

gene name	gene label	gene position	Predicted -10 box	score of predicted box	Space -10 box to start of translation or 1st nt of RNA
>dnaN	pro0001	174..1331	TAGAAT	score: 3.565336720	81
>dnaN	pro0001	174..1331	TAAATT	score: 3.968301383	86
>pro0008	pro0008	10521..11270	TAAACT	score: 4.702840244	23
>pro0008	pro0008	10521..11270	TAAATT	score: 3.968301383	46
>pro0008	pro0008	10521..11270	TATTCT	score: 4.565336720	54
>pro0013	pro0013	16279..17037	TACATT	score: 3.465801047	23
>pro0013	pro0013	16279..17037	TAATTT	score: 3.830797859	50
>pro0013	pro0013	16279..17037	TAAAAT	score: 4.482874556	85
>pro0015	pro0015	18102..18602	TAGGGT	score: 4.090156995	28
>pro0015	pro0015	18102..18602	TACATT	score: 3.465801047	34
>pro0015	pro0015	18102..18602	CATTTT	score: 2.717339814	48
>pro0015	pro0015	18102..18602	TAGGCT	score: 4.090156995	83
>grpE	pro0016	18707..19435	CAATAT	score: 3.231912987	26
>grpE	pro0016	18707..19435	TACTCT	score: 4.062836384	38
>gapA	pro0023	24618..25640	TAGGAT	score: 3.870191306	36
>gapA	pro0023	24618..25640	TAAAAT	score: 4.482874556	73
>pro0029	pro0029	29973..30119	TAATTT	score: 3.830797859	26
>pro0029	pro0029	29973..30119	TATTTT	score: 3.830797859	35
>pro0029	pro0029	29973..30119	CATGCT	score: 3.894236785	46
>pro0029	pro0029	29973..30119	CAAAAT	score: 3.369416510	68
>pro0034	pro0034	32121..32492	CATGGT	score: 3.894236785	71
>pro0035	pro0035	32863..33150	TAAGTT	score: 4.273155969	80
>cbiD	pro0037	34418..35563	TAAGTT	score: 4.273155969	84
>pro0039	pro0039	38158..38769	TATTTT	score: 3.830797859	24
>pro0039	pro0039	38158..38769	CATAAT	score: 3.369416510	33
>pro0039	pro0039	38158..38769	TAGACT	score: 3.785302409	52
>pro0039	pro0039	38158..38769	TATTTT	score: 3.830797859	60
>pro0039	pro0039	38158..38769	TAAACT	score: 4.702840244	91
>alaS	pro0048	49984..52662	TATTGT	score: 4.565336720	47
>alaS	pro0048	49984..52662	GAAGCT	score: 2.572308690	67
>alaS	pro0048	49984..52662	TAGATT	score: 3.050763548	79
>ndk	pro0050	54704..55216	GAAGAT	score: 2.352343001	54
>ndk	pro0050	54704..55216	CAAGTT	score: 3.159697923	89
>gatB	pro0052	56478..57956	TAGTAT	score: 3.427833197	27
>gatB	pro0052	56478..57956	CATAGT	score: 3.589382199	29
>gatB	pro0052	56478..57956	TATTTT	score: 3.830797859	36
>gatB	pro0052	56478..57956	CAATTT	score: 2.717339814	47
>gatB	pro0052	56478..57956	CATGAT	score: 3.674271096	60
>gatB	pro0052	56478..57956	TAATTT	score: 3.830797859	80
>argJ	pro0054	58642..59883	CAGGAT	score: 2.756733261	30
>hupE	pro0055	60286..60918	CAGAAT	score: 2.451878675	36
>hupE	pro0055	60286..60918	TATTCT	score: 4.565336720	53
>hupE	pro0055	60286..60918	TACTGT	score: 4.062836384	80
>rfaG	pro0057	63339..64562	TACTCT	score: 4.062836384	43
>rfaG	pro0057	63339..64562	CAATCT	score: 3.451878675	86
>arnT	pro0059	66592..68190	TATAAT	score: 4.482874556	23
>arnT	pro0059	66592..68190	TACTCT	score: 4.062836384	28
>arnT	pro0059	66592..68190	TAGGTT	score: 3.355618133	33
>arnT	pro0059	66592..68190	TATATT	score: 3.968301383	38
>arnT	pro0059	66592..68190	TAAAAT	score: 4.482874556	53
>wcaA	pro0060	68269..69663	CATAGT	score: 3.589382199	25

>wcaA	pro0060	68269..69663	TAGTAT	score: 3.427833197	31
>wcaA	pro0060	68269..69663	TAGAAT	score: 3.565336720	47
>arnT	pro0062	70715..73054	TATTTT	score: 3.830797859	23
>arnT	pro0062	70715..73054	TATTAT	score: 4.345371032	26
>arnT	pro0062	70715..73054	TAATAT	score: 4.345371032	29
>arnT	pro0062	70715..73054	TAAAAT	score: 4.482874556	52
>arnT	pro0062	70715..73054	CAATTT	score: 2.717339814	67
>gmd	pro0063	73141..74268	TAGATT	score: 3.050763548	23
>gmd	pro0063	73141..74268	TATGCT	score: 5.007694830	47
>gmd	pro0063	73141..74268	CATTGT	score: 3.451878675	58
>pro0065	pro0065	75660..76808	TATTCT	score: 4.565336720	54
>pro0065	pro0065	75660..76808	TATATT	score: 3.968301383	56
>pro0065	pro0065	75660..76808	CAAAAT	score: 3.369416510	69
>pro0068	pro0068	77901..78029	TACATT	score: 3.465801047	56
>pro0069	pro0069	78177..78383	TAGTCT	score: 3.647798885	26
>pro0069	pro0069	78177..78383	TATAGT	score: 4.702840244	28
>pro0069	pro0069	78177..78383	TATTAT	score: 4.345371032	31
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>pro0069	pro0069	78177..78383	TATGTT	score: 4.273155969	47
>pro0069	pro0069	78177..78383	TATTTT	score: 3.830797859	78
>pro0069	pro0069	78177..78383	TAGTGT	score: 3.647798885	85
>smc	pro0071	78939..82493	CAAGAT	score: 3.674271096	65
>smc	pro0071	78939..82493	TAATCT	score: 4.565336720	78
>pro0072	pro0072	82558..83631	CAAAAT	score: 3.369416510	31
>accC	pro0074	85161..86510	TACGAT	score: 4.285228806	25
>accC	pro0074	85161..86510	TACGTT	score: 3.770655633	56
>accC	pro0074	85161..86510	TACGGT	score: 4.505194494	63
>accC	pro0074	85161..86510	GATGAT	score: 2.352343001	73
>psbX	pro0076	86930..87097	TAAGAT	score: 4.787729142	31
>psbX	pro0076	86930..87097	TAAATT	score: 3.968301383	50
>pro0077	pro0077	87184..88242	TATGTT	score: 4.273155969	50
>pro0077	pro0077	87184..88242	TAGACT	score: 3.785302409	55
>dAP2	pro0082	91942..93900	TATTTT	score: 3.830797859	23
>dAP2	pro0082	91942..93900	TAATTT	score: 3.830797859	33
>dAP2	pro0082	91942..93900	TAATGT	score: 4.565336720	50
>dAP2	pro0082	91942..93900	CAAGTT	score: 3.159697923	81
>pro0087	pro0087	98697..99074	TAGGTT	score: 3.355618133	28
>pro0087	pro0087	98697..99074	CATGGT	score: 3.894236785	39
>pro0088	pro0088	99371..100468	TACTAT	score: 3.842870696	32
>pro0088	pro0088	99371..100468	GAAGAT	score: 2.352343001	37
>pgm	pro0090	100718..102376	GATGGT	score: 2.572308690	26
>bcp	pro0093	104471..104938	TACTCT	score: 4.062836384	25
>bcp	pro0093	104471..104938	TATTTT	score: 3.830797859	91
>ndh	pro0096	106440..107624	TAGGTT	score: 3.355618133	27
>ndh	pro0096	106440..107624	CATTAT	score: 3.231912987	43
>ndh	pro0096	106440..107624	CAATTT	score: 2.717339814	73
>citT	pro0097	107726..109546	TACTTT	score: 3.328297523	32
>citT	pro0097	107726..109546	GATGAT	score: 2.352343001	40
>citT	pro0097	107726..109546	CATGCT	score: 3.894236785	50
>pro0102	pro0102	113338..113703	TAGATT	score: 3.050763548	30
>pro0102	pro0102	113338..113703	CAATTT	score: 2.717339814	37
>pro0102	pro0102	113338..113703	CAATCT	score: 3.451878675	55
>pro0102	pro0102	113338..113703	CAAATT	score: 2.854843338	62
>pro0102	pro0102	113338..113703	TAATCT	score: 4.565336720	78
>pro0102	pro0102	113338..113703	TATTTT	score: 3.830797859	89

>uup	pro0105	114223..115932	TATATT	score: 3.968301383	25
>uup	pro0105	114223..115932	TAGTTT	score: 2.913260024	34
>uup	pro0105	114223..115932	CAATAT	score: 3.231912987	40
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>uup	pro0105	114223..115932	TAGTAT	score: 3.427833197	60
>uup	pro0105	114223..115932	TAAGAT	score: 4.787729142	83
>uup	pro0105	114223..115932	CATTAT	score: 3.231912987	90
>pro0107	pro0107	117173..117349	TATTTT	score: 3.830797859	34
>pro0107	pro0107	117173..117349	CATTTT	score: 2.717339814	39
>pro0107	pro0107	117173..117349	TAATTT	score: 3.830797859	51
>pro0107	pro0107	117173..117349	TAGTTT	score: 2.913260024	64
>hli4	pro0110	118186..118335	TAGAAT	score: 3.565336720	22
>pro0118	pro0118	125392..126051	CAATTT	score: 2.717339814	83
>miaB	pro0121	128876..130180	TAATTT	score: 3.830797859	25
>miaB	pro0121	128876..130180	TACTCT	score: 4.062836384	31
>miaB	pro0121	128876..130180	TATTTT	score: 3.830797859	88
>aroK	pro0128	134061..134633	CAAGAT	score: 3.674271096	35
>pro0131	pro0131	135674..135880	CAGAGT	score: 2.671844363	30
>pro0131	pro0131	135674..135880	CAAGGT	score: 3.894236785	36
>pro0131	pro0131	135674..135880	TAAAGT	score: 4.702840244	54
>pro0131	pro0131	135674..135880	TAGAGT	score: 3.785302409	67
>pro0131	pro0131	135674..135880	CAAATT	score: 2.854843338	75
>pro0131	pro0131	135674..135880	CAAAAT	score: 3.369416510	91
>iscA	pro0137	140806..141201	TAAAGT	score: 4.702840244	26
>iscA	pro0137	140806..141201	CAAAAT	score: 3.369416510	46
>iscA	pro0137	140806..141201	TAATGT	score: 4.565336720	82
>iscA	pro0137	140806..141201	CAGTCT	score: 2.534340839	90
>pro0144	pro0144	145956..146219	TATTTT	score: 3.830797859	47
>pro0144	pro0144	145956..146219	TACTAT	score: 3.842870696	50
>pro0144	pro0144	145956..146219	CATACT	score: 3.589382199	52
>ompR	pro0150	150619..151386	TAAATT	score: 3.968301383	33
>ompR	pro0150	150619..151386	TACAAT	score: 3.980374220	65
>ompR	pro0150	150619..151386	CAAAAT	score: 3.369416510	87
>pro0154	pro0154	155480..156001	GATGGT	score: 2.572308690	26
>pro0154	pro0154	155480..156001	CAGGAT	score: 2.756733261	29
>pro0154	pro0154	155480..156001	TATTTT	score: 3.830797859	84
>ompR	pro0156	157514..158257	TAAGAT	score: 4.787729142	33
>ompR	pro0156	157514..158257	GATGAT	score: 2.352343001	53
>ompR	pro0156	157514..158257	TAGTTT	score: 2.913260024	63
>plsC	pro0160	161650..162240	TAGTTT	score: 2.913260024	25
>pcnB	pro0164	163750..164997	CATGTT	score: 3.159697923	56
>pcnB	pro0164	163750..164997	TAAGTT	score: 4.273155969	76
>pcnB	pro0164	163750..164997	CAAAAT	score: 3.369416510	89
>pro0168	pro0168	167991..168338	TATTTT	score: 3.830797859	26
>pro0168	pro0168	167991..168338	TAAAAT	score: 4.482874556	51
>pro0168	pro0168	167991..168338	TAGATT	score: 3.050763548	85
>pro0171	pro0171	170042..170779	TAAATT	score: 3.968301383	58
>pro0171	pro0171	170042..170779	CACACT	score: 3.086881863	64
>nuoM	pro0173	172918..174591	TACACT	score: 4.200339908	26
>pro0174	pro0174	174835..175719	TATTTT	score: 3.830797859	74
>pro0174	pro0174	174835..175719	TAGTTT	score: 2.913260024	81
>csgD	pro0177	177893..178174	TAATAT	score: 4.345371032	26
>csgD	pro0177	177893..178174	TACTAT	score: 3.842870696	57
>csgD	pro0177	177893..178174	CAATTT	score: 2.717339814	77
>csgD	pro0177	177893..178174	CAGAAT	score: 2.451878675	89
>pspE	pro0187	185719..186072	CATGTT	score: 3.159697923	71

>sUI1	pro0189	187391..187714	GAAGAT	score: 2.352343001	28
>sUI1	pro0189	187391..187714	CAGGAT	score: 2.756733261	77
>sUI1	pro0189	187391..187714	CAAGAT	score: 3.674271096	83
>nagA	pro0192	189010..190167	CACGTT	score: 2.657197587	75
>nifS	pro0195	191750..192901	CAGGAT	score: 2.756733261	33
>nifS	pro0195	191750..192901	CAATAT	score: 3.231912987	43
>nifS	pro0195	191750..192901	TAAGGT	score: 5.007694830	58
>nuoD	pro0197	193865..195049	TAATAT	score: 4.345371032	28
>nuoD	pro0197	193865..195049	CAATCT	score: 3.451878675	60
>menF	pro0202	198765..200186	TAGTCT	score: 3.647798885	23
>menF	pro0202	198765..200186	TATGTT	score: 4.273155969	29
>menF	pro0202	198765..200186	TACGGT	score: 4.505194494	42
>menF	pro0202	198765..200186	TAGTCT	score: 3.647798885	52
>menF	pro0202	198765..200186	TAGGTT	score: 3.355618133	74
>menF	pro0202	198765..200186	CATTTT	score: 2.717339814	89
>prfB	pro0205	201482..202552	CAGAAT	score: 2.451878675	39
>prfB	pro0205	201482..202552	CAGGAT	score: 2.756733261	49
>prfB	pro0205	201482..202552	TAGTTT	score: 2.913260024	64
>prfB	pro0205	201482..202552	TATTTT	score: 3.830797859	81
>prfB	pro0205	201482..202552	TATGCT	score: 5.007694830	90
>pro0215	pro0215	210522..210980	CATTCT	score: 3.451878675	33
>pro0215	pro0215	210522..210980	TACGAT	score: 4.285228806	45
>pro0215	pro0215	210522..210980	TAAACT	score: 4.702840244	71
>pro0218	pro0218	214959..216581	CAGGCT	score: 2.976698949	87
>pgk	pro0221	218921..220129	TATTTT	score: 3.830797859	49
>pgk	pro0221	218921..220129	GATGAT	score: 2.352343001	76
>pgk	pro0221	218921..220129	TATGGT	score: 5.007694830	84
>murG	pro0223	220991..222064	TAATTT	score: 3.830797859	55
>murG	pro0223	220991..222064	TATTTT	score: 3.830797859	65
>murG	pro0223	220991..222064	TAGGAT	score: 3.870191306	91
>eno	pro0235	231829..233127	TAAGAT	score: 4.787729142	23
>eno	pro0235	231829..233127	TAAGTT	score: 4.273155969	47
>trxB	pro0239	236020..236976	TATGCT	score: 5.007694830	41
>trxB	pro0239	236020..236976	TATTTT	score: 3.830797859	61
>trxB	pro0239	236020..236976	CAATAT	score: 3.231912987	64
>hemB	pro0243	240195..241199	TACGAT	score: 4.285228806	28
>hemB	pro0243	240195..241199	TATTAT	score: 4.345371032	43
>hemB	pro0243	240195..241199	CATATT	score: 2.854843338	45
>hemB	pro0243	240195..241199	CAGACT	score: 2.671844363	54
>hemB	pro0243	240195..241199	TATTTT	score: 3.830797859	81
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>obg	pro0246	244212..245201	TAGGTT	score: 3.355618133	28
>obg	pro0246	244212..245201	TAGTCT	score: 3.647798885	42
>obg	pro0246	244212..245201	CATGCT	score: 3.894236785	58
>aspA	pro0251	247653..248576	TATTTT	score: 3.830797859	31
>aspA	pro0251	247653..248576	TATTTT	score: 3.830797859	42
>aspA	pro0251	247653..248576	CAAAAT	score: 3.369416510	47
>psbA	pro0252	248725..249807	TAATGT	score: 4.565336720	27
>psbA	pro0252	248725..249807	CATAAT	score: 3.369416510	29
>psbA	pro0252	248725..249807	TAATAT	score: 4.345371032	44
>psbA	pro0252	248725..249807	TAAACT	score: 4.702840244	62
>psbA	pro0252	248725..249807	CAAACT	score: 3.589382199	74
>aroC	pro0253	249977..251065	TAGTCT	score: 3.647798885	42
>aroC	pro0253	249977..251065	TATTTT	score: 3.830797859	74
>pro0260	pro0260	257725..257925	TATGTT	score: 4.273155969	71
>pro0261	pro0261	258008..258343	TATTTT	score: 3.830797859	42

>pro0264	pro0264	260097..260897	CAAAAT	score: 3.369416510	26
>pro0264	pro0264	260097..260897	CATTAT	score: 3.231912987	55
>pro0264	pro0264	260097..260897	CAAGTT	score: 3.159697923	72
>pro0267	pro0267	262583..263131	CAAAAT	score: 3.369416510	27
>pro0267	pro0267	262583..263131	TAAACT	score: 4.702840244	38
>pro0267	pro0267	262583..263131	CAGAAT	score: 2.451878675	55
>pro0267	pro0267	262583..263131	TATTTT	score: 3.830797859	71
>pro0270	pro0270	266820..267461	GAAGCT	score: 2.572308690	25
>pro0270	pro0270	266820..267461	TATTAT	score: 4.345371032	38
>pro0270	pro0270	266820..267461	CACTAT	score: 2.729412650	41
>pro0270	pro0270	266820..267461	TAATCT	score: 4.565336720	51
>pro0270	pro0270	266820..267461	TATTAT	score: 4.345371032	57
>pro0270	pro0270	266820..267461	CAATTT	score: 2.717339814	66
>trxA	pro0272	269007..269576	TATTCT	score: 4.565336720	36
>trxA	pro0272	269007..269576	CAAGCT	score: 3.894236785	41
>trxA	pro0272	269007..269576	CAAATT	score: 2.854843338	83
>trxA	pro0272	269007..269576	TAAATT	score: 3.968301383	90
>ntcA	pro0277	271665..272399	CATTTT	score: 2.717339814	54
>ntcA	pro0277	271665..272399	CATTCT	score: 3.451878675	75
>psbN	pro0284	275354..275494	CAGGCT	score: 2.976698949	27
>psbN	pro0284	275354..275494	TATTGT	score: 4.565336720	43
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>psbI	pro0285	275624..275752	TACATT	score: 3.465801047	25
>psbI	pro0285	275624..275752	TAAGAT	score: 4.787729142	30
>pro0286	pro0286	275871..277928	TATTGT	score: 4.565336720	38
>pro0286	pro0286	275871..277928	CAATTT	score: 2.717339814	44
>pro0286	pro0286	275871..277928	TAGGTT	score: 3.355618133	54
>pro0286	pro0286	275871..277928	TATTAT	score: 4.345371032	60
>pro0291	pro0291	282855..283112	TAGGAT	score: 3.870191306	30
>pro0291	pro0291	282855..283112	CAAGGT	score: 3.894236785	70
>sfsA	pro0294	285201..285956	CAATAT	score: 3.231912987	22
>sfsA	pro0294	285201..285956	TAGATT	score: 3.050763548	32
>sfsA	pro0294	285201..285956	CATGCT	score: 3.894236785	80
>amtB	pro0295	286257..287765	CATATT	score: 2.854843338	59
>amtB	pro0295	286257..287765	TATTTT	score: 3.830797859	68
>lytB	pro0296	287863..289080	TAGAGT	score: 3.785302409	22
>lytB	pro0296	287863..289080	CAAGCT	score: 3.894236785	54
>pro0297	pro0297	289209..289772	TAATAT	score: 4.345371032	22
>pro0297	pro0297	289209..289772	CAAAAT	score: 3.369416510	60
>pro0297	pro0297	289209..289772	TACGTT	score: 3.770655633	67
>pro0297	pro0297	289209..289772	TAGTTT	score: 2.913260024	84
>baeS	pro0301	292769..293887	CATTTT	score: 2.717339814	27
>baeS	pro0301	292769..293887	TACTTT	score: 3.328297523	62
>baeS	pro0301	292769..293887	TAAATT	score: 3.968301383	86
>tgt	pro0303	294742..295860	TAGGTT	score: 3.355618133	53
>tgt	pro0303	294742..295860	CAGAAT	score: 2.451878675	91
>manB	pro0310	301635..303077	CAATTT	score: 2.717339814	31
>manB	pro0310	301635..303077	TAATTT	score: 3.830797859	48
>manB	pro0310	301635..303077	TAGGTT	score: 3.355618133	53
>manB	pro0310	301635..303077	TATTGT	score: 4.565336720	73
>manB	pro0310	301635..303077	TAGTAT	score: 3.427833197	76
>manB	pro0310	301635..303077	TATTGT	score: 4.565336720	91
>trxA	pro0315	306829..307449	TATTTT	score: 3.830797859	29
>chlD	pro0319	309998..312121	TAAACT	score: 4.702840244	28
>chlD	pro0319	309998..312121	CATTGT	score: 3.451878675	44
>pro0322	pro0322	313970..315298	CAAGAT	score: 3.674271096	38

>pro0326	pro0326	317028..317459	TAGAGT	score: 3.785302409	23
>pro0326	pro0326	317028..317459	TAAGGT	score: 5.007694830	41
>pro0326	pro0326	317028..317459	TAGTTT	score: 2.913260024	57
>psbE	pro0328	318588..318836	TAGTAT	score: 3.427833197	25
>psbE	pro0328	318588..318836	CATGCT	score: 3.894236785	65
>ndh	pro0333	320315..322477	CAATCT	score: 3.451878675	31
>ndh	pro0333	320315..322477	CAAGAT	score: 3.674271096	50
>ndh	pro0333	320315..322477	CATTTT	score: 2.717339814	64
>cpeB	pro0337	326768..327316	TAGGTT	score: 3.355618133	70
>cpeB	pro0337	326768..327316	TAGAGT	score: 3.785302409	76
>cpeY	pro0341	329467..330786	TATATT	score: 3.968301383	26
>cpeY	pro0341	329467..330786	TAGAGT	score: 3.785302409	87
>pro0355	pro0355	341973..342125	TAAGAT	score: 4.787729142	23
>pro0355	pro0355	341973..342125	CAGGGT	score: 2.976698949	75
>psbM	pro0357	342693..342845	TAGTCT	score: 3.647798885	37
>psbM	pro0357	342693..342845	TATAGT	score: 4.702840244	39
>psbM	pro0357	342693..342845	CAAGCT	score: 3.894236785	74
>petB	pro0367	349948..350604	TAGACT	score: 3.785302409	32
>petB	pro0367	349948..350604	CACATT	score: 2.352343001	41
>petB	pro0367	349948..350604	TACAGT	score: 4.200339908	85
>petD	pro0368	350685..351167	CATTCT	score: 3.451878675	37
>16S_rRNA	RNA_41	353331..354795	TAGGGT	score: 4.090156995	27
>16S_rRNA	RNA_41	353331..354795	CATTCT	score: 3.451878675	64
>ile-tRNA	RNA_6	354973..355046	TAAACT	score: 4.702840244	31
>ile-tRNA	RNA_6	354973..355046	TATTTT	score: 3.830797859	44
>ile-tRNA	RNA_6	354973..355046	TAGTTT	score: 2.913260024	51
>ile-tRNA	RNA_6	354973..355046	CAAAGT	score: 3.589382199	91
>23S_rRNA	RNA_42	355462..358334	TAAAAT	score: 4.482874556	36
>23S_rRNA	RNA_42	355462..358334	CATATT	score: 2.854843338	45
>5S_rRNA	RNA_43	358430..358543	TAAGCT	score: 5.007694830	65
>pro0372	pro0372	359810..360853	CAGAAT	score: 2.451878675	50
>pro0372	pro0372	359810..360853	TAAGAT	score: 4.787729142	91
>pro0378	pro0378	365281..366000	TAAAAT	score: 4.482874556	34
>wcaA	pro0380	366770..367723	TACTAT	score: 3.842870696	29
>wcaA	pro0380	366770..367723	CACTGT	score: 2.949378339	69
>wcaA	pro0380	366770..367723	TATGTT	score: 4.273155969	80
>wcaA	pro0380	366770..367723	CATTTT	score: 2.717339814	89
>aroQ	pro0384	370779..371228	TACGAT	score: 4.285228806	28
>aroQ	pro0384	370779..371228	TATGTT	score: 4.273155969	56
>aroQ	pro0384	370779..371228	CAATTT	score: 2.717339814	68
>pro0387	pro0387	372703..373179	TATTGT	score: 4.565336720	40
>pro0388	pro0388	373321..374691	TATTGT	score: 4.565336720	24
>pro0388	pro0388	373321..374691	TATTGT	score: 4.565336720	42
>pro0388	pro0388	373321..374691	TAGGTT	score: 3.355618133	67
>pro0388	pro0388	373321..374691	CAATTT	score: 2.717339814	73
>pro0390	pro0390	375745..376017	TATTAT	score: 4.345371032	34
>pro0392	pro0392	376833..377402	TAATCT	score: 4.565336720	57
>pro0392	pro0392	376833..377402	CATTTT	score: 2.717339814	77
>pro0392	pro0392	376833..377402	TACATT	score: 3.465801047	79
>lipB	pro0398	381560..382234	CAAGAT	score: 3.674271096	50
>aceF	pro0401	384875..386257	TAAGAT	score: 4.787729142	26
>pro0407	pro0407	392552..392794	TAGATT	score: 3.050763548	22
>pro0407	pro0407	392552..392794	GAAGGT	score: 2.572308690	59
>pro0410	pro0410	394190..394429	CATGCT	score: 3.894236785	59
>pro0416	pro0416	398503..398748	TATTCT	score: 4.565336720	30
>pro0416	pro0416	398503..398748	CATTTT	score: 2.717339814	69

>mqaA	pro0418	399080..400570	TATGTG	score: 4.565336720	53
>mqaA	pro0418	399080..400570	CATTGT	score: 3.451878675	80
>lepA	pro0419	400642..402450	TAGGGT	score: 4.090156995	38
>dppC	pro0420	402761..403630	TATTAT	score: 4.345371032	24
>dppC	pro0420	402761..403630	TAAATT	score: 3.968301383	40
>dppC	pro0420	402761..403630	TATATT	score: 3.968301383	60
>dppC	pro0420	402761..403630	CATGTT	score: 3.159697923	83
>sun	pro0422	404610..405926	TAAATT	score: 3.968301383	39
>sun	pro0422	404610..405926	TAAGTT	score: 4.273155969	47
>sun	pro0422	404610..405926	TAAAAT	score: 4.482874556	53
>hisF	pro0426	409032..409805	TAAGAT	score: 4.787729142	76
>hisF	pro0426	409032..409805	TATTCT	score: 4.565336720	84
>ubiE	pro0427	409919..410620	TAAAGT	score: 4.702840244	37
>ubiE	pro0427	409919..410620	TAATTT	score: 3.830797859	47
>ubiE	pro0427	409919..410620	TATGCT	score: 5.007694830	53
>ubiE	pro0427	409919..410620	TAATAT	score: 4.345371032	56
>ubiE	pro0427	409919..410620	TACAGT	score: 4.200339908	72
>birA	pro0429	411284..412045	TAAGTT	score: 4.273155969	37
>birA	pro0429	411284..412045	TATGCT	score: 5.007694830	43
>birA	pro0429	411284..412045	TAAAAT	score: 4.482874556	58
>birA	pro0429	411284..412045	TAGATT	score: 3.050763548	63
>ribC	pro0438	421781..422449	TAGATT	score: 3.050763548	44
>ribC	pro0438	421781..422449	TAATTT	score: 3.830797859	59
>ribC	pro0438	421781..422449	TAATCT	score: 4.565336720	79
>ctaA	pro0443	426296..427234	TAAGGT	score: 5.007694830	67
>ctaA	pro0443	426296..427234	CAATTT	score: 2.717339814	72
>ccmA	pro0445	428321..429334	TAGATT	score: 3.050763548	35
>ccmA	pro0445	428321..429334	TACTAT	score: 3.842870696	42
>ccmA	pro0445	428321..429334	TAATTT	score: 3.830797859	53
>ccmA	pro0445	428321..429334	TACACT	score: 4.200339908	59
>ccmA	pro0445	428321..429334	CAAAAT	score: 3.369416510	64
>pro0449	pro0449	432666..432839	TAGATT	score: 3.050763548	42
>ispD	pro0453	435322..436002	TAAGTT	score: 4.273155969	36
>ispD	pro0453	435322..436002	CAGTGT	score: 2.534340839	46
>ispD	pro0453	435322..436002	TAAATT	score: 3.968301383	56
>ispD	pro0453	435322..436002	TAGTTT	score: 2.913260024	75
>gppA	pro0456	437834..439510	TAAGGT	score: 5.007694830	33
>pro0461	pro0461	443011..443364	TACTCT	score: 4.062836384	32
>pro0461	pro0461	443011..443364	CATTAT	score: 3.231912987	50
>pro0461	pro0461	443011..443364	CATAAT	score: 3.369416510	62
>gmk	pro0465	446371..446925	TATGAT	score: 4.787729142	59
>qRI7	pro0468	447763..448833	CAGGAT	score: 2.756733261	36
>nhaP	pro0470	449249..450445	CATTTT	score: 2.717339814	35
>nhaP	pro0470	449249..450445	CAAGAT	score: 3.674271096	41
>nhaP	pro0470	449249..450445	TAGTCT	score: 3.647798885	51
>nhaP	pro0470	449249..450445	TAAGGT	score: 5.007694830	60
>nhaP	pro0470	449249..450445	CAGAAAT	score: 2.451878675	72
>nhaP	pro0470	449249..450445	CAAACT	score: 3.589382199	82
>pro0474	pro0474	453066..453248	TATGTG	score: 4.565336720	31
>pro0474	pro0474	453066..453248	TATTTT	score: 3.830797859	46
>pro0474	pro0474	453066..453248	CAATTT	score: 2.717339814	52
>pro0474	pro0474	453066..453248	TACAAT	score: 3.980374220	54
>pro0474	pro0474	453066..453248	TATTTT	score: 3.830797859	82
>map	pro0475	453442..454278	CAAGCT	score: 3.894236785	42
>pta	pro0477	455240..456310	TAAGAT	score: 4.787729142	44
>pta	pro0477	455240..456310	GATGAT	score: 2.352343001	50

