

TBLASTN 2.10.1+

Query: lcl|KP202363.1_prot_AJF96734.1_1 [gene=CENH3] [protein=CENH3] [protein_id=A

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

18 hits found

lcl KP202. Chr12	52.174	115	51	2	62	176	1.3E+07
lcl KP202. Chr12	47.826	115	56	2	62	176	1.3E+07
lcl KP202. Chr1	56.566	99	41	1	77	175	3.8E+07
lcl KP202. Chr6	56	100	42	1	77	176	3040837
lcl KP202. Chr6	56	100	42	1	77	176	3056279
lcl KP202. Chr6	56	100	42	1	77	176	3055514
lcl KP202. Chr6	57	100	41	1	77	176	1646006
lcl KP202. Chr6	56	100	42	1	77	176	3046867
lcl KP202. Chr11	56	100	42	1	77	176	2626112
lcl KP202. Chr5	56	100	42	1	77	176	2.1E+07
lcl KP202. Chr5	60	40	16	0	73	112	2.4E+07
lcl KP202. Chr4	56	100	42	1	77	176	2.1E+07
lcl KP202. Chr4	35.028	177	49	4	60	176	2.2E+07
lcl KP202. Chr2	38.462	117	42	1	90	176	1.5E+07
lcl KP202. Chr2	60	35	14	0	142	176	1.5E+07
lcl KP202. Chr3	62.857	35	13	0	142	176	1.6E+07
lcl KP202. Chr3	55.556	27	12	0	91	117	1.6E+07
lcl KP202. Chr3	68.75	16	5	0	77	92	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KP177475.1_prot_AJD07128.1_1 [gene=CenH3] [protein=CenH3] [protein_id=A

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

lcl KP177. Chr1	60	95	37	1	54	148	3.8E+07
lcl KP177. Chr1	32.53	83	48	2	75	149	2.6E+07
lcl KP177. Chr6	60	95	37	1	54	148	3056288
lcl KP177. Chr6	60	95	37	1	54	148	3040828
lcl KP177. Chr6	60	95	37	1	54	148	3055505
lcl KP177. Chr6	60	95	37	1	54	148	3046858
lcl KP177. Chr6	58.947	95	38	1	54	148	1645997
lcl KP177. Chr5	60	95	37	1	54	148	2.1E+07
lcl KP177. Chr5	66.667	33	11	0	54	86	2.4E+07
lcl KP177. Chr5	46.429	28	15	0	85	112	2.4E+07
lcl KP177. Chr5	57.143	28	12	0	110	137	2.4E+07
lcl KP177. Chr11	60	95	37	1	54	148	2626103
lcl KP177. Chr4	60	95	37	1	54	148	2.1E+07
lcl KP177. Chr4	41.739	115	36	1	65	148	2.2E+07
lcl KP177. Chr12	55.102	98	37	2	54	148	1.3E+07
lcl KP177. Chr12	50.526	95	46	1	54	148	1.3E+07
lcl KP177. Chr3	66	50	17	0	99	148	1.6E+07
lcl KP177. Chr3	48.571	35	18	0	65	99	1.6E+07

lcl KP177.Chr2	39.655	116	39	1	64	148	1.5E+07
lcl KP177.Chr2	62	50	19	0	99	148	1.5E+07
lcl KP177.Chr2	51.724	29	14	0	65	93	1.5E+07
lcl KP177.Chr2	30.263	76	50	2	66	141	2140530

TBLASTN 2.10.1+

Query: lcl|KP177470.1_prot_AJD07123.1_1 [gene=CenH3] [protein=CenH3] [protein_id=A

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

25 hits found

lcl KP177.Chr11	56.637	113	48	1	36	148	2626157
lcl KP177.Chr6	56.637	113	48	1	36	148	3040882
lcl KP177.Chr6	56.637	113	48	1	36	148	3055559
lcl KP177.Chr6	56.637	113	48	1	36	148	3046912
lcl KP177.Chr6	56.637	113	48	1	36	148	3056234
lcl KP177.Chr6	58.491	106	43	1	43	148	1646030
lcl KP177.Chr5	56.637	113	48	1	36	148	2.2E+07
lcl KP177.Chr5	63.158	38	14	0	49	86	2.4E+07
lcl KP177.Chr5	42.857	28	16	0	85	112	2.4E+07
lcl KP177.Chr5	57.143	28	12	0	110	137	2.4E+07
lcl KP177.Chr1	57.522	113	44	2	36	148	3.8E+07
lcl KP177.Chr4	56.637	113	48	1	36	148	2.1E+07
lcl KP177.Chr4	36.527	167	45	2	43	148	2.2E+07
lcl KP177.Chr12	52.632	114	47	2	38	148	1.3E+07
lcl KP177.Chr12	47.748	111	57	1	38	148	1.3E+07
lcl KP177.Chr3	68	50	16	0	99	148	1.6E+07
lcl KP177.Chr3	45.714	35	19	0	65	99	1.6E+07
lcl KP177.Chr3	50	24	12	0	43	66	1.6E+07
lcl KP177.Chr3	46.667	30	16	0	74	103	3.6E+07
lcl KP177.Chr2	64	50	18	0	99	148	1.5E+07
lcl KP177.Chr2	51.724	29	14	0	65	93	1.5E+07
lcl KP177.Chr2	40.517	116	38	2	64	148	1.5E+07
lcl KP177.Chr2	63.158	19	7	0	50	68	2E+07
lcl KP177.Chr2	41.304	46	17	2	105	148	2E+07
lcl KP177.Chr7	45.833	24	13	0	109	132	2.6E+07

TBLASTN 2.10.1+

Query: lcl|KP177464.1_prot_AJD07117.1_1 [gene=CenH3] [protein=CenH3] [protein_id=A

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

24 hits found

lcl KP177.Chr1	60.606	99	38	1	50	148	3.8E+07
lcl KP177.Chr6	60	100	39	1	49	148	3040843
lcl KP177.Chr6	60	100	39	1	49	148	3056273
lcl KP177.Chr6	60	100	39	1	49	148	3055520
lcl KP177.Chr6	60	100	39	1	49	148	3046873
lcl KP177.Chr6	59	100	40	1	49	148	1646012
lcl KP177.Chr11	60	100	39	1	49	148	2626118

lcl KP177.Chr5	60	100	39	1	49	148	2.1E+07
lcl KP177.Chr5	63.889	36	13	0	51	86	2.4E+07
lcl KP177.Chr5	46.429	28	15	0	85	112	2.4E+07
lcl KP177.Chr5	57.143	28	12	0	110	137	2.4E+07
lcl KP177.Chr4	60	100	39	1	49	148	2.1E+07
lcl KP177.Chr4	36.25	160	41	2	50	148	2.2E+07
lcl KP177.Chr12	56.311	103	38	2	49	148	1.3E+07
lcl KP177.Chr12	52	100	47	1	49	148	1.3E+07
lcl KP177.Chr3	68	50	16	0	99	148	1.6E+07
lcl KP177.Chr3	48.571	35	18	0	65	99	1.6E+07
lcl KP177.Chr3	50	18	9	0	49	66	1.6E+07
lcl KP177.Chr2	40.87	115	37	1	65	148	1.5E+07
lcl KP177.Chr2	64	50	18	0	99	148	1.5E+07
lcl KP177.Chr2	51.724	29	14	0	65	93	1.5E+07
lcl KP177.Chr2	66.667	18	6	0	51	68	2E+07
lcl KP177.Chr2	41.304	46	17	2	105	148	2E+07
lcl KP177.Chr7	45.833	24	13	0	109	132	2.6E+07

TBLASTN 2.10.1+

Query: lcl|KP177463.1_prot_AJD07116.1_1 [gene=CenH3] [protein=CenH3] [protein_id=A

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

26 hits found

lcl KP177.Chr11	58.407	113	46	1	36	148	2626157
lcl KP177.Chr6	58.407	113	46	1	36	148	3040882
lcl KP177.Chr6	58.407	113	46	1	36	148	3055559
lcl KP177.Chr6	58.407	113	46	1	36	148	3046912
lcl KP177.Chr6	58.407	113	46	1	36	148	3056234
lcl KP177.Chr6	59.434	106	42	1	43	148	1646030
lcl KP177.Chr5	58.407	113	46	1	36	148	2.2E+07
lcl KP177.Chr5	68.421	38	12	0	49	86	2.4E+07
lcl KP177.Chr5	42.857	28	16	0	85	112	2.4E+07
lcl KP177.Chr5	57.143	28	12	0	110	137	2.4E+07
lcl KP177.Chr4	58.407	113	46	1	36	148	2.1E+07
lcl KP177.Chr4	37.126	167	44	2	43	148	2.2E+07
lcl KP177.Chr1	58.407	113	46	1	36	148	3.8E+07
lcl KP177.Chr12	53.509	114	46	2	38	148	1.3E+07
lcl KP177.Chr12	49.55	111	55	1	38	148	1.3E+07
lcl KP177.Chr3	68	50	16	0	99	148	1.6E+07
lcl KP177.Chr3	48.571	35	18	0	65	99	1.6E+07
lcl KP177.Chr3	50	24	12	0	43	66	1.6E+07
lcl KP177.Chr2	41.379	116	37	1	64	148	1.5E+07
lcl KP177.Chr2	64	50	18	0	99	148	1.5E+07
lcl KP177.Chr2	55.172	29	13	0	65	93	1.5E+07
lcl KP177.Chr2	68.421	19	6	0	50	68	2E+07
lcl KP177.Chr2	41.304	46	17	2	105	148	2E+07
lcl KP177.Chr2	27.632	76	52	2	66	141	2140530

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lcl|KP177.Chr2      50      24      12      0      43      66 1.5E+07
lcl|KP177.Chr7     45.833     24      13      0     109     132 2.6E+07
# TBLASTN 2.10.1+
# Query: lcl|KP177462.1_prot_AJD07115.1_1 [gene=CenH3] [protein=CenH3] [protein_id=A
# Database: Nippon
# Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens
# 26 hits found
lcl|KP177.Chr11     54.867     113      50      1      36     148 2626157
lcl|KP177.Chr6      54.867     113      50      1      36     148 3055559
lcl|KP177.Chr6      54.867     113      50      1      36     148 3040882
lcl|KP177.Chr6      54.867     113      50      1      36     148 3046912
lcl|KP177.Chr6      54.867     113      50      1      36     148 3056234
lcl|KP177.Chr6      56.604     106      45      1      43     148 1646030
lcl|KP177.Chr5      54.867     113      50      1      36     148 2.2E+07
lcl|KP177.Chr5      63.158      38      14      0      49      86 2.4E+07
lcl|KP177.Chr5      42.857      28      16      0      85     112 2.4E+07
lcl|KP177.Chr5      53.571      28      13      0     110     137 2.4E+07
lcl|KP177.Chr1      55.752     113      46      2      36     148 3.8E+07
lcl|KP177.Chr4      54.867     113      50      1      36     148 2.1E+07
lcl|KP177.Chr4      35.329     167      47      2      43     148 2.2E+07
lcl|KP177.Chr12     51.351     111      53      1      38     148 1.3E+07
lcl|KP177.Chr12     46.847     111      58      1      38     148 1.3E+07
lcl|KP177.Chr3       66      50      17      0      99     148 1.6E+07
lcl|KP177.Chr3       50      24      12      0      43      66 1.6E+07
lcl|KP177.Chr3     53.846      26      12      0      65      90 1.6E+07
lcl|KP177.Chr3       50      30      15      0      74     103 3.6E+07
lcl|KP177.Chr3     43.333      30      17      0      74     103 3.6E+07
lcl|KP177.Chr2     39.655     116      39      2      64     148 1.5E+07
lcl|KP177.Chr2       62      50      19      0      99     148 1.5E+07
lcl|KP177.Chr2     51.852      27      13      0      64      90 1.5E+07
lcl|KP177.Chr2     63.158      19       7      0      50      68 2E+07
lcl|KP177.Chr2     41.304      46      17      2     105     148 2E+07
lcl|KP177.Chr10     32.692      52      35      0      54     105 9042169
# TBLASTN 2.10.1+
# Query: lcl|KP177459.1_prot_AJD07112.1_1 [gene=CenH3] [protein=CenH3] [protein_id=A
# Database: Nippon
# Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens
# 28 hits found
lcl|KP177.Chr11     55.752     113      49      1      36     148 2626157
lcl|KP177.Chr6      55.752     113      49      1      36     148 3040882
lcl|KP177.Chr6      55.752     113      49      1      36     148 3056234
lcl|KP177.Chr6      55.752     113      49      1      36     148 3055559
lcl|KP177.Chr6      55.752     113      49      1      36     148 3046912
lcl|KP177.Chr6      57.547     106      44      1      43     148 1646030
lcl|KP177.Chr5      55.752     113      49      1      36     148 2.2E+07
lcl|KP177.Chr5      60.526      38      15      0      49      86 2.4E+07

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lcl KP177.Chr5	42.857	28	16	0	85	112	2.4E+07
lcl KP177.Chr5	57.143	28	12	0	110	137	2.4E+07
lcl KP177.Chr5	37.288	59	34	2	34	92	2.8E+07
lcl KP177.Chr1	55.752	113	49	1	36	148	3.8E+07
lcl KP177.Chr4	55.752	113	49	1	36	148	2.1E+07
lcl KP177.Chr4	35.928	167	46	2	43	148	2.2E+07
lcl KP177.Chr12	53.211	109	44	2	43	148	1.3E+07
lcl KP177.Chr12	50	106	52	1	43	148	1.3E+07
lcl KP177.Chr3	68	50	16	0	99	148	1.6E+07
lcl KP177.Chr3	45.714	35	19	0	65	99	1.6E+07
lcl KP177.Chr3	45.833	24	13	0	43	66	1.6E+07
lcl KP177.Chr3	46.667	30	16	0	74	103	3.6E+07
lcl KP177.Chr2	40.517	116	38	2	64	148	1.5E+07
lcl KP177.Chr2	64	50	18	0	99	148	1.5E+07
lcl KP177.Chr2	51.724	29	14	0	65	93	1.5E+07
lcl KP177.Chr2	57.895	19	8	0	50	68	2E+07
lcl KP177.Chr2	41.304	46	17	2	105	148	2E+07
lcl KP177.Chr2	33.898	59	38	1	55	112	7812463
lcl KP177.Chr8	42.424	33	19	0	34	66	2.4E+07
lcl KP177.Chr7	45.833	24	13	0	109	132	2.6E+07

TBLASTN 2.10.1+

Query: lcl|KP177458.1_prot_AJD07111.1_1 [gene=CenH3] [protein=CenH3] [protein_id=A

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

25 hits found

lcl KP177.Chr11	54.867	113	50	1	36	148	2626157
lcl KP177.Chr6	54.867	113	50	1	36	148	3040882
lcl KP177.Chr6	54.867	113	50	1	36	148	3055559
lcl KP177.Chr6	54.867	113	50	1	36	148	3046912
lcl KP177.Chr6	54.867	113	50	1	36	148	3056234
lcl KP177.Chr6	56.604	106	45	1	43	148	1646030
lcl KP177.Chr5	54.867	113	50	1	36	148	2.2E+07
lcl KP177.Chr5	63.158	38	14	0	49	86	2.4E+07
lcl KP177.Chr5	46.429	28	15	0	85	112	2.4E+07
lcl KP177.Chr5	50	28	14	0	110	137	2.4E+07
lcl KP177.Chr1	55.752	113	46	2	36	148	3.8E+07
lcl KP177.Chr4	54.867	113	50	1	36	148	2.1E+07
lcl KP177.Chr4	35.329	167	47	2	43	148	2.2E+07
lcl KP177.Chr12	50.877	114	49	2	38	148	1.3E+07
lcl KP177.Chr12	45.946	111	59	1	38	148	1.3E+07
lcl KP177.Chr3	64	50	18	0	99	148	1.6E+07
lcl KP177.Chr3	48.571	35	18	0	65	99	1.6E+07
lcl KP177.Chr3	50	24	12	0	43	66	1.6E+07
lcl KP177.Chr2	38.793	116	40	1	64	148	1.5E+07
lcl KP177.Chr2	60	50	20	0	99	148	1.5E+07
lcl KP177.Chr2	51.724	29	14	0	65	93	1.5E+07

lcl KP177.Chr2	63.158	19	7	0	50	68	2E+07
lcl KP177.Chr2	39.13	46	18	2	105	148	2E+07
lcl KP177.Chr2	30.137	73	49	2	55	125	7812463
lcl KP177.Chr2	27.632	76	52	2	66	141	2140530

TBLASTN 2.10.1+

Query: lcl|GQ849334.1_prot_ACX30895.1_1 [gene=CenH3] [protein=CENH3] [protein_id=,

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

25 hits found

lcl GQ849.Chr6	68	100	31	1	65	164	3040837
lcl GQ849.Chr6	68	100	31	1	65	164	3055514
lcl GQ849.Chr6	68	100	31	1	65	164	3056279
lcl GQ849.Chr6	68	100	31	1	65	164	3046867
lcl GQ849.Chr6	68	100	31	1	65	164	1646006
lcl GQ849.Chr11	68	100	31	1	65	164	2626112
lcl GQ849.Chr5	68	100	31	1	65	164	2.1E+07
lcl GQ849.Chr5	95.122	41	2	0	60	100	2.4E+07
lcl GQ849.Chr5	100	16	0	0	100	115	2.4E+07
lcl GQ849.Chr5	100	32	0	0	1	32	2.4E+07
lcl GQ849.Chr5	100	22	0	0	128	149	2.4E+07
lcl GQ849.Chr5	62.069	29	4	1	138	166	2.4E+07
lcl GQ849.Chr4	68	100	31	1	65	164	2.1E+07
lcl GQ849.Chr4	40.994	161	34	2	65	164	2.2E+07
lcl GQ849.Chr1	68.367	98	30	1	65	162	3.8E+07
lcl GQ849.Chr12	61.165	103	33	2	65	164	1.3E+07
lcl GQ849.Chr12	61	100	38	1	65	164	1.3E+07
lcl GQ849.Chr2	47.458	118	31	1	78	164	1.5E+07
lcl GQ849.Chr2	72.222	36	10	0	129	164	1.5E+07
lcl GQ849.Chr2	66.667	30	10	0	78	107	1.5E+07
lcl GQ849.Chr2	77.778	18	4	0	65	82	2E+07
lcl GQ849.Chr3	72.973	37	10	0	129	165	1.6E+07
lcl GQ849.Chr3	57.143	35	15	0	79	113	1.6E+07
lcl GQ849.Chr3	68.75	16	5	0	65	80	1.6E+07
lcl GQ849.Chr7	60	20	8	0	94	113	1.2E+07

TBLASTN 2.10.1+

Query: lcl|GQ849333.1_prot_ACX30894.1_1 [gene=CenH3] [protein=CENH3] [protein_id=,

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

26 hits found

lcl GQ849.Chr6	68	100	31	1	65	164	3040837
lcl GQ849.Chr6	68	100	31	1	65	164	3055514
lcl GQ849.Chr6	68	100	31	1	65	164	3056279
lcl GQ849.Chr6	68	100	31	1	65	164	3046867
lcl GQ849.Chr6	68	100	31	1	65	164	1646006
lcl GQ849.Chr11	68	100	31	1	65	164	2626112
lcl GQ849.Chr5	68	100	31	1	65	164	2.1E+07

lcl GQ849 Chr5	93.023	43	3	0	58	100	2.4E+07
lcl GQ849 Chr5	100	16	0	0	100	115	2.4E+07
lcl GQ849 Chr5	96.875	32	1	0	1	32	2.4E+07
lcl GQ849 Chr5	100	22	0	0	128	149	2.4E+07
lcl GQ849 Chr5	62.069	29	4	1	138	166	2.4E+07
lcl GQ849 Chr4	68	100	31	1	65	164	2.1E+07
lcl GQ849 Chr4	40.994	161	34	2	65	164	2.2E+07
lcl GQ849 Chr1	68.367	98	30	1	65	162	3.8E+07
lcl GQ849 Chr12	61.165	103	33	2	65	164	1.3E+07
lcl GQ849 Chr12	61	100	38	1	65	164	1.3E+07
lcl GQ849 Chr2	46.61	118	32	1	78	164	1.5E+07
lcl GQ849 Chr2	72.222	36	10	0	129	164	1.5E+07
lcl GQ849 Chr2	63.333	30	11	0	78	107	1.5E+07
lcl GQ849 Chr2	83.333	18	3	0	65	82	2E+07
lcl GQ849 Chr2	75	16	4	0	65	80	1.5E+07
lcl GQ849 Chr3	72.973	37	10	0	129	165	1.6E+07
lcl GQ849 Chr3	54.286	35	16	0	79	113	1.6E+07
lcl GQ849 Chr3	66.667	18	6	0	65	82	1.6E+07
lcl GQ849 Chr7	60	20	8	0	94	113	1.2E+07

TBLASTN 2.10.1+

Query: lcl|GQ849332.1_prot_ACX30893.1_1 [gene=CenH3] [protein=CENH3] [protein_id=

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

26 hits found

lcl GQ849 Chr6	71	100	28	1	62	161	3040837
lcl GQ849 Chr6	71	100	28	1	62	161	3055514
lcl GQ849 Chr6	71	100	28	1	62	161	3056279
lcl GQ849 Chr6	71	100	28	1	62	161	3046867
lcl GQ849 Chr6	71	100	28	1	62	161	1646006
lcl GQ849 Chr11	71	100	28	1	62	161	2626112
lcl GQ849 Chr5	71	100	28	1	62	161	2.1E+07
lcl GQ849 Chr5	95.349	43	2	0	55	97	2.4E+07
lcl GQ849 Chr5	100	16	0	0	97	112	2.4E+07
lcl GQ849 Chr5	78.788	33	6	1	1	33	2.4E+07
lcl GQ849 Chr5	95.455	22	1	0	125	146	2.4E+07
lcl GQ849 Chr5	58.621	29	5	1	135	163	2.4E+07
lcl GQ849 Chr4	71	100	28	1	62	161	2.1E+07
lcl GQ849 Chr4	42.857	161	31	2	62	161	2.2E+07
lcl GQ849 Chr1	71.429	98	27	1	62	159	3.8E+07
lcl GQ849 Chr12	62.963	108	31	3	62	164	1.3E+07
lcl GQ849 Chr12	62.857	105	36	2	62	164	1.3E+07
lcl GQ849 Chr2	48.305	118	30	1	75	161	1.5E+07
lcl GQ849 Chr2	54.43	79	19	1	100	161	1.5E+07
lcl GQ849 Chr2	66.667	30	10	0	75	104	1.5E+07
lcl GQ849 Chr2	83.333	18	3	0	62	79	2E+07
lcl GQ849 Chr2	75	16	4	0	62	77	1.5E+07

lcl GQ849 Chr3	73.81	42	8	1	126	164	1.6E+07
lcl GQ849 Chr3	57.143	35	15	0	76	110	1.6E+07
lcl GQ849 Chr3	75	16	4	0	62	77	1.6E+07
lcl GQ849 Chr7	60	20	8	0	91	110	1.2E+07

TBLASTN 2.10.1+

Query: lcl|GQ849328.1_prot_ACX30889.1_1 [gene=CenH3] [protein=CENH3] [protein_id=,

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

26 hits found

lcl GQ849 Chr6	71	100	28	1	62	161	3040837
lcl GQ849 Chr6	71	100	28	1	62	161	3055514
lcl GQ849 Chr6	71	100	28	1	62	161	3056279
lcl GQ849 Chr6	71	100	28	1	62	161	3046867
lcl GQ849 Chr6	71	100	28	1	62	161	1646006
lcl GQ849 Chr11	71	100	28	1	62	161	2626112
lcl GQ849 Chr5	71	100	28	1	62	161	2.1E+07
lcl GQ849 Chr5	95.349	43	2	0	55	97	2.4E+07
lcl GQ849 Chr5	100	16	0	0	97	112	2.4E+07
lcl GQ849 Chr5	87.879	33	3	1	1	33	2.4E+07
lcl GQ849 Chr5	95.455	22	1	0	125	146	2.4E+07
lcl GQ849 Chr5	58.621	29	5	1	135	163	2.4E+07
lcl GQ849 Chr4	71	100	28	1	62	161	2.1E+07
lcl GQ849 Chr4	42.857	161	31	2	62	161	2.2E+07
lcl GQ849 Chr1	71.429	98	27	1	62	159	3.8E+07
lcl GQ849 Chr12	62.963	108	31	3	62	164	1.3E+07
lcl GQ849 Chr12	62.857	105	36	2	62	164	1.3E+07
lcl GQ849 Chr2	48.305	118	30	1	75	161	1.5E+07
lcl GQ849 Chr2	54.43	79	19	1	100	161	1.5E+07
lcl GQ849 Chr2	66.667	30	10	0	75	104	1.5E+07
lcl GQ849 Chr2	83.333	18	3	0	62	79	2E+07
lcl GQ849 Chr2	75	16	4	0	62	77	1.5E+07
lcl GQ849 Chr3	73.81	42	8	1	126	164	1.6E+07
lcl GQ849 Chr3	57.143	35	15	0	76	110	1.6E+07
lcl GQ849 Chr3	75	16	4	0	62	77	1.6E+07
lcl GQ849 Chr7	60	20	8	0	91	110	1.2E+07

TBLASTN 2.10.1+

Query: lcl|KJ651124.1_prot_AJO61187.1_1 [protein=CenH3] [protein_id=AJO61187.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

20 hits found

lcl KJ6511 Chr6	49.533	107	53	1	12	118	1646033
lcl KJ6511 Chr6	49.533	107	53	1	12	118	3040864
lcl KJ6511 Chr6	49.533	107	53	1	12	118	3055541
lcl KJ6511 Chr6	49.533	107	53	1	12	118	3056252
lcl KJ6511 Chr6	49.533	107	53	1	12	118	3046894
lcl KJ6511 Chr5	49.533	107	53	1	12	118	2.2E+07

lcl KJ6511Chr5	56.098	41	18	0	16	56	2.4E+07
lcl KJ6511Chr5	59.259	27	11	0	56	82	2.4E+07
lcl KJ6511Chr5	50	30	15	0	78	107	2.4E+07
lcl KJ6511Chr11	49.533	107	53	1	12	118	2626139
lcl KJ6511Chr4	49.533	107	53	1	12	118	2.1E+07
lcl KJ6511Chr4	32.143	168	53	3	12	118	2.2E+07
lcl KJ6511Chr1	49.533	107	53	1	12	118	3.8E+07
lcl KJ6511Chr12	47.664	107	55	1	12	118	1.3E+07
lcl KJ6511Chr12	47.959	98	50	1	21	118	1.3E+07
lcl KJ6511Chr2	36.207	116	43	1	34	118	1.5E+07
lcl KJ6511Chr2	40.299	67	35	1	52	118	1.5E+07
lcl KJ6511Chr2	60	30	12	0	34	63	1.5E+07
lcl KJ6511Chr3	52	50	24	0	69	118	1.6E+07
lcl KJ6511Chr3	58.621	29	12	0	35	63	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KJ651120.1_prot_AJO61183.1_1 [protein=CenH3] [protein_id=AJO61183.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

lcl KJ6511Chr5	50	100	48	2	12	110	2.2E+07
lcl KJ6511Chr5	58.537	41	16	1	16	55	2.4E+07
lcl KJ6511Chr5	59.259	27	11	0	55	81	2.4E+07
lcl KJ6511Chr5	50	30	15	0	77	106	2.4E+07
lcl KJ6511Chr6	50	100	48	2	12	110	3040864
lcl KJ6511Chr6	50	100	48	2	12	110	3056252
lcl KJ6511Chr6	50	100	48	2	12	110	3055541
lcl KJ6511Chr6	49	100	49	2	12	110	1646033
lcl KJ6511Chr6	50	100	48	2	12	110	3046894
lcl KJ6511Chr1	50	100	48	2	12	110	3.8E+07
lcl KJ6511Chr11	50	100	48	2	12	110	2626139
lcl KJ6511Chr4	50	100	48	2	12	110	2.1E+07
lcl KJ6511Chr4	37.037	108	37	2	34	110	2.2E+07
lcl KJ6511Chr4	24.419	86	53	2	16	89	358622
lcl KJ6511Chr12	48	100	50	2	12	110	1.3E+07
lcl KJ6511Chr12	47	100	51	2	12	110	1.3E+07
lcl KJ6511Chr3	51.163	43	21	0	68	110	1.6E+07
lcl KJ6511Chr3	48.571	35	18	0	34	68	1.6E+07
lcl KJ6511Chr2	33.945	109	41	1	33	110	1.5E+07
lcl KJ6511Chr2	38.333	60	32	1	51	110	1.5E+07
lcl KJ6511Chr2	58.621	29	12	0	34	62	1.5E+07
lcl KJ6511Chr8	41.935	31	18	0	54	84	2.4E+07

TBLASTN 2.10.1+

Query: lcl|KJ651113.1_prot_AJO61176.1_1 [protein=CenH3] [protein_id=AJO61176.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

lcl KJ6511Chr6	53.846	91	41	1	20	110	3056279
lcl KJ6511Chr6	51	100	48	1	11	110	3040864
lcl KJ6511Chr6	53.846	91	41	1	20	110	3055514
lcl KJ6511Chr6	53.846	91	41	1	20	110	1646006
lcl KJ6511Chr6	53.846	91	41	1	20	110	3046867
lcl KJ6511Chr5	51	100	48	1	11	110	2.2E+07
lcl KJ6511Chr5	67.568	37	12	0	19	55	2.4E+07
lcl KJ6511Chr5	59.259	27	11	0	55	81	2.4E+07
lcl KJ6511Chr5	53.333	30	14	0	77	106	2.4E+07
lcl KJ6511Chr11	53.846	91	41	1	20	110	2626112
lcl KJ6511Chr1	53.846	91	41	1	20	110	3.8E+07
lcl KJ6511Chr4	53.846	91	41	1	20	110	2.1E+07
lcl KJ6511Chr4	32.895	152	41	3	20	110	2.2E+07
lcl KJ6511Chr12	51.648	91	43	1	20	110	1.3E+07
lcl KJ6511Chr12	50.549	91	44	1	20	110	1.3E+07
lcl KJ6511Chr3	51.163	43	21	0	68	110	1.6E+07
lcl KJ6511Chr3	58.621	29	12	0	34	62	1.6E+07
lcl KJ6511Chr3	71.429	14	4	0	20	33	1.6E+07
lcl KJ6511Chr3	40	35	21	0	2	36	1.3E+07
lcl KJ6511Chr2	34.862	109	40	1	33	110	1.5E+07
lcl KJ6511Chr2	38.333	60	32	1	51	110	1.5E+07
lcl KJ6511Chr2	60	30	12	0	33	62	1.5E+07
lcl KJ6511Chr2	30.986	71	35	1	20	76	2E+07

TBLASTN 2.10.1+

Query: lcl|KJ651193.1_prot_AJO61254.1_1 [protein=CenH3] [protein_id=AJO61254.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

25 hits found

lcl KJ6511Chr11	57.143	98	41	1	17	114	2626112
lcl KJ6511Chr11	38.235	34	21	0	58	91	2.8E+07
lcl KJ6511Chr6	57.143	98	41	1	17	114	3056279
lcl KJ6511Chr6	57.143	98	41	1	17	114	3040837
lcl KJ6511Chr6	57.143	98	41	1	17	114	1646006
lcl KJ6511Chr6	57.143	98	41	1	17	114	3055514
lcl KJ6511Chr6	57.143	98	41	1	17	114	3046867
lcl KJ6511Chr12	53.211	109	50	1	17	125	1.3E+07
lcl KJ6511Chr12	51.376	109	52	1	17	125	1.3E+07
lcl KJ6511Chr12	22.785	79	51	2	49	127	4809489
lcl KJ6511Chr5	57.143	98	41	1	17	114	2.1E+07
lcl KJ6511Chr5	63.158	38	14	0	15	52	2.4E+07
lcl KJ6511Chr5	54.545	33	14	1	52	83	2.4E+07
lcl KJ6511Chr5	60	30	12	0	74	103	2.4E+07
lcl KJ6511Chr1	57.143	98	41	1	17	114	3.8E+07
lcl KJ6511Chr4	57.143	98	41	1	17	114	2.1E+07
lcl KJ6511Chr4	35.849	159	41	3	17	114	2.2E+07
lcl KJ6511Chr2	38.793	116	40	2	30	114	1.5E+07

lcl KJ6511Chr2	54	50	23	0	65	114	1.5E+07
lcl KJ6511Chr2	56.667	30	13	0	30	59	1.5E+07
lcl KJ6511Chr2	33.333	42	28	0	59	100	1.1E+07
lcl KJ6511Chr3	58	50	21	0	65	114	1.6E+07
lcl KJ6511Chr3	40.323	62	34	2	31	92	1.6E+07
lcl KJ6511Chr3	71.429	14	4	0	17	30	1.6E+07
lcl KJ6511Chr3	33.333	42	28	0	59	100	9963056

TBLASTN 2.10.1+

Query: lcl|KJ651190.1_prot_AJO61251.1_1 [protein=CenH3] [protein_id=AJO61251.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

lcl KJ6511Chr6	54.082	98	44	1	17	114	3056279
lcl KJ6511Chr6	54.082	98	44	1	17	114	3040837
lcl KJ6511Chr6	54.082	98	44	1	17	114	3055514
lcl KJ6511Chr6	54.082	98	44	1	17	114	1646006
lcl KJ6511Chr6	54.082	98	44	1	17	114	3046867
lcl KJ6511Chr11	54.082	98	44	1	17	114	2626112
lcl KJ6511Chr12	54.082	98	44	1	17	114	1.3E+07
lcl KJ6511Chr12	51.02	98	47	1	17	114	1.3E+07
lcl KJ6511Chr5	54.082	98	44	1	17	114	2.1E+07
lcl KJ6511Chr5	58.696	46	17	1	7	52	2.4E+07
lcl KJ6511Chr5	51.515	33	15	1	52	83	2.4E+07
lcl KJ6511Chr5	60	30	12	0	74	103	2.4E+07
lcl KJ6511Chr1	54.082	98	44	1	17	114	3.8E+07
lcl KJ6511Chr4	54.082	98	44	1	17	114	2.1E+07
lcl KJ6511Chr4	33.962	159	44	3	17	114	2.2E+07
lcl KJ6511Chr2	38.793	116	40	2	30	114	1.5E+07
lcl KJ6511Chr2	54	50	23	0	65	114	1.5E+07
lcl KJ6511Chr2	59.259	27	11	0	30	56	1.5E+07
lcl KJ6511Chr2	26.23	61	45	0	40	100	1.1E+07
lcl KJ6511Chr3	58	50	21	0	65	114	1.6E+07
lcl KJ6511Chr3	37.097	62	36	2	31	92	1.6E+07
lcl KJ6511Chr3	64.286	14	5	0	17	30	1.6E+07
lcl KJ6511Chr3	33.333	39	26	0	62	100	9963065

TBLASTN 2.10.1+

Query: lcl|KJ651189.1_prot_AJO61250.1_1 [protein=CenH3] [protein_id=AJO61250.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

lcl KJ6511Chr6	55.102	98	43	1	17	114	3056279
lcl KJ6511Chr6	55.102	98	43	1	17	114	3040837
lcl KJ6511Chr6	55.102	98	43	1	17	114	3055514
lcl KJ6511Chr6	55.102	98	43	1	17	114	1646006
lcl KJ6511Chr6	55.102	98	43	1	17	114	3046867
lcl KJ6511Chr11	55.102	98	43	1	17	114	2626112

lcl KJ6511Chr12	55.102	98	43	1	17	114	1.3E+07
lcl KJ6511Chr12	52.041	98	46	1	17	114	1.3E+07
lcl KJ6511Chr5	55.102	98	43	1	17	114	2.1E+07
lcl KJ6511Chr5	60.87	46	16	1	7	52	2.4E+07
lcl KJ6511Chr5	51.515	33	15	1	52	83	2.4E+07
lcl KJ6511Chr5	60	30	12	0	74	103	2.4E+07
lcl KJ6511Chr4	55.102	98	43	1	17	114	2.1E+07
lcl KJ6511Chr4	34.591	159	43	3	17	114	2.2E+07
lcl KJ6511Chr1	55.102	98	43	1	17	114	3.8E+07
lcl KJ6511Chr2	38.793	116	40	2	30	114	1.5E+07
lcl KJ6511Chr2	54	50	23	0	65	114	1.5E+07
lcl KJ6511Chr2	55.172	29	13	0	30	58	1.5E+07
lcl KJ6511Chr2	33.333	39	26	0	62	100	1.1E+07
lcl KJ6511Chr3	58	50	21	0	65	114	1.6E+07
lcl KJ6511Chr3	35.938	64	38	2	31	94	1.6E+07
lcl KJ6511Chr3	71.429	14	4	0	17	30	1.6E+07
lcl KJ6511Chr3	33.333	39	26	0	62	100	9963065

TBLASTN 2.10.1+

Query: lcl|KJ651187.1_prot_AJO61248.1_1 [protein=CenH3] [protein_id=AJO61248.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

24 hits found

lcl KJ6511Chr6	55.102	98	43	1	17	114	3056279
lcl KJ6511Chr6	55.102	98	43	1	17	114	3040837
lcl KJ6511Chr6	55.102	98	43	1	17	114	1646006
lcl KJ6511Chr6	55.102	98	43	1	17	114	3055514
lcl KJ6511Chr6	55.102	98	43	1	17	114	3046867
lcl KJ6511Chr11	55.102	98	43	1	17	114	2626112
lcl KJ6511Chr12	55.102	98	43	1	17	114	1.3E+07
lcl KJ6511Chr12	52.041	98	46	1	17	114	1.3E+07
lcl KJ6511Chr5	55.102	98	43	1	17	114	2.1E+07
lcl KJ6511Chr5	60.976	41	16	0	12	52	2.4E+07
lcl KJ6511Chr5	51.515	33	15	1	52	83	2.4E+07
lcl KJ6511Chr5	60	30	12	0	74	103	2.4E+07
lcl KJ6511Chr1	55.102	98	43	1	17	114	3.8E+07
lcl KJ6511Chr4	55.102	98	43	1	17	114	2.1E+07
lcl KJ6511Chr4	34.591	159	43	3	17	114	2.2E+07
lcl KJ6511Chr2	37.931	116	41	2	30	114	1.5E+07
lcl KJ6511Chr2	54	50	23	0	65	114	1.5E+07
lcl KJ6511Chr2	57.143	28	12	0	30	57	1.5E+07
lcl KJ6511Chr2	41.935	31	18	0	4	34	1.2E+07
lcl KJ6511Chr2	33.333	39	26	0	62	100	1.1E+07
lcl KJ6511Chr3	58	50	21	0	65	114	1.6E+07
lcl KJ6511Chr3	37.097	62	36	2	31	92	1.6E+07
lcl KJ6511Chr3	71.429	14	4	0	17	30	1.6E+07
lcl KJ6511Chr3	33.333	39	26	0	62	100	9963065

TBLASTN 2.10.1+

Query: lcl|KJ651185.1_prot_AJO61246.1_1 [protein=CenH3] [protein_id=AJO61246.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

lcl KJ6511Chr6	55.102	98	43	1	17	114	3040837
lcl KJ6511Chr6	55.102	98	43	1	17	114	3056279
lcl KJ6511Chr6	55.102	98	43	1	17	114	1646006
lcl KJ6511Chr6	55.102	98	43	1	17	114	3055514
lcl KJ6511Chr6	55.102	98	43	1	17	114	3046867
lcl KJ6511Chr11	55.102	98	43	1	17	114	2626112
lcl KJ6511Chr5	55.102	98	43	1	17	114	2.1E+07
lcl KJ6511Chr5	58.696	46	17	1	7	52	2.4E+07
lcl KJ6511Chr5	51.515	33	15	1	52	83	2.4E+07
lcl KJ6511Chr5	60	30	12	0	74	103	2.4E+07
lcl KJ6511Chr12	55.102	98	43	1	17	114	1.3E+07
lcl KJ6511Chr12	52.041	98	46	1	17	114	1.3E+07
lcl KJ6511Chr1	55.102	98	43	1	17	114	3.8E+07
lcl KJ6511Chr4	55.102	98	43	1	17	114	2.1E+07
lcl KJ6511Chr4	34.591	159	43	3	17	114	2.2E+07
lcl KJ6511Chr2	37.931	116	41	2	30	114	1.5E+07
lcl KJ6511Chr2	54	50	23	0	65	114	1.5E+07
lcl KJ6511Chr2	55.172	29	13	0	30	58	1.5E+07
lcl KJ6511Chr2	30.435	69	37	2	43	100	1.1E+07
lcl KJ6511Chr3	58	50	21	0	65	114	1.6E+07
lcl KJ6511Chr3	35.938	64	38	2	31	94	1.6E+07
lcl KJ6511Chr3	71.429	14	4	0	17	30	1.6E+07
lcl KJ6511Chr3	33.333	39	26	0	62	100	9963065

TBLASTN 2.10.1+

Query: lcl|KJ651184.1_prot_AJO61245.1_1 [protein=CenH3] [protein_id=AJO61245.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

20 hits found

lcl KJ6511Chr11	53.846	91	41	1	24	114	2626091
lcl KJ6511Chr6	53.846	91	41	1	24	114	3040816
lcl KJ6511Chr6	53.846	91	41	1	24	114	3056300
lcl KJ6511Chr6	53.846	91	41	1	24	114	3055493
lcl KJ6511Chr6	53.846	91	41	1	24	114	3046846
lcl KJ6511Chr6	53.846	91	41	1	24	114	1645985
lcl KJ6511Chr5	53.846	91	41	1	24	114	2.1E+07
lcl KJ6511Chr5	68.966	29	9	0	24	52	2.4E+07
lcl KJ6511Chr5	48.485	33	16	1	52	83	2.4E+07
lcl KJ6511Chr5	60	30	12	0	74	103	2.4E+07
lcl KJ6511Chr1	53.846	91	41	1	24	114	3.8E+07
lcl KJ6511Chr4	53.846	91	41	1	24	114	2.1E+07
lcl KJ6511Chr4	40	115	38	2	31	114	2.2E+07

lcl KJ6511Chr12	52.747	91	42	1	24	114	1.3E+07
lcl KJ6511Chr12	50.549	91	44	1	24	114	1.3E+07
lcl KJ6511Chr2	38.261	115	40	2	31	114	1.5E+07
lcl KJ6511Chr2	54	50	23	0	65	114	1.5E+07
lcl KJ6511Chr2	53.571	28	13	0	31	58	1.5E+07
lcl KJ6511Chr3	58	50	21	0	65	114	1.6E+07
lcl KJ6511Chr3	35.938	64	38	2	31	94	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KJ651182.1_prot_AJO61244.1_1 [protein=CenH3] [protein_id=AJO61244.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

20 hits found

lcl KJ6511Chr11	53.846	91	41	1	24	114	2626091
lcl KJ6511Chr6	53.846	91	41	1	24	114	3040816
lcl KJ6511Chr6	53.846	91	41	1	24	114	3056300
lcl KJ6511Chr6	53.846	91	41	1	24	114	3055493
lcl KJ6511Chr6	53.846	91	41	1	24	114	3046846
lcl KJ6511Chr6	53.846	91	41	1	24	114	1645985
lcl KJ6511Chr5	53.846	91	41	1	24	114	2.1E+07
lcl KJ6511Chr5	65.517	29	10	0	24	52	2.4E+07
lcl KJ6511Chr5	51.515	33	15	1	52	83	2.4E+07
lcl KJ6511Chr5	60	30	12	0	74	103	2.4E+07
lcl KJ6511Chr1	53.846	91	41	1	24	114	3.8E+07
lcl KJ6511Chr4	53.846	91	41	1	24	114	2.1E+07
lcl KJ6511Chr4	39.13	115	39	2	31	114	2.2E+07
lcl KJ6511Chr12	52.747	91	42	1	24	114	1.3E+07
lcl KJ6511Chr12	50.549	91	44	1	24	114	1.3E+07
lcl KJ6511Chr2	38.261	115	40	2	31	114	1.5E+07
lcl KJ6511Chr2	54	50	23	0	65	114	1.5E+07
lcl KJ6511Chr2	53.571	28	13	0	31	58	1.5E+07
lcl KJ6511Chr3	58	50	21	0	65	114	1.6E+07
lcl KJ6511Chr3	35.938	64	38	2	31	94	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KJ651181.1_prot_AJO61243.1_1 [protein=CenH3] [protein_id=AJO61243.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

25 hits found

lcl KJ6511Chr11	47.761	134	49	2	1	114	2626220
lcl KJ6511Chr11	41.176	34	20	0	58	91	2.8E+07
lcl KJ6511Chr6	47.761	134	49	2	1	114	3040945
lcl KJ6511Chr6	47.761	134	49	2	1	114	3055622
lcl KJ6511Chr6	47.761	134	49	2	1	114	3056171
lcl KJ6511Chr6	57.143	98	41	1	17	114	1646006
lcl KJ6511Chr6	57.143	98	41	1	17	114	3046867
lcl KJ6511Chr5	47.761	134	49	2	1	114	2.2E+07
lcl KJ6511Chr5	60.87	46	16	1	7	52	2.4E+07

lcl KJ6511Chr5	54.545	33	14	1	52	83	2.4E+07
lcl KJ6511Chr5	60	30	12	0	74	103	2.4E+07
lcl KJ6511Chr12	58.163	98	40	1	17	114	1.3E+07
lcl KJ6511Chr12	54.082	98	44	1	17	114	1.3E+07
lcl KJ6511Chr4	47.761	134	49	2	1	114	2.1E+07
lcl KJ6511Chr4	35.849	159	41	3	17	114	2.2E+07
lcl KJ6511Chr1	57.143	98	41	1	17	114	3.8E+07
lcl KJ6511Chr2	40.517	116	38	2	30	114	1.5E+07
lcl KJ6511Chr2	54	50	23	0	65	114	1.5E+07
lcl KJ6511Chr2	62.069	29	11	0	30	58	1.5E+07
lcl KJ6511Chr2	33.333	39	26	0	62	100	1.1E+07
lcl KJ6511Chr3	58	50	21	0	65	114	1.6E+07
lcl KJ6511Chr3	37.5	64	37	2	31	94	1.6E+07
lcl KJ6511Chr3	71.429	14	4	0	17	30	1.6E+07
lcl KJ6511Chr3	33.333	39	26	0	62	100	9963065
lcl KJ6511Chr8	38.636	44	26	1	11	54	2.4E+07

