144	Genetic diversities of 21 non-CODIS autosomal STRs of a Chinese Tibetan ethnic minority group in Lhasa. International Journal of Legal Medicine, 2011, 125, 581-585.	1.2	39

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145	Population genetic analysis of 15 autosomal STR loci in the Russian population of northeastern Inner-Mongolia, China. Molecular Biology Reports, 2010, 37, 3889-3895.	1.0	22
146	Distributions of HLA-A and -B alleles and haplotypes in the Yi ethnic minority of Yunnan, China: relationship to other populations. Journal of Zhejiang University: Science B, 2010, 11, 127-135.	1.3	21
147	Allelic diversity and haplotype structure of HLA loci in the Chinese Han population living in the Guanzhong region of the Shaanxi province. Human Immunology, 2010, 71, 627-633.	1.2	23
148	Killer cell immunoglobulin-like receptor gene diversity in the Tibetan ethnic minority group of China. Human Immunology, 2010, 71, 1116-1123.	1.2	13
149	Allele Polymorphism and Haplotype Diversity of HLA-A, -B and -DRB1 Loci in Sequence-Based Typing for Chinese Uyghur Ethnic Group. PLoS ONE, 2010, 5, e13458.	1.1	43
150	Population genetic analysis of 15 STR loci of Chinese Tu ethnic minority group. Forensic Science International, 2008, 174, 255-258.	1.3	25
151	Population data of 15 STR loci of Chinese Yi ethnic minority group. Legal Medicine, 2008, 10, 220-224.	0.6	36
152	Genetic analysis of 17 Y-chromosomal STRs haplotypes of Chinese Tibetan ethnic group residing in Qinghai province of China. Forensic Science International, 2008, 175, 238-243.	1.3	58
153	Genetic polymorphisms of 15 STR loci of Chinese Dongxiang and Salar ethnic minority living in Qinghai Province of China. Legal Medicine, 2007, 9, 38-42.	0.6	24
154	Population genetic polymorphisms for 17 Y-chromosomal STRs haplotypes of Chinese Salar ethnic minority group. Legal Medicine, 2007, 9, 203-209.	0.6	24
155	Genetic Analysis for Y Chromosome Short Tandem Repeat Haplotypes of Chinese Han Population Residing in the Ningxia Province of China. Journal of Forensic Sciences, 2006, 51, 1417-1420.	0.9	14
156	Population genetics for Y-chromosomal STRs haplotypes of Chinese Tibetan ethnic minority group in Tibet. Forensic Science International, 2006, 161, 78-83.	1.3	28
157	Genetic polymorphisms for 11 Y-STRs haplotypes of Chinese Yi ethnic minority group. Forensic Science International, 2006, 158, 229-233.	1.3	26
158	Y-STRs haplotypes of Chinese Mongol ethnic group using Y-PLEXâ"¢ 12. Forensic Science International, 2005, 153, 260-263.	1.3	37
159	Population Genetics for Y-STRs Haplotypes of Chinese Ewenki Ethnic Minority Group. Journal of Forensic Sciences, 2005, 50, 1-3.	0.9	6
160	Genetic Analysis of 15 STR Loci of Chinese Uigur Ethnic Population. Journal of Forensic Sciences, 2005, 50, 1-2.	0.9	19
161	Population Data of 15 STR in Chinese Han Population From North of Guangdong. Journal of Forensic Sciences, 2005, 50, 1-2.	0.9	20
162	Population genetics for Y-STRs haplotypes of Chinese Ewenki ethnic minority group. Journal of Forensic Sciences, 2005, 50, 969-71.	0.9	1

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163	Genetic analysis of 15 STR loci of Chinese Uigur ethnic population. Journal of Forensic Sciences, 2005, 50, 1235-6.	0.9	13
164	Genetic polymorphisms of 44 Y chromosomal genetic markers in the Inner Mongolia Han population and its genetic relationship analysis with other reference populations. Forensic Sciences Research, 0, , 1-15.	0.9	0
165	An interpretation of the genetic polymorphism and population genetic background of Ankang Han population via a novel InDel panel. Forensic Sciences Research, 0, , 1-8.	0.9	0
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