>pta	pro0477	455240..456310	TACTAT	score: 3.842870696	70
>pta	pro0477	455240..456310	TATTTT	score: 3.830797859	82
>pta	pro0477	455240..456310	CAAATT	score: 2.854843338	87
>pro0479	pro0479	456999..457496	TAGAAT	score: 3.565336720	26
>pro0479	pro0479	456999..457496	TATTGT	score: 4.565336720	44
>pro0479	pro0479	456999..457496	TAGGCT	score: 4.090156995	61
>pro0480	pro0480	457554..457766	TATGTT	score: 4.273155969	22
>pro0484	pro0484	461279..461602	TAGGGT	score: 4.090156995	23
>pro0484	pro0484	461279..461602	TAGAAT	score: 3.565336720	28
>pro0484	pro0484	461279..461602	TAGGTT	score: 3.355618133	44
>pro0484	pro0484	461279..461602	CACAGT	score: 3.086881863	59
>pro0484	pro0484	461279..461602	CAAGTT	score: 3.159697923	73
>pro0484	pro0484	461279..461602	TACATT	score: 3.465801047	80
>pro0485	pro0485	461662..462285	TAGATT	score: 3.050763548	28
>pro0486	pro0486	462410..463636	TAAAAT	score: 4.482874556	37
>pro0486	pro0486	462410..463636	CATAAT	score: 3.369416510	57
>pro0486	pro0486	462410..463636	CAAACT	score: 3.589382199	82
>pro0492	pro0492	468584..470125	TAAGAT	score: 4.787729142	39
>pro0492	pro0492	468584..470125	TATTTT	score: 3.830797859	44
>pro0492	pro0492	468584..470125	TAAACT	score: 4.702840244	67
>pro0496	pro0496	473310..473480	TAGTTT	score: 2.913260024	71
>pro0496	pro0496	473310..473480	TATGTT	score: 4.273155969	84
>pro0501	pro0501	478452..478637	TAATTT	score: 3.830797859	40
>pro0501	pro0501	478452..478637	CATGTT	score: 3.159697923	48
>cobK	pro0503	479143..479937	CATTTT	score: 2.717339814	25
>cobK	pro0503	479143..479937	TACTTT	score: 3.328297523	58
>pro0509	pro0509	485140..485565	TAATTT	score: 3.830797859	28
>pro0509	pro0509	485140..485565	TAGTTT	score: 2.913260024	41
>ppa	pro0510	485907..486437	CAATTT	score: 2.717339814	27
>ppa	pro0510	485907..486437	TATTTT	score: 3.830797859	60
>lepB	pro0513	488450..489118	TAAATT	score: 3.968301383	45
>lepB	pro0513	488450..489118	TAAATT	score: 3.968301383	70
>lepB	pro0513	488450..489118	TATGGT	score: 5.007694830	83
>pro0516	pro0516	491811..493169	TAATCT	score: 4.565336720	54
>pro0516	pro0516	491811..493169	CACTGT	score: 2.949378339	65
>pro0516	pro0516	491811..493169	TACACT	score: 4.200339908	67
>pro0517	pro0517	493254..493721	TAATGT	score: 4.565336720	27
>pro0517	pro0517	493254..493721	GAAGAT	score: 2.352343001	32
>mipB	pro0519	495609..496616	CATAAT	score: 3.369416510	42
>hemH	pro0525	501339..502514	TAAGCT	score: 5.007694830	24
>hemH	pro0525	501339..502514	TACATT	score: 3.465801047	45
>hemH	pro0525	501339..502514	TAAAGT	score: 4.702840244	74
>ilvB	pro0526	502652..504406	TAATTT	score: 3.830797859	74
>pro0531	pro0531	507847..508680	CATTGT	score: 3.451878675	27
>pro0531	pro0531	507847..508680	TAATGT	score: 4.565336720	48
>pro0531	pro0531	507847..508680	TAGGTT	score: 3.355618133	83
>pro0532	pro0532	508768..509481	TACACT	score: 4.200339908	28
>pro0532	pro0532	508768..509481	TATTTT	score: 3.830797859	47
>pro0532	pro0532	508768..509481	CAAACT	score: 3.589382199	52
>pro0533	pro0533	509626..510669	TAATCT	score: 4.565336720	49
>pro0533	pro0533	509626..510669	TAATTT	score: 3.830797859	73
>spoIVFB	pro0539	513931..515196	TAGGAT	score: 3.870191306	45
>spoIVFB	pro0539	513931..515196	CAAACT	score: 3.589382199	70
>spoIVFB	pro0539	513931..515196	CATAGT	score: 3.589382199	76
>spoIVFB	pro0539	513931..515196	GATGCT	score: 2.572308690	90
>psaM	pro0541	516085..516189	TAAGTT	score: 4.273155969	28

>psaM	pro0541	516085..516189	CATTTT	score: 2.717339814	42
>psaM	pro0541	516085..516189	CAGGGT	score: 2.976698949	62
>pro0542	pro0542	516255..516671	CACTGT	score: 2.949378339	37
>pro0548	pro0548	522339..523112	TAAGGT	score: 5.007694830	52
>pro0548	pro0548	522339..523112	GAAGAT	score: 2.352343001	71
>pro0548	pro0548	522339..523112	TATGCT	score: 5.007694830	87
>csoS1B	pro0550	524074..524385	CATTGT	score: 3.451878675	39
>csoS1B	pro0550	524074..524385	TAGTAT	score: 3.427833197	54
>csoS1B	pro0550	524074..524385	TAGTGT	score: 3.647798885	85
>rbcS	pro0552	525970..526311	TACTTT	score: 3.328297523	23
>rbcS	pro0552	525970..526311	CATACT	score: 3.589382199	25
>rbcS	pro0552	525970..526311	CAAACCT	score: 3.589382199	36
>dnaA	pro0567	537957..539342	TAGATT	score: 3.050763548	35
>dnaA	pro0567	537957..539342	CATGCT	score: 3.894236785	41
>gPro	pro0569	540650..542011	TAAGCT	score: 5.007694830	75
>pyrC	pro0571	543290..544369	TATTTT	score: 3.830797859	51
>pyrC	pro0571	543290..544369	CAATTT	score: 2.717339814	90
>Leu1-tRNA	RNA_2	544514..544599	TATGAT	score: 4.787729142	32
>ndhL	pro0572	544847..545083	TAGAAT	score: 3.565336720	33
>ndhL	pro0572	544847..545083	TAATGT	score: 4.565336720	44
>ndhL	pro0572	544847..545083	TAGTAT	score: 3.427833197	50
>ndhL	pro0572	544847..545083	TAATTT	score: 3.830797859	86
>trpA	pro0574	545500..546303	TAAATT	score: 3.968301383	29
>trpA	pro0574	545500..546303	TAAGCT	score: 5.007694830	39
>trpA	pro0574	545500..546303	TAGATT	score: 3.050763548	44
>pro0576	pro0576	546894..547163	TAAGTT	score: 4.273155969	28
>pro0576	pro0576	546894..547163	TAAAAT	score: 4.482874556	75
>pro0576	pro0576	546894..547163	TAAATT	score: 3.968301383	88
>pro0581	pro0581	549417..549899	TATTTT	score: 3.830797859	60
>pro0581	pro0581	549417..549899	CACTAT	score: 2.729412650	63
>pro0581	pro0581	549417..549899	TATTCT	score: 4.565336720	90
>pro0583	pro0583	550708..551193	CATTTT	score: 2.717339814	29
>pro0583	pro0583	550708..551193	CATAAT	score: 3.369416510	54
>pro0583	pro0583	550708..551193	TATTCT	score: 4.565336720	65
>pro0583	pro0583	550708..551193	CATATT	score: 2.854843338	67
>Lys-tRNA	RNA_3	554563..554634	CAAGAT	score: 3.674271096	45
>Lys-tRNA	RNA_3	554563..554634	CATTTT	score: 2.717339814	57
>pro0589	pro0589	555785..556087	TAAGGT	score: 5.007694830	25
>pro0589	pro0589	555785..556087	TATTTT	score: 3.830797859	33
>pro0589	pro0589	555785..556087	CACTAT	score: 2.729412650	36
>pro0589	pro0589	555785..556087	TAAATT	score: 3.968301383	45
>pro0589	pro0589	555785..556087	TATTCT	score: 4.565336720	53
>pro0589	pro0589	555785..556087	CAAATT	score: 2.854843338	58
>pro0592	pro0592	557128..557337	CATACT	score: 3.589382199	26
>pro0592	pro0592	557128..557337	CAGAGT	score: 2.671844363	58
>pro0592	pro0592	557128..557337	TAATAT	score: 4.345371032	69
>pro0593	pro0593	557401..557751	TAATTT	score: 3.830797859	35
>pro1-tRNA	RNA_4	562384..562460	TAAGCT	score: 5.007694830	90
>pro0605	pro0605	565292..565459	TATTTT	score: 3.830797859	36
>pro0605	pro0605	565292..565459	TAGTAT	score: 3.427833197	39
>pro0605	pro0605	565292..565459	TACGTT	score: 3.770655633	54
>pro0605	pro0605	565292..565459	CATGGT	score: 3.894236785	90
>pro0610	pro0610	571124..571642	TAAAAT	score: 4.482874556	77
>pro0617	pro0617	584182..584373	TATTCT	score: 4.565336720	37
>pro0617	pro0617	584182..584373	CATTCT	score: 3.451878675	44
>pro0617	pro0617	584182..584373	TAAAAT	score: 4.482874556	55

>pro0624	pro0624	586717..586875	TACGGT	score: 4.505194494	57
>pro0624	pro0624	586717..586875	TACTAT	score: 3.842870696	63
>pro0624	pro0624	586717..586875	TATACT	score: 4.702840244	65
>pro0624	pro0624	586717..586875	TACATT	score: 3.465801047	71
>pro0625	pro0625	586958..587416	TAGAGT	score: 3.785302409	33
>pro0631	pro0631	594914..595705	CAGAGT	score: 2.671844363	69
>pro0633	pro0633	596166..596642	CAATTT	score: 2.717339814	27
>pro0635	pro0635	597305..597727	CAGAAT	score: 2.451878675	34
>pro0635	pro0635	597305..597727	CAAGAT	score: 3.674271096	87
>pro0640	pro0640	600113..600295	TAAAAT	score: 4.482874556	50
>pro0641	pro0641	600609..601028	TAGGGT	score: 4.090156995	67
>pro0643	pro0643	601603..602019	TAAGCT	score: 5.007694830	28
>pro0643	pro0643	601603..602019	TAGGGT	score: 4.090156995	60
>pro0643	pro0643	601603..602019	TACTAT	score: 3.842870696	70
>pro0649	pro0649	604253..604534	TACTTT	score: 3.328297523	41
>pro0649	pro0649	604253..604534	TACTAT	score: 3.842870696	86
>pro0652	pro0652	605761..605964	TAAGTT	score: 4.273155969	37
>pro0652	pro0652	605761..605964	TAGATT	score: 3.050763548	46
>pro0655	pro0655	606580..607020	CATAAT	score: 3.369416510	26
>pro0656	pro0656	607118..607219	TACAAT	score: 3.980374220	62
>pro0660	pro0660	609021..609194	CATGCT	score: 3.894236785	47
>pro0660	pro0660	609021..609194	TATTTT	score: 3.830797859	77
>pro0661	pro0661	609841..610272	TAGATT	score: 3.050763548	26
>pro0661	pro0661	609841..610272	CAGGAT	score: 2.756733261	33
>pro0661	pro0661	609841..610272	TACTTT	score: 3.328297523	57
>pro0661	pro0661	609841..610272	TAGATT	score: 3.050763548	78
>pro0661	pro0661	609841..610272	TAAGCT	score: 5.007694830	86
>pro0663	pro0663	612367..612552	TATTTT	score: 3.830797859	73
>pro0663	pro0663	612367..612552	TAGATT	score: 3.050763548	83
>pro0666	pro0666	614078..614473	TATGGT	score: 5.007694830	41
>pro0666	pro0666	614078..614473	CATGGT	score: 3.894236785	55
>pro0667	pro0667	614554..614826	CATGTT	score: 3.159697923	43
>pro0668	pro0668	615231..615425	CAAGTT	score: 3.159697923	53
>pro0670	pro0670	616298..616528	TAAGCT	score: 5.007694830	38
>pro0670	pro0670	616298..616528	TACGTT	score: 3.770655633	69
>pro0672	pro0672	617076..617714	TAAGGT	score: 5.007694830	30
>pro0672	pro0672	617076..617714	TATTTT	score: 3.830797859	45
>pro0672	pro0672	617076..617714	TAAACT	score: 4.702840244	66
>pro0672	pro0672	617076..617714	TAGACT	score: 3.785302409	75
>pro0677	pro0677	623197..623781	GATGCT	score: 2.572308690	31
>pro0677	pro0677	623197..623781	TAGATT	score: 3.050763548	52
>pro0677	pro0677	623197..623781	TATTTT	score: 3.830797859	66
>pro0677	pro0677	623197..623781	TATTAT	score: 4.345371032	69
>pro0677	pro0677	623197..623781	TAGTTT	score: 2.913260024	83
>pro0677	pro0677	623197..623781	CAAGCT	score: 3.894236785	91
>pro0678	pro0678	623897..624106	TAAACT	score: 4.702840244	26
>pro0678	pro0678	623897..624106	TAAAAT	score: 4.482874556	34
>pro0678	pro0678	623897..624106	CAAAAT	score: 3.369416510	44
>pro0678	pro0678	623897..624106	TAAAAT	score: 4.482874556	75
>pro0687	pro0687	632104..632349	TATAGT	score: 4.702840244	35
>pro0687	pro0687	632104..632349	TATTTT	score: 3.830797859	49
>pro0687	pro0687	632104..632349	TACTAT	score: 3.842870696	52
>pro0687	pro0687	632104..632349	TAAATT	score: 3.968301383	60
>pro0695	pro0695	636428..636811	TAGACT	score: 3.785302409	49
>pro0695	pro0695	636428..636811	TATAAT	score: 4.482874556	91
>pro0698	pro0698	638341..638922	TACTTT	score: 3.328297523	23

>pro0698	pro0698	638341..638922	CATTGT	score: 3.451878675	57
>pro0698	pro0698	638341..638922	TATTTT	score: 3.830797859	78
>pro0701	pro0701	642190..642519	CATGAT	score: 3.674271096	29
>pro0701	pro0701	642190..642519	TAATTT	score: 3.830797859	41
>pro0705	pro0705	647448..647588	TAGTTT	score: 2.913260024	44
>pro0705	pro0705	647448..647588	TATAGT	score: 4.702840244	46
>pro0705	pro0705	647448..647588	TATGAT	score: 4.787729142	57
>pro0705	pro0705	647448..647588	TAAGCT	score: 5.007694830	62
>pro0705	pro0705	647448..647588	TAAAAT	score: 4.482874556	72
>pro0705	pro0705	647448..647588	CATTCT	score: 3.451878675	91
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>gly1-tRNA	RNA_5	651118..651189	CATTGT	score: 3.451878675	55
>fabG	pro0710	651677..652342	TAGAGT	score: 3.785302409	62
>fabG	pro0710	651677..652342	CATTGT	score: 3.451878675	68
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>pro0711	pro0711	652463..652648	TAGGTT	score: 3.355618133	84
>pro0713	pro0713	653296..653439	CATTTT	score: 2.717339814	86
>pro0717	pro0717	655047..655301	TAAAGT	score: 4.702840244	53
>pro0721	pro0721	657313..657864	TAGTTT	score: 2.913260024	35
>pro0721	pro0721	657313..657864	CAAAGT	score: 3.589382199	43
>pro0721	pro0721	657313..657864	TAGTTT	score: 2.913260024	69
>pro0725	pro0725	659846..660052	TATGAT	score: 4.787729142	23
>amyA	pro0728	662087..663865	CAGAAT	score: 2.451878675	24
>amyA	pro0728	662087..663865	TAAAGT	score: 4.702840244	50
>amyA	pro0728	662087..663865	CATACT	score: 3.589382199	83
>pro0731	pro0731	665755..665982	TATTTT	score: 3.830797859	40
>pro0732	pro0732	666151..666528	CATACT	score: 3.589382199	24
>pro0732	pro0732	666151..666528	TATATT	score: 3.968301383	41
>pro0732	pro0732	666151..666528	TATTGT	score: 4.565336720	78
>pro0733	pro0733	666626..666760	TAAATT	score: 3.968301383	22
>pro0733	pro0733	666626..666760	TATTTT	score: 3.830797859	52
>pro0733	pro0733	666626..666760	TATATT	score: 3.968301383	54
>pro0733	pro0733	666626..666760	TATTAT	score: 4.345371032	69
>bacA	pro0735	667190..668059	TAAAGT	score: 4.702840244	32
>bacA	pro0735	667190..668059	TAGGAT	score: 3.870191306	37
>bacA	pro0735	667190..668059	TACTTT	score: 3.328297523	43
>bacA	pro0735	667190..668059	TAGTTT	score: 2.913260024	64
>bacA	pro0735	667190..668059	CATGAT	score: 3.674271096	83
>pro0743	pro0743	674156..674461	TACGGT	score: 4.505194494	45
>pro0743	pro0743	674156..674461	TATATT	score: 3.968301383	54
>pro0743	pro0743	674156..674461	CAATTT	score: 2.717339814	59
>pro0743	pro0743	674156..674461	TAGTAT	score: 3.427833197	71
>trpD	pro0744	674580..675605	TAAATT	score: 3.968301383	76
>pro0749	pro0749	679040..679270	TAATAT	score: 4.345371032	22
>pro0749	pro0749	679040..679270	TAGTTT	score: 2.913260024	45
>dnaE	pro0751	681024..684530	TATATT	score: 3.968301383	27
>dnaE	pro0751	681024..684530	CACTGT	score: 2.949378339	32
>dnaE	pro0751	681024..684530	TATTTT	score: 3.830797859	44
>dnaE	pro0751	681024..684530	TATATT	score: 3.968301383	46
>dnaE	pro0751	681024..684530	CATTGT	score: 3.451878675	73
>dnaG	pro0757	687410..689470	TAGTTT	score: 2.913260024	83
>ksgA	pro0763	692833..693672	GATGCT	score: 2.572308690	60
>ksgA	pro0763	692833..693672	TACTCT	score: 4.062836384	89
>ksgA	pro0763	692833..693672	CATACT	score: 3.589382199	91
>acoB	pro0766	695189..696172	CACACT	score: 3.086881863	52
>acoB	pro0766	695189..696172	TACATT	score: 3.465801047	79

>acoB	pro0766	695189..696172	TATCT	score: 4.565336720	88
>pro0773	pro0773	701466..702191	CATAGT	score: 3.589382199	34
>rsbW	pro0774	702305..702748	TAAGCT	score: 5.007694830	69
>rsbW	pro0774	702305..702748	TAAGCT	score: 5.007694830	78
>dnaQ	pro0777	703846..704556	TAGGCT	score: 4.090156999	42
>dnaQ	pro0777	703846..704556	TATAAT	score: 4.482874556	47
>dnaQ	pro0777	703846..704556	TATGTT	score: 4.273155969	89
>pro0778	pro0778	704687..704926	CAGTCT	score: 2.534340839	34
>pro0778	pro0778	704687..704926	TAGGTT	score: 3.355618133	68
>hisS	pro0779	705071..706336	TAGAAT	score: 3.565336720	63
>hisS	pro0779	705071..706336	TACTAT	score: 3.842870696	69
>pro0782	pro0782	707091..707312	TATCT	score: 4.565336720	27
>pro0782	pro0782	707091..707312	TAGGGT	score: 4.090156999	84
>pcbA	pro0783	707932..708987	TAGTGT	score: 3.647798889	30
>pcbA	pro0783	707932..708987	TATTTT	score: 3.830797859	48
>pcbA	pro0783	707932..708987	CAATGT	score: 3.451878679	78
>pcbA	pro0783	707932..708987	CACAAT	score: 2.866916174	80
>gltS	pro0784	709152..710534	TATCT	score: 4.565336720	32
>gltS	pro0784	709152..710534	TATTTT	score: 3.830797859	37
>gltS	pro0784	709152..710534	TATATT	score: 3.968301383	78
>pro0785	pro0785	710600..710857	CAATAT	score: 3.231912987	34
>pro0787	pro0787	711684..712241	TAAATT	score: 3.968301383	28
>pro0787	pro0787	711684..712241	TATAAT	score: 4.482874556	58
>pro0788	pro0788	712345..712605	TATTTT	score: 3.830797859	25
>pro0788	pro0788	712345..712605	TAGTTT	score: 2.913260024	56
>pro0788	pro0788	712345..712605	TATTTT	score: 3.830797859	61
>pro0788	pro0788	712345..712605	CATTAT	score: 3.231912987	64
>por	pro0791	714903..715907	TATTAT	score: 4.345371032	25
>por	pro0791	714903..715907	TAAGAT	score: 4.787729142	36
>por	pro0791	714903..715907	TAAATT	score: 3.968301383	64
>fur	pro0794	717794..718300	TAAATT	score: 3.968301383	58
>fur	pro0794	717794..718300	TAGTAT	score: 3.427833197	73
>fur	pro0794	717794..718300	CATTTT	score: 2.717339814	89
>pro0797	pro0797	720713..722245	TATGTT	score: 4.273155969	31
>pro0797	pro0797	720713..722245	TAAAAT	score: 4.482874556	38
>pro0797	pro0797	720713..722245	TATTTT	score: 3.830797859	44
>pro0797	pro0797	720713..722245	TATGTT	score: 4.273155969	51
>pro0797	pro0797	720713..722245	TATGAT	score: 4.787729142	57
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>pro0797	pro0797	720713..722245	TAGAAT	score: 3.565336720	71
>pro0798	pro0798	722345..723496	TATTAT	score: 4.345371032	22
>pro0798	pro0798	722345..723496	TATTAT	score: 4.345371032	25
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>pro0798	pro0798	722345..723496	TATAAT	score: 4.482874556	37
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>pro0799	pro0799	723575..724279	TATCT	score: 4.565336720	24
>pro0799	pro0799	723575..724279	TATTAT	score: 4.345371032	27
>pro0806	pro0806	730556..731605	CACGAT	score: 3.171770760	26
>pro0806	pro0806	730556..731605	TAGATT	score: 3.050763548	45
>pro0806	pro0806	730556..731605	CACGAT	score: 3.171770760	83
>pro0806	pro0806	730556..731605	TATTGT	score: 4.565336720	90
>pro0807	pro0807	731998..732255	CAAATT	score: 2.854843338	72
>pro0810	pro0810	734416..734892	TATTTT	score: 3.830797859	22
>pro0810	pro0810	734416..734892	TAAAAT	score: 4.482874556	44

>pro0810	pro0810	734416..734892	TAAGAT	score: 4.787729142	77
>pro0810	pro0810	734416..734892	TAAATT	score: 3.968301383	86
>pro0813	pro0813	736371..736565	CATAAT	score: 3.369416510	22
>pro0813	pro0813	736371..736565	TAATTT	score: 3.830797859	32
>pro0813	pro0813	736371..736565	CAAGCT	score: 3.894236785	62
>smtA	pro0816	739564..740256	CAGTGT	score: 2.534340839	34
>smtA	pro0816	739564..740256	CAAGTT	score: 3.159697923	57
>smtA	pro0816	739564..740256	CAGGCT	score: 2.976698949	83
>pcyA	pro0819	742912..743655	CATGTG	score: 3.451878675	27
>pcyA	pro0819	742912..743655	CAAAGT	score: 3.589382199	35
>pcyA	pro0819	742912..743655	CAGAGT	score: 2.671844363	48
>pcyA	pro0819	742912..743655	TAATTT	score: 3.830797859	76
>wcaA	pro0824	746717..747649	TACTTT	score: 3.328297523	26
>wcaA	pro0824	746717..747649	TAAGAT	score: 4.787729142	55
>rpsB	pro0825	747785..748501	TAAATT	score: 3.968301383	61
>rpsB	pro0825	747785..748501	CAAAGT	score: 3.589382199	66
>ddpX	pro0829	753064..753741	TATTCT	score: 4.565336720	25
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>ddpX	pro0829	753064..753741	CAGTGT	score: 2.534340839	53
>ddpX	pro0829	753064..753741	TATTTT	score: 3.830797859	70
>ddpX	pro0829	753064..753741	TAAATT	score: 3.968301383	75
>glyS	pro0831	755581..757746	TAAAGT	score: 4.702840244	23
>glyS	pro0831	755581..757746	TACTTT	score: 3.328297523	45
>glyS	pro0831	755581..757746	CATACT	score: 3.589382199	47
>glyS	pro0831	755581..757746	CAAATT	score: 2.854843338	65
>vanY	pro0833	759211..759969	TACGAT	score: 4.285228806	25
>vanY	pro0833	759211..759969	TACTCT	score: 4.062836384	54
>vanY	pro0833	759211..759969	TATTTT	score: 3.830797859	81
>vanY	pro0833	759211..759969	TATTCT	score: 4.565336720	87
>vanY	pro0833	759211..759969	TATATT	score: 3.968301383	89
>typA	pro0834	760056..761858	TATTCT	score: 4.565336720	49
>pro0836	pro0836	762434..763162	TATTTT	score: 3.830797859	66
>pro0836	pro0836	762434..763162	TAAATT	score: 3.968301383	87
>glpX	pro0840	766305..767309	TATTCT	score: 4.565336720	42
>glpX	pro0840	766305..767309	CAAGCT	score: 3.894236785	47
>glpX	pro0840	766305..767309	CACATT	score: 2.352343001	70
>glgC	pro0842	768769..770064	TAGGTT	score: 3.355618133	24
>glgC	pro0842	768769..770064	CAAATT	score: 2.854843338	53
>gnd	pro0843	770220..771638	CACACT	score: 3.086881863	25
>pro0845	pro0845	772434..772988	TAAGTT	score: 4.273155969	28
>pro0850	pro0850	776110..776622	TAAATT	score: 3.968301383	27
>pro0850	pro0850	776110..776622	GATGAT	score: 2.352343001	62
>pro0850	pro0850	776110..776622	CATGAT	score: 3.674271096	65
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>purS	pro0853	778133..778405	GAAGCT	score: 2.572308690	29
>purS	pro0853	778133..778405	TAATTT	score: 3.830797859	64
>pro0875	pro0875	797810..798394	TAATTT	score: 3.830797859	48
>pro0875	pro0875	797810..798394	CATGTG	score: 3.451878675	73
>pro0875	pro0875	797810..798394	TACATT	score: 3.465801047	75
>pro0875	pro0875	797810..798394	TATGCT	score: 5.007694830	82
>potA	pro0881	801199..802263	CAATTT	score: 2.717339814	41
>potA	pro0881	801199..802263	CATTAT	score: 3.231912987	47
>potA	pro0881	801199..802263	TAGGAT	score: 3.870191306	72
>ftn	pro0882	802582..803127	TAGAGT	score: 3.785302409	35
>ftn	pro0882	802582..803127	CAAGTT	score: 3.159697923	51
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>ftn	pro0882	802582..803127	TAATTT	score: 3.830797859	86
>pro0886	pro0886	805599..806330	CAATCT	score: 3.451878675	43
>pro0886	pro0886	805599..806330	TAATTT	score: 3.830797859	53
>pro0886	pro0886	805599..806330	TATAAT	score: 4.482874556	55
>pro0886	pro0886	805599..806330	TATGTT	score: 4.273155969	66
>pro0886	pro0886	805599..806330	TAGATT	score: 3.050763548	72
>pro0886	pro0886	805599..806330	TAATAT	score: 4.345371032	82
>pcbG	pro0892	809662..810723	TATTTT	score: 3.830797859	45
>pcbG	pro0892	809662..810723	TAAATT	score: 3.968301383	60
>carB	pro0897	813913..817239	TAGTAT	score: 3.427833197	85
>pro0900	pro0900	819317..819532	TAGATT	score: 3.050763548	34
>pro0900	pro0900	819317..819532	GAAGCT	score: 2.572308690	39
>pro0900	pro0900	819317..819532	TAGTTT	score: 2.913260024	48
>pro0900	pro0900	819317..819532	TAAATT	score: 3.968301383	60
>pro0908	pro0908	828364..828969	TATACT	score: 4.702840244	32
>pro0908	pro0908	828364..828969	CACTAT	score: 2.729412650	35
>pro0908	pro0908	828364..828969	CAAACT	score: 3.589382199	44
>pro0908	pro0908	828364..828969	CACTAT	score: 2.729412650	65
>pro0910	pro0910	829645..829995	CAAAAT	score: 3.369416510	27
>pro0911	pro0911	830615..830929	CATGCT	score: 3.894236785	22
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>pro0911	pro0911	830615..830929	TAAAGT	score: 4.702840244	67
>pro0911	pro0911	830615..830929	TAAGAT	score: 4.787729142	76
>pro0911	pro0911	830615..830929	CATATT	score: 2.854843338	82
>pro0915	pro0915	832805..833074	TAATTT	score: 3.830797859	22
>pro0915	pro0915	832805..833074	TATAAT	score: 4.482874556	24
>pro0915	pro0915	832805..833074	TACTAT	score: 3.842870696	27
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>pro0915	pro0915	832805..833074	TAATTT	score: 3.830797859	67
>pro0915	pro0915	832805..833074	CACAAT	score: 2.866916174	76
>pro0915	pro0915	832805..833074	TAATTT	score: 3.830797859	87
>pro0918	pro0918	834283..834384	TATAAT	score: 4.482874556	22
>pro0918	pro0918	834283..834384	TATGAT	score: 4.787729142	29
>pro0918	pro0918	834283..834384	TAATAT	score: 4.345371032	45
>pro0918	pro0918	834283..834384	TACTTT	score: 3.328297523	50
>pro0918	pro0918	834283..834384	CATTAT	score: 3.231912987	76
>clpP	pro0920	835259..835849	TAGTAT	score: 3.427833197	23
>clpP	pro0920	835259..835849	CAATAT	score: 3.231912987	35
>clpP	pro0920	835259..835849	TAAAAT	score: 4.482874556	63
>clpP	pro0920	835259..835849	TAGTTT	score: 2.913260024	87
>mazG	pro0924	840991..841320	CATTTT	score: 2.717339814	30
>dxs	pro0928	843898..845829	TAGATT	score: 3.050763548	22
>dxs	pro0928	843898..845829	TAATCT	score: 4.565336720	51
>dxs	pro0928	843898..845829	CATTTT	score: 2.717339814	68
>dxs	pro0928	843898..845829	TACTAT	score: 3.842870696	75
>ser1-tRNA RNA_1		852209..852295	TAGATT	score: 3.050763548	25
>ser1-tRNA RNA_1		852209..852295	CATATT	score: 2.854843338	37
>ser1-tRNA RNA_1		852209..852295	GATGAT	score: 2.352343001	44
>ser1-tRNA RNA_1		852209..852295	TAAATT	score: 3.968301383	51
>ser1-tRNA RNA_1		852209..852295	TAGTTT	score: 2.913260024	79
>dnaK	pro0938	852504..854504	TAGTTT	score: 2.913260024	22
>dnaK	pro0938	852504..854504	CATAAT	score: 3.369416510	91
>ppiB	pro0942	856901..857338	TATAAT	score: 4.482874556	26

>ppiB	pro0942	856901..857338	TAGTAT	score: 3.427833197	29
>ppiB	pro0942	856901..857338	TATGTT	score: 4.273155969	39
>ppiB	pro0942	856901..857338	CAATTT	score: 2.717339814	46
>argC	pro0944	859086..860165	TAGTTT	score: 2.913260024	24
>argC	pro0944	859086..860165	CATAGT	score: 3.589382199	26
>argC	pro0944	859086..860165	TAAGTT	score: 4.273155969	32
>argC	pro0944	859086..860165	TAAAGT	score: 4.702840244	39
>argC	pro0944	859086..860165	TATTGT	score: 4.565336720	56
>pgi	pro0946	860990..862591	CATAAT	score: 3.369416510	38
>pgi	pro0946	860990..862591	TATTTT	score: 3.830797859	58
>dapF	pro0948	865323..866180	TATATT	score: 3.968301383	26
>dapF	pro0948	865323..866180	TATTAT	score: 4.345371032	33
>dapF	pro0948	865323..866180	TATATT	score: 3.968301383	35
>dapF	pro0948	865323..866180	GAAGCT	score: 2.572308690	42
>dapF	pro0948	865323..866180	TATTAT	score: 4.345371032	53
>dapF	pro0948	865323..866180	TATTAT	score: 4.345371032	56
>dapF	pro0948	865323..866180	TAATAT	score: 4.345371032	59
>pro0953	pro0953	869857..870339	TATTTT	score: 3.830797859	40
>pro0953	pro0953	869857..870339	GATGGT	score: 2.572308690	48
>pro0953	pro0953	869857..870339	TAATTT	score: 3.830797859	64
>pro0953	pro0953	869857..870339	CATAAT	score: 3.369416510	66
>pro0953	pro0953	869857..870339	CAGGGT	score: 2.976698949	82
>pro0955	pro0955	872378..872944	TAATAT	score: 4.345371032	30
>pro0955	pro0955	872378..872944	TATTTT	score: 3.830797859	71
>ilvE	pro0958	877443..878357	TATTAT	score: 4.345371032	63
>ilvE	pro0958	877443..878357	GAAGAT	score: 2.352343001	90
>aPA2	pro0961	882714..883556	TAAATT	score: 3.968301383	32
>aPA2	pro0961	882714..883556	TAAAAT	score: 4.482874556	37
>aPA2	pro0961	882714..883556	TATGAT	score: 4.787729142	48
>aPA2	pro0961	882714..883556	TAATAT	score: 4.345371032	51
>aPA2	pro0961	882714..883556	CATAAT	score: 3.369416510	74
>pro0963	pro0963	883950..885014	CAATAT	score: 3.231912987	70
>pro0963	pro0963	883950..885014	TACTCT	score: 4.062836384	78
>pro0964	pro0964	885291..885527	TAATTT	score: 3.830797859	39
>pro0964	pro0964	885291..885527	TAGATT	score: 3.050763548	52
>pro0964	pro0964	885291..885527	CAATTT	score: 2.717339814	57
>pro0964	pro0964	885291..885527	TAATAT	score: 4.345371032	71
>rpmG	pro0967	889575..889772	CAAAGT	score: 3.589382199	25
>rpmG	pro0967	889575..889772	TAGGTT	score: 3.355618133	34
>rpmG	pro0967	889575..889772	TAGGAT	score: 3.870191306	41
>rpmG	pro0967	889575..889772	TACACT	score: 4.200339908	55
>rpmG	pro0967	889575..889772	TACGGT	score: 4.505194494	83
>vacB	pro0969	890081..891379	TAGTTT	score: 2.913260024	24
>metG	pro0970	891444..892967	TACTAT	score: 3.842870696	23
>metG	pro0970	891444..892967	CAATAT	score: 3.231912987	36
>pro0973	pro0973	894365..894676	CAATAT	score: 3.231912987	23
>pro0973	pro0973	894365..894676	CAAAAT	score: 3.369416510	42
>pro0973	pro0973	894365..894676	CATAAT	score: 3.369416510	61
>pro0973	pro0973	894365..894676	TACTAT	score: 3.842870696	68
>pro0973	pro0973	894365..894676	TAAGGT	score: 5.007694830	79
>met1-tRNA	RNA_19	896720..896793	TATTTT	score: 3.830797859	37
>met1-tRNA	RNA_19	896720..896793	TACTAT	score: 3.842870696	40
>met1-tRNA	RNA_19	896720..896793	TATTGT	score: 4.565336720	45
>met1-tRNA	RNA_19	896720..896793	TAATAT	score: 4.345371032	84
>ahpC	pro0978	897258..897851	TAAAAT	score: 4.482874556	26
>ahpC	pro0978	897258..897851	TAAAAT	score: 4.482874556	45