TBLASTN 2.10.1+

Query: lcl|KJ651179.1_prot_AJO61241.1_1 [protein=CenH3] [protein_id=AJO61241.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

25 hits found

lcl KJ6511Chr11	47.015	134	50	2	1	114	2626220
lcl KJ6511Chr11	40	35	21	0	57	91	2.8E+07
lcl KJ6511Chr6	47.015	134	50	2	1	114	3040945
lcl KJ6511Chr6	47.015	134	50	2	1	114	3055622
lcl KJ6511Chr6	47.015	134	50	2	1	114	3056171
lcl KJ6511Chr6	56.122	98	42	1	17	114	3046867
lcl KJ6511Chr6	56.122	98	42	1	17	114	1646006
lcl KJ6511Chr5	47.015	134	50	2	1	114	2.2E+07
lcl KJ6511Chr5	60.87	46	16	1	7	52	2.4E+07
lcl KJ6511Chr5	54.545	33	14	1	52	83	2.4E+07
lcl KJ6511Chr5	60	30	12	0	74	103	2.4E+07
lcl KJ6511Chr12	57.143	98	41	1	17	114	1.3E+07
lcl KJ6511Chr12	53.061	98	45	1	17	114	1.3E+07
lcl KJ6511Chr4	47.015	134	50	2	1	114	2.1E+07
lcl KJ6511Chr4	35.22	159	42	3	17	114	2.2E+07
lcl KJ6511Chr1	56.122	98	42	1	17	114	3.8E+07
lcl KJ6511Chr3	56	50	22	0	65	114	1.6E+07
lcl KJ6511Chr3	68	25	8	0	31	55	1.6E+07
lcl KJ6511Chr3	71.429	14	4	0	17	30	1.6E+07
lcl KJ6511Chr3	31.818	44	30	0	57	100	9963050
lcl KJ6511Chr2	39.655	116	39	2	30	114	1.5E+07
lcl KJ6511Chr2	52	50	24	0	65	114	1.5E+07
lcl KJ6511Chr2	69.231	26	8	0	30	55	1.5E+07
lcl KJ6511Chr2	31.818	44	30	0	57	100	1.1E+07
lcl KJ6511Chr8	38.776	49	29	1	11	59	2.4E+07

TBLASTN 2.10.1+

Query: lcl|KJ651178.1_prot_AJO61240.1_1 [protein=CenH3] [protein_id=AJO61240.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

20 hits found

lcl KJ6511Chr6	53.061	98	45	1	17	114	3040837
lcl KJ6511Chr6	53.061	98	45	1	17	114	3056279
lcl KJ6511Chr6	53.061	98	45	1	17	114	3055514
lcl KJ6511Chr6	53.061	98	45	1	17	114	3046867
lcl KJ6511Chr6	53.061	98	45	1	17	114	1646006
lcl KJ6511Chr5	53.061	98	45	1	17	114	2.1E+07
lcl KJ6511Chr5	58.14	43	18	0	10	52	2.4E+07
lcl KJ6511Chr5	51.515	33	15	1	52	83	2.4E+07
lcl KJ6511Chr5	60	30	12	0	74	103	2.4E+07
lcl KJ6511Chr11	53.061	98	45	1	17	114	2626112
lcl KJ6511Chr11	38.71	31	19	0	29	59	1.9E+07
lcl KJ6511Chr4	53.061	98	45	1	17	114	2.1E+07
lcl KJ6511Chr4	32.075	159	47	2	17	114	2.2E+07
lcl KJ6511Chr1	53.061	98	45	1	17	114	3.8E+07
lcl KJ6511Chr12	53.061	98	45	1	17	114	1.3E+07
lcl KJ6511Chr12	50	98	48	1	17	114	1.3E+07
lcl KJ6511Chr2	37.931	116	41	2	30	114	1.5E+07
lcl KJ6511Chr2	54	50	23	0	65	114	1.5E+07
lcl KJ6511Chr2	45.455	33	18	0	30	62	1.5E+07
lcl KJ6511Chr3	58	50	21	0	65	114	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KJ651174.1_prot_AJO61236.1_1 [protein=CenH3] [protein_id=AJO61236.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

21 hits found

lcl KJ6511Chr6	54.082	98	44	1	17	114	3056279
lcl KJ6511Chr6	54.082	98	44	1	17	114	1646006
lcl KJ6511Chr6	54.082	98	44	1	17	114	3040837
lcl KJ6511Chr6	54.082	98	44	1	17	114	3055514
lcl KJ6511Chr6	54.082	98	44	1	17	114	3046867
lcl KJ6511Chr11	54.082	98	44	1	17	114	2626112
lcl KJ6511Chr12	54.082	98	44	1	17	114	1.3E+07
lcl KJ6511Chr12	51.02	98	47	1	17	114	1.3E+07
lcl KJ6511Chr5	54.082	98	44	1	17	114	2.1E+07
lcl KJ6511Chr5	60.87	46	16	1	7	52	2.4E+07
lcl KJ6511Chr5	53.125	32	14	1	52	82	2.4E+07
lcl KJ6511Chr5	56.667	30	13	0	74	103	2.4E+07
lcl KJ6511Chr4	54.082	98	44	1	17	114	2.1E+07
lcl KJ6511Chr4	33.962	159	44	3	17	114	2.2E+07
lcl KJ6511Chr1	54.082	98	44	1	17	114	3.8E+07
lcl KJ6511Chr2	37.931	116	41	2	30	114	1.5E+07

lcl KJ6511Chr2	52	50	24	0	65	114	1.5E+07
lcl KJ6511Chr2	55.172	29	13	0	30	58	1.5E+07
lcl KJ6511Chr3	56	50	22	0	65	114	1.6E+07
lcl KJ6511Chr3	37.097	62	36	2	31	92	1.6E+07
lcl KJ6511Chr3	71.429	14	4	0	17	30	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KJ651169.1_prot_AJO61231.1_1 [protein=CenH3] [protein_id=AJO61231.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

20 hits found

lcl KJ6511Chr11	50	134	52	3	1	120	2626220
lcl KJ6511Chr6	50	134	52	3	1	120	3040945
lcl KJ6511Chr6	50	134	52	3	1	120	3055622
lcl KJ6511Chr6	50	134	52	3	1	120	3056171
lcl KJ6511Chr6	59.574	94	37	1	27	120	3046855
lcl KJ6511Chr6	58.511	94	38	1	27	120	1645994
lcl KJ6511Chr5	50	134	52	3	1	120	2.2E+07
lcl KJ6511Chr5	81.25	32	6	0	27	58	2.4E+07
lcl KJ6511Chr5	56.522	23	10	0	87	109	2.4E+07
lcl KJ6511Chr4	50	134	52	3	1	120	2.1E+07
lcl KJ6511Chr4	33.974	156	42	2	26	120	2.2E+07
lcl KJ6511Chr1	59.574	94	37	1	27	120	3.8E+07
lcl KJ6511Chr12	45.522	134	58	3	1	120	1.3E+07
lcl KJ6511Chr12	43.284	134	61	3	1	120	1.3E+07
lcl KJ6511Chr2	38.793	116	40	1	36	120	1.5E+07
lcl KJ6511Chr2	55.882	34	15	0	87	120	1.5E+07
lcl KJ6511Chr2	53.125	32	15	0	36	67	1.5E+07
lcl KJ6511Chr3	61.765	34	13	0	87	120	1.6E+07
lcl KJ6511Chr3	45.714	35	19	0	37	71	1.6E+07
lcl KJ6511Chr3	80	10	2	0	27	36	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KJ651166.1_prot_AJO61228.1_1 [protein=CenH3] [protein_id=AJO61228.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

21 hits found

lcl KJ6511Chr6	49.153	118	58	2	8	124	3040897
lcl KJ6511Chr6	49.153	118	58	2	8	124	3055574
lcl KJ6511Chr6	49.153	118	58	2	8	124	3056219
lcl KJ6511Chr6	50	112	54	2	14	124	3046909
lcl KJ6511Chr6	52.83	106	48	2	20	124	1646030
lcl KJ6511Chr6	50	28	14	0	9	36	1833569
lcl KJ6511Chr11	49.153	118	58	2	8	124	2626172
lcl KJ6511Chr5	49.153	118	58	2	8	124	2.2E+07
lcl KJ6511Chr5	60.976	41	16	0	22	62	2.4E+07
lcl KJ6511Chr5	56.522	23	10	0	91	113	2.4E+07
lcl KJ6511Chr5	46.429	28	15	0	90	117	1E+07

lcl KJ6511Chr4	49.153	118	58	2	8	124	2.1E+07
lcl KJ6511Chr4	39.13	115	39	2	41	124	2.2E+07
lcl KJ6511Chr1	50	112	54	2	14	124	3.8E+07
lcl KJ6511Chr12	51.546	97	46	1	28	124	1.3E+07
lcl KJ6511Chr12	44.167	120	65	2	6	124	1.3E+07
lcl KJ6511Chr2	37.069	116	42	1	40	124	1.5E+07
lcl KJ6511Chr2	46.269	67	31	1	58	124	1.5E+07
lcl KJ6511Chr2	53.571	28	13	0	40	67	1.5E+07
lcl KJ6511Chr3	61.765	34	13	0	91	124	1.6E+07
lcl KJ6511Chr3	42.857	35	20	0	41	75	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KJ651163.1_prot_AJO61225.1_1 [protein=CenH3] [protein_id=AJO61225.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

20 hits found

lcl KJ6511Chr6	53.061	98	45	1	27	124	3040837
lcl KJ6511Chr6	53.061	98	45	1	27	124	3056279
lcl KJ6511Chr6	53.061	98	45	1	27	124	3055514
lcl KJ6511Chr6	53.061	98	45	1	27	124	3046867
lcl KJ6511Chr6	54.082	98	44	1	27	124	1646006
lcl KJ6511Chr5	53.061	98	45	1	27	124	2.1E+07
lcl KJ6511Chr5	53.191	47	22	0	16	62	2.4E+07
lcl KJ6511Chr5	56.522	23	10	0	91	113	2.4E+07
lcl KJ6511Chr5	46.429	28	15	0	90	117	1E+07
lcl KJ6511Chr11	53.061	98	45	1	27	124	2626112
lcl KJ6511Chr1	53.061	98	45	1	27	124	3.8E+07
lcl KJ6511Chr4	53.061	98	45	1	27	124	2.1E+07
lcl KJ6511Chr4	40	115	38	2	41	124	2.2E+07
lcl KJ6511Chr12	52.041	98	46	1	27	124	1.3E+07
lcl KJ6511Chr12	48.98	98	49	1	27	124	1.3E+07
lcl KJ6511Chr2	37.931	116	41	1	40	124	1.5E+07
lcl KJ6511Chr2	47.761	67	30	1	58	124	1.5E+07
lcl KJ6511Chr2	46.875	32	17	0	40	71	1.5E+07
lcl KJ6511Chr3	61.765	34	13	0	91	124	1.6E+07
lcl KJ6511Chr3	42.857	35	20	0	41	75	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KJ651160.1_prot_AJO61222.1_1 [protein=CenH3] [protein_id=AJO61222.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

24 hits found

lcl KJ6511Chr6	58.242	91	37	1	24	114	1645985
lcl KJ6511Chr6	57.143	91	38	1	24	114	3040816
lcl KJ6511Chr6	57.143	91	38	1	24	114	3055493
lcl KJ6511Chr6	57.143	91	38	1	24	114	3056300
lcl KJ6511Chr6	57.143	91	38	1	24	114	3046846
lcl KJ6511Chr11	57.143	91	38	1	24	114	2626091

lcl KJ6511Chr11	38.235	34	21	0	58	91	2.8E+07
lcl KJ6511Chr5	57.143	91	38	1	24	114	2.1E+07
lcl KJ6511Chr5	79.31	29	6	0	24	52	2.4E+07
lcl KJ6511Chr5	51.351	37	17	1	52	87	2.4E+07
lcl KJ6511Chr5	54.545	33	15	0	71	103	2.4E+07
lcl KJ6511Chr4	57.143	91	38	1	24	114	2.1E+07
lcl KJ6511Chr4	40.87	115	37	2	31	114	2.2E+07
lcl KJ6511Chr1	57.143	91	38	1	24	114	3.8E+07
lcl KJ6511Chr1	26.923	78	48	2	42	114	3.1E+07
lcl KJ6511Chr12	56.044	91	39	1	24	114	1.3E+07
lcl KJ6511Chr12	53.846	91	41	1	24	114	1.3E+07
lcl KJ6511Chr2	40.517	116	38	2	30	114	1.5E+07
lcl KJ6511Chr2	46.269	67	31	1	48	114	1.5E+07
lcl KJ6511Chr2	65.385	26	9	0	30	55	1.5E+07
lcl KJ6511Chr2	35.897	39	25	0	62	100	1.1E+07
lcl KJ6511Chr3	60	50	20	0	65	114	1.6E+07
lcl KJ6511Chr3	35.938	64	38	2	31	94	1.6E+07
lcl KJ6511Chr3	35.897	39	25	0	62	100	9963065

TBLASTN 2.10.1+

Query: lcl|KJ651157.1_prot_AJO61219.1_1 [protein=CenH3] [protein_id=AJO61219.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

21 hits found

lcl KJ6511Chr12	52.577	97	45	1	22	118	1.3E+07
lcl KJ6511Chr12	48.454	97	49	1	22	118	1.3E+07
lcl KJ6511Chr6	51.546	97	46	1	22	118	1646003
lcl KJ6511Chr6	51.546	97	46	1	22	118	3040834
lcl KJ6511Chr6	52.128	94	44	1	25	118	3055502
lcl KJ6511Chr6	51.546	97	46	1	22	118	3056282
lcl KJ6511Chr6	51.546	97	46	1	22	118	3046864
lcl KJ6511Chr11	52.128	94	44	1	25	118	2626100
lcl KJ6511Chr5	51.546	97	46	1	22	118	2.1E+07
lcl KJ6511Chr5	57.5	40	17	0	17	56	2.4E+07
lcl KJ6511Chr5	51.852	27	13	0	56	82	2.4E+07
lcl KJ6511Chr5	51.515	33	16	0	75	107	2.4E+07
lcl KJ6511Chr4	51.546	97	46	1	22	118	2.1E+07
lcl KJ6511Chr4	31.361	169	55	3	11	118	2.2E+07
lcl KJ6511Chr1	51.546	97	46	1	22	118	3.8E+07
lcl KJ6511Chr2	35.345	116	44	1	34	118	1.5E+07
lcl KJ6511Chr2	47.761	67	30	1	52	118	1.5E+07
lcl KJ6511Chr2	32.609	46	29	1	28	71	3450588
lcl KJ6511Chr3	60	50	20	0	69	118	1.6E+07
lcl KJ6511Chr3	30.882	68	45	1	35	100	2.6E+07
lcl KJ6511Chr10	32.075	53	28	1	34	86	2E+07

TBLASTN 2.10.1+

Query: lcl|KJ651154.1_prot_AJO61216.1_1 [protein=CenH3] [protein_id=AJO61216.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

19 hits found

lcl KJ6511Chr11	57.143	91	38	1	24	114	2626091
lcl KJ6511Chr6	57.143	91	38	1	24	114	3040816
lcl KJ6511Chr6	57.143	91	38	1	24	114	3055493
lcl KJ6511Chr6	57.143	91	38	1	24	114	3046846
lcl KJ6511Chr6	57.143	91	38	1	24	114	3056300
lcl KJ6511Chr6	58.242	91	37	1	24	114	1645985
lcl KJ6511Chr5	57.143	91	38	1	24	114	2.1E+07
lcl KJ6511Chr5	82.759	29	5	0	24	52	2.4E+07
lcl KJ6511Chr5	59.091	22	9	0	82	103	2.4E+07
lcl KJ6511Chr4	57.143	91	38	1	24	114	2.1E+07
lcl KJ6511Chr4	40.87	115	37	2	31	114	2.2E+07
lcl KJ6511Chr12	57.143	91	38	1	24	114	1.3E+07
lcl KJ6511Chr12	53.846	91	41	1	24	114	1.3E+07
lcl KJ6511Chr1	57.143	91	38	1	24	114	3.8E+07
lcl KJ6511Chr2	40.517	116	38	2	30	114	1.5E+07
lcl KJ6511Chr2	54.545	33	15	0	82	114	1.5E+07
lcl KJ6511Chr2	58.621	29	12	0	30	58	1.5E+07
lcl KJ6511Chr3	60.606	33	13	0	82	114	1.6E+07
lcl KJ6511Chr3	35.484	62	37	1	31	92	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KJ651153.1_prot_AJO61215.1_1 [protein=CenH3] [protein_id=AJO61215.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

lcl KJ6511Chr6	56.044	91	39	1	24	114	1645985
lcl KJ6511Chr6	54.945	91	40	1	24	114	3040816
lcl KJ6511Chr6	54.945	91	40	1	24	114	3055493
lcl KJ6511Chr6	54.945	91	40	1	24	114	3056300
lcl KJ6511Chr6	54.945	91	40	1	24	114	3046846
lcl KJ6511Chr11	54.945	91	40	1	24	114	2626091
lcl KJ6511Chr12	54.945	91	40	1	24	114	1.3E+07
lcl KJ6511Chr12	51.648	91	43	1	24	114	1.3E+07
lcl KJ6511Chr5	54.945	91	40	1	24	114	2.1E+07
lcl KJ6511Chr5	82.759	29	5	0	24	52	2.4E+07
lcl KJ6511Chr5	58.333	36	14	1	52	86	2.4E+07
lcl KJ6511Chr5	48.485	33	17	0	71	103	2.4E+07
lcl KJ6511Chr4	54.945	91	40	1	24	114	2.1E+07
lcl KJ6511Chr4	39.13	115	39	2	31	114	2.2E+07
lcl KJ6511Chr4	41.463	41	23	1	39	79	3.4E+07
lcl KJ6511Chr1	54.945	91	40	1	24	114	3.8E+07
lcl KJ6511Chr1	31.034	58	31	2	42	94	3.1E+07
lcl KJ6511Chr2	39.655	116	39	2	30	114	1.5E+07
lcl KJ6511Chr2	44.776	67	32	1	48	114	1.5E+07

lcl KJ6511Chr2	58.621	29	12	0	30	58	1.5E+07
lcl KJ6511Chr3	56	50	22	0	65	114	1.6E+07
lcl KJ6511Chr3	37.097	62	36	2	31	92	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KJ651146.1_prot_AJO61208.1_1 [protein=CenH3] [protein_id=AJO61208.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

lcl KJ6511Chr6	58.242	91	37	1	24	114	1645985
lcl KJ6511Chr6	57.143	91	38	1	24	114	3040816
lcl KJ6511Chr6	57.143	91	38	1	24	114	3055493
lcl KJ6511Chr6	57.143	91	38	1	24	114	3056300
lcl KJ6511Chr6	57.143	91	38	1	24	114	3046846
lcl KJ6511Chr11	57.143	91	38	1	24	114	2626091
lcl KJ6511Chr11	38.235	34	21	0	58	91	2.8E+07
lcl KJ6511Chr5	57.143	91	38	1	24	114	2.1E+07
lcl KJ6511Chr5	82.759	29	5	0	24	52	2.4E+07
lcl KJ6511Chr5	51.351	37	17	1	52	87	2.4E+07
lcl KJ6511Chr5	54.545	33	15	0	71	103	2.4E+07
lcl KJ6511Chr4	57.143	91	38	1	24	114	2.1E+07
lcl KJ6511Chr4	40.87	115	37	2	31	114	2.2E+07
lcl KJ6511Chr1	57.143	91	38	1	24	114	3.8E+07
lcl KJ6511Chr12	56.044	91	39	1	24	114	1.3E+07
lcl KJ6511Chr12	53.846	91	41	1	24	114	1.3E+07
lcl KJ6511Chr2	39.655	116	39	2	30	114	1.5E+07
lcl KJ6511Chr2	46.269	67	31	1	48	114	1.5E+07
lcl KJ6511Chr2	58.621	29	12	0	30	58	1.5E+07
lcl KJ6511Chr2	35.897	39	25	0	62	100	1.1E+07
lcl KJ6511Chr3	60	50	20	0	65	114	1.6E+07
lcl KJ6511Chr3	35.938	64	38	2	31	94	1.6E+07
lcl KJ6511Chr3	35.897	39	25	0	62	100	9963065

TBLASTN 2.10.1+

Query: lcl|KJ651142.1_prot_AJO61205.1_1 [protein=CenH3] [protein_id=AJO61205.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

lcl KJ6511Chr6	57.143	91	38	1	24	114	1645985
lcl KJ6511Chr6	56.044	91	39	1	24	114	3040816
lcl KJ6511Chr6	56.044	91	39	1	24	114	3055493
lcl KJ6511Chr6	56.044	91	39	1	24	114	3056300
lcl KJ6511Chr6	56.044	91	39	1	24	114	3046846
lcl KJ6511Chr11	56.044	91	39	1	24	114	2626091
lcl KJ6511Chr5	56.044	91	39	1	24	114	2.1E+07
lcl KJ6511Chr5	79.31	29	6	0	24	52	2.4E+07
lcl KJ6511Chr5	51.351	37	17	1	52	87	2.4E+07
lcl KJ6511Chr5	55.882	34	15	0	70	103	2.4E+07

lcl KJ6511Chr4	56.044	91	39	1	24	114	2.1E+07
lcl KJ6511Chr4	40	115	38	2	31	114	2.2E+07
lcl KJ6511Chr4	41.026	39	22	1	39	77	3.4E+07
lcl KJ6511Chr1	56.044	91	39	1	24	114	3.8E+07
lcl KJ6511Chr12	54.945	91	40	1	24	114	1.3E+07
lcl KJ6511Chr12	51.648	91	43	1	24	114	1.3E+07
lcl KJ6511Chr2	38.793	116	40	2	30	114	1.5E+07
lcl KJ6511Chr2	44.776	67	32	1	48	114	1.5E+07
lcl KJ6511Chr2	65.385	26	9	0	30	55	1.5E+07
lcl KJ6511Chr2	34.091	44	29	0	57	100	1.1E+07
lcl KJ6511Chr3	58	50	21	0	65	114	1.6E+07
lcl KJ6511Chr3	35.938	64	38	1	31	94	1.6E+07
lcl KJ6511Chr3	34.091	44	29	0	57	100	9963050

TBLASTN 2.10.1+

Query: lcl|KJ651141.1_prot_AJO61204.1_1 [protein=CenH3] [protein_id=AJO61204.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

19 hits found

lcl KJ6511Chr6	57.143	91	38	1	24	114	3040816
lcl KJ6511Chr6	57.143	91	38	1	24	114	3055493
lcl KJ6511Chr6	57.143	91	38	1	24	114	3046846
lcl KJ6511Chr6	57.143	91	38	1	24	114	3056300
lcl KJ6511Chr6	58.242	91	37	1	24	114	1645985
lcl KJ6511Chr11	57.143	91	38	1	24	114	2626091
lcl KJ6511Chr5	57.143	91	38	1	24	114	2.1E+07
lcl KJ6511Chr5	79.31	29	6	0	24	52	2.4E+07
lcl KJ6511Chr5	63.636	22	8	0	82	103	2.4E+07
lcl KJ6511Chr4	57.143	91	38	1	24	114	2.1E+07
lcl KJ6511Chr4	40.87	115	37	2	31	114	2.2E+07
lcl KJ6511Chr1	57.143	91	38	1	24	114	3.8E+07
lcl KJ6511Chr12	56.044	91	39	1	24	114	1.3E+07
lcl KJ6511Chr12	52.747	91	42	1	24	114	1.3E+07
lcl KJ6511Chr2	40.517	116	38	2	30	114	1.5E+07
lcl KJ6511Chr2	54.545	33	15	0	82	114	1.5E+07
lcl KJ6511Chr2	55.882	34	13	1	30	61	1.5E+07
lcl KJ6511Chr3	60.606	33	13	0	82	114	1.6E+07
lcl KJ6511Chr3	64	25	9	0	31	55	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KJ651140.1_prot_AJO61203.1_1 [protein=CenH3] [protein_id=AJO61203.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

lcl KJ6511Chr6	56.044	91	39	1	24	114	1645985
lcl KJ6511Chr6	54.945	91	40	1	24	114	3040816
lcl KJ6511Chr6	54.945	91	40	1	24	114	3055493
lcl KJ6511Chr6	54.945	91	40	1	24	114	3056300

lcl KJ6511Chr6	54.945	91	40	1	24	114	3046846
lcl KJ6511Chr6	52.632	19	9	0	32	50	1.7E+07
lcl KJ6511Chr11	54.945	91	40	1	24	114	2626091
lcl KJ6511Chr5	54.945	91	40	1	24	114	2.1E+07
lcl KJ6511Chr5	82.759	29	5	0	24	52	2.4E+07
lcl KJ6511Chr5	56.667	30	13	0	52	81	2.4E+07
lcl KJ6511Chr5	48.485	33	17	0	71	103	2.4E+07
lcl KJ6511Chr4	54.945	91	40	1	24	114	2.1E+07
lcl KJ6511Chr4	37.391	115	41	1	31	114	2.2E+07
lcl KJ6511Chr1	57.143	91	38	1	24	114	3.8E+07
lcl KJ6511Chr1	38.462	39	19	1	42	75	3.1E+07
lcl KJ6511Chr12	54.945	91	40	1	24	114	1.3E+07
lcl KJ6511Chr12	52.747	91	42	1	24	114	1.3E+07
lcl KJ6511Chr2	37.931	116	41	1	30	114	1.5E+07
lcl KJ6511Chr2	43.284	67	33	1	48	114	1.5E+07
lcl KJ6511Chr2	54.545	33	15	0	30	62	1.5E+07
lcl KJ6511Chr3	50.82	61	30	0	54	114	1.6E+07
lcl KJ6511Chr3	45.714	35	19	0	31	65	1.6E+07
lcl KJ6511Chr10	37.778	45	27	1	32	75	1887345

TBLASTN 2.10.1+

Query: lcl|KJ651136.1_prot_AJO61199.1_1 [protein=CenH3] [protein_id=AJO61199.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

lcl KJ6511Chr6	57.143	91	38	1	24	114	1645985
lcl KJ6511Chr6	56.044	91	39	1	24	114	3040816
lcl KJ6511Chr6	56.044	91	39	1	24	114	3055493
lcl KJ6511Chr6	56.044	91	39	1	24	114	3056300
lcl KJ6511Chr6	56.044	91	39	1	24	114	3046846
lcl KJ6511Chr11	56.044	91	39	1	24	114	2626091
lcl KJ6511Chr11	38.235	34	21	0	58	91	2.8E+07
lcl KJ6511Chr5	56.044	91	39	1	24	114	2.1E+07
lcl KJ6511Chr5	79.31	29	6	0	24	52	2.4E+07
lcl KJ6511Chr5	52.778	36	16	1	52	86	2.4E+07
lcl KJ6511Chr5	54.545	33	15	0	71	103	2.4E+07
lcl KJ6511Chr4	56.044	91	39	1	24	114	2.1E+07
lcl KJ6511Chr4	40	115	38	2	31	114	2.2E+07
lcl KJ6511Chr1	56.044	91	39	1	24	114	3.8E+07
lcl KJ6511Chr1	31.034	58	31	2	42	94	3.1E+07
lcl KJ6511Chr12	54.945	91	40	1	24	114	1.3E+07
lcl KJ6511Chr12	52.747	91	42	1	24	114	1.3E+07
lcl KJ6511Chr2	39.655	116	39	2	30	114	1.5E+07
lcl KJ6511Chr2	44.776	67	32	1	48	114	1.5E+07
lcl KJ6511Chr2	54.839	31	14	0	30	60	1.5E+07
lcl KJ6511Chr3	58	50	21	0	65	114	1.6E+07
lcl KJ6511Chr3	35.938	64	38	2	31	94	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KJ651133.1_prot_AJO61196.1_1 [protein=CenH3] [protein_id=AJO61196.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

lcl KJ6511Chr6	56.044	91	39	1	24	114	1645985
lcl KJ6511Chr6	54.945	91	40	1	24	114	3040816
lcl KJ6511Chr6	54.945	91	40	1	24	114	3055493
lcl KJ6511Chr6	54.945	91	40	1	24	114	3056300
lcl KJ6511Chr6	54.945	91	40	1	24	114	3046846
lcl KJ6511Chr11	54.945	91	40	1	24	114	2626091
lcl KJ6511Chr5	54.945	91	40	1	24	114	2.1E+07
lcl KJ6511Chr5	79.31	29	6	0	24	52	2.4E+07
lcl KJ6511Chr5	56.667	30	13	0	52	81	2.4E+07
lcl KJ6511Chr5	51.515	33	16	0	71	103	2.4E+07
lcl KJ6511Chr4	54.945	91	40	1	24	114	2.1E+07
lcl KJ6511Chr4	37.391	115	41	1	31	114	2.2E+07
lcl KJ6511Chr1	57.143	91	38	1	24	114	3.8E+07
lcl KJ6511Chr1	38.462	39	19	1	42	75	3.1E+07
lcl KJ6511Chr12	54.945	91	40	1	24	114	1.3E+07
lcl KJ6511Chr12	52.747	91	42	1	24	114	1.3E+07
lcl KJ6511Chr2	37.931	116	41	1	30	114	1.5E+07
lcl KJ6511Chr2	43.284	67	33	1	48	114	1.5E+07
lcl KJ6511Chr2	54.545	33	15	0	30	62	1.5E+07
lcl KJ6511Chr3	50.82	61	30	0	54	114	1.6E+07
lcl KJ6511Chr3	45.714	35	19	0	31	65	1.6E+07
lcl KJ6511Chr10	40	45	26	1	32	75	1887345

TBLASTN 2.10.1+

Query: lcl|KJ651128.1_prot_AJO61191.1_1 [protein=CenH3] [protein_id=AJO61191.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

lcl KJ6511Chr6	47.664	107	55	1	12	118	1646033
lcl KJ6511Chr6	51.087	92	44	1	27	118	3040819
lcl KJ6511Chr6	47.664	107	55	1	12	118	3056252
lcl KJ6511Chr6	47.664	107	55	1	12	118	3055541
lcl KJ6511Chr6	47.664	107	55	1	12	118	3046894
lcl KJ6511Chr5	47.664	107	55	1	12	118	2.2E+07
lcl KJ6511Chr5	70	30	9	0	27	56	2.4E+07
lcl KJ6511Chr5	55.556	27	12	0	56	82	2.4E+07
lcl KJ6511Chr5	50	30	15	0	78	107	2.4E+07
lcl KJ6511Chr11	51.087	92	44	1	27	118	2626094
lcl KJ6511Chr4	47.664	107	55	1	12	118	2.1E+07
lcl KJ6511Chr4	36.522	115	42	2	35	118	2.2E+07
lcl KJ6511Chr1	50	98	48	1	21	118	3.8E+07
lcl KJ6511Chr12	50	92	45	1	27	118	1.3E+07

lcl KJ6511Chr12	48.352	91	46	1	28	118	1.3E+07
lcl KJ6511Chr2	34.483	116	45	1	34	118	1.5E+07
lcl KJ6511Chr2	40.299	67	35	1	52	118	1.5E+07
lcl KJ6511Chr2	53.333	30	14	0	34	63	1.5E+07
lcl KJ6511Chr3	52	50	24	0	69	118	1.6E+07
lcl KJ6511Chr3	51.724	29	14	0	35	63	1.6E+07
lcl KJ6511Chr3	29.31	58	34	1	16	66	2.1E+07
lcl KJ6511Chr3	30.769	117	52	6	1	91	2E+07
lcl KJ6511Chr9	46.154	39	19	1	37	75	1.5E+07

TBLASTN 2.10.1+

Query: lcl|KJ651123.1_prot_AJO61186.1_1 [protein=CenH3] [protein_id=AJO61186.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

20 hits found

lcl KJ6511Chr6	47.664	107	55	1	12	118	1646033
lcl KJ6511Chr6	47.664	107	55	1	12	118	3040864
lcl KJ6511Chr6	47.664	107	55	1	12	118	3056252
lcl KJ6511Chr6	47.664	107	55	1	12	118	3055541
lcl KJ6511Chr6	47.664	107	55	1	12	118	3046894
lcl KJ6511Chr5	47.664	107	55	1	12	118	2.2E+07
lcl KJ6511Chr5	34.066	91	48	3	14	94	2.4E+07
lcl KJ6511Chr5	55.556	27	12	0	56	82	2.4E+07
lcl KJ6511Chr5	50	30	15	0	78	107	2.4E+07
lcl KJ6511Chr11	47.664	107	55	1	12	118	2626139
lcl KJ6511Chr4	47.664	107	55	1	12	118	2.1E+07
lcl KJ6511Chr4	35.652	115	43	1	35	118	2.2E+07
lcl KJ6511Chr1	50	98	48	1	21	118	3.8E+07
lcl KJ6511Chr12	48.98	98	49	1	21	118	1.3E+07
lcl KJ6511Chr12	46.939	98	51	1	21	118	1.3E+07
lcl KJ6511Chr2	36.207	116	43	2	34	118	1.5E+07
lcl KJ6511Chr2	40.299	67	35	1	52	118	1.5E+07
lcl KJ6511Chr2	56.667	30	13	0	34	63	1.5E+07
lcl KJ6511Chr3	52	50	24	0	69	118	1.6E+07
lcl KJ6511Chr3	45.714	35	19	0	35	69	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KJ651119.1_prot_AJO61182.1_1 [protein=CenH3] [protein_id=AJO61182.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

lcl KJ6511Chr6	50.467	107	52	1	12	118	1646033
lcl KJ6511Chr6	50.467	107	52	1	12	118	3056252
lcl KJ6511Chr6	50.467	107	52	1	12	118	3040864
lcl KJ6511Chr6	50.467	107	52	1	12	118	3055541
lcl KJ6511Chr6	50.467	107	52	1	12	118	3046894
lcl KJ6511Chr5	50.467	107	52	1	12	118	2.2E+07
lcl KJ6511Chr5	66.667	36	12	0	21	56	2.4E+07

lcl KJ6511Chr5	51.852	27	13	0	56	82	2.4E+07
lcl KJ6511Chr5	50	30	15	0	78	107	2.4E+07
lcl KJ6511Chr11	50.467	107	52	1	12	118	2626139
lcl KJ6511Chr4	50.467	107	52	1	12	118	2.1E+07
lcl KJ6511Chr4	33.333	168	51	3	12	118	2.2E+07
lcl KJ6511Chr1	50.467	107	52	1	12	118	3.8E+07
lcl KJ6511Chr12	48.598	107	54	1	12	118	1.3E+07
lcl KJ6511Chr12	46.729	107	56	1	12	118	1.3E+07
lcl KJ6511Chr3	52	50	24	0	69	118	1.6E+07
lcl KJ6511Chr3	48.571	35	18	0	35	69	1.6E+07
lcl KJ6511Chr3	52.174	23	11	0	12	34	1.6E+07
lcl KJ6511Chr3	29.31	58	34	1	16	66	2.1E+07
lcl KJ6511Chr2	37.069	116	42	2	34	118	1.5E+07
lcl KJ6511Chr2	40.299	67	35	1	52	118	1.5E+07
lcl KJ6511Chr2	56.667	30	13	0	34	63	1.5E+07

TBLASTN 2.10.1+

Query: lcl|KJ651117.1_prot_AJO61180.1_1 [protein=CenH3] [protein_id=AJO61180.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

lcl KJ6511Chr6	49.533	107	53	1	12	118	1646033
lcl KJ6511Chr6	49.533	107	53	1	12	118	3056252
lcl KJ6511Chr6	49.533	107	53	1	12	118	3040864
lcl KJ6511Chr6	49.533	107	53	1	12	118	3055541
lcl KJ6511Chr6	49.074	108	54	1	11	118	3046897
lcl KJ6511Chr5	49.533	107	53	1	12	118	2.2E+07
lcl KJ6511Chr5	54.167	48	15	1	21	61	2.4E+07
lcl KJ6511Chr5	55.556	27	12	0	56	82	2.4E+07
lcl KJ6511Chr5	46.667	30	16	0	78	107	2.4E+07
lcl KJ6511Chr4	49.533	107	53	1	12	118	2.1E+07
lcl KJ6511Chr4	32.143	168	53	3	12	118	2.2E+07
lcl KJ6511Chr11	49.533	107	53	1	12	118	2626139
lcl KJ6511Chr1	49.533	107	53	1	12	118	3.8E+07
lcl KJ6511Chr12	48.598	107	54	1	12	118	1.3E+07
lcl KJ6511Chr12	46.729	107	56	1	12	118	1.3E+07
lcl KJ6511Chr3	50	50	25	0	69	118	1.6E+07
lcl KJ6511Chr3	55.172	29	13	0	35	63	1.6E+07
lcl KJ6511Chr3	52.174	23	11	0	12	34	1.6E+07
lcl KJ6511Chr3	29.31	58	34	1	16	66	2.1E+07
lcl KJ6511Chr2	34.483	116	45	1	34	118	1.5E+07
lcl KJ6511Chr2	38.806	67	36	1	52	118	1.5E+07
lcl KJ6511Chr2	56.667	30	13	0	34	63	1.5E+07

TBLASTN 2.10.1+

Query: lcl|KJ651116.1_prot_AJO61179.1_1 [protein=CenH3] [protein_id=AJO61179.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

lcl KJ6511Chr6	49.533	107	53	1	12	118	3040864
lcl KJ6511Chr6	49.533	107	53	1	12	118	3056252
lcl KJ6511Chr6	49.533	107	53	1	12	118	3055541
lcl KJ6511Chr6	49.533	107	53	1	12	118	1646033
lcl KJ6511Chr6	49.533	107	53	1	12	118	3046894
lcl KJ6511Chr5	49.533	107	53	1	12	118	2.2E+07
lcl KJ6511Chr5	36.047	86	46	2	16	94	2.4E+07
lcl KJ6511Chr5	59.259	27	11	0	56	82	2.4E+07
lcl KJ6511Chr5	50	30	15	0	78	107	2.4E+07
lcl KJ6511Chr11	49.533	107	53	1	12	118	2626139
lcl KJ6511Chr4	49.533	107	53	1	12	118	2.1E+07
lcl KJ6511Chr4	32.143	168	53	3	12	118	2.2E+07
lcl KJ6511Chr1	49.533	107	53	1	12	118	3.8E+07
lcl KJ6511Chr12	48.598	107	54	1	12	118	1.3E+07
lcl KJ6511Chr12	47.959	98	50	1	21	118	1.3E+07
lcl KJ6511Chr2	36.207	116	43	1	34	118	1.5E+07
lcl KJ6511Chr2	40.299	67	35	1	52	118	1.5E+07
lcl KJ6511Chr2	60	30	12	0	34	63	1.5E+07
lcl KJ6511Chr3	52	50	24	0	69	118	1.6E+07
lcl KJ6511Chr3	58.621	29	12	0	35	63	1.6E+07
lcl KJ6511Chr3	27.869	61	41	2	18	77	9249068
lcl KJ6511Chr3	29.06	117	54	5	1	91	2E+07

TBLASTN 2.10.1+

Query: lcl|KJ651112.1_prot_AJO61175.1_1 [protein=CenH3] [protein_id=AJO61175.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

lcl KJ6511Chr6	55.102	98	43	1	17	114	1646006
lcl KJ6511Chr6	55.102	98	43	1	17	114	3056279
lcl KJ6511Chr6	55.102	98	43	1	17	114	3040837
lcl KJ6511Chr6	55.102	98	43	1	17	114	3055514
lcl KJ6511Chr6	55.102	98	43	1	17	114	3046867
lcl KJ6511Chr11	55.102	98	43	1	17	114	2626112
lcl KJ6511Chr5	55.102	98	43	1	17	114	2.1E+07
lcl KJ6511Chr5	65.116	43	15	0	10	52	2.4E+07
lcl KJ6511Chr5	50	36	17	1	52	86	2.4E+07
lcl KJ6511Chr5	60	30	12	0	74	103	2.4E+07
lcl KJ6511Chr4	55.102	98	43	1	17	114	2.1E+07
lcl KJ6511Chr4	33.333	159	45	2	17	114	2.2E+07
lcl KJ6511Chr1	55.102	98	43	1	17	114	3.8E+07
lcl KJ6511Chr1	26.923	78	48	2	42	114	3.1E+07
lcl KJ6511Chr12	55.102	98	43	1	17	114	1.3E+07
lcl KJ6511Chr12	52.041	98	46	1	17	114	1.3E+07
lcl KJ6511Chr12	23.81	105	76	3	16	118	9050848
lcl KJ6511Chr3	58	50	21	0	65	114	1.6E+07

lcl KJ6511Chr3	45.714	35	19	0	31	65	1.6E+07
lcl KJ6511Chr3	64.286	14	5	0	17	30	1.6E+07
lcl KJ6511Chr2	39.655	116	39	2	30	114	1.5E+07
lcl KJ6511Chr2	44.776	67	32	1	48	114	1.5E+07
lcl KJ6511Chr2	51.515	33	16	0	30	62	1.5E+07

TBLASTN 2.10.1+

Query: lcl|KJ651108.1_prot_AJO61171.1_1 [protein=CenH3] [protein_id=AJO61171.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

lcl KJ6511Chr6	56.044	91	39	1	24	114	1645985
lcl KJ6511Chr6	54.945	91	40	1	24	114	3040816
lcl KJ6511Chr6	54.945	91	40	1	24	114	3055493
lcl KJ6511Chr6	54.945	91	40	1	24	114	3056300
lcl KJ6511Chr6	54.945	91	40	1	24	114	3046846
lcl KJ6511Chr11	54.945	91	40	1	24	114	2626091
lcl KJ6511Chr11	38.235	34	21	0	58	91	2.8E+07
lcl KJ6511Chr5	54.945	91	40	1	24	114	2.1E+07
lcl KJ6511Chr5	75.862	29	7	0	24	52	2.4E+07
lcl KJ6511Chr5	51.351	37	17	1	52	87	2.4E+07
lcl KJ6511Chr5	51.515	33	16	0	71	103	2.4E+07
lcl KJ6511Chr12	54.945	91	40	1	24	114	1.3E+07
lcl KJ6511Chr12	52.747	91	42	1	24	114	1.3E+07
lcl KJ6511Chr4	54.945	91	40	1	24	114	2.1E+07
lcl KJ6511Chr4	39.13	115	39	2	31	114	2.2E+07
lcl KJ6511Chr1	54.945	91	40	1	24	114	3.8E+07
lcl KJ6511Chr1	26.923	78	48	2	42	114	3.1E+07
lcl KJ6511Chr2	38.793	116	40	2	30	114	1.5E+07
lcl KJ6511Chr2	44.776	67	32	1	48	114	1.5E+07
lcl KJ6511Chr2	55.172	29	13	0	30	58	1.5E+07
lcl KJ6511Chr3	58	50	21	0	65	114	1.6E+07
lcl KJ6511Chr3	35.484	62	37	2	31	92	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KJ651107.1_prot_AJO61170.1_1 [protein=CenH3] [protein_id=AJO61170.1] [loc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

21 hits found

lcl KJ6511Chr12	52.041	98	46	1	21	118	1.3E+07
lcl KJ6511Chr12	50	98	48	1	21	118	1.3E+07
lcl KJ6511Chr5	52.041	98	46	1	21	118	2.1E+07
lcl KJ6511Chr5	66.667	36	12	0	21	56	2.4E+07
lcl KJ6511Chr5	51.852	27	13	0	56	82	2.4E+07
lcl KJ6511Chr5	53.333	30	14	0	78	107	2.4E+07
lcl KJ6511Chr6	52.041	98	46	1	21	118	3056279
lcl KJ6511Chr6	52.041	98	46	1	21	118	3040837
lcl KJ6511Chr6	49.533	107	53	1	12	118	1646033

lcl KJ6511Chr6	52.041	98	46	1	21	118	3055514
lcl KJ6511Chr6	52.041	98	46	1	21	118	3046867
lcl KJ6511Chr11	52.041	98	46	1	21	118	2626112
lcl KJ6511Chr4	52.041	98	46	1	21	118	2.1E+07
lcl KJ6511Chr4	32.143	168	53	3	12	118	2.2E+07
lcl KJ6511Chr1	52.041	98	46	1	21	118	3.8E+07
lcl KJ6511Chr2	37.069	116	42	2	34	118	1.5E+07
lcl KJ6511Chr2	43.284	67	33	1	52	118	1.5E+07
lcl KJ6511Chr2	53.333	30	14	0	34	63	1.5E+07
lcl KJ6511Chr3	54	50	23	0	69	118	1.6E+07
lcl KJ6511Chr3	42.857	35	20	0	35	69	1.6E+07
lcl KJ6511Chr3	64.286	14	5	0	21	34	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KJ507244.1_prot_AHW98238.1_1 [gene=CenH3] [protein=centromeric histone]