>ahpC	pro0978	897258..897851	TAAATT	score: 3.968301383	63
>ahpC	pro0978	897258..897851	TATGTT	score: 4.273155969	68
>ahpC	pro0978	897258..897851	CACAAT	score: 2.866916174	85
>ahpC	pro0978	897258..897851	TACACT	score: 4.200339908	91
>rpmF	pro0981	900624..900797	CACGAT	score: 3.171770760	25
>rpmF	pro0981	900624..900797	CAATTT	score: 2.717339814	50
>rpmF	pro0981	900624..900797	TACAAT	score: 3.980374220	52
>rpmF	pro0981	900624..900797	CAAAAT	score: 3.369416510	61
>rpmF	pro0981	900624..900797	TAGTAT	score: 3.427833197	80
>rpmF	pro0981	900624..900797	CATAGT	score: 3.589382199	82
>recJ	pro0984	901954..903834	TAAAAT	score: 4.482874556	25
>recJ	pro0984	901954..903834	TATAAT	score: 4.482874556	36
>recJ	pro0984	901954..903834	CAAGAT	score: 3.674271096	85
>pro0985	pro0985	904075..904434	TAATTT	score: 3.830797859	40
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>pro0985	pro0985	904075..904434	TAAGAT	score: 4.787729142	61
>pro0985	pro0985	904075..904434	TATTAT	score: 4.345371032	86
>vacB	pro0988	905204..907510	TAAATT	score: 3.968301383	27
>vacB	pro0988	905204..907510	TAATTT	score: 3.830797859	50
>vacB	pro0988	905204..907510	TATAAT	score: 4.482874556	52
>vacB	pro0988	905204..907510	TAGAAT	score: 3.565336720	57
>vacB	pro0988	905204..907510	TAGTGT	score: 3.647798885	65
>pro0992	pro0992	909422..910465	TATTAT	score: 4.345371032	22
>pro0992	pro0992	909422..910465	CACGCT	score: 3.391736448	63
>pro0992	pro0992	909422..910465	TAAATT	score: 3.968301383	80
>pro0999	pro0999	915984..916694	TAGATT	score: 3.050763548	38
>pro0999	pro0999	915984..916694	TATGGT	score: 5.007694830	74
>mfd	pro1000	916759..920271	TAATCT	score: 4.565336720	28
>mfd	pro1000	916759..920271	TAAATT	score: 3.968301383	34
>pro1002	pro1002	921350..921514	CAAATT	score: 2.854843338	38
>pro1002	pro1002	921350..921514	CATGCT	score: 3.894236785	67
>pro1007	pro1007	923453..923668	TACACT	score: 4.200339908	34
>pro1007	pro1007	923453..923668	TAAGCT	score: 5.007694830	43
>pro1007	pro1007	923453..923668	TAGAAT	score: 3.565336720	57
>pro1007	pro1007	923453..923668	TAATAT	score: 4.345371032	62
>pro1007	pro1007	923453..923668	CATTCT	score: 3.451878675	69
>aroB	pro1009	925914..927017	TAAAGT	score: 4.702840244	72
>aroB	pro1009	925914..927017	TATTTT	score: 3.830797859	86
>pro1011	pro1011	928257..929048	CAAGGT	score: 3.894236785	47
>nadA	pro1013	929980..931011	CAGGAT	score: 2.756733261	75
>pro1018	pro1018	934763..935944	CAAAGT	score: 3.589382199	47
>pro1018	pro1018	934763..935944	TAAGGT	score: 5.007694830	67
>pro1018	pro1018	934763..935944	TATAAT	score: 4.482874556	76
>pro1018	pro1018	934763..935944	CATGTT	score: 3.159697923	89
>cbiO	pro1026	941991..942620	TATGAT	score: 4.787729142	29
>cbiO	pro1026	941991..942620	CATTAT	score: 3.231912987	32
>cbiO	pro1026	941991..942620	TAATTT	score: 3.830797859	70
>bioY	pro1031	946328..946912	TACTTT	score: 3.328297523	24
>bioY	pro1031	946328..946912	TAAAAT	score: 4.482874556	48
>bioY	pro1031	946328..946912	TACTTT	score: 3.328297523	63
>cumB	pro1036	950547..951041	TATGGT	score: 5.007694830	27
>cumB	pro1036	950547..951041	TATATT	score: 3.968301383	69
>cumB	pro1036	950547..951041	TATGTT	score: 4.273155969	84
>glnA	pro1038	952441..953862	TAATTT	score: 3.830797859	26
>glnA	pro1038	952441..953862	TACGGT	score: 4.505194494	35
>glnA	pro1038	952441..953862	TAAGTT	score: 4.273155969	44

>glnA	pro1038	952441..953862	CAAAAT	score: 3.369416510	49
>pro1039	pro1039	953966..954262	TATAAT	score: 4.482874556	28
>pro1039	pro1039	953966..954262	CAAGGT	score: 3.894236785	56
>pro1039	pro1039	953966..954262	TATTAT	score: 4.345371032	65
>pro1039	pro1039	953966..954262	TAATAT	score: 4.345371032	68
>pro1039	pro1039	953966..954262	TAAAAT	score: 4.482874556	75
>ubiD	pro1047	962406..963971	CAGAGT	score: 2.671844363	32
>ubiD	pro1047	962406..963971	CAATCT	score: 3.451878675	52
>lepB	pro1055	973448..974038	TAATCT	score: 4.565336720	43
>pro1062	pro1062	979891..980460	CAAAAT	score: 3.369416510	32
>nuoM	pro1067	985503..987074	TAAGGT	score: 5.007694830	22
>pro1074	pro1074	996048..996641	TAATCT	score: 4.565336720	75
>hemE	pro1079	1001451..1002506	TACTTT	score: 3.328297523	44
>hemE	pro1079	1001451..1002506	GAAGAT	score: 2.352343001	71
>clpA	pro1082	1004268..1006862	TATTTT	score: 3.830797859	36
>clpA	pro1082	1004268..1006862	CAAGTT	score: 3.159697923	84
>pro1084	pro1084	1007703..1007975	TAAAAT	score: 4.482874556	48
>pro1084	pro1084	1007703..1007975	CAAGTT	score: 3.159697923	58
>pro1084	pro1084	1007703..1007975	CAAAAT	score: 3.369416510	64
>pro1084	pro1084	1007703..1007975	TAATGT	score: 4.565336720	77
>pdxJ	pro1089	1010005..1010745	TAAACT	score: 4.702840244	27
>pdxJ	pro1089	1010005..1010745	CAAATT	score: 2.854843338	47
>srnB	pro1094	1020284..1022095	CACGGT	score: 3.391736448	60
>recR	pro1098	1024995..1025504	CAATTT	score: 2.717339814	45
>rimI	pro1106	1032104..1032565	TAAATT	score: 3.968301383	22
>rimI	pro1106	1032104..1032565	TAAGGT	score: 5.007694830	48
>rimI	pro1106	1032104..1032565	CAAAAT	score: 3.369416510	78
>clpA	pro1107	1032758..1035328	TAGAGT	score: 3.785302409	22
>clpA	pro1107	1032758..1035328	TAAATT	score: 3.968301383	27
>clpA	pro1107	1032758..1035328	CAAACT	score: 3.589382199	47
>clpA	pro1107	1032758..1035328	TACGGT	score: 4.505194494	77
>clpA	pro1107	1032758..1035328	CAAGAT	score: 3.674271096	83
>aarF	pro1113	1040409..1042055	CACAGT	score: 3.086881863	37
>aarF	pro1113	1040409..1042055	TACTTT	score: 3.328297523	52
>aarF	pro1113	1040409..1042055	TAGAAT	score: 3.565336720	87
>rsuA	pro1114	1042125..1042838	TAAACT	score: 4.702840244	28
>pro1121	pro1121	1048119..1049264	TAAGGT	score: 5.007694830	28
>petH	pro1123	1050143..1051237	TAAAGT	score: 4.702840244	38
>petH	pro1123	1050143..1051237	CAATCT	score: 3.451878675	80
>petH	pro1123	1050143..1051237	CAGACT	score: 2.671844363	91
>zwf	pro1124	1051431..1052951	CAATTT	score: 2.717339814	49
>pro1131	pro1131	1059598..1061718	CAGGCT	score: 2.976698949	22
>pro1131	pro1131	1059598..1061718	TAAGTT	score: 4.273155969	36
>pro1131	pro1131	1059598..1061718	CAAATT	score: 2.854843338	41
>pro1131	pro1131	1059598..1061718	CAAGTT	score: 3.159697923	77
>pro1135	pro1135	1064271..1065836	TATATT	score: 3.968301383	39
>pro1135	pro1135	1064271..1065836	TATCTT	score: 4.565336720	48
>pro1135	pro1135	1064271..1065836	TAATGT	score: 4.565336720	57
>pro1135	pro1135	1064271..1065836	TAAACT	score: 4.702840244	79
>guaB	pro1138	1070538..1071701	TAGTTT	score: 2.913260024	23
>guaB	pro1138	1070538..1071701	CAAGAT	score: 3.674271096	37
>guaB	pro1138	1070538..1071701	CAATCT	score: 3.451878675	65
>guaB	pro1138	1070538..1071701	TAATCT	score: 4.565336720	78
>trxA	pro1139	1071876..1072199	CAAAAT	score: 3.369416510	35
>cccA	pro1143	1073603..1074019	CAGAGT	score: 2.671844363	46
>chlI	pro1146	1075942..1077030	TAAGCT	score: 5.007694830	51

>pro1151	pro1151	1080082..1080282	CACATT	score: 2.352343001	32
>proP	pro1155	1084544..1085818	CAGAAT	score: 2.451878675	29
>proP	pro1155	1084544..1085818	CAATTT	score: 2.717339814	43
>proP	pro1155	1084544..1085818	CAAAAT	score: 3.369416510	90
>rbsK	pro1157	1086518..1087342	TAATTT	score: 3.830797859	36
>rbsK	pro1157	1086518..1087342	TATATT	score: 3.968301383	53
>rbsK	pro1157	1086518..1087342	TAAGAT	score: 4.787729142	66
>pro1163	pro1163	1089611..1089814	TAGGAT	score: 3.870191306	48
>pro1163	pro1163	1089611..1089814	TAGAAT	score: 3.565336720	54
>pro1163	pro1163	1089611..1089814	TATTGT	score: 4.565336720	60
>pro1163	pro1163	1089611..1089814	CAGAAT	score: 2.451878675	70
>pro1168	pro1168	1092962..1093177	TAGGTT	score: 3.355618133	24
>pro1168	pro1168	1092962..1093177	TAAAGT	score: 4.702840244	31
>pro1168	pro1168	1092962..1093177	TAGATT	score: 3.050763548	80
>pro1168	pro1168	1092962..1093177	TATTTT	score: 3.830797859	89
>pro1170	pro1170	1094438..1094743	TAATTT	score: 3.830797859	28
>pro1170	pro1170	1094438..1094743	CATAAT	score: 3.369416510	30
>pro1170	pro1170	1094438..1094743	CAGAAT	score: 2.451878675	82
>pro1171	pro1171	1094967..1095203	TAAAGT	score: 4.702840244	65
>pro1171	pro1171	1094967..1095203	CAAGTT	score: 3.159697923	91
>pro1173	pro1173	1095606..1095773	GAAGGT	score: 2.572308690	50
>pro1173	pro1173	1095606..1095773	TAAATT	score: 3.968301383	61
>hli8	pro1175	1097458..1097565	CAAAAT	score: 3.369416510	35
>pro1177	pro1177	1098074..1098397	TAAATT	score: 3.968301383	23
>pro1177	pro1177	1098074..1098397	TAAAGT	score: 4.702840244	28
>pro1177	pro1177	1098074..1098397	TATTGT	score: 4.565336720	52
>pro1177	pro1177	1098074..1098397	TAATTT	score: 3.830797859	58
>pro1177	pro1177	1098074..1098397	TAGAAT	score: 3.565336720	63
>pro1177	pro1177	1098074..1098397	TAATAT	score: 4.345371032	76
>pro1178	pro1178	1098837..1099067	TAAATT	score: 3.968301383	51
>pro1182	pro1182	1100638..1100841	TAATAT	score: 4.345371032	22
>pro1182	pro1182	1100638..1100841	TAAGTT	score: 4.273155969	27
>pro1182	pro1182	1100638..1100841	TAGTTT	score: 2.913260024	38
>purT	pro1184	1101411..1102592	TAGGTT	score: 3.355618133	44
>purT	pro1184	1101411..1102592	TAAGGT	score: 5.007694830	62
>purT	pro1184	1101411..1102592	TATATT	score: 3.968301383	74
>purT	pro1184	1101411..1102592	TAAGAT	score: 4.787729142	85
>pro1185	pro1185	1102737..1103039	CATTGT	score: 3.451878675	37
>pro1186	pro1186	1103247..1103366	TAAAAT	score: 4.482874556	30
>pro1186	pro1186	1103247..1103366	TAATAT	score: 4.345371032	55
>pro1186	pro1186	1103247..1103366	TATAAT	score: 4.482874556	61
>pro1186	pro1186	1103247..1103366	CAGACT	score: 2.671844363	72
>pro1186	pro1186	1103247..1103366	CACAGT	score: 3.086881863	83
>pro1186	pro1186	1103247..1103366	TAATGT	score: 4.565336720	90
>pro1188	pro1188	1104450..1104635	CAATTT	score: 2.717339814	28
>pro1188	pro1188	1104450..1104635	TAAATT	score: 3.968301383	69
>tas	pro1192	1105916..1106875	CATGAT	score: 3.674271096	23
>pro1195	pro1195	1107661..1107978	TACTCT	score: 4.062836384	29
>pro1195	pro1195	1107661..1107978	TATACT	score: 4.702840244	31
>pro1195	pro1195	1107661..1107978	TACTAT	score: 3.842870696	34
>pro1195	pro1195	1107661..1107978	CAATTT	score: 2.717339814	43
>pro1195	pro1195	1107661..1107978	TACAAT	score: 3.980374220	45
>pro1195	pro1195	1107661..1107978	CACACT	score: 3.086881863	53
>uup	pro1196	1108136..1110067	TATTGT	score: 4.565336720	29
>uup	pro1196	1108136..1110067	TACTTT	score: 3.328297523	35
>uup	pro1196	1108136..1110067	TAGAAT	score: 3.565336720	87

>pro1198	pro1198	1110734..1111165	GAAGAT	score: 2.352343001	29
>pro1199	pro1199	1111490..1111699	TATATT	score: 3.968301383	28
>pro1199	pro1199	1111490..1111699	CAAGTT	score: 3.159697923	55
>pro1202	pro1202	1113529..1113774	CATTGT	score: 3.451878675	46
>pro1202	pro1202	1113529..1113774	TAGTTT	score: 2.913260024	62
>mntH	pro1203	1113963..1115270	TATTTT	score: 3.830797859	62
>mntH	pro1203	1113963..1115270	TAAAAT	score: 4.482874556	72
>mntH	pro1203	1113963..1115270	TAGTCT	score: 3.647798885	79
>pro1215	pro1215	1122633..1122854	CATAAT	score: 3.369416510	48
>pro1217	pro1217	1123812..1124009	CAGTCT	score: 2.534340839	35
>pro1217	pro1217	1123812..1124009	CAAGTT	score: 3.159697923	56
>pro1219	pro1219	1124867..1125454	CAATTT	score: 2.717339814	31
>pro1222	pro1222	1126677..1126838	TAATTT	score: 3.830797859	25
>pro1222	pro1222	1126677..1126838	TAATCT	score: 4.565336720	45
>pro1222	pro1222	1126677..1126838	CATGAT	score: 3.674271096	80
>pro1223	pro1223	1127426..1127827	TAAGAT	score: 4.787729142	23
>pro1223	pro1223	1127426..1127827	CAATTT	score: 2.717339814	44
>pro1223	pro1223	1127426..1127827	CAATAT	score: 3.231912987	60
>pro1223	pro1223	1127426..1127827	TAAGGT	score: 5.007694830	66
>prfB	pro1225	1128356..1128787	TAAACT	score: 4.702840244	26
>prfB	pro1225	1128356..1128787	CAAGGT	score: 3.894236785	64
>mmsB	pro1229	1131357..1132253	TAGTAT	score: 3.427833197	28
>mmsB	pro1229	1131357..1132253	TATAGT	score: 4.702840244	30
>mmsB	pro1229	1131357..1132253	TAAGTT	score: 4.273155969	47
>mmsB	pro1229	1131357..1132253	TAGTCT	score: 3.647798885	57
>tata	pro1230	1132446..1132703	TATTAT	score: 4.345371032	39
>tata	pro1230	1132446..1132703	TAGAGT	score: 3.785302409	79
>pro1231	pro1231	1133344..1133961	TATTAT	score: 4.345371032	47
>pro1231	pro1231	1133344..1133961	TATATT	score: 3.968301383	49
>pro1231	pro1231	1133344..1133961	TAAGTT	score: 4.273155969	57
>pro1231	pro1231	1133344..1133961	CAATTT	score: 2.717339814	65
>pro1231	pro1231	1133344..1133961	CACAAT	score: 2.866916174	67
>pro1231	pro1231	1133344..1133961	TATATT	score: 3.968301383	78
>pro1231	pro1231	1133344..1133961	TAGAAT	score: 3.565336720	87
>acrA	pro1233	1135226..1136287	CAAACCT	score: 3.589382199	75
>acrA	pro1233	1135226..1136287	TATTCT	score: 4.565336720	84
>pro1243	pro1243	1146615..1147196	CATTTT	score: 2.717339814	74
>pro1244	pro1244	1147398..1147640	CAATGT	score: 3.451878675	39
>pro1244	pro1244	1147398..1147640	CAAGTT	score: 3.159697923	65
>trxB	pro1245	1147746..1149104	TATATT	score: 3.968301383	26
>trxB	pro1245	1147746..1149104	TAATAT	score: 4.345371032	29
>trxB	pro1245	1147746..1149104	TAGGAT	score: 3.870191306	52
>mhpC	pro1250	1151116..1152090	CAATTT	score: 2.717339814	62
>mhpC	pro1250	1151116..1152090	TAGTCT	score: 3.647798885	77
>mhpC	pro1250	1151116..1152090	TAAATT	score: 3.968301383	89
>psbD	pro1254	1154108..1155184	TAAAGT	score: 4.702840244	37
>pro1258	pro1258	1157248..1157655	CATATT	score: 2.854843338	36
>pro1258	pro1258	1157248..1157655	CAATAT	score: 3.231912987	57
>pro1258	pro1258	1157248..1157655	TACTTT	score: 3.328297523	70
>pro1258	pro1258	1157248..1157655	TATACT	score: 4.702840244	72
>pro1258	pro1258	1157248..1157655	CATTTT	score: 2.717339814	84
>pro1258	pro1258	1157248..1157655	TACATT	score: 3.465801047	86
>pro1264	pro1264	1163872..1164573	TATGAT	score: 4.787729142	23
>pro1264	pro1264	1163872..1164573	CAGACT	score: 2.671844363	36
>pro1264	pro1264	1163872..1164573	CAAGGT	score: 3.894236785	63
>pro1265	pro1265	1164742..1167198	TAATTT	score: 3.830797859	32

>pro1265	pro1265	1164742..1167198	CACTAT	score: 2.729412650	65
>pro1265	pro1265	1164742..1167198	TAAGTT	score: 4.273155969	85
>pro1267	pro1267	1167975..1168856	TAATTT	score: 3.830797859	30
>pro1267	pro1267	1167975..1168856	TAAATT	score: 3.968301383	35
>pro1267	pro1267	1167975..1168856	TAAAAT	score: 4.482874556	47
>pro1267	pro1267	1167975..1168856	CATATT	score: 2.854843338	52
>pro1269	pro1269	1169899..1171452	TAGGCT	score: 4.090156995	36
>pro1269	pro1269	1169899..1171452	TAGAAT	score: 3.565336720	41
>afuA	pro1272	1172770..1173798	TATTAT	score: 4.345371032	24
>afuA	pro1272	1172770..1173798	TAAAAT	score: 4.482874556	29
>afuA	pro1272	1172770..1173798	TACTTT	score: 3.328297523	81
>afuA	pro1272	1172770..1173798	TATGAT	score: 4.787729142	86
>ser2-tRNA	RNA_17	1173899..1173985	TAAATT	score: 3.968301383	33
>ser2-tRNA	RNA_17	1173899..1173985	TATTAT	score: 4.345371032	43
>ser2-tRNA	RNA_17	1173899..1173985	TATGTT	score: 4.273155969	52
>ser2-tRNA	RNA_17	1173899..1173985	CAGAAT	score: 2.451878675	62
>pro1274	pro1274	1174866..1176800	TAAATT	score: 3.968301383	28
>pro1274	pro1274	1174866..1176800	TATTGT	score: 4.565336720	73
>pro1276	pro1276	1177675..1178226	TATACT	score: 4.702840244	36
>smtA	pro1277	1178442..1179323	TAGAAT	score: 3.565336720	26
>smtA	pro1277	1178442..1179323	TAAAAT	score: 4.482874556	42
>smtA	pro1277	1178442..1179323	GATGAT	score: 2.352343001	55
>smtA	pro1277	1178442..1179323	TAAAAT	score: 4.482874556	77
>smtA	pro1277	1178442..1179323	CAATTT	score: 2.717339814	82
>smtA	pro1277	1178442..1179323	TACTCT	score: 4.062836384	88
>pro1278	pro1278	1179653..1180312	TAAGCT	score: 5.007694830	22
>pro1278	pro1278	1179653..1180312	TATTAT	score: 4.345371032	27
>pro1278	pro1278	1179653..1180312	TATTAT	score: 4.345371032	48
>pro1278	pro1278	1179653..1180312	TAGGTT	score: 3.355618133	53
>pro1278	pro1278	1179653..1180312	TAATGT	score: 4.565336720	82
>pcbF	pro1288	1188562..1189626	CATGTT	score: 3.159697923	23
>pcbF	pro1288	1188562..1189626	TAGTGT	score: 3.647798885	34
>pcbF	pro1288	1188562..1189626	CAATTT	score: 2.717339814	84
>sppA	pro1296	1197664..1198473	TAAACT	score: 4.702840244	23
>sppA	pro1296	1197664..1198473	TATTTT	score: 3.830797859	29
>yidC	pro1302	1200654..1201802	CATAGT	score: 3.589382199	35
>yidC	pro1302	1200654..1201802	TATTAT	score: 4.345371032	50
>spoVK	pro1303	1201885..1203363	TATTTT	score: 3.830797859	37
>spoVK	pro1303	1201885..1203363	TATTAT	score: 4.345371032	52
>rpsN	pro1306	1205795..1206094	TAAAAT	score: 4.482874556	29
>pnp	pro1307	1206287..1208455	CAATGT	score: 3.451878675	26
>pnp	pro1307	1206287..1208455	CATATT	score: 2.854843338	61
>pnp	pro1307	1206287..1208455	TAAAAT	score: 4.482874556	78
>pnp	pro1307	1206287..1208455	CAAAC	score: 3.589382199	86
>pro1309	pro1309	1209387..1210304	CAAATT	score: 2.854843338	34
>pro1309	pro1309	1209387..1210304	CAAATT	score: 2.854843338	43
>pro1309	pro1309	1209387..1210304	TAAGTT	score: 4.273155969	56
>pro1309	pro1309	1209387..1210304	CAGAAT	score: 2.451878675	88
>arg2-tRNA	RNA_16	1212078..1212151	TACTCT	score: 4.062836384	51
>arg2-tRNA	RNA_16	1212078..1212151	TAAAGT	score: 4.702840244	83
>wza	pro1316	1217122..1218336	TATAGT	score: 4.702840244	76
>wza	pro1316	1217122..1218336	TATTGT	score: 4.565336720	81
>hisB	pro1318	1219466..1220125	TAAGTT	score: 4.273155969	42
>hisB	pro1318	1219466..1220125	TACATT	score: 3.465801047	47
>hisB	pro1318	1219466..1220125	GAAGCT	score: 2.572308690	78
>hisB	pro1318	1219466..1220125	TAAATT	score: 3.968301383	84

>wcaG	pro1323	1224296..1225243	TAGATT	score: 3.050763548	51
>gumC	pro1330	1231308..1233065	TATAAT	score: 4.482874556	23
>gumC	pro1330	1231308..1233065	CAGGAT	score: 2.756733261	52
>pro1334	pro1334	1237463..1238422	TAAAAT	score: 4.482874556	52
>pro1334	pro1334	1237463..1238422	CATAGT	score: 3.589382199	68
>pro1334	pro1334	1237463..1238422	TAAAAT	score: 4.482874556	78
>pro1342	pro1342	1245934..1247238	TAAGAT	score: 4.787729142	91
>surE	pro1345	1249282..1250070	TAATTT	score: 3.830797859	22
>surE	pro1345	1249282..1250070	CAAACT	score: 3.589382199	46
>ribF	pro1347	1250700..1251617	CAAACT	score: 3.589382199	32
>ribF	pro1347	1250700..1251617	CAAAAAT	score: 3.369416510	54
>thiE	pro1348	1251780..1252820	CAAAAAT	score: 3.369416510	56
>thiE	pro1348	1251780..1252820	CACATT	score: 2.352343001	70
>pro1350	pro1350	1253279..1253446	TAAGTT	score: 4.273155969	24
>pro1350	pro1350	1253279..1253446	CACAGT	score: 3.086881863	30
>pro1350	pro1350	1253279..1253446	CAATAT	score: 3.231912987	56
>pro1350	pro1350	1253279..1253446	TATTTT	score: 3.830797859	79
>pro1350	pro1350	1253279..1253446	TATATT	score: 3.968301383	81
>pro1351	pro1351	1253515..1253649	TATAAT	score: 4.482874556	37
>pro1356	pro1356	1257003..1257521	CACAGT	score: 3.086881863	25
>pro1356	pro1356	1257003..1257521	CATAGT	score: 3.589382199	46
>pro1356	pro1356	1257003..1257521	TAATGT	score: 4.565336720	55
>acoA	pro1362	1263536..1264630	TAAAGT	score: 4.702840244	23
>acoA	pro1362	1263536..1264630	CAAACT	score: 3.589382199	73
>acoA	pro1362	1263536..1264630	CAAGCT	score: 3.894236785	88
>trmU	pro1365	1267363..1268583	GAAGAT	score: 2.352343001	85
>fkpA	pro1367	1270179..1270772	TAGTTT	score: 2.913260024	68
>pro1368	pro1368	1270861..1271334	TAATGT	score: 4.565336720	26
>murA	pro1374	1276078..1277451	CAAACT	score: 3.589382199	88
>miaB	pro1379	1282845..1284245	TATTGT	score: 4.565336720	26
>ddlA	pro1380	1284301..1285356	TATTTT	score: 3.830797859	25
>ftsZ	pro1383	1286755..1287870	CATAAT	score: 3.369416510	37
>panB	pro1384	1288028..1288798	TAAAGT	score: 4.702840244	33
>pro1386	pro1386	1290126..1291235	TAGATT	score: 3.050763548	51
>pro1386	pro1386	1290126..1291235	CATATT	score: 2.854843338	69
>ilvC	pro1389	1292746..1293741	CAAGCT	score: 3.894236785	31
>ilvC	pro1389	1292746..1293741	TATTTT	score: 3.830797859	40
>ilvC	pro1389	1292746..1293741	TAATTT	score: 3.830797859	45
>ilvC	pro1389	1292746..1293741	TATAAT	score: 4.482874556	47
>ilvC	pro1389	1292746..1293741	TAATTT	score: 3.830797859	85
>pro1394	pro1394	1297539..1297703	TAGAGT	score: 3.785302409	28
>pro1394	pro1394	1297539..1297703	TAAGTT	score: 4.273155969	55
>pro1394	pro1394	1297539..1297703	TAAGTT	score: 4.273155969	64
>pro1394	pro1394	1297539..1297703	CAAGCT	score: 3.894236785	70
>pro1394	pro1394	1297539..1297703	TATTTT	score: 3.830797859	86
>pro1394	pro1394	1297539..1297703	TAATAT	score: 4.345371032	89
>pulA	pro1403	1302061..1304166	CAAAAAT	score: 3.369416510	31
>pulA	pro1403	1302061..1304166	CAGAGT	score: 2.671844363	61
>pulA	pro1403	1302061..1304166	TAATTT	score: 3.830797859	73
>pulA	pro1403	1302061..1304166	CAATCT	score: 3.451878675	80
>melB	pro1404	1304392..1305750	TAAATT	score: 3.968301383	28
>melB	pro1404	1304392..1305750	CATTAT	score: 3.231912987	72
>pro1412	pro1412	1311115..1311717	TATTTT	score: 3.830797859	34
>pro1412	pro1412	1311115..1311717	TATTTT	score: 3.830797859	52
>pro1412	pro1412	1311115..1311717	TATAAT	score: 4.482874556	58
>pro1412	pro1412	1311115..1311717	TAATTT	score: 3.830797859	83

>purD	pro1421	1320693..1322030	CAAGCT	score: 3.894236785	28
>rplU	pro1425	1326239..1326697	CATTTT	score: 2.717339814	43
>rplU	pro1425	1326239..1326697	CAGGCT	score: 2.976698949	57
>truB	pro1428	1327826..1328767	TAAACT	score: 4.702840244	59
>elaC	pro1430	1330159..1331121	CAAGTT	score: 3.159697923	39
>elaC	pro1430	1330159..1331121	TAAAGT	score: 4.702840244	50
>elaC	pro1430	1330159..1331121	TAATTT	score: 3.830797859	76
>elaC	pro1430	1330159..1331121	TAATAT	score: 4.345371032	89
>pro1431	pro1431	1331190..1331744	TATGTT	score: 4.273155969	35
>pro1437	pro1437	1335813..1336376	CAGAAT	score: 2.451878675	23
>pro1437	pro1437	1335813..1336376	TAAACT	score: 4.702840244	72
>vall-tRNA	RNA_15	1337241..1337312	TAAATT	score: 3.968301383	29
>pro1440	pro1440	1338872..1339186	TATATT	score: 3.968301383	22
>pro1440	pro1440	1338872..1339186	TATTAT	score: 4.345371032	35
>pro1440	pro1440	1338872..1339186	CAAAAT	score: 3.369416510	42
>pro1440	pro1440	1338872..1339186	CATATT	score: 2.854843338	77
>pro1440	pro1440	1338872..1339186	CACAAT	score: 2.866916174	84
>pro1442	pro1442	1339696..1339878	CAAATT	score: 2.854843338	24
>pro1442	pro1442	1339696..1339878	GATGCT	score: 2.572308690	48
>pro1442	pro1442	1339696..1339878	CAAGGT	score: 3.894236785	65
>pro1442	pro1442	1339696..1339878	TAAAGT	score: 4.702840244	71
>pro1442	pro1442	1339696..1339878	TAATTT	score: 3.830797859	84
>pro1443	pro1443	1340096..1340263	CAATTT	score: 2.717339814	50
>pro1443	pro1443	1340096..1340263	CAAGTT	score: 3.159697923	63
>pro1443	pro1443	1340096..1340263	TAGACT	score: 3.785302409	80
>apt	pro1445	1340747..1341265	TATATT	score: 3.968301383	29
>apt	pro1445	1340747..1341265	CAAAGT	score: 3.589382199	34
>pro1446	pro1446	1341579..1341872	GAAGCT	score: 2.572308690	35
>pro1446	pro1446	1341579..1341872	CATTAT	score: 3.231912987	59
>pro1446	pro1446	1341579..1341872	TACATT	score: 3.465801047	61
>pro1455	pro1455	1349413..1349610	CATACT	score: 3.589382199	74
>wecE	pro1456	1349704..1350894	TAATCT	score: 4.565336720	22
>wecE	pro1456	1349704..1350894	TAAAAT	score: 4.482874556	33
>wecE	pro1456	1349704..1350894	TAATTT	score: 3.830797859	43
>wecE	pro1456	1349704..1350894	TAAATT	score: 3.968301383	48
>pro1457	pro1457	1351142..1351417	CAAGCT	score: 3.894236785	22
>pro1457	pro1457	1351142..1351417	CAATCT	score: 3.451878675	71
>pro1458	pro1458	1351770..1351952	TAAGAT	score: 4.787729142	25
>pro1458	pro1458	1351770..1351952	TAAAAT	score: 4.482874556	37
>pro1458	pro1458	1351770..1351952	CAATAT	score: 3.231912987	54
>gloB	pro1462	1356227..1357129	CAAATT	score: 2.854843338	45
>gloB	pro1462	1356227..1357129	TAAAAT	score: 4.482874556	51
>pro1464	pro1464	1357861..1358007	CAAATT	score: 2.854843338	60
>pro1467	pro1467	1360473..1360754	CAAGCT	score: 3.894236785	66
>pro1469	pro1469	1361334..1361486	TATGCT	score: 5.007694830	32
>pro1469	pro1469	1361334..1361486	TAGTAT	score: 3.427833197	39
>pro1469	pro1469	1361334..1361486	CATAGT	score: 3.589382199	44
>pro1469	pro1469	1361334..1361486	TATAAT	score: 4.482874556	50
>pro1469	pro1469	1361334..1361486	TATTTT	score: 3.830797859	64
>pro1469	pro1469	1361334..1361486	CAAAC	score: 3.589382199	69
>pro1470	pro1470	1361592..1361756	CATAGT	score: 3.589382199	37
>pro1470	pro1470	1361592..1361756	TAAGCT	score: 5.007694830	53
>pro1471	pro1471	1362033..1362758	CAAGCT	score: 3.894236785	46
>pro1471	pro1471	1362033..1362758	TAAAGT	score: 4.702840244	52
>pro1471	pro1471	1362033..1362758	TAGAAT	score: 3.565336720	57
>pro1471	pro1471	1362033..1362758	CACGTT	score: 2.657197587	68