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

24 hits found

lcl KJ5072Chr12	53.608	97	44	1	22	118	1.3E+07
lcl KJ5072Chr12	49.485	97	48	1	22	118	1.3E+07
lcl KJ5072Chr11	53.191	94	43	1	25	118	2626100
lcl KJ5072Chr6	52.577	97	45	1	22	118	3040834
lcl KJ5072Chr6	52.577	97	45	1	22	118	1646003
lcl KJ5072Chr6	53.191	94	43	1	25	118	3055502
lcl KJ5072Chr6	49.074	108	54	1	11	118	3056249
lcl KJ5072Chr6	52.577	97	45	1	22	118	3046864
lcl KJ5072Chr5	49.074	108	54	1	11	118	2.2E+07
lcl KJ5072Chr5	60	40	16	0	17	56	2.4E+07
lcl KJ5072Chr5	51.852	27	13	0	56	82	2.4E+07
lcl KJ5072Chr5	51.515	33	16	0	75	107	2.4E+07
lcl KJ5072Chr4	52.577	97	45	1	22	118	2.1E+07
lcl KJ5072Chr4	32.911	158	45	3	22	118	2.2E+07
lcl KJ5072Chr4	24.793	121	66	5	20	119	1121700
lcl KJ5072Chr1	52.577	97	45	1	22	118	3.8E+07
lcl KJ5072Chr2	36.207	116	43	1	34	118	1.5E+07
lcl KJ5072Chr2	47.761	67	30	1	52	118	1.5E+07
lcl KJ5072Chr2	50	26	13	0	34	59	1.5E+07
lcl KJ5072Chr2	30	60	42	0	12	71	2.8E+07
lcl KJ5072Chr3	60	50	20	0	69	118	1.6E+07
lcl KJ5072Chr3	37.143	35	22	0	35	69	1.6E+07
lcl KJ5072Chr3	45.833	24	13	0	11	34	1.6E+07
lcl KJ5072Chr8	50	28	14	0	20	47	2.5E+07

TBLASTN 2.10.1+

Query: lcl|KJ507242.1_prot_AHW98236.1_1 [gene=CenH3] [protein=centromeric histone]

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

24 hits found

lcl KJ5072 Chr12	54.639	97	43	1	22	118	1.3E+07
lcl KJ5072 Chr12	50.515	97	47	1	22	118	1.3E+07
lcl KJ5072 Chr11	54.255	94	42	1	25	118	2626100
lcl KJ5072 Chr11	42.857	42	23	1	8	48	4447208
lcl KJ5072 Chr6	53.608	97	44	1	22	118	1646003
lcl KJ5072 Chr6	53.608	97	44	1	22	118	3040834
lcl KJ5072 Chr6	54.255	94	42	1	25	118	3055502
lcl KJ5072 Chr6	53.608	97	44	1	22	118	3056282
lcl KJ5072 Chr6	53.608	97	44	1	22	118	3046864
lcl KJ5072 Chr6	52	25	12	0	5	29	6305245
lcl KJ5072 Chr5	53.608	97	44	1	22	118	2.1E+07
lcl KJ5072 Chr5	58.537	41	17	0	16	56	2.4E+07
lcl KJ5072 Chr5	51.852	27	13	0	56	82	2.4E+07
lcl KJ5072 Chr5	54.545	33	15	0	75	107	2.4E+07
lcl KJ5072 Chr4	53.608	97	44	1	22	118	2.1E+07
lcl KJ5072 Chr4	33.544	158	44	3	22	118	2.2E+07
lcl KJ5072 Chr4	24.793	121	66	5	20	119	1121700
lcl KJ5072 Chr1	53.608	97	44	1	22	118	3.8E+07
lcl KJ5072 Chr2	37.069	116	42	1	34	118	1.5E+07
lcl KJ5072 Chr2	49.254	67	29	1	52	118	1.5E+07
lcl KJ5072 Chr2	50	26	13	0	34	59	1.5E+07
lcl KJ5072 Chr3	62	50	19	0	69	118	1.6E+07
lcl KJ5072 Chr3	37.143	35	22	0	35	69	1.6E+07
lcl KJ5072 Chr3	69.231	13	4	0	22	34	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KJ507235.1_prot_AHW98229.1_1 [gene=CenH3] [protein=centromeric histone]

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

21 hits found

lcl KJ5072 Chr6	60.748	107	40	2	47	152	3040864
lcl KJ5072 Chr6	60.748	107	40	2	47	152	3056252
lcl KJ5072 Chr6	60.748	107	40	2	47	152	3055541
lcl KJ5072 Chr6	60.748	107	40	2	47	152	3046894
lcl KJ5072 Chr6	61.682	107	39	2	47	152	1646033
lcl KJ5072 Chr5	60.748	107	40	2	47	152	2.2E+07
lcl KJ5072 Chr5	60	40	16	0	51	90	2.4E+07
lcl KJ5072 Chr5	68.75	16	5	0	90	105	2.4E+07
lcl KJ5072 Chr5	66.667	21	7	0	121	141	2.4E+07
lcl KJ5072 Chr11	60.748	107	40	2	47	152	2626139
lcl KJ5072 Chr1	60.748	107	40	2	47	152	3.8E+07
lcl KJ5072 Chr4	62.245	98	36	1	55	152	2.1E+07
lcl KJ5072 Chr4	38.69	168	41	3	47	152	2.2E+07
lcl KJ5072 Chr12	61.224	98	37	1	55	152	1.3E+07
lcl KJ5072 Chr12	58.163	98	40	1	55	152	1.3E+07
lcl KJ5072 Chr2	43.966	116	34	1	68	152	1.5E+07
lcl KJ5072 Chr2	58.209	67	23	1	86	152	1.5E+07

lcl KJ5072 Chr2	50	32	16	0	68	99	1.5E+07
lcl KJ5072 Chr3	75	32	8	0	121	152	1.6E+07
lcl KJ5072 Chr3	48.571	35	18	0	69	103	1.6E+07
lcl KJ5072 Chr3	44.444	27	14	1	47	72	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KJ507234.1_prot_AHW98228.1_1 [gene=CenH3] [protein=centromeric histone]

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

20 hits found

lcl KJ5072 Chr6	59.813	107	41	2	47	152	3040864
lcl KJ5072 Chr6	59.813	107	41	2	47	152	3056252
lcl KJ5072 Chr6	59.813	107	41	2	47	152	3055541
lcl KJ5072 Chr6	59.813	107	41	2	47	152	3046894
lcl KJ5072 Chr6	60.748	107	40	2	47	152	1646033
lcl KJ5072 Chr5	59.813	107	41	2	47	152	2.2E+07
lcl KJ5072 Chr5	64.103	39	14	0	52	90	2.4E+07
lcl KJ5072 Chr5	56.25	16	7	0	90	105	2.4E+07
lcl KJ5072 Chr5	72.222	18	5	0	124	141	2.4E+07
lcl KJ5072 Chr11	59.813	107	41	2	47	152	2626139
lcl KJ5072 Chr1	59.813	107	41	2	47	152	3.8E+07
lcl KJ5072 Chr4	59.813	107	41	2	47	152	2.1E+07
lcl KJ5072 Chr4	38.69	168	41	3	47	152	2.2E+07
lcl KJ5072 Chr12	59.184	98	39	1	55	152	1.3E+07
lcl KJ5072 Chr12	56.122	98	42	1	55	152	1.3E+07
lcl KJ5072 Chr2	43.103	116	35	1	68	152	1.5E+07
lcl KJ5072 Chr2	56.716	67	24	1	86	152	1.5E+07
lcl KJ5072 Chr2	50	32	16	0	68	99	1.5E+07
lcl KJ5072 Chr3	75.862	29	7	0	124	152	1.6E+07
lcl KJ5072 Chr3	48.571	35	18	0	69	103	1.6E+07

TBLASTN 2.10.1+

Query: lcl|HM582916.1_prot_ADN92693.1_1 [gene=CENH3] [protein=centromere-specific]

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

lcl HM58: Chr6	53.211	109	49	1	71	179	1646033
lcl HM58: Chr6	53.211	109	49	2	71	179	3040864
lcl HM58: Chr6	52.294	109	50	1	71	179	3056252
lcl HM58: Chr6	53.211	109	49	2	71	179	3055541
lcl HM58: Chr6	52.294	109	50	1	71	179	3046894
lcl HM58: Chr1	52.778	108	49	1	71	178	3.8E+07
lcl HM58: Chr5	53.211	109	49	2	71	179	2.2E+07
lcl HM58: Chr5	60.976	41	16	0	75	115	2.4E+07
lcl HM58: Chr5	51.724	29	13	1	114	142	2.4E+07
lcl HM58: Chr5	51.613	31	15	0	140	170	2.4E+07
lcl HM58: Chr11	53.211	109	49	2	71	179	2626139
lcl HM58: Chr4	52.294	109	50	1	71	179	2.1E+07

lcl HM58:Chr4	35.329	167	46	3	74	179	2.2E+07
lcl HM58:Chr12	50.893	112	47	2	71	179	1.3E+07
lcl HM58:Chr12	48.624	109	48	2	74	179	1.3E+07
lcl HM58:Chr3	60.784	51	20	0	129	179	1.6E+07
lcl HM58:Chr3	51.724	29	14	0	94	122	1.6E+07
lcl HM58:Chr3	44.444	27	15	0	71	97	1.6E+07
lcl HM58:Chr2	39.831	118	39	2	93	179	1.5E+07
lcl HM58:Chr2	58.824	51	21	0	129	179	1.5E+07
lcl HM58:Chr2	53.333	30	14	0	93	122	1.5E+07
lcl HM58:Chr2	36.842	38	24	0	125	162	2.5E+07

TBLASTN 2.10.1+

Query: lcl|MN625524.1_prot_QGY64363.1_1 [gene=CENH3] [protein=histone H3-like cent

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

lcl MN62:Chr11	60.909	110	40	2	45	154	2626139
lcl MN62:Chr6	60.909	110	40	2	45	154	3040864
lcl MN62:Chr6	60.909	110	40	2	45	154	3055541
lcl MN62:Chr6	59.821	112	42	2	43	154	3046900
lcl MN62:Chr6	60.909	110	40	2	45	154	3056252
lcl MN62:Chr6	60	110	41	2	45	154	1646033
lcl MN62:Chr5	61.468	109	39	2	46	154	2.2E+07
lcl MN62:Chr5	74.419	43	11	0	49	91	2.4E+07
lcl MN62:Chr5	57.692	26	11	0	120	145	2.4E+07
lcl MN62:Chr1	62.037	108	38	2	46	153	3.8E+07
lcl MN62:Chr4	60.909	110	40	2	45	154	2.1E+07
lcl MN62:Chr4	38.824	170	41	3	46	154	2.2E+07
lcl MN62:Chr12	61.818	110	39	2	45	154	1.3E+07
lcl MN62:Chr12	58.716	109	42	2	46	154	1.3E+07
lcl MN62:Chr2	43.697	119	32	2	69	154	1.5E+07
lcl MN62:Chr2	65.714	35	12	0	120	154	1.5E+07
lcl MN62:Chr2	56.667	30	13	0	69	98	1.5E+07
lcl MN62:Chr2	76.471	17	4	0	56	72	2E+07
lcl MN62:Chr2	50	32	14	1	40	71	1.5E+07
lcl MN62:Chr3	68.571	35	11	0	120	154	1.6E+07
lcl MN62:Chr3	48.571	35	18	0	70	104	1.6E+07
lcl MN62:Chr3	53.571	28	11	1	46	73	1.6E+07

TBLASTN 2.10.1+

Query: lcl|MN625523.1_prot_QGY64362.1_1 [gene=CENH3] [protein=histone H3-like cent

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

lcl MN62:Chr11	61.818	110	39	2	45	154	2626139
lcl MN62:Chr6	61.818	110	39	2	45	154	3040864
lcl MN62:Chr6	61.818	110	39	2	45	154	3055541
lcl MN62:Chr6	60.714	112	41	2	43	154	3046900

lcl MN62! Chr6	61.818	110	39	2	45	154	3056252
lcl MN62! Chr6	60.909	110	40	2	45	154	1646033
lcl MN62! Chr5	61.818	110	39	2	45	154	2.2E+07
lcl MN62! Chr5	76.744	43	10	0	49	91	2.4E+07
lcl MN62! Chr5	57.692	26	11	0	120	145	2.4E+07
lcl MN62! Chr4	61.818	110	39	2	45	154	2.1E+07
lcl MN62! Chr4	39.412	170	40	3	46	154	2.2E+07
lcl MN62! Chr1	62.963	108	37	2	46	153	3.8E+07
lcl MN62! Chr12	62.727	110	38	2	45	154	1.3E+07
lcl MN62! Chr12	58.182	110	43	2	45	154	1.3E+07
lcl MN62! Chr2	43.697	119	32	2	69	154	1.5E+07
lcl MN62! Chr2	65.714	35	12	0	120	154	1.5E+07
lcl MN62! Chr2	56.667	30	13	0	69	98	1.5E+07
lcl MN62! Chr2	77.778	18	4	0	56	73	2E+07
lcl MN62! Chr2	53.125	32	13	1	40	71	1.5E+07
lcl MN62! Chr3	68.571	35	11	0	120	154	1.6E+07
lcl MN62! Chr3	48.571	35	18	0	70	104	1.6E+07
lcl MN62! Chr3	61.538	26	8	1	46	71	1.6E+07

TBLASTN 2.10.1+

Query: lcl|MN625521.1_prot_QGY64360.1_1 [gene=CENH3] [protein=histone H3-like cent

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

20 hits found

lcl MN62! Chr12	57.547	106	44	1	40	145	1.3E+07
lcl MN62! Chr12	53.774	106	48	1	40	145	1.3E+07
lcl MN62! Chr11	48.276	145	64	3	1	145	2626220
lcl MN62! Chr6	48.276	145	64	3	1	145	3055622
lcl MN62! Chr6	48.276	145	64	3	1	145	3040945
lcl MN62! Chr6	56.604	106	45	1	40	145	3046888
lcl MN62! Chr6	56.604	106	45	1	40	145	1646027
lcl MN62! Chr6	48.276	145	64	3	1	145	3056171
lcl MN62! Chr5	48.276	145	64	3	1	145	2.2E+07
lcl MN62! Chr5	74.286	35	9	0	48	82	2.4E+07
lcl MN62! Chr4	48.276	145	64	3	1	145	2.1E+07
lcl MN62! Chr4	37.126	167	44	3	40	145	2.2E+07
lcl MN62! Chr1	48.611	144	63	3	1	144	3.8E+07
lcl MN62! Chr3	57.692	26	11	0	61	86	1.6E+07
lcl MN62! Chr3	52	25	12	0	40	64	1.6E+07
lcl MN62! Chr3	66.667	21	7	0	125	145	1.6E+07
lcl MN62! Chr2	40.171	117	39	1	60	145	1.5E+07
lcl MN62! Chr2	55.556	27	12	0	60	86	1.5E+07
lcl MN62! Chr2	45.946	37	20	0	45	81	2E+07
lcl MN62! Chr2	61.905	21	8	0	125	145	1.5E+07

TBLASTN 2.10.1+

Query: lcl|MN625520.1_prot_QGY64359.1_1 [gene=CENH3] [protein=histone H3-like cent

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

24 hits found

lcl MN62! Chr11	51.389	144	60	3	1	144	2626220
lcl MN62! Chr6	51.389	144	60	3	1	144	3055622
lcl MN62! Chr6	51.389	144	60	3	1	144	3040945
lcl MN62! Chr6	51.389	144	60	3	1	144	3056171
lcl MN62! Chr6	57.944	107	44	1	38	144	3046891
lcl MN62! Chr6	57.009	107	45	1	38	144	1646030
lcl MN62! Chr5	51.389	144	60	3	1	144	2.2E+07
lcl MN62! Chr5	60.87	46	18	0	35	80	2.4E+07
lcl MN62! Chr5	44.444	27	15	0	81	107	2.4E+07
lcl MN62! Chr5	54.545	33	15	0	103	135	2.4E+07
lcl MN62! Chr4	51.389	144	60	3	1	144	2.1E+07
lcl MN62! Chr4	37.278	169	43	4	38	144	2.2E+07
lcl MN62! Chr4	25.472	106	73	2	24	124	2.3E+07
lcl MN62! Chr1	51.748	143	59	3	1	143	3.8E+07
lcl MN62! Chr12	48.98	147	59	4	1	144	1.3E+07
lcl MN62! Chr12	46.259	147	63	5	1	144	1.3E+07
lcl MN62! Chr3	60.784	51	20	0	94	144	1.6E+07
lcl MN62! Chr3	43.333	30	17	0	38	67	1.6E+07
lcl MN62! Chr3	57.692	26	11	0	60	85	1.6E+07
lcl MN62! Chr2	39.316	117	40	1	59	144	1.5E+07
lcl MN62! Chr2	58.824	51	21	0	94	144	1.5E+07
lcl MN62! Chr2	45	40	22	0	59	98	1.5E+07
lcl MN62! Chr2	40.678	59	33	1	46	102	2E+07
lcl MN62! Chr2	45.161	31	17	0	31	61	1.5E+07

TBLASTN 2.10.1+

Query: lcl|MN625519.1_prot_QGY64358.1_1 [gene=CENH3] [protein=histone H3-like cent

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

24 hits found

lcl MN62! Chr11	52.482	141	57	3	1	141	2626220
lcl MN62! Chr6	52.482	141	57	3	1	141	3055622
lcl MN62! Chr6	52.482	141	57	3	1	141	3040945
lcl MN62! Chr6	52.482	141	57	3	1	141	3056171
lcl MN62! Chr6	59.615	104	41	1	38	141	3046891
lcl MN62! Chr6	58.654	104	42	1	38	141	1646030
lcl MN62! Chr5	52.482	141	57	3	1	141	2.2E+07
lcl MN62! Chr5	60.87	46	18	0	35	80	2.4E+07
lcl MN62! Chr5	44.444	27	15	0	81	107	2.4E+07
lcl MN62! Chr5	51.515	33	16	0	103	135	2.4E+07
lcl MN62! Chr4	52.482	141	57	3	1	141	2.1E+07
lcl MN62! Chr4	37.952	166	40	4	38	141	2.2E+07
lcl MN62! Chr4	25.439	114	79	2	16	124	2.3E+07
lcl MN62! Chr1	52.482	141	57	3	1	141	3.8E+07
lcl MN62! Chr12	49.306	144	57	4	1	141	1.3E+07

lcl MN62! Chr12	48.592	142	57	5	1	139	1.3E+07
lcl MN62! Chr3	64.583	48	17	0	94	141	1.6E+07
lcl MN62! Chr3	48.148	27	14	0	38	64	1.6E+07
lcl MN62! Chr3	57.692	26	11	0	60	85	1.6E+07
lcl MN62! Chr2	42.105	114	35	1	59	141	1.5E+07
lcl MN62! Chr2	66.667	48	16	0	94	141	1.5E+07
lcl MN62! Chr2	45	40	22	0	59	98	1.5E+07
lcl MN62! Chr2	40.678	59	33	1	46	102	2E+07
lcl MN62! Chr2	45.161	31	17	0	31	61	1.5E+07

TBLASTN 2.10.1+

Query: lcl|MG384774.1_prot_AUN88460.1_1 [gene=CENH3] [protein=alpha centromeric h

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

53 hits found

lcl MG38! Chr11	64	100	35	1	65	164	2626112
lcl MG38! Chr11	40.909	44	25	1	86	129	1.8E+07
lcl MG38! Chr11	43.182	44	24	1	86	129	2.4E+07
lcl MG38! Chr6	64	100	35	1	65	164	3040837
lcl MG38! Chr6	64	100	35	1	65	164	3055514
lcl MG38! Chr6	64	100	35	1	65	164	3056279
lcl MG38! Chr6	64	100	35	1	65	164	3046867
lcl MG38! Chr6	63	100	36	1	65	164	1646006
lcl MG38! Chr6	38.636	44	26	1	86	129	2.8E+07
lcl MG38! Chr6	38.636	44	26	1	86	129	1.6E+07
lcl MG38! Chr6	38.636	44	26	1	86	129	1.5E+07
lcl MG38! Chr6	38.636	44	26	1	86	129	2.4E+07
lcl MG38! Chr5	64	100	35	1	65	164	2.1E+07
lcl MG38! Chr5	84.211	38	6	0	63	100	2.4E+07
lcl MG38! Chr5	48.148	27	14	0	100	126	2.4E+07
lcl MG38! Chr5	76.923	26	6	0	124	149	2.4E+07
lcl MG38! Chr5	85	20	3	0	1	20	2.4E+07
lcl MG38! Chr5	55.172	29	12	1	139	166	2.4E+07
lcl MG38! Chr5	38.636	44	26	1	86	129	1.2E+07
lcl MG38! Chr5	38.636	44	26	1	86	129	7739575
lcl MG38! Chr5	36.364	44	27	1	86	129	8333986
lcl MG38! Chr5	38.636	44	26	1	86	129	1.2E+07
lcl MG38! Chr5	38.636	44	26	1	86	129	7092135
lcl MG38! Chr4	64	100	35	1	65	164	2.1E+07
lcl MG38! Chr4	39.752	161	36	3	65	164	2.2E+07
lcl MG38! Chr4	38.636	44	26	1	86	129	6034854
lcl MG38! Chr4	38.636	44	26	1	86	129	6358900
lcl MG38! Chr1	64.286	98	34	1	65	162	3.8E+07
lcl MG38! Chr1	40.909	44	25	1	86	129	1E+07
lcl MG38! Chr12	59	100	40	1	65	164	1.3E+07
lcl MG38! Chr12	57	100	42	1	65	164	1.3E+07
lcl MG38! Chr12	38.636	44	26	1	86	129	2.7E+07

lcl MG38: Chr2	42.857	119	37	2	78	165	1.5E+07
lcl MG38: Chr2	62.264	53	20	0	113	165	1.5E+07
lcl MG38: Chr2	56.667	30	13	0	78	107	1.5E+07
lcl MG38: Chr2	51.429	35	17	0	65	99	2E+07
lcl MG38: Chr2	39.583	48	19	2	119	164	2E+07
lcl MG38: Chr2	75	16	4	0	65	80	1.5E+07
lcl MG38: Chr2	38.636	44	26	1	86	129	1.5E+07
lcl MG38: Chr3	65.385	52	18	0	113	164	1.6E+07
lcl MG38: Chr3	54.286	35	16	0	79	113	1.6E+07
lcl MG38: Chr3	44.444	45	17	2	65	102	1.6E+07
lcl MG38: Chr3	38.636	44	26	1	86	129	2E+07
lcl MG38: Chr3	38.636	44	26	1	86	129	1.9E+07
lcl MG38: Chr3	38.636	44	26	1	86	129	1.9E+07
lcl MG38: Chr10	38.636	44	26	1	86	129	6630385
lcl MG38: Chr10	38.636	44	26	1	86	129	9325176
lcl MG38: Chr10	38.636	44	26	1	86	129	1.1E+07
lcl MG38: Chr10	38.636	44	26	1	86	129	1.3E+07
lcl MG38: Chr10	38.636	44	26	1	86	129	7380895
lcl MG38: Chr9	38.636	44	26	1	86	129	7580887
lcl MG38: Chr7	52.174	23	11	0	107	129	4633593
lcl MG38: Chr8	38.636	44	26	1	86	129	9874145

TBLASTN 2.10.1+

Query: lcl|KT600804.1_prot_AMH40810.1_1 [gene=CENH3] [protein=centromere-specific

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

lcl KT600: Chr6	57.609	92	38	1	74	165	3040813
lcl KT600: Chr6	57.609	92	38	1	74	165	3056303
lcl KT600: Chr6	57.609	92	38	1	74	165	3055490
lcl KT600: Chr6	57.609	92	38	1	74	165	3046843
lcl KT600: Chr6	57.609	92	38	1	74	165	1645982
lcl KT600: Chr11	57.609	92	38	1	74	165	2626088
lcl KT600: Chr5	57.609	92	38	1	74	165	2.1E+07
lcl KT600: Chr5	78.571	28	6	0	74	101	2.4E+07
lcl KT600: Chr5	70.37	27	8	0	101	127	2.4E+07
lcl KT600: Chr5	61.538	26	10	0	125	150	2.4E+07
lcl KT600: Chr5	65	20	7	0	148	167	2.4E+07
lcl KT600: Chr5	42.105	38	21	1	3	39	5980000
lcl KT600: Chr1	57.778	90	37	1	74	163	3.8E+07
lcl KT600: Chr4	57.609	92	38	1	74	165	2.1E+07
lcl KT600: Chr4	42.735	117	36	2	80	165	2.2E+07
lcl KT600: Chr12	55.435	92	40	1	74	165	1.3E+07
lcl KT600: Chr12	54.945	91	40	1	75	165	1.3E+07
lcl KT600: Chr2	41.525	118	38	2	79	165	1.5E+07
lcl KT600: Chr2	46.835	79	25	2	104	165	1.5E+07
lcl KT600: Chr2	63.333	30	10	1	79	107	1.5E+07

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lcl|KT600:Chr3      61.538      52      20      0      114      165 1.6E+07
lcl|KT600:Chr3      59.259      27      11      0      80      106 1.6E+07
# TBLASTN 2.10.1+
# Query: lcl|KT600803.1_prot_AMH40809.1_1 [gene=CENH3] [protein=centromere-specific
# Database: Nippon
# Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens
# 33 hits found
lcl|KT600:Chr6      59.375      96      38      1      70      165 3040825
lcl|KT600:Chr6      42.424      165     65      4      1      165 3055622
lcl|KT600:Chr6      59.375      96      38      1      70      165 3056291
lcl|KT600:Chr6      59.375      96      38      1      70      165 3046855
lcl|KT600:Chr6      58.333      96      39      1      70      165 1645994
lcl|KT600:Chr6      33.333      60      38      1      54      113 1.2E+07
lcl|KT600:Chr11     42.424      165     65      4      1      165 2626220
lcl|KT600:Chr5      59.375      96      38      1      70      165 2.1E+07
lcl|KT600:Chr5      68.889      45      14      0      57      101 2.4E+07
lcl|KT600:Chr5      70.37      27      8       0      101     127 2.4E+07
lcl|KT600:Chr5      61.538      26      10      0      125     150 2.4E+07
lcl|KT600:Chr5      76.471      17      4       0      151     167 2.4E+07
lcl|KT600:Chr5      42.105      38      21      1      3       39 5980000
lcl|KT600:Chr1      59.574      94      37      1      70      163 3.8E+07
lcl|KT600:Chr1      31.707      41      26      1      95      135 1E+07
lcl|KT600:Chr1      36.842      38      22      1      25      62 1E+07
lcl|KT600:Chr4      59.375      96      38      1      70      165 2.1E+07
lcl|KT600:Chr4      36.943      157     38      3      70      165 2.2E+07
lcl|KT600:Chr4      34.426      61      38      1      54      114 1.1E+07
lcl|KT600:Chr4      35         60      37      1      54      113 9964857
lcl|KT600:Chr12     57.292      96      40      1      70      165 1.3E+07
lcl|KT600:Chr12     48.062      129     62      4      38      165 1.3E+07
lcl|KT600:Chr12     33.333      60      38      1      54      113 1.1E+07
lcl|KT600:Chr2      41.525      118     38      2      79      165 1.5E+07
lcl|KT600:Chr2      46.835      79      25      2      104     165 1.5E+07
lcl|KT600:Chr2      63.333      30      10      1      79      107 1.5E+07
lcl|KT600:Chr2      48.485      33      15      1      50      82 2E+07
lcl|KT600:Chr2      36         50      22      2      120     167 2E+07
lcl|KT600:Chr3      61.538      52      20      0      114     165 1.6E+07
lcl|KT600:Chr3      59.259      27      11      0      80      106 1.6E+07
lcl|KT600:Chr8      38.333      60      35      1      54      113 2.2E+07
lcl|KT600:Chr8      33.333      60      38      1      54      113 2.3E+07
lcl|KT600:Chr8      23.622      127     91      2      40      162 2.7E+07
# TBLASTN 2.10.1+
# Query: lcl|KP878239.1_prot_AK132619.1_1 [gene=CENH3] [protein=centromere specific hi
# Database: Nippon
# Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens
# 31 hits found
lcl|KP878:Chr6      52.542      118     52      3      38      154 3046915

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lcl KP878.Chr6	58.333	96	39	1	59	154	3040825
lcl KP878.Chr6	58.333	96	39	1	59	154	3055502
lcl KP878.Chr6	58.333	96	39	1	59	154	3056291
lcl KP878.Chr6	57.292	96	40	1	59	154	1645994
lcl KP878.Chr6	42.5	40	11	1	38	65	7680155
lcl KP878.Chr11	58.333	96	39	1	59	154	2626100
lcl KP878.Chr5	58.333	96	39	1	59	154	2.1E+07
lcl KP878.Chr5	65.306	49	16	1	43	90	2.4E+07
lcl KP878.Chr5	66.667	27	9	0	90	116	2.4E+07
lcl KP878.Chr5	61.538	26	10	0	114	139	2.4E+07
lcl KP878.Chr5	68.421	19	6	0	138	156	2.4E+07
lcl KP878.Chr4	58.333	96	39	1	59	154	2.1E+07
lcl KP878.Chr4	32.804	189	59	4	34	154	2.2E+07
lcl KP878.Chr4	33.871	62	35	2	46	103	1.1E+07
lcl KP878.Chr4	32.203	59	38	1	46	102	2.1E+07
lcl KP878.Chr1	58.511	94	38	1	59	152	3.8E+07
lcl KP878.Chr12	43.949	157	63	5	1	154	1.3E+07
lcl KP878.Chr12	55.208	96	42	1	59	154	1.3E+07
lcl KP878.Chr12	32.787	61	35	2	46	102	1.1E+07
lcl KP878.Chr12	32.292	96	59	3	8	103	2433708
lcl KP878.Chr2	40.678	118	39	2	68	154	1.5E+07
lcl KP878.Chr2	45.57	79	26	2	93	154	1.5E+07
lcl KP878.Chr2	63.333	30	10	1	68	96	1.5E+07
lcl KP878.Chr2	37.255	51	22	2	108	156	2E+07
lcl KP878.Chr2	84.615	13	2	0	59	71	2E+07
lcl KP878.Chr3	59.615	52	21	0	103	154	1.6E+07
lcl KP878.Chr3	55.172	29	13	0	69	97	1.6E+07
lcl KP878.Chr8	35.593	59	36	1	46	102	2.2E+07
lcl KP878.Chr10	28.125	96	58	2	31	120	8621404
lcl KP878.Chr7	28.169	71	47	2	88	156	2.8E+07

TBLASTN 2.10.1+

Query: lcl|KP878237.1_prot_AKI32617.1_1 [gene=CENH3] [protein=centromere specific hi

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

13 hits found

lcl KP878.Chr5	54.762	42	18	1	43	83	2.4E+07
lcl KP878.Chr5	75	20	5	0	59	78	2.1E+07
lcl KP878.Chr12	33.333	99	39	5	1	93	1.3E+07
lcl KP878.Chr12	47.368	38	17	1	59	93	1.3E+07
lcl KP878.Chr6	50	42	18	2	38	78	3046915
lcl KP878.Chr6	47.368	38	17	1	59	93	3056291
lcl KP878.Chr6	75	20	5	0	59	78	3040825
lcl KP878.Chr6	44.737	38	18	1	59	93	1645994
lcl KP878.Chr6	75	20	5	0	59	78	3055502
lcl KP878.Chr6	42.5	40	11	1	38	65	7680155
lcl KP878.Chr4	47.368	38	17	1	59	93	2.1E+07

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lcl|KP878.Chr11      75      20      5      0      59      78 2626100
lcl|KP878.Chr1       75      20      5      0      59      78 3.8E+07
# TBLASTN 2.10.1+
# Query: lcl|KP878236.1_prot_AKI32616.1_1 [gene=CENH3] [protein=centromere specific hi
# Database: Nippon
# Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens
# 23 hits found
lcl|KP878.Chr6        50      118      55      3      38      154 3046915
lcl|KP878.Chr6       55.208     96      42      1      59      154 3040825
lcl|KP878.Chr6       55.208     96      42      1      59      154 3056291
lcl|KP878.Chr6       55.208     96      42      1      59      154 3055502
lcl|KP878.Chr6       54.167     96      43      1      59      154 1645994
lcl|KP878.Chr6        42.5      40      11      1      38       65 7680155
lcl|KP878.Chr11     55.208     96      42      1      59      154 2626100
lcl|KP878.Chr5     55.208     96      42      1      59      154 2.1E+07
lcl|KP878.Chr5     63.265     49      17      1      43       90 2.4E+07
lcl|KP878.Chr5     62.963     27      10      0      90      116 2.4E+07
lcl|KP878.Chr5     61.538     26      10      0     114      139 2.4E+07
lcl|KP878.Chr1     56.383     94      40      1      59      152 3.8E+07
lcl|KP878.Chr4     55.208     96      42      1      59      154 2.1E+07
lcl|KP878.Chr4     31.217    189      62      4      34      154 2.2E+07
lcl|KP878.Chr12    43.312    157      64      5       1      154 1.3E+07
lcl|KP878.Chr12    54.167     96      43      1      59      154 1.3E+07
lcl|KP878.Chr2     38.136    118      42      2      68      154 1.5E+07
lcl|KP878.Chr2     44.304     79      27      2      93      154 1.5E+07
lcl|KP878.Chr2     56.667     30      12      1      68       96 1.5E+07
lcl|KP878.Chr2     38.776     49      20      2     108      154 2E+07
lcl|KP878.Chr2     76.923     13       3      0      59       71 2E+07
lcl|KP878.Chr3     57.692     52      22      0     103      154 1.6E+07
lcl|KP878.Chr3        50      28      14      0      70       97 1.6E+07
# TBLASTN 2.10.1+
# Query: lcl|KP878232.1_prot_AKI32612.1_1 [gene=CENH3] [protein=centromere specific hi
# Database: Nippon
# Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens
# 21 hits found
lcl|KP878.Chr6       52.055     73      34      1      74      146 3040813
lcl|KP878.Chr6       52.055     73      34      1      74      146 3055490
lcl|KP878.Chr6       52.055     73      34      1      74      146 3056303
lcl|KP878.Chr6       52.055     73      34      1      74      146 3046843
lcl|KP878.Chr6       52.055     73      34      1      74      146 1645982
lcl|KP878.Chr11     52.055     73      34      1      74      146 2626088
lcl|KP878.Chr5     52.055     73      34      1      74      146 2.1E+07
lcl|KP878.Chr5     78.571     28       6      0      74      101 2.4E+07
lcl|KP878.Chr5      70.37      27       8      0     101      127 2.4E+07
lcl|KP878.Chr5     46.429     28      15      0     125      152 2.4E+07
lcl|KP878.Chr5     42.105     38      21      1       3       39 5980000

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lcl KP878.Chr1	52.778	72	33	1	74	145	3.8E+07
lcl KP878.Chr4	48.75	80	40	1	74	153	2.1E+07
lcl KP878.Chr4	34.286	105	38	2	80	153	2.2E+07
lcl KP878.Chr12	52.055	73	34	1	74	146	1.3E+07
lcl KP878.Chr12	51.389	72	34	1	75	146	1.3E+07
lcl KP878.Chr2	33.962	106	39	2	79	153	1.5E+07
lcl KP878.Chr2	42.5	40	23	0	114	153	1.5E+07
lcl KP878.Chr2	63.333	30	10	1	79	107	1.5E+07
lcl KP878.Chr3	53.125	32	15	0	114	145	1.6E+07
lcl KP878.Chr3	59.259	27	11	0	80	106	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KP878228.1_prot_AKI32608.1_1 [gene=CENH3] [protein=centromere specific hi

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

8 hits found

lcl KP878.Chr11	52	25	12	0	47	71	5306225
lcl KP878.Chr5	42.105	38	21	1	3	39	5980000
lcl KP878.Chr5	42.857	42	20	1	27	68	1.2E+07
lcl KP878.Chr12	40.476	42	25	0	28	69	2141632
lcl KP878.Chr2	30.137	73	46	2	4	71	1.2E+07
lcl KP878.Chr6	42.424	33	19	0	39	71	2.5E+07
lcl KP878.Chr3	40.541	37	21	1	3	38	3.5E+07
lcl KP878.Chr10	35.714	28	18	0	42	69	1.7E+07

TBLASTN 2.10.1+

Query: lcl|KP878222.1_prot_AKI32602.1_1 [gene=CENH3] [protein=centromere specific hi

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

20 hits found

lcl KP878.Chr6	57.609	92	38	1	65	156	3040813
lcl KP878.Chr6	57.609	92	38	1	65	156	3056303
lcl KP878.Chr6	57.609	92	38	1	65	156	3055490
lcl KP878.Chr6	57.609	92	38	1	65	156	3046843
lcl KP878.Chr6	57.609	92	38	1	65	156	1645982
lcl KP878.Chr11	57.609	92	38	1	65	156	2626088
lcl KP878.Chr5	57.609	92	38	1	65	156	2.1E+07
lcl KP878.Chr5	78.571	28	6	0	65	92	2.4E+07
lcl KP878.Chr5	70.37	27	8	0	92	118	2.4E+07
lcl KP878.Chr5	61.538	26	10	0	116	141	2.4E+07
lcl KP878.Chr1	57.778	90	37	1	65	154	3.8E+07
lcl KP878.Chr4	57.609	92	38	1	65	156	2.1E+07
lcl KP878.Chr4	42.735	117	36	2	71	156	2.2E+07
lcl KP878.Chr12	56.522	92	39	1	65	156	1.3E+07
lcl KP878.Chr12	56.044	91	39	1	66	156	1.3E+07
lcl KP878.Chr2	41.525	118	38	2	70	156	1.5E+07
lcl KP878.Chr2	46.835	79	25	2	95	156	1.5E+07
lcl KP878.Chr2	63.333	30	10	1	70	98	1.5E+07

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lcl|KP878.Chr3      61.538      52      20      0      105      156 1.6E+07
lcl|KP878.Chr3      59.259      27      11      0      71      97 1.6E+07
# TBLASTN 2.10.1+
# Query: lcl|KP878221.1_prot_AKI32601.1_1 [gene=CENH3] [protein=centromere specific hi
# Database: Nippon
# Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens
# 23 hits found
lcl|KP878.Chr6      59.375      96      38      1      59      154 3040825
lcl|KP878.Chr6      45.455      154     65      4      1      154 3055622
lcl|KP878.Chr6      59.375      96      38      1      59      154 3056291
lcl|KP878.Chr6      59.375      96      38      1      59      154 3046855
lcl|KP878.Chr6      58.333      96      39      1      59      154 1645994
lcl|KP878.Chr11     45.455      154     65      4      1      154 2626220
lcl|KP878.Chr5      59.375      96      38      1      59      154 2.1E+07
lcl|KP878.Chr5      70.732      41      12      0      50      90 2.4E+07
lcl|KP878.Chr5      70.37      27      8      0      90      116 2.4E+07
lcl|KP878.Chr5      61.538      26      10      0      114     139 2.4E+07
lcl|KP878.Chr5      65      20      7      0      137     156 2.4E+07
lcl|KP878.Chr1      59.574      94      37      1      59      152 3.8E+07
lcl|KP878.Chr4      59.375      96      38      1      59      154 2.1E+07
lcl|KP878.Chr4      36.943      157     38      3      59      154 2.2E+07
lcl|KP878.Chr12     57.292      96      40      1      59      154 1.3E+07
lcl|KP878.Chr12     56.25      96      41      1      59      154 1.3E+07
lcl|KP878.Chr2      41.525      118     38      2      68      154 1.5E+07
lcl|KP878.Chr2      46.835      79      25      2      93      154 1.5E+07
lcl|KP878.Chr2      63.333      30      10      1      68      96 1.5E+07
lcl|KP878.Chr2      84.615      13      2      0      59      71 2E+07
lcl|KP878.Chr2      36      50      22      2      109     156 2E+07
lcl|KP878.Chr3      61.538      52      20      0      103     154 1.6E+07
lcl|KP878.Chr3      45.714      35      19      0      69      103 1.6E+07
# TBLASTN 2.10.1+
# Query: lcl|KP878220.1_prot_AKI32600.1_1 [gene=CENH3] [protein=centromere specific hi
# Database: Nippon
# Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens
# 30 hits found
lcl|KP878.Chr6      47.436      156     74      6      11      165 3040987
lcl|KP878.Chr6      59.375      96      38      1      70      165 3056291
lcl|KP878.Chr6      59.375      96      38      1      70      165 3055502
lcl|KP878.Chr6      59.375      96      38      1      70      165 3046855
lcl|KP878.Chr6      58.333      96      39      1      70      165 1645994
lcl|KP878.Chr6      33.333      60      38      1      54      113 1.2E+07
lcl|KP878.Chr11     59.375      96      38      1      70      165 2626100
lcl|KP878.Chr5      59.375      96      38      1      70      165 2.1E+07
lcl|KP878.Chr5      68.889      45      14      0      57      101 2.4E+07
lcl|KP878.Chr5      58.333      36      14      1      101     135 2.4E+07
lcl|KP878.Chr5      61.538      26      10      0      125     150 2.4E+07

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lcl KP878.Chr5	65	20	7	0	148	167	2.4E+07
lcl KP878.Chr1	59.574	94	37	1	70	163	3.8E+07
lcl KP878.Chr4	59.375	96	38	1	70	165	2.1E+07
lcl KP878.Chr4	36.943	157	38	3	70	165	2.2E+07
lcl KP878.Chr4	34.426	61	38	1	54	114	1.1E+07
lcl KP878.Chr4	35	60	37	1	54	113	9964857
lcl KP878.Chr12	57.292	96	40	1	70	165	1.3E+07
lcl KP878.Chr12	48.062	129	62	4	38	165	1.3E+07
lcl KP878.Chr12	33.333	60	38	1	54	113	1.1E+07
lcl KP878.Chr2	41.525	118	38	2	79	165	1.5E+07
lcl KP878.Chr2	46.835	79	25	2	104	165	1.5E+07
lcl KP878.Chr2	63.333	30	10	1	79	107	1.5E+07
lcl KP878.Chr2	48.485	33	15	1	50	82	2E+07
lcl KP878.Chr2	36	50	22	2	120	167	2E+07
lcl KP878.Chr3	61.538	52	20	0	114	165	1.6E+07
lcl KP878.Chr3	59.259	27	11	0	80	106	1.6E+07
lcl KP878.Chr8	38.333	60	35	1	54	113	2.2E+07
lcl KP878.Chr8	33.333	60	38	1	54	113	2.3E+07
lcl KP878.Chr8	23.256	129	93	2	38	162	2.7E+07

TBLASTN 2.10.1+

Query: lcl|AB770164.1_prot_BAP26971.1_1 [gene=CENH3] [protein=centromeric histone I

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

lcl AB770 Chr11	64.356	101	35	1	68	168	2626115
lcl AB770 Chr6	64.356	101	35	1	68	168	3040840
lcl AB770 Chr6	64.356	101	35	1	68	168	3055517
lcl AB770 Chr6	64.356	101	35	1	68	168	3046870
lcl AB770 Chr6	64.356	101	35	1	68	168	3056276
lcl AB770 Chr6	65.347	101	34	1	68	168	1646009
lcl AB770 Chr5	64.356	101	35	1	68	168	2.1E+07
lcl AB770 Chr5	80.556	36	7	0	69	104	2.4E+07
lcl AB770 Chr5	75	16	4	0	104	119	2.4E+07
lcl AB770 Chr5	77.778	27	6	0	1	27	2.4E+07
lcl AB770 Chr5	68.182	22	7	0	132	153	2.4E+07
lcl AB770 Chr4	64.356	101	35	1	68	168	2.1E+07
lcl AB770 Chr4	40.123	162	36	2	68	168	2.2E+07
lcl AB770 Chr1	64.646	99	34	1	68	166	3.8E+07
lcl AB770 Chr12	59.406	101	40	1	68	168	1.3E+07
lcl AB770 Chr12	58.416	101	41	1	68	168	1.3E+07
lcl AB770 Chr2	44.068	118	35	1	82	168	1.5E+07
lcl AB770 Chr2	64.865	37	13	0	133	169	1.5E+07
lcl AB770 Chr2	58.065	31	13	0	81	111	1.5E+07
lcl AB770 Chr2	73.684	19	5	0	68	86	2E+07
lcl AB770 Chr3	69.444	36	11	0	133	168	1.6E+07
lcl AB770 Chr3	54.286	35	16	0	83	117	1.6E+07

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lcl|AB770 Chr3      70.588      17      5      0      68      84 1.6E+07
# TBLASTN 2.10.1+
# Query: lcl|AB770163.1_prot_BAP26970.1_1 [gene=CENH3] [protein=centromeric histone I
# Database: Nippon
# Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens
# 23 hits found
lcl|AB770 Chr11     64.356      101      35      1      61      161 2626115
lcl|AB770 Chr6      64.356      101      35      1      61      161 3040840
lcl|AB770 Chr6      64.356      101      35      1      61      161 3055517
lcl|AB770 Chr6      64.356      101      35      1      61      161 3046870
lcl|AB770 Chr6      64.356      101      35      1      61      161 3056276
lcl|AB770 Chr6      65.347      101      34      1      61      161 1646009
lcl|AB770 Chr5      64.356      101      35      1      61      161 2.1E+07
lcl|AB770 Chr5      80.556       36       7      0      62       97 2.4E+07
lcl|AB770 Chr5       75       16       4      0      97      112 2.4E+07
lcl|AB770 Chr5      77.778       27       6      0       1       27 2.4E+07
lcl|AB770 Chr5      68.182       22       7      0     125      146 2.4E+07
lcl|AB770 Chr4      64.356      101      35      1      61      161 2.1E+07
lcl|AB770 Chr4      40.123      162      36      2      61      161 2.2E+07
lcl|AB770 Chr1      64.646       99      34      1      61      159 3.8E+07
lcl|AB770 Chr12     59.406      101      40      1      61      161 1.3E+07
lcl|AB770 Chr12     58.416      101      41      1      61      161 1.3E+07
lcl|AB770 Chr2      44.068      118      35      1      75      161 1.5E+07
lcl|AB770 Chr2      64.865       37      13      0     126      162 1.5E+07
lcl|AB770 Chr2      58.065       31      13      0      74      104 1.5E+07
lcl|AB770 Chr2      73.684       19       5      0      61       79 2E+07
lcl|AB770 Chr3      69.444       36      11      0     126      161 1.6E+07
lcl|AB770 Chr3      54.286       35      16      0      76      110 1.6E+07
lcl|AB770 Chr3      70.588       17       5      0      61       77 1.6E+07
# TBLASTN 2.10.1+
# Query: lcl|JF969287.1_prot_AEH95352.1_1 [gene=CENH3] [protein=centromeric histone 3
# Database: Nippon
# Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens
# 56 hits found
lcl|JF9692 Chr6      62       100      37      1      62      161 3040837
lcl|JF9692 Chr6      62       100      37      1      62      161 3055514
lcl|JF9692 Chr6      62       100      37      1      62      161 3056279
lcl|JF9692 Chr6      62       100      37      1      62      161 3046867
lcl|JF9692 Chr6      61       100      38      1      62      161 1646006
lcl|JF9692 Chr6     38.636       44      26      1      83      126 2.8E+07
lcl|JF9692 Chr6     38.636       44      26      1      83      126 1.6E+07
lcl|JF9692 Chr6     38.636       44      26      1      83      126 1.5E+07
lcl|JF9692 Chr6     38.636       44      26      1      83      126 2.4E+07
lcl|JF9692 Chr11     62       100      37      1      62      161 2626112
lcl|JF9692 Chr11     40.909       44      25      1      83      126 1.8E+07
lcl|JF9692 Chr11     43.182       44      24      1      83      126 2.4E+07

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lcl JF9692 Chr5	62	100	37	1	62	161	2.1E+07
lcl JF9692 Chr5	78.947	38	8	0	60	97	2.4E+07
lcl JF9692 Chr5	48.148	27	14	0	97	123	2.4E+07
lcl JF9692 Chr5	76.923	26	6	0	121	146	2.4E+07
lcl JF9692 Chr5	66.667	30	6	1	1	26	2.4E+07
lcl JF9692 Chr5	55.172	29	12	1	136	163	2.4E+07
lcl JF9692 Chr5	38.636	44	26	1	83	126	1.2E+07
lcl JF9692 Chr5	38.636	44	26	1	83	126	7739575
lcl JF9692 Chr5	36.364	44	27	1	83	126	8333986
lcl JF9692 Chr5	38.636	44	26	1	83	126	1.2E+07
lcl JF9692 Chr5	38.636	44	26	1	83	126	7092135
lcl JF9692 Chr4	62	100	37	1	62	161	2.1E+07
lcl JF9692 Chr4	38.509	161	38	3	62	161	2.2E+07
lcl JF9692 Chr4	38.636	44	26	1	83	126	6034854
lcl JF9692 Chr4	38.636	44	26	1	83	126	6358900
lcl JF9692 Chr4	38.636	44	26	1	83	126	1.7E+07
lcl JF9692 Chr1	62.245	98	36	1	62	159	3.8E+07
lcl JF9692 Chr1	40.909	44	25	1	83	126	1E+07
lcl JF9692 Chr12	58	100	41	1	62	161	1.3E+07
lcl JF9692 Chr12	56	100	43	1	62	161	1.3E+07
lcl JF9692 Chr12	38.636	44	26	1	83	126	2.7E+07
lcl JF9692 Chr2	41.176	119	39	2	75	162	1.5E+07
lcl JF9692 Chr2	62.264	53	20	0	110	162	1.5E+07
lcl JF9692 Chr2	50	30	15	0	75	104	1.5E+07
lcl JF9692 Chr2	54.286	35	16	0	62	96	2E+07
lcl JF9692 Chr2	39.583	48	19	2	116	161	2E+07
lcl JF9692 Chr2	75	16	4	0	62	77	1.5E+07
lcl JF9692 Chr2	38.636	44	26	1	83	126	1.5E+07
lcl JF9692 Chr3	65.385	52	18	0	110	161	1.6E+07
lcl JF9692 Chr3	48.571	35	18	0	76	110	1.6E+07
lcl JF9692 Chr3	38.636	44	26	1	83	126	2E+07
lcl JF9692 Chr3	38.636	44	26	1	83	126	1.9E+07
lcl JF9692 Chr3	44.444	45	17	2	62	99	1.6E+07
lcl JF9692 Chr3	38.636	44	26	1	83	126	1.9E+07
lcl JF9692 Chr10	38.636	44	26	1	83	126	6630385
lcl JF9692 Chr10	38.636	44	26	1	83	126	9325176
lcl JF9692 Chr10	38.636	44	26	1	83	126	1.1E+07
lcl JF9692 Chr10	38.636	44	26	1	83	126	1.3E+07
lcl JF9692 Chr10	38.636	44	26	1	83	126	7380895
lcl JF9692 Chr9	38.636	44	26	1	83	126	7580887
lcl JF9692 Chr9	36.364	44	27	1	83	126	2880881
lcl JF9692 Chr7	38.636	44	26	1	83	126	4633533
lcl JF9692 Chr8	38.636	44	26	1	83	126	9874145
lcl JF9692 Chr8	47.826	23	12	0	104	126	1.3E+07

TBLASTN 2.10.1+

Query: lcl|JF969285.1_prot_AEH95350.1_1 [gene=CENH3] [protein=centromeric histone 3]

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

53 hits found

lcl JF9692 Chr6	63	100	36	1	65	164	3040837
lcl JF9692 Chr6	63	100	36	1	65	164	3055514
lcl JF9692 Chr6	63	100	36	1	65	164	3056279
lcl JF9692 Chr6	63	100	36	1	65	164	3046867
lcl JF9692 Chr6	62	100	37	1	65	164	1646006
lcl JF9692 Chr6	38.636	44	26	1	86	129	2.8E+07
lcl JF9692 Chr6	38.636	44	26	1	86	129	1.6E+07
lcl JF9692 Chr6	38.636	44	26	1	86	129	1.5E+07
lcl JF9692 Chr6	38.636	44	26	1	86	129	2.4E+07
lcl JF9692 Chr11	63	100	36	1	65	164	2626112
lcl JF9692 Chr11	40.909	44	25	1	86	129	1.8E+07
lcl JF9692 Chr11	44.186	43	23	1	86	128	2.4E+07
lcl JF9692 Chr5	63	100	36	1	65	164	2.1E+07
lcl JF9692 Chr5	81.579	38	7	0	63	100	2.4E+07
lcl JF9692 Chr5	48.148	27	14	0	100	126	2.4E+07
lcl JF9692 Chr5	76.923	26	6	0	124	149	2.4E+07
lcl JF9692 Chr5	85	20	3	0	1	20	2.4E+07
lcl JF9692 Chr5	55.172	29	12	1	139	166	2.4E+07
lcl JF9692 Chr5	38.636	44	26	1	86	129	1.2E+07
lcl JF9692 Chr5	38.636	44	26	1	86	129	7739575
lcl JF9692 Chr5	36.364	44	27	1	86	129	8333986
lcl JF9692 Chr5	38.636	44	26	1	86	129	1.2E+07
lcl JF9692 Chr5	38.636	44	26	1	86	129	7092135
lcl JF9692 Chr4	63	100	36	1	65	164	2.1E+07
lcl JF9692 Chr4	39.13	161	37	3	65	164	2.2E+07
lcl JF9692 Chr4	38.636	44	26	1	86	129	6034854
lcl JF9692 Chr4	38.636	44	26	1	86	129	6358900
lcl JF9692 Chr1	63.265	98	35	1	65	162	3.8E+07
lcl JF9692 Chr1	40.909	44	25	1	86	129	1E+07
lcl JF9692 Chr12	58	100	41	1	65	164	1.3E+07
lcl JF9692 Chr12	56	100	43	1	65	164	1.3E+07
lcl JF9692 Chr12	38.636	44	26	1	86	129	2.7E+07
lcl JF9692 Chr2	42.017	119	38	2	78	165	1.5E+07
lcl JF9692 Chr2	62.264	53	20	0	113	165	1.5E+07
lcl JF9692 Chr2	53.333	30	14	0	78	107	1.5E+07
lcl JF9692 Chr2	51.429	35	17	0	65	99	2E+07
lcl JF9692 Chr2	39.583	48	19	2	119	164	2E+07
lcl JF9692 Chr2	75	16	4	0	65	80	1.5E+07
lcl JF9692 Chr2	38.636	44	26	1	86	129	1.5E+07
lcl JF9692 Chr3	65.385	52	18	0	113	164	1.6E+07
lcl JF9692 Chr3	51.429	35	17	0	79	113	1.6E+07
lcl JF9692 Chr3	38.636	44	26	1	86	129	2E+07
lcl JF9692 Chr3	44.444	45	17	2	65	102	1.6E+07

lcl JF9692 Chr3	38.636	44	26	1	86	129	1.9E+07
lcl JF9692 Chr3	38.636	44	26	1	86	129	1.9E+07
lcl JF9692 Chr10	38.636	44	26	1	86	129	6630385
lcl JF9692 Chr10	38.636	44	26	1	86	129	9325176
lcl JF9692 Chr10	38.636	44	26	1	86	129	1.1E+07
lcl JF9692 Chr10	38.636	44	26	1	86	129	1.3E+07
lcl JF9692 Chr10	38.636	44	26	1	86	129	7380895
lcl JF9692 Chr9	38.636	44	26	1	86	129	7580887
lcl JF9692 Chr7	38.636	44	26	1	86	129	4633533
lcl JF9692 Chr8	38.636	44	26	1	86	129	9874145

TBLASTN 2.10.1+

Query: lcl|JF419330.1_prot_AEK21394.1_1 [gene=CENH3] [protein=beta centromeric histc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

26 hits found

lcl JF4193 Chr11	51.825	137	53	3	1	130	2626220
lcl JF4193 Chr6	51.825	137	53	3	1	130	3055622
lcl JF4193 Chr6	51.825	137	53	3	1	130	3040945
lcl JF4193 Chr6	61.386	101	33	1	30	130	1646006
lcl JF4193 Chr6	51.825	137	53	3	1	130	3056171
lcl JF4193 Chr6	60.396	101	34	1	30	130	3046867
lcl JF4193 Chr5	53.285	137	51	4	1	130	2.2E+07
lcl JF4193 Chr5	75.61	41	10	0	25	65	2.4E+07
lcl JF4193 Chr5	67.742	31	10	0	89	119	2.4E+07
lcl JF4193 Chr1	53.285	137	51	4	1	130	3.8E+07
lcl JF4193 Chr4	51.825	137	53	3	1	130	2.1E+07
lcl JF4193 Chr4	38.217	157	41	2	30	130	2.2E+07
lcl JF4193 Chr4	45.946	37	20	0	16	52	3.2E+07
lcl JF4193 Chr12	48.905	137	57	4	1	130	1.3E+07
lcl JF4193 Chr12	46.377	138	61	4	1	131	1.3E+07
lcl JF4193 Chr12	28.788	66	47	0	12	77	3562813
lcl JF4193 Chr12	41.176	34	20	0	102	135	3718543
lcl JF4193 Chr3	68.182	44	14	0	87	130	1.6E+07
lcl JF4193 Chr3	72.414	29	8	0	44	72	1.6E+07
lcl JF4193 Chr3	68.75	16	5	0	30	45	1.6E+07
lcl JF4193 Chr2	44.737	114	37	1	43	130	1.5E+07
lcl JF4193 Chr2	65.909	44	15	0	87	130	1.5E+07
lcl JF4193 Chr2	70	30	9	0	43	72	1.5E+07
lcl JF4193 Chr2	75	20	5	0	30	49	2E+07
lcl JF4193 Chr2	42.857	28	16	0	8	35	2.7E+07
lcl JF4193 Chr8	38.095	42	24	1	21	62	4507089

TBLASTN 2.10.1+

Query: lcl|JF419329.1_prot_AEK21393.1_1 [gene=CENH3] [protein=beta centromeric histc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

lcl JF4193 Chr11	57.547	106	34	3	34	137	2626103
lcl JF4193 Chr6	57.547	106	34	3	34	137	3040828
lcl JF4193 Chr6	57.547	106	34	3	34	137	3055505
lcl JF4193 Chr6	57.547	106	34	3	34	137	3046858
lcl JF4193 Chr6	57.143	105	36	2	34	137	3056288
lcl JF4193 Chr6	57	100	35	1	34	133	1645997
lcl JF4193 Chr5	57.143	105	36	2	34	137	2.1E+07
lcl JF4193 Chr5	55.357	56	25	0	32	87	2.4E+07
lcl JF4193 Chr5	61.29	31	12	0	92	122	2.4E+07
lcl JF4193 Chr4	57.143	105	36	2	34	137	2.1E+07
lcl JF4193 Chr4	37.179	156	44	3	32	133	2.2E+07
lcl JF4193 Chr1	56.863	102	36	2	32	133	3.8E+07
lcl JF4193 Chr1	30.337	89	51	4	39	117	1.7E+07
lcl JF4193 Chr12	54	100	38	1	34	133	1.3E+07
lcl JF4193 Chr12	50.495	101	42	1	34	134	1.3E+07
lcl JF4193 Chr2	44.737	114	39	2	44	133	1.5E+07
lcl JF4193 Chr2	72.093	43	12	0	91	133	1.5E+07
lcl JF4193 Chr2	60	30	12	0	44	73	1.5E+07
lcl JF4193 Chr2	76.471	17	4	0	34	50	2E+07
lcl JF4193 Chr3	69.767	43	13	0	91	133	1.6E+07
lcl JF4193 Chr3	62.069	29	11	0	45	73	1.6E+07
lcl JF4193 Chr3	60	15	6	0	32	46	1.6E+07
lcl JF4193 Chr7	43.75	32	14	1	111	138	1.6E+07

TBLASTN 2.10.1+

Query: lcl|GU166744.1_prot_ACZ04984.1_1 [gene=CENH3] [protein=centromere-specific I

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

lcl GU166 Chr6	53.774	106	47	1	72	177	1646024
lcl GU166 Chr6	53.774	106	47	2	72	177	3040855
lcl GU166 Chr6	52.83	106	48	1	72	177	3056261
lcl GU166 Chr6	53.774	106	47	2	72	177	3055532
lcl GU166 Chr6	52.83	106	48	1	72	177	3046885
lcl GU166 Chr1	53.333	105	47	1	72	176	3.8E+07
lcl GU166 Chr5	53.774	106	47	2	72	177	2.2E+07
lcl GU166 Chr5	60.976	41	16	0	73	113	2.4E+07
lcl GU166 Chr5	51.724	29	13	1	112	140	2.4E+07
lcl GU166 Chr5	48.387	31	16	0	138	168	2.4E+07
lcl GU166 Chr11	53.774	106	47	2	72	177	2626130
lcl GU166 Chr11	32.308	65	39	2	104	164	1069460
lcl GU166 Chr4	52.83	106	48	1	72	177	2.1E+07
lcl GU166 Chr4	34.731	167	47	3	72	177	2.2E+07
lcl GU166 Chr12	51.376	109	45	2	72	177	1.3E+07
lcl GU166 Chr12	48.113	106	53	1	72	177	1.3E+07
lcl GU166 Chr3	58.824	51	21	0	127	177	1.6E+07
lcl GU166 Chr3	51.724	29	14	0	92	120	1.6E+07

lcl GU166 Chr3	50	24	12	0	72	95	1.6E+07
lcl GU166 Chr2	38.983	118	40	2	91	177	1.5E+07
lcl GU166 Chr2	56.863	51	22	0	127	177	1.5E+07
lcl GU166 Chr2	53.333	30	14	0	91	120	1.5E+07
lcl GU166 Chr2	29.688	64	42	1	97	160	2.5E+07

TBLASTN 2.10.1+

Query: lcl|GU166742.1_prot_ACZ04982.1_1 [gene=CENH3] [protein=centromere-specific I

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

lcl GU166 Chr6	52.294	109	50	1	72	180	1646033
lcl GU166 Chr6	49.242	132	65	2	49	180	3055610
lcl GU166 Chr6	49.242	132	65	2	49	180	3040933
lcl GU166 Chr6	51.376	109	51	1	72	180	3056252
lcl GU166 Chr6	51.376	109	51	1	72	180	3046894
lcl GU166 Chr1	51.852	108	50	1	72	179	3.8E+07
lcl GU166 Chr11	49.242	132	65	2	49	180	2626208
lcl GU166 Chr5	52.294	109	50	2	72	180	2.2E+07
lcl GU166 Chr5	60.976	41	16	0	76	116	2.4E+07
lcl GU166 Chr5	55.172	29	12	1	115	143	2.4E+07
lcl GU166 Chr5	48.387	31	16	0	141	171	2.4E+07
lcl GU166 Chr4	51.376	109	51	1	72	180	2.1E+07
lcl GU166 Chr4	34.118	170	50	3	72	180	2.2E+07
lcl GU166 Chr12	45	140	69	2	44	180	1.3E+07
lcl GU166 Chr12	42.336	137	77	1	44	180	1.3E+07
lcl GU166 Chr3	58.824	51	21	0	130	180	1.6E+07
lcl GU166 Chr3	51.724	29	14	0	95	123	1.6E+07
lcl GU166 Chr3	48	25	13	0	72	96	1.6E+07
lcl GU166 Chr2	38.983	118	40	2	94	180	1.5E+07
lcl GU166 Chr2	56.863	51	22	0	130	180	1.5E+07
lcl GU166 Chr2	53.333	30	14	0	94	123	1.5E+07
lcl GU166 Chr2	29.688	64	42	1	100	163	2.5E+07

TBLASTN 2.10.1+

Query: lcl|GU166740.1_prot_ACZ04980.1_1 [gene=CENH3] [protein=centromere-specific I

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

19 hits found

lcl GU166 Chr6	53.211	109	49	1	70	178	1646033
lcl GU166 Chr6	52.294	109	50	1	70	178	3040864
lcl GU166 Chr6	52.294	109	50	1	70	178	3055541
lcl GU166 Chr6	52.294	109	50	1	70	178	3046894
lcl GU166 Chr6	52.294	109	50	1	70	178	3056252
lcl GU166 Chr11	52.294	109	50	1	70	178	2626139
lcl GU166 Chr1	52.778	108	49	1	70	177	3.8E+07
lcl GU166 Chr5	52.294	109	50	1	70	178	2.2E+07
lcl GU166 Chr5	60.976	41	16	0	74	114	2.4E+07

lcl GU166 Chr5	52	25	12	0	145	169	2.4E+07
lcl GU166 Chr4	52.294	109	50	1	70	178	2.1E+07
lcl GU166 Chr4	34.911	169	50	3	70	178	2.2E+07
lcl GU166 Chr12	53.774	106	47	1	73	178	1.3E+07
lcl GU166 Chr12	50	106	51	1	73	178	1.3E+07
lcl GU166 Chr2	39.316	117	41	1	92	178	1.5E+07
lcl GU166 Chr2	62.857	35	13	0	144	178	1.5E+07
lcl GU166 Chr3	65.714	35	12	0	144	178	1.6E+07
lcl GU166 Chr3	44.444	27	15	0	70	96	1.6E+07
lcl GU166 Chr3	51.852	27	13	0	93	119	1.6E+07

TBLASTN 2.10.1+

Query: lcl|GU166738.1_prot_ACZ04978.1_1 [gene=CENH3] [protein=centromere-specific I

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

19 hits found

lcl GU166 Chr6	58.333	96	38	1	63	158	1645994
lcl GU166 Chr6	57.292	96	39	1	63	158	3056291
lcl GU166 Chr6	57.292	96	39	1	63	158	3046855
lcl GU166 Chr6	57.292	96	39	1	63	158	3040825
lcl GU166 Chr6	57.292	96	39	1	63	158	3055502
lcl GU166 Chr5	57.292	96	39	1	63	158	2.1E+07
lcl GU166 Chr5	75	32	8	0	63	94	2.4E+07
lcl GU166 Chr5	50	26	13	0	124	149	2.4E+07
lcl GU166 Chr11	57.292	96	39	1	63	158	2626100
lcl GU166 Chr1	57.895	95	38	1	63	157	3.8E+07
lcl GU166 Chr4	57.292	96	39	1	63	158	2.1E+07
lcl GU166 Chr4	36.538	156	39	3	63	158	2.2E+07
lcl GU166 Chr12	57.292	96	39	1	63	158	1.3E+07
lcl GU166 Chr12	53.125	96	43	1	63	158	1.3E+07
lcl GU166 Chr2	40.171	117	40	1	72	158	1.5E+07
lcl GU166 Chr2	65.714	35	12	0	124	158	1.5E+07
lcl GU166 Chr3	68.571	35	11	0	124	158	1.6E+07
lcl GU166 Chr3	51.852	27	13	0	73	99	1.6E+07
lcl GU166 Chr3	64.286	14	5	0	63	76	1.6E+07

TBLASTN 2.10.1+

Query: lcl|MH329772.1_prot_QBB85873.1_1 [gene=CENH3] [protein=centromere specific

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

lcl MH32! Chr6	53.774	106	47	1	75	180	1646024
lcl MH32! Chr6	53.774	106	47	2	75	180	3040855
lcl MH32! Chr6	53.774	106	47	2	75	180	3055532
lcl MH32! Chr6	52.83	106	48	1	75	180	3046885
lcl MH32! Chr6	52.83	106	48	1	75	180	3056261
lcl MH32! Chr1	53.333	105	47	1	75	179	3.8E+07
lcl MH32! Chr11	53.774	106	47	2	75	180	2626130

lcl MH32! Chr11	32.308	65	39	2	107	167	1069460
lcl MH32! Chr5	53.774	106	47	2	75	180	2.2E+07
lcl MH32! Chr5	60.976	41	16	0	76	116	2.4E+07
lcl MH32! Chr5	55.172	29	12	1	115	143	2.4E+07
lcl MH32! Chr5	48.387	31	16	0	141	171	2.4E+07
lcl MH32! Chr4	52.83	106	48	1	75	180	2.1E+07
lcl MH32! Chr4	34.731	167	47	3	75	180	2.2E+07
lcl MH32! Chr12	51.376	109	45	2	75	180	1.3E+07
lcl MH32! Chr12	48.113	106	53	1	75	180	1.3E+07
lcl MH32! Chr3	58.824	51	21	0	130	180	1.6E+07
lcl MH32! Chr3	51.724	29	14	0	95	123	1.6E+07
lcl MH32! Chr3	50	24	12	0	75	98	1.6E+07
lcl MH32! Chr2	38.983	118	40	2	94	180	1.5E+07
lcl MH32! Chr2	56.863	51	22	0	130	180	1.5E+07
lcl MH32! Chr2	53.333	30	14	0	94	123	1.5E+07
lcl MH32! Chr2	29.688	64	42	1	100	163	2.5E+07

TBLASTN 2.10.1+

Query: lcl|MH329770.1_prot_QBB85871.1_1 [gene=CENH3] [protein=centromere specific

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

lcl MH32! Chr6	51.818	110	51	1	65	174	1646036
lcl MH32! Chr6	51.818	110	51	2	65	174	3040867
lcl MH32! Chr6	50.909	110	52	1	65	174	3056249
lcl MH32! Chr6	51.818	110	51	2	65	174	3055544
lcl MH32! Chr6	51.376	109	51	1	66	174	3046894
lcl MH32! Chr1	51.376	109	51	1	65	173	3.8E+07
lcl MH32! Chr11	51.818	110	51	2	65	174	2626142
lcl MH32! Chr11	32.308	65	39	2	101	161	1069460
lcl MH32! Chr5	51.818	110	51	2	65	174	2.2E+07
lcl MH32! Chr5	60.976	41	16	0	70	110	2.4E+07
lcl MH32! Chr5	55.172	29	12	1	109	137	2.4E+07
lcl MH32! Chr5	48.387	31	16	0	135	165	2.4E+07
lcl MH32! Chr4	50.909	110	52	1	65	174	2.1E+07
lcl MH32! Chr4	33.918	171	51	3	65	174	2.2E+07
lcl MH32! Chr12	49.558	113	49	2	65	174	1.3E+07
lcl MH32! Chr12	46.364	110	57	1	65	174	1.3E+07
lcl MH32! Chr3	58.824	51	21	0	124	174	1.6E+07
lcl MH32! Chr3	51.724	29	14	0	89	117	1.6E+07
lcl MH32! Chr3	46.154	26	14	0	65	90	1.6E+07
lcl MH32! Chr2	38.983	118	40	2	88	174	1.5E+07
lcl MH32! Chr2	56.863	51	22	0	124	174	1.5E+07
lcl MH32! Chr2	53.333	30	14	0	88	117	1.5E+07
lcl MH32! Chr2	29.688	64	42	1	94	157	2.5E+07

TBLASTN 2.10.1+

Query: lcl|KT932954.1_prot_AOR06535.1_1 [gene=CENH3] [protein=centromere histone h

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

lcl KT932! Chr6	67	100	32	1	73	172	3040837
lcl KT932! Chr6	67	100	32	1	73	172	3055514
lcl KT932! Chr6	67	100	32	1	73	172	3056279
lcl KT932! Chr6	67	100	32	1	73	172	3046867
lcl KT932! Chr6	68	100	31	1	73	172	1646006
lcl KT932! Chr11	67	100	32	1	73	172	2626112
lcl KT932! Chr5	67	100	32	1	73	172	2.1E+07
lcl KT932! Chr5	70.732	41	12	0	68	108	2.4E+07
lcl KT932! Chr5	73.333	15	4	0	108	122	2.4E+07
lcl KT932! Chr5	61.905	21	8	0	137	157	2.4E+07
lcl KT932! Chr1	68.367	98	30	1	73	170	3.8E+07
lcl KT932! Chr4	67	100	32	1	73	172	2.1E+07
lcl KT932! Chr4	40.994	161	34	2	73	172	2.2E+07
lcl KT932! Chr12	63	100	36	1	73	172	1.3E+07
lcl KT932! Chr12	60	100	39	1	73	172	1.3E+07
lcl KT932! Chr2	46.218	119	33	2	86	173	1.5E+07
lcl KT932! Chr2	67.568	37	12	0	137	173	1.5E+07
lcl KT932! Chr2	56.667	30	13	0	86	115	1.5E+07
lcl KT932! Chr2	40.476	42	25	0	66	107	2E+07
lcl KT932! Chr2	41.667	36	13	1	137	172	2E+07
lcl KT932! Chr3	75	36	9	0	137	172	1.6E+07
lcl KT932! Chr3	51.429	35	17	0	87	121	1.6E+07
lcl KT932! Chr3	68.75	16	5	0	73	88	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KT932953.1_prot_AOR06534.1_1 [gene=CENH3] [protein=centromere histone t

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

lcl KT932! Chr6	67	100	32	1	81	180	3040837
lcl KT932! Chr6	67	100	32	1	81	180	3055514
lcl KT932! Chr6	67	100	32	1	81	180	3056279
lcl KT932! Chr6	67	100	32	1	81	180	3046867
lcl KT932! Chr6	68	100	31	1	81	180	1646006
lcl KT932! Chr11	67	100	32	1	81	180	2626112
lcl KT932! Chr5	67	100	32	1	81	180	2.1E+07
lcl KT932! Chr5	70.732	41	12	0	76	116	2.4E+07
lcl KT932! Chr5	73.333	15	4	0	116	130	2.4E+07
lcl KT932! Chr5	61.905	21	8	0	145	165	2.4E+07
lcl KT932! Chr1	68.367	98	30	1	81	178	3.8E+07
lcl KT932! Chr4	67	100	32	1	81	180	2.1E+07
lcl KT932! Chr4	40.994	161	34	2	81	180	2.2E+07
lcl KT932! Chr12	63	100	36	1	81	180	1.3E+07
lcl KT932! Chr12	60	100	39	1	81	180	1.3E+07

lcl KT932! Chr2	46.218	119	33	2	94	181	1.5E+07
lcl KT932! Chr2	67.568	37	12	0	145	181	1.5E+07
lcl KT932! Chr2	56.667	30	13	0	94	123	1.5E+07
lcl KT932! Chr2	40.476	42	25	0	74	115	2E+07
lcl KT932! Chr2	41.667	36	13	1	145	180	2E+07
lcl KT932! Chr3	75	36	9	0	145	180	1.6E+07
lcl KT932! Chr3	51.429	35	17	0	95	129	1.6E+07
lcl KT932! Chr3	68.75	16	5	0	81	96	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KU837266.1_prot_AOH73624.1_1 [gene=CENH3] [protein=centromere-specific]

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

lcl KU837 Chr6	53.211	109	49	1	81	189	1646033
lcl KU837 Chr6	53.211	109	49	2	81	189	3040864
lcl KU837 Chr6	52.294	109	50	1	81	189	3056252
lcl KU837 Chr6	53.211	109	49	2	81	189	3055541
lcl KU837 Chr6	52.294	109	50	1	81	189	3046894
lcl KU837 Chr1	52.778	108	49	1	81	188	3.8E+07
lcl KU837 Chr5	53.211	109	49	2	81	189	2.2E+07
lcl KU837 Chr5	60.976	41	16	0	85	125	2.4E+07
lcl KU837 Chr5	51.724	29	13	1	124	152	2.4E+07
lcl KU837 Chr5	51.613	31	15	0	150	180	2.4E+07
lcl KU837 Chr11	53.211	109	49	2	81	189	2626139
lcl KU837 Chr4	52.294	109	50	1	81	189	2.1E+07
lcl KU837 Chr4	35.329	167	46	3	84	189	2.2E+07
lcl KU837 Chr12	50.893	112	47	2	81	189	1.3E+07
lcl KU837 Chr12	49.057	106	52	1	84	189	1.3E+07
lcl KU837 Chr3	60.784	51	20	0	139	189	1.6E+07
lcl KU837 Chr3	51.724	29	14	0	104	132	1.6E+07
lcl KU837 Chr3	48	25	13	0	81	105	1.6E+07
lcl KU837 Chr2	39.831	118	39	2	103	189	1.5E+07
lcl KU837 Chr2	58.824	51	21	0	139	189	1.5E+07
lcl KU837 Chr2	53.333	30	14	0	103	132	1.5E+07
lcl KU837 Chr2	29.688	64	42	1	109	172	2.5E+07

TBLASTN 2.10.1+

Query: lcl|KU837264.1_prot_AOH73622.1_1 [gene=CENH3] [protein=centromere-specific]

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

21 hits found

lcl KU837 Chr6	53.211	109	49	1	67	175	1646033
lcl KU837 Chr6	53.211	109	49	2	67	175	3040864
lcl KU837 Chr6	52.294	109	50	1	67	175	3056252
lcl KU837 Chr6	53.211	109	49	2	67	175	3055541
lcl KU837 Chr6	52.294	109	50	1	67	175	3046894
lcl KU837 Chr1	52.778	108	49	1	67	174	3.8E+07

lcl KU837 Chr11	53.211	109	49	2	67	175	2626139
lcl KU837 Chr5	53.211	109	49	2	67	175	2.2E+07
lcl KU837 Chr5	60.976	41	16	0	71	111	2.4E+07
lcl KU837 Chr5	51.724	29	13	1	110	138	2.4E+07
lcl KU837 Chr5	51.613	31	15	0	136	166	2.4E+07
lcl KU837 Chr4	52.294	109	50	1	67	175	2.1E+07
lcl KU837 Chr4	34.706	170	49	3	67	175	2.2E+07
lcl KU837 Chr12	52.294	109	44	2	70	175	1.3E+07
lcl KU837 Chr12	48.624	109	48	2	70	175	1.3E+07
lcl KU837 Chr3	60.784	51	20	0	125	175	1.6E+07
lcl KU837 Chr3	51.724	29	14	0	90	118	1.6E+07
lcl KU837 Chr3	44.444	27	15	0	67	93	1.6E+07
lcl KU837 Chr2	39.831	118	39	2	89	175	1.5E+07
lcl KU837 Chr2	58.824	51	21	0	125	175	1.5E+07
lcl KU837 Chr2	53.333	30	14	0	89	118	1.5E+07

TBLASTN 2.10.1+

Query: lcl|KU837263.1_prot_AOH73621.1_1 [gene=CENH3] [protein=centromere-specific

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

19 hits found

lcl KU837 Chr6	51.786	112	52	1	67	178	1646042
lcl KU837 Chr6	52.101	119	52	2	63	178	3040894
lcl KU837 Chr6	51.786	112	52	1	67	178	3046903
lcl KU837 Chr6	52.101	119	52	2	63	178	3055571
lcl KU837 Chr6	52.101	119	52	2	63	178	3056222
lcl KU837 Chr5	52.101	119	52	2	63	178	2.2E+07
lcl KU837 Chr5	60.976	41	16	0	74	114	2.4E+07
lcl KU837 Chr5	56	25	11	0	145	169	2.4E+07
lcl KU837 Chr11	52.101	119	52	2	63	178	2626169
lcl KU837 Chr1	52.542	118	51	2	63	177	3.8E+07
lcl KU837 Chr4	52.101	119	52	2	63	178	2.1E+07
lcl KU837 Chr4	34.884	172	52	3	67	178	2.2E+07
lcl KU837 Chr12	51.818	110	51	1	69	178	1.3E+07
lcl KU837 Chr12	48.182	110	55	1	69	178	1.3E+07
lcl KU837 Chr2	39.316	117	41	1	92	178	1.5E+07
lcl KU837 Chr2	62.857	35	13	0	144	178	1.5E+07
lcl KU837 Chr3	65.714	35	12	0	144	178	1.6E+07
lcl KU837 Chr3	42.857	28	16	0	69	96	1.6E+07
lcl KU837 Chr3	51.852	27	13	0	93	119	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KU837262.1_prot_AOH73620.1_1 [gene=CENH3] [protein=centromere-specific

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

19 hits found

lcl KU837 Chr11	56.25	96	40	1	62	157	2626100
lcl KU837 Chr6	57.292	96	39	1	62	157	1645994

lcl KU837 Chr6	56.25	96	40	1	62	157	3056291
lcl KU837 Chr6	56.25	96	40	1	62	157	3040825
lcl KU837 Chr6	56.25	96	40	1	62	157	3055502
lcl KU837 Chr6	56.25	96	40	1	62	157	3046855
lcl KU837 Chr1	56.842	95	39	1	62	156	3.8E+07
lcl KU837 Chr5	56.25	96	40	1	62	157	2.1E+07
lcl KU837 Chr5	75	32	8	0	62	93	2.4E+07
lcl KU837 Chr5	46.154	26	14	0	123	148	2.4E+07
lcl KU837 Chr4	56.25	96	40	1	62	157	2.1E+07
lcl KU837 Chr4	35.897	156	40	3	62	157	2.2E+07
lcl KU837 Chr12	57.292	96	39	1	62	157	1.3E+07
lcl KU837 Chr12	53.125	96	43	1	62	157	1.3E+07
lcl KU837 Chr2	39.316	117	41	1	71	157	1.5E+07
lcl KU837 Chr2	62.857	35	13	0	123	157	1.5E+07
lcl KU837 Chr3	65.714	35	12	0	123	157	1.6E+07
lcl KU837 Chr3	51.852	27	13	0	72	98	1.6E+07
lcl KU837 Chr3	64.286	14	5	0	62	75	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KU674827.1_prot_AOH73617.1_1 [gene=CENH3] [protein=centromere-specific

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

20 hits found

lcl KU674 Chr6	57	100	41	1	81	180	3040837
lcl KU674 Chr6	58	100	40	1	81	180	1646006
lcl KU674 Chr6	57	100	41	1	81	180	3056279
lcl KU674 Chr6	57	100	41	1	81	180	3055514
lcl KU674 Chr6	57	100	41	1	81	180	3046867
lcl KU674 Chr5	57	100	41	1	81	180	2.1E+07
lcl KU674 Chr5	62.5	40	15	0	77	116	2.4E+07
lcl KU674 Chr5	52	25	12	0	147	171	2.4E+07
lcl KU674 Chr11	57	100	41	1	81	180	2626112
lcl KU674 Chr4	57	100	41	1	81	180	2.1E+07
lcl KU674 Chr4	36.646	161	40	4	81	180	2.2E+07
lcl KU674 Chr1	57.576	99	40	1	81	179	3.8E+07
lcl KU674 Chr12	57	100	41	1	81	180	1.3E+07
lcl KU674 Chr12	53	100	45	1	81	180	1.3E+07
lcl KU674 Chr2	40.833	120	35	2	94	180	1.5E+07
lcl KU674 Chr2	60	35	14	0	146	180	1.5E+07
lcl KU674 Chr2	60	30	12	0	94	123	1.5E+07
lcl KU674 Chr3	62.857	35	13	0	146	180	1.6E+07
lcl KU674 Chr3	55.172	29	13	0	95	123	1.6E+07
lcl KU674 Chr3	61.111	18	7	0	81	98	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KR029619.1_prot_ALF04640.1_1 [gene=CENH3] [protein=centromeric histone H

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

25 hits found

lcl KR029 Chr11	59.2	125	41	2	54	176	2626166
lcl KR029 Chr6	59.2	125	41	2	54	176	3040891
lcl KR029 Chr6	59.2	125	41	2	54	176	3055568
lcl KR029 Chr6	65.347	101	35	0	76	176	3056273
lcl KR029 Chr6	65.347	101	35	0	76	176	3046873
lcl KR029 Chr6	65.385	104	36	0	73	176	1646021
lcl KR029 Chr5	59.2	125	41	2	54	176	2.2E+07
lcl KR029 Chr5	75.61	41	10	0	73	113	2.4E+07
lcl KR029 Chr5	78.947	19	4	0	143	161	2.4E+07
lcl KR029 Chr4	65.347	101	35	0	76	176	2.1E+07
lcl KR029 Chr4	40.659	182	36	4	57	176	2.2E+07
lcl KR029 Chr1	65.657	99	34	0	76	174	3.8E+07
lcl KR029 Chr1	41.935	31	17	1	149	178	2E+07
lcl KR029 Chr12	48.921	139	54	4	47	178	1.3E+07
lcl KR029 Chr12	54.902	102	46	0	75	176	1.3E+07
lcl KR029 Chr3	65.517	58	20	0	119	176	1.6E+07
lcl KR029 Chr3	58.621	29	12	0	92	120	1.6E+07
lcl KR029 Chr3	61.905	21	8	0	73	93	1.6E+07
lcl KR029 Chr2	47.059	119	31	1	91	177	1.5E+07
lcl KR029 Chr2	67.273	55	18	0	123	177	1.5E+07
lcl KR029 Chr2	60	30	12	0	91	120	1.5E+07
lcl KR029 Chr2	44.186	43	24	0	70	112	2E+07
lcl KR029 Chr2	50	34	9	1	143	176	2E+07
lcl KR029 Chr2	35.556	45	27	1	63	105	2.9E+07
lcl KR029 Chr2	47.5	40	11	2	54	93	1.5E+07

TBLASTN 2.10.1+

Query: lcl|KR029618.1_prot_ALF04639.1_1 [gene=CENH3] [protein=centromeric histone H

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

25 hits found

lcl KR029 Chr6	64.356	101	36	0	76	176	3040843
lcl KR029 Chr6	62.5	104	39	0	73	176	3055529
lcl KR029 Chr6	64.356	101	36	0	76	176	3056273
lcl KR029 Chr6	64.356	101	36	0	76	176	3046873
lcl KR029 Chr6	66.337	101	34	0	76	176	1646012
lcl KR029 Chr11	64.356	101	36	0	76	176	2626118
lcl KR029 Chr5	64.356	101	36	0	76	176	2.1E+07
lcl KR029 Chr5	76.19	42	10	0	72	113	2.4E+07
lcl KR029 Chr5	73.684	19	5	0	143	161	2.4E+07
lcl KR029 Chr4	64.356	101	36	0	76	176	2.1E+07
lcl KR029 Chr4	40.659	182	36	4	57	176	2.2E+07
lcl KR029 Chr1	64.646	99	35	0	76	174	3.8E+07
lcl KR029 Chr1	41.935	31	17	1	149	178	2E+07
lcl KR029 Chr12	51.2	125	49	3	56	178	1.3E+07
lcl KR029 Chr12	53.922	102	47	0	75	176	1.3E+07

lcl KR029 Chr3	63.793	58	21	0	119	176	1.6E+07
lcl KR029 Chr3	58.621	29	12	0	92	120	1.6E+07
lcl KR029 Chr3	61.905	21	8	0	73	93	1.6E+07
lcl KR029 Chr2	46.218	119	32	1	91	177	1.5E+07
lcl KR029 Chr2	65.455	55	19	0	123	177	1.5E+07
lcl KR029 Chr2	60	30	12	0	91	120	1.5E+07
lcl KR029 Chr2	44.186	43	24	0	70	112	2E+07
lcl KR029 Chr2	47.059	34	10	1	143	176	2E+07
lcl KR029 Chr2	35.556	45	27	1	63	105	2.9E+07
lcl KR029 Chr2	68.421	19	6	0	75	93	1.5E+07

TBLASTN 2.10.1+

Query: lcl|KF214777.1_prot_AHH01567.1_1 [gene=CenH3] [protein=centromere-specific h

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

20 hits found

lcl KF214' Chr6	65.306	98	33	1	57	154	3040837
lcl KF214' Chr6	65.306	98	33	1	57	154	3056279
lcl KF214' Chr6	65.306	98	33	1	57	154	3055514
lcl KF214' Chr6	65.306	98	33	1	57	154	3046867
lcl KF214' Chr6	65.306	98	33	1	57	154	1646006
lcl KF214' Chr11	65.306	98	33	1	57	154	2626112
lcl KF214' Chr5	65.306	98	33	1	57	154	2.1E+07
lcl KF214' Chr5	66.667	39	13	0	54	92	2.4E+07
lcl KF214' Chr5	65.217	23	8	0	121	143	2.4E+07
lcl KF214' Chr4	65.306	98	33	1	57	154	2.1E+07
lcl KF214' Chr4	40.881	159	33	2	57	154	2.2E+07
lcl KF214' Chr1	65.306	98	33	1	57	154	3.8E+07
lcl KF214' Chr12	63.265	98	35	1	57	154	1.3E+07
lcl KF214' Chr12	58.163	98	40	1	57	154	1.3E+07
lcl KF214' Chr2	45.69	116	32	2	70	154	1.5E+07
lcl KF214' Chr2	70.588	34	10	0	121	154	1.5E+07
lcl KF214' Chr2	52.778	36	15	1	70	105	1.5E+07
lcl KF214' Chr3	76.471	34	8	0	121	154	1.6E+07
lcl KF214' Chr3	51.429	35	17	0	71	105	1.6E+07
lcl KF214' Chr3	68.75	16	5	0	57	72	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KC491791.1_prot_AGQ21573.1_1 [gene=CENH3] [protein=centromere specific l

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

20 hits found

lcl KC491 Chr6	60.204	98	38	1	61	158	3040837
lcl KC491 Chr6	60.204	98	38	1	61	158	3056279
lcl KC491 Chr6	60.204	98	38	1	61	158	3055514
lcl KC491 Chr6	60.204	98	38	1	61	158	3046867
lcl KC491 Chr6	60.204	98	38	1	61	158	1646006
lcl KC491 Chr11	60.204	98	38	1	61	158	2626112

lcl KC491 Chr5	60.204	98	38	1	61	158	2.1E+07
lcl KC491 Chr5	61.538	39	15	0	58	96	2.4E+07
lcl KC491 Chr5	62.5	16	6	0	96	111	2.4E+07
lcl KC491 Chr1	60.204	98	38	1	61	158	3.8E+07
lcl KC491 Chr4	60.204	98	38	1	61	158	2.1E+07
lcl KC491 Chr4	44.348	115	33	1	75	158	2.2E+07
lcl KC491 Chr12	59.184	98	39	1	61	158	1.3E+07
lcl KC491 Chr12	55.102	98	43	1	61	158	1.3E+07
lcl KC491 Chr2	42.241	116	36	1	74	158	1.5E+07
lcl KC491 Chr2	70	30	9	0	129	158	1.5E+07
lcl KC491 Chr2	50	32	16	0	74	105	1.5E+07
lcl KC491 Chr3	76.667	30	7	0	129	158	1.6E+07
lcl KC491 Chr3	48.571	35	18	0	75	109	1.6E+07
lcl KC491 Chr3	52.174	23	11	0	66	88	2.9E+07

TBLASTN 2.10.1+

Query: lcl|AY438639.1_prot_AAR85315.1_1 [gene=CenH3] [protein=centromeric histone 3]