>pro1471	pro1471	1362033..1362758	TACTAT	score: 3.842870696	88
>pro1473	pro1473	1363484..1363789	TAA AAT	score: 4.482874556	35
>pro1473	pro1473	1363484..1363789	CAA AAT	score: 3.369416510	47
>pro1474	pro1474	1363871..1364041	TAA ACT	score: 4.702840244	23
>pro1474	pro1474	1363871..1364041	CAT TTT	score: 2.717339814	43
>pro1476	pro1476	1364365..1364904	TAT TCT	score: 4.565336720	26
>pro1476	pro1476	1364365..1364904	TAA ATT	score: 3.968301383	31
>pro1476	pro1476	1364365..1364904	TA A TTT	score: 3.830797859	55
>pro1481	pro1481	1367464..1367691	TAT TGT	score: 4.565336720	33
>pro1481	pro1481	1367464..1367691	CA A GTT	score: 3.159697923	46
>pro1481	pro1481	1367464..1367691	TAA ACT	score: 4.702840244	87
>pro1485	pro1485	1369029..1369196	TACTAT	score: 3.842870696	27
>pro1485	pro1485	1369029..1369196	TAT AGT	score: 4.702840244	40
>pro1485	pro1485	1369029..1369196	CA CTCT	score: 2.949378339	45
>pro1485	pro1485	1369029..1369196	CAA ATT	score: 2.854843338	82
>pro1486	pro1486	1369386..1369544	CA ATAT	score: 3.231912987	46
>pro1486	pro1486	1369386..1369544	TAG ATT	score: 3.050763548	86
>pro1488	pro1488	1370461..1370958	TAG ATT	score: 3.050763548	48
>pro1493	pro1493	1373189..1373797	TAC ATT	score: 3.465801047	65
>pro1493	pro1493	1373189..1373797	TA A GCT	score: 5.007694830	83
>pro1495	pro1495	1374888..1375127	CA ATCT	score: 3.451878675	27
>pro1495	pro1495	1374888..1375127	TAT ATT	score: 3.968301383	59
>pro1495	pro1495	1374888..1375127	CAG GGT	score: 2.976698949	64
>pro1495	pro1495	1374888..1375127	CA ATCT	score: 3.451878675	77
>pro1497	pro1497	1375405..1375575	TAT TCT	score: 4.565336720	47
>pro1497	pro1497	1375405..1375575	CAT TGT	score: 3.451878675	64
>fur	pro1502	1378553..1378960	TAT TGT	score: 4.565336720	25
>fur	pro1502	1378553..1378960	CA A TTT	score: 2.717339814	64
>lraI	pro1504	1379762..1381264	TAG TAT	score: 3.427833197	26
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>lraI	pro1504	1379762..1381264	CAT TAT	score: 3.231912987	31
>lraI	pro1504	1379762..1381264	TA A GAT	score: 4.787729142	50
>lraI	pro1504	1379762..1381264	CAA ACT	score: 3.589382199	89
>pro1509	pro1509	1385685..1385849	CAT GGT	score: 3.894236785	54
>pro1509	pro1509	1385685..1385849	CAT TGT	score: 3.451878675	66
>pro1509	pro1509	1385685..1385849	CA A GAT	score: 3.674271096	72
>pro1509	pro1509	1385685..1385849	TAT TAT	score: 4.345371032	78
>hli13	pro1512	1387252..1387371	TAT TTT	score: 3.830797859	22
>hli13	pro1512	1387252..1387371	TAT ATT	score: 3.968301383	24
>hli13	pro1512	1387252..1387371	CAT TAT	score: 3.231912987	34
>hli13	pro1512	1387252..1387371	CAC ACT	score: 3.086881863	46
>hli13	pro1512	1387252..1387371	TAG GCT	score: 4.090156995	68
>pro1515	pro1515	1387748..1387921	CA A TTT	score: 2.717339814	53
>hli1	pro1516	1388012..1388131	TAA ACT	score: 4.702840244	36
>pro1517	pro1517	1388593..1388769	TAC GTT	score: 3.770655633	47
>pro1518	pro1518	1388887..1389012	CAA AAT	score: 3.369416510	63
>pro1518	pro1518	1388887..1389012	CAT GGT	score: 3.894236785	73
>pro1519	pro1519	1389227..1389415	TAT TCT	score: 4.565336720	34
>pro1519	pro1519	1389227..1389415	CAT ATT	score: 2.854843338	36
>pro1519	pro1519	1389227..1389415	CAT TCT	score: 3.451878675	48
>pro1519	pro1519	1389227..1389415	TAC ATT	score: 3.465801047	69
>pro1521	pro1521	1390206..1391906	TAA AGT	score: 4.702840244	30
>pro1521	pro1521	1390206..1391906	TA A TGT	score: 4.565336720	57
>pro1521	pro1521	1390206..1391906	CAC AGT	score: 3.086881863	65
>pro1523	pro1523	1393972..1394328	TAG GCT	score: 4.090156995	40
>pro1523	pro1523	1393972..1394328	TAA ATT	score: 3.968301383	71

>pro1523	pro1523	1393972..1394328	CATGTG	score: 3.451878675	78
>pro1523	pro1523	1393972..1394328	CACATT	score: 2.352343001	80
>pro1524	pro1524	1394488..1395066	TATTTT	score: 3.830797859	52
>pro1524	pro1524	1394488..1395066	TATATT	score: 3.968301383	54
>pro1525	pro1525	1395300..1395974	TAATCT	score: 4.565336720	70
>hli12	pro1528	1397333..1397440	TATGGT	score: 5.007694830	29
>hli12	pro1528	1397333..1397440	CATGTG	score: 3.451878675	79
>pro1531	pro1531	1398832..1399155	CATGCT	score: 3.894236785	34
>pstS	pro1533	1400147..1401139	TATAAT	score: 4.482874556	29
>pstS	pro1533	1400147..1401139	CATAAT	score: 3.369416510	46
>alsT	pro1538	1405931..1407325	TATTTT	score: 3.830797859	65
>pro1542	pro1542	1409678..1410265	TATTCT	score: 4.565336720	41
>pro1542	pro1542	1409678..1410265	TAATAT	score: 4.345371032	44
>pro1542	pro1542	1409678..1410265	GAAGGT	score: 2.572308690	53
>pro1542	pro1542	1409678..1410265	CAAGAT	score: 3.674271096	68
>pro1549	pro1549	1415923..1416150	TATTTT	score: 3.830797859	52
>pro1549	pro1549	1415923..1416150	CAATGT	score: 3.451878675	65
>pro1550	pro1550	1416262..1416468	TAAAAT	score: 4.482874556	75
>pro1551	pro1551	1416584..1416748	TACTGT	score: 4.062836384	35
>pro1551	pro1551	1416584..1416748	CACAAT	score: 2.866916174	41
>pro1554	pro1554	1418096..1418389	CAAAAT	score: 3.369416510	24
>pro1554	pro1554	1418096..1418389	TATATT	score: 3.968301383	69
>pro1557	pro1557	1419823..1419987	CAATCT	score: 3.451878675	23
>pro1557	pro1557	1419823..1419987	CACTGT	score: 2.949378339	34
>pro1557	pro1557	1419823..1419987	TACGAT	score: 4.285228806	40
>pro1559	pro1559	1420774..1420965	TAGATT	score: 3.050763548	22
>pro1559	pro1559	1420774..1420965	TAGTCT	score: 3.647798885	62
>pro1559	pro1559	1420774..1420965	CAAATT	score: 2.854843338	67
>pro1559	pro1559	1420774..1420965	CAAATT	score: 2.854843338	87
>pro1560	pro1560	1421155..1421547	CATTAT	score: 3.231912987	32
>pro1560	pro1560	1421155..1421547	TAAATT	score: 3.968301383	38
>pro1560	pro1560	1421155..1421547	CAGGCT	score: 2.976698949	84
>pro1561	pro1561	1422025..1422663	TAAATT	score: 3.968301383	27
>pro1561	pro1561	1422025..1422663	CAGTGT	score: 2.534340839	33
>pro1561	pro1561	1422025..1422663	TAGTTT	score: 2.913260024	49
>pro1561	pro1561	1422025..1422663	TATTAT	score: 4.345371032	67
>pro1561	pro1561	1422025..1422663	CATATT	score: 2.854843338	69
>pro1561	pro1561	1422025..1422663	TAGTAT	score: 3.427833197	77
>pro1563	pro1563	1424836..1425504	TAAAAT	score: 4.482874556	26
>pro1563	pro1563	1424836..1425504	TAGATT	score: 3.050763548	39
>pro1563	pro1563	1424836..1425504	TATTTT	score: 3.830797859	48
>pro1563	pro1563	1424836..1425504	TACAAT	score: 3.980374220	69
>pro1563	pro1563	1424836..1425504	CAATTT	score: 2.717339814	74
>pro1563	pro1563	1424836..1425504	TAAAAT	score: 4.482874556	86
>pro1567	pro1567	1427121..1427906	TAAGGT	score: 5.007694830	26
>pro1567	pro1567	1427121..1427906	CAAAAT	score: 3.369416510	60
>pro1567	pro1567	1427121..1427906	TATTGT	score: 4.565336720	74
>pro1567	pro1567	1427121..1427906	TAATCT	score: 4.565336720	83
>ampC	pro1570	1429681..1430868	TATACT	score: 4.702840244	28
>ampC	pro1570	1429681..1430868	CAAACT	score: 3.589382199	35
>ampC	pro1570	1429681..1430868	GATGCT	score: 2.572308690	61
>pro1571	pro1571	1431094..1431471	CAAGAT	score: 3.674271096	33
>pro1571	pro1571	1431094..1431471	CAAAAT	score: 3.369416510	44
>pro1571	pro1571	1431094..1431471	CATACT	score: 3.589382199	52
>pro1573	pro1573	1432160..1432426	TACTCT	score: 4.062836384	83
>pro1573	pro1573	1432160..1432426	TAAAAT	score: 4.482874556	88

>pstS	pro1575	1433553..1434542	TAGAAT	score: 3.565336720	27
>pstS	pro1575	1433553..1434542	TATGGT	score: 5.007694830	74
>arsR	pro1578	1437040..1437351	TAAAAT	score: 4.482874556	27
>arsR	pro1578	1437040..1437351	CAATCT	score: 3.451878675	58
>arsR	pro1578	1437040..1437351	TAGTAT	score: 3.427833197	86
>arsR	pro1578	1437040..1437351	CATAGT	score: 3.589382195	88
>pro1581	pro1581	1438918..1439391	CAAAAT	score: 3.369416510	49
>pro1581	pro1581	1438918..1439391	CAAATT	score: 2.854843338	59
>pro1581	pro1581	1438918..1439391	CAAAAT	score: 3.369416510	85
>dnaK	pro1585	1440663..1442246	TACTCT	score: 4.062836384	69
>dnaK	pro1585	1440663..1442246	TAGTAT	score: 3.427833197	78
>dnaK	pro1585	1440663..1442246	TAAATT	score: 3.968301383	90
>gpmI	pro1587	1442975..1444597	TAATTT	score: 3.830797859	40
>gpmI	pro1587	1442975..1444597	TAATCT	score: 4.565336720	64
>gpmI	pro1587	1442975..1444597	GATGAT	score: 2.352343001	75
>gpmI	pro1587	1442975..1444597	GAAGAT	score: 2.352343001	78
>atpD	pro1591	1447640..1449106	TACTTT	score: 3.328297523	32
>atpD	pro1591	1447640..1449106	TAGTCT	score: 3.647798885	57
>atpD	pro1591	1447640..1449106	CAGGGT	score: 2.976698949	65
>tlyC	pro1596	1452421..1453407	TAAAGT	score: 4.702840244	38
>tlyC	pro1596	1452421..1453407	CATAGT	score: 3.589382195	50
>ftsW	pro1611	1465888..1467126	CATTTT	score: 2.717339814	38
>ftsW	pro1611	1465888..1467126	CAAATT	score: 2.854843338	45
>ftsW	pro1611	1465888..1467126	TATCTC	score: 4.565336720	70
>ccdA	pro1612	1467225..1467878	TAGATT	score: 3.050763548	50
>pro1615	pro1615	1469770..1469997	TATCTC	score: 4.565336720	38
>pro1615	pro1615	1469770..1469997	CATTAT	score: 3.231912987	41
>bioF	pro1622	1477252..1478397	CAATAT	score: 3.231912987	44
>bioA	pro1626	1480761..1482065	TACTTT	score: 3.328297523	36
>bioA	pro1626	1480761..1482065	CATTTT	score: 2.717339814	63
>bioA	pro1626	1480761..1482065	TAAGCT	score: 5.007694830	72
>bioA	pro1626	1480761..1482065	CATATT	score: 2.854843338	87
>gidB	pro1629	1482894..1483655	CAAGCT	score: 3.894236785	27
>gidB	pro1629	1482894..1483655	CAATAT	score: 3.231912987	62
>hisD	pro1643	1501001..1502323	CAAAC	score: 3.589382195	84
>pro1646	pro1646	1504390..1504857	TAGAAT	score: 3.565336720	86
>pro1652	pro1652	1511883..1513508	CACTAT	score: 2.729412650	30
>pro1652	pro1652	1511883..1513508	CATGAT	score: 3.674271096	36
>pro1656	pro1656	1516036..1518720	TACGAT	score: 4.285228806	23
>pro1656	pro1656	1516036..1518720	TATACT	score: 4.702840244	64
>cafA	pro1657	1518963..1520798	TAATTT	score: 3.830797859	33
>cafA	pro1657	1518963..1520798	CAAATT	score: 2.854843338	38
>pheA	pro1660	1521967..1522809	CATGAT	score: 3.674271096	30
>pheA	pro1660	1521967..1522809	CATGAT	score: 3.674271096	51
>pheA	pro1660	1521967..1522809	CAATTT	score: 2.717339814	82
>glsF	pro1668	1529478..1534052	CAATCT	score: 3.451878675	33
>glsF	pro1668	1529478..1534052	TATTTT	score: 3.830797859	40
>glsF	pro1668	1529478..1534052	CACTAT	score: 2.729412650	43
>glsF	pro1668	1529478..1534052	CACACT	score: 3.086881863	45
>glsF	pro1668	1529478..1534052	TAGAAT	score: 3.565336720	65
>psaA	pro1672	1537494..1539815	TAGATT	score: 3.050763548	74
>psaA	pro1672	1537494..1539815	CAATTT	score: 2.717339814	85
>spr	pro1675	1543060..1543812	CAGGAT	score: 2.756733261	37
>spr	pro1675	1543060..1543812	CAAAAT	score: 3.369416510	51
>psaI	pro1678	1545356..1545472	TACAGT	score: 4.200339908	25
>psaI	pro1678	1545356..1545472	CACGTT	score: 2.657197587	38

>psaI	pro1678	1545356..1545472	TACGTT	score: 3.770655633	51
>pro1680	pro1680	1546214..1546354	CAATTT	score: 2.717339814	34
>pro1680	pro1680	1546214..1546354	GAAGGT	score: 2.572308690	57
>mcrA	pro1682	1547801..1548313	GATGAT	score: 2.352343001	22
>mcrA	pro1682	1547801..1548313	TATGAT	score: 4.787729142	25
>mcrA	pro1682	1547801..1548313	CAAGAT	score: 3.674271096	56
>mcrA	pro1682	1547801..1548313	CAATTT	score: 2.717339814	87
>pro1713	pro1713	1565298..1565756	CAGAAT	score: 2.451878675	32
>pro1713	pro1713	1565298..1565756	CAAAGT	score: 3.589382199	53
>pro1713	pro1713	1565298..1565756	TACACT	score: 4.200339908	70
>pro1713	pro1713	1565298..1565756	TAGAAT	score: 3.565336720	75
>gln-tRNA	RNA_10	1566956..1567027	TATTTT	score: 3.830797859	42
>gln-tRNA	RNA_10	1566956..1567027	CAATGT	score: 3.451878675	53
>gln-tRNA	RNA_10	1566956..1567027	CACAAT	score: 2.866916174	55
>recA	pro1716	1567932..1569071	CAAGCT	score: 3.894236785	69
>tyrA	pro1719	1570909..1571775	TATAGT	score: 4.702840244	41
>tyrA	pro1719	1570909..1571775	TAATTT	score: 3.830797859	53
>tyrA	pro1719	1570909..1571775	GAAGAT	score: 2.352343001	58
>tyrA	pro1719	1570909..1571775	TATATT	score: 3.968301383	77
>pro1721	pro1721	1573302..1574192	CATAAT	score: 3.369416510	35
>pro1721	pro1721	1573302..1574192	TACAAT	score: 3.980374220	56
>pro1723	pro1723	1574688..1575215	TAATCT	score: 4.565336720	71
>arg1-tRNA	RNA_11	1580265..1580338	TAAGCT	score: 5.007694830	52
>hemF	pro1737	1590897..1591928	CATGTG	score: 3.451878675	83
>rnd	pro1740	1593460..1594104	TAAATT	score: 3.968301383	70
>cys-tRNA	RNA_12	1595707..1595777	TACGAT	score: 4.285228806	31
>cmk	pro1746	1598748..1600307	CAGACT	score: 2.671844363	38
>cmk	pro1746	1598748..1600307	TATTTT	score: 3.830797859	53
>cmk	pro1746	1598748..1600307	TACTAT	score: 3.842870696	56
>cmk	pro1746	1598748..1600307	CAATGT	score: 3.451878675	70
>icd	pro1752	1603833..1605257	TATTCT	score: 4.565336720	31
>icd	pro1752	1603833..1605257	CATATT	score: 2.854843338	33
>glgP	pro1759	1613224..1615746	CAAGAT	score: 3.674271096	47
>rnpB	RNA_45	1616782..1617168	TACGGT	score: 4.505194494	77
>rimM	pro1764	1618196..1618726	CACTAT	score: 2.729412650	27
>rimM	pro1764	1618196..1618726	CAAAAT	score: 3.369416510	44
>rimM	pro1764	1618196..1618726	CAAGAT	score: 3.674271096	68
>rimM	pro1764	1618196..1618726	GAAGAT	score: 2.352343001	79
>acpP	pro1768	1622599..1622841	CACTCT	score: 2.949378339	50
>acpP	pro1768	1622599..1622841	CAATTT	score: 2.717339814	89
>tkkA	pro1770	1624148..1626157	CAGAAT	score: 2.451878675	22
>smpB	pro1776	1631109..1631606	CATACT	score: 3.589382199	47
>smpB	pro1776	1631109..1631606	CACAAT	score: 2.866916174	56
>ssb	pro1784	1637412..1637801	TATAGT	score: 4.702840244	30
>pro1787	pro1787	1639954..1640460	CATAAT	score: 3.369416510	32
>pro1787	pro1787	1639954..1640460	GATGCT	score: 2.572308690	49
>pro1787	pro1787	1639954..1640460	CAAAAT	score: 3.369416510	81
>mhpC	pro1790	1642645..1643556	CATGCT	score: 3.894236785	27
>mhpC	pro1790	1642645..1643556	GAAGAT	score: 2.352343001	53
>mhpC	pro1790	1642645..1643556	CAATTT	score: 2.717339814	75
>mhpC	pro1790	1642645..1643556	CAATGT	score: 3.451878675	89
>pro1799	pro1799	1651060..1652046	TATTGT	score: 4.565336720	27
>pro1799	pro1799	1651060..1652046	CATAAT	score: 3.369416510	55
>pro1799	pro1799	1651060..1652046	TAAGCT	score: 5.007694830	72
>mutS	pro1805	1657339..1660083	TACGAT	score: 4.285228806	30
>holA	pro1807	1660814..1661830	CATGAT	score: 3.674271096	27

>holA	pro1807	1660814..1661830	GATGAT	score: 2.352343001	76
>mesJ	pro1811	1666648..1667658	CAAAGT	score: 3.589382199	25
>tig	pro1815	1671820..1673223	TAGTGT	score: 3.647798885	34
>tig	pro1815	1671820..1673223	TACTCT	score: 4.062836384	44
>tig	pro1815	1671820..1673223	GATGGT	score: 2.572308690	52
>tig	pro1815	1671820..1673223	GAAGCT	score: 2.572308690	70
>clpX	pro1817	1674037..1675389	CATTAT	score: 3.231912987	42
>dnaX	pro1818	1675533..1677212	TATCTC	score: 4.565336720	22
>dnaX	pro1818	1675533..1677212	TAGAGT	score: 3.785302409	40
>dnaX	pro1818	1675533..1677212	CAAATT	score: 2.854843338	61
>rpmI	pro1821	1680231..1680428	TAGAGT	score: 3.785302409	29
>rpmI	pro1821	1680231..1680428	CAATTT	score: 2.717339814	57
>rplT	pro1822	1680493..1680840	TAATTT	score: 3.830797859	24
>pro1823	pro1823	1680948..1681505	TAAAGT	score: 4.702840244	33
>pro1823	pro1823	1680948..1681505	TATAAT	score: 4.482874556	39
>pro1823	pro1823	1680948..1681505	TAAAGT	score: 4.702840244	53
>pro1823	pro1823	1680948..1681505	TATATT	score: 3.968301383	58
>pro1823	pro1823	1680948..1681505	TACTTT	score: 3.328297523	70
>pro1823	pro1823	1680948..1681505	TATACT	score: 4.702840244	72
>hli14	pro1825	1682409..1682573	CATATT	score: 2.854843338	23
>wcaG	pro1826	1682637..1683833	TACTTT	score: 3.328297523	32
>oLE1	pro1833	1690865..1691797	TATAAT	score: 4.482874556	23
>oLE1	pro1833	1690865..1691797	TACTAT	score: 3.842870696	26
>dnaB	pro1835	1692385..1693800	CAAAGT	score: 3.589382199	25
>ubiC	pro1837	1695924..1696430	CAATCT	score: 3.451878675	47
>pro1840	pro1840	1697731..1698153	TAAAGT	score: 4.702840244	37
>pro1840	pro1840	1697731..1698153	TAGTCT	score: 3.647798885	49
>pro1840	pro1840	1697731..1698153	CATAGT	score: 3.589382199	65
>pro1840	pro1840	1697731..1698153	CATTCT	score: 3.451878675	79
>pro1846	pro1846	1704422..1704673	TAGATT	score: 3.050763548	31
>pro1846	pro1846	1704422..1704673	TAAAAT	score: 4.482874556	37
>pro1847	pro1847	1705247..1706077	CAGGCT	score: 2.976698949	69
>pro1847	pro1847	1705247..1706077	CAAGTT	score: 3.159697923	75
>gcvT	pro1851	1708285..1709406	CAAGAT	score: 3.674271096	58
>gcvT	pro1851	1708285..1709406	CAAACG	score: 3.589382199	81
>aspS	pro1852	1709479..1711296	TACATT	score: 3.465801047	39
>pyrG	pro1853	1711409..1713064	CAATAT	score: 3.231912987	70
>trpD	pro1859	1717442..1718497	CAGGAT	score: 2.756733261	50
>proP	pro1861	1719055..1720314	TATCTC	score: 4.565336720	47
>proP	pro1861	1719055..1720314	CAAATT	score: 2.854843338	82
>ppk	pro1862	1720403..1722514	CAATCT	score: 3.451878675	34
>ppk	pro1862	1720403..1722514	TATAAT	score: 4.482874556	46
>ppk	pro1862	1720403..1722514	TAATGT	score: 4.565336720	52
>ppk	pro1862	1720403..1722514	TATAAT	score: 4.482874556	54
>rpoD	pro1863	1722731..1723750	TAAGTT	score: 4.273155969	32
>rpoD	pro1863	1722731..1723750	TATTTT	score: 3.830797859	50
>rpoD	pro1863	1722731..1723750	CACTGT	score: 2.949378339	56
>rpoD	pro1863	1722731..1723750	GAAGAT	score: 2.352343001	90
>acnB	pro1866	1725643..1728234	TAGGCT	score: 4.090156995	24
>acnB	pro1866	1725643..1728234	TAAGTT	score: 4.273155969	37
>acnB	pro1866	1725643..1728234	CACAAT	score: 2.866916174	42
>acnB	pro1866	1725643..1728234	TAGATT	score: 3.050763548	57
>acnB	pro1866	1725643..1728234	CAAAGT	score: 3.589382199	63
>acnB	pro1866	1725643..1728234	TAGAAT	score: 3.565336720	69
>pro1870	pro1870	1732706..1733788	CATTAT	score: 3.231912987	55
>pro1870	pro1870	1732706..1733788	TAAAGT	score: 4.702840244	89

>aroE	pro1872	1735798..1736700	TAAATT	score: 3.968301383	82
>pro1877	pro1877	1739373..1739624	TATGTT	score: 4.273155969	25
>pro1877	pro1877	1739373..1739624	CATTAT	score: 3.231912987	28
>pro1877	pro1877	1739373..1739624	CATAAT	score: 3.369416510	35
>pro1877	pro1877	1739373..1739624	TAGACT	score: 3.785302409	41
>aarF	pro1883	1747375..1749222	TAATCT	score: 4.565336720	59
>aarF	pro1883	1747375..1749222	CACAGT	score: 3.086881863	72
>gyrA	pro0005	complement 5992..8478	TACTGT	score: 4.062836384	35
>pro0007	pro0007	complement 9433..10395	CAAAAT	score: 3.369416510	22
>pro0007	pro0007	complement 9433..10395	TAGAAT	score: 3.565336720	66
>pro0007	pro0007	complement 9433..10395	CAATTT	score: 2.717339814	74
>pro0007	pro0007	complement 9433..10395	CACAAT	score: 2.866916174	76
>pro0014	pro0014	complement 17049..18050	CATTCT	score: 3.451878675	29
>pro0014	pro0014	complement 17049..18050	TAAGAT	score: 4.787729142	46
>ppiB	pro0025	complement 26670..27746	CATGTG	score: 3.451878675	60
>wcaG	pro0030	complement 30137..31030	GAAGGT	score: 2.572308690	53
>mcrA	pro0032	complement 31287..31679	TACATT	score: 3.465801047	47
>mcrA	pro0032	complement 31287..31679	CAGTGT	score: 2.534340839	57
>pro0033	pro0033	complement 31805..32068	CAGGAT	score: 2.756733261	26
>pro0033	pro0033	complement 31805..32068	CAATTT	score: 2.717339814	59
>pro0036	pro0036	complement 33189..34343	TAAGAT	score: 4.787729142	22
>pro0036	pro0036	complement 33189..34343	TAGTTT	score: 2.913260024	30
>pro0036	pro0036	complement 33189..34343	CAATTT	score: 2.717339814	42
>pro0042	pro0042	complement 40976..41209	TACACT	score: 4.200339908	24
>pro0042	pro0042	complement 40976..41209	TAGGTT	score: 3.355618133	43
>pro0042	pro0042	complement 40976..41209	TATTTT	score: 3.830797859	62
>dfa1	pro0045	complement 43837..45609	TAAAAT	score: 4.482874556	23
>dfa1	pro0045	complement 43837..45609	TAAATT	score: 3.968301383	70
>dfa1	pro0045	complement 43837..45609	TAAATT	score: 3.968301383	81
>hepA	pro0047	complement 46600..49788	CAAATT	score: 2.854843338	25
>hepA	pro0047	complement 46600..49788	TATTTT	score: 3.830797859	60
>hepA	pro0047	complement 46600..49788	CATTAT	score: 3.231912987	63
>hepA	pro0047	complement 46600..49788	CATTAT	score: 3.231912987	91
>speA	pro0049	complement 52665..54611	TAAAAT	score: 4.482874556	36
>speA	pro0049	complement 52665..54611	TAGATT	score: 3.050763548	55
>speA	pro0049	complement 52665..54611	TAGGAT	score: 3.870191306	77
>dadA	pro0051	complement 55259..56371	CAAAAT	score: 3.369416510	22
>dadA	pro0051	complement 55259..56371	CATGGT	score: 3.894236785	38
>dadA	pro0051	complement 55259..56371	CAAATT	score: 2.854843338	54
>dadA	pro0051	complement 55259..56371	TAAGAT	score: 4.787729142	60
>dadA	pro0051	complement 55259..56371	TACTAT	score: 3.842870696	72
>dadA	pro0051	complement 55259..56371	CATACT	score: 3.589382199	74
>dadA	pro0051	complement 55259..56371	CAAGAT	score: 3.674271096	91
>coaE	pro0053	complement 57964..58596	TAAACT	score: 4.702840244	22
>coaE	pro0053	complement 57964..58596	GATGAT	score: 2.352343001	59
>asnB	pro0058	complement 64567..66531	TAGAGT	score: 3.785302409	27
>asnB	pro0058	complement 64567..66531	TATTAT	score: 4.345371032	32
>asnB	pro0058	complement 64567..66531	TATATT	score: 3.968301383	34
>asnB	pro0058	complement 64567..66531	TACGAT	score: 4.285228806	40
>asnB	pro0058	complement 64567..66531	TAGTTT	score: 2.913260024	90
>tmRNA	RNA_46	complement 75321..75579	CAAAAT	score: 3.369416510	31
>tmRNA	RNA_46	complement 75321..75579	TAGTTT	score: 2.913260024	60
>tmRNA	RNA_46	complement 75321..75579	TAGGTT	score: 3.355618133	89
>pro0067	pro0067	complement 77192..77656	TAGGCT	score: 4.090156995	22
>pro0067	pro0067	complement 77192..77656	TAGAAT	score: 3.565336720	40
>pro0067	pro0067	complement 77192..77656	TATTAT	score: 4.345371032	77

>pro0067	pro0067	complement	77192..77656	TACTGT	score: 4.062836384	84
>Leu4-tRNA	RNA_27	complement	84970..85051	TATGAT	score: 4.787729142	34
>Leu4-tRNA	RNA_27	complement	84970..85051	CATTCT	score: 3.451878675	55
>pro0075	pro0075	complement	86523..86843	TACGAT	score: 4.285228806	24
>pro0079	pro0079	complement	88537..90525	TAAGTT	score: 4.273155969	30
>pro0079	pro0079	complement	88537..90525	TAGATT	score: 3.050763548	39
>pro0079	pro0079	complement	88537..90525	TACAAT	score: 3.980374220	45
>hit	pro0080	complement	90732..91073	TAATTT	score: 3.830797859	38
>hit	pro0080	complement	90732..91073	TATAAT	score: 4.482874556	40
>hit	pro0080	complement	90732..91073	TAAGTT	score: 4.273155969	64
>hit	pro0080	complement	90732..91073	TAAACT	score: 4.702840244	73
>def	pro0081	complement	91268..91879	TAAAAT	score: 4.482874556	25
>def	pro0081	complement	91268..91879	TAAAAT	score: 4.482874556	34
>def	pro0081	complement	91268..91879	TATTTT	score: 3.830797859	72
>def	pro0081	complement	91268..91879	CAGAAT	score: 2.451878675	81
>sufB	pro0086	complement	97172..98614	CATTTT	score: 2.717339814	30
>sufB	pro0086	complement	97172..98614	TATGCT	score: 5.007694830	44
>sufB	pro0086	complement	97172..98614	TAGGAT	score: 3.870191306	56
>sufB	pro0086	complement	97172..98614	TAATTT	score: 3.830797859	72
>sufB	pro0086	complement	97172..98614	TAAAAT	score: 4.482874556	77
>pro0092	pro0092	complement	103816..104472	TAATTT	score: 3.830797859	55
>cysH	pro0095	complement	105629..106393	GATGAT	score: 2.352343001	25
>cysH	pro0095	complement	105629..106393	TAGACT	score: 3.785302409	50
>cysH	pro0095	complement	105629..106393	CATTTT	score: 2.717339814	65
>pro0101	pro0101	complement	112874..113173	TACACT	score: 4.200339908	28
>pro0101	pro0101	complement	112874..113173	TACTAT	score: 3.842870696	49
>pro0101	pro0101	complement	112874..113173	CATAGT	score: 3.589382199	61
>pro0101	pro0101	complement	112874..113173	CAAAAT	score: 3.369416510	70
>pro0101	pro0101	complement	112874..113173	TAATCT	score: 4.565336720	76
>pro0104	pro0104	complement	113950..114129	TAAACT	score: 4.702840244	23
>pro0104	pro0104	complement	113950..114129	CAAACT	score: 3.589382199	37
>pro0104	pro0104	complement	113950..114129	TAATAT	score: 4.345371032	49
>pro0104	pro0104	complement	113950..114129	TAAACT	score: 4.702840244	54
>pro0104	pro0104	complement	113950..114129	TATATT	score: 3.968301383	60
>pro0104	pro0104	complement	113950..114129	CAATAT	score: 3.231912987	63
>degQ	pro0106	complement	115973..117148	TATACT	score: 4.702840244	69
>rbn	pro0114	complement	120179..121120	TAAAAT	score: 4.482874556	24
>rbn	pro0114	complement	120179..121120	TACACT	score: 4.200339908	29
>rbn	pro0114	complement	120179..121120	TATATT	score: 3.968301383	35
>rbn	pro0114	complement	120179..121120	TACTAT	score: 3.842870696	38
>rbn	pro0114	complement	120179..121120	CAATTT	score: 2.717339814	43
>rbn	pro0114	complement	120179..121120	GAAGCT	score: 2.572308690	57
>rbn	pro0114	complement	120179..121120	TAAAAT	score: 4.482874556	65
>rbn	pro0114	complement	120179..121120	TAATCT	score: 4.565336720	82
>pro0117	pro0117	complement	123683..125080	CAATTT	score: 2.717339814	32
>pro0117	pro0117	complement	123683..125080	TACAAT	score: 3.980374220	34
>pro0117	pro0117	complement	123683..125080	CAAGCT	score: 3.894236785	91
>pro0120	pro0120	complement	127743..128684	TAAAAT	score: 4.482874556	31
>pro0120	pro0120	complement	127743..128684	TACTAT	score: 3.842870696	40
>pro0120	pro0120	complement	127743..128684	TAAATT	score: 3.968301383	58
>pro0120	pro0120	complement	127743..128684	CATTTT	score: 2.717339814	63
>pro0120	pro0120	complement	127743..128684	TAATTT	score: 3.830797859	75
>pro0120	pro0120	complement	127743..128684	TATAAT	score: 4.482874556	77
>pro0120	pro0120	complement	127743..128684	CAATGT	score: 3.451878675	87
>folP	pro0123	complement	130443..130838	CAAGCT	score: 3.894236785	40
>folP	pro0123	complement	130443..130838	CAAAAT	score: 3.369416510	57