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

26 hits found

lcl AY438 Chr6	69	100	30	1	63	162	3040837
lcl AY438 Chr6	69	100	30	1	63	162	3055514
lcl AY438 Chr6	69	100	30	1	63	162	3056279
lcl AY438 Chr6	69	100	30	1	63	162	3046867
lcl AY438 Chr6	69	100	30	1	63	162	1646006
lcl AY438 Chr11	69	100	30	1	63	162	2626112
lcl AY438 Chr5	69	100	30	1	63	162	2.1E+07
lcl AY438 Chr5	100	43	0	0	56	98	2.4E+07
lcl AY438 Chr5	100	16	0	0	98	113	2.4E+07
lcl AY438 Chr5	100	32	0	0	1	32	2.4E+07
lcl AY438 Chr5	100	22	0	0	126	147	2.4E+07
lcl AY438 Chr5	62.069	29	4	1	136	164	2.4E+07
lcl AY438 Chr4	69	100	30	1	63	162	2.1E+07
lcl AY438 Chr4	41.615	161	33	2	63	162	2.2E+07
lcl AY438 Chr1	69.388	98	29	1	63	160	3.8E+07
lcl AY438 Chr12	62.136	103	32	2	63	162	1.3E+07
lcl AY438 Chr12	62	100	37	1	63	162	1.3E+07
lcl AY438 Chr2	47.458	118	31	1	76	162	1.5E+07
lcl AY438 Chr2	72.222	36	10	0	127	162	1.5E+07
lcl AY438 Chr2	66.667	30	10	0	76	105	1.5E+07
lcl AY438 Chr2	83.333	18	3	0	63	80	2E+07
lcl AY438 Chr2	75	16	4	0	63	78	1.5E+07
lcl AY438 Chr3	72.973	37	10	0	127	163	1.6E+07
lcl AY438 Chr3	57.143	35	15	0	77	111	1.6E+07
lcl AY438 Chr3	75	16	4	0	63	78	1.6E+07
lcl AY438 Chr7	60	20	8	0	92	111	1.2E+07

TBLASTN 2.10.1+

Query: lcl|AF519807.2_prot_AAM74226.1_1 [protein=centromeric histone H3-like protein

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

lcl AF519:Chr6	67.677	99	28	2	58	155	3040828
lcl AF519:Chr6	67.677	99	28	2	58	155	3055505
lcl AF519:Chr6	67.677	99	28	2	58	155	3046858
lcl AF519:Chr6	67.677	99	28	2	58	155	3056288
lcl AF519:Chr6	68.687	99	27	2	58	155	1645997
lcl AF519:Chr11	67.677	99	28	2	58	155	2626103
lcl AF519:Chr5	67.677	99	28	2	58	155	2.1E+07
lcl AF519:Chr5	71.429	42	11	1	49	90	2.4E+07
lcl AF519:Chr5	72.727	22	6	0	119	140	2.4E+07
lcl AF519:Chr5	80	25	5	0	1	25	2.4E+07
lcl AF519:Chr4	67.677	99	28	2	58	155	2.1E+07
lcl AF519:Chr4	39.752	161	37	3	55	155	2.2E+07
lcl AF519:Chr1	68.041	97	27	2	58	153	3.8E+07
lcl AF519:Chr12	61.224	98	36	1	58	155	1.3E+07
lcl AF519:Chr12	59.184	98	38	1	58	155	1.3E+07
lcl AF519:Chr2	46.61	118	33	1	68	155	1.5E+07
lcl AF519:Chr2	70.27	37	11	0	120	156	1.5E+07
lcl AF519:Chr2	69.231	26	8	0	68	93	1.5E+07
lcl AF519:Chr2	65.217	23	8	0	50	72	2E+07
lcl AF519:Chr3	77.778	36	8	0	120	155	1.6E+07
lcl AF519:Chr3	72	25	7	0	69	93	1.6E+07
lcl AF519:Chr3	76.923	13	3	0	58	70	1.6E+07

TBLASTN 2.10.1+

Query: lcl|HM988988.1_prot_ADM18965.1_1 [gene=CENH3-B] [protein=centromeric histone H3-like protein

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

lcl HM98:Chr6	63.542	96	34	1	80	175	3040837
lcl HM98:Chr6	63.542	96	34	1	80	175	3056279
lcl HM98:Chr6	63.542	96	34	1	80	175	3055514
lcl HM98:Chr6	51.493	134	61	3	43	175	3046975
lcl HM98:Chr6	64.583	96	33	1	80	175	1646006
lcl HM98:Chr1	63.542	96	34	1	80	175	3.8E+07
lcl HM98:Chr11	60	110	42	2	67	175	2626154
lcl HM98:Chr5	63.542	96	34	1	80	175	2.1E+07
lcl HM98:Chr5	70	40	12	0	76	115	2.4E+07
lcl HM98:Chr5	73.333	15	4	0	115	129	2.4E+07
lcl HM98:Chr5	59.091	22	9	0	143	164	2.4E+07
lcl HM98:Chr4	63.542	96	34	1	80	175	2.1E+07
lcl HM98:Chr4	39.881	168	37	5	71	175	2.2E+07
lcl HM98:Chr12	61.458	96	36	1	80	175	1.3E+07
lcl HM98:Chr12	57.143	98	41	1	80	177	1.3E+07

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lcl|HM98:Chr2      45.614      114      31      2      93      175 1.5E+07
lcl|HM98:Chr2      71.875      32       9      0     144      175 1.5E+07
lcl|HM98:Chr2      54.054      37      15      1      93      127 1.5E+07
lcl|HM98:Chr2      42.857      35      20      0      80      114 2E+07
lcl|HM98:Chr3      78.125      32       7      0     144      175 1.6E+07
lcl|HM98:Chr3        60      25      10      0      94      118 1.6E+07
lcl|HM98:Chr3     41.463      41      18      2      80      115 1.6E+07
# TBLASTN 2.10.1+
# Query: lcl|MH094618.1_prot_AYA72175.1_1 [protein=centromeric-specific histone H3 var
# Database: Nippon
# Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens
# 23 hits found
lcl|MH09:Chr11     51.282      156      50      3       1      151 2626220
lcl|MH09:Chr6      51.282      156      50      3       1      151 3040945
lcl|MH09:Chr6      51.282      156      50      3       1      151 3055622
lcl|MH09:Chr6      51.282      156      50      3       1      151 3056171
lcl|MH09:Chr6      64.706      102      35      1      50      151 3046873
lcl|MH09:Chr6      64.706      102      35      1      50      151 1646012
lcl|MH09:Chr5      51.282      156      50      3       1      151 2.2E+07
lcl|MH09:Chr5      77.273      44      10      0      44       87 2.4E+07
lcl|MH09:Chr5       70.37      27       8      0      87      113 2.4E+07
lcl|MH09:Chr5      57.692      26      11      0     111      136 2.4E+07
lcl|MH09:Chr4      51.282      156      50      3       1      151 2.1E+07
lcl|MH09:Chr4      40.491      163      36      2      50      151 2.2E+07
lcl|MH09:Chr1      51.299      154      49      3       1      149 3.8E+07
lcl|MH09:Chr12     48.993      149      60      3       1      149 1.3E+07
lcl|MH09:Chr12     49.007      151      61      4       1      151 1.3E+07
lcl|MH09:Chr2      45.763      118      33      1      65      151 1.5E+07
lcl|MH09:Chr2      61.538      52      20      0     100      151 1.5E+07
lcl|MH09:Chr2      80.769      26       5      0      65       90 1.5E+07
lcl|MH09:Chr2      66.667      27       6      1      46       69 2E+07
lcl|MH09:Chr2      38.776      49      20      2     108      154 2E+07
lcl|MH09:Chr3      65.385      52      18      0     100      151 1.6E+07
lcl|MH09:Chr3      57.143      35      15      0      66      100 1.6E+07
lcl|MH09:Chr3      66.667      18       6      0      50       67 1.6E+07
# TBLASTN 2.10.1+
# Query: lcl|MH182682.1_prot_AYA72192.1_1 [protein=centromeric-specific histone H3 var
# Database: Nippon
# Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens
# 24 hits found
lcl|MH18:Chr6      49.359      156      53      3       1      151 3040945
lcl|MH18:Chr6      49.359      156      53      3       1      151 3056171
lcl|MH18:Chr6      49.359      156      53      3       1      151 3055622
lcl|MH18:Chr6      63.725      102      36      1      50      151 3046873
lcl|MH18:Chr6      59.483      116      40      2      36      151 1646036
lcl|MH18:Chr11     49.359      156      53      3       1      151 2626220

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lcl MH18:Chr5	49.359	156	53	3	1	151	2.2E+07
lcl MH18:Chr5	68.182	44	14	0	44	87	2.4E+07
lcl MH18:Chr5	70.37	27	8	0	87	113	2.4E+07
lcl MH18:Chr5	57.692	26	11	0	111	136	2.4E+07
lcl MH18:Chr4	49.359	156	53	3	1	151	2.1E+07
lcl MH18:Chr4	39.548	177	40	3	36	151	2.2E+07
lcl MH18:Chr1	49.351	154	52	3	1	149	3.8E+07
lcl MH18:Chr12	49.032	155	55	4	1	151	1.3E+07
lcl MH18:Chr12	57.843	102	42	1	50	151	1.3E+07
lcl MH18:Chr2	46.61	118	32	2	65	151	1.5E+07
lcl MH18:Chr2	61.538	52	20	0	100	151	1.5E+07
lcl MH18:Chr2	76.923	26	6	0	65	90	1.5E+07
lcl MH18:Chr2	68.421	19	6	0	51	69	2E+07
lcl MH18:Chr2	36.735	49	21	2	108	154	2E+07
lcl MH18:Chr2	66.667	18	6	0	50	67	1.5E+07
lcl MH18:Chr3	65.385	52	18	0	100	151	1.6E+07
lcl MH18:Chr3	76	25	6	0	66	90	1.6E+07
lcl MH18:Chr3	66.667	18	6	0	50	67	1.6E+07

TBLASTN 2.10.1+

Query: lcl|MH153697.1_prot_AYA72176.1_1 [protein=centromeric-specific histone H3 var

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

25 hits found

lcl MH15:Chr11	54.305	151	53	4	1	151	2626220
lcl MH15:Chr6	54.305	151	53	4	1	151	3040945
lcl MH15:Chr6	54.305	151	53	4	1	151	3055622
lcl MH15:Chr6	54.305	151	53	4	1	151	3056171
lcl MH15:Chr6	55.944	143	55	4	12	151	3046984
lcl MH15:Chr6	63.636	110	35	2	42	151	1646024
lcl MH15:Chr6	27.5	40	29	0	66	105	3153949
lcl MH15:Chr5	54.305	151	53	4	1	151	2.2E+07
lcl MH15:Chr5	71.111	45	13	0	43	87	2.4E+07
lcl MH15:Chr5	62.963	27	10	0	87	113	2.4E+07
lcl MH15:Chr5	65.385	26	9	0	111	136	2.4E+07
lcl MH15:Chr4	54.305	151	53	4	1	151	2.1E+07
lcl MH15:Chr4	40.341	176	40	3	37	151	2.2E+07
lcl MH15:Chr1	55.034	149	51	4	1	149	3.8E+07
lcl MH15:Chr12	48.344	151	62	3	1	151	1.3E+07
lcl MH15:Chr12	46.154	156	58	3	1	151	1.3E+07
lcl MH15:Chr2	44.068	118	35	1	65	151	1.5E+07
lcl MH15:Chr2	61.538	52	20	0	100	151	1.5E+07
lcl MH15:Chr2	76	25	6	0	65	89	1.5E+07
lcl MH15:Chr2	33.721	86	47	2	45	128	2E+07
lcl MH15:Chr2	72.222	18	5	0	50	67	1.5E+07
lcl MH15:Chr2	35.294	51	23	2	106	154	2E+07
lcl MH15:Chr3	65.385	52	18	0	100	151	1.6E+07

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lcl|MH15:Chr3      79.167      24      5      0      66      89 1.6E+07
lcl|MH15:Chr3      61.538      26      6      1      42      67 1.6E+07
# TBLASTN 2.10.1+
# Query: lcl|MG384788.1_prot_AUN88474.1_1 [gene=betaCENH3] [protein=centromeric his
# Database: Nippon
# Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens
# 25 hits found
lcl|MG38:Chr11     65.306      98      32      1      52      149 2626103
lcl|MG38:Chr6      65.306      98      32      1      52      149 3040828
lcl|MG38:Chr6      65.306      98      32      1      52      149 3055505
lcl|MG38:Chr6      65.306      98      32      1      52      149 3046858
lcl|MG38:Chr6      64      100      34      1      50      149 3056282
lcl|MG38:Chr6      64.286      98      33      1      52      149 1645997
lcl|MG38:Chr5      64      100      34      1      50      149 2.1E+07
lcl|MG38:Chr5      80      35      7      0      50      84 2.4E+07
lcl|MG38:Chr5      42.857      28      15      1      84      111 2.4E+07
lcl|MG38:Chr5      78.571      28      6      0      107     134 2.4E+07
lcl|MG38:Chr5      55.172      29      6      1      123     151 2.4E+07
lcl|MG38:Chr4      64      100      34      1      50      149 2.1E+07
lcl|MG38:Chr4      40.881     159      32      4      52      149 2.2E+07
lcl|MG38:Chr4      36.364      33      21      0      64      96 2E+07
lcl|MG38:Chr1      64.286      98      33      1      50      147 3.8E+07
lcl|MG38:Chr12     60      100      38      1      50      149 1.3E+07
lcl|MG38:Chr12     59      100      39      1      50      149 1.3E+07
lcl|MG38:Chr2      47.059     119      33      4      62      150 1.5E+07
lcl|MG38:Chr2      60      60      21      1      94      150 1.5E+07
lcl|MG38:Chr2      73.077      26      7      0      62      87 1.5E+07
lcl|MG38:Chr2      80      15      3      0      52      66 2E+07
lcl|MG38:Chr2      37.5      48      20      2     104     149 2E+07
lcl|MG38:Chr3      66.667      51      17      0      99      149 1.6E+07
lcl|MG38:Chr3      65.625      32      11      0      63      94 1.6E+07
lcl|MG38:Chr3      60      15      6      0      50      64 1.6E+07
# TBLASTN 2.10.1+
# Query: lcl|MG384783.1_prot_AUN88469.1_1 [gene=betaCENH3] [protein=beta centrome
# Database: Nippon
# Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens
# 25 hits found
lcl|MG38:Chr6      66.327      98      31      2      52      149 3040828
lcl|MG38:Chr6      66.327      98      31      2      52      149 3055505
lcl|MG38:Chr6      65      100      33      2      50      149 3056282
lcl|MG38:Chr6      66.327      98      31      2      52      149 3046858
lcl|MG38:Chr6      65.306      98      32      2      52      149 1645997
lcl|MG38:Chr11     66.327      98      31      2      52      149 2626103
lcl|MG38:Chr5      65      100      33      2      50      149 2.1E+07
lcl|MG38:Chr5      80      35      7      0      50      84 2.4E+07
lcl|MG38:Chr5      42.857      28      15      1      84      111 2.4E+07

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lcl MG38·Chr5	78.571	28	6	0	107	134	2.4E+07
lcl MG38·Chr5	73.684	19	5	0	133	151	2.4E+07
lcl MG38·Chr4	65	100	33	2	50	149	2.1E+07
lcl MG38·Chr4	41.509	159	31	4	52	149	2.2E+07
lcl MG38·Chr4	33.333	33	22	0	64	96	2E+07
lcl MG38·Chr1	65.306	98	32	2	50	147	3.8E+07
lcl MG38·Chr12	60	100	38	1	50	149	1.3E+07
lcl MG38·Chr12	59	100	39	1	50	149	1.3E+07
lcl MG38·Chr2	45.833	120	33	3	62	150	1.5E+07
lcl MG38·Chr2	58.333	60	22	1	94	150	1.5E+07
lcl MG38·Chr2	73.077	26	7	0	62	87	1.5E+07
lcl MG38·Chr2	80	15	3	0	52	66	2E+07
lcl MG38·Chr2	37.5	48	20	2	104	149	2E+07
lcl MG38·Chr3	66.667	51	17	0	99	149	1.6E+07
lcl MG38·Chr3	65.625	32	11	0	63	94	1.6E+07
lcl MG38·Chr3	60	15	6	0	50	64	1.6E+07

TBLASTN 2.10.1+

Query: lcl|MG384777.1_prot_AUN88463.1_1 [gene=betaCENH3-2] [protein=beta centron

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

24 hits found

lcl MG38·Chr11	66.327	98	31	2	54	151	2626103
lcl MG38·Chr6	66.327	98	31	2	54	151	3040828
lcl MG38·Chr6	66.327	98	31	2	54	151	3055505
lcl MG38·Chr6	65	100	33	2	52	151	3056282
lcl MG38·Chr6	65	100	33	2	52	151	3046864
lcl MG38·Chr6	65.306	98	32	2	54	151	1645997
lcl MG38·Chr5	65	100	33	2	52	151	2.1E+07
lcl MG38·Chr5	74.286	35	9	0	52	86	2.4E+07
lcl MG38·Chr5	46.429	28	14	1	86	113	2.4E+07
lcl MG38·Chr5	74.194	31	8	0	106	136	2.4E+07
lcl MG38·Chr5	55.172	29	6	1	125	153	2.4E+07
lcl MG38·Chr4	65	100	33	2	52	151	2.1E+07
lcl MG38·Chr4	40.373	161	34	4	52	151	2.2E+07
lcl MG38·Chr1	65.306	98	32	2	52	149	3.8E+07
lcl MG38·Chr12	58	100	40	1	52	151	1.3E+07
lcl MG38·Chr12	57	100	41	1	52	151	1.3E+07
lcl MG38·Chr2	45.833	120	33	3	64	152	1.5E+07
lcl MG38·Chr2	52.113	71	28	1	82	152	1.5E+07
lcl MG38·Chr2	65.385	26	9	0	64	89	1.5E+07
lcl MG38·Chr2	80	15	3	0	54	68	2E+07
lcl MG38·Chr2	41.304	46	17	2	108	151	2E+07
lcl MG38·Chr3	68.627	51	16	0	101	151	1.6E+07
lcl MG38·Chr3	59.375	32	13	0	65	96	1.6E+07
lcl MG38·Chr3	66.667	15	5	0	52	66	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KR676382.1_prot_ALK04343.1_1 [protein=centromeric histone H3 protein] [prc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

21 hits found

lcl KR676. Chr11	48.529	136	49	3	44	172	2626184
lcl KR676. Chr6	48.529	136	49	3	44	172	3040909
lcl KR676. Chr6	48.529	136	49	3	44	172	3055586
lcl KR676. Chr6	49.219	128	63	1	45	172	3046951
lcl KR676. Chr6	47.482	139	52	3	41	172	3056198
lcl KR676. Chr6	55.963	109	46	1	64	172	1646033
lcl KR676. Chr5	48.529	136	49	3	44	172	2.2E+07
lcl KR676. Chr5	65	40	14	0	69	108	2.4E+07
lcl KR676. Chr5	56	25	11	0	139	163	2.4E+07
lcl KR676. Chr1	47.826	138	51	3	41	171	3.8E+07
lcl KR676. Chr4	47.482	139	52	3	41	172	2.1E+07
lcl KR676. Chr4	37.87	169	45	4	64	172	2.2E+07
lcl KR676. Chr12	55.046	109	47	1	64	172	1.3E+07
lcl KR676. Chr12	51.376	109	51	1	64	172	1.3E+07
lcl KR676. Chr2	42.735	117	37	2	86	172	1.5E+07
lcl KR676. Chr2	65.714	35	12	0	138	172	1.5E+07
lcl KR676. Chr2	41.667	36	21	0	54	89	2E+07
lcl KR676. Chr2	55.172	29	13	0	86	114	1.5E+07
lcl KR676. Chr2	75	16	4	0	73	88	1.5E+07
lcl KR676. Chr3	68.571	35	11	0	138	172	1.6E+07
lcl KR676. Chr3	38.776	49	23	1	64	105	1.6E+07

TBLASTN 2.10.1+

Query: lcl|KR676380.1_prot_ALK04341.1_1 [protein=centromeric histone H3 protein] [prc

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

21 hits found

lcl KR676. Chr1	56.566	99	41	1	71	169	3.8E+07
lcl KR676. Chr6	57	100	41	1	71	170	1646006
lcl KR676. Chr6	56	100	42	1	71	170	3056279
lcl KR676. Chr6	56	100	42	1	71	170	3040837
lcl KR676. Chr6	56	100	42	1	71	170	3055514
lcl KR676. Chr6	56	100	42	1	71	170	3046867
lcl KR676. Chr12	57	100	41	1	71	170	1.3E+07
lcl KR676. Chr12	52	100	46	1	71	170	1.3E+07
lcl KR676. Chr4	56	100	42	1	71	170	2.1E+07
lcl KR676. Chr4	37.5	160	40	3	71	170	2.2E+07
lcl KR676. Chr5	56	100	42	1	71	170	2.1E+07
lcl KR676. Chr5	67.5	40	13	0	67	106	2.4E+07
lcl KR676. Chr5	48.276	29	14	1	105	133	2.4E+07
lcl KR676. Chr5	54.839	31	14	0	131	161	2.4E+07
lcl KR676. Chr11	56	100	42	1	71	170	2626112
lcl KR676. Chr3	62.745	51	19	0	120	170	1.6E+07

lcl KR676 Chr3	56	25	11	0	85	109	1.6E+07
lcl KR676 Chr3	61.111	18	7	0	71	88	1.6E+07
lcl KR676 Chr2	60.784	51	20	0	120	170	1.5E+07
lcl KR676 Chr2	57.692	26	11	0	84	109	1.5E+07
lcl KR676 Chr2	40.171	117	40	2	84	170	1.5E+07

TBLASTN 2.10.1+

Query: lcl|AB793504.1_prot_BAO51832.1_1 [gene=TbCENH3] [protein=centromere specif

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

lcl AB793 Chr11	54.73	148	53	4	1	148	2626220
lcl AB793 Chr6	54.73	148	53	4	1	148	3055622
lcl AB793 Chr6	54.73	148	53	4	1	148	3040945
lcl AB793 Chr6	54.73	148	53	4	1	148	3056171
lcl AB793 Chr6	58.929	112	45	1	37	148	3046906
lcl AB793 Chr6	60.185	108	42	1	41	148	1646033
lcl AB793 Chr5	54.73	148	53	4	1	148	2.2E+07
lcl AB793 Chr5	70.27	37	11	0	49	85	2.4E+07
lcl AB793 Chr5	53.846	26	12	0	114	139	2.4E+07
lcl AB793 Chr4	54.73	148	53	4	1	148	2.1E+07
lcl AB793 Chr4	38.462	169	43	2	41	148	2.2E+07
lcl AB793 Chr1	54.422	147	53	3	1	147	3.8E+07
lcl AB793 Chr12	56.481	108	46	1	41	148	1.3E+07
lcl AB793 Chr12	52.778	108	50	1	41	148	1.3E+07
lcl AB793 Chr2	41.88	117	37	1	63	148	1.5E+07
lcl AB793 Chr2	62.857	35	13	0	114	148	1.5E+07
lcl AB793 Chr2	60	30	12	0	63	92	1.5E+07
lcl AB793 Chr2	51.22	41	19	1	25	65	1.5E+07
lcl AB793 Chr3	65.714	35	12	0	114	148	1.6E+07
lcl AB793 Chr3	51.429	35	17	0	64	98	1.6E+07
lcl AB793 Chr3	37.5	64	28	2	33	87	1.6E+07
lcl AB793 Chr7	38.462	39	24	0	33	71	4666485

TBLASTN 2.10.1+

Query: lcl|AF465802.1_prot_AAL86777.1_1 [gene=HTR12] [protein=centromeric histone h

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

20 hits found

lcl AF465: Chr11	59	100	39	1	73	172	2626112
lcl AF465: Chr6	59	100	39	1	73	172	3040837
lcl AF465: Chr6	59	100	39	1	73	172	3055514
lcl AF465: Chr6	59	100	39	1	73	172	3046867
lcl AF465: Chr6	59	100	39	1	73	172	3056279
lcl AF465: Chr6	58	100	40	1	73	172	1646006
lcl AF465: Chr1	59.596	99	38	1	73	171	3.8E+07
lcl AF465: Chr5	59	100	39	1	73	172	2.1E+07
lcl AF465: Chr5	72.973	37	10	0	72	108	2.4E+07

lcl AF465: Chr5	53.846	26	12	0	138	163	2.4E+07
lcl AF465: Chr4	59	100	39	1	73	172	2.1E+07
lcl AF465: Chr4	36.875	160	41	3	73	172	2.2E+07
lcl AF465: Chr12	59	100	39	1	73	172	1.3E+07
lcl AF465: Chr12	55	100	43	1	73	172	1.3E+07
lcl AF465: Chr2	41.026	117	39	2	86	172	1.5E+07
lcl AF465: Chr2	65.714	35	12	0	138	172	1.5E+07
lcl AF465: Chr2	82.353	17	3	0	73	89	2E+07
lcl AF465: Chr3	68.571	35	11	0	138	172	1.6E+07
lcl AF465: Chr3	68.75	16	5	0	73	88	1.6E+07
lcl AF465: Chr3	51.852	27	13	0	87	113	1.6E+07

TBLASTN 2.10.1+

Query: lcl|AF465800.1_prot_AAL86775.1_1 [gene=HTR12] [protein=centromeric histone H

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

18 hits found

lcl AF465: Chr6	53.982	113	49	2	63	174	3040876
lcl AF465: Chr6	53.982	113	49	2	63	174	3055553
lcl AF465: Chr6	53.043	115	51	2	61	174	3056234
lcl AF465: Chr6	56.311	103	43	1	72	174	3046876
lcl AF465: Chr6	57.282	103	42	1	72	174	1646015
lcl AF465: Chr11	53.982	113	49	2	63	174	2626151
lcl AF465: Chr1	53.509	114	50	2	61	173	3.8E+07
lcl AF465: Chr5	53.982	113	49	2	63	174	2.2E+07
lcl AF465: Chr5	67.568	37	12	0	74	110	2.4E+07
lcl AF465: Chr5	53.846	26	12	0	140	165	2.4E+07
lcl AF465: Chr4	53.043	115	51	2	61	174	2.1E+07
lcl AF465: Chr4	36.257	171	48	4	65	174	2.2E+07
lcl AF465: Chr12	50.847	118	54	3	63	178	1.3E+07
lcl AF465: Chr12	48.673	113	55	2	63	174	1.3E+07
lcl AF465: Chr2	40.171	117	40	2	88	174	1.5E+07
lcl AF465: Chr2	65.714	35	12	0	140	174	1.5E+07
lcl AF465: Chr2	46.154	39	18	1	53	91	2E+07
lcl AF465: Chr3	68.571	35	11	0	140	174	1.6E+07

TBLASTN 2.10.1+

Query: lcl|AF465801.1_prot_AAL86776.1_1 [gene=HTR12] [protein=centromeric histone H

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

20 hits found

lcl AF465: Chr11	59	100	39	1	73	172	2626112
lcl AF465: Chr6	59	100	39	1	73	172	3040837
lcl AF465: Chr6	59	100	39	1	73	172	3055514
lcl AF465: Chr6	59	100	39	1	73	172	3046867
lcl AF465: Chr6	59	100	39	1	73	172	3056279
lcl AF465: Chr6	58	100	40	1	73	172	1646006
lcl AF465: Chr1	59.596	99	38	1	73	171	3.8E+07

lcl AF465:Chr5	59	100	39	1	73	172	2.1E+07
lcl AF465:Chr5	72.973	37	10	0	72	108	2.4E+07
lcl AF465:Chr5	53.846	26	12	0	138	163	2.4E+07
lcl AF465:Chr4	59	100	39	1	73	172	2.1E+07
lcl AF465:Chr4	36.875	160	41	3	73	172	2.2E+07
lcl AF465:Chr12	59	100	39	1	73	172	1.3E+07
lcl AF465:Chr12	55	100	43	1	73	172	1.3E+07
lcl AF465:Chr2	41.026	117	39	2	86	172	1.5E+07
lcl AF465:Chr2	65.714	35	12	0	138	172	1.5E+07
lcl AF465:Chr2	82.353	17	3	0	73	89	2E+07
lcl AF465:Chr3	68.571	35	11	0	138	172	1.6E+07
lcl AF465:Chr3	68.75	16	5	0	73	88	1.6E+07
lcl AF465:Chr3	51.852	27	13	0	87	113	1.6E+07

TBLASTN 2.10.1+

Query: tr|A0A0G3YJC7|A0A0G3YJC7_AEGTA Centromeric histone H3 OS=Aegilops tauschii

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

50 hits found

tr A0A0G Chr11	55.714	140	56	4	1	139	2626220
tr A0A0G Chr11	40.909	44	25	1	61	104	1.8E+07
tr A0A0G Chr11	37.037	27	17	0	88	114	1.4E+07
tr A0A0G Chr11	44.186	43	23	1	61	103	2.4E+07
tr A0A0G Chr6	55.714	140	56	4	1	139	3040945
tr A0A0G Chr6	55.714	140	56	4	1	139	3055622
tr A0A0G Chr6	55.714	140	56	4	1	139	3056171
tr A0A0G Chr6	60.748	107	39	2	33	139	3046882
tr A0A0G Chr6	60	100	39	1	40	139	1646006
tr A0A0G Chr6	52.174	23	11	0	82	104	2.8E+07
tr A0A0G Chr6	52.174	23	11	0	82	104	1.6E+07
tr A0A0G Chr5	55.714	140	56	4	1	139	2.2E+07
tr A0A0G Chr5	75	40	10	0	36	75	2.4E+07
tr A0A0G Chr5	48.148	27	14	0	75	101	2.4E+07
tr A0A0G Chr5	76.923	26	6	0	99	124	2.4E+07
tr A0A0G Chr5	58.333	36	11	1	1	32	2.4E+07
tr A0A0G Chr5	55.172	29	12	1	114	141	2.4E+07
tr A0A0G Chr5	50	28	14	0	63	90	8282467
tr A0A0G Chr5	47.826	23	12	0	82	104	8334046
tr A0A0G Chr5	52.174	23	11	0	82	104	7739635
tr A0A0G Chr5	52.174	23	11	0	82	104	7092075
tr A0A0G Chr5	52.174	23	11	0	82	104	1.2E+07
tr A0A0G Chr4	55.714	140	56	4	1	139	2.1E+07
tr A0A0G Chr4	37.572	173	45	4	28	139	2.2E+07
tr A0A0G Chr4	52.174	23	11	0	82	104	6034914
tr A0A0G Chr4	31.707	41	26	1	76	114	1.6E+07
tr A0A0G Chr4	31.707	41	26	1	76	114	1.6E+07
tr A0A0G Chr1	55.797	138	55	4	1	137	3.8E+07

tr A0A0G Chr1	40.909	44	25	1	61	104	1E+07
tr A0A0G Chr12	49.306	144	65	4	1	141	1.3E+07
tr A0A0G Chr12	48.571	140	66	3	1	139	1.3E+07
tr A0A0G Chr12	52.174	23	11	0	82	104	2.7E+07
tr A0A0G Chr3	65.385	52	18	0	88	139	1.6E+07
tr A0A0G Chr3	48.571	35	18	0	54	88	1.6E+07
tr A0A0G Chr3	78.571	14	3	0	40	53	1.6E+07
tr A0A0G Chr3	52.174	23	11	0	82	104	2E+07
tr A0A0G Chr3	52.174	23	11	0	82	104	1.9E+07
tr A0A0G Chr2	41.176	119	39	2	53	140	1.5E+07
tr A0A0G Chr2	62.264	53	20	0	88	140	1.5E+07
tr A0A0G Chr2	50	30	15	0	53	82	1.5E+07
tr A0A0G Chr2	36.364	66	42	0	9	74	2E+07
tr A0A0G Chr2	39.583	48	19	2	94	139	2E+07
tr A0A0G Chr2	68.75	16	5	0	40	55	1.5E+07
tr A0A0G Chr7	38.636	44	26	1	61	104	4633533
tr A0A0G Chr7	30.508	59	41	0	25	83	1.1E+07
tr A0A0G Chr7	27.273	44	30	1	73	114	1.2E+07
tr A0A0G Chr8	47.826	23	12	0	82	104	1.3E+07
tr A0A0G Chr9	52.174	23	11	0	82	104	7580827
tr A0A0G Chr10	52.174	23	11	0	82	104	1.3E+07
tr A0A0G Chr10	52.174	23	11	0	82	104	9325236

TBLASTN 2.10.1+

Query: tr|A0A0B6VLZ9|A0A0B6VLZ9_AVESA Centromere specific histone H3 (Fragment) O

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

25 hits found

tr A0A0B Chr11	67.708	96	28	2	66	160	2626109
tr A0A0B Chr6	67.708	96	28	2	66	160	3040834
tr A0A0B Chr6	67.708	96	28	2	66	160	3055511
tr A0A0B Chr6	67.708	96	28	2	66	160	3046864
tr A0A0B Chr6	67.708	96	28	2	66	160	3056282
tr A0A0B Chr6	66.667	96	29	2	66	160	1646003
tr A0A0B Chr5	67.708	96	28	2	66	160	2.1E+07
tr A0A0B Chr5	88.571	35	4	0	66	100	2.4E+07
tr A0A0B Chr5	51.852	27	13	0	100	126	2.4E+07
tr A0A0B Chr5	75	28	7	0	122	149	2.4E+07
tr A0A0B Chr5	61.111	36	14	0	1	36	2.4E+07
tr A0A0B Chr1	67.708	96	28	2	66	160	3.8E+07
tr A0A0B Chr4	67.708	96	28	2	66	160	2.1E+07
tr A0A0B Chr4	41.667	156	30	3	66	160	2.2E+07
tr A0A0B Chr12	67.368	95	30	1	66	160	1.3E+07
tr A0A0B Chr12	64.211	95	33	1	66	160	1.3E+07
tr A0A0B Chr2	44.737	114	32	1	78	160	1.5E+07
tr A0A0B Chr2	64.583	48	17	0	113	160	1.5E+07
tr A0A0B Chr2	73.077	26	7	0	78	103	1.5E+07

tr A0A0B Chr2	82.353	17	3	0	66	82	2E+07
tr A0A0B Chr2	73.333	15	4	0	66	80	1.5E+07
tr A0A0B Chr3	68.75	48	15	0	113	160	1.6E+07
tr A0A0B Chr3	76	25	6	0	79	103	1.6E+07
tr A0A0B Chr3	43.182	44	17	2	66	102	1.6E+07
tr A0A0B Chr9	42.222	45	22	2	79	121	1018147

TBLASTN 2.10.1+

Query: tr|A0A0B6VNT5|A0A0B6VNT5_AVESA Centromere specific histone H3 (Fragment)

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

25 hits found

tr A0A0B Chr11	67.01	97	29	2	62	157	2626112
tr A0A0B Chr6	67.01	97	29	2	62	157	3040837
tr A0A0B Chr6	67.01	97	29	2	62	157	3055514
tr A0A0B Chr6	67.01	97	29	2	62	157	3046867
tr A0A0B Chr6	67.01	97	29	2	62	157	3056279
tr A0A0B Chr6	65.306	98	31	2	61	157	1646009
tr A0A0B Chr5	67.01	97	29	2	62	157	2.1E+07
tr A0A0B Chr5	80.488	41	8	0	57	97	2.4E+07
tr A0A0B Chr5	51.852	27	13	0	97	123	2.4E+07
tr A0A0B Chr5	75	28	7	0	119	146	2.4E+07
tr A0A0B Chr5	72.727	22	6	0	1	22	2.4E+07
tr A0A0B Chr1	67.01	97	29	2	62	157	3.8E+07
tr A0A0B Chr12	66.667	96	31	1	62	157	1.3E+07
tr A0A0B Chr12	63.542	96	34	1	62	157	1.3E+07
tr A0A0B Chr4	66.327	98	30	2	61	157	2.1E+07
tr A0A0B Chr4	40.506	158	33	3	61	157	2.2E+07
tr A0A0B Chr2	44.737	114	32	1	75	157	1.5E+07
tr A0A0B Chr2	64.583	48	17	0	110	157	1.5E+07
tr A0A0B Chr2	73.077	26	7	0	75	100	1.5E+07
tr A0A0B Chr2	78.947	19	4	0	61	79	2E+07
tr A0A0B Chr2	64.706	17	6	0	61	77	1.5E+07
tr A0A0B Chr3	68.75	48	15	0	110	157	1.6E+07
tr A0A0B Chr3	76	25	6	0	76	100	1.6E+07
tr A0A0B Chr3	42.222	45	18	2	62	99	1.6E+07
tr A0A0B Chr9	42.222	45	22	2	76	118	1018147

TBLASTN 2.10.1+

Query: tr|A0A0G3YJC9|A0A0G3YJC9_AEGSP Centromeric histone H3 OS=Aegilops speltoid

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

tr A0A0G Chr11	64.356	101	33	3	52	151	2626112
tr A0A0G Chr6	64.356	101	33	3	52	151	3040837
tr A0A0G Chr6	64.356	101	33	3	52	151	3055514
tr A0A0G Chr6	64.356	101	33	3	52	151	3056279
tr A0A0G Chr6	64.356	101	33	3	52	151	1646006

tr A0A0G Chr6	64.356	101	33	3	52	151	3046867
tr A0A0G Chr5	64.356	101	33	3	52	151	2.1E+07
tr A0A0G Chr5	75.676	37	9	0	50	86	2.4E+07
tr A0A0G Chr5	74.194	31	8	0	106	136	2.4E+07
tr A0A0G Chr5	41.176	34	20	0	120	153	2.4E+07
tr A0A0G Chr4	64.356	101	33	3	52	151	2.1E+07
tr A0A0G Chr4	39.752	161	36	3	52	151	2.2E+07
tr A0A0G Chr1	64.646	99	32	3	52	149	3.8E+07
tr A0A0G Chr12	57.426	101	40	2	52	151	1.3E+07
tr A0A0G Chr12	57.426	101	40	2	52	151	1.3E+07
tr A0A0G Chr3	66.667	51	17	0	101	151	1.6E+07
tr A0A0G Chr3	62.5	32	11	1	66	96	1.6E+07
tr A0A0G Chr3	55.556	18	8	0	52	69	1.6E+07
tr A0A0G Chr2	45.833	120	32	4	65	152	1.5E+07
tr A0A0G Chr2	58.333	60	22	1	96	152	1.5E+07
tr A0A0G Chr2	72.727	22	6	0	65	86	1.5E+07
tr A0A0G Chr2	72.222	18	5	0	52	69	2E+07
tr A0A0G Chr2	36	50	22	2	104	151	2E+07

TBLASTN 2.10.1+

Query: tr|A0A0B6VJW4|A0A0B6VJW4_AVES Centromere specific histone H3 (Fragment)

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

26 hits found

tr A0A0B Chr11	70.833	96	25	2	66	160	2626109
tr A0A0B Chr11	29.851	67	32	1	67	118	8742263
tr A0A0B Chr6	70.833	96	25	2	66	160	3040834
tr A0A0B Chr6	70.833	96	25	2	66	160	3055511
tr A0A0B Chr6	70.833	96	25	2	66	160	3046864
tr A0A0B Chr6	70.833	96	25	2	66	160	3056282
tr A0A0B Chr6	69.792	96	26	2	66	160	1646003
tr A0A0B Chr5	70.833	96	25	2	66	160	2.1E+07
tr A0A0B Chr5	85.714	35	5	0	66	100	2.4E+07
tr A0A0B Chr5	59.259	27	11	0	100	126	2.4E+07
tr A0A0B Chr5	75	28	7	0	122	149	2.4E+07
tr A0A0B Chr5	61.111	36	14	0	1	36	2.4E+07
tr A0A0B Chr1	70.833	96	25	2	66	160	3.8E+07
tr A0A0B Chr4	70.833	96	25	2	66	160	2.1E+07
tr A0A0B Chr4	42.949	156	28	3	66	160	2.2E+07
tr A0A0B Chr12	69.474	95	28	1	66	160	1.3E+07
tr A0A0B Chr12	66.316	95	31	1	66	160	1.3E+07
tr A0A0B Chr2	45.614	114	31	2	78	160	1.5E+07
tr A0A0B Chr2	66.667	48	16	0	113	160	1.5E+07
tr A0A0B Chr2	76.923	26	6	0	78	103	1.5E+07
tr A0A0B Chr2	82.353	17	3	0	66	82	2E+07
tr A0A0B Chr2	37.647	85	37	4	78	160	2E+07
tr A0A0B Chr2	73.333	15	4	0	66	80	1.5E+07

tr A0A0B1Chr3	70.833	48	14	0	113	160	1.6E+07
tr A0A0B1Chr3	75.862	29	6	1	79	106	1.6E+07
tr A0A0B1Chr3	43.182	44	17	2	66	102	1.6E+07

TBLASTN 2.10.1+

Query: tr|A0A0H3VKW3|A0A0H3VKW3_9POAL Centromeric histone H3 isoform B (Fragment)

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

tr A0A0H1Chr6	58.929	112	39	2	55	166	3040867
tr A0A0H1Chr6	58.929	112	39	2	55	166	3056249
tr A0A0H1Chr6	58.929	112	39	2	55	166	3055544
tr A0A0H1Chr6	52.143	140	55	5	29	166	3046972
tr A0A0H1Chr6	59.821	112	38	2	55	166	1646036
tr A0A0H1Chr11	58.929	112	39	2	55	166	2626142
tr A0A0H1Chr5	58.929	112	39	2	55	166	2.2E+07
tr A0A0H1Chr5	67.5	40	13	0	67	106	2.4E+07
tr A0A0H1Chr5	73.333	15	4	0	106	120	2.4E+07
tr A0A0H1Chr5	63.636	22	8	0	134	155	2.4E+07
tr A0A0H1Chr1	58.929	112	39	2	55	166	3.8E+07
tr A0A0H1Chr4	58.929	112	39	2	55	166	2.1E+07
tr A0A0H1Chr4	39.655	174	36	5	55	166	2.2E+07
tr A0A0H1Chr12	56.14	114	43	2	53	166	1.3E+07
tr A0A0H1Chr12	53.043	115	47	2	53	167	1.3E+07
tr A0A0H1Chr2	45.614	114	31	2	84	166	1.5E+07
tr A0A0H1Chr2	71.875	32	9	0	135	166	1.5E+07
tr A0A0H1Chr2	54.054	37	15	1	84	118	1.5E+07
tr A0A0H1Chr2	42.857	35	20	0	71	105	2E+07
tr A0A0H1Chr2	50	32	10	1	55	86	1.5E+07
tr A0A0H1Chr3	78.125	32	7	0	135	166	1.6E+07
tr A0A0H1Chr3	60	25	10	0	85	109	1.6E+07
tr A0A0H1Chr3	38.596	57	23	3	55	106	1.6E+07

TBLASTN 2.10.1+

Query: tr|A0A0H3VKW8|A0A0H3VKW8_9POAL Centromeric histone H3 isoform A (Fragment)

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

24 hits found

tr A0A0H1Chr6	55.455	110	48	1	55	164	3056237
tr A0A0H1Chr6	57.407	108	45	1	57	164	1646042
tr A0A0H1Chr6	55.455	110	48	1	55	164	3040879
tr A0A0H1Chr6	55.455	110	48	1	55	164	3055556
tr A0A0H1Chr6	61.458	96	36	1	69	164	3046867
tr A0A0H1Chr1	55.963	109	47	1	56	164	3.8E+07
tr A0A0H1Chr12	51.24	121	58	1	44	164	1.3E+07
tr A0A0H1Chr12	50	116	57	1	50	165	1.3E+07
tr A0A0H1Chr4	55.455	110	48	1	55	164	2.1E+07
tr A0A0H1Chr4	35.882	170	48	3	56	164	2.2E+07

tr A0A0H Chr5	55.455	110	48	1	55	164	2.2E+07
tr A0A0H Chr5	72.5	40	11	0	65	104	2.4E+07
tr A0A0H Chr5	57.576	33	12	1	104	134	2.4E+07
tr A0A0H Chr5	53.333	30	14	0	126	155	2.4E+07
tr A0A0H Chr11	55.455	110	48	1	55	164	2626154
tr A0A0H Chr2	42.982	114	34	2	82	164	1.5E+07
tr A0A0H Chr2	55.357	56	25	0	109	164	1.5E+07
tr A0A0H Chr2	51.351	37	16	1	82	116	1.5E+07
tr A0A0H Chr2	39.062	64	37	2	49	112	2E+07
tr A0A0H Chr2	42.857	42	14	2	125	164	2E+07
tr A0A0H Chr3	57.627	59	25	0	106	164	1.6E+07
tr A0A0H Chr3	60	25	10	0	83	107	1.6E+07
tr A0A0H Chr3	37.778	45	23	1	56	95	1.6E+07
tr A0A0H Chr3	37.736	53	32	1	43	94	2.5E+07

TBLASTN 2.10.1+

Query: tr|A0A0H3VKW4|A0A0H3VKW4_9POAL Centromeric histone H3 isoform A (Fragment)

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

24 hits found

tr A0A0H Chr1	58.333	96	39	1	66	161	3.8E+07
tr A0A0H Chr1	42.857	42	23	1	75	115	4816782
tr A0A0H Chr6	58.333	96	39	1	66	161	3056279
tr A0A0H Chr6	60.417	96	37	1	66	161	1646006
tr A0A0H Chr6	58.333	96	39	1	66	161	3040837
tr A0A0H Chr6	58.333	96	39	1	66	161	3055514
tr A0A0H Chr6	58.333	96	39	1	66	161	3046867
tr A0A0H Chr4	58.333	96	39	1	66	161	2.1E+07
tr A0A0H Chr4	36.943	157	38	3	66	161	2.2E+07
tr A0A0H Chr11	58.333	96	39	1	66	161	2626112
tr A0A0H Chr5	58.333	96	39	1	66	161	2.1E+07
tr A0A0H Chr5	72.5	40	11	0	62	101	2.4E+07
tr A0A0H Chr5	59.259	27	11	0	101	127	2.4E+07
tr A0A0H Chr5	42.105	38	22	0	115	152	2.4E+07
tr A0A0H Chr12	44.776	134	71	2	28	161	1.3E+07
tr A0A0H Chr12	52.577	97	45	1	66	162	1.3E+07
tr A0A0H Chr3	62.5	48	18	0	114	161	1.6E+07
tr A0A0H Chr3	64	25	9	0	80	104	1.6E+07
tr A0A0H Chr3	57.143	21	9	0	61	81	1.6E+07
tr A0A0H Chr2	41.228	114	36	2	79	161	1.5E+07
tr A0A0H Chr2	58.333	48	20	0	114	161	1.5E+07
tr A0A0H Chr2	51.351	37	16	1	79	113	1.5E+07
tr A0A0H Chr2	36.842	57	35	1	66	122	2E+07
tr A0A0H Chr2	50	34	14	1	9	42	7595248

TBLASTN 2.10.1+

Query: tr|A0A0H3VKW7|A0A0H3VKW7_9POAL Centromeric histone H3 isoform A (Fragment)

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

tr A0A0H Chr1	55.046	109	48	1	56	164	3.8E+07
tr A0A0H Chr6	56.481	108	46	1	57	164	1646042
tr A0A0H Chr6	54.545	110	49	1	55	164	3056237
tr A0A0H Chr6	54.545	110	49	1	55	164	3040879
tr A0A0H Chr6	54.545	110	49	1	55	164	3055556
tr A0A0H Chr6	60.417	96	37	1	69	164	3046867
tr A0A0H Chr5	54.545	110	49	1	55	164	2.2E+07
tr A0A0H Chr5	76.316	38	9	0	67	104	2.4E+07
tr A0A0H Chr5	57.576	33	12	1	104	134	2.4E+07
tr A0A0H Chr5	56.667	30	13	0	126	155	2.4E+07
tr A0A0H Chr4	54.545	110	49	1	55	164	2.1E+07
tr A0A0H Chr4	35.882	170	48	2	56	164	2.2E+07
tr A0A0H Chr11	54.545	110	49	1	55	164	2626154
tr A0A0H Chr12	50.413	121	59	1	44	164	1.3E+07
tr A0A0H Chr12	50	116	57	1	50	165	1.3E+07
tr A0A0H Chr2	43.86	114	33	2	82	164	1.5E+07
tr A0A0H Chr2	62.5	48	18	0	117	164	1.5E+07
tr A0A0H Chr2	54.054	37	15	1	82	116	1.5E+07
tr A0A0H Chr2	47.368	38	19	1	49	86	2E+07
tr A0A0H Chr3	66.667	48	16	0	117	164	1.6E+07
tr A0A0H Chr3	64	25	9	0	83	107	1.6E+07
tr A0A0H Chr3	34.568	81	43	4	56	129	1.6E+07

TBLASTN 2.10.1+

Query: tr|A0A0H3VKV8|A0A0H3VKV8_9POAL Centromeric histone H3 isoform A (Fragmer

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

25 hits found

tr A0A0H Chr6	47.368	152	72	2	13	164	3056132
tr A0A0H Chr6	47.368	152	72	2	13	164	3040984
tr A0A0H Chr6	58.333	108	44	1	57	164	1646042
tr A0A0H Chr6	50.37	135	59	2	30	164	3055610
tr A0A0H Chr6	54.31	116	52	1	49	164	3046927
tr A0A0H Chr1	54.783	115	51	1	50	164	3.8E+07
tr A0A0H Chr5	50.37	135	59	2	30	164	2.2E+07
tr A0A0H Chr5	75	40	10	0	65	104	2.4E+07
tr A0A0H Chr5	57.576	33	12	1	104	134	2.4E+07
tr A0A0H Chr5	53.333	30	14	0	126	155	2.4E+07
tr A0A0H Chr4	50.37	135	59	2	30	164	2.1E+07
tr A0A0H Chr4	36.471	170	47	3	56	164	2.2E+07
tr A0A0H Chr11	50.37	135	59	2	30	164	2626208
tr A0A0H Chr12	51.24	121	58	1	44	164	1.3E+07
tr A0A0H Chr12	50	116	57	1	50	165	1.3E+07
tr A0A0H Chr3	57.627	59	25	0	106	164	1.6E+07
tr A0A0H Chr3	64	25	9	0	83	107	1.6E+07

tr A0A0H Chr3	44.828	29	16	0	56	84	1.6E+07
tr A0A0H Chr3	37.736	53	32	1	43	94	2.5E+07
tr A0A0H Chr3	38.095	42	21	1	54	95	2.3E+07
tr A0A0H Chr2	43.86	114	33	2	82	164	1.5E+07
tr A0A0H Chr2	54.386	57	26	0	108	164	1.5E+07
tr A0A0H Chr2	54.054	37	15	1	82	116	1.5E+07
tr A0A0H Chr2	39.062	64	37	2	49	112	2E+07
tr A0A0H Chr2	42.857	42	14	2	125	164	2E+07

TBLASTN 2.10.1+

Query: tr|A0A0H3VKW5|A0A0H3VKW5_9POAL Centromeric histone H3 isoform A (Fragme

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

25 hits found

tr A0A0H Chr1	54.128	109	49	1	56	164	3.8E+07
tr A0A0H Chr6	55.556	108	47	1	57	164	1646042
tr A0A0H Chr6	53.636	110	50	1	55	164	3056237
tr A0A0H Chr6	53.636	110	50	1	55	164	3040879
tr A0A0H Chr6	53.636	110	50	1	55	164	3055556
tr A0A0H Chr6	59.375	96	38	1	69	164	3046867
tr A0A0H Chr4	53.636	110	50	1	55	164	2.1E+07
tr A0A0H Chr4	35.294	170	49	2	56	164	2.2E+07
tr A0A0H Chr5	53.636	110	50	1	55	164	2.2E+07
tr A0A0H Chr5	72.5	40	11	0	65	104	2.4E+07
tr A0A0H Chr5	54.545	33	13	1	104	134	2.4E+07
tr A0A0H Chr5	53.333	30	14	0	126	155	2.4E+07
tr A0A0H Chr11	53.636	110	50	1	55	164	2626154
tr A0A0H Chr12	49.587	121	60	1	44	164	1.3E+07
tr A0A0H Chr12	50	116	57	1	50	165	1.3E+07
tr A0A0H Chr2	42.982	114	34	2	82	164	1.5E+07
tr A0A0H Chr2	60.417	48	19	0	117	164	1.5E+07
tr A0A0H Chr2	54.054	37	15	1	82	116	1.5E+07
tr A0A0H Chr2	47.368	38	19	1	49	86	2E+07
tr A0A0H Chr2	41.463	41	14	2	126	164	2E+07
tr A0A0H Chr2	50	34	14	1	9	42	7595248
tr A0A0H Chr3	64.583	48	17	0	117	164	1.6E+07
tr A0A0H Chr3	64	25	9	0	83	107	1.6E+07
tr A0A0H Chr3	37.736	53	32	1	43	94	2.5E+07
tr A0A0H Chr3	35.185	54	29	2	56	104	1.6E+07

TBLASTN 2.10.1+

Query: tr|A0A0H3VKX0|A0A0H3VKX0_9POAL Centromeric histone H3 isoform A (Fragmen

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

tr A0A0H Chr1	53.211	109	50	1	56	164	3.8E+07
tr A0A0H Chr6	54.63	108	48	1	57	164	1646042
tr A0A0H Chr6	52.727	110	51	1	55	164	3056237

tr A0A0H Chr6	52.727	110	51	1	55	164	3040879
tr A0A0H Chr6	52.727	110	51	1	55	164	3055556
tr A0A0H Chr6	58.333	96	39	1	69	164	3046867
tr A0A0H Chr4	52.727	110	51	1	55	164	2.1E+07
tr A0A0H Chr4	34.706	170	50	2	56	164	2.2E+07
tr A0A0H Chr5	52.727	110	51	1	55	164	2.2E+07
tr A0A0H Chr5	77.5	40	9	0	65	104	2.4E+07
tr A0A0H Chr5	57.576	33	12	1	104	134	2.4E+07
tr A0A0H Chr5	53.333	30	14	0	126	155	2.4E+07
tr A0A0H Chr11	52.727	110	51	1	55	164	2626154
tr A0A0H Chr12	47.934	121	62	1	44	164	1.3E+07
tr A0A0H Chr12	47.414	116	60	1	50	165	1.3E+07
tr A0A0H Chr2	42.105	114	35	2	82	164	1.5E+07
tr A0A0H Chr2	58.333	48	20	0	117	164	1.5E+07
tr A0A0H Chr2	54.054	37	15	1	82	116	1.5E+07
tr A0A0H Chr2	44.737	38	20	1	49	86	2E+07
tr A0A0H Chr2	50	34	14	1	9	42	7595248
tr A0A0H Chr3	62.5	48	18	0	117	164	1.6E+07
tr A0A0H Chr3	64	25	9	0	83	107	1.6E+07
tr A0A0H Chr3	34.568	81	43	4	56	129	1.6E+07

TBLASTN 2.10.1+

Query: tr|A0A0H3VKX1|A0A0H3VKX1_9POAL Centromeric histone H3 isoform A (Fragmen

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

26 hits found

tr A0A0H Chr1	54.128	109	49	1	56	164	3.8E+07
tr A0A0H Chr6	46.053	152	74	3	13	164	3056132
tr A0A0H Chr6	46.053	152	74	3	13	164	3040984
tr A0A0H Chr6	55.556	108	47	1	57	164	1646042
tr A0A0H Chr6	52.459	122	54	2	46	164	3055592
tr A0A0H Chr6	54.545	110	49	1	55	164	3046909
tr A0A0H Chr4	52.459	122	54	2	46	164	2.1E+07
tr A0A0H Chr4	35.294	170	49	2	56	164	2.2E+07
tr A0A0H Chr11	52.459	122	54	2	46	164	2626190
tr A0A0H Chr5	52.459	122	54	2	46	164	2.2E+07
tr A0A0H Chr5	75	40	10	0	65	104	2.4E+07
tr A0A0H Chr5	57.576	33	12	1	104	134	2.4E+07
tr A0A0H Chr5	53.333	30	14	0	126	155	2.4E+07
tr A0A0H Chr12	49.587	121	60	1	44	164	1.3E+07
tr A0A0H Chr12	49.138	116	58	1	50	165	1.3E+07
tr A0A0H Chr2	42.982	114	34	2	82	164	1.5E+07
tr A0A0H Chr2	60.417	48	19	0	117	164	1.5E+07
tr A0A0H Chr2	54.054	37	15	1	82	116	1.5E+07
tr A0A0H Chr2	47.368	38	19	1	49	86	2E+07
tr A0A0H Chr2	42.857	42	14	2	125	164	2E+07
tr A0A0H Chr3	64.583	48	17	0	117	164	1.6E+07

tr A0A0H Chr3	64	25	9	0	83	107	1.6E+07
tr A0A0H Chr3	37.736	53	32	1	43	94	2.5E+07
tr A0A0H Chr3	34.568	81	43	4	56	129	1.6E+07
tr A0A0H Chr3	35.714	42	22	1	54	95	2.3E+07
tr A0A0H Chr10	43.59	39	18	1	49	83	1.9E+07

TBLASTN 2.10.1+

Query: tr|A0A0H3VKV7|A0A0H3VKV7_9POAL Centromeric histone H3 isoform A (Fragmer

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

24 hits found

tr A0A0H Chr1	55.046	109	48	1	56	164	3.8E+07
tr A0A0H Chr6	57.407	108	45	1	57	164	1646042
tr A0A0H Chr6	54.545	110	49	1	55	164	3040879
tr A0A0H Chr6	55.455	110	48	1	55	164	3056237
tr A0A0H Chr6	54.545	110	49	1	55	164	3055556
tr A0A0H Chr6	60.417	96	37	1	69	164	3046867
tr A0A0H Chr4	54.545	110	49	1	55	164	2.1E+07
tr A0A0H Chr4	36.471	170	47	3	56	164	2.2E+07
tr A0A0H Chr5	54.545	110	49	1	55	164	2.2E+07
tr A0A0H Chr5	72.5	40	11	0	65	104	2.4E+07
tr A0A0H Chr5	54.545	33	13	1	104	134	2.4E+07
tr A0A0H Chr5	44.737	38	21	0	118	155	2.4E+07
tr A0A0H Chr5	35.556	45	27	1	106	150	1.2E+07
tr A0A0H Chr11	54.545	110	49	1	55	164	2626154
tr A0A0H Chr12	49.587	121	60	1	44	164	1.3E+07
tr A0A0H Chr12	48.276	116	59	1	50	165	1.3E+07
tr A0A0H Chr3	66.667	48	16	0	117	164	1.6E+07
tr A0A0H Chr3	64	25	9	0	83	107	1.6E+07
tr A0A0H Chr3	44.828	29	16	0	56	84	1.6E+07
tr A0A0H Chr2	42.982	114	34	2	82	164	1.5E+07
tr A0A0H Chr2	62.5	48	18	0	117	164	1.5E+07
tr A0A0H Chr2	51.351	37	16	1	82	116	1.5E+07
tr A0A0H Chr2	33.333	81	49	3	49	126	2E+07
tr A0A0H Chr2	50	34	14	1	9	42	7595248

TBLASTN 2.10.1+

Query: tr|A0A0H3VKW2|A0A0H3VKW2_9POAL Centromeric histone H3 isoform B (Fragme

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

24 hits found

tr A0A0H Chr1	62.5	96	35	1	64	159	3.8E+07
tr A0A0H Chr6	47.297	148	64	3	12	159	3040954
tr A0A0H Chr6	62.5	96	35	1	64	159	3056279
tr A0A0H Chr6	47.887	142	60	3	18	159	3055613
tr A0A0H Chr6	62.5	96	35	1	64	159	3046867
tr A0A0H Chr6	63.542	96	34	1	64	159	1646006
tr A0A0H Chr11	47.887	142	60	3	18	159	2626211

tr A0A0H Chr5	62.5	96	35	1	64	159	2.1E+07
tr A0A0H Chr5	70.732	41	12	0	59	99	2.4E+07
tr A0A0H Chr5	66.667	27	9	0	99	125	2.4E+07
tr A0A0H Chr5	57.143	28	12	0	121	148	2.4E+07
tr A0A0H Chr4	62.5	96	35	1	64	159	2.1E+07
tr A0A0H Chr4	38.854	157	35	3	64	159	2.2E+07
tr A0A0H Chr12	47.183	142	61	3	18	159	1.3E+07
tr A0A0H Chr12	44.755	143	65	3	18	160	1.3E+07
tr A0A0H Chr2	43.86	114	33	2	77	159	1.5E+07
tr A0A0H Chr2	66.667	48	16	0	112	159	1.5E+07
tr A0A0H Chr2	56.667	30	13	0	77	106	1.5E+07
tr A0A0H Chr2	33.333	81	38	4	81	159	2E+07
tr A0A0H Chr2	37.288	59	35	1	64	120	2E+07
tr A0A0H Chr2	21.739	46	36	0	79	124	2.6E+07
tr A0A0H Chr3	70.833	48	14	0	112	159	1.6E+07
tr A0A0H Chr3	42.857	35	20	0	78	112	1.6E+07
tr A0A0H Chr3	29.508	61	43	0	96	156	1.7E+07

TBLASTN 2.10.1+

Query: tr|A0A0H3VKX2|A0A0H3VKX2_LUZMU Centromeric histone H3 isoform B (Fragment)

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

24 hits found

tr A0A0H Chr1	62.5	96	35	1	70	165	3.8E+07
tr A0A0H Chr6	62.5	96	35	1	70	165	3040837
tr A0A0H Chr6	62.5	96	35	1	70	165	3056279
tr A0A0H Chr6	62.5	96	35	1	70	165	3055514
tr A0A0H Chr6	62.5	96	35	1	70	165	3046867
tr A0A0H Chr6	63.542	96	34	1	70	165	1646006
tr A0A0H Chr11	62.5	96	35	1	70	165	2626112
tr A0A0H Chr5	62.5	96	35	1	70	165	2.1E+07
tr A0A0H Chr5	70.732	41	12	0	65	105	2.4E+07
tr A0A0H Chr5	66.667	27	9	0	105	131	2.4E+07
tr A0A0H Chr5	57.143	28	12	0	127	154	2.4E+07
tr A0A0H Chr4	62.5	96	35	1	70	165	2.1E+07
tr A0A0H Chr4	38.854	157	35	3	70	165	2.2E+07
tr A0A0H Chr12	53.448	116	45	2	50	165	1.3E+07
tr A0A0H Chr12	56.701	97	41	1	70	166	1.3E+07
tr A0A0H Chr2	43.86	114	33	2	83	165	1.5E+07
tr A0A0H Chr2	66.667	48	16	0	118	165	1.5E+07
tr A0A0H Chr2	56.667	30	13	0	83	112	1.5E+07
tr A0A0H Chr2	33.333	81	38	4	87	165	2E+07
tr A0A0H Chr2	37.288	59	35	1	70	126	2E+07
tr A0A0H Chr2	21.739	46	36	0	85	130	2.6E+07
tr A0A0H Chr3	70.833	48	14	0	118	165	1.6E+07
tr A0A0H Chr3	42.857	35	20	0	84	118	1.6E+07
tr A0A0H Chr3	29.508	61	43	0	102	162	1.7E+07

TBLASTN 2.10.1+

Query: tr|A0A0H3VKW9|A0A0H3VKW9_9POAL Centromeric histone H3 isoform B (Fragment)

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

24 hits found

tr A0A0H Chr1	62.5	96	35	1	70	165	3.8E+07
tr A0A0H Chr6	62.5	96	35	1	70	165	3056279
tr A0A0H Chr6	62.5	96	35	1	70	165	3040837
tr A0A0H Chr6	62.5	96	35	1	70	165	3055514
tr A0A0H Chr6	62.5	96	35	1	70	165	3046867
tr A0A0H Chr6	58.182	110	37	2	56	165	1646024
tr A0A0H Chr5	62.5	96	35	1	70	165	2.1E+07
tr A0A0H Chr5	70.732	41	12	0	65	105	2.4E+07
tr A0A0H Chr5	66.667	27	9	0	105	131	2.4E+07
tr A0A0H Chr5	57.143	28	12	0	127	154	2.4E+07
tr A0A0H Chr11	62.5	96	35	1	70	165	2626112
tr A0A0H Chr4	62.5	96	35	1	70	165	2.1E+07
tr A0A0H Chr4	38.854	157	35	3	70	165	2.2E+07
tr A0A0H Chr12	59.375	96	38	1	70	165	1.3E+07
tr A0A0H Chr12	56.701	97	41	1	70	166	1.3E+07
tr A0A0H Chr2	43.86	114	33	2	83	165	1.5E+07
tr A0A0H Chr2	66.667	48	16	0	118	165	1.5E+07
tr A0A0H Chr2	56.667	30	13	0	83	112	1.5E+07
tr A0A0H Chr2	33.333	81	38	4	87	165	2E+07
tr A0A0H Chr2	37.288	59	35	1	70	126	2E+07
tr A0A0H Chr2	21.739	46	36	0	85	130	2.6E+07
tr A0A0H Chr3	70.833	48	14	0	118	165	1.6E+07
tr A0A0H Chr3	42.857	35	20	0	84	118	1.6E+07
tr A0A0H Chr3	29.508	61	43	0	102	162	1.7E+07

TBLASTN 2.10.1+

Query: tr|A0A0H3VKW0|A0A0H3VKW0_9POAL Centromeric histone H3 isoform A (Fragment)

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

25 hits found

tr A0A0H Chr1	60.417	96	37	1	66	161	3.8E+07
tr A0A0H Chr1	42.857	42	23	1	75	115	4816782
tr A0A0H Chr6	60.417	96	37	1	66	161	3056279
tr A0A0H Chr6	62.5	96	35	1	66	161	1646006
tr A0A0H Chr6	60.417	96	37	1	66	161	3040837
tr A0A0H Chr6	60.417	96	37	1	66	161	3055514
tr A0A0H Chr6	60.417	96	37	1	66	161	3046867
tr A0A0H Chr4	60.417	96	37	1	66	161	2.1E+07
tr A0A0H Chr4	38.217	157	36	3	66	161	2.2E+07
tr A0A0H Chr11	60.417	96	37	1	66	161	2626112
tr A0A0H Chr5	60.417	96	37	1	66	161	2.1E+07
tr A0A0H Chr5	72.5	40	11	0	62	101	2.4E+07

tr A0A0H Chr5	54.545	33	13	1	101	131	2.4E+07
tr A0A0H Chr5	44.737	38	21	0	115	152	2.4E+07
tr A0A0H Chr5	35.556	45	27	1	103	147	1.2E+07
tr A0A0H Chr5	32.895	76	47	1	76	147	2715650
tr A0A0H Chr12	48.031	127	63	2	35	161	1.3E+07
tr A0A0H Chr12	54.639	97	43	1	66	162	1.3E+07
tr A0A0H Chr3	66.667	48	16	0	114	161	1.6E+07
tr A0A0H Chr3	64	25	9	0	80	104	1.6E+07
tr A0A0H Chr3	57.143	21	9	0	61	81	1.6E+07
tr A0A0H Chr2	42.982	114	34	2	79	161	1.5E+07
tr A0A0H Chr2	62.5	48	18	0	114	161	1.5E+07
tr A0A0H Chr2	51.351	37	16	1	79	113	1.5E+07
tr A0A0H Chr2	36.066	61	35	2	66	123	2E+07

TBLASTN 2.10.1+

Query: tr|A0A0H3VKW6|A0A0H3VKW6_9POAL Centromeric histone H3 isoform B (Fragment)

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

24 hits found

tr A0A0H Chr1	62.5	96	35	1	75	170	3.8E+07
tr A0A0H Chr6	62.5	96	35	1	75	170	3040837
tr A0A0H Chr6	62.5	96	35	1	75	170	3056279
tr A0A0H Chr6	62.5	96	35	1	75	170	3055514
tr A0A0H Chr6	62.5	96	35	1	75	170	3046867
tr A0A0H Chr6	58.182	110	37	2	61	170	1646024
tr A0A0H Chr11	62.5	96	35	1	75	170	2626112
tr A0A0H Chr5	62.5	96	35	1	75	170	2.1E+07
tr A0A0H Chr5	70.732	41	12	0	70	110	2.4E+07
tr A0A0H Chr5	66.667	27	9	0	110	136	2.4E+07
tr A0A0H Chr5	57.143	28	12	0	132	159	2.4E+07
tr A0A0H Chr4	62.5	96	35	1	75	170	2.1E+07
tr A0A0H Chr4	39.241	158	33	4	75	170	2.2E+07
tr A0A0H Chr12	59.375	96	38	1	75	170	1.3E+07
tr A0A0H Chr12	57.732	97	40	1	75	171	1.3E+07
tr A0A0H Chr2	43.86	114	33	2	88	170	1.5E+07
tr A0A0H Chr2	66.667	48	16	0	123	170	1.5E+07
tr A0A0H Chr2	51.351	37	16	1	88	122	1.5E+07
tr A0A0H Chr2	33.333	81	38	4	92	170	2E+07
tr A0A0H Chr2	37.288	59	35	1	75	131	2E+07
tr A0A0H Chr2	21.739	46	36	0	90	135	2.6E+07
tr A0A0H Chr3	70.833	48	14	0	123	170	1.6E+07
tr A0A0H Chr3	42.857	35	20	0	89	123	1.6E+07
tr A0A0H Chr3	27.869	61	44	0	107	167	1.7E+07

TBLASTN 2.10.1+

Query: tr|A0A0H3VKV9|A0A0H3VKV9_9POAL Centromeric histone H3 isoform B (Fragment)

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

24 hits found

tr A0A0H Chr1	62.5	96	35	1	70	165	3.8E+07
tr A0A0H Chr6	62.5	96	35	1	70	165	3056279
tr A0A0H Chr6	62.5	96	35	1	70	165	3040837
tr A0A0H Chr6	62.5	96	35	1	70	165	3055514
tr A0A0H Chr6	62.5	96	35	1	70	165	3046867
tr A0A0H Chr6	63.542	96	34	1	70	165	1646006
tr A0A0H Chr5	62.5	96	35	1	70	165	2.1E+07
tr A0A0H Chr5	70.732	41	12	0	65	105	2.4E+07
tr A0A0H Chr5	66.667	27	9	0	105	131	2.4E+07
tr A0A0H Chr5	57.143	28	12	0	127	154	2.4E+07
tr A0A0H Chr11	62.5	96	35	1	70	165	2626112
tr A0A0H Chr4	62.5	96	35	1	70	165	2.1E+07
tr A0A0H Chr4	37.58	157	37	2	70	165	2.2E+07
tr A0A0H Chr12	59.375	96	38	1	70	165	1.3E+07
tr A0A0H Chr12	57.732	97	40	1	70	166	1.3E+07
tr A0A0H Chr2	43.86	114	33	2	83	165	1.5E+07
tr A0A0H Chr2	66.667	48	16	0	118	165	1.5E+07
tr A0A0H Chr2	51.351	37	16	1	83	117	1.5E+07
tr A0A0H Chr2	43.182	44	15	2	124	165	2E+07
tr A0A0H Chr2	45.714	35	19	0	70	104	2E+07
tr A0A0H Chr2	21.739	46	36	0	85	130	2.6E+07
tr A0A0H Chr3	70.833	48	14	0	118	165	1.6E+07
tr A0A0H Chr3	42.857	35	20	0	84	118	1.6E+07
tr A0A0H Chr3	29.508	61	43	0	102	162	1.7E+07

TBLASTN 2.10.1+

Query: tr|A0A0G3YLA7|A0A0G3YLA7_TRIUA Centromeric histone H3 OS=Triticum urartu C

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

26 hits found

tr A0A0G Chr6	64.286	98	33	2	52	149	3040828
tr A0A0G Chr6	64.286	98	33	2	52	149	3055505
tr A0A0G Chr6	64.286	98	33	2	52	149	3056288
tr A0A0G Chr6	64.286	98	33	2	52	149	3046858
tr A0A0G Chr6	63.265	98	34	2	52	149	1645997
tr A0A0G Chr11	64.286	98	33	2	52	149	2626103
tr A0A0G Chr5	64.286	98	33	2	52	149	2.1E+07
tr A0A0G Chr5	74.286	35	9	0	50	84	2.4E+07
tr A0A0G Chr5	46.429	28	14	1	84	111	2.4E+07
tr A0A0G Chr5	74.194	31	8	0	104	134	2.4E+07
tr A0A0G Chr5	45.455	33	18	0	119	151	2.4E+07
tr A0A0G Chr4	64.286	98	33	2	52	149	2.1E+07
tr A0A0G Chr4	39.13	161	36	4	50	149	2.2E+07
tr A0A0G Chr1	63.265	98	34	2	50	147	3.8E+07
tr A0A0G Chr1	28.571	49	35	0	96	144	3E+07
tr A0A0G Chr12	58.163	98	39	1	52	149	1.3E+07

tr A0A0G Chr12	58.163	98	39	1	52	149	1.3E+07
tr A0A0G Chr3	65.385	52	18	0	99	150	1.6E+07
tr A0A0G Chr3	59.375	32	13	0	63	94	1.6E+07
tr A0A0G Chr3	58.824	17	7	0	50	66	1.6E+07
tr A0A0G Chr2	45.378	119	33	4	62	149	1.5E+07
tr A0A0G Chr2	57.627	59	22	1	94	149	1.5E+07
tr A0A0G Chr2	65.385	26	9	0	62	87	1.5E+07
tr A0A0G Chr2	80	15	3	0	52	66	2E+07
tr A0A0G Chr2	39.13	46	18	2	106	149	2E+07
tr A0A0G Chr10	30.556	36	25	0	77	112	1.8E+07

TBLASTN 2.10.1+

Query: tr|G1C1P4|G1C1P4_HORMA Beta centromeric histone H3 (Fragment) OS=Hordeun

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

23 hits found

tr G1C1P Chr6	65.934	91	29	2	1	91	3040807
tr G1C1P Chr6	65.934	91	29	2	1	91	3056309
tr G1C1P Chr6	65.934	91	29	2	1	91	3055484
tr G1C1P Chr6	65.934	91	29	2	1	91	3046837
tr G1C1P Chr6	65.934	91	29	2	1	91	1645976
tr G1C1P Chr11	65.934	91	29	2	1	91	2626082
tr G1C1P Chr5	65.934	91	29	2	1	91	2.1E+07
tr G1C1P Chr5	75	28	7	0	49	76	2.4E+07
tr G1C1P Chr5	84.615	26	4	0	1	26	2.4E+07
tr G1C1P Chr5	42.857	28	15	1	26	53	2.4E+07
tr G1C1P Chr5	51.724	29	7	1	65	93	2.4E+07
tr G1C1P Chr4	65.934	91	29	2	1	91	2.1E+07
tr G1C1P Chr4	48.305	118	29	3	5	91	2.2E+07
tr G1C1P Chr1	66.292	89	28	2	1	89	3.8E+07
tr G1C1P Chr1	26.531	49	36	0	38	86	3E+07
tr G1C1P Chr12	61.538	91	33	1	1	91	1.3E+07
tr G1C1P Chr12	60.44	91	34	1	1	91	1.3E+07
tr G1C1P Chr2	46.667	120	32	3	4	92	1.5E+07
tr G1C1P Chr2	50.704	71	29	1	22	92	1.5E+07
tr G1C1P Chr2	73.077	26	7	0	4	29	1.5E+07
tr G1C1P Chr2	38	50	21	2	44	91	2E+07
tr G1C1P Chr3	66.667	51	17	0	41	91	1.6E+07
tr G1C1P Chr3	65.625	32	11	0	5	36	1.6E+07

TBLASTN 2.10.1+

Query: tr|A0A0A9F0R2|A0A0A9F0R2_ARUDO CenH3 OS=Arundo donax OX=35708 PE=3 S'

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

22 hits found

tr A0A0A: Chr6	50.538	93	42	2	32	123	1646006
tr A0A0A: Chr6	49.462	93	43	2	32	123	3040837
tr A0A0A: Chr6	49.462	93	43	2	32	123	3046867

tr A0A0A: Chr6	49.462	93	43	2	32	123	3055514
tr A0A0A: Chr6	49.462	93	43	2	32	123	3056279
tr A0A0A: Chr5	49.462	93	43	2	32	123	2.1E+07
tr A0A0A: Chr5	70.213	47	13	1	21	67	2.4E+07
tr A0A0A: Chr5	68.182	22	6	1	71	92	2.4E+07
tr A0A0A: Chr5	45.946	37	14	1	52	82	2.1E+07
tr A0A0A: Chr11	49.462	93	43	2	32	123	2626112
tr A0A0A: Chr11	37.5	32	20	0	71	102	1.4E+07
tr A0A0A: Chr11	45.946	37	14	1	52	82	2.5E+07
tr A0A0A: Chr4	49.462	93	43	2	32	123	2.1E+07
tr A0A0A: Chr4	30.263	152	46	2	32	123	2.2E+07
tr A0A0A: Chr1	49.462	93	43	2	32	123	3.8E+07
tr A0A0A: Chr12	46.237	93	46	2	32	123	1.3E+07
tr A0A0A: Chr12	45.161	93	47	2	32	123	1.3E+07
tr A0A0A: Chr3	44.186	43	24	0	81	123	1.6E+07
tr A0A0A: Chr3	45.946	37	17	2	46	81	1.6E+07
tr A0A0A: Chr3	85.714	14	2	0	32	45	1.6E+07
tr A0A0A: Chr3	36.508	63	38	1	20	82	2880168
tr A0A0A: Chr2	48.718	39	20	0	31	69	2E+07

TBLASTN 2.10.1+

Query: tr|A0A0A9RZT3|A0A0A9RZT3_ARUDO CenH3 OS=Arundo donax OX=35708 PE=3 S'

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

34 hits found

tr A0A0A: Chr4	39.844	128	74	1	222	346	1.7E+07
tr A0A0A: Chr4	51.111	90	43	1	29	118	2.1E+07
tr A0A0A: Chr4	32.099	162	47	4	20	118	2.2E+07
tr A0A0A: Chr4	42	50	23	1	358	401	1.7E+07
tr A0A0A: Chr4	30.682	88	48	2	316	390	2.2E+07
tr A0A0A: Chr4	30	80	52	2	316	392	1.2E+07
tr A0A0A: Chr4	32.468	77	48	2	319	392	2.6E+07
tr A0A0A: Chr1	51.136	88	42	1	31	118	3.8E+07
tr A0A0A: Chr1	31.25	80	51	2	316	392	4E+07
tr A0A0A: Chr1	31.25	80	51	2	316	392	2.5E+07
tr A0A0A: Chr11	51.111	90	43	1	29	118	2626127
tr A0A0A: Chr11	31.25	80	51	2	316	392	1480527
tr A0A0A: Chr6	51.111	90	43	1	29	118	3046882
tr A0A0A: Chr6	52.273	88	41	1	31	118	1646015
tr A0A0A: Chr6	51.111	90	43	1	29	118	3040852
tr A0A0A: Chr6	51.111	90	43	1	29	118	3055529
tr A0A0A: Chr6	51.111	90	43	1	29	118	3056264
tr A0A0A: Chr5	51.111	90	43	1	29	118	2.2E+07
tr A0A0A: Chr5	55.814	43	19	0	27	69	2.4E+07
tr A0A0A: Chr5	62.963	27	10	0	69	95	2.4E+07
tr A0A0A: Chr5	46.154	52	23	1	69	120	2.4E+07
tr A0A0A: Chr12	42.453	106	59	2	13	118	1.3E+07

tr A0A0A: Chr12	42.453	106	59	2	13	118	1.3E+07
tr A0A0A: Chr3	57.895	38	16	0	81	118	1.6E+07
tr A0A0A: Chr3	52	25	12	0	48	72	1.6E+07
tr A0A0A: Chr3	57.895	19	8	0	31	49	1.6E+07
tr A0A0A: Chr3	32.5	80	50	2	316	392	30807
tr A0A0A: Chr3	32.5	80	50	2	316	392	2.7E+07
tr A0A0A: Chr2	52.632	38	18	0	81	118	1.5E+07
tr A0A0A: Chr2	53.846	26	12	0	47	72	1.5E+07
tr A0A0A: Chr2	33.01	103	38	1	47	118	1.5E+07
tr A0A0A: Chr2	31.25	80	51	2	316	392	1.7E+07
tr A0A0A: Chr7	28.916	83	52	2	15	93	1.8E+07
tr A0A0A: Chr8	29.412	85	56	2	311	392	1103493

TBLASTN 2.10.1+

Query: tr|A0A0K0PMX0|A0A0K0PMX0_LOLPR CENH3 (Fragment) OS=Lolium perenne OX=

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

17 hits found

tr A0A0KI Chr6	94.444	18	1	0	61	78	3040840
tr A0A0KI Chr6	94.444	18	1	0	61	78	3055517
tr A0A0KI Chr6	94.444	18	1	0	61	78	3046870
tr A0A0KI Chr6	94.444	18	1	0	61	78	3056276
tr A0A0KI Chr6	88.889	18	2	0	61	78	1646009
tr A0A0KI Chr11	94.444	18	1	0	61	78	2626115
tr A0A0KI Chr12	94.444	18	1	0	61	78	1.3E+07
tr A0A0KI Chr12	77.778	18	4	0	61	78	1.3E+07
tr A0A0KI Chr5	94.444	18	1	0	61	78	2.1E+07
tr A0A0KI Chr5	76.19	21	5	0	58	78	2.4E+07
tr A0A0KI Chr5	45.161	31	17	0	1	31	2.4E+07
tr A0A0KI Chr1	94.444	18	1	0	61	78	3.8E+07
tr A0A0KI Chr4	94.444	18	1	0	61	78	2.1E+07
tr A0A0KI Chr4	72.222	18	5	0	61	78	2.2E+07
tr A0A0KI Chr2	83.333	18	3	0	61	78	2E+07
tr A0A0KI Chr2	76.471	17	4	0	61	77	1.5E+07
tr A0A0KI Chr3	76.471	17	4	0	61	77	1.6E+07