>folP	pro0123	complement	130443..130838	TATCT	score: 4.565336720	66
>pro0127	pro0127	complement	133098..134006	TAAGAT	score: 4.787729142	23
>pro0127	pro0127	complement	133098..134006	CAATTT	score: 2.717339814	63
>pro0127	pro0127	complement	133098..134006	TAATTT	score: 3.830797859	90
>gst	pro0130	complement	134889..135614	TACTCT	score: 4.062836384	24
>gst	pro0130	complement	134889..135614	CATTGT	score: 3.451878675	56
>pro0136	pro0136	complement	139235..140695	TATTGT	score: 4.565336720	33
>pro0136	pro0136	complement	139235..140695	CAATTT	score: 2.717339814	60
>pro0140	pro0140	complement	142902..143840	CACTCT	score: 2.949378339	28
>pro0140	pro0140	complement	142902..143840	CAATTT	score: 2.717339814	38
>pro0140	pro0140	complement	142902..143840	TACAAT	score: 3.980374220	45
>pro0140	pro0140	complement	142902..143840	TACTCT	score: 4.062836384	54
>pro0140	pro0140	complement	142902..143840	TAAAAAT	score: 4.482874556	59
>pro0140	pro0140	complement	142902..143840	CAATTT	score: 2.717339814	64
>pro0140	pro0140	complement	142902..143840	CAATCT	score: 3.451878675	72
>cysK	pro0143	complement	144878..145846	CAAGTT	score: 3.159697923	36
>cysK	pro0143	complement	144878..145846	TAGTAT	score: 3.427833197	52
>pro0147	pro0147	complement	148013..148735	TACACT	score: 4.200339908	26
>pro0147	pro0147	complement	148013..148735	TAGAGT	score: 3.785302409	31
>pro0147	pro0147	complement	148013..148735	TATCT	score: 4.565336720	36
>pro0147	pro0147	complement	148013..148735	TATTAT	score: 4.345371032	39
>pro0147	pro0147	complement	148013..148735	TATATT	score: 3.968301383	41
>pro0147	pro0147	complement	148013..148735	CATTCT	score: 3.451878675	46
>pro0149	pro0149	complement	149466..150461	TAATCT	score: 4.565336720	25
>pro0149	pro0149	complement	149466..150461	TATTTT	score: 3.830797859	65
>pro0149	pro0149	complement	149466..150461	TATTAT	score: 4.345371032	68
>pro0149	pro0149	complement	149466..150461	TATTGT	score: 4.565336720	87
>zntA	pro0153	complement	153014..155338	TAATTT	score: 3.830797859	69
>sms	pro0155	complement	156021..157406	TAAAAAT	score: 4.482874556	52
>sms	pro0155	complement	156021..157406	CAATCT	score: 3.451878675	70
>sms	pro0155	complement	156021..157406	CAAAGT	score: 3.589382199	76
>pro0163	pro0163	complement	163506..163757	TACTAT	score: 3.842870696	23
>pro0163	pro0163	complement	163506..163757	CAGGCT	score: 2.976698949	77
>pds	pro0167	complement	166480..167889	TAAAGT	score: 4.702840244	23
>pds	pro0167	complement	166480..167889	CAAAAT	score: 3.369416510	70
>rbcR	pro0170	complement	168990..169943	CATGTT	score: 3.159697923	22
>rbcR	pro0170	complement	168990..169943	TAATTT	score: 3.830797859	35
>rbcR	pro0170	complement	168990..169943	TAGAGT	score: 3.785302409	47
>rbcR	pro0170	complement	168990..169943	CAATTT	score: 2.717339814	70
>metF	pro0176	complement	176919..177812	TAGGGT	score: 4.090156995	35
>metF	pro0176	complement	176919..177812	CAAGCT	score: 3.894236785	40
>metF	pro0176	complement	176919..177812	CATATT	score: 2.854843338	49
>pro0178	pro0178	complement	178128..178328	TATATT	score: 3.968301383	55
>nuoI	pro0183	complement	180819..181478	TAGGTT	score: 3.355618133	25
>nuoI	pro0183	complement	180819..181478	TAAGAT	score: 4.787729142	39
>nuoI	pro0183	complement	180819..181478	CATTTT	score: 2.717339814	81
>nuoI	pro0183	complement	180819..181478	TACATT	score: 3.465801047	83
>nuoI	pro0183	complement	180819..181478	CAATTT	score: 2.717339814	88
>gltA	pro0185	complement	182790..183968	CAGAAT	score: 2.451878675	41
>pro0186	pro0186	complement	184043..185644	GAAGGT	score: 2.572308690	24
>pro0186	pro0186	complement	184043..185644	TATTTT	score: 3.830797859	63
>trpB	pro0188	complement	186094..187344	TAATCT	score: 4.565336720	25
>trpB	pro0188	complement	186094..187344	CATTTT	score: 2.717339814	43
>trpB	pro0188	complement	186094..187344	CAATTT	score: 2.717339814	57
>trpB	pro0188	complement	186094..187344	CAAATT	score: 2.854843338	68
>trpB	pro0188	complement	186094..187344	CAAATT	score: 2.854843338	77

>trpB	pro0188	complement	186094..187344	TATTTT	score: 3.830797859	86
>trpB	pro0188	complement	186094..187344	TATTAT	score: 4.345371032	89
>purE	pro0191	complement	188395..188886	CATTAT	score: 3.231912987	71
>pro0194	pro0194	complement	190935..191663	CAATAT	score: 3.231912987	51
>menA	pro0201	complement	197720..198685	CAGACT	score: 2.671844363	22
>menA	pro0201	complement	197720..198685	CACAAT	score: 2.866916174	72
>grxC	pro0204	complement	201082..201345	TAAGAT	score: 4.787729142	23
>grxC	pro0204	complement	201082..201345	CACAAT	score: 2.866916174	75
>grxC	pro0204	complement	201082..201345	TAAGAT	score: 4.787729142	85
>nadC	pro0213	complement	208099..208962	CAATTT	score: 2.717339814	87
>thdF	pro0214	complement	209078..210445	TAAACT	score: 4.702840244	51
>spoT	pro0217	complement	212585..214915	TAAATT	score: 3.968301383	50
>spoT	pro0217	complement	212585..214915	TAATAT	score: 4.345371032	83
>pro0220	pro0220	complement	217549..218412	CAGTGT	score: 2.534340839	48
>pro0220	pro0220	complement	217549..218412	CAATAT	score: 3.231912987	84
>pro0220	pro0220	complement	217549..218412	CATGAT	score: 3.674271096	90
>pro0222	pro0222	complement	220171..220941	TAAGTT	score: 4.273155969	24
>pro0222	pro0222	complement	220171..220941	TATATT	score: 3.968301383	29
>rnhA	pro0226	complement	224331..224828	CAGAAT	score: 2.451878675	47
>rplJ	pro0228	complement	225357..225884	TATTTT	score: 3.830797859	54
>rplJ	pro0228	complement	225357..225884	CAAATT	score: 2.854843338	90
>rplA	pro0229	complement	226123..226827	CATGTT	score: 3.159697923	23
>rplA	pro0229	complement	226123..226827	TAAAGT	score: 4.702840244	62
>rplK	pro0230	complement	226918..227343	CAATTT	score: 2.717339814	22
>rplK	pro0230	complement	226918..227343	TAAACT	score: 4.702840244	43
>rplK	pro0230	complement	226918..227343	TAGGTT	score: 3.355618133	67
>secE	pro0232	complement	228175..228417	CAATGT	score: 3.451878675	38
>gloA	pro0234	complement	231281..231682	TAGTTT	score: 2.913260024	23
>gloA	pro0234	complement	231281..231682	CAAAAT	score: 3.369416510	34
>gloA	pro0234	complement	231281..231682	CAAGCT	score: 3.894236785	63
>gloA	pro0234	complement	231281..231682	TAGTTT	score: 2.913260024	89
>pro0238	pro0238	complement	235194..235760	TAGATT	score: 3.050763548	26
>pro0238	pro0238	complement	235194..235760	TAAACT	score: 4.702840244	39
>pro0238	pro0238	complement	235194..235760	TAGAGT	score: 3.785302409	48
>pro0238	pro0238	complement	235194..235760	CAGTCT	score: 2.534340839	54
>sUL1	pro0242	complement	238336..239991	TAGGCT	score: 4.090156995	33
>sUL1	pro0242	complement	238336..239991	CAAGAT	score: 3.674271096	38
>sUL1	pro0242	complement	238336..239991	CAATCT	score: 3.451878675	72
>sUL1	pro0242	complement	238336..239991	CAATTT	score: 2.717339814	86
>sUL1	pro0242	complement	238336..239991	TACAAT	score: 3.980374220	88
>pro0248	pro0248	complement	245525..245743	TAATGT	score: 4.565336720	36
>pro0248	pro0248	complement	245525..245743	CAAATT	score: 2.854843338	45
>pro0248	pro0248	complement	245525..245743	CATATT	score: 2.854843338	55
>eCM4	pro0250	complement	246621..247598	CAAAAT	score: 3.369416510	38
>mET3	pro0256	complement	253642..254814	TAGACT	score: 3.785302409	43
>mET3	pro0256	complement	253642..254814	TAGTTT	score: 2.913260024	50
>mET3	pro0256	complement	253642..254814	TACTCT	score: 4.062836384	55
>mET3	pro0256	complement	253642..254814	CATACT	score: 3.589382199	57
>mET3	pro0256	complement	253642..254814	CAATCT	score: 3.451878675	63
>psbO	pro0257	complement	254963..255754	TAAGCT	score: 5.007694830	61
>pro0259	pro0259	complement	257249..257473	TAGAAT	score: 3.565336720	62
>pro0259	pro0259	complement	257249..257473	CAAGCT	score: 3.894236785	91
>mpg	pro0263	complement	259376..260038	TATTTT	score: 3.830797859	27
>mpg	pro0263	complement	259376..260038	TATATT	score: 3.968301383	29
>mpg	pro0263	complement	259376..260038	CAATAT	score: 3.231912987	32
>mpg	pro0263	complement	259376..260038	CAAGTT	score: 3.159697923	74

>Leu5-tRNA RNA_31	complement	262281..262362	TATATT	score: 3.968301383	43
>Leu5-tRNA RNA_31	complement	262281..262362	TAAGCT	score: 5.007694830	55
>pro0269 pro0269	complement	266124..266750	CACTAT	score: 2.729412650	66
>pro0269 pro0269	complement	266124..266750	CATGTT	score: 3.159697923	76
>manB pro0271	complement	267518..268903	TAAGCT	score: 5.007694830	31
>manB pro0271	complement	267518..268903	CAGAAT	score: 2.451878675	62
>manB pro0271	complement	267518..268903	CATTTT	score: 2.717339814	68
>pro0276 pro0276	complement	271396..271599	GAAGCT	score: 2.572308690	27
>psbH pro0283	complement	275064..275267	CAATAT	score: 3.231912987	36
>psbH pro0283	complement	275064..275267	TACAAT	score: 3.980374220	38
>psbH pro0283	complement	275064..275267	CAATGT	score: 3.451878675	60
>glyA pro0290	complement	281325..282584	TACTAT	score: 3.842870696	35
>glyA pro0290	complement	281325..282584	CATTTT	score: 2.717339814	65
>arg4-tRNA RNA_30	complement	282704..282777	TATAGT	score: 4.702840244	37
>mviN pro0293	complement	283501..285117	TATATT	score: 3.968301383	56
>purH pro0298	complement	289813..291369	TAAGTT	score: 4.273155969	29
>purH pro0298	complement	289813..291369	CAAATT	score: 2.854843338	49
>purH pro0298	complement	289813..291369	CAGAAT	score: 2.451878675	84
>purH pro0298	complement	289813..291369	CAATTT	score: 2.717339814	90
>pro0300 pro0300	complement	292047..292415	CACTCT	score: 2.949378339	33
>pro0300 pro0300	complement	292047..292415	TAATTT	score: 3.830797859	52
>pro0300 pro0300	complement	292047..292415	TAAATT	score: 3.968301383	79
>pro0300 pro0300	complement	292047..292415	TAATTT	score: 3.830797859	88
>cobS pro0302	complement	293868..294647	TACGTT	score: 3.770655633	31
>met2-tRNA RNA_29	complement	298481..298553	CAAATT	score: 2.854843338	32
>met2-tRNA RNA_29	complement	298481..298553	TATTAT	score: 4.345371032	53
>pro0309 pro0309	complement	300107..301570	TAAATT	score: 3.968301383	28
>pro0309 pro0309	complement	300107..301570	CAAATT	score: 2.854843338	89
>fabI pro0314	complement	305936..306718	TAGTTT	score: 2.913260024	71
>fabI pro0314	complement	305936..306718	CAAAAT	score: 3.369416510	76
>pro0317 pro0317	complement	308737..309297	TAAAAT	score: 4.482874556	26
>folK pro0318	complement	309369..309950	CATTTT	score: 2.717339814	25
>folK pro0318	complement	309369..309950	TACTCT	score: 4.062836384	75
>ttg2A pro0321	complement	312981..313793	TACTTT	score: 3.328297523	25
>ttg2A pro0321	complement	312981..313793	TAAAAT	score: 4.482874556	46
>ttg2A pro0321	complement	312981..313793	TATTGT	score: 4.565336720	60
>ttg2A pro0321	complement	312981..313793	CAATTT	score: 2.717339814	75
>nuoA pro0325	complement	316580..316942	CAAACT	score: 3.589382199	23
>nuoA pro0325	complement	316580..316942	CAGTCT	score: 2.534340839	73
>pnp pro0332	complement	319367..320311	CAAAGT	score: 3.589382199	87
>pcnB pro0334	complement	322503..323753	TAAAAT	score: 4.482874556	30
>uvrD pro0335	complement	323818..326241	TATTTT	score: 3.830797859	24
>uvrD pro0335	complement	323818..326241	TAAAAT	score: 4.482874556	39
>pro0336 pro0336	complement	326319..326525	CAAGCT	score: 3.894236785	36
>pro0336 pro0336	complement	326319..326525	TAAGTT	score: 4.273155969	71
>pro0336 pro0336	complement	326319..326525	CAAAAT	score: 3.369416510	85
>mpeX pro0340	complement	328493..329389	CAAACT	score: 3.589382199	30
>mpeX pro0340	complement	328493..329389	TATGAT	score: 4.787729142	41
>pucC pro0346	complement	332950..334245	TAGGCT	score: 4.090156995	23
>pucC pro0346	complement	332950..334245	GATGCT	score: 2.572308690	29
>pro0347 pro0347	complement	334411..334641	CAAGGT	score: 3.894236785	36
>pro0347 pro0347	complement	334411..334641	TACTTT	score: 3.328297523	57
>pro0347 pro0347	complement	334411..334641	TAAAGT	score: 4.702840244	89
>phe-tRNA RNA_28	complement	334895..334970	TAAGAT	score: 4.787729142	29
>rpsA pro0351	complement	338390..339493	TAGGTT	score: 3.355618133	55
>pro0352 pro0352	complement	339588..340061	TAAATT	score: 3.968301383	24

>pro0352	pro0352	complement	339588..340061	TACATT	score: 3.465801047	30
>pro0352	pro0352	complement	339588..340061	TAGTAT	score: 3.427833197	83
>psbB	pro0354	complement	340387..341940	CATAAT	score: 3.369416510	29
>psbB	pro0354	complement	340387..341940	TACGAT	score: 4.285228806	50
>thr3-tRNA	RNA_37	complement	345079..345150	TAAAAT	score: 4.482874556	51
>thr3-tRNA	RNA_37	complement	345079..345150	CAATCT	score: 3.451878675	67
>minD	pro0363	complement	345602..346417	CATTGT	score: 3.451878675	45
>minD	pro0363	complement	345602..346417	TAATTT	score: 3.830797859	55
>minD	pro0363	complement	345602..346417	TAATTT	score: 3.830797859	61
>minD	pro0363	complement	345602..346417	TAAATT	score: 3.968301383	69
>minD	pro0363	complement	345602..346417	CAATCT	score: 3.451878675	74
>prc	pro0366	complement	348504..349883	CAGTCT	score: 2.534340839	27
>pro0369	pro0369	complement	351176..352621	TATGAT	score: 4.787729142	52
>pro0369	pro0369	complement	351176..352621	TATTCT	score: 4.565336720	59
>pro0369	pro0369	complement	351176..352621	TAATTT	score: 3.830797859	86
>psaE	pro0371	complement	359478..359687	TAATCT	score: 4.565336720	27
>psaE	pro0371	complement	359478..359687	CACGAT	score: 3.171770760	32
>psaE	pro0371	complement	359478..359687	CATTCT	score: 3.451878675	67
>pro0373	pro0373	complement	360884..361759	CAAAAT	score: 3.369416510	42
>pro0373	pro0373	complement	360884..361759	TACAAT	score: 3.980374220	59
>pro0375	pro0375	complement	363268..363654	TATGAT	score: 4.787729142	30
>pro0375	pro0375	complement	363268..363654	CATTCT	score: 3.451878675	40
>pro0375	pro0375	complement	363268..363654	TACATT	score: 3.465801047	42
>pro0375	pro0375	complement	363268..363654	CATAAT	score: 3.369416510	51
>pro0376	pro0376	complement	363741..364982	TATTCT	score: 4.565336720	26
>pro0379	pro0379	complement	366104..366286	CATTTT	score: 2.717339814	22
>pro0379	pro0379	complement	366104..366286	TAATCT	score: 4.565336720	32
>pseudo-tRNRNA_36		complement	366467..366539	CAAGGT	score: 3.894236785	35
>pseudo-tRNRNA_36		complement	366467..366539	CAATGT	score: 3.451878675	45
>pseudo-tRNRNA_36		complement	366467..366539	TAAATT	score: 3.968301383	70
>pseudo-tRNRNA_36		complement	366467..366539	CAATAT	score: 3.231912987	82
>pro0383	pro0383	complement	369606..369950	CAAATT	score: 2.854843338	41
>pro0383	pro0383	complement	369606..369950	TAAAAT	score: 4.482874556	48
>tyr-tRNA	RNA_34	complement	370586..370670	CATATT	score: 2.854843338	44
>tyr-tRNA	RNA_34	complement	370586..370670	CACGAT	score: 3.171770760	61
>rfaG	pro0394	complement	378246..379403	GAAGAT	score: 2.352343001	48
>pro0397	pro0397	complement	380947..381534	TAAATT	score: 3.968301383	31
>pro0397	pro0397	complement	380947..381534	GATGGT	score: 2.572308690	84
>cysK	pro0403	complement	387417..388403	CAAATT	score: 2.854843338	34
>cysK	pro0403	complement	387417..388403	CAGAAT	score: 2.451878675	51
>metC/MetB	pro0405	complement	389961..391130	TAGAAT	score: 3.565336720	34
>metC/MetB	pro0405	complement	389961..391130	TAGATT	score: 3.050763548	62
>metC/MetB	pro0405	complement	389961..391130	TATTAT	score: 4.345371032	68
>pro0406	pro0406	complement	391296..392276	TAAAAT	score: 4.482874556	36
>pro0406	pro0406	complement	391296..392276	CAAGGT	score: 3.894236785	55
>pro0406	pro0406	complement	391296..392276	CATAAT	score: 3.369416510	63
>pro0408	pro0408	complement	392945..393247	TACGTT	score: 3.770655633	26
>pro0408	pro0408	complement	392945..393247	GAAGCT	score: 2.572308690	49
>rpsD	pro0409	complement	393478..394086	TAAATT	score: 3.968301383	80
>rpsD	pro0409	complement	393478..394086	TAGAAT	score: 3.565336720	88
>csdB	pro0413	complement	396275..397468	TAAATT	score: 3.968301383	48
>pro0414	pro0414	complement	397549..397773	TATGAT	score: 4.787729142	26
>pro0414	pro0414	complement	397549..397773	CAAAAT	score: 3.369416510	49
>pro0414	pro0414	complement	397549..397773	TACTTT	score: 3.328297523	56
>pro0414	pro0414	complement	397549..397773	TATAAT	score: 4.482874556	69
>pro0414	pro0414	complement	397549..397773	TACAAT	score: 3.980374220	84

>pro0414	pro0414	complement	397549..397773	CAAGAT	score: 3.674271096	90
>pro0417	pro0417	complement	398766..399011	TAGGCT	score: 4.090156995	29
>spoU	pro0421	complement	403671..404360	TAGGCT	score: 4.090156995	58
>spoU	pro0421	complement	403671..404360	TAGATT	score: 3.050763548	77
>pro0425	pro0425	complement	408747..408980	TATAGT	score: 4.702840244	35
>pro0425	pro0425	complement	408747..408980	CAATTT	score: 2.717339814	40
>pro0425	pro0425	complement	408747..408980	CATAAT	score: 3.369416510	48
>pro0428	pro0428	complement	410622..411149	CAAGTT	score: 3.159697923	29
>pro0428	pro0428	complement	410622..411149	TAAACT	score: 4.702840244	59
>pro0428	pro0428	complement	410622..411149	TAATCT	score: 4.565336720	66
>nuoN	pro0431	complement	412751..414325	TAGAGT	score: 3.785302409	30
>nuoN	pro0431	complement	412751..414325	CATATT	score: 2.854843338	48
>nuoN	pro0431	complement	412751..414325	CATAGT	score: 3.589382199	65
>nuoN	pro0431	complement	412751..414325	CAAAAT	score: 3.369416510	79
>pro0437	pro0437	complement	420520..421656	TAAGAT	score: 4.787729142	41
>pro0437	pro0437	complement	420520..421656	CAATCT	score: 3.451878675	75
>pro0437	pro0437	complement	420520..421656	CATAAT	score: 3.369416510	89
>pro0439	pro0439	complement	422496..422873	CAGAAT	score: 2.451878675	25
>pro0439	pro0439	complement	422496..422873	CACAAT	score: 2.866916174	44
>pro0439	pro0439	complement	422496..422873	CATGGT	score: 3.894236785	57
>cyoA	pro0442	complement	425227..426060	CATGCT	score: 3.894236785	38
>cyoA	pro0442	complement	425227..426060	TACATT	score: 3.465801047	51
>cyoA	pro0442	complement	425227..426060	CAAAAT	score: 3.369416510	56
>groL	pro0448	complement	430833..432524	CAAATT	score: 2.854843338	23
>groL	pro0448	complement	430833..432524	CAAGCT	score: 3.894236785	50
>groL	pro0448	complement	430833..432524	TAAAAT	score: 4.482874556	89
>fabG	pro0452	complement	434454..435206	TACGTT	score: 3.770655633	30
>fabG	pro0452	complement	434454..435206	CAAACCT	score: 3.589382199	35
>fabG	pro0452	complement	434454..435206	TAGGCT	score: 4.090156995	46
>fabG	pro0452	complement	434454..435206	TAATTT	score: 3.830797859	54
>ubiA	pro0455	complement	436888..437778	CAAAAT	score: 3.369416510	44
>ubiA	pro0455	complement	436888..437778	TAATTT	score: 3.830797859	86
>qcrA	pro0460	complement	442387..442923	CATAAT	score: 3.369416510	32
>qcrA	pro0460	complement	442387..442923	TATTTT	score: 3.830797859	65
>qcrA	pro0460	complement	442387..442923	CATATT	score: 2.854843338	79
>tatC	pro0462	complement	443330..444082	TAGTAT	score: 3.427833197	43
>tatC	pro0462	complement	443330..444082	TAATAT	score: 4.345371032	52
>tatC	pro0462	complement	443330..444082	TATTAT	score: 4.345371032	58
>tatC	pro0462	complement	443330..444082	TATTTT	score: 3.830797859	63
>tatC	pro0462	complement	443330..444082	TAATCT	score: 4.565336720	74
>pro0464	pro0464	complement	444591..446306	CATGTG	score: 3.451878675	74
>pro0464	pro0464	complement	444591..446306	TACTAT	score: 3.842870696	85
>psaF	pro0467	complement	447133..447684	TACTGT	score: 4.062836384	84
>asp-tRNA	RNA_33	complement	451916..451989	CAGACT	score: 2.671844363	52
>asp-tRNA	RNA_33	complement	451916..451989	TAGGTT	score: 3.355618133	72
>trp-tRNA	RNA_32	complement	452382..452454	CATGTG	score: 3.451878675	29
>rplS	pro0473	complement	452517..452999	TACAAT	score: 3.980374220	30
>rplS	pro0473	complement	452517..452999	TATTAT	score: 4.345371032	58
>rplS	pro0473	complement	452517..452999	CAAAAT	score: 3.369416510	63
>fabG	pro0476	complement	454301..455062	TAAATT	score: 3.968301383	25
>fabG	pro0476	complement	454301..455062	CAATCT	score: 3.451878675	37
>fabG	pro0476	complement	454301..455062	CAAAGT	score: 3.589382199	56
>fabG	pro0476	complement	454301..455062	TAATTT	score: 3.830797859	85
>fabG	pro0476	complement	454301..455062	CAAAAT	score: 3.369416510	90
>hemL	pro0482	complement	458766..460067	CATTAT	score: 3.231912987	36
>hemL	pro0482	complement	458766..460067	TAGACT	score: 3.785302409	60

>xthA	pro0483	complement	460386..461216	TATCT	score: 4.565336720	29
>xthA	pro0483	complement	460386..461216	TATGCT	score: 5.007694830	52
>xthA	pro0483	complement	460386..461216	TATTTT	score: 3.830797859	85
>xthA	pro0483	complement	460386..461216	TATATT	score: 3.968301383	87
>pro0491	pro0491	complement	467660..468220	TACTAT	score: 3.842870696	31
>pro0491	pro0491	complement	467660..468220	TAGAGT	score: 3.785302409	44
>hemC	pro0494	complement	470762..471709	TAAGGT	score: 5.007694830	22
>hemC	pro0494	complement	470762..471709	TAAGGT	score: 5.007694830	41
>hemC	pro0494	complement	470762..471709	TAAAGT	score: 4.702840244	71
>rpoD	pro0495	complement	471863..473179	CAAAAT	score: 3.369416510	30
>rpoD	pro0495	complement	471863..473179	TATTTT	score: 3.830797859	36
>rpoD	pro0495	complement	471863..473179	CATATT	score: 2.854843338	38
>rpoD	pro0495	complement	471863..473179	TAGGCT	score: 4.090156999	66
>pro0500	pro0500	complement	477849..478400	CAAACT	score: 3.589382199	33
>pro0500	pro0500	complement	477849..478400	TAAGAT	score: 4.787729142	79
>ssb	pro0502	complement	478656..479114	CAAGAT	score: 3.674271096	22
>ssb	pro0502	complement	478656..479114	TAATTT	score: 3.830797859	42
>ssb	pro0502	complement	478656..479114	TAATAT	score: 4.345371032	64
>proS	pro0508	complement	483185..484996	TATTAT	score: 4.345371032	30
>proS	pro0508	complement	483185..484996	CAAATT	score: 2.854843338	44
>pro0512	pro0512	complement	486820..488313	TACTTT	score: 3.328297523	35
>pro0512	pro0512	complement	486820..488313	CATATT	score: 2.854843338	45
>pro0512	pro0512	complement	486820..488313	CAATTT	score: 2.717339814	61
>pro0512	pro0512	complement	486820..488313	TAATTT	score: 3.830797859	86
>pro0512	pro0512	complement	486820..488313	TAAGAT	score: 4.787729142	91
>gpmB	pro0515	complement	490376..491704	CAGTGT	score: 2.534340839	34
>gpmB	pro0515	complement	490376..491704	TAGGTT	score: 3.355618133	42
>gpmB	pro0515	complement	490376..491704	CAAGAT	score: 3.674271096	48
>pyrH	pro0522	complement	498408..499121	CACGAT	score: 3.171770760	82
>pro0524	pro0524	complement	500108..501268	TACTTT	score: 3.328297523	59
>pro0524	pro0524	complement	500108..501268	TAAAAT	score: 4.482874556	64
>rpsA	pro0530	complement	506532..507785	TAATTT	score: 3.830797859	47
>trpF	pro0538	complement	513192..513851	GATGGT	score: 2.572308690	48
>trpF	pro0538	complement	513192..513851	GAAGAT	score: 2.352343001	51
>trpF	pro0538	complement	513192..513851	TAAGCT	score: 5.007694830	58
>trpF	pro0538	complement	513192..513851	CAAATT	score: 2.854843338	76
>lplA	pro0540	complement	515103..515945	CAAAAT	score: 3.369416510	30
>lplA	pro0540	complement	515103..515945	TAAATT	score: 3.968301383	42
>chlN	pro0546	complement	520461..521717	TATATT	score: 3.968301383	78
>chlN	pro0546	complement	520461..521717	CAAAAT	score: 3.369416510	85
>pro0547	pro0547	complement	521869..522240	TAAATT	score: 3.968301383	36
>pro0549	pro0549	complement	523130..523714	CAATTT	score: 2.717339814	32
>pro0549	pro0549	complement	523130..523714	TACTCT	score: 4.062836384	44
>pro0549	pro0549	complement	523130..523714	TAAGTT	score: 4.273155969	49
>pro0559	pro0559	complement	531759..531983	TAGATT	score: 3.050763548	22
>pro0559	pro0559	complement	531759..531983	TATTGT	score: 4.565336720	29
>pro0559	pro0559	complement	531759..531983	CACTAT	score: 2.729412650	32
>pro0559	pro0559	complement	531759..531983	CACACT	score: 3.086881863	34
>tdcF	pro0560	complement	532072..532470	TAGGAT	score: 3.870191306	25
>gloB	pro0561	complement	532524..533285	CAGAGT	score: 2.671844363	89
>pro0566	pro0566	complement	537058..537702	CAGGAT	score: 2.756733261	60
>pro0566	pro0566	complement	537058..537702	GAAGCT	score: 2.572308690	79
>gst	pro0568	complement	539358..540608	CAAAAT	score: 3.369416510	38
>gst	pro0568	complement	539358..540608	TACAAT	score: 3.980374220	62
>eCM27	pro0570	complement	542066..543145	CAAATT	score: 2.854843338	49
>eCM27	pro0570	complement	542066..543145	TAAAAT	score: 4.482874556	88

>pro0575	pro0575	complement	546430..546789	TATTTT	score: 3.830797859	24
>pro0575	pro0575	complement	546430..546789	TATGTT	score: 4.273155969	29
>pro0575	pro0575	complement	546430..546789	CAAGCT	score: 3.894236785	41
>pro0575	pro0575	complement	546430..546789	CACAAT	score: 2.866916174	50
>pro0575	pro0575	complement	546430..546789	TACAAT	score: 3.980374220	66
>rpoD	pro0580	complement	548286..549218	TACGAT	score: 4.285228806	25
>rpoD	pro0580	complement	548286..549218	TACTTT	score: 3.328297523	36
>rpoD	pro0580	complement	548286..549218	TAAAAT	score: 4.482874556	79
>hisI	pro0582	complement	549957..550637	CAAAAT	score: 3.369416510	36
>hisI	pro0582	complement	549957..550637	CATATT	score: 2.854843338	58
>hisI	pro0582	complement	549957..550637	TAATTT	score: 3.830797859	80
>psbY	pro0586	complement	554236..554358	TAAAAT	score: 4.482874556	22
>psbY	pro0586	complement	554236..554358	TATTTT	score: 3.830797859	31
>rpsU	pro0590	complement	556189..556368	CAATAT	score: 3.231912987	53
>rpsU	pro0590	complement	556189..556368	CAAGTT	score: 3.159697923	79
>pro0591	pro0591	complement	556786..557040	TACTCT	score: 4.062836384	24
>pro0591	pro0591	complement	556786..557040	CATACT	score: 3.589382199	26
>pro0591	pro0591	complement	556786..557040	GAAGCT	score: 2.572308690	48
>pro0594	pro0594	complement	557760..558110	CACATT	score: 2.352343001	46
>pro0594	pro0594	complement	557760..558110	TACTTT	score: 3.328297523	66
>pro0595	pro0595	complement	558478..558675	TAATAT	score: 4.345371032	37
>pro0595	pro0595	complement	558478..558675	TAAACT	score: 4.702840244	45
>pro0595	pro0595	complement	558478..558675	TATTTT	score: 3.830797859	51
>pro0595	pro0595	complement	558478..558675	TATATT	score: 3.968301383	53
>pro0595	pro0595	complement	558478..558675	TATAAT	score: 4.482874556	68
>pro0595	pro0595	complement	558478..558675	TAATCT	score: 4.565336720	73
>pro0595	pro0595	complement	558478..558675	TAGATT	score: 3.050763548	82
>pro0595	pro0595	complement	558478..558675	TATTTT	score: 3.830797859	87
>pro0595	pro0595	complement	558478..558675	TAATAT	score: 4.345371032	90
>pstC	pro0598	complement	560650..561600	TAGATT	score: 3.050763548	22
>pro0599	pro0599	complement	561803..561931	CAAGAT	score: 3.674271096	25
>pro0599	pro0599	complement	561803..561931	TAATTT	score: 3.830797859	65
>pro0599	pro0599	complement	561803..561931	TAAAAT	score: 4.482874556	89
>pro0603	pro0603	complement	563865..564173	TACTTT	score: 3.328297523	50
>pro0603	pro0603	complement	563865..564173	CATACT	score: 3.589382199	52
>pro0604	pro0604	complement	564321..564986	CAATGT	score: 3.451878675	44
>pro0609	pro0609	complement	570126..570731	CAAGGT	score: 3.894236785	85
>pro0614	pro0614	complement	574963..577755	TACAGT	score: 4.200339908	55
>pro0614	pro0614	complement	574963..577755	CAAAGT	score: 3.589382199	88
>pro0615	pro0615	complement	578131..579900	TAAATT	score: 3.968301383	62
>pro0616	pro0616	complement	580239..583571	TAAATT	score: 3.968301383	62
>pro0621	pro0621	complement	585381..585884	CAATTT	score: 2.717339814	52
>pro0621	pro0621	complement	585381..585884	TACGGT	score: 4.505194494	61
>pro0630	pro0630	complement	591847..594594	TAGTTT	score: 2.913260024	22
>pro0630	pro0630	complement	591847..594594	TATAGT	score: 4.702840244	24
>pro0630	pro0630	complement	591847..594594	TAAAAT	score: 4.482874556	37
>pro0630	pro0630	complement	591847..594594	TAGGAT	score: 3.870191306	51
>pro0636	pro0636	complement	597918..598535	TATAAT	score: 4.482874556	23
>pro0636	pro0636	complement	597918..598535	TATAAT	score: 4.482874556	38
>pro0636	pro0636	complement	597918..598535	CAAATT	score: 2.854843338	51
>pro0636	pro0636	complement	597918..598535	TAAAAT	score: 4.482874556	64
>pro0639	pro0639	complement	599677..599916	CAAGCT	score: 3.894236785	28
>pro0639	pro0639	complement	599677..599916	TATTGT	score: 4.565336720	60
>pro0642	pro0642	complement	601045..601263	CACAAT	score: 2.866916174	28
>pro0642	pro0642	complement	601045..601263	TAAGTT	score: 4.273155969	66
>pro0642	pro0642	complement	601045..601263	CACAAT	score: 2.866916174	71

>iscA	pro0644	complement	602429..602767	TAAAAT	score: 4.482874556	25
>iscA	pro0644	complement	602429..602767	TAATCT	score: 4.565336720	30
>iscA	pro0644	complement	602429..602767	CAAAAT	score: 3.369416510	74
>iscA	pro0644	complement	602429..602767	CAAAC	score: 3.589382199	83
>pro0646	pro0646	complement	603118..603303	TAGAGT	score: 3.785302409	27
>pro0647	pro0647	complement	603394..603591	CAAATT	score: 2.854843338	55
>pro0647	pro0647	complement	603394..603591	CAAAC	score: 3.589382199	88
>pro0648	pro0648	complement	603905..604117	CATAT	score: 3.231912987	25
>pro0648	pro0648	complement	603905..604117	TAATCT	score: 4.565336720	39
>pro0648	pro0648	complement	603905..604117	CATGTT	score: 3.159697923	66
>pro0648	pro0648	complement	603905..604117	TACTTT	score: 3.328297523	84
>pro0651	pro0651	complement	604975..605196	TAAAAT	score: 4.482874556	26
>pro0651	pro0651	complement	604975..605196	TAGTCT	score: 3.647798885	37
>pro0654	pro0654	complement	606274..606450	GATGGT	score: 2.572308690	44
>pro0654	pro0654	complement	606274..606450	CATGAT	score: 3.674271096	47
>pro0654	pro0654	complement	606274..606450	TAATTT	score: 3.830797859	59
>pro0654	pro0654	complement	606274..606450	CAAGAT	score: 3.674271096	90
>pro0658	pro0658	complement	607985..608257	TATGAT	score: 4.787729142	27
>pro0658	pro0658	complement	607985..608257	TACACT	score: 4.200339908	48
>pro0658	pro0658	complement	607985..608257	TAAAGT	score: 4.702840244	63
>pro0658	pro0658	complement	607985..608257	TATTTT	score: 3.830797859	85
>pro0659	pro0659	complement	608429..608797	TAGATT	score: 3.050763548	58
>pro0659	pro0659	complement	608429..608797	TACTTT	score: 3.328297523	91
>pro0662	pro0662	complement	610371..611435	TACATT	score: 3.465801047	30
>pro0662	pro0662	complement	610371..611435	CAAAAT	score: 3.369416510	44
>pro0664	pro0664	complement	612889..613047	TAAGCT	score: 5.007694830	23
>pro0664	pro0664	complement	612889..613047	TAGATT	score: 3.050763548	28
>pro0664	pro0664	complement	612889..613047	TAAGAT	score: 4.787729142	40
>pro0665	pro0665	complement	613294..613473	CAATCT	score: 3.451878675	25
>pro0665	pro0665	complement	613294..613473	CACTGT	score: 2.949378339	31
>pro0665	pro0665	complement	613294..613473	TAATTT	score: 3.830797859	49
>pro0665	pro0665	complement	613294..613473	CAAAC	score: 3.589382199	77
>pro0669	pro0669	complement	615718..616089	TAAATT	score: 3.968301383	53
>pro0671	pro0671	complement	616559..616747	TATTGT	score: 4.565336720	25
>pro0676	pro0676	complement	620558..621610	TAGAAT	score: 3.565336720	30
>pro0679	pro0679	complement	624259..626154	TATTTT	score: 3.830797859	33
>pro0679	pro0679	complement	624259..626154	CATATT	score: 2.854843338	35
>pro0679	pro0679	complement	624259..626154	TATATT	score: 3.968301383	48
>rfaG	pro0682	complement	628144..629292	CAAAAT	score: 3.369416510	32
>rfaG	pro0682	complement	628144..629292	TAGATT	score: 3.050763548	71
>pro0683	pro0683	complement	629584..630120	TAGTAT	score: 3.427833197	62
>pro0684	pro0684	complement	630215..630391	CACTCT	score: 2.949378339	22
>pro0684	pro0684	complement	630215..630391	TACACT	score: 4.200339908	24
>pro0684	pro0684	complement	630215..630391	GAAGAT	score: 2.352343001	33
>pro0684	pro0684	complement	630215..630391	CACATT	score: 2.352343001	74
>pro0684	pro0684	complement	630215..630391	CAAGGT	score: 3.894236785	81
>pro0685	pro0685	complement	630559..630756	TAGTAT	score: 3.427833197	23
>pro0685	pro0685	complement	630559..630756	TAGACT	score: 3.785302409	28
>pro0685	pro0685	complement	630559..630756	GAAGGT	score: 2.572308690	54
>pro0685	pro0685	complement	630559..630756	TAAATT	score: 3.968301383	69
>pro0685	pro0685	complement	630559..630756	GAAGAT	score: 2.352343001	79
>pro0688	pro0688	complement	632352..632552	TAAATT	score: 3.968301383	80
>pro0688	pro0688	complement	632352..632552	TAAAGT	score: 4.702840244	85
>pro0689	pro0689	complement	633210..633563	TAGGCT	score: 4.090156995	50
>pro0689	pro0689	complement	633210..633563	TATTGT	score: 4.565336720	58
>pro0689	pro0689	complement	633210..633563	TATATT	score: 3.968301383	87

>pro0690	pro0690	complement	634024..634422	GAAGCT	score: 2.572308690	38
>pro0690	pro0690	complement	634024..634422	CAAATT	score: 2.854843338	57
>pro0690	pro0690	complement	634024..634422	CAATTT	score: 2.717339814	67
>pro0690	pro0690	complement	634024..634422	CATTTT	score: 2.717339814	87
>pro0690	pro0690	complement	634024..634422	CACATT	score: 2.352343001	89
>pro0691	pro0691	complement	634861..635037	TAAACT	score: 4.702840244	24
>pro0691	pro0691	complement	634861..635037	GAAGCT	score: 2.572308690	38
>pro0691	pro0691	complement	634861..635037	CATTTT	score: 2.717339814	52
>pro0692	pro0692	complement	635119..635319	TACTTT	score: 3.328297523	48
>pro0692	pro0692	complement	635119..635319	CATACT	score: 3.589382199	50
>pro0693	pro0693	complement	635488..635604	TATGAT	score: 4.787729142	63
>pro0693	pro0693	complement	635488..635604	CAATTT	score: 2.717339814	68
>pro0693	pro0693	complement	635488..635604	TAATTT	score: 3.830797859	81
>pro0694	pro0694	complement	635829..636029	TATGTT	score: 4.273155969	28
>pro0694	pro0694	complement	635829..636029	CAATCT	score: 3.451878679	36
>pro0694	pro0694	complement	635829..636029	TACATT	score: 3.465801047	42
>pro0694	pro0694	complement	635829..636029	TAAATT	score: 3.968301383	48
>pro0694	pro0694	complement	635829..636029	TATTTT	score: 3.830797859	89
>pro0696	pro0696	complement	636868..637368	TAAGAT	score: 4.787729142	25
>pro0696	pro0696	complement	636868..637368	CATGCT	score: 3.894236789	54
>pro0696	pro0696	complement	636868..637368	TAATTT	score: 3.830797859	72
>pro0697	pro0697	complement	637643..637822	CAAAAT	score: 3.369416510	30
>pro0697	pro0697	complement	637643..637822	TAATTT	score: 3.830797859	72
>sbcd	pro0703	complement	645540..646724	TAAATT	score: 3.968301383	47
>hsdM	pro0708	complement	649203..650945	CAAAAT	score: 3.369416510	24
>hsdM	pro0708	complement	649203..650945	CAAATT	score: 2.854843338	71
>pro0709	pro0709	complement	651296..651523	TAAACT	score: 4.702840244	28
>pro0709	pro0709	complement	651296..651523	TAAGTT	score: 4.273155969	37
>pro0709	pro0709	complement	651296..651523	CACTCT	score: 2.949378339	86
>pro0709	pro0709	complement	651296..651523	CACACT	score: 3.086881863	88
>pro0712	pro0712	complement	652685..653206	CATGTG	score: 3.451878679	57
>pro0712	pro0712	complement	652685..653206	GATGCT	score: 2.572308690	70
>pro0712	pro0712	complement	652685..653206	TATAAT	score: 4.482874556	78
>pro0712	pro0712	complement	652685..653206	TATTAT	score: 4.345371032	81
>pro0712	pro0712	complement	652685..653206	TACTAT	score: 3.842870696	84
>pro0712	pro0712	complement	652685..653206	CATACT	score: 3.589382199	86
>pro0714	pro0714	complement	653491..653664	TATTTT	score: 3.830797859	58
>pro0714	pro0714	complement	653491..653664	TAGTAT	score: 3.427833197	61
>pro0715	pro0715	complement	653864..654106	TAATAT	score: 4.345371032	57
>pro0715	pro0715	complement	653864..654106	CAAAAT	score: 2.854843338	62
>pro0715	pro0715	complement	653864..654106	TATCTC	score: 4.565336720	68
>pro0715	pro0715	complement	653864..654106	CAGGCT	score: 2.976698949	80
>pro0719	pro0719	complement	655664..656167	TAAGCT	score: 5.007694830	28
>pro0719	pro0719	complement	655664..656167	TAAACT	score: 4.702840244	40
>pro0719	pro0719	complement	655664..656167	CAAGCT	score: 3.894236789	45
>pro0719	pro0719	complement	655664..656167	GAAGAT	score: 2.352343001	68
>pro0720	pro0720	complement	656300..657079	CAATTT	score: 2.717339814	28
>pro0720	pro0720	complement	656300..657079	TATTTT	score: 3.830797859	52
>pro0720	pro0720	complement	656300..657079	CAAGGT	score: 3.894236789	59
>pro0720	pro0720	complement	656300..657079	TATAGT	score: 4.702840244	70
>pro0720	pro0720	complement	656300..657079	TATCTC	score: 4.565336720	83
>pro0722	pro0722	complement	657874..658251	TAAAGT	score: 4.702840244	24
>pro0722	pro0722	complement	657874..658251	GAAGGT	score: 2.572308690	56
>pro0722	pro0722	complement	657874..658251	CAAAAT	score: 3.369416510	66
>pro0722	pro0722	complement	657874..658251	CAAAAT	score: 3.369416510	83
>pro0723	pro0723	complement	658375..658575	TAAAAA	score: 4.482874556	34

>pro0723	pro0723	complement	658375..658575	TATAAT	score: 4.482874556	42
>pro0723	pro0723	complement	658375..658575	TAGATT	score: 3.050763548	73
>pro0723	pro0723	complement	658375..658575	TAATTT	score: 3.830797859	91
>pro0724	pro0724	complement	658863..659183	TAATAT	score: 4.345371032	76
>pro0724	pro0724	complement	658863..659183	TATAAT	score: 4.482874556	85
>pro0724	pro0724	complement	658863..659183	TAAAAT	score: 4.482874556	90
>pro0726	pro0726	complement	660478..660657	TACGCT	score: 4.505194494	33
>pro0726	pro0726	complement	660478..660657	TAAGAT	score: 4.787729142	41
>wcaA	pro0727	complement	660844..662040	CAGGAT	score: 2.756733261	41
>wcaA	pro0727	complement	660844..662040	TACTTT	score: 3.328297523	50
>pro0734	pro0734	complement	666828..667103	TAAACT	score: 4.702840244	51
>pro0734	pro0734	complement	666828..667103	TAAATT	score: 3.968301383	77
>pro0737	pro0737	complement	668400..669743	TATTCT	score: 4.565336720	47
>pro0737	pro0737	complement	668400..669743	TAAACT	score: 4.702840244	72
>pro0738	pro0738	complement	670322..670666	TAAAAT	score: 4.482874556	30
>pro0738	pro0738	complement	670322..670666	TAAAAT	score: 4.482874556	37
>pro0738	pro0738	complement	670322..670666	TAATTT	score: 3.830797859	47
>pro0738	pro0738	complement	670322..670666	TATAAT	score: 4.482874556	49
>pro0738	pro0738	complement	670322..670666	CATAAT	score: 3.369416510	58
>pro0738	pro0738	complement	670322..670666	TACTTT	score: 3.328297523	72
>pro0738	pro0738	complement	670322..670666	TAAAAT	score: 4.482874556	77
>pro2-tRNA	RNA_38	complement	670781..670854	TAGATT	score: 3.050763548	48
>pro2-tRNA	RNA_38	complement	670781..670854	TAAAAT	score: 4.482874556	62
>pro0741	pro0741	complement	671971..672222	TAAGCT	score: 5.007694830	37
>pro0741	pro0741	complement	671971..672222	GAAGAT	score: 2.352343001	42
>pro0741	pro0741	complement	671971..672222	TACATT	score: 3.465801047	49
>pro0741	pro0741	complement	671971..672222	TATTTT	score: 3.830797859	58
>pro0741	pro0741	complement	671971..672222	TATATT	score: 3.968301383	60
>mdlB	pro0742	complement	672319..674070	CAATAT	score: 3.231912987	26
>rpsO	pro0753	complement	684948..685217	TAAGCT	score: 5.007694830	28
>rhaT	pro0756	complement	686395..687282	TAAGTT	score: 4.273155969	69
>umuD	pro0760	complement	691340..691771	TACATT	score: 3.465801047	24
>umuD	pro0760	complement	691340..691771	TATGGT	score: 5.007694830	29
>pro0762	pro0762	complement	692310..692693	CAAAAT	score: 3.369416510	29
>pro0762	pro0762	complement	692310..692693	TAGAGT	score: 3.785302409	45
>pro0762	pro0762	complement	692310..692693	CATTTT	score: 2.717339814	55
>pro0762	pro0762	complement	692310..692693	TACAAT	score: 3.980374220	64
>perM	pro0770	complement	698877..699854	TATTCT	score: 4.565336720	25
>perM	pro0770	complement	698877..699854	TATTTT	score: 3.830797859	50
>perM	pro0770	complement	698877..699854	TATTTT	score: 3.830797859	77
>psb28	pro0771	complement	699968..700321	TACTAT	score: 3.842870696	22
>psb28	pro0771	complement	699968..700321	CATTTT	score: 2.717339814	31
>pro0772	pro0772	complement	700385..701428	GATGCT	score: 2.572308690	54
>pro0772	pro0772	complement	700385..701428	TATATT	score: 3.968301383	64
>pro0776	pro0776	complement	702956..703687	TAATTT	score: 3.830797859	47
>pro0776	pro0776	complement	702956..703687	CATATT	score: 2.854843338	61
>pro0776	pro0776	complement	702956..703687	TACAAT	score: 3.980374220	90
>gst	pro0786	complement	710887..711588	TATAAT	score: 4.482874556	29
>gst	pro0786	complement	710887..711588	CATTAT	score: 3.231912987	86
>crtL-e, Lcpro0790		complement	713347..714633	TAAGTT	score: 4.273155969	27
>crtL-e, Lcpro0790		complement	713347..714633	TAAAGT	score: 4.702840244	33
>crtL-e, Lcpro0790		complement	713347..714633	TAAAGT	score: 4.702840244	66
>mscS	pro0792	complement	715924..716940	CATAAT	score: 3.369416510	26
>mscS	pro0792	complement	715924..716940	TAATGT	score: 4.565336720	32
>mscS	pro0792	complement	715924..716940	CAAATT	score: 2.854843338	61
>mscS	pro0792	complement	715924..716940	TAGTTT	score: 2.913260024	79

>mscS	pro0792	complement	715924..716940	TATAGT	score: 4.702840244	81
>mscS	pro0792	complement	715924..716940	TAATAT	score: 4.345371032	84
>pncA	pro0793	complement	717090..717644	CAAAAT	score: 3.369416510	55
>pncA	pro0793	complement	717090..717644	TAATCT	score: 4.565336720	77
>pncA	pro0793	complement	717090..717644	TAATTT	score: 3.830797859	86
>pro0796	pro0796	complement	719298..720527	TATAAT	score: 4.482874556	26
>pro0796	pro0796	complement	719298..720527	TAGTAT	score: 3.427833197	29
>pro0796	pro0796	complement	719298..720527	CATATT	score: 2.854843338	71
>pro0803	pro0803	complement	727144..727425	CAATAT	score: 3.231912987	63
>glcD	pro0805	complement	729183..730469	CAAAAT	score: 3.369416510	38
>pro0809	pro0809	complement	733949..734251	TAAAGT	score: 4.702840244	54
>pro0809	pro0809	complement	733949..734251	TAAAAT	score: 4.482874556	65
>pro0809	pro0809	complement	733949..734251	TAAAAT	score: 4.482874556	75
>pro0812	pro0812	complement	735265..735774	TATTAT	score: 4.345371032	23
>pro0812	pro0812	complement	735265..735774	TATATT	score: 3.968301383	25
>pro0812	pro0812	complement	735265..735774	CATGCT	score: 3.894236785	38
>pro0812	pro0812	complement	735265..735774	CAGGGT	score: 2.976698949	51
>pro0812	pro0812	complement	735265..735774	TAGACT	score: 3.785302409	62
>pro0812	pro0812	complement	735265..735774	TAATAT	score: 4.345371032	75
>ser4-tRNA RNA_39	pro0814	complement	736098..736184	TAAAAT	score: 4.482874556	48
>ser4-tRNA RNA_39	pro0814	complement	736098..736184	CACTCT	score: 2.949378339	66
>pro0814	pro0814	complement	736618..736884	TAATAT	score: 4.345371032	91
>pro0815	pro0815	complement	737110..739503	TAGTGT	score: 3.647798885	37
>pro0815	pro0815	complement	737110..739503	CACGTT	score: 2.657197587	64
>pqqL	pro0818	complement	741583..742860	CACTAT	score: 2.729412650	37
>sir	pro0830	complement	753696..755492	TATGAT	score: 4.787729142	33
>sir	pro0830	complement	753696..755492	TACAAT	score: 3.980374220	46
>sir	pro0830	complement	753696..755492	GAAGAT	score: 2.352343001	51
>chlP	pro0832	complement	757756..759099	TAAAAT	score: 4.482874556	25
>chlP	pro0832	complement	757756..759099	TAGGTT	score: 3.355618133	32
>chlP	pro0832	complement	757756..759099	TAGAGT	score: 3.785302409	52
>rpe	pro0839	complement	765353..766096	TAGAAT	score: 3.565336720	23
>upp	pro0849	complement	775424..776041	CACGTT	score: 2.657197587	23
>upp	pro0849	complement	775424..776041	TAATTT	score: 3.830797859	36
>upp	pro0849	complement	775424..776041	TAGAAT	score: 3.565336720	63
>upp	pro0849	complement	775424..776041	TAATTT	score: 3.830797859	75
>fba	pro0855	complement	779131..780204	TAAAGT	score: 4.702840244	60
>fba	pro0856	complement	780355..781422	CATGAT	score: 3.674271096	38
>fba	pro0856	complement	780355..781422	TATTTT	score: 3.830797859	84
>pulO	pro0860	complement	783996..784580	TACTTT	score: 3.328297523	39
>pulO	pro0860	complement	783996..784580	TAAATT	score: 3.968301383	45
>prkB	pro0861	complement	784660..785559	TACTAT	score: 3.842870696	43
>pro0868	pro0868	complement	790478..791512	TACTTT	score: 3.328297523	35
>pro0868	pro0868	complement	790478..791512	TACATT	score: 3.465801047	53
>pro0869	pro0869	complement	791603..792772	TATTTT	score: 3.830797859	29
>pro0869	pro0869	complement	791603..792772	TATTAT	score: 4.345371032	32
>pro0869	pro0869	complement	791603..792772	TAGAAT	score: 3.565336720	37
>pro0869	pro0869	complement	791603..792772	TATAAT	score: 4.482874556	43
>pro0869	pro0869	complement	791603..792772	TAATAT	score: 4.345371032	46
>hisA	pro0872	complement	795218..795988	CAGGAT	score: 2.756733261	22
>hisA	pro0872	complement	795218..795988	TACTTT	score: 3.328297523	74
>pgsA	pro0874	complement	796982..797524	CAAATT	score: 2.854843338	48
>pgsA	pro0874	complement	796982..797524	TAATAT	score: 4.345371032	70
>pgsA	pro0874	complement	796982..797524	TAATGT	score: 4.565336720	86
>pgsA	pro0874	complement	796982..797524	TATAAT	score: 4.482874556	88
>pro0879	pro0879	complement	799764..800441	TAATAT	score: 4.345371032	30

>pro0879	pro0879	complement	799764..800441	TAAAGT	score: 4.702840244	36
>pro0879	pro0879	complement	799764..800441	CAAAAT	score: 3.369416510	41
>pro0879	pro0879	complement	799764..800441	CACAGT	score: 3.086881863	52
>nth	pro0880	complement	800525..801178	CATTAT	score: 3.231912987	24
>nth	pro0880	complement	800525..801178	TAGGTT	score: 3.355618133	47
>crp	pro0884	complement	803442..804035	TATTCT	score: 4.565336720	26
>crp	pro0884	complement	803442..804035	TATTTT	score: 3.830797859	38
>crp	pro0884	complement	803442..804035	TAGTGT	score: 3.647798885	43
>crp	pro0884	complement	803442..804035	CATGTT	score: 3.159697923	83
>pcbD	pro0885	complement	804325..805380	TACTTT	score: 3.328297523	27
>pcbD	pro0885	complement	804325..805380	GAAGCT	score: 2.572308690	37
>pcbD	pro0885	complement	804325..805380	CAATGT	score: 3.451878675	66
>pcbD	pro0885	complement	804325..805380	TACAAT	score: 3.980374220	81
>hcaE	pro0890	complement	807436..808773	CAAAAT	score: 3.369416510	25
>hcaE	pro0890	complement	807436..808773	TACGCT	score: 4.505194494	35
>hcaE	pro0890	complement	807436..808773	TAATAT	score: 4.345371032	47
>hcaE	pro0890	complement	807436..808773	TACTGT	score: 4.062836384	52
>hcaE	pro0890	complement	807436..808773	TAAATT	score: 3.968301383	88
>pro0891	pro0891	complement	808984..809166	TAAGAT	score: 4.787729142	68
>pro0891	pro0891	complement	808984..809166	TAATCT	score: 4.565336720	73
>pro0891	pro0891	complement	808984..809166	TATAAT	score: 4.482874556	75
>pro0891	pro0891	complement	808984..809166	TAAATT	score: 3.968301383	84
>pro0896	pro0896	complement	813155..813790	TAAGTT	score: 4.273155969	23
>pro0896	pro0896	complement	813155..813790	GATGCT	score: 2.572308690	75
>pro0898	pro0898	complement	817254..817481	CAAAGT	score: 3.589382199	27
>pro0898	pro0898	complement	817254..817481	TAATAT	score: 4.345371032	33
>mdlB	pro0899	complement	817556..819298	CATTTT	score: 2.717339814	38
>mdlB	pro0899	complement	817556..819298	CAGACT	score: 2.671844363	58
>chlH	pro0903	complement	821126..825139	TAGGCT	score: 4.090156995	27
>chlH	pro0903	complement	821126..825139	CACAGT	score: 3.086881863	50
>chlH	pro0903	complement	821126..825139	TAAAAT	score: 4.482874556	83
>pro0912	pro0912	complement	831289..831669	TAAGAT	score: 4.787729142	26
>pro0912	pro0912	complement	831289..831669	TAAAAT	score: 4.482874556	49
>pro0912	pro0912	complement	831289..831669	TAGAAT	score: 3.565336720	58
>pro0912	pro0912	complement	831289..831669	TATAAT	score: 4.482874556	63
>pro0913	pro0913	complement	831770..831964	TAAAAT	score: 4.482874556	22
>pro0913	pro0913	complement	831770..831964	TATGAT	score: 4.787729142	27
>pro0913	pro0913	complement	831770..831964	CAATTT	score: 2.717339814	32
>pro0913	pro0913	complement	831770..831964	TAAAAT	score: 4.482874556	74
>pro0913	pro0913	complement	831770..831964	CATGTT	score: 3.159697923	86
>pro0914	pro0914	complement	832234..832617	TATATT	score: 3.968301383	48
>pro0914	pro0914	complement	832234..832617	TAAGAT	score: 4.787729142	53
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>pro0914	pro0914	complement	832234..832617	CAATAT	score: 3.231912987	61
>pro0914	pro0914	complement	832234..832617	TATTCT	score: 4.565336720	85
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>pro0917	pro0917	complement	833911..834186	TAAAGT	score: 4.702840244	41
>pro0917	pro0917	complement	833911..834186	CATATT	score: 2.854843338	59
>pro0917	pro0917	complement	833911..834186	TAAATT	score: 3.968301383	71
>pro0917	pro0917	complement	833911..834186	TAAGGT	score: 5.007694830	84
>pro0919	pro0919	complement	834537..835181	TAAGGT	score: 5.007694830	23
>pro0919	pro0919	complement	834537..835181	TATATT	score: 3.968301383	37
>pro0919	pro0919	complement	834537..835181	CACGAT	score: 3.171770760	52
>pro0919	pro0919	complement	834537..835181	TAAAAT	score: 4.482874556	69
>pro0919	pro0919	complement	834537..835181	CATTAT	score: 3.231912987	74
>hflB	pro0921	complement	835861..837777	TATTCT	score: 4.565336720	29

>hflB	pro0921	complement	835861..837777	TATATT	score: 3.968301383	31
>hflB	pro0921	complement	835861..837777	TAAAAT	score: 4.482874556	52
>pykF	pro0923	complement	839129..840913	TATTTT	score: 3.830797859	23
>pykF	pro0923	complement	839129..840913	CAAGAT	score: 3.674271096	31
>pykF	pro0923	complement	839129..840913	CAAAAT	score: 3.369416510	42
>pykF	pro0923	complement	839129..840913	CATGAT	score: 3.674271096	74
>pykF	pro0923	complement	839129..840913	TAAGGT	score: 5.007694830	81
>pro0926	pro0926	complement	841669..842151	CAAAAT	score: 3.369416510	27
>ilvA	pro0927	complement	842240..843781	CAAAAT	score: 3.369416510	43
>ilvA	pro0927	complement	842240..843781	TACGGT	score: 4.505194494	84
>ilvA	pro0927	complement	842240..843781	CAATCT	score: 3.451878675	89
>htpG	pro0934	complement	847814..849715	TAAAAT	score: 4.482874556	29
>htpG	pro0934	complement	847814..849715	TAATTT	score: 3.830797859	34
>htpG	pro0934	complement	847814..849715	CAAATT	score: 2.854843338	39
>htpG	pro0934	complement	847814..849715	TAAATT	score: 3.968301383	47
>suhB	pro0937	complement	851248..852111	CAAATT	score: 2.854843338	42
>suhB	pro0937	complement	851248..852111	TAATAT	score: 4.345371032	55
>suhB	pro0937	complement	851248..852111	CAAAAT	score: 3.369416510	73
>ribB	pro0943	complement	857355..858995	TAAACT	score: 4.702840244	48
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>ribB	pro0943	complement	857355..858995	TAGAAT	score: 3.565336720	77
>ribB	pro0943	complement	857355..858995	CACAAT	score: 2.866916174	83
>purN	pro0945	complement	860174..860812	CACAAT	score: 2.866916174	47
>purN	pro0945	complement	860174..860812	TATAAT	score: 4.482874556	56
>purN	pro0945	complement	860174..860812	TATTCT	score: 4.565336720	65
>purN	pro0945	complement	860174..860812	CAAAAT	score: 3.369416510	89
>leuS	pro0947	complement	862588..865200	TAGGAT	score: 3.870191306	39
>leuS	pro0947	complement	862588..865200	TAATAT	score: 4.345371032	59
>leuS	pro0947	complement	862588..865200	CATAAT	score: 3.369416510	64
>leuS	pro0947	complement	862588..865200	TAATAT	score: 4.345371032	82
>leuS	pro0947	complement	862588..865200	TAATAT	score: 4.345371032	91
>coaD	pro0952	complement	869302..869787	CAAGCT	score: 3.894236785	53
>cobN	pro0957	complement	873619..877368	CACGCT	score: 3.391736448	31
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>pro0960	pro0960	complement	881948..882178	TATGTT	score: 4.273155969	89
>pro0962	pro0962	complement	883553..883750	CAATAT	score: 3.231912987	54
>pro0962	pro0962	complement	883553..883750	TATGAT	score: 4.787729142	60
>pro0962	pro0962	complement	883553..883750	CAAAAT	score: 3.369416510	82
>pro0962	pro0962	complement	883553..883750	TAGGTT	score: 3.355618133	91
>pheT	pro0966	complement	886946..889459	TAGGAT	score: 3.870191306	22
>pheT	pro0966	complement	886946..889459	TACTTT	score: 3.328297523	35
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>pheT	pro0966	complement	886946..889459	TACTTT	score: 3.328297523	85
>pheT	pro0966	complement	886946..889459	TACGAT	score: 4.285228806	90
>pro0972	pro0972	complement	893610..894179	CACGAT	score: 3.171770760	22
>pro0972	pro0972	complement	893610..894179	TAGTTT	score: 2.913260024	50
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>pro0976	pro0976	complement	895780..896379	TATTCT	score: 4.565336720	25
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>pro0977	pro0977	complement	896976..897131	TATTGT	score: 4.565336720	36
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>pro0977	pro0977	complement	896976..897131	TAGGCT	score: 4.090156995	87
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>hflB	pro0980	complement	898722..900476	TATTTT	score: 3.830797859	44
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>hflB	pro0980	complement	898722..900476	TATACT	score: 4.702840244	62
>hflB	pro0980	complement	898722..900476	TATTTT	score: 3.830797859	81
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>pro0983	pro0983	complement	901144..901896	TAAAAT	score: 4.482874556	33
>pro0983	pro0983	complement	901144..901896	TAAGAT	score: 4.787729142	38
>pro0983	pro0983	complement	901144..901896	TATTAT	score: 4.345371032	51
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>pro0983	pro0983	complement	901144..901896	TATGTT	score: 4.273155969	85
>pro0994	pro0994	complement	910857..911189	TATTAT	score: 4.345371032	31
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>pro0994	pro0994	complement	910857..911189	TAAGTT	score: 4.273155969	76
>terC	pro0998	complement	915168..915890	TAAGCT	score: 5.007694830	45
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>terC	pro0998	complement	915168..915890	TATGCT	score: 5.007694830	85
>pro1001	pro1001	complement	920877..921122	TATGGT	score: 5.007694830	62
>pro1006	pro1006	complement	922787..923227	TAGATT	score: 3.050763548	25
>pro1006	pro1006	complement	922787..923227	TAAAAT	score: 4.482874556	31
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>pro1006	pro1006	complement	922787..923227	TAAATT	score: 3.968301383	83
>purK	pro1008	complement	924662..925831	CAAATT	score: 2.854843338	77
>pro1010	pro1010	complement	927021..928226	CATGTT	score: 3.159697923	27
>pro1010	pro1010	complement	927021..928226	TAAAAT	score: 4.482874556	63
>pro1010	pro1010	complement	927021..928226	CAAATT	score: 2.854843338	80
>pro1012	pro1012	complement	929138..929920	CATTTT	score: 2.717339814	56
>pro1012	pro1012	complement	929138..929920	CAATTT	score: 2.717339814	70
>pro1017	pro1017	complement	934269..934670	TAGTGT	score: 3.647798885	32
>pro1017	pro1017	complement	934269..934670	CATTTT	score: 2.717339814	89
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>pro1037	pro1037	complement	951036..952202	TAGGCT	score: 4.090156995	26
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>acs	pro1041	complement	955620..957596	CATGTT	score: 3.159697923	80
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>znuA	pro1060	complement	977289..978161	TATATT	score: 3.968301383	54
>znuA	pro1060	complement	977289..978161	TAGATT	score: 3.050763548	60
>znuA	pro1060	complement	977289..978161	TATATT	score: 3.968301383	72
>znuA	pro1060	complement	977289..978161	TAAATT	score: 3.968301383	77
>znuA	pro1060	complement	977289..978161	TATGGT	score: 5.007694830	82
>pro1061	pro1061	complement	978296..979642	TAATTT	score: 3.830797859	35
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>pro1061	pro1061	complement	978296..979642	TAGTCT	score: 3.647798885	73
>pro1061	pro1061	complement	978296..979642	TATAGT	score: 4.702840244	75
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>pro1073	pro1073	complement	991996..995925	TATAGT	score: 4.702840244	89
>ompR	pro1083	complement	1006867..1007628	TACAGT	score: 4.200339908	43
>ompR	pro1083	complement	1006867..1007628	GATGAT	score: 2.352343001	63
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>plsC	pro1088	complement	1009168..1009851	TAAGTT	score: 4.273155969	26
>psbP	pro1097	complement	1024233..1024790	TACATT	score: 3.465801047	32
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>lysA	pro1105	complement	1030664..1032031	TAAATT	score: 3.968301383	46
>lysA	pro1105	complement	1030664..1032031	CATGAT	score: 3.674271096	52
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>ldcC	pro1112	complement	1038919..1040241	TAATCT	score: 4.565336720	31
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>malQ	pro1116	complement	1043407..1044957	TATGAT	score: 4.787729142	54
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>pro1117	pro1117	complement	1045272..1045817	TATGCT	score: 5.007694830	51
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>pro1117	pro1117	complement	1045272..1045817	CACGGT	score: 3.391736448	82
>pro1119	pro1119	complement	1046909..1047343	CATTCT	score: 3.451878675	25
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>pro1119	pro1119	complement	1046909..1047343	CACTAT	score: 2.729412650	73
>pro1120	pro1120	complement	1047452..1048006	TACTCT	score: 4.062836384	28
>pro1122	pro1122	complement	1049395..1049916	TAAATT	score: 3.968301383	54
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>pro1122	pro1122	complement	1049395..1049916	TATFGT	score: 4.565336720	84
>fold	pro1130	complement	1058637..1059545	TAAGCT	score: 5.007694830	85
>pro1132	pro1132	complement	1061781..1062173	TAATTT	score: 3.830797859	22
>pro1132	pro1132	complement	1061781..1062173	TATAGT	score: 4.702840244	28
>pro1132	pro1132	complement	1061781..1062173	TAGTTT	score: 2.913260024	35
>pro1132	pro1132	complement	1061781..1062173	TAATTT	score: 3.830797859	56
>leuA	pro1134	complement	1062576..1064186	TAGAAT	score: 3.565336720	31
>leuA	pro1134	complement	1062576..1064186	TATAGT	score: 4.702840244	37