TBLASTN 2.10.1+

Query: tr|A0A0K0PMV8|A0A0K0PMV8_9POAL CENH3 (Fragment) OS=Glyceria maxima OX=

Database: Nippon

0 hits found

TBLASTN 2.10.1+

Query: tr|A0A0K0PMC2|A0A0K0PMC2_9POAL CENH3 (Fragment) OS=Glyceria lithuanica C

Database: Nippon

0 hits found

TBLASTN 2.10.1+

Query: tr|A0A0K0PNL1|A0A0K0PNL1_9POAL CENH3 (Fragment) OS=Glyceria alnasteretur

Database: Nippon

0 hits found

```

# TBLASTN 2.10.1+
# Query: tr|A0A0K0PMD0|A0A0K0PMD0_9POAL CENH3.M2 (Fragment) OS=Melica nutans C
# Database: Nippon
# Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens
# 1 hits found
tr|A0A0KI Chr5      77.778      18      2      1      1      16  2.4E+07
# TBLASTN 2.10.1+
# Query: tr|A0A0K0PMC7|A0A0K0PMC7_9POAL CENH3 (Fragment) OS=Glyceria triflora OX=
# Database: Nippon
# Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens
# 12 hits found
tr|A0A0KI Chr11     92.857      14      1      0      26      39 2626103
tr|A0A0KI Chr6      92.857      14      1      0      26      39 3055505
tr|A0A0KI Chr6      92.857      14      1      0      26      39 3046858
tr|A0A0KI Chr6      85.714      14      2      0      26      39 1645997
tr|A0A0KI Chr6      92.857      14      1      0      26      39 3056288
tr|A0A0KI Chr6      92.857      14      1      0      26      39 3040828
tr|A0A0KI Chr1      92.857      14      1      0      26      39 3.8E+07
tr|A0A0KI Chr5      92.857      14      1      0      26      39 2.4E+07
tr|A0A0KI Chr5      92.857      14      1      0      26      39 2.1E+07
tr|A0A0KI Chr2      85.714      14      2      0      26      39 2E+07
tr|A0A0KI Chr12     85.714      14      2      0      26      39 1.3E+07
tr|A0A0KI Chr4      92.857      14      1      0      26      39 2.1E+07
# TBLASTN 2.10.1+
# Query: tr|A0A0A9IDC5|A0A0A9IDC5_ARUDO CenH3 OS=Arundo donax OX=35708 PE=4 SV
# Database: Nippon
# Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens
# 6 hits found
tr|A0A0A: Chr3      45.161      31      16      1      8      37 1.6E+07
tr|A0A0A: Chr12     38.235      34      21      0      1      34 5339559
tr|A0A0A: Chr5      46.875      32      17      0      3      34 1.5E+07
tr|A0A0A: Chr5      41.667      24      14      0      12      35 1.3E+07
tr|A0A0A: Chr8      46.429      28      13      1      19      44 1.9E+07
tr|A0A0A: Chr8      42.308      26      15      0      12      37 5362996
# TBLASTN 2.10.1+
# Query: tr|A0A0K0PME4|A0A0K0PME4_GLYFL CENH3 (Fragment) OS=Glyceria fluitans OX=
# Database: Nippon
# 0 hits found
# TBLASTN 2.10.1+
# Query: tr|A0A0K0PMW4|A0A0K0PMW4_9POAL CENH3 (Fragment) OS=Melica nutans OX=
# Database: Nippon
# Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens
# 20 hits found
tr|A0A0KI Chr5      66.667      27      8      1      23      49 2.4E+07
tr|A0A0KI Chr5      82.353      17      3      0      33      49 2.1E+07
tr|A0A0KI Chr1      82.353      17      3      0      33      49 3.8E+07

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tr A0A0KI Chr1	39.394	33	20	0	2	34	7848565
tr A0A0KI Chr1	40	25	14	1	24	48	6071688
tr A0A0KI Chr6	82.353	17	3	0	33	49	3040837
tr A0A0KI Chr6	82.353	17	3	0	33	49	3056279
tr A0A0KI Chr6	82.353	17	3	0	33	49	3046867
tr A0A0KI Chr6	82.353	17	3	0	33	49	3055514
tr A0A0KI Chr6	82.353	17	3	0	33	49	1646006
tr A0A0KI Chr11	82.353	17	3	0	33	49	2626112
tr A0A0KI Chr4	82.353	17	3	0	33	49	2.1E+07
tr A0A0KI Chr4	64.706	17	6	0	33	49	2.2E+07
tr A0A0KI Chr12	76.471	17	4	0	33	49	1.3E+07
tr A0A0KI Chr2	76.471	17	4	0	33	49	2E+07
tr A0A0KI Chr2	68.75	16	5	0	33	48	1.5E+07
tr A0A0KI Chr10	58.333	24	7	1	23	46	2.3E+07
tr A0A0KI Chr10	45.238	42	18	2	3	39	2.1E+07
tr A0A0KI Chr3	68.75	16	5	0	33	48	1.6E+07
tr A0A0KI Chr7	71.429	14	4	0	22	35	4467810

TBLASTN 2.10.1+

Query: tr|A0A0K0PME8|A0A0K0PME8_9POAL CENH3 (Fragment) OS=Pleuropogon sabine

Database: Nippon

0 hits found

TBLASTN 2.10.1+

Query: tr|A0A0A9LKJ7|A0A0A9LKJ7_ARUDO CenH3 OS=Arundo donax OX=35708 PE=4 SV=

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

3 hits found

tr A0A0A: Chr5	75	16	4	0	17	32	2.4E+07
tr A0A0A: Chr3	33.333	42	23	1	5	41	1.4E+07
tr A0A0A: Chr9	34.884	43	24	1	6	44	1.8E+07

TBLASTN 2.10.1+

Query: tr|A0A0A9AVD8|A0A0A9AVD8_ARUDO CenH3 OS=Arundo donax OX=35708 PE=4 SV=

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

6 hits found

tr A0A0A: Chr2	40	75	28	4	10	78	2.2E+07
tr A0A0A: Chr1	43.243	37	21	0	10	46	2973164
tr A0A0A: Chr11	33.929	56	36	1	12	67	2.6E+07
tr A0A0A: Chr11	45.833	24	13	0	31	54	8612620
tr A0A0A: Chr6	43.243	37	21	0	10	46	2.9E+07
tr A0A0A: Chr9	35.185	54	27	2	28	75	5182979

TBLASTN 2.10.1+

Query: tr|A0A0A9NFP0|A0A0A9NFP0_ARUDO CenH3 OS=Arundo donax OX=35708 PE=4 SV=

Database: Nippon

0 hits found

TBLASTN 2.10.1+

Query: tr|A0A0A9N0H4|A0A0A9N0H4_ARUDO CenH3 OS=Arundo donax OX=35708 PE=4 SV=

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

6 hits found

tr A0A0A: Chr12	37.5	40	25	0	30	69	1.3E+07
tr A0A0A: Chr11	43.902	41	19	2	22	62	1.6E+07
tr A0A0A: Chr4	41.379	29	17	0	29	57	2.1E+07
tr A0A0A: Chr10	41.379	29	17	0	32	60	7780241
tr A0A0A: Chr10	51.852	27	13	0	24	50	1.2E+07
tr A0A0A: Chr6	27.419	62	42	1	6	67	2815080

TBLASTN 2.10.1+

Query: tr|A0A0A9NCE1|A0A0A9NCE1_ARUDO CenH3 OS=Arundo donax OX=35708 PE=4 S

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

17 hits found

tr A0A0A: Chr6	61.765	34	13	0	1	34	3056544
tr A0A0A: Chr6	57.692	26	11	0	1	26	3040572
tr A0A0A: Chr6	57.692	26	11	0	1	26	3046602
tr A0A0A: Chr6	53.846	26	12	0	1	26	3055249
tr A0A0A: Chr6	58.333	24	10	0	1	24	1645741
tr A0A0A: Chr5	54.054	37	17	0	5	41	2.4E+07
tr A0A0A: Chr5	52	25	12	0	1	25	2.1E+07
tr A0A0A: Chr3	56.757	37	16	0	1	37	1.6E+07
tr A0A0A: Chr12	56.25	32	14	0	1	32	1.3E+07
tr A0A0A: Chr12	48.649	37	19	0	1	37	1.3E+07
tr A0A0A: Chr4	57.692	26	11	0	1	26	2.2E+07
tr A0A0A: Chr4	56	25	11	0	1	25	2.1E+07
tr A0A0A: Chr2	52	25	12	0	2	26	1.5E+07
tr A0A0A: Chr2	54.167	24	11	0	2	25	1.5E+07
tr A0A0A: Chr1	52	25	12	0	1	25	3.8E+07
tr A0A0A: Chr1	38.462	39	23	1	3	40	3.3E+07
tr A0A0A: Chr11	52	25	12	0	1	25	2625847

TBLASTN 2.10.1+

Query: tr|A0A0A9P9H2|A0A0A9P9H2_ARUDO CenH3 OS=Arundo donax OX=35708 PE=4 S

Database: Nippon

0 hits found

TBLASTN 2.10.1+

Query: tr|A0A0A9LV64|A0A0A9LV64_ARUDO CenH3 OS=Arundo donax OX=35708 PE=4 S

Database: Nippon

0 hits found

TBLASTN 2.10.1+

Query: tr|A0A0A9AYD3|A0A0A9AYD3_ARUDO CenH3 OS=Arundo donax OX=35708 PE=4 S

Database: Nippon

Fields: query acc.ver, subject acc.ver, % identity, alignment length, mismatches, gap opens

7 hits found

tr A0A0A: Chr1	47.826	23	12	0	1	23	1.2E+07
tr A0A0A: Chr2	40	30	18	0	3	32	2.1E+07

tr A0A0A:Chr2	60	20	8	0	5	24	1.7E+07
tr A0A0A:Chr12	55	20	9	0	1	20	2.1E+07
tr A0A0A:Chr4	59.091	22	9	0	4	25	2.8E+07
tr A0A0A:Chr3	41.379	29	14	1	5	30	1.8E+07
tr A0A0A:Chr11	46.875	32	15	1	1	32	5525746

BLAST processed 148 queries

JF96734.1] [location=join(1..55,167..207,315..366,492..526,609..645,730..842,1206..1283,14

, q. start, q. end, s. start, s. end, evaluate, bit score

1.3E+07	9.55E-21	91.7
1.3E+07	2.62E-17	81.6
3.8E+07	2.75E-20	90.5
3040544	4.86E-20	89.7
3056572	7.28E-20	89
3055221	9.90E-20	88.6
1645713	1.56E-19	88.2
3046574	2.00E-19	87.8
2625819	6.30E-20	89.4
2.1E+07	7.71E-20	89
2.4E+07	7.20E-07	51.6
2.1E+07	1.75E-19	88.2
2.2E+07	2.10E-11	64.7
1.5E+07	3.58E-08	55.1
1.5E+07	5.74E-07	51.6
1.6E+07	5.32E-07	52
1.6E+07	0.073	27.7
1.6E+07	0.073	26.9

JD07128.1] [location=join(161..212,310..361,947..978,1115..1233,1579..1653,2099..2174,27

, q. start, q. end, s. start, s. end, evaluate, bit score

3.8E+07	3.72E-28	111
2.6E+07	7.3	30
3056569	4.39E-28	111
3040547	5.98E-28	111
3055224	8.80E-28	110
3046577	1.35E-27	110
1645716	6.79E-27	108
2.1E+07	5.43E-28	111
2.4E+07	4.67E-09	47.4
2.4E+07	4.67E-09	32.3
2.4E+07	0.33	33.9
2625822	6.34E-28	110
2.1E+07	1.04E-27	110
2.2E+07	1.29E-16	78.6
1.3E+07	2.99E-24	100
1.3E+07	7.26E-21	90.9
1.6E+07	9.58E-16	70.5
1.6E+07	9.58E-16	32

1.5E+07	1.26E-15	75.9
1.5E+07	5.89E-15	69.7
1.5E+07	5.89E-15	30
2140312	4.8	30.4

JD07123.1] [location=join(161..212,310..361,946..977,1114..1232,1590..1664,2109..2184,27

, q. start, q. end, s. start, s. end, eval, bit score

2625822	6.74E-32	122
3040547	9.10E-32	122
3055224	9.46E-32	122
3046577	1.07E-31	121
3056569	1.24E-31	121
1645716	2.01E-31	120
2.1E+07	9.64E-32	122
2.4E+07	3.23E-10	52
2.4E+07	3.23E-10	31.6
2.4E+07	0.06	36.2
3.8E+07	1.38E-31	121
2.1E+07	2.24E-31	120
2.2E+07	1.02E-21	93.2
1.3E+07	8.23E-28	110
1.3E+07	8.01E-24	99.4
1.6E+07	8.63E-19	72
1.6E+07	8.63E-19	31.2
1.6E+07	8.63E-19	29.3
3.6E+07	5	30.4
1.5E+07	1.15E-15	72
1.5E+07	1.15E-15	30
1.5E+07	1.95E-15	75.1
2E+07	0.19	28.9
2E+07	0.19	23.9
2.6E+07	5.1	30.4

JD07117.1] [location=join(149..200,298..349,936..967,1104..1222,1568..1642,2087..2162,27

, q. start, q. end, s. start, s. end, eval, bit score

3.8E+07	9.11E-31	119
3040547	9.57E-31	119
3056569	9.66E-31	119
3055224	1.37E-30	118
3046577	2.62E-30	117
1645716	1.32E-29	115
2625822	1.02E-30	119

2.1E+07	1.10E-30	119
2.4E+07	3.56E-10	51.2
2.4E+07	3.56E-10	32.3
2.4E+07	0.11	35.4
2.1E+07	2.59E-30	117
2.2E+07	1.79E-18	84
1.3E+07	2.43E-27	109
1.3E+07	5.60E-24	99.8
1.6E+07	5.69E-18	72
1.6E+07	5.69E-18	32.3
1.6E+07	5.69E-18	25.4
1.5E+07	2.38E-16	77.8
1.5E+07	1.71E-15	71.6
1.5E+07	1.71E-15	30
2E+07	0.14	28.9
2E+07	0.14	24.3
2.6E+07	6.1	30.4

JD07116.1] [location=join(149..200,289..340,928..959,1096..1214,1570..1644,2093..2168,27

, q. start, q. end, s. start, s. end, eval, bit score

2625822	4.43E-34	128
3040547	6.27E-34	128
3055224	6.65E-34	128
3046577	8.89E-34	127
3056569	1.35E-33	127
1645716	1.34E-32	124
2.1E+07	9.79E-34	127
2.4E+07	2.63E-11	55.8
2.4E+07	2.63E-11	31.6
2.4E+07	0.06	36.2
2.1E+07	3.10E-33	126
2.2E+07	2.87E-23	97.8
3.8E+07	4.57E-33	125
1.3E+07	3.86E-29	114
1.3E+07	2.30E-25	103
1.6E+07	8.18E-20	72
1.6E+07	8.18E-20	32.7
1.6E+07	8.18E-20	30.8
1.5E+07	4.24E-16	77
1.5E+07	4.80E-16	72
1.5E+07	4.80E-16	31.6
2E+07	0.032	32
2E+07	0.032	23.5
2140312	5.2	30.4

1.5E+07	5.7	30.4
2.6E+07	5.2	30.4

JD07115.1] [location=join(149..200,298..349,927..958,1095..1213,1569..1643,2088..2163,26

, q. start, q. end, s. start, s. end, eval, bit score

2625822	3.30E-30	117
3055224	3.67E-30	117
3040547	4.73E-30	117
3046577	4.77E-30	117
3056569	5.36E-30	117
1645716	8.70E-30	116
2.1E+07	5.11E-30	117
2.4E+07	9.82E-10	52.4
2.4E+07	9.82E-10	29.6
2.4E+07	0.39	33.9
3.8E+07	6.38E-30	116
2.1E+07	1.20E-29	115
2.2E+07	4.51E-20	88.6
1.3E+07	5.59E-27	108
1.3E+07	3.84E-23	97.4
1.6E+07	1.79E-17	69.7
1.6E+07	1.79E-17	29.3
1.6E+07	1.79E-17	28.9
3.6E+07	0.95	32.7
3.6E+07	3.6	30.8
1.5E+07	7.67E-15	73.6
1.5E+07	1.49E-14	69.7
1.5E+07	1.49E-14	28.9
2E+07	0.22	28.9
2E+07	0.22	23.5
9042014	4.7	30.4

JD07112.1] [location=join(149..200,298..349,941..972,1109..1227,1584..1658,2102..2177,27

, q. start, q. end, s. start, s. end, eval, bit score

2625822	5.05E-31	119
3040547	6.13E-31	119
3056569	6.75E-31	119
3055224	7.29E-31	119
3046577	9.66E-31	119
1645716	1.08E-30	119
2.1E+07	7.02E-31	119
2.4E+07	1.30E-09	50.1

2.4E+07	1.30E-09	31.6
2.4E+07	0.06	36.2
2.8E+07	6.4	30
3.8E+07	8.04E-31	119
2.1E+07	1.32E-30	118
2.2E+07	1.17E-20	90.1
1.3E+07	8.64E-27	107
1.3E+07	3.32E-24	100
1.6E+07	2.97E-18	72
1.6E+07	2.97E-18	30.8
1.6E+07	2.97E-18	27.3
3.6E+07	4.2	30.8
1.5E+07	6.52E-17	79.3
1.5E+07	1.23E-15	72
1.5E+07	1.23E-15	30
2E+07	0.39	27.3
2E+07	0.39	23.9
7812287	3.8	30.8
2.4E+07	1.9	31.6
2.6E+07	5	30.4

JD07111.1] [location=join(149..200,298..349,927..958,1097..1215,1571..1645,2090..2165,27

, q. start, q. end, s. start, s. end, eval, bit score

2625822	1.28E-30	118
3040547	1.66E-30	118
3055224	1.69E-30	118
3046577	2.08E-30	118
3056569	2.52E-30	117
1645716	4.13E-30	117
2.1E+07	2.04E-30	118
2.4E+07	1.40E-10	52.4
2.4E+07	1.40E-10	32.7
2.4E+07	1	32.7
3.8E+07	2.45E-30	117
2.1E+07	4.73E-30	117
2.2E+07	2.02E-20	89.7
1.3E+07	2.61E-26	106
1.3E+07	2.07E-22	95.1
1.6E+07	4.81E-18	68.2
1.6E+07	4.81E-18	32.3
1.6E+07	4.81E-18	29.3
1.5E+07	3.13E-15	74.7
1.5E+07	1.44E-14	68.2
1.5E+07	1.44E-14	30

2E+07	0.58	28.9
2E+07	0.58	21.6
7812245	5.1	30.4
2140312	9.6	29.6

ACX30895.1] [location=join(1..103,198..223,338..374,1443..1573,1667..1741,2185..2260,264

, q. start, q. end, s. start, s. end, evaluate, bit score

3040541	9.76E-30	116
3055218	2.33E-29	115
3056575	2.49E-29	115
3046571	5.73E-29	114
1645710	8.02E-28	111
2625816	1.41E-29	116
2.1E+07	1.81E-29	115
2.4E+07	5.82E-20	80.1
2.4E+07	5.82E-20	37
2.4E+07	1.79E-11	64.3
2.4E+07	8.56E-07	50.8
2.4E+07	0.013	38.5
2.1E+07	5.96E-29	114
2.2E+07	2.81E-16	78.2
3.8E+07	6.01E-29	114
1.3E+07	4.40E-24	100
1.3E+07	3.98E-23	97.8
1.5E+07	1.24E-13	70.5
1.5E+07	3.27E-09	57.8
1.5E+07	0.003	40
2E+07	1	32.7
1.6E+07	3.03E-09	57.8
1.6E+07	7.32E-06	40.4
1.6E+07	7.32E-06	28.5
1.2E+07	7	30.4

ACX30894.1] [location=join(1..103,201..226,354..390,971..1101,1197..1271,1694..1769,2167

, q. start, q. end, s. start, s. end, evaluate, bit score

3040541	2.45E-30	118
3055218	4.21E-30	117
3056575	8.05E-30	117
3046571	1.12E-29	116
1645710	1.83E-28	113
2625816	2.83E-30	118
2.1E+07	4.42E-30	117

2.4E+07	1.75E-20	81.6
2.4E+07	1.75E-20	37.4
2.4E+07	9.14E-11	62.4
2.4E+07	8.56E-07	50.8
2.4E+07	0.016	38.1
2.1E+07	1.76E-29	116
2.2E+07	2.19E-17	81.3
3.8E+07	2.62E-29	115
1.3E+07	9.30E-25	102
1.3E+07	5.83E-24	100
1.5E+07	7.90E-14	71.2
1.5E+07	3.12E-09	57.8
1.5E+07	0.01	38.9
2E+07	0.11	35.8
1.5E+07	2.6	31.6
1.6E+07	3.43E-09	57.8
1.6E+07	2.23E-06	39.3
1.6E+07	2.23E-06	31.6
1.2E+07	7.4	30.4

ACX30893.1] [location=join(1..106,240..265,381..405,1067..1197,1294..1368,1444..1519,160

, q. start, q. end, s. start, s. end, evalule, bit score

3040541	1.43E-31	122
3055218	2.64E-31	121
3056575	4.44E-31	120
3046571	6.67E-31	120
1645710	1.16E-29	116
2625816	1.62E-31	121
2.1E+07	2.61E-31	121
2.4E+07	6.48E-21	83.2
2.4E+07	6.48E-21	37
2.4E+07	7.33E-07	50.8
2.4E+07	1.86E-06	49.7
2.4E+07	0.059	36.6
2.1E+07	1.18E-30	119
2.2E+07	6.76E-19	85.5
3.8E+07	1.34E-30	119
1.3E+07	2.10E-26	107
1.3E+07	1.81E-25	104
1.5E+07	5.38E-15	74.3
1.5E+07	6.69E-15	59.3
1.5E+07	6.69E-15	40.4
2E+07	0.11	35.8
1.5E+07	2.5	31.6

1.6E+07	5.87E-10	60.1
1.6E+07	1.07E-06	40.4
1.6E+07	1.07E-06	31.2
1.2E+07	7.5	30

ACX30889.1] [location=join(1..106,237..262,378..402,1074..1204,1301..1375,1450..1525,160

, q. start, q. end, s. start, s. end, evaluate, bit score

3040541	1.26E-31	122
3055218	2.96E-31	120
3056575	4.49E-31	120
3046571	8.09E-31	119
1645710	1.34E-29	116
2625816	1.77E-31	121
2.1E+07	2.69E-31	121
2.4E+07	5.73E-21	83.6
2.4E+07	5.73E-21	37
2.4E+07	1.38E-08	55.8
2.4E+07	1.86E-06	49.7
2.4E+07	0.058	36.6
2.1E+07	1.09E-30	119
2.2E+07	6.83E-19	85.5
3.8E+07	1.49E-30	119
1.3E+07	1.80E-26	107
1.3E+07	2.14E-25	104
1.5E+07	5.13E-15	74.3
1.5E+07	6.80E-15	59.7
1.5E+07	6.80E-15	40.4
2E+07	0.11	35.8
1.5E+07	2.5	31.6
1.6E+07	5.54E-10	60.1
1.6E+07	1.02E-06	40.4
1.6E+07	1.02E-06	31.6
1.2E+07	7.2	30.4

ation=join(26..68,189..310,551..625,9869..9944,10062..10117)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

1645716	9.99E-24	97.8
3040547	1.79E-23	97.1
3055224	2.05E-23	96.7
3056569	2.07E-23	96.7
3046577	3.20E-23	96.3
2.1E+07	1.93E-23	97.1

2.4E+07	5.93E-11	49.7
2.4E+07	5.93E-11	35.4
2.4E+07	0.18	33.9
2625822	2.11E-23	96.7
2.1E+07	3.33E-23	96.3
2.2E+07	1.90E-14	71.2
3.8E+07	5.25E-23	95.5
1.3E+07	1.33E-21	91.7
1.3E+07	2.38E-18	82.4
1.5E+07	1.93E-13	68.2
1.5E+07	1.97E-09	57
1.5E+07	0.02	36.6
1.6E+07	2.42E-12	55.5
1.6E+07	2.42E-12	34.7

ation=join(6..48,187..305,583..657,9709..9784,9872..9927)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

2.1E+07	2.21E-19	85.1
2.4E+07	1.23E-09	47
2.4E+07	1.23E-09	33.9
2.4E+07	0.31	33.1
3040568	2.32E-19	85.1
3056548	2.46E-19	85.1
3055245	3.53E-19	84.7
1645737	5.79E-19	84
3046598	6.08E-19	84
3.8E+07	3.08E-19	84.7
2625843	3.67E-19	84.7
2.1E+07	4.00E-19	84.3
2.2E+07	3.23E-10	58.9
358879	4.7	29.6
1.3E+07	6.68E-18	80.9
1.3E+07	1.50E-15	74.3
1.6E+07	5.42E-10	47.8
1.6E+07	5.42E-10	34.3
1.5E+07	6.18E-10	58.2
1.5E+07	4.35E-06	47.4
1.5E+07	0.1	34.7
2.4E+07	9.4	28.9

ation=join(6..45,184..305,585..659,9308..9383,9471..9526)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3056548	2.39E-22	93.6
3040568	2.43E-22	93.6
3055245	3.49E-22	93.2
1645737	3.52E-22	93.2
3046598	6.12E-22	92.4
2.1E+07	2.53E-22	93.6
2.4E+07	8.05E-12	54.3
2.4E+07	8.05E-12	33.9
2.4E+07	0.051	35.4
2625843	3.04E-22	93.6
3.8E+07	3.66E-22	93.2
2.1E+07	5.24E-22	92.8
2.2E+07	5.61E-12	63.9
1.3E+07	1.30E-20	88.6
1.3E+07	1.84E-18	82.4
1.6E+07	5.23E-12	48.9
1.6E+07	5.23E-12	34.3
1.6E+07	5.23E-12	24.6
1.3E+07	9.9	28.9
1.5E+07	2.06E-11	62.4
1.5E+07	8.74E-07	49.3
1.5E+07	0.021	36.6
2E+07	4.2	30

ation=join(97..127,273..394,521..595,3268..3343,3633..3733)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

2625822	8.71E-26	103
2.8E+07	7.3	29.6
3056569	9.78E-26	103
3040547	1.04E-25	103
1645716	1.04E-25	103
3055224	1.18E-25	103
3046577	1.18E-25	103
1.3E+07	1.21E-25	103
1.3E+07	1.09E-21	92.4
4809283	4.7	30
2.1E+07	1.40E-25	103
2.4E+07	1.51E-11	53.9
2.4E+07	1.51E-11	33.9
2.4E+07	0.051	35.8
3.8E+07	1.59E-25	103
2.1E+07	1.65E-25	103
2.2E+07	7.76E-16	75.5
1.5E+07	4.41E-13	67.8

1.5E+07	3.77E-12	56.2
1.5E+07	3.77E-12	33.5
1.1E+07	6.1	29.6
1.6E+07	6.42E-11	61.6
1.6E+07	0.002	35.4
1.6E+07	0.002	23.9
9963181	6.1	29.6

ation=join(88..118,248..369,662..736,2209..2284,2501..2556)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3056569	5.33E-24	98.2
3040547	5.33E-24	98.2
3055224	7.19E-24	97.8
1645716	1.02E-23	97.4
3046577	1.04E-23	97.4
2625822	5.38E-24	98.2
1.3E+07	7.63E-24	97.8
1.3E+07	5.71E-20	86.7
2.1E+07	7.78E-24	97.8
2.4E+07	1.40E-10	52.4
2.4E+07	1.40E-10	31.6
2.4E+07	0.019	36.6
3.8E+07	1.18E-23	97.4
2.1E+07	1.34E-23	97.1
2.2E+07	8.09E-14	69.3
1.5E+07	1.19E-12	65.9
1.5E+07	4.78E-11	55.5
1.5E+07	4.78E-11	30
1.1E+07	4.4	29.6
1.6E+07	9.19E-11	60.5
1.6E+07	0.023	33.1
1.6E+07	0.023	21.9
9963181	9.8	28.9

ation=join(86..116,246..367,660..734,2208..2283,2500..2555)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3056569	1.07E-24	100
3040547	1.21E-24	100
3055224	1.44E-24	99.8
1645716	1.58E-24	99.8
3046577	1.66E-24	99.8
2625822	1.17E-24	100

1.3E+07	1.46E-24	99.8
1.3E+07	9.03E-21	89
2.1E+07	1.63E-24	99.8
2.4E+07	1.63E-11	55.8
2.4E+07	1.63E-11	31.6
2.4E+07	0.019	36.6
2.1E+07	2.10E-24	99.4
2.2E+07	9.38E-15	72
3.8E+07	2.14E-24	99.4
1.5E+07	8.15E-13	66.2
1.5E+07	3.04E-11	55.5
1.5E+07	3.04E-11	30.8
1.1E+07	9.8	28.9
1.6E+07	8.03E-11	60.5
1.6E+07	0.007	33.5
1.6E+07	0.007	23.5
9963181	9.8	28.9

ation=join(56..86,216..337,440..514,2117..2192,2284..2339)) [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3056569	1.23E-24	100
3040547	1.41E-24	99.8
1645716	1.60E-24	99.8
3055224	1.68E-24	99.8
3046577	1.80E-24	99.8
2625822	1.42E-24	99.8
1.3E+07	1.68E-24	99.8
1.3E+07	9.85E-21	89
2.1E+07	1.69E-24	99.8
2.4E+07	4.51E-11	54.7
2.4E+07	4.51E-11	30.8
2.4E+07	0.02	36.6
3.8E+07	2.00E-24	99.4
2.1E+07	2.29E-24	99.4
2.2E+07	1.34E-14	71.2
1.5E+07	3.60E-12	64.3
1.5E+07	2.39E-11	55.5
1.5E+07	2.39E-11	31.2
1.2E+07	7.8	29.3
1.1E+07	9.8	28.9
1.6E+07	7.95E-11	60.8
1.6E+07	0.006	33.9
1.6E+07	0.006	23.5
9963181	9.8	28.9

ation=join(56..86,216..337,440..514,2117..2192,2284..2339)) [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3040547	8.42E-25	100
3056569	8.50E-25	100
1645716	9.65E-25	100
3055224	1.08E-24	100
3046577	1.45E-24	99.8
2625822	1.00E-24	100
2.1E+07	1.25E-24	100
2.4E+07	1.10E-10	53.5
2.4E+07	1.10E-10	30.8
2.4E+07	0.019	36.6
1.3E+07	1.38E-24	100
1.3E+07	8.27E-21	89.4
3.8E+07	1.58E-24	99.8
2.1E+07	1.85E-24	99.8
2.2E+07	1.23E-14	71.6
1.5E+07	2.96E-12	64.7
1.5E+07	2.20E-11	55.5
1.5E+07	2.20E-11	31.2
1.1E+07	8.6	28.9
1.6E+07	7.14E-11	60.8
1.6E+07	0.007	33.9
1.6E+07	0.007	23.1
9963181	9.8	28.9

ation=join(108..138,279..400,562..636,3452..3527,3766..3821)) [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

2625822	1.26E-23	97.1
3040547	1.26E-23	97.1
3056569	1.43E-23	97.1
3055224	1.55E-23	97.1
3046577	2.67E-23	96.3
1645716	3.57E-23	95.9
2.1E+07	1.84E-23	96.7
2.4E+07	1.66E-08	46.2
2.4E+07	1.66E-08	30.4
2.4E+07	0.019	36.6
3.8E+07	4.01E-23	95.9
2.1E+07	6.03E-23	95.1
2.2E+07	2.34E-15	73.6

1.3E+07	7.54E-23	95.1
1.3E+07	3.68E-19	84.3
1.5E+07	4.56E-14	70.1
1.5E+07	7.63E-12	57.8
1.5E+07	7.63E-12	30.4
1.6E+07	5.83E-11	61.2
1.6E+07	0.025	36.2

ation=join(108..138,279..400,562..636,3452..3527,3766..3821)) [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

2625822	1.26E-23	97.1
3040547	1.26E-23	97.1
3056569	1.43E-23	97.1
3055224	1.55E-23	97.1
3046577	2.67E-23	96.3
1645716	3.57E-23	95.9
2.1E+07	1.84E-23	96.7
2.4E+07	1.69E-08	45.8
2.4E+07	1.69E-08	31.2
2.4E+07	0.019	36.6
3.8E+07	4.01E-23	95.9
2.1E+07	6.03E-23	95.1
2.2E+07	2.98E-15	73.2
1.3E+07	7.54E-23	95.1
1.3E+07	3.68E-19	84.3
1.5E+07	4.56E-14	70.1
1.5E+07	7.63E-12	57.8
1.5E+07	7.63E-12	30.4
1.6E+07	5.83E-11	61.2
1.6E+07	0.025	36.2

ation=join(114..144,281..402,535..609,3406..3481,3717..3772)) [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

2625822	2.15E-26	105
2.8E+07	3.6	30
3040547	2.28E-26	105
3055224	2.56E-26	104
3056569	3.26E-26	104
1645716	9.76E-26	103
3046577	1.07E-25	103
2.1E+07	3.52E-26	104
2.4E+07	4.21E-12	55.5

2.4E+07	4.21E-12	33.5
2.4E+07	0.021	36.6
1.3E+07	6.95E-26	103
1.3E+07	4.68E-22	92.8
2.1E+07	1.07E-25	103
2.2E+07	4.95E-16	75.5
3.8E+07	1.24E-25	102
1.5E+07	2.52E-13	67.8
1.5E+07	6.60E-12	55.1
1.5E+07	6.60E-12	33.5
1.1E+07	9.8	28.9
1.6E+07	5.44E-11	61.2
1.6E+07	0.002	35.4
1.6E+07	0.002	23.5
9963181	9.8	28.9
2.4E+07	9.5	28.9

ation=join(114..144,281..402,535..609,3406..3481,3717..3772)) [gbkey=CDS]

, q. start, q. end, s. start, s. end, evalue, bit score

2625822	1.91E-25	102
2.8E+07	1.7	31.2
3040547	2.18E-25	102
3055224	2.29E-25	102
3056569	3.04E-25	101
3046577	1.13E-24	100
1645716	1.15E-24	100
2.1E+07	3.22E-25	101
2.4E+07	1.82E-11	55.5
2.4E+07	1.82E-11	31.6
2.4E+07	0.026	36.2
1.3E+07	8.50E-25	100
1.3E+07	6.24E-21	89.4
2.1E+07	8.67E-25	100
2.2E+07	9.38E-15	72
3.8E+07	9.46E-25	100
1.6E+07	1.39E-14	59.3
1.6E+07	1.39E-14	33.9
1.6E+07	1.39E-14	23.5
9963181	4.5	29.6
1.5E+07	3.48E-14	70.1
1.5E+07	5.18E-13	58.9
1.5E+07	5.18E-13	33.5
1.1E+07	4.5	29.6
2.4E+07	1	31.6

ation=join(130..160,311..432,556..630,2941..3016,3291..3346)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3040547	2.45E-24	99.4
3056569	2.55E-24	99.4
3055224	2.81E-24	99
3046577	3.65E-24	98.6
1645716	7.55E-24	97.8
2.1E+07	2.73E-24	99
2.4E+07	5.26E-11	53.5
2.4E+07	5.26E-11	32
2.4E+07	0.019	36.6
2625822	2.86E-24	99
1.9E+07	3	30.4
2.1E+07	4.65E-24	98.6
2.2E+07	3.30E-13	67.4
3.8E+07	5.64E-24	98.2
1.3E+07	3.57E-23	95.9
1.3E+07	5.94E-20	86.7
1.5E+07	8.96E-12	63.5
1.5E+07	9.50E-11	55.1
1.5E+07	9.50E-11	29.6
1.6E+07	1.58E-10	59.7

ation=join(100..130,240..361,492..566,2828..2903,2994..3049)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3056569	2.33E-23	96.3
1645716	2.37E-23	96.3
3040547	2.54E-23	96.3
3055224	3.00E-23	96.3
3046577	3.78E-23	95.9
2625822	2.59E-23	96.3
1.3E+07	3.21E-23	95.9
1.3E+07	8.59E-20	86.3
2.1E+07	3.30E-23	95.9
2.4E+07	5.84E-11	53.9
2.4E+07	5.84E-11	31.2
2.4E+07	0.072	35
2.1E+07	4.13E-23	95.9
2.2E+07	9.27E-14	68.9
3.8E+07	5.16E-23	95.5
1.5E+07	9.59E-12	63.2

1.5E+07	2.18E-10	54.3
1.5E+07	2.18E-10	29.3
1.6E+07	2.81E-10	58.9
1.6E+07	0.021	32
1.6E+07	0.021	23.5

ation=join(123..171,268..389,1598..1672,3898..3973,4767..4822)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

2625822	5.31E-24	98.6
3040547	7.60E-24	98.2
3055224	7.68E-24	98.2
3056569	4.19E-23	95.9
3046577	2.65E-22	93.6
1645716	1.86E-21	91.3
2.1E+07	1.84E-23	97.1
2.4E+07	1.12E-08	54.7
2.4E+07	0.62	32.3
2.1E+07	4.62E-23	95.9
2.2E+07	4.34E-09	55.8
3.8E+07	1.89E-22	94
1.3E+07	2.08E-19	85.5
1.3E+07	2.24E-16	76.6
1.5E+07	2.84E-09	56.6
1.5E+07	1.59E-05	45.8
1.5E+07	0.096	34.7
1.6E+07	7.73E-06	46.6
1.6E+07	0.026	32.7
1.6E+07	0.026	22.3

ation=join(20..74,155..282,2036..2110,3866..3941,5009..5064)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3040547	2.64E-20	88.2
3055224	2.85E-20	88.2
3056569	5.15E-20	87.4
3046577	1.75E-19	85.9
1645716	9.36E-19	83.6
1833486	5.6	29.6
2625822	2.77E-20	88.2
2.1E+07	3.27E-20	87.8
2.4E+07	6.82E-07	49.7
2.4E+07	0.88	32
1E+07	7.2	29.6

2.1E+07	6.63E-20	87
2.2E+07	2.87E-08	53.9
3.8E+07	8.70E-20	86.7
1.3E+07	2.26E-16	77
1.3E+07	5.00E-14	70.1
1.5E+07	2.61E-08	53.9
1.5E+07	2.63E-06	48.1
1.5E+07	2.1	31.2
1.6E+07	2.99E-06	48.1
1.6E+07	0.25	33.9

ation=join(106..160,251..378,2114..2188,3968..4043,5071..5126)) [gbkey=CDS]

, q. start, q. end, s. start, s. end, evalue, bit score

3040547	6.80E-19	84.3
3056569	8.66E-19	84
3055224	1.41E-18	83.2
3046577	1.79E-18	82.8
1645716	5.26E-18	81.6
2.1E+07	9.83E-19	83.6
2.4E+07	4.75E-08	53.1
2.4E+07	0.66	32.3
1E+07	7.2	29.6
2625822	1.01E-18	83.6
3.8E+07	1.01E-18	83.6
2.1E+07	1.02E-18	83.6
2.2E+07	7.40E-08	52.8
1.3E+07	3.57E-16	76.3
1.3E+07	7.23E-14	69.7
1.5E+07	1.06E-07	52
1.5E+07	2.49E-06	48.1
1.5E+07	7.9	29.3
1.6E+07	2.09E-05	45.4
1.6E+07	9.3	29.3

ation=join(143..173,315..436,574..648,3469..3544,3777..3832)) [gbkey=CDS]

, q. start, q. end, s. start, s. end, evalue, bit score

1645716	7.85E-24	97.8
3040547	1.11E-23	97.4
3055224	1.20E-23	97.4
3056569	1.50E-23	97.1
3046577	2.35E-23	96.3
2625822	1.08E-23	97.4

2.8E+07	9	28.9
2.1E+07	1.94E-23	96.7
2.4E+07	7.20E-11	49.3
2.4E+07	7.20E-11	35.8
2.4E+07	0.024	36.2
2.1E+07	2.44E-23	96.3
2.2E+07	3.22E-14	70.5
3.8E+07	3.78E-23	95.9
3.1E+07	2.5	30.4
1.3E+07	6.52E-23	95.1
1.3E+07	1.57E-19	85.5
1.5E+07	8.95E-16	74.7
1.5E+07	5.22E-13	60.8
1.5E+07	5.22E-13	31.6
1.1E+07	7.6	29.3
1.6E+07	2.02E-11	62.4
1.6E+07	0.66	32.3
9963181	7.6	29.3

ation=join(55..97,220..341,1621..1695,4522..4597,5523..5578)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

1.3E+07	7.00E-25	100
1.3E+07	2.17E-20	88.2
1645716	2.03E-24	99.8
3040547	2.57E-24	99.4
3055224	3.15E-24	99
3056569	3.57E-24	99
3046577	4.92E-24	98.6
2625822	2.54E-24	99.4
2.1E+07	3.64E-24	99
2.4E+07	3.23E-09	46.6
2.4E+07	3.23E-09	32.7
2.4E+07	0.01	37.7
2.1E+07	5.11E-24	98.6
2.2E+07	2.00E-14	71.2
3.8E+07	6.65E-24	98.2
1.5E+07	8.89E-14	69.3
1.5E+07	1.65E-13	68.6
3450725	5.3	29.6
1.6E+07	5.35E-13	67
2.6E+07	4.9	29.6
2E+07	4.3	30

ation=join(38..68,190..311,450..524,2427..2502,2783..2838)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

2625822	2.86E-18	82
3040547	3.27E-18	81.6
3055224	3.82E-18	81.6
3046577	5.07E-18	81.3
3056569	6.71E-18	80.9
1645716	1.42E-17	80.1
2.1E+07	5.16E-18	81.3
2.4E+07	1.70E-07	51.2
2.4E+07	2.2	30.8
2.1E+07	7.92E-18	80.5
2.2E+07	6.72E-08	52.4
1.3E+07	1.62E-17	79.7
1.3E+07	7.08E-15	72.4
3.8E+07	1.76E-17	79.7
1.5E+07	1.50E-08	54.3
1.5E+07	1.07E-04	43.1
1.5E+07	0.23	33.5
1.6E+07	3.05E-05	44.7
1.6E+07	0.15	34.3

ation=join(38..68,190..311,450..524,2427..2502,2783..2838)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

1645716	1.03E-22	94.7
3040547	2.03E-22	93.6
3055224	2.46E-22	93.6
3056569	2.91E-22	93.2
3046577	3.74E-22	92.8
2625822	1.82E-22	94
1.3E+07	2.24E-22	93.6
1.3E+07	8.01E-19	83.6
2.1E+07	2.69E-22	93.6
2.4E+07	1.87E-12	51.2
2.4E+07	1.87E-12	39.3
2.4E+07	0.66	32.3
2.1E+07	3.63E-22	93.2
2.2E+07	3.75E-13	67.4
3.4E+07	5.6	29.6
3.8E+07	5.73E-22	92.4
3.1E+07	6.9	29.3
1.5E+07	2.97E-13	67.8
1.5E+07	2.19E-09	56.6

1.5E+07	0.98	31.6
1.6E+07	1.32E-09	57
1.6E+07	0.1	34.7

ation=join(38..68,209..330,472..546,2261..2336,2565..2620)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

1645716	2.81E-24	99
3040547	5.38E-24	98.2
3055224	5.48E-24	98.2
3056569	6.16E-24	98.2
3046577	9.44E-24	97.4
2625822	4.34E-24	98.6
2.8E+07	8.5	28.9
2.1E+07	6.04E-24	98.2
2.4E+07	4.77E-11	50.8
2.4E+07	4.77E-11	34.7
2.4E+07	0.025	36.2
2.1E+07	1.04E-23	97.4
2.2E+07	1.66E-14	71.2
3.8E+07	1.24E-23	97.1
1.3E+07	2.62E-23	96.3
1.3E+07	5.49E-20	86.7
1.5E+07	1.00E-13	68.9
1.5E+07	1.16E-10	60.1
1.5E+07	0.3	33.1
1.1E+07	8.8	28.9
1.6E+07	1.98E-11	62.4
1.6E+07	0.27	33.5
9963181	8.8	28.9

ation=join(38..68,210..331,471..545,2958..3033,3309..3364)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

1645716	1.81E-22	94
3040547	1.99E-22	94
3055224	2.49E-22	93.6
3056569	2.59E-22	93.6
3046577	4.24E-22	92.8
2625822	1.90E-22	94
2.1E+07	3.70E-22	93.2
2.4E+07	5.07E-10	48.9
2.4E+07	5.07E-10	33.1
2.4E+07	0.011	37.4

2.1E+07	4.81E-22	92.8
2.2E+07	1.13E-12	65.9
3.4E+07	7.1	29.3
3.8E+07	6.63E-22	92.4
1.3E+07	1.84E-21	90.9
1.3E+07	6.71E-18	80.9
1.5E+07	7.78E-14	69.3
1.5E+07	9.97E-12	56.6
1.5E+07	9.97E-12	31.2
1.1E+07	5.3	29.6
1.6E+07	1.80E-10	59.7
1.6E+07	0.76	32
9963181	5.3	29.6

ation=join(38..68,210..331,452..526,3494..3569,3845..3900)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3040547	6.08E-17	78.2
3055224	7.38E-17	77.8
3046577	9.98E-17	77.4
3056569	1.22E-16	77.4
1645716	2.48E-16	76.3
2625822	6.38E-17	78.2
2.1E+07	9.69E-17	77.4
2.4E+07	1.34E-06	48.5
2.4E+07	0.65	32.3
2.1E+07	1.49E-16	77
2.2E+07	9.55E-07	48.9
3.8E+07	2.99E-16	76.3
1.3E+07	1.13E-15	74.3
1.3E+07	4.78E-13	67
1.5E+07	1.03E-07	51.6
1.5E+07	1.88E-04	42.4
1.5E+07	1.2	31.6
1.6E+07	4.41E-05	44.3
1.6E+07	1.5	31.2

ation=join(42..72,215..336,549..623,1557..1632,1915..1970)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

1645716	1.83E-24	99.8
3040547	4.26E-24	98.6
3055224	4.56E-24	98.6
3056569	5.93E-24	98.2

3046577	7.19E-24	97.8
1.7E+07	2.6	30.4
2625822	3.51E-24	99
2.1E+07	6.72E-24	97.8
2.4E+07	1.27E-11	52.8
2.4E+07	1.27E-11	35
2.4E+07	0.062	35
2.1E+07	8.99E-24	97.4
2.2E+07	6.86E-14	69.3
3.8E+07	1.53E-23	97.1
3.1E+07	3.1	30.4
1.3E+07	1.76E-23	96.7
1.3E+07	3.99E-20	87
1.5E+07	4.10E-14	70.1
1.5E+07	1.80E-10	59.7
1.5E+07	0.056	35.4
1.6E+07	4.23E-11	61.6
1.6E+07	0.38	32.7
1887211	5.3	29.6

ation=join(38..68,213..334,452..526,3607..3682,3961..4016)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evalue, bit score

1645716	2.97E-23	96.3
3040547	3.64E-23	95.9
3055224	4.01E-23	95.9
3056569	4.59E-23	95.5
3046577	7.76E-23	95.1
2625822	3.50E-23	95.9
2.8E+07	8.7	28.9
2.1E+07	6.58E-23	95.1
2.4E+07	7.32E-11	49.3
2.4E+07	7.32E-11	35.8
2.4E+07	0.022	36.6
2.1E+07	8.39E-23	94.7
2.2E+07	1.22E-13	68.6
3.8E+07	1.67E-22	94
3.1E+07	3.7	30
1.3E+07	2.28E-22	93.6
1.3E+07	6.16E-19	84
1.5E+07	2.40E-13	67.8
1.5E+07	3.03E-10	58.9
1.5E+07	1	31.6
1.6E+07	1.01E-10	60.5
1.6E+07	0.53	32.3

ation=join(42..72,215..336,548..622,3079..3154,3455..3510)) [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

1645716	5.38E-24	98.2
3040547	1.07E-23	97.4
3055224	1.16E-23	97.4
3056569	1.37E-23	97.1
3046577	1.97E-23	96.7
2625822	9.44E-24	97.4
2.1E+07	1.67E-23	96.7
2.4E+07	3.99E-11	50.8
2.4E+07	3.99E-11	35
2.4E+07	0.017	37
2.1E+07	2.24E-23	96.7
2.2E+07	1.71E-13	68.2
3.8E+07	3.47E-23	95.9
3.1E+07	2.9	30.4
1.3E+07	7.39E-23	95.1
1.3E+07	1.65E-19	85.5
1.5E+07	2.20E-13	67.8
1.5E+07	1.66E-10	59.7
1.5E+07	0.18	33.9
1.6E+07	2.98E-11	62
1.6E+07	1.5	31.2
1887211	2.3	30.8

ation=join(33..75,167..288,453..527,1327..1402,1523..1578)) [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

1645716	8.59E-22	92
3040547	1.32E-21	91.7
3056569	1.46E-21	91.7
3055224	1.54E-21	91.3
3046577	2.75E-21	90.9
2.1E+07	1.41E-21	91.7
2.4E+07	1.02E-09	46.2
2.4E+07	1.02E-09	34.7
2.4E+07	0.24	33.5
2625822	1.45E-21	91.7
2.1E+07	2.57E-21	90.9
2.2E+07	1.00E-12	66.2
3.8E+07	2.97E-21	90.5
1.3E+07	1.55E-20	88.6

1.3E+07	4.60E-17	78.6
1.5E+07	1.04E-12	66.2
1.5E+07	1.15E-09	57.4
1.5E+07	0.17	33.9
1.6E+07	1.27E-11	55.8
1.6E+07	1.27E-11	32
2.1E+07	6.5	29.3
2E+07	8.8	28.9
1.5E+07	10	28.9

ation=join(27..69,179..300,1448..1522,2923..2998,3117..3172)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