>leuA	pro1134	complement	1062576..1064186	TAGGAT	score: 3.870191306	53
>leuA	pro1134	complement	1062576..1064186	CAAGTT	score: 3.159697923	81
>gyrA	pro1137	complement	1067068..1069695	TATTTT	score: 3.830797859	50
>gyrA	pro1137	complement	1067068..1069695	TAGTAT	score: 3.427833197	53
>gyrA	pro1137	complement	1067068..1069695	CAAATT	score: 2.854843338	72
>pro1154	pro1154	complement	1082940..1084571	CAATTT	score: 2.717339814	32
>pro1154	pro1154	complement	1082940..1084571	TATTGT	score: 4.565336720	47
>pro1154	pro1154	complement	1082940..1084571	CATATT	score: 2.854843338	49
>pro1154	pro1154	complement	1082940..1084571	GATGCT	score: 2.572308690	64
>pro1156	pro1156	complement	1085824..1086120	TAATTT	score: 3.830797859	43
>pro1156	pro1156	complement	1085824..1086120	TACTAT	score: 3.842870696	85
>pro1159	pro1159	complement	1087742..1088026	CATGTT	score: 3.159697923	52
>pro1160	pro1160	complement	1088118..1088312	TAAATT	score: 3.968301383	22
>pro1160	pro1160	complement	1088118..1088312	TATATT	score: 3.968301383	74
>pro1161	pro1161	complement	1088437..1088988	CATGAT	score: 3.674271096	33
>pro1161	pro1161	complement	1088437..1088988	TATGTT	score: 4.273155969	57
>pro1161	pro1161	complement	1088437..1088988	TATAT	score: 4.345371032	60
>pro1161	pro1161	complement	1088437..1088988	TAATTT	score: 3.830797859	89
>pro1162	pro1162	complement	1089113..1089295	CATTTT	score: 2.717339814	23
>pro1162	pro1162	complement	1089113..1089295	TATATT	score: 3.968301383	30
>pro1162	pro1162	complement	1089113..1089295	TAGTAT	score: 3.427833197	68
>pro1162	pro1162	complement	1089113..1089295	TAGGCT	score: 4.090156995	85
>isiB	pro1164	complement	1089871..1090392	CAGGAT	score: 2.756733261	31
>isiB	pro1164	complement	1089871..1090392	CATTCT	score: 3.451878675	41
>isiB	pro1164	complement	1089871..1090392	TAAACT	score: 4.702840244	69
>isiB	pro1164	complement	1089871..1090392	TAAGAT	score: 4.787729142	75
>pro1165	pro1165	complement	1090497..1090763	TATTTT	score: 3.830797859	66
>pro1166	pro1166	complement	1090875..1091018	TAAAAT	score: 4.482874556	76
>pro1166	pro1166	complement	1090875..1091018	TAAAAT	score: 4.482874556	81
>pcbC	pro1167	complement	1091282..1092367	TAATCT	score: 4.565336720	33
>pcbC	pro1167	complement	1091282..1092367	CAGTGT	score: 2.534340839	38
>pcbC	pro1167	complement	1091282..1092367	CACAGT	score: 3.086881863	40
>pcbC	pro1167	complement	1091282..1092367	TATTCT	score: 4.565336720	62
>pcbC	pro1167	complement	1091282..1092367	CAAAC	score: 3.589382199	85
>pcbB	pro1169	complement	1093355..1094404	TAGTGT	score: 3.647798885	37
>pcbB	pro1169	complement	1093355..1094404	CATTTT	score: 2.717339814	57
>pcbB	pro1169	complement	1093355..1094404	TACATT	score: 3.465801047	59
>pro1179	pro1179	complement	1099132..1099347	CATTTT	score: 2.717339814	24
>pro1179	pro1179	complement	1099132..1099347	TATATT	score: 3.968301383	33
>pro1179	pro1179	complement	1099132..1099347	CATTTT	score: 2.717339814	39
>pro1179	pro1179	complement	1099132..1099347	CAAATT	score: 2.854843338	45
>pro1179	pro1179	complement	1099132..1099347	TAAAAT	score: 4.482874556	66
>pro1179	pro1179	complement	1099132..1099347	CAATTT	score: 2.717339814	73
>pro1179	pro1179	complement	1099132..1099347	TAAGCT	score: 5.007694830	86
>pro1181	pro1181	complement	1099793..1100455	CATTTT	score: 2.717339814	24
>pro1181	pro1181	complement	1099793..1100455	TAGGAT	score: 3.870191306	31
>pro1181	pro1181	complement	1099793..1100455	TATGAT	score: 4.787729142	60
>pro1181	pro1181	complement	1099793..1100455	CATAT	score: 3.231912987	63
>pro1181	pro1181	complement	1099793..1100455	CACATT	score: 2.352343001	65
>pro1181	pro1181	complement	1099793..1100455	CATACT	score: 3.589382199	73
>pro1181	pro1181	complement	1099793..1100455	TAATCT	score: 4.565336720	84
>pro1183	pro1183	complement	1100854..1101069	TAAATT	score: 3.968301383	25
>pro1183	pro1183	complement	1100854..1101069	TAGATT	score: 3.050763548	33
>pro1183	pro1183	complement	1100854..1101069	TATTTT	score: 3.830797859	51
>pro1183	pro1183	complement	1100854..1101069	TAGTAT	score: 3.427833197	54
>pro1183	pro1183	complement	1100854..1101069	TAGTGT	score: 3.647798885	71

>pro1183	pro1183	complement	1100854..1101069	TAATTT	score: 3.830797859	91
>pro1187	pro1187	complement	1103408..1104157	TAAAGT	score: 4.702840244	24
>pro1187	pro1187	complement	1103408..1104157	TATGCT	score: 5.007694830	35
>pro1187	pro1187	complement	1103408..1104157	CAATAT	score: 3.231912987	38
>pro1187	pro1187	complement	1103408..1104157	TAAATT	score: 3.968301383	46
>pro1190	pro1190	complement	1104944..1105120	TAAAGT	score: 4.702840244	22
>pro1191	pro1191	complement	1105175..1105651	TAATAT	score: 4.345371032	31
>pro1191	pro1191	complement	1105175..1105651	TATAAT	score: 4.482874556	36
>pro1191	pro1191	complement	1105175..1105651	TAATGT	score: 4.565336720	43
>pro1191	pro1191	complement	1105175..1105651	CAAATT	score: 2.854843338	58
>pro1191	pro1191	complement	1105175..1105651	CAGGAT	score: 2.756733261	64
>pro1193	pro1193	complement	1106880..1107155	CATTTT	score: 2.717339814	42
>pro1193	pro1193	complement	1106880..1107155	TAGGTT	score: 3.355618133	59
>pro1194	pro1194	complement	1107344..1107517	TAAAAT	score: 4.482874556	26
>pro1194	pro1194	complement	1107344..1107517	TAGTTT	score: 2.913260024	38
>pro1194	pro1194	complement	1107344..1107517	TATAGT	score: 4.702840244	40
>pro1194	pro1194	complement	1107344..1107517	TAATAT	score: 4.345371032	43
>pro1194	pro1194	complement	1107344..1107517	TAAAAT	score: 4.482874556	67
>pro1194	pro1194	complement	1107344..1107517	TAGACT	score: 3.785302409	75
>pro1197	pro1197	complement	1110206..1110502	TAAGCT	score: 5.007694830	71
>pro1197	pro1197	complement	1110206..1110502	TAGATT	score: 3.050763548	81
>pro1204	pro1204	complement	1115324..1115662	CATTTT	score: 2.717339814	22
>pro1204	pro1204	complement	1115324..1115662	TAAGTT	score: 4.273155969	29
>pro1206	pro1206	complement	1116150..1116266	TATCTC	score: 4.565336720	49
>pro1206	pro1206	complement	1116150..1116266	TAGTTT	score: 2.913260024	82
>pro1206	pro1206	complement	1116150..1116266	TATAGT	score: 4.702840244	84
>pro1207	pro1207	complement	1116464..1116724	TAAGAT	score: 4.787729142	29
>pro1207	pro1207	complement	1116464..1116724	CATATT	score: 2.854843338	55
>pro1207	pro1207	complement	1116464..1116724	TAAGGT	score: 5.007694830	68
>pro1207	pro1207	complement	1116464..1116724	TAAATT	score: 3.968301383	77
>desA	pro1208	complement	1116904..1118016	CAAACT	score: 3.589382199	24
>desA	pro1208	complement	1116904..1118016	CAAGTT	score: 3.159697923	51
>desA	pro1208	complement	1116904..1118016	CAATCT	score: 3.451878675	71
>pro1209	pro1209	complement	1118372..1118620	TATTTT	score: 3.830797859	22
>pro1209	pro1209	complement	1118372..1118620	TAAAAT	score: 4.482874556	54
>pro1209	pro1209	complement	1118372..1118620	CACTAT	score: 2.729412650	81
>pro1211	pro1211	complement	1119493..1119879	CATTTT	score: 2.717339814	27
>pro1211	pro1211	complement	1119493..1119879	TAGAAT	score: 3.565336720	39
>pro1212	pro1212	complement	1119968..1120459	TAGAGT	score: 3.785302409	31
>pro1212	pro1212	complement	1119968..1120459	TAAGCT	score: 5.007694830	60
>pro1212	pro1212	complement	1119968..1120459	TAAAAT	score: 4.482874556	65
>pro1212	pro1212	complement	1119968..1120459	CATTGT	score: 3.451878675	71
>pro1213	pro1213	complement	1120744..1120974	TATAAT	score: 4.482874556	63
>desA	pro1214	complement	1121144..1122250	TATTTT	score: 3.830797859	68
>desA	pro1214	complement	1121144..1122250	TAAATT	score: 3.968301383	83
>pro1216	pro1216	complement	1122990..1123322	CATACT	score: 3.589382199	23
>pro1216	pro1216	complement	1122990..1123322	TAAATT	score: 3.968301383	29
>pro1216	pro1216	complement	1122990..1123322	TAATTT	score: 3.830797859	34
>pro1216	pro1216	complement	1122990..1123322	TAAATT	score: 3.968301383	48
>pro1216	pro1216	complement	1122990..1123322	CAATTT	score: 2.717339814	53
>pro1216	pro1216	complement	1122990..1123322	CATGTT	score: 3.159697923	70
>pro1224	pro1224	complement	1127972..1128268	TAGTGT	score: 3.647798885	51
>pro1224	pro1224	complement	1127972..1128268	TAGTTT	score: 2.913260024	56
>pro1226	pro1226	complement	1129473..1129760	TATTAT	score: 4.345371032	30
>pro1226	pro1226	complement	1129473..1129760	TAGTTT	score: 2.913260024	87
>pro1226	pro1226	complement	1129473..1129760	TATAGT	score: 4.702840244	89

>pro1228	pro1228	complement	1130800..1131051	TAGGGT	score: 4.090156995	89
>pro1232	pro1232	complement	1134012..1135103	CAGAAT	score: 2.451878675	33
>pro1232	pro1232	complement	1134012..1135103	TAGTTT	score: 2.913260024	42
>pro1232	pro1232	complement	1134012..1135103	TAGTTT	score: 2.913260024	84
>pro1242	pro1242	complement	1146508..1146630	CATTCT	score: 3.451878675	91
>infA	pro1246	complement	1149118..1149399	TAAGGT	score: 5.007694830	27
>infA	pro1246	complement	1149118..1149399	TAGAAT	score: 3.565336720	33
>pro1247	pro1247	complement	1149471..1149686	TAGTTT	score: 2.913260024	32
>petM	pro1249	complement	1150769..1150867	CAAATT	score: 2.854843338	55
>petM	pro1249	complement	1150769..1150867	TAAGTT	score: 4.273155965	86
>pro1253	pro1253	complement	1153349..1153930	CATGTT	score: 3.159697923	45
>maf	pro1257	complement	1156646..1157272	TATTCT	score: 4.565336720	24
>maf	pro1257	complement	1156646..1157272	TAATAT	score: 4.345371032	27
>maf	pro1257	complement	1156646..1157272	TAGAAT	score: 3.565336720	72
>pro1262	pro1262	complement	1160963..1163053	GATGCT	score: 2.572308690	61
>pro1263	pro1263	complement	1163358..1163720	TACGAT	score: 4.285228806	40
>pro1263	pro1263	complement	1163358..1163720	TAATTT	score: 3.830797859	68
>pro1263	pro1263	complement	1163358..1163720	TATTAT	score: 4.345371032	75
>pro1270	pro1270	complement	1171620..1171862	CACAAT	score: 2.866916174	25
>pro1270	pro1270	complement	1171620..1171862	CATTGT	score: 3.451878675	39
>pro1270	pro1270	complement	1171620..1171862	CAAGTT	score: 3.159697923	67
>piuC	pro1271	complement	1171958..1172623	TATGTT	score: 4.273155965	50
>piuC	pro1271	complement	1171958..1172623	TATGAT	score: 4.787729142	72
>piuC	pro1271	complement	1171958..1172623	GAAGCT	score: 2.572308690	84
>pro1275	pro1275	complement	1177065..1177238	CATATT	score: 2.854843338	38
>pro1289	pro1289	complement	1189952..1190803	TAATTT	score: 3.830797859	27
>pro1291	pro1291	complement	1191765..1192997	TAATTT	score: 3.830797859	24
>pro1291	pro1291	complement	1191765..1192997	TATAAT	score: 4.482874556	26
>pro1291	pro1291	complement	1191765..1192997	TATAAT	score: 4.482874556	54
>pro1291	pro1291	complement	1191765..1192997	CATTTT	score: 2.717339814	59
>pro1291	pro1291	complement	1191765..1192997	TAATTT	score: 3.830797859	72
>pro1292	pro1292	complement	1193100..1193279	TAATTT	score: 3.830797859	32
>pro1292	pro1292	complement	1193100..1193279	CAGTGT	score: 2.534340839	87
>cysQ	pro1308	complement	1208471..1209385	CAGAAT	score: 2.451878675	47
>cysQ	pro1308	complement	1208471..1209385	CAAGGT	score: 3.894236785	86
>pro1311	pro1311	complement	1210574..1211299	TAGGTT	score: 3.355618133	26
>pro1311	pro1311	complement	1210574..1211299	CAAAGT	score: 3.589382199	31
>pro1311	pro1311	complement	1210574..1211299	CACATT	score: 2.352343001	49
>pro1311	pro1311	complement	1210574..1211299	CATTTT	score: 2.717339814	56
>pro1311	pro1311	complement	1210574..1211299	CACATT	score: 2.352343001	58
>pro1311	pro1311	complement	1210574..1211299	CATTCT	score: 3.451878675	65
>pro1311	pro1311	complement	1210574..1211299	GATGGT	score: 2.572308690	88
>wcaG	pro1313	complement	1213586..1214509	TACAAT	score: 3.980374220	28
>wcaG	pro1313	complement	1213586..1214509	TAATCT	score: 4.565336720	40
>wcaG	pro1313	complement	1213586..1214509	TAAAAT	score: 4.482874556	46
>wcaG	pro1313	complement	1213586..1214509	TATGCT	score: 5.007694830	54
>wcaG	pro1313	complement	1213586..1214509	TAAATT	score: 3.968301383	77
>galE	pro1314	complement	1214631..1215674	TATGAT	score: 4.787729142	36
>galE	pro1314	complement	1214631..1215674	TAGTTT	score: 2.913260024	67
>galE	pro1314	complement	1214631..1215674	TAATTT	score: 3.830797859	72
>galE	pro1314	complement	1214631..1215674	TAAGCT	score: 5.007694830	87
>pro1317	pro1317	complement	1218351..1219040	TAATAT	score: 4.345371032	26
>pro1317	pro1317	complement	1218351..1219040	TAAACT	score: 4.702840244	31
>pro1317	pro1317	complement	1218351..1219040	CACTGT	score: 2.949378339	44
>pro1317	pro1317	complement	1218351..1219040	GAAGAT	score: 2.352343001	91
>mdlB	pro1332	complement	1234364..1236145	TACAAT	score: 3.980374220	23

>mdlB	pro1332	complement	1234364..1236145	TAATAT	score: 4.345371032	29
>mdlB	pro1332	complement	1234364..1236145	TAGATT	score: 3.050763548	40
>mdlB	pro1332	complement	1234364..1236145	CAATAT	score: 3.231912987	47
>mdlB	pro1332	complement	1234364..1236145	TACAAT	score: 3.980374220	49
>mdlB	pro1332	complement	1234364..1236145	TACTTT	score: 3.328297523	54
>ala2-tRNA	RNA_20	complement	1237213..1237285	CAAGTT	score: 3.159697923	48
>ala2-tRNA	RNA_20	complement	1237213..1237285	CACTAT	score: 2.729412650	64
>ala2-tRNA	RNA_20	complement	1237213..1237285	CAAATT	score: 2.854843338	84
>lexA	pro1336	complement	1240339..1240947	TATGTG	score: 4.565336720	27
>hflB	pro1338	complement	1242030..1243895	TAGTTT	score: 2.913260024	24
>hflB	pro1338	complement	1242030..1243895	TAATTT	score: 3.830797859	56
>pro1341	pro1341	complement	1245607..1245873	TAGATT	score: 3.050763548	23
>pro1341	pro1341	complement	1245607..1245873	TAGATT	score: 3.050763548	36
>pro1341	pro1341	complement	1245607..1245873	TATGTG	score: 4.565336720	70
>pro1341	pro1341	complement	1245607..1245873	TATATT	score: 3.968301383	72
>pro1341	pro1341	complement	1245607..1245873	CAGAAT	score: 2.451878675	79
>pheS	pro1344	complement	1248203..1249210	TAAAGT	score: 4.702840244	22
>pheS	pro1344	complement	1248203..1249210	TAAAAT	score: 4.482874556	86
>pro1346	pro1346	complement	1250076..1250639	CAAGTT	score: 3.159697923	24
>pro1346	pro1346	complement	1250076..1250639	CAATTT	score: 2.717339814	44
>pro1346	pro1346	complement	1250076..1250639	CAAGAT	score: 3.674271096	57
>pro1346	pro1346	complement	1250076..1250639	CAGAGT	score: 2.671844363	68
>era	pro1355	complement	1256009..1256953	TATTTT	score: 3.830797859	38
>era	pro1355	complement	1256009..1256953	TACAGT	score: 4.200339908	44
>pro1357	pro1357	complement	1257588..1258325	CAAAGT	score: 3.589382199	23
>pro1357	pro1357	complement	1257588..1258325	TATTTT	score: 3.830797859	36
>ffh	pro1360	complement	1259847..1261304	TAAGCT	score: 5.007694830	30
>pro1361	pro1361	complement	1261377..1263434	TAAAGT	score: 4.702840244	25
>pro1361	pro1361	complement	1261377..1263434	CAGTCT	score: 2.534340839	87
>rpoD	pro1363	complement	1264686..1265627	TACGTT	score: 3.770655633	90
>pro1364	pro1364	complement	1265759..1267318	TAATTT	score: 3.830797859	30
>lnt	pro1366	complement	1268586..1270070	TACTTT	score: 3.328297523	43
>lnt	pro1366	complement	1268586..1270070	TAAGGT	score: 5.007694830	55
>lnt	pro1366	complement	1268586..1270070	GAAGAT	score: 2.352343001	68
>pro1370	pro1370	complement	1271704..1272372	CAAAGT	score: 3.589382199	40
>pro1370	pro1370	complement	1271704..1272372	TAAGTT	score: 4.273155969	69
>spoU	pro1373	complement	1274836..1275630	GATGAT	score: 2.352343001	60
>spoU	pro1373	complement	1274836..1275630	TACGAT	score: 4.285228806	63
>spoU	pro1373	complement	1274836..1275630	CAAAAT	score: 3.369416510	68
>Leu3-tRNA	RNA_22	complement	1275825..1275907	TATTTT	score: 3.830797859	25
>Leu3-tRNA	RNA_22	complement	1275825..1275907	TACTTT	score: 3.328297523	44
>Leu3-tRNA	RNA_22	complement	1275825..1275907	TATTCT	score: 4.565336720	55
>Leu3-tRNA	RNA_22	complement	1275825..1275907	TAGTTT	score: 2.913260024	77
>ssnA	pro1378	complement	1281331..1282629	CAAATT	score: 2.854843338	27
>ffs	RNA_44	complement	1287889..1287985	CAAGTT	score: 3.159697923	73
>hemN	pro1385	complement	1288767..1290017	TAATCT	score: 4.565336720	52
>hemN	pro1385	complement	1288767..1290017	CATGTG	score: 3.451878675	65
>nuoL	pro1393	complement	1296804..1297247	TAATGT	score: 4.565336720	25
>nuoL	pro1393	complement	1296804..1297247	TATTTT	score: 3.830797859	61
>nuoL	pro1393	complement	1296804..1297247	TATTTT	score: 3.830797859	66
>nuoL	pro1393	complement	1296804..1297247	TATTTT	score: 3.830797859	89
>pro1397	pro1397	complement	1298276..1298521	TAGTAT	score: 3.427833197	25
>pro1397	pro1397	complement	1298276..1298521	TAAGTT	score: 4.273155969	42
>pro1397	pro1397	complement	1298276..1298521	GATGAT	score: 2.352343001	78
>pro1398	pro1398	complement	1299121..1299417	TAGAAT	score: 3.565336720	22
>pro1398	pro1398	complement	1299121..1299417	TATAAT	score: 4.482874556	27

>pro1398	pro1398	complement	1299121..1299417	TAATTT	score: 3.830797859	56
>pro1398	pro1398	complement	1299121..1299417	TAATGT	score: 4.565336720	64
>pro1398	pro1398	complement	1299121..1299417	TAATTT	score: 3.830797859	75
>glnS	pro1400	complement	1299901..1300851	TATTTT	score: 3.830797859	56
>glnS	pro1400	complement	1299901..1300851	TAGATT	score: 3.050763548	61
>himA	pro1401	complement	1300942..1301217	GATGAT	score: 2.352343001	54
>himA	pro1401	complement	1300942..1301217	TACGAT	score: 4.285228806	78
>gloB	pro1402	complement	1301377..1302012	TATTTT	score: 3.830797859	28
>gloB	pro1402	complement	1301377..1302012	CATAGT	score: 3.589382199	34
>gloB	pro1402	complement	1301377..1302012	CAAGCT	score: 3.894236785	45
>gly2-tRNA	RNA_21	complement	1304181..1304251	CAAATT	score: 2.854843338	42
>gly2-tRNA	RNA_21	complement	1304181..1304251	CAAGGT	score: 3.894236785	69
>pro1411	pro1411	complement	1310635..1310955	CAATTT	score: 2.717339814	43
>pro1411	pro1411	complement	1310635..1310955	CAAAAT	score: 3.369416510	72
>pro1411	pro1411	complement	1310635..1310955	TAAATT	score: 3.968301383	82
>pro1419	pro1419	complement	1317250..1319742	TAAATT	score: 3.968301383	31
>kaiB	pro1424	complement	1325722..1326075	TAAAGT	score: 4.702840244	22
>kaiB	pro1424	complement	1325722..1326075	CAAGAT	score: 3.674271096	42
>kaiB	pro1424	complement	1325722..1326075	CACTCT	score: 2.949378339	64
>kaiB	pro1424	complement	1325722..1326075	CAAGAT	score: 3.674271096	78
>kaiB	pro1424	complement	1325722..1326075	CACAAT	score: 2.866916174	91
>pro1427	pro1427	complement	1326981..1327739	TAAGTT	score: 4.273155969	23
>pro1427	pro1427	complement	1326981..1327739	TATTTT	score: 3.830797859	47
>pro1427	pro1427	complement	1326981..1327739	TACTAT	score: 3.842870696	90
>spoIID	pro1429	complement	1328787..1330046	TAGATT	score: 3.050763548	26
>spoIID	pro1429	complement	1328787..1330046	CAAATT	score: 2.854843338	31
>spoIID	pro1429	complement	1328787..1330046	CATGTT	score: 3.159697923	75
>pro1432	pro1432	complement	1331835..1332029	GAAGAT	score: 2.352343001	83
>fdx	pro1434	complement	1332720..1333019	TATTTT	score: 3.830797859	38
>fdx	pro1434	complement	1332720..1333019	TAATAT	score: 4.345371032	41
>fdx	pro1434	complement	1332720..1333019	CAGTGT	score: 2.534340839	67
>fdx	pro1434	complement	1332720..1333019	TACAGT	score: 4.200339908	69
>fdx	pro1434	complement	1332720..1333019	CACATT	score: 2.352343001	83
>serA	pro1436	complement	1334126..1335712	TAAAGT	score: 4.702840244	25
>serA	pro1436	complement	1334126..1335712	TAAATT	score: 3.968301383	74
>pro1441	pro1441	complement	1339217..1339555	TATTAT	score: 4.345371032	23
>pro1441	pro1441	complement	1339217..1339555	TATATT	score: 3.968301383	25
>pro1441	pro1441	complement	1339217..1339555	TATTAT	score: 4.345371032	46
>pro1441	pro1441	complement	1339217..1339555	CAAATT	score: 2.854843338	51
>pro1444	pro1444	complement	1340376..1340540	TAAGTT	score: 4.273155969	22
>pro1444	pro1444	complement	1340376..1340540	TATGGT	score: 5.007694830	50
>pro1444	pro1444	complement	1340376..1340540	TACTTT	score: 3.328297523	59
>pro1444	pro1444	complement	1340376..1340540	GATGGT	score: 2.572308690	82
>pro1444	pro1444	complement	1340376..1340540	TATGAT	score: 4.787729142	85
>pro1444	pro1444	complement	1340376..1340540	CAATAT	score: 3.231912987	88
>smtA	pro1447	complement	1342211..1342858	TAGACT	score: 3.785302409	30
>smtA	pro1447	complement	1342211..1342858	TAAGTT	score: 4.273155969	36
>smtA	pro1447	complement	1342211..1342858	CAAGTT	score: 3.159697923	53
>pro1448	pro1448	complement	1342960..1343442	TATGTT	score: 4.273155969	27
>pro1448	pro1448	complement	1342960..1343442	TAAGAT	score: 4.787729142	43
>pro1448	pro1448	complement	1342960..1343442	GATGAT	score: 2.352343001	62
>pcbE	pro1450	complement	1344165..1345250	TAATCT	score: 4.565336720	33
>pcbE	pro1450	complement	1344165..1345250	CAAAAT	score: 3.369416510	44
>guaA	pro1451	complement	1345466..1346194	GAAGCT	score: 2.572308690	25
>guaA	pro1451	complement	1345466..1346194	TAATTT	score: 3.830797859	53
>guaA	pro1451	complement	1345466..1346194	TAATTT	score: 3.830797859	68

>pro1452	pro1452	complement	1346303..1347634	CATAAT	score: 3.369416510	34
>pro1452	pro1452	complement	1346303..1347634	TATGGT	score: 5.007694830	59
>pro1453	pro1453	complement	1347811..1348098	TAATTT	score: 3.830797859	81
>pro1453	pro1453	complement	1347811..1348098	CATTAT	score: 3.231912987	91
>pro1454	pro1454	complement	1348751..1348924	TAAATT	score: 3.968301383	23
>pro1454	pro1454	complement	1348751..1348924	TAAATT	score: 3.968301383	42
>pro1454	pro1454	complement	1348751..1348924	CAAATC	score: 3.589382199	51
>pro1454	pro1454	complement	1348751..1348924	GATGAT	score: 2.352343001	78
>pro1454	pro1454	complement	1348751..1348924	CAGGAT	score: 2.756733261	81
>pro1459	pro1459	complement	1352512..1352868	TATTAT	score: 4.345371032	24
>pro1459	pro1459	complement	1352512..1352868	TAAGTT	score: 4.273155969	29
>pro1459	pro1459	complement	1352512..1352868	TATTGT	score: 4.565336720	49
>pro1459	pro1459	complement	1352512..1352868	TAATAT	score: 4.345371032	58
>pro1459	pro1459	complement	1352512..1352868	TACATT	score: 3.465801047	80
>pro1460	pro1460	complement	1353842..1354342	GAAGCT	score: 2.572308690	26
>pro1460	pro1460	complement	1353842..1354342	CAAGCT	score: 3.894236785	49
>pro1460	pro1460	complement	1353842..1354342	TACAGT	score: 4.200339908	88
>pro1461	pro1461	complement	1355770..1355922	TATTCT	score: 4.565336720	24
>pro1461	pro1461	complement	1355770..1355922	TACTAT	score: 3.842870696	27
>pro1461	pro1461	complement	1355770..1355922	TAAAAT	score: 4.482874556	36
>pro1461	pro1461	complement	1355770..1355922	TATTAT	score: 4.345371032	49
>pro1461	pro1461	complement	1355770..1355922	TAAATT	score: 3.968301383	58
>pro1461	pro1461	complement	1355770..1355922	TATTAT	score: 4.345371032	70
>pro1461	pro1461	complement	1355770..1355922	TAGTCT	score: 3.647798885	91
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>pro1465	pro1465	complement	1358173..1358577	TAGTCT	score: 3.647798885	53
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>pro1468	pro1468	complement	1360831..1361190	TAGTTT	score: 2.913260024	69
>pro1468	pro1468	complement	1360831..1361190	TATGAT	score: 4.787729142	91
>pro1472	pro1472	complement	1362868..1363053	TAATCT	score: 4.565336720	34
>rhaT	pro1477	complement	1364916..1365590	TACTTT	score: 3.328297523	37
>rhaT	pro1477	complement	1364916..1365590	TAATAT	score: 4.345371032	44
>rhaT	pro1477	complement	1364916..1365590	TATTTT	score: 3.830797859	56
>rhaT	pro1477	complement	1364916..1365590	TATATT	score: 3.968301383	58
>rhaT	pro1477	complement	1364916..1365590	CATTAT	score: 3.231912987	61
>rhaT	pro1477	complement	1364916..1365590	TATAAT	score: 4.482874556	73
>pro1478	pro1478	complement	1365865..1366206	TAATGT	score: 4.565336720	44
>pro1479	pro1479	complement	1366361..1366561	TAATTT	score: 3.830797859	34
>pro1479	pro1479	complement	1366361..1366561	TAGATT	score: 3.050763548	67
>abrB	pro1480	complement	1366724..1367245	CAGAAT	score: 2.451878675	69
>pro1482	pro1482	complement	1368037..1368201	GAAGGT	score: 2.572308690	44
>pro1482	pro1482	complement	1368037..1368201	TAGTCT	score: 3.647798885	60
>pro1482	pro1482	complement	1368037..1368201	TAGGAT	score: 3.870191306	78
>pro1482	pro1482	complement	1368037..1368201	CAAATT	score: 2.854843338	88
>pro1483	pro1483	complement	1368430..1368624	TATTTT	score: 3.830797859	30
>pro1483	pro1483	complement	1368430..1368624	TAAGTT	score: 4.273155969	35
>pro1484	pro1484	complement	1368694..1368873	CAAATT	score: 2.854843338	41
>pro1484	pro1484	complement	1368694..1368873	TAAATT	score: 3.968301383	69
>pro1487	pro1487	complement	1369651..1370079	CAATAT	score: 3.231912987	41
>pro1487	pro1487	complement	1369651..1370079	TATTAT	score: 4.345371032	69
>pro1487	pro1487	complement	1369651..1370079	CATTTT	score: 2.717339814	78
>pro1490	pro1490	complement	1371586..1371729	TAGGTT	score: 3.355618133	67
>pro1490	pro1490	complement	1371586..1371729	TATAGT	score: 4.702840244	72
>pro1491	pro1491	complement	1371971..1372252	TAATTT	score: 3.830797859	31
>pro1491	pro1491	complement	1371971..1372252	CATAAT	score: 3.369416510	33

>pro1492	pro1492	complement	1372352..1372528	TATGGT	score: 5.007694830	47
>pro1494	pro1494	complement	1373904..1374194	TAAAAT	score: 4.482874556	63
>pro1494	pro1494	complement	1373904..1374194	CAAAAT	score: 3.369416510	72
>pro1496	pro1496	complement	1375179..1375460	CATTTT	score: 2.717339814	67
>pro1496	pro1496	complement	1375179..1375460	CATAAT	score: 3.369416510	78
>pro1499	pro1499	complement	1376001..1376264	TAAATT	score: 3.968301383	22
>pro1499	pro1499	complement	1376001..1376264	CAATCT	score: 3.451878675	74
>pro1500	pro1500	complement	1376732..1376914	TATATAT	score: 4.345371032	36
>pro1500	pro1500	complement	1376732..1376914	TAATGT	score: 4.565336720	65
>pro1500	pro1500	complement	1376732..1376914	CAAATT	score: 2.854843338	70
>znuB	pro1501	complement	1377714..1378505	CAAGAT	score: 3.674271096	44
>znuB	pro1501	complement	1377714..1378505	TAATTT	score: 3.830797859	72
>znuC	pro1503	complement	1378977..1379678	CAATCT	score: 3.451878675	29
>znuC	pro1503	complement	1378977..1379678	TATAAT	score: 4.482874556	47
>znuC	pro1503	complement	1378977..1379678	TACTAT	score: 3.842870696	50
>znuC	pro1503	complement	1378977..1379678	TATACT	score: 4.702840244	52
>znuC	pro1503	complement	1378977..1379678	TATTTT	score: 3.830797859	59
>znuC	pro1503	complement	1378977..1379678	CAAATT	score: 2.854843338	70
>znuC	pro1503	complement	1378977..1379678	TATGCT	score: 5.007694830	77
>znuC	pro1503	complement	1378977..1379678	CATTAT	score: 3.231912987	80
>pro1510	pro1510	complement	1385987..1386139	TAATGT	score: 4.565336720	31
>pro1510	pro1510	complement	1385987..1386139	TATAAT	score: 4.482874556	33
>pro1510	pro1510	complement	1385987..1386139	TATTGT	score: 4.565336720	50
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>pro1511	pro1511	complement	1386430..1386912	TAGTCT	score: 3.647798885	24
>pro1511	pro1511	complement	1386430..1386912	TATTTT	score: 3.830797859	44
>pro1511	pro1511	complement	1386430..1386912	TATATT	score: 3.968301383	46
>pro1511	pro1511	complement	1386430..1386912	TAAGTT	score: 4.273155969	69
>pro1520	pro1520	complement	1389491..1389721	TATATT	score: 3.968301383	34
>pro1520	pro1520	complement	1389491..1389721	TATTTT	score: 3.830797859	47
>pro1520	pro1520	complement	1389491..1389721	CAATAT	score: 3.231912987	50
>pro1520	pro1520	complement	1389491..1389721	TAGTCT	score: 3.647798885	85
>kch	pro1527	complement	1396295..1397062	CAATTT	score: 2.717339814	60
>kch	pro1527	complement	1396295..1397062	GATGGT	score: 2.572308690	67
>kch	pro1527	complement	1396295..1397062	TAGATT	score: 3.050763548	88
>pro1530	pro1530	complement	1398618..1398800	GATGAT	score: 2.352343001	23
>pro1530	pro1530	complement	1398618..1398800	TACGAT	score: 4.285228806	26
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>pro1530	pro1530	complement	1398618..1398800	CAAATT	score: 2.854843338	63
>pro1530	pro1530	complement	1398618..1398800	CACGAT	score: 3.171770760	83
>pro1534	pro1534	complement	1401141..1401356	CACTAT	score: 2.729412650	26
>pro1534	pro1534	complement	1401141..1401356	TATTGT	score: 4.565336720	34
>pro1534	pro1534	complement	1401141..1401356	TATATT	score: 3.968301383	36
>pro1534	pro1534	complement	1401141..1401356	GAAGCT	score: 2.572308690	76
>pro1535	pro1535	complement	1401550..1401681	CACAGT	score: 3.086881863	29
>pro1535	pro1535	complement	1401550..1401681	TATAAT	score: 4.482874556	70
>pro1535	pro1535	complement	1401550..1401681	TATTTT	score: 3.830797859	81
>pro1535	pro1535	complement	1401550..1401681	GATGAT	score: 2.352343001	86
>pro1536	pro1536	complement	1402126..1404240	TATGTT	score: 4.273155969	59
>pro1536	pro1536	complement	1402126..1404240	TAATCT	score: 4.565336720	72
>por	pro1537	complement	1404505..1405452	TATTAT	score: 4.345371032	26
>por	pro1537	complement	1404505..1405452	TAAAGT	score: 4.702840244	68
>murA	pro1539	complement	1407516..1408799	TAGAAT	score: 3.565336720	39
>pro1541	pro1541	complement	1409143..1409571	TATTAT	score: 4.345371032	36
>pro1546	pro1546	complement	1413396..1413668	TAGTAT	score: 3.427833197	23
>pro1546	pro1546	complement	1413396..1413668	GATGCT	score: 2.572308690	78

>pro1548	pro1548	complement	1414690..1415310	TAGGTT	score: 3.355618133	27
>pro1548	pro1548	complement	1414690..1415310	TATATT	score: 3.968301383	40
>pro1548	pro1548	complement	1414690..1415310	TAGTTT	score: 2.913260024	49
>pro1548	pro1548	complement	1414690..1415310	TAAATT	score: 3.968301383	72
>pro1548	pro1548	complement	1414690..1415310	CAAGAT	score: 3.674271096	89
>pro1553	pro1553	complement	1417723..1417887	CAATTT	score: 2.717339814	41
>pro1553	pro1553	complement	1417723..1417887	CACTAT	score: 2.729412650	50
>pro1553	pro1553	complement	1417723..1417887	TACTTT	score: 3.328297523	64
>pro1553	pro1553	complement	1417723..1417887	CAGTCT	score: 2.534340839	73
>pro1553	pro1553	complement	1417723..1417887	TACAGT	score: 4.200339908	75
>pro1556	pro1556	complement	1419437..1419631	CAGGAT	score: 2.756733261	59
>pro1556	pro1556	complement	1419437..1419631	GATGAT	score: 2.352343001	65
>pro1562	pro1562	complement	1423583..1424221	TATGAT	score: 4.787729142	25
>pro1562	pro1562	complement	1423583..1424221	TAATTT	score: 3.830797859	55
>pro1562	pro1562	complement	1423583..1424221	TATAAT	score: 4.482874556	57
>pro1562	pro1562	complement	1423583..1424221	TAAGCT	score: 5.007694830	72
>pro1564	pro1564	complement	1425901..1426029	TATTCT	score: 4.565336720	25
>pro1564	pro1564	complement	1425901..1426029	TATTCT	score: 4.565336720	33
>pro1564	pro1564	complement	1425901..1426029	TACATT	score: 3.465801047	48
>hli3	pro1566	complement	1426348..1426440	TATTAT	score: 4.345371032	26
>hli3	pro1566	complement	1426348..1426440	TATATT	score: 3.968301383	28
>hli3	pro1566	complement	1426348..1426440	TAGTAT	score: 3.427833197	31
>hli3	pro1566	complement	1426348..1426440	TACACT	score: 4.200339908	46
>pro1572	pro1572	complement	1431811..1432005	CAATTT	score: 2.717339814	38
>pro1572	pro1572	complement	1431811..1432005	CAATGT	score: 3.451878675	46
>pro1572	pro1572	complement	1431811..1432005	TACAAT	score: 3.980374220	54
>pro1572	pro1572	complement	1431811..1432005	TATTTT	score: 3.830797859	61
>crp	pro1574	complement	1432575..1433198	TATTAT	score: 4.345371032	22
>crp	pro1574	complement	1432575..1433198	TATATT	score: 3.968301383	24
>crp	pro1574	complement	1432575..1433198	GATGAT	score: 2.352343001	29
>crp	pro1574	complement	1432575..1433198	TATGAT	score: 4.787729142	32
>crp	pro1574	complement	1432575..1433198	TATTAT	score: 4.345371032	41
>crp	pro1574	complement	1432575..1433198	CATTCT	score: 3.451878675	57
>crp	pro1574	complement	1432575..1433198	TACATT	score: 3.465801047	59
>crp	pro1574	complement	1432575..1433198	CATGCT	score: 3.894236785	87
>gapA	pro1577	complement	1435895..1436920	TACTAT	score: 3.842870696	26
>gapA	pro1577	complement	1435895..1436920	TATACT	score: 4.702840244	28
>gapA	pro1577	complement	1435895..1436920	TAATTT	score: 3.830797859	88
>folE	pro1579	complement	1437601..1438347	TAGGGT	score: 4.090156995	52
>folE	pro1579	complement	1437601..1438347	TAATGT	score: 4.565336720	60
>folE	pro1579	complement	1437601..1438347	CAAAAT	score: 3.369416510	73
>folE	pro1579	complement	1437601..1438347	TAATTT	score: 3.830797859	85
>pro1582	pro1582	complement	1439395..1439667	TAATTT	score: 3.830797859	61
>rpoZ	pro1584	complement	1440339..1440566	TAGAGT	score: 3.785302409	22
>rpoZ	pro1584	complement	1440339..1440566	TATTTT	score: 3.830797859	75
>rpoZ	pro1584	complement	1440339..1440566	CATGGT	score: 3.894236785	80
>groS	pro1590	complement	1447105..1447416	TAAGGT	score: 5.007694830	62
>groS	pro1590	complement	1447105..1447416	TATGTT	score: 4.273155969	76
>ycf65	pro1593	complement	1449659..1450039	CAAATT	score: 2.854843338	44
>pepP	pro1595	complement	1450999..1452318	TATGTT	score: 4.273155969	44
>pepP	pro1595	complement	1450999..1452318	CACTAT	score: 2.729412650	47
>pepP	pro1595	complement	1450999..1452318	TATTTT	score: 3.830797859	54
>atpF	pro1607	complement	1463171..1463632	CAATTT	score: 2.717339814	62
>atpF	pro1607	complement	1463171..1463632	CACAAT	score: 2.866916174	64
>atpE	pro1608	complement	1463765..1464013	TAAACT	score: 4.702840244	54
>atpB	pro1609	complement	1464186..1464911	CAATGT	score: 3.451878675	28

>atpB	pro1609	complement	1464186..1464911	CACAAT	score: 2.866916174	30
>pro1610	pro1610	complement	1464995..1465474	TAGATT	score: 3.050763548	27
>pro1610	pro1610	complement	1464995..1465474	CATGGT	score: 3.894236785	32
>pro1610	pro1610	complement	1464995..1465474	CAATGT	score: 3.451878675	81
>pro1614	pro1614	complement	1469169..1469576	TATTTT	score: 3.830797859	24
>pro1617	pro1617	complement	1470367..1471179	TAAGTT	score: 4.273155969	41
>pro1617	pro1617	complement	1470367..1471179	CAAAAT	score: 3.369416510	50
>pro1617	pro1617	complement	1470367..1471179	TAGATT	score: 3.050763548	59
>pro1621	pro1621	complement	1474361..1477138	CATATT	score: 2.854843338	64
>cbpA	pro1628	complement	1482278..1482820	TAGAAT	score: 3.565336720	48
>pro1634	pro1634	complement	1485933..1486742	TATGTT	score: 4.273155969	57
>rpoC	pro1639	complement	1494174..1496078	CATTTT	score: 2.717339814	22
>rpoB	pro1640	complement	1496129..1499419	CAAGAT	score: 3.674271096	33
>rpoB	pro1640	complement	1496129..1499419	CAGAAT	score: 2.451878675	75
>tatD	pro1641	complement	1499696..1500484	CAATTT	score: 2.717339814	24
>rpsT	pro1642	complement	1500568..1500867	TAGAAT	score: 3.565336720	31
>rpsT	pro1642	complement	1500568..1500867	TAGGCT	score: 4.090156995	36
>rpsT	pro1642	complement	1500568..1500867	TAGTTT	score: 2.913260024	44
>rpsT	pro1642	complement	1500568..1500867	TATTTT	score: 3.830797859	57
>rpsT	pro1642	complement	1500568..1500867	CAAGAT	score: 3.674271096	62
>degQ	pro1645	complement	1503055..1504170	TAAAAT	score: 4.482874556	28
>degQ	pro1645	complement	1503055..1504170	TAGATT	score: 3.050763548	74
>pro1650	pro1650	complement	1510153..1510389	CAAAAT	score: 3.369416510	91
>pro1651	pro1651	complement	1511302..1511661	TATATT	score: 3.968301383	31
>pro1651	pro1651	complement	1511302..1511661	TAATAT	score: 4.345371032	36
>pro1651	pro1651	complement	1511302..1511661	TATTCT	score: 4.565336720	42
>pro1651	pro1651	complement	1511302..1511661	TATTTT	score: 3.830797859	50
>pro1651	pro1651	complement	1511302..1511661	TATTTT	score: 3.830797859	59
>pro1654	pro1654	complement	1514341..1514652	TACATT	score: 3.465801047	23
>pro1655	pro1655	complement	1514714..1515940	CAATTT	score: 2.717339814	58
>pro1662	pro1662	complement	1523740..1524402	TAGTAT	score: 3.427833197	23
>pro1662	pro1662	complement	1523740..1524402	CAAGAT	score: 3.674271096	34
>rpsJ	pro1663	complement	1524466..1524786	TATTTT	score: 3.830797859	38
>rpsJ	pro1663	complement	1524466..1524786	TAGTCT	score: 3.647798885	71
>rpsJ	pro1663	complement	1524466..1524786	TAAATT	score: 3.968301383	91
>fusA	pro1665	complement	1526167..1528242	TAGAGT	score: 3.785302409	38
>fusA	pro1665	complement	1526167..1528242	TACTTT	score: 3.328297523	64
>rpsL	pro1667	complement	1528848..1529222	GAAGAT	score: 2.352343001	40
>rpsL	pro1667	complement	1528848..1529222	TAGAAT	score: 3.565336720	47
>cobJ	pro1671	complement	1535300..1537063	CAGAGT	score: 2.671844363	34
>cobJ	pro1671	complement	1535300..1537063	CAAATT	score: 2.854843338	82
>pro1674	pro1674	complement	1542127..1543041	TATTTT	score: 3.830797859	30
>pro1674	pro1674	complement	1542127..1543041	CAAGCT	score: 3.894236785	35
>pro1674	pro1674	complement	1542127..1543041	TATTAT	score: 4.345371032	82
>pro1674	pro1674	complement	1542127..1543041	TATTAT	score: 4.345371032	85
>pro1674	pro1674	complement	1542127..1543041	TAATAT	score: 4.345371032	88
>pro1677	pro1677	complement	1544762..1545229	TAGAGT	score: 3.785302409	89
>alr	pro1681	complement	1546581..1547741	CATACT	score: 3.589382199	26
>alr	pro1681	complement	1546581..1547741	TAATTT	score: 3.830797859	40
>alr	pro1681	complement	1546581..1547741	CATTCT	score: 3.451878675	56
>alr	pro1681	complement	1546581..1547741	TAAGAT	score: 4.787729142	85
>rplM	pro1686	complement	1550185..1550637	TACTCT	score: 4.062836384	56
>rpsK	pro1690	complement	1553076..1553468	GAAGGT	score: 2.572308690	36
>rpsM	pro1691	complement	1553538..1553903	CAGAGT	score: 2.671844363	31
>rpsM	pro1691	complement	1553538..1553903	CAATCT	score: 3.451878675	49
>rpsM	pro1691	complement	1553538..1553903	TACTTT	score: 3.328297523	61

>rpsM	pro1691	complement	1553538..1553903	TAAGGT	score: 5.007694830	81
>secY	pro1694	complement	1554763..1556082	CATTTT	score: 2.717339814	32
>secY	pro1694	complement	1554763..1556082	TACATT	score: 3.465801047	34
>rplC	pro1712	complement	1564246..1564905	TAAGTT	score: 4.273155969	41
>rplC	pro1712	complement	1564246..1564905	CAATAT	score: 3.231912987	46
>rplC	pro1712	complement	1564246..1564905	CAGGGT	score: 2.976698949	71
>pro1717	pro1717	complement	1569088..1569339	TAGAAT	score: 3.565336720	22
>dinG	pro1718	complement	1569396..1570826	TACTAT	score: 3.842870696	36
>dinG	pro1718	complement	1569396..1570826	TAATCT	score: 4.565336720	76
>pro1722	pro1722	complement	1574201..1574566	TACACT	score: 4.200339908	32
>pro1722	pro1722	complement	1574201..1574566	CAATGT	score: 3.451878675	61
>pro1722	pro1722	complement	1574201..1574566	CATTAT	score: 3.231912987	75
>pro1722	pro1722	complement	1574201..1574566	CAGGGT	score: 2.976698949	85
>btuR	pro1725	complement	1576382..1577590	GAAGAT	score: 2.352343001	50
>btuR	pro1725	complement	1576382..1577590	TACTTT	score: 3.328297523	67
>btuR	pro1725	complement	1576382..1577590	CATGTT	score: 3.159697923	74
>recF	pro1728	complement	1579064..1580131	TAAGAT	score: 4.787729142	52
>recF	pro1728	complement	1579064..1580131	TAGAGT	score: 3.785302409	82
>trpE	pro1732	complement	1584958..1586475	TAGGTT	score: 3.355618133	33
>psaD	pro1733	complement	1586540..1586965	TACTTT	score: 3.328297523	35
>psaD	pro1733	complement	1586540..1586965	TAAAGT	score: 4.702840244	65
>psaD	pro1733	complement	1586540..1586965	GAAGGT	score: 2.572308690	79
>mrp	pro1736	complement	1589731..1590810	TAGGAT	score: 3.870191306	22
>mrp	pro1736	complement	1589731..1590810	TATTTT	score: 3.830797859	67
>mrp	pro1736	complement	1589731..1590810	CAATTT	score: 2.717339814	73
>pro1739	pro1739	complement	1592704..1593258	TAAAGT	score: 4.702840244	39
>pro1739	pro1739	complement	1592704..1593258	TATTTT	score: 3.830797859	77
>pro1742	pro1742	complement	1594423..1595700	TAAAAT	score: 4.482874556	82
>pro1744	pro1744	complement	1596781..1597401	GAAGCT	score: 2.572308690	30
>pro1744	pro1744	complement	1596781..1597401	GAAGAT	score: 2.352343001	43
>pro1744	pro1744	complement	1596781..1597401	GATGAT	score: 2.352343001	81
>pro1744	pro1744	complement	1596781..1597401	GATGAT	score: 2.352343001	84
>purM	pro1745	complement	1597573..1598610	CACATT	score: 2.352343001	62
>purM	pro1745	complement	1597573..1598610	TAGTAT	score: 3.427833197	74
>wzb	pro1747	complement	1600300..1600770	TATTGT	score: 4.565336720	34
>wzb	pro1747	complement	1600300..1600770	TATTTT	score: 3.830797859	55
>pebA	pro1749	complement	1601635..1602360	TATTTT	score: 3.830797859	24
>pebA	pro1749	complement	1601635..1602360	TATGTT	score: 4.273155969	43
>pebA	pro1749	complement	1601635..1602360	TATTAT	score: 4.345371032	46
>pebA	pro1749	complement	1601635..1602360	TAATTT	score: 3.830797859	51
>pebA	pro1749	complement	1601635..1602360	TAAATT	score: 3.968301383	56
>hol	pro1750	complement	1602445..1603158	TACTCT	score: 4.062836384	29
>hol	pro1750	complement	1602445..1603158	TAGAGT	score: 3.785302409	40
>pro1751	pro1751	complement	1603248..1603673	CATTGT	score: 3.451878675	25
>pro1751	pro1751	complement	1603248..1603673	CACATT	score: 2.352343001	73
>l1dD	pro1754	complement	1606671..1607843	TAGAAT	score: 3.565336720	26
>l1dD	pro1754	complement	1606671..1607843	CACGTT	score: 2.657197587	38
>l1dD	pro1754	complement	1606671..1607843	CAAATT	score: 2.854843338	76
>l1dD	pro1754	complement	1606671..1607843	TACACT	score: 4.200339908	89
>d1d	pro1755	complement	1607961..1609661	CATGAT	score: 3.674271096	23
>d1d	pro1755	complement	1607961..1609661	TATTTT	score: 3.830797859	32
>d1d	pro1755	complement	1607961..1609661	GATGAT	score: 2.352343001	38
>d1d	pro1755	complement	1607961..1609661	TATTTT	score: 3.830797859	79
>d1d	pro1755	complement	1607961..1609661	TAGATT	score: 3.050763548	88
>mhpC	pro1757	complement	1610658..1611563	TATTTT	score: 3.830797859	26
>mhpC	pro1757	complement	1610658..1611563	TAGTAT	score: 3.427833197	29

>mhpC	pro1757	complement	1610658..1611563	CAAATT	score: 2.854843338	38
>kefB	pro1758	complement	1611686..1613059	TAAGTT	score: 4.273155969	27
>kefB	pro1758	complement	1611686..1613059	TAATTT	score: 3.830797859	32
>kefB	pro1758	complement	1611686..1613059	TATGGT	score: 5.007694830	64
>kefB	pro1758	complement	1611686..1613059	TACAGT	score: 4.200339908	77
>pro1760	pro1760	complement	1615754..1616212	CATGAT	score: 3.674271096	24
>pro1760	pro1760	complement	1615754..1616212	CAAGAT	score: 3.674271096	32
>pro1761	pro1761	complement	1616283..1616579	CACTCT	score: 2.949378339	32
>pro1761	pro1761	complement	1616283..1616579	CACACT	score: 3.086881863	34
>arg3-tRNA	RNA_23	complement	1616670..1616743	CATAAT	score: 3.369416510	26
>pro1763	pro1763	complement	1617963..1618148	TAAAAT	score: 4.482874556	22
>pro1763	pro1763	complement	1617963..1618148	TAGAAT	score: 3.565336720	28
>pro1763	pro1763	complement	1617963..1618148	TATTTT	score: 3.830797859	37
>pro1763	pro1763	complement	1617963..1618148	CATGAT	score: 3.674271096	44
>pro1763	pro1763	complement	1617963..1618148	TAATCT	score: 4.565336720	57
>glmS	pro1766	complement	1620235..1622139	TAGTTT	score: 2.913260024	45
>psaC	pro1767	complement	1622219..1622464	TAAAGT	score: 4.702840244	31
>psaC	pro1767	complement	1622219..1622464	CAAATT	score: 2.854843338	40
>psaC	pro1767	complement	1622219..1622464	TATGTT	score: 4.273155969	50
>psaC	pro1767	complement	1622219..1622464	TAATCT	score: 4.565336720	59
>ruvB	pro1775	complement	1629988..1631058	TACTCT	score: 4.062836384	34
>ruvB	pro1775	complement	1629988..1631058	CATTTT	score: 2.717339814	47
>ruvB	pro1775	complement	1629988..1631058	TAGTTT	score: 2.913260024	80
>lysU	pro1779	complement	1632353..1633861	CAAGGT	score: 3.894236785	23
>lysU	pro1779	complement	1632353..1633861	TAGGCT	score: 4.090156995	29
>pro1780	pro1780	complement	1633934..1634743	TATAGT	score: 4.702840244	25
>pro1780	pro1780	complement	1633934..1634743	TAATTT	score: 3.830797859	75
>mreB	pro1783	complement	1636228..1637280	TAAGTT	score: 4.273155969	23
>mreB	pro1783	complement	1636228..1637280	TAGTGT	score: 3.647798885	28
>mreB	pro1783	complement	1636228..1637280	TAGTTT	score: 2.913260024	37
>mreB	pro1783	complement	1636228..1637280	TATGTT	score: 4.273155969	52
>mreB	pro1783	complement	1636228..1637280	CATGTT	score: 3.159697923	74
>sAM1	pro1786	complement	1638488..1639918	CACGTT	score: 2.657197587	32
>sAM1	pro1786	complement	1638488..1639918	TAGAGT	score: 3.785302409	75
>mutY	pro1789	complement	1641463..1642665	CAAAAT	score: 3.369416510	69
>rpoD	pro1791	complement	1643541..1644527	TAGAGT	score: 3.785302409	23
>rpoD	pro1791	complement	1643541..1644527	TATTCT	score: 4.565336720	42
>rpoD	pro1791	complement	1643541..1644527	TACAGT	score: 4.200339908	57
>rpoD	pro1791	complement	1643541..1644527	TATTTT	score: 3.830797859	72
>gyrB	pro1796	complement	1647189..1649165	TAAATT	score: 3.968301383	36
>gyrB	pro1796	complement	1647189..1649165	TAAATT	score: 3.968301383	70
>secA	pro1801	complement	1652820..1655660	TAGTCT	score: 3.647798885	27
>secA	pro1801	complement	1652820..1655660	CAAGGT	score: 3.894236785	44
>secA	pro1801	complement	1652820..1655660	CATATT	score: 2.854843338	81
>gly3-tRNA	RNA_26	complement	1656288..1656359	CATGCT	score: 3.894236785	30
>psbZ	pro1804	complement	1656981..1657178	CATTGT	score: 3.451878675	78
>cobH	pro1806	complement	1660088..1660750	TAGATT	score: 3.050763548	51
>cobH	pro1806	complement	1660088..1660750	CAAAAT	score: 3.369416510	91
>pro1810	pro1810	complement	1665781..1666563	TAATAT	score: 4.345371032	28
>pro1810	pro1810	complement	1665781..1666563	CACTAT	score: 2.729412650	63
>pro1810	pro1810	complement	1665781..1666563	CATATT	score: 2.854843338	81
>pro1812	pro1812	complement	1667692..1669635	CAAGCT	score: 3.894236785	22
>asd	pro1814	complement	1670623..1671654	TACAGT	score: 4.200339908	37
>asd	pro1814	complement	1670623..1671654	CAAATT	score: 2.854843338	45
>asd	pro1814	complement	1670623..1671654	TAGTTT	score: 2.913260024	63
>spoIID	pro1820	complement	1678583..1680121	CAAAAT	score: 3.369416510	48

>spoIID	pro1820	complement	1678583..1680121	TACTCT	score: 4.062836384	75
>spoIID	pro1820	complement	1678583..1680121	CAATCT	score: 3.451878675	83
>spoIID	pro1820	complement	1678583..1680121	TACAAT	score: 3.980374220	85
>pro1828	pro1828	complement	1685012..1685314	CAAAAT	score: 3.369416510	27
>pro1828	pro1828	complement	1685012..1685314	TAAATT	score: 3.968301383	45
>pro1832	pro1832	complement	1690045..1690794	TATAGT	score: 4.702840244	39
>pro1832	pro1832	complement	1690045..1690794	TATTAT	score: 4.345371032	42
>pro1832	pro1832	complement	1690045..1690794	CACATT	score: 2.352343001	67
>pro1832	pro1832	complement	1690045..1690794	CACGCT	score: 3.391736448	79
>pro1838	pro1838	complement	1696436..1696951	CATTTT	score: 2.717339814	37
>pro1838	pro1838	complement	1696436..1696951	CATGAT	score: 3.674271096	76
>pro1839	pro1839	complement	1697056..1697604	CAGAAT	score: 2.451878675	42
>pro1839	pro1839	complement	1697056..1697604	TATGTT	score: 4.273155969	53
>pro1839	pro1839	complement	1697056..1697604	CACTAT	score: 2.729412650	56
>pro1839	pro1839	complement	1697056..1697604	CACAGT	score: 3.086881863	62
>valS	pro1844	complement	1701033..1703834	TAGTGT	score: 3.647798885	33
>pro1845	pro1845	complement	1703899..1704357	TAATTT	score: 3.830797859	23
>pro1845	pro1845	complement	1703899..1704357	TAGTAT	score: 3.427833197	55
>pro1845	pro1845	complement	1703899..1704357	CATGAT	score: 3.674271096	61
>val2-tRNA RNA_25	pro1845	complement	1704853..1704924	TAATTT	score: 3.830797859	38
>val2-tRNA RNA_25	pro1845	complement	1704853..1704924	TATTTT	score: 3.830797859	67
>val2-tRNA RNA_25	pro1845	complement	1704853..1704924	GAAGAT	score: 2.352343001	89
>pro1850	pro1850	complement	1707913..1708143	TAATGT	score: 4.565336720	25
>pro1850	pro1850	complement	1707913..1708143	CATATT	score: 2.854843338	64
>pro1850	pro1850	complement	1707913..1708143	CACAAT	score: 2.866916174	71
>pro1850	pro1850	complement	1707913..1708143	CAATCT	score: 3.451878675	79
>pro1850	pro1850	complement	1707913..1708143	TACAAT	score: 3.980374220	81
>cysG	pro1858	complement	1716658..1717443	TAGTTT	score: 2.913260024	65
>wecD	pro1860	complement	1718532..1719023	TAGTTT	score: 2.913260024	23
>wecD	pro1860	complement	1718532..1719023	CATAAT	score: 3.369416510	28
>wecD	pro1860	complement	1718532..1719023	TACTTT	score: 3.328297523	58
>wecD	pro1860	complement	1718532..1719023	CAGAGT	score: 2.671844363	67
>wecD	pro1860	complement	1718532..1719023	TAAAGT	score: 4.702840244	88
>aroG	pro1865	complement	1724418..1725491	TAGTTT	score: 2.913260024	30
>aroG	pro1865	complement	1724418..1725491	TAATTT	score: 3.830797859	37
>aroG	pro1865	complement	1724418..1725491	TAATGT	score: 4.565336720	46
>aroG	pro1865	complement	1724418..1725491	CAAGTT	score: 3.159697923	54
>aroG	pro1865	complement	1724418..1725491	TAATCT	score: 4.565336720	89
>aroG	pro1865	complement	1724418..1725491	TATAAT	score: 4.482874556	91
>rfaL	pro1869	complement	1731226..1732521	CAGGAT	score: 2.756733261	34
>rfaL	pro1869	complement	1731226..1732521	TACTCT	score: 4.062836384	68
>dnaK	pro1871	complement	1733789..1735690	TACACT	score: 4.200339908	51
>dnaK	pro1871	complement	1733789..1735690	TAAGTT	score: 4.273155969	88
>pro1876	pro1876	complement	1739121..1739315	CATAAT	score: 3.369416510	24
>pro1876	pro1876	complement	1739121..1739315	TACTTT	score: 3.328297523	44
>pro1876	pro1876	complement	1739121..1739315	CAAATT	score: 2.854843338	51
>rfaG	pro1880	complement	1741024..1742418	TAAATT	score: 3.968301383	29
>rfaG	pro1880	complement	1741024..1742418	CAAAAT	score: 3.369416510	34
>rfaG	pro1880	complement	1741024..1742418	TAGATT	score: 3.050763548	49
>rfaG	pro1880	complement	1741024..1742418	TATGCT	score: 5.007694830	60
>rfaG	pro1880	complement	1741024..1742418	TAGAAT	score: 3.565336720	69
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>recN	pro1882	complement	1745611..1747299	GATGGT	score: 2.572308690	64
>recN	pro1882	complement	1745611..1747299	CATTTT	score: 2.717339814	72
>recN	pro1882	complement	1745611..1747299	CAAGTT	score: 3.159697923	85