1645716	8.78E-23	95.1
3040547	1.56E-22	94.4
3056569	1.65E-22	94.4
3055224	2.00E-22	94
3046577	3.07E-22	93.6
2.1E+07	1.37E-22	94.4
2.4E+07	3.93E-07	50.4
2.4E+07	0.093	34.7
2.4E+07	0.24	33.5
2625822	1.89E-22	94
2.1E+07	3.13E-22	93.6
2.2E+07	4.53E-13	67.4
3.8E+07	3.73E-22	93.2
1.3E+07	4.97E-21	90.1
1.3E+07	6.11E-18	81.3
1.5E+07	4.40E-13	67.4
1.5E+07	2.41E-09	56.6
1.5E+07	0.057	35.4
1.6E+07	5.56E-12	55.1
1.6E+07	5.56E-12	33.9

ation=join(26..68,188..309,517..591,3224..3299,3418..3473)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

1645716	2.49E-24	99.4
3056569	3.06E-24	99
3040547	4.05E-24	99
3055224	5.75E-24	98.2
3046577	8.64E-24	97.8
2.1E+07	3.86E-24	99
2.4E+07	1.42E-10	50.1

2.4E+07	1.42E-10	33.9
2.4E+07	0.15	34.3
2625822	5.02E-24	98.6
2.1E+07	5.37E-24	98.6
2.2E+07	7.94E-15	72.4
3.8E+07	6.65E-24	98.2
1.3E+07	1.10E-22	94.7
1.3E+07	4.76E-19	84.3
1.6E+07	1.83E-13	55.8
1.6E+07	1.83E-13	33.9
1.6E+07	1.83E-13	23.5
2.1E+07	9.8	28.9
1.5E+07	4.45E-13	67.4
1.5E+07	1.57E-09	57
1.5E+07	0.049	35.4

ation=join(26..68,188..309,517..591,3224..3299,3418..3473)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

1645716	1.70E-22	94.4
3056569	2.36E-22	93.6
3040547	2.39E-22	93.6
3055224	3.59E-22	93.2
3046577	4.11E-22	93.2
2.1E+07	2.32E-22	94
2.4E+07	1.32E-10	50.1
2.4E+07	1.32E-10	33.9
2.4E+07	5.9	29.6
2.1E+07	3.26E-22	93.2
2.2E+07	2.09E-13	68.2
2625822	3.29E-22	93.2
3.8E+07	3.80E-22	93.2
1.3E+07	4.34E-21	90.1
1.3E+07	1.07E-17	80.5
1.6E+07	5.62E-12	51.2
1.6E+07	5.62E-12	33.1
1.6E+07	5.62E-12	23.1
2.1E+07	9.8	28.9
1.5E+07	1.86E-11	62.8
1.5E+07	4.67E-08	52.8
1.5E+07	0.055	35.4

ation=join(26..68,189..310,549..623,2260..2335,2453..2508)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3040547	9.99E-24	97.8
3056569	1.30E-23	97.4
3055224	1.38E-23	97.4
1645716	1.38E-23	97.4
3046577	2.15E-23	96.7
2.1E+07	1.10E-23	97.4
2.4E+07	5.67E-07	49.7
2.4E+07	0.057	35.4
2.4E+07	0.26	33.5
2625822	1.19E-23	97.4
2.1E+07	2.88E-23	96.3
2.2E+07	2.86E-14	70.9
3.8E+07	3.49E-23	96.3
1.3E+07	7.95E-22	92.4
1.3E+07	1.63E-18	82.8
1.5E+07	2.85E-13	67.8
1.5E+07	3.19E-09	56.2
1.5E+07	0.02	36.6
1.6E+07	2.68E-12	55.1
1.6E+07	2.68E-12	34.7
9249244	3.7	30
2E+07	9.1	28.9

ation=join(13..43,159..280,432..506,2692..2767,3048..3103)) [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

1645716	2.55E-25	102
3056569	3.80E-25	101
3040547	3.99E-25	101
3055224	4.94E-25	101
3046577	8.75E-25	100
2625822	4.39E-25	101
2.1E+07	4.84E-25	101
2.4E+07	1.71E-13	57
2.4E+07	1.71E-13	37
2.4E+07	0.019	36.6
2.1E+07	6.17E-25	100
2.2E+07	9.63E-14	68.9
3.8E+07	1.09E-24	100
3.1E+07	7.9	29.3
1.3E+07	1.54E-24	99.8
1.3E+07	1.04E-20	89
9051156	6.5	29.3
1.6E+07	1.41E-14	61.6

1.6E+07	1.41E-14	32.3
1.6E+07	1.41E-14	23.1
1.5E+07	9.07E-13	66.2
1.5E+07	1.88E-10	59.7
1.5E+07	1.1	31.6

ation=join(103..133,278..399,517..591,2974..3049,3309..3364)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evalue, bit score

1645716	6.64E-23	95.1
3040547	1.01E-22	94.7
3055224	1.19E-22	94.4
3056569	1.34E-22	94.4
3046577	1.86E-22	94
2625822	8.98E-23	94.7
2.8E+07	8.8	28.9
2.1E+07	1.67E-22	94
2.4E+07	1.69E-10	48.1
2.4E+07	1.69E-10	35.8
2.4E+07	0.085	34.7
1.3E+07	1.70E-22	94
1.3E+07	4.34E-19	84.3
2.1E+07	2.09E-22	93.6
2.2E+07	2.62E-13	67.8
3.8E+07	3.30E-22	93.2
3.1E+07	2.8	30.4
1.5E+07	3.71E-13	67.4
1.5E+07	1.55E-10	59.7
1.5E+07	2.6	30.4
1.6E+07	5.83E-11	61.2
1.6E+07	1.8	30.8

ation=join(35..77,194..315,580..654,3340..3415,3533..3588)] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evalue, bit score

1.3E+07	1.84E-22	94
1.3E+07	3.56E-19	84.7
2.1E+07	3.59E-22	93.2
2.4E+07	4.42E-10	50.8
2.4E+07	4.42E-10	31.2
2.4E+07	0.61	32.3
3056569	3.88E-22	93.2
3040547	4.15E-22	93.2
1645716	4.66E-22	92.8

3055224	5.29E-22	92.8
3046577	8.76E-22	92
2625822	4.85E-22	92.8
2.1E+07	6.42E-22	92.4
2.2E+07	4.45E-13	67.4
3.8E+07	8.42E-22	92
1.5E+07	2.57E-12	65.1
1.5E+07	1.86E-09	57
1.5E+07	2.2	30.8
1.6E+07	5.23E-11	54.7
1.6E+07	5.23E-11	28.9
1.6E+07	5.23E-11	21.2

3] [protein_id=AHW98238.1] [location=1..372] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

1.3E+07	5.95E-26	103
1.3E+07	2.33E-21	90.9
2625822	2.50E-25	102
3040547	2.63E-25	102
1645716	3.13E-25	102
3055224	3.28E-25	102
3056569	3.69E-25	101
3046577	5.13E-25	101
2.1E+07	2.84E-25	102
2.4E+07	6.62E-10	49.7
2.4E+07	6.62E-10	32
2.4E+07	0.012	37.4
2.1E+07	5.93E-25	101
2.2E+07	1.52E-14	71.6
1121350	8.4	29.3
3.8E+07	7.94E-25	100
1.5E+07	1.29E-14	71.6
1.5E+07	4.15E-14	68.2
1.5E+07	4.15E-14	27.7
2.8E+07	9.1	28.9
1.6E+07	1.87E-14	67
1.6E+07	1.87E-14	27.3
1.6E+07	1.87E-14	21.9
2.5E+07	8	29.3

3] [protein_id=AHW98236.1] [location=1..372] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

1.3E+07	2.66E-26	105
1.3E+07	9.74E-22	92
2625822	1.04E-25	103
4447083	8.5	29.3
1645716	1.08E-25	103
3040547	1.22E-25	103
3055224	1.44E-25	102
3056569	1.70E-25	102
3046577	2.38E-25	102
6305171	0.74	32.3
2.1E+07	1.76E-25	102
2.4E+07	5.96E-10	49.7
2.4E+07	5.96E-10	32.3
2.4E+07	0.006	38.5
2.1E+07	2.58E-25	102
2.2E+07	7.28E-15	72.4
1121350	7.6	29.3
3.8E+07	3.69E-25	101
1.5E+07	5.99E-15	72.8
1.5E+07	2.25E-14	69.3
1.5E+07	2.25E-14	27.7
1.6E+07	1.10E-14	68.2
1.6E+07	1.10E-14	27.3
1.6E+07	1.10E-14	21.9

3] [protein_id=AHW98229.1] [location=1..474] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3040547	3.00E-22	95.1
3056569	3.82E-22	94.7
3055224	4.54E-22	94.4
3046577	8.19E-22	93.6
1645716	2.09E-21	92.4
2.1E+07	3.40E-22	94.7
2.4E+07	3.10E-08	50.4
2.4E+07	3.10E-08	26.6
2.4E+07	2.6	31.6
2625822	3.46E-22	94.7
3.8E+07	7.88E-22	94
2.1E+07	1.41E-21	93.2
2.2E+07	4.85E-11	62.8
1.3E+07	2.20E-19	86.7
1.3E+07	5.13E-18	82.8
1.5E+07	1.83E-09	58.2
1.5E+07	1.21E-07	53.1

1.5E+07	0.61	33.5
1.6E+07	7.50E-07	50.8
1.6E+07	0.008	37.4
1.6E+07	0.008	20.4

3] [protein_id=AHW98228.1] [location=1..474] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

3040547	1.31E-20	90.1
3056569	1.80E-20	89.7
3055224	2.19E-20	89.7
3046577	3.91E-20	89
1645716	5.64E-20	88.6
2.1E+07	1.39E-20	90.1
2.4E+07	6.47E-08	52
2.4E+07	6.47E-08	23.9
2.4E+07	8.9	29.6
2625822	1.55E-20	90.1
3.8E+07	2.32E-20	89.7
2.1E+07	3.13E-20	89.4
2.2E+07	3.61E-10	60.5
1.3E+07	2.60E-17	80.9
1.3E+07	3.69E-16	77.4
1.5E+07	3.99E-08	54.3
1.5E+07	1.91E-06	49.7
1.5E+07	1.4	32.3
1.6E+07	5.00E-06	48.1
1.6E+07	0.059	36.2

: H3 variant protein] [protein_id=ADN92693.1] [location=153..704] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

1645713	4.73E-28	112
3040544	2.99E-27	110
3056572	3.32E-27	110
3055221	4.27E-27	110
3046574	4.84E-27	109
3.8E+07	2.22E-27	110
2.1E+07	3.29E-27	110
2.4E+07	1.45E-10	51.6
2.4E+07	1.45E-10	33.9
2.4E+07	0.29	34.7
2625819	3.36E-27	110
2.1E+07	3.96E-27	110

2.2E+07	2.94E-18	84.7
1.3E+07	6.42E-26	106
1.3E+07	2.23E-23	99.4
1.6E+07	3.44E-17	68.9
1.6E+07	3.44E-17	29.6
1.6E+07	3.44E-17	28.9
1.5E+07	2.66E-16	79
1.5E+07	1.09E-14	68.9
1.5E+07	1.09E-14	30.8
2.5E+07	9.8	30

romeric protein B] [protein_id=QGY64363.1] [location=24..500] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

2625819	4.13E-27	108
3040544	4.77E-27	108
3055221	6.38E-27	108
3046574	6.83E-27	108
3056572	1.80E-26	107
1645713	1.01E-25	105
2.1E+07	9.13E-27	107
2.4E+07	1.06E-12	67.8
2.4E+07	1.3	32.3
3.8E+07	5.57E-26	105
2.1E+07	6.50E-26	105
2.2E+07	8.97E-17	79.3
1.3E+07	5.20E-25	102
1.3E+07	1.11E-22	96.3
1.5E+07	5.53E-12	65.5
1.5E+07	8.00E-07	50.4
1.5E+07	0.02	37.7
2E+07	1.3	32.3
1.5E+07	4	30.8
1.6E+07	8.47E-07	50.4
1.6E+07	6.43E-06	38.1
1.6E+07	6.43E-06	30.8

romeric protein A] [protein_id=QGY64362.1] [location=24..500] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

2625819	5.06E-28	111
3040544	5.36E-28	111
3055221	7.45E-28	110
3046574	8.78E-28	110

3056572	1.70E-27	110
1645713	1.22E-26	107
2.1E+07	1.14E-27	110
2.4E+07	1.68E-13	70.1
2.4E+07	1.2	32.3
2.1E+07	5.85E-27	108
2.2E+07	1.13E-17	82
3.8E+07	5.96E-27	108
1.3E+07	1.08E-25	104
1.3E+07	9.00E-23	96.7
1.5E+07	3.29E-12	66.2
1.5E+07	9.96E-07	50.4
1.5E+07	0.01	38.5
2E+07	0.19	34.7
1.5E+07	0.63	33.1
1.6E+07	9.59E-07	50.4
1.6E+07	1.45E-06	38.5
1.6E+07	1.45E-06	32.7

romeric protein 2] [protein_id=QGY64360.1] [location=106..555] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

1.3E+07	3.53E-15	74.3
1.3E+07	3.85E-11	62.8
2625819	4.80E-15	73.9
3055221	5.24E-15	73.9
3040544	6.00E-15	73.6
3046574	1.01E-14	73.2
1645713	1.43E-14	72.8
3056572	1.70E-14	72.4
2.1E+07	7.42E-15	73.6
2.4E+07	3.90E-09	57
2.1E+07	3.87E-14	71.2
2.2E+07	4.40E-06	48.1
3.8E+07	7.82E-14	70.5
1.6E+07	2.59E-04	33.5
1.6E+07	2.59E-04	29.3
1.6E+07	2.2	31.6
1.5E+07	0.002	40
1.5E+07	0.44	33.5
2E+07	0.6	33.1
1.5E+07	1.7	32

romeric protein 1A] [protein_id=QGY64359.1] [location=123..569] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

2625819	2.22E-33	126
3055221	2.49E-33	126
3040544	3.21E-33	125
3056572	6.14E-33	125
3046574	8.72E-32	122
1645713	5.88E-31	119
2.1E+07	5.91E-33	125
2.4E+07	4.47E-12	58.9
2.4E+07	4.47E-12	30.8
2.4E+07	0.006	38.9
2.1E+07	7.75E-33	124
2.2E+07	8.89E-21	90.5
2.3E+07	3.6	30.8
3.8E+07	2.68E-32	123
1.3E+07	3.30E-30	117
1.3E+07	2.91E-25	103
1.6E+07	1.01E-17	63.2
1.6E+07	1.01E-17	34.3
1.6E+07	1.01E-17	31.2
1.5E+07	1.16E-14	72.8
1.5E+07	1.98E-13	62
1.5E+07	1.98E-13	32.7
2E+07	0.18	34.7
1.5E+07	0.63	33.1

romeric protein 1B] [protein_id=QGY64358.1] [location=161..607] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

2625828	2.09E-33	126
3055230	2.45E-33	126
3040553	3.50E-33	125
3056563	6.96E-33	125
3046583	9.07E-32	121
1645722	5.44E-31	119
2.1E+07	6.90E-33	125
2.4E+07	4.15E-12	59.3
2.4E+07	4.15E-12	30.8
2.4E+07	0.015	37.7
2.1E+07	1.01E-32	124
2.2E+07	7.39E-21	90.5
2.3E+07	2.3	31.6
3.8E+07	2.89E-32	123
1.3E+07	9.66E-30	115

1.3E+07	1.16E-25	104
1.6E+07	1.23E-17	62.8
1.6E+07	1.23E-17	34.3
1.6E+07	1.23E-17	31.2
1.5E+07	2.43E-15	74.7
1.5E+07	5.70E-14	63.5
1.5E+07	5.70E-14	32.7
2E+07	0.13	35
1.5E+07	0.56	33.1

histone H3] [protein_id=AUN88460.1] [location=1..501] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

2625816	1.18E-33	128
1.8E+07	0.14	35.4
2.4E+07	1.4	32.3
3040541	1.33E-33	127
3055218	2.14E-33	127
3056575	5.32E-33	126
3046571	7.11E-33	125
1645710	3.44E-32	124
2.8E+07	1.7	32.3
1.6E+07	2.8	31.6
1.5E+07	4.1	31.2
2.4E+07	5.3	30.8
2.1E+07	2.76E-33	127
2.4E+07	1.85E-17	69.3
2.4E+07	1.85E-17	39.3
2.4E+07	3.20E-06	49.3
2.4E+07	0.091	35.8
2.4E+07	0.57	33.5
1.2E+07	2.2	32
7739703	2.2	32
8334114	4	31.2
1.2E+07	4.5	30.8
7092007	5.3	30.8
2.1E+07	2.27E-32	124
2.2E+07	1.05E-22	96.7
6034982	1.3	32.7
6359028	9.1	30
3.8E+07	2.98E-32	124
1E+07	0.93	33.1
1.3E+07	2.64E-29	115
1.3E+07	1.76E-27	110
2.7E+07	2	32

1.5E+07	6.32E-18	82.8
1.5E+07	2.32E-17	71.6
1.5E+07	2.32E-17	36.6
2E+07	1.37E-04	36.6
2E+07	1.37E-04	27.7
1.5E+07	2.7	31.6
1.5E+07	5.6	30.8
1.6E+07	5.79E-17	70.1
1.6E+07	5.79E-17	37
1.6E+07	1.3	32.3
2E+07	1.5	32.3
1.9E+07	2.3	32
1.9E+07	9.1	30
6630257	2.5	31.6
9325304	3.4	31.2
1.1E+07	3.8	31.2
1.3E+07	6.7	30.4
7380767	6.9	30.4
7580759	3.9	31.2
4633661	5.7	30.4
9874017	6.8	30.4

histone 3] [protein_id=AMH40810.1] [location=1..504] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

3040541	9.56E-26	105
3056575	1.51E-25	104
3055218	1.71E-25	104
3046571	5.94E-25	103
1645710	3.22E-24	100
2625816	1.21E-25	105
2.1E+07	2.54E-25	104
2.4E+07	3.52E-12	45.4
2.4E+07	3.52E-12	45.1
2.4E+07	0.002	40.8
2.4E+07	3.8	31.2
5979887	7.2	30.4
3.8E+07	3.42E-25	103
2.1E+07	8.99E-25	102
2.2E+07	9.41E-17	79.7
1.3E+07	2.32E-22	95.9
1.3E+07	8.46E-22	94
1.5E+07	4.15E-18	83.6
1.5E+07	2.36E-15	69.3
1.5E+07	2.36E-15	32.3

1.6E+07	6.23E-15	68.9
1.6E+07	6.23E-15	31.2

histone 3] [protein_id=AMH40809.1] [location=1..504] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3040541	3.26E-29	115
3055218	6.41E-29	114
3056575	8.41E-29	114
3046571	3.10E-28	112
1645710	4.92E-27	108
1.2E+07	9.3	30
2625816	4.57E-29	115
2.1E+07	1.52E-28	113
2.4E+07	7.68E-17	60.8
2.4E+07	7.68E-17	45.8
2.4E+07	0.002	40.8
2.4E+07	4.6	30.8
5979887	7.5	30.4
3.8E+07	2.58E-28	112
1E+07	7	28.9
1E+07	7	17.7
2.1E+07	5.81E-28	111
2.2E+07	1.07E-16	79.3
1.1E+07	1.3	32.7
9964684	6.3	30.4
1.3E+07	7.16E-26	105
1.3E+07	7.00E-25	102
1.1E+07	1.7	32.3
1.5E+07	1.11E-15	76.6
1.5E+07	1.52E-15	70.5
1.5E+07	1.52E-15	32
2E+07	0.076	28.9
2E+07	0.076	25.8
1.6E+07	5.56E-15	69.7
1.6E+07	5.56E-15	30.8
2.2E+07	2.5	31.6
2.3E+07	4.2	31.2
2.7E+07	5.2	30.8

histone 3] [protein_id=AKI32619.1] [location=1..471] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3046571	9.44E-29	113
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3040541	2.07E-28	112
3055218	3.32E-28	112
3056575	4.27E-28	111
1645710	1.35E-26	107
7680274	7.4	30
2625816	2.11E-28	112
2.1E+07	4.94E-28	111
2.4E+07	1.27E-15	58.9
2.4E+07	1.27E-15	43.5
2.4E+07	0.002	40.8
2.4E+07	4.3	30.8
2.1E+07	2.26E-27	109
2.2E+07	2.65E-18	83.6
1.1E+07	3.1	31.2
2.1E+07	7.1	30
3.8E+07	2.37E-27	109
1.3E+07	2.79E-26	106
1.3E+07	3.26E-24	100
1.1E+07	2.4	31.6
2433977	9.5	29.6
1.5E+07	1.02E-16	79
1.5E+07	2.67E-15	68.9
1.5E+07	2.67E-15	32
2E+07	0.033	29.3
2E+07	0.033	26.6
1.6E+07	9.18E-15	68.2
1.6E+07	9.18E-15	30.8
2.2E+07	1	32.7
8621132	1.3	32.3
2.8E+07	9.6	29.6

[stone 3] [protein_id=AKI32617.1] [location=1..306] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

2.4E+07	1.18E-04	42.4
2.1E+07	0.4	32.3
1.3E+07	0.006	37.4
1.3E+07	0.079	34.3
3046796	0.012	36.6
3056404	0.04	35
3040766	0.045	35
1645881	0.19	33.1
3055443	0.75	31.6
7680274	3.1	29.6
2.1E+07	0.048	35

2626041	0.053	34.7
3.8E+07	0.067	34.3

stone 3] [protein_id=AKI32616.1] [location=1..471] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

3046571	1.58E-26	107
3040541	3.32E-26	106
3056575	4.44E-26	105
3055218	4.75E-26	105
1645710	1.20E-24	101
7680274	7.2	30
2625816	2.93E-26	106
2.1E+07	7.49E-26	105
2.4E+07	3.23E-14	56.2
2.4E+07	3.23E-14	41.2
2.4E+07	0.002	40.8
3.8E+07	1.50E-25	104
2.1E+07	2.24E-25	103
2.2E+07	1.33E-16	78.6
1.3E+07	7.14E-25	102
1.3E+07	6.34E-23	97.1
1.5E+07	4.87E-15	74.3
1.5E+07	7.30E-14	68.6
1.5E+07	7.30E-14	27.7
2E+07	0.2	29.3
2E+07	0.2	23.5
1.6E+07	2.57E-13	67.8
1.6E+07	2.57E-13	26.6

stone 3] [protein_id=AKI32612.1] [location=1..471] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

3040598	1.65E-16	78.6
3055275	2.31E-16	78.2
3056518	3.50E-16	77.4
3046628	6.19E-16	77
1645767	2.01E-15	75.5
2625873	1.68E-16	78.6
2.1E+07	4.54E-16	77.4
2.4E+07	2.85E-12	45.4
2.4E+07	2.85E-12	45.4
2.4E+07	0.84	32.7
5979887	8.9	29.6

3.8E+07	4.63E-16	77
2.1E+07	1.59E-15	75.5
2.2E+07	1.10E-07	53.1
1.3E+07	3.16E-14	72
1.3E+07	2.79E-13	69.3
1.5E+07	1.03E-08	56.2
1.5E+07	1.82E-07	41.6
1.5E+07	1.82E-07	32.3
1.6E+07	2.30E-07	42.4
1.6E+07	2.30E-07	31.6

stone 3] [protein_id=AKI32608.1] [location=1..219] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

5306151	1.1	29.6
5979887	1.6	29.3
1.2E+07	3.2	28.5
2141507	6.4	27.7
1.2E+07	6.4	27.7
2.5E+07	7.1	27.7
3.5E+07	8.1	27.3
1.7E+07	9.2	27.3

stone 3] [protein_id=AKI32602.1] [location=1..477] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3040541	4.09E-26	106
3056575	6.76E-26	105
3055218	8.45E-26	105
3046571	2.24E-25	103
1645710	9.76E-25	102
2625816	5.68E-26	105
2.1E+07	1.08E-25	104
2.4E+07	2.67E-12	45.8
2.4E+07	2.67E-12	45.1
2.4E+07	0.003	40
3.8E+07	1.92E-25	104
2.1E+07	3.47E-25	103
2.2E+07	7.46E-17	79.7
1.3E+07	1.86E-23	98.6
1.3E+07	5.77E-23	97.1
1.5E+07	1.56E-18	84.3
1.5E+07	1.21E-15	70.1
1.5E+07	1.21E-15	32.3

1.6E+07	2.77E-15	69.7
1.6E+07	2.77E-15	31.2

stone 3] [protein_id=AKI32601.1] [location=1..471] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

3040541	7.27E-29	114
3055218	1.07E-28	113
3056575	1.24E-28	113
3046571	3.45E-28	112
1645710	3.70E-27	108
2625816	8.01E-29	113
2.1E+07	2.07E-28	112
2.4E+07	1.75E-15	56.6
2.4E+07	1.75E-15	45.1
2.4E+07	0.002	40.8
2.4E+07	3	31.2
3.8E+07	5.18E-28	111
2.1E+07	8.33E-28	110
2.2E+07	6.92E-17	79.7
1.3E+07	5.04E-26	105
1.3E+07	9.09E-25	102
1.5E+07	6.57E-18	82.4
1.5E+07	2.69E-15	69.7
1.5E+07	2.69E-15	31.6
2E+07	0.19	26.6
2E+07	0.19	26.2
1.6E+07	5.82E-15	69.3
1.6E+07	5.82E-15	30.4

stone 3] [protein_id=AKI32600.1] [location=1..504] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

3040541	5.34E-29	114
3056575	1.25E-28	113
3055218	1.61E-28	113
3046571	5.54E-28	111
1645710	8.46E-27	108
1.2E+07	9.7	30
2625816	1.15E-28	114
2.1E+07	2.37E-28	112
2.4E+07	7.08E-17	60.8
2.4E+07	7.08E-17	45.8
2.4E+07	0.001	41.6

2.4E+07	4.8	30.8
3.8E+07	3.76E-28	112
2.1E+07	9.07E-28	111
2.2E+07	1.92E-16	78.6
1.1E+07	1.2	32.7
9964684	6.1	30.4
1.3E+07	2.86E-26	107
1.3E+07	1.00E-24	102
1.1E+07	1.7	32.3
1.5E+07	5.93E-18	83.2
1.5E+07	2.08E-15	70.1
1.5E+07	2.08E-15	32
2E+07	0.099	28.9
2E+07	0.099	25.4
1.6E+07	8.35E-15	68.9
1.6E+07	8.35E-15	30.8
2.2E+07	2.6	31.6
2.3E+07	4.4	30.8
2.7E+07	8.4	30

H3 isoform b] [protein_id=BAP26971.1] [location=1..513] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evalue, bit score

2625816	2.60E-27	110
3040541	2.86E-27	110
3055218	3.68E-27	109
3046571	4.60E-27	109
3056575	1.37E-26	107
1645710	2.44E-26	107
2.1E+07	8.36E-27	108
2.4E+07	5.20E-12	61.6
2.4E+07	5.20E-12	28.9
2.4E+07	0.001	41.6
2.4E+07	0.009	38.9
2.1E+07	6.06E-26	106
2.2E+07	7.22E-16	77
3.8E+07	1.52E-25	105
1.3E+07	1.60E-22	96.3
1.3E+07	1.30E-21	93.6
1.5E+07	5.50E-10	60.1
1.5E+07	2.62E-07	52.4
1.5E+07	0.18	35
2E+07	0.44	33.9
1.6E+07	7.36E-07	51.2
1.6E+07	3.95E-06	38.1

1.6E+07 3.95E-06 31.6

H3 isoform a] [protein_id=BAP26970.1] [location=1..492] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

2625816	2.03E-27	110
3040541	2.23E-27	110
3055218	2.87E-27	109
3046571	3.59E-27	109
3056575	1.07E-26	107
1645710	1.91E-26	107
2.1E+07	6.54E-27	108
2.4E+07	4.70E-12	61.6
2.4E+07	4.70E-12	28.9
2.4E+07	0.001	41.6
2.4E+07	0.008	38.9
2.1E+07	4.74E-26	106
2.2E+07	5.80E-16	77
3.8E+07	1.19E-25	105
1.3E+07	1.26E-22	96.3
1.3E+07	1.03E-21	93.6
1.5E+07	4.53E-10	60.1
1.5E+07	2.20E-07	52.4
1.5E+07	0.16	35
2E+07	0.39	33.9
1.6E+07	6.20E-07	51.2
1.6E+07	3.58E-06	38.1
1.6E+07	3.58E-06	31.6

] [protein_id=AEH95352.1] [location=1..492] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

3040541	9.03E-33	125
3055218	1.46E-32	124
3056575	3.78E-32	123
3046571	5.05E-32	123
1645710	2.94E-31	120
2.8E+07	1.4	32.3
1.6E+07	1.7	32
1.5E+07	2.7	31.6
2.4E+07	3.5	31.2
2625816	9.56E-33	125
1.8E+07	0.12	35.4
2.4E+07	0.93	32.7

2.1E+07	1.88E-32	124
2.4E+07	8.10E-17	67
2.4E+07	8.10E-17	39.3
2.4E+07	6.07E-06	48.1
2.4E+07	0.021	37.7
2.4E+07	0.29	34.3
1.2E+07	1.4	32.3
7739703	1.6	32.3
8334114	3	31.2
1.2E+07	3.3	31.2
7092007	3.6	31.2
2.1E+07	1.51E-31	122
2.2E+07	8.14E-22	94
6034982	1	32.7
6359028	6.3	30.4
1.7E+07	7.8	30
3.8E+07	2.28E-31	121
1E+07	0.69	33.1
1.3E+07	7.22E-29	114
1.3E+07	5.34E-27	108
2.7E+07	1.5	32.3
1.5E+07	4.40E-19	86.3
1.5E+07	1.03E-16	71.6
1.5E+07	1.03E-16	34.3
2E+07	1.15E-04	37
2E+07	1.15E-04	27.7
1.5E+07	2.6	31.6
1.5E+07	3.8	31.2
1.6E+07	2.81E-16	70.1
1.6E+07	2.81E-16	34.7
2E+07	0.98	32.7
1.9E+07	1.6	32.3
1.6E+07	1.8	32
1.9E+07	6.3	30.4
6630257	2	32
9325304	2.3	31.6
1.1E+07	2.8	31.6
1.3E+07	4.8	30.8
7380767	5	30.8
7580759	3	31.2
2881009	7.1	30.4
4633661	3.9	31.2
9874017	5.4	30.4
1.3E+07	9	30

] [protein_id=AEH95350.1] [location=1..501] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

3040541	3.22E-33	126
3055218	4.92E-33	126
3056575	1.57E-32	124
3046571	1.98E-32	124
1645710	1.10E-31	122
2.8E+07	1.7	32.3
1.6E+07	2.6	31.6
1.5E+07	3.7	31.2
2.4E+07	4.8	30.8
2625816	3.28E-33	126
1.8E+07	0.15	35.4
2.4E+07	1.2	32.7
2.1E+07	6.71E-33	125
2.4E+07	3.59E-17	68.6
2.4E+07	3.59E-17	39.3
2.4E+07	5.05E-06	48.5
2.4E+07	0.078	36.2
2.4E+07	0.51	33.9
1.2E+07	2	32
7739703	2.1	32
8334114	3.9	31.2
1.2E+07	4.8	30.8
7092007	5.4	30.8
2.1E+07	5.75E-32	123
2.2E+07	2.72E-22	95.5
6034982	1.4	32.3
6359028	8.7	30
3.8E+07	7.39E-32	122
1E+07	0.85	33.1
1.3E+07	5.62E-29	114
1.3E+07	4.48E-27	109
2.7E+07	2.1	32
1.5E+07	1.41E-19	87.8
1.5E+07	4.32E-17	71.6
1.5E+07	4.32E-17	35.8
2E+07	1.67E-04	36.2
2E+07	1.67E-04	27.7
1.5E+07	2.5	31.6
1.5E+07	5	30.8
1.6E+07	1.27E-16	70.1
1.6E+07	1.27E-16	35.8
2E+07	1.4	32.3
1.6E+07	1.9	32

1.9E+07	2.2	32
1.9E+07	8.4	30
6630257	2.5	31.6
9325304	3	31.6
1.1E+07	3.8	31.2
1.3E+07	5.9	30.4
7380767	6.7	30.4
7580759	3.7	31.2
4633661	5.6	30.8
9874017	6.7	30.4

one H3] [protein_id=AEK21394.1] [location=1..411] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

2625828	9.83E-31	118
3055230	1.41E-30	117
3040553	1.64E-30	117
1645722	4.46E-30	116
3056563	9.78E-30	115
3046583	4.79E-29	113
2.1E+07	3.64E-30	116
2.4E+07	1.31E-12	66.6
2.4E+07	1.08E-06	49.7
3.8E+07	1.87E-29	114
2.1E+07	2.43E-29	114
2.2E+07	1.10E-19	86.7
3.2E+07	0.19	34.3
1.3E+07	5.23E-27	107
1.3E+07	5.11E-23	96.3
3562616	0.83	32.3
3718644	6.4	29.6
1.6E+07	6.71E-18	63.2
1.6E+07	6.71E-18	37.4
1.6E+07	6.71E-18	28.1
1.5E+07	1.50E-17	80.5
1.5E+07	2.03E-16	63.2
1.5E+07	2.03E-16	41.2
2E+07	0.27	33.9
2.7E+07	4.8	30
4506970	4.7	30

one H3] [protein_id=AEK21393.1] [location=44..463] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

2625813	2.77E-27	108
3040538	3.93E-27	108
3055215	4.37E-27	108
3046568	9.31E-27	107
3056578	1.13E-26	106
1645722	2.70E-26	105
2.1E+07	9.22E-27	107
2.4E+07	2.45E-10	60.1
2.4E+07	3.13E-05	45.4
2.1E+07	2.58E-26	105
2.2E+07	1.68E-16	77.8
3.8E+07	2.60E-26	105
1.7E+07	4.7	30.4
1.3E+07	4.67E-25	102
1.3E+07	3.54E-21	91.3
1.5E+07	4.13E-16	76.6
1.5E+07	2.73E-11	62.8
1.5E+07	0.007	38.5
2E+07	2	31.2
1.6E+07	1.40E-10	60.8
1.6E+07	2.93E-04	38.1
1.6E+07	2.93E-04	24.3
1.6E+07	7	29.6

H3 variant protein] [protein_id=ACZ04984.1] [location=1..546] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

1645713	1.27E-27	111
3040544	7.62E-27	109
3056572	8.31E-27	108
3055221	9.60E-27	108
3046574	1.09E-26	108
3.8E+07	6.34E-27	109
2.1E+07	8.31E-27	108
2.4E+07	1.47E-10	51.6
2.4E+07	1.47E-10	33.9
2.4E+07	0.33	34.7
2625819	8.47E-27	108
1069651	0.57	33.9
2.1E+07	1.36E-26	108
2.2E+07	8.12E-18	83.2
1.3E+07	1.23E-25	105
1.3E+07	4.52E-23	98.2
1.6E+07	6.26E-17	68.2
1.6E+07	6.26E-17	29.6

1.6E+07	6.26E-17	28.5
1.5E+07	3.37E-16	78.6
1.5E+07	1.34E-14	68.2
1.5E+07	1.34E-14	30.8
2.5E+07	8.4	30.4

H3 variant protein] [protein_id=ACZ04982.1] [location=1..555] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

1645713	7.86E-28	112
3055221	2.41E-27	110
3040544	2.73E-27	110
3056572	4.34E-27	110
3046574	6.56E-27	109
3.8E+07	1.82E-27	111
2625819	1.91E-27	110
2.1E+07	4.82E-27	109
2.4E+07	4.23E-11	51.6
2.4E+07	4.23E-11	35.8
2.4E+07	0.3	34.7
2.1E+07	6.20E-27	109
2.2E+07	1.84E-18	85.1
1.3E+07	1.38E-26	108
1.3E+07	8.56E-24	100
1.6E+07	3.49E-17	68.6
1.6E+07	3.49E-17	30
1.6E+07	3.49E-17	28.9
1.5E+07	1.54E-16	79.7
1.5E+07	9.29E-15	68.6
1.5E+07	9.29E-15	31.2
2.5E+07	6.9	30.8

H3 variant protein] [protein_id=ACZ04980.1] [location=1..549] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

1645713	1.66E-20	90.9
3040544	3.20E-20	90.1
3055221	3.39E-20	90.1
3046574	3.46E-20	90.1
3056572	3.73E-20	90.1
2625819	2.72E-20	90.5
3.8E+07	3.56E-20	90.1
2.1E+07	3.92E-20	90.1
2.4E+07	2.66E-07	52.8

2.4E+07	5.2	30.8
2.1E+07	6.21E-20	89.4
2.2E+07	5.05E-12	66.6
1.3E+07	3.65E-19	87
1.3E+07	1.02E-17	82.8
1.5E+07	6.15E-09	57.4
1.5E+07	2.29E-07	52.8
1.6E+07	1.91E-07	53.1
1.6E+07	0.031	28.5
1.6E+07	0.031	27.7

H3 variant protein] [protein_id=ACZ04978.1] [location=1..489] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

1645713	2.17E-19	87
3056572	3.13E-19	86.7
3046574	3.65E-19	86.3
3040544	3.69E-19	86.3
3055221	3.76E-19	86.3
2.1E+07	3.04E-19	86.7
2.4E+07	2.25E-06	49.3
2.4E+07	3.7	31.2
2625819	3.22E-19	86.7
3.8E+07	4.14E-19	86.3
2.1E+07	6.45E-19	85.5
2.2E+07	5.19E-10	60.1
1.3E+07	1.81E-18	84.3
1.3E+07	6.87E-17	79.7
1.5E+07	3.56E-09	57.8
1.5E+07	4.93E-08	54.3
1.6E+07	4.19E-08	54.3
1.6E+07	0.58	27.7
1.6E+07	0.58	23.1

histone H3] [protein_id=QBB85873.1] [location=join(1..52,159..205,292..343,424..461,556..589)]

, q. start, q. end, s. start, s. end, eval, bit score

1645713	1.32E-27	111
3040544	8.68E-27	108
3055221	1.01E-26	108
3046574	1.08E-26	108
3056572	1.13E-26	108
3.8E+07	6.76E-27	109
2625819	7.37E-27	109

1069651	0.75	33.5
2.1E+07	1.00E-26	108
2.4E+07	5.13E-11	51.6
2.4E+07	5.13E-11	35.4
2.4E+07	0.3	34.7
2.1E+07	1.53E-26	108
2.2E+07	3.54E-18	84.3
1.3E+07	1.37E-25	105
1.3E+07	4.40E-23	98.6
1.6E+07	6.06E-17	68.2
1.6E+07	6.06E-17	30
1.6E+07	6.06E-17	28.5
1.5E+07	3.19E-16	78.6
1.5E+07	1.30E-14	68.2
1.5E+07	1.30E-14	31.2
2.5E+07	6.6	30.8

histone H3-3 variant] [protein_id=QBB85871.1] [location=1..537] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

1645713	4.14E-28	112
3040544	2.88E-27	110
3056572	3.43E-27	110
3055221	4.00E-27	109
3046574	5.67E-27	109
3.8E+07	2.24E-27	110
2625819	3.06E-27	110
1069651	0.86	33.1
2.1E+07	3.50E-27	110
2.4E+07	5.24E-11	51.6
2.4E+07	5.24E-11	35.4
2.4E+07	0.34	34.7
2.1E+07	4.33E-27	109
2.2E+07	2.33E-18	84.7
1.3E+07	6.21E-26	106
1.3E+07	2.25E-23	99
1.6E+07	2.82E-17	68.6
1.6E+07	2.82E-17	30
1.6E+07	2.82E-17	29.3
1.5E+07	2.97E-16	78.6
1.5E+07	1.29E-14	68.2
1.5E+07	1.29E-14	30.8
2.5E+07	6.5	30.8

+3 variant 2] [protein_id=AOR06535.1] [location=1..525] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

3040541	7.58E-31	120
3055218	1.92E-30	119
3056575	2.39E-30	119
3046571	3.56E-30	118
1645710	1.56E-29	116
2625816	1.42E-30	119
2.1E+07	2.05E-30	119
2.4E+07	6.05E-13	65.9
2.4E+07	6.05E-13	27.7
2.4E+07	5.1	30.8
3.8E+07	3.23E-30	118
2.1E+07	1.03E-29	117
2.2E+07	7.01E-20	89
1.3E+07	9.21E-26	105
1.3E+07	1.41E-23	99.4
1.5E+07	1.03E-14	73.9
1.5E+07	2.32E-09	58.5
1.5E+07	0.002	41.6
2E+07	0.003	33.1
2E+07	0.003	26.6
1.6E+07	3.06E-09	58.2
1.6E+07	1.00E-06	43.1
1.6E+07	1.00E-06	28.9

+3 variant 1] [protein_id=AOR06534.1] [location=1..549] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

3040541	1.37E-30	120
3055218	2.61E-30	119
3056575	3.02E-30	119
3046571	4.45E-30	118
1645710	1.70E-29	116
2625816	1.81E-30	119
2.1E+07	2.82E-30	119
2.4E+07	7.25E-13	65.9
2.4E+07	7.25E-13	27.7
2.4E+07	5.6	30.8
3.8E+07	4.20E-30	118
2.1E+07	1.25E-29	117
2.2E+07	4.66E-20	89.7
1.3E+07	2.74E-25	104
1.3E+07	2.25E-23	99.4

1.5E+07	4.41E-15	75.5
1.5E+07	2.72E-09	58.5
1.5E+07	0.002	41.6
2E+07	0.003	33.1
2E+07	0.003	26.6
1.6E+07	4.09E-09	58.2
1.6E+07	1.08E-06	43.1
1.6E+07	1.08E-06	28.9

histone H3-4 variant] [protein_id=AOH73624.1] [location=124..705] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

1645713	5.02E-28	113
3040544	2.82E-27	110
3056572	4.23E-27	110
3055221	4.27E-27	110
3046574	4.31E-27	110
3.8E+07	2.64E-27	110
2.1E+07	2.99E-27	110
2.4E+07	1.21E-10	52
2.4E+07	1.21E-10	33.9
2.4E+07	0.37	34.7
2625819	3.13E-27	110
2.1E+07	4.70E-27	110
2.2E+07	1.90E-18	85.5
1.3E+07	6.71E-26	107
1.3E+07	2.60E-23	99.4
1.6E+07	2.13E-17	69.3
1.6E+07	2.13E-17	30
1.6E+07	2.13E-17	29.3
1.5E+07	2.14E-16	79.7
1.5E+07	8.31E-15	68.9
1.5E+07	8.31E-15	31.2
2.5E+07	6.5	30.8

histone H3-2] [protein_id=AOH73622.1] [location=72..611] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

1645713	5.25E-28	112
3040544	2.76E-27	110
3056572	3.99E-27	109
3055221	4.35E-27	109
3046574	5.92E-27	109
3.8E+07	2.21E-27	110

2625819	3.55E-27	110
2.1E+07	4.43E-27	109
2.4E+07	1.22E-10	51.6
2.4E+07	1.22E-10	33.9
2.4E+07	0.19	35.4
2.1E+07	4.98E-27	109
2.2E+07	1.82E-18	85.1
1.3E+07	6.87E-26	106
1.3E+07	1.92E-23	99.4
1.6E+07	3.29E-17	68.9
1.6E+07	3.29E-17	29.6
1.6E+07	3.29E-17	28.9
1.5E+07	1.82E-16	79.3
1.5E+07	9.19E-15	68.9
1.5E+07	9.19E-15	30.8

histone H3-2] [protein_id=AOH73621.1] [location=107..655] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

1645713	5.39E-21	92.4
3040544	6.60E-21	92
3046574	6.73E-21	92
3055221	7.06E-21	92
3056572	7.27E-21	92
2.1E+07	5.50E-21	92.4
2.4E+07	6.79E-07	51.6
2.4E+07	2.1	32.3
2625819	6.11E-21	92.4
3.8E+07	1.02E-20	91.7
2.1E+07	1.25E-20	91.3
2.2E+07	3.32E-12	67
1.3E+07	7.39E-20	89.4
1.3E+07	2.00E-18	85.1
1.5E+07	1.71E-08	56.2
1.5E+07	1.06E-07	53.9
1.6E+07	8.90E-08	54.3
1.6E+07	0.023	28.9
1.6E+07	0.023	27.7

histone H3] [protein_id=AOH73620.1] [location=167..652] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

2625819	3.30E-19	86.3
1645713	3.30E-19	86.3

3056572	3.53E-19	86.3
3040544	3.71E-19	86.3
3055221	4.00E-19	86.3
3046574	5.05E-19	85.9
3.8E+07	4.37E-19	86.3
2.1E+07	4.72E-19	85.9
2.4E+07	1.88E-06	49.7
2.4E+07	5.6	30.4
2.1E+07	7.01E-19	85.5
2.2E+07	4.67E-10	60.1
1.3E+07	2.21E-18	84
1.3E+07	7.92E-17	79.7
1.5E+07	1.02E-08	56.2
1.5E+07	1.02E-07	53.1
1.6E+07	6.57E-08	53.9
1.6E+07	0.5	27.7
1.6E+07	0.5	23.1

histone H3] [protein_id=AOH73617.1] [location=1..555] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3040544	1.53E-19	88.2
1645713	2.06E-19	87.8
3056572	2.22E-19	87.8
3055221	2.52E-19	87.8
3046574	2.91E-19	87.4
2.1E+07	1.65E-19	88.2
2.4E+07	4.26E-07	52.4
2.4E+07	7.7	30.4
2625819	1.94E-19	88.2
2.1E+07	2.31E-19	87.8
2.2E+07	3.42E-09	58.5
3.8E+07	2.42E-19	87.8
1.3E+07	1.49E-18	85.5
1.3E+07	1.90E-17	82.4
1.5E+07	1.13E-10	62.8
1.5E+07	1.77E-06	50.4
1.5E+07	0.2	35.4
1.6E+07	1.63E-06	50.4
1.6E+07	0.011	31.6
1.6E+07	0.011	26.2

13 variant 2] [protein_id=ALF04640.1] [location=29..565] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

2625816	3.96E-31	121
3040541	3.96E-31	121
3055218	5.55E-31	120
3056575	1.25E-30	119
3046571	1.68E-30	119
1645710	1.99E-30	119
2.1E+07	5.60E-31	120
2.4E+07	6.21E-12	66.2
2.4E+07	0.034	37.4
2.1E+07	4.02E-30	118
2.2E+07	2.30E-20	90.5
3.8E+07	7.90E-30	117
2E+07	2.2	32
1.3E+07	2.52E-25	104
1.3E+07	2.81E-23	99
1.6E+07	5.37E-18	60.5
1.6E+07	5.37E-18	38.5
1.6E+07	5.37E-18	31.2
1.5E+07	8.11E-17	80.1
1.5E+07	2.28E-15	61.6
1.5E+07	2.28E-15	40.4
2E+07	8.65E-05	36.2
2E+07	8.65E-05	29.3
2.9E+07	0.76	33.5
1.5E+07	1.4	32.7

13 variant 1] [protein_id=ALF04639.1] [location=29..565] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3040541	4.07E-31	121
3055218	1.04E-30	120
3056575	1.40E-30	119
3046571	1.91E-30	119
1645710	2.58E-30	119
2625816	6.86E-31	120
2.1E+07	7.85E-31	120
2.4E+07	1.16E-12	68.2
2.4E+07	0.051	37
2.1E+07	3.79E-30	118
2.2E+07	3.58E-20	89.7
3.8E+07	6.77E-30	117
2E+07	1.8	32.3
1.3E+07	5.29E-25	103
1.3E+07	3.44E-23	98.6

1.6E+07	6.05E-18	60.1
1.6E+07	6.05E-18	38.5
1.6E+07	6.05E-18	31.6
1.5E+07	1.38E-16	79.7
1.5E+07	2.67E-15	61.2
1.5E+07	2.67E-15	40.4
2E+07	4.92E-05	35.8
2E+07	4.92E-05	30.4
2.9E+07	1.8	32.3
1.5E+07	2.5	32

histone H3 variant] [protein_id=AHH01567.1] [location=61..540] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3040547	1.84E-25	104
3056569	2.19E-25	103
3055224	3.32E-25	103
3046577	3.99E-25	103
1645716	1.49E-24	101
2625822	2.01E-25	104
2.1E+07	2.07E-25	103
2.4E+07	3.41E-08	54.7
2.4E+07	0.45	33.9
2.1E+07	2.99E-25	103
2.2E+07	1.09E-16	79
3.8E+07	3.63E-25	103
1.3E+07	2.47E-22	95.5
1.3E+07	2.33E-19	86.7
1.5E+07	1.04E-13	70.5
1.5E+07	4.62E-09	57
1.5E+07	0.037	37
1.6E+07	2.09E-09	58.2
1.6E+07	6.41E-04	37.7
1.6E+07	6.41E-04	24.3

histone H3 variant] [protein_id=AGQ21573.1] [location=66..557] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3040547	2.91E-21	92.4
3056569	3.57E-21	92
3055224	5.20E-21	91.7
3046577	9.18E-21	90.9
1645716	1.74E-20	90.1
2625822	3.53E-21	92

2.1E+07	4.28E-21	92
2.4E+07	6.14E-08	50.1
2.4E+07	6.14E-08	25.8
3.8E+07	4.54E-21	92
2.1E+07	6.74E-21	91.3
2.2E+07	3.19E-11	63.5
1.3E+07	5.01E-18	83.2
1.3E+07	4.64E-17	80.5
1.5E+07	3.26E-09	57.8
1.5E+07	9.43E-07	50.4
1.5E+07	0.029	37.4
1.6E+07	9.16E-07	50.4
1.6E+07	0.005	39.7
2.9E+07	6.3	30.4

3] [protein_id=AAR85315.1] [location=68..562] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evalue, bit score

3040541	6.54E-31	120
3055218	1.30E-30	119
3056575	2.09E-30	118
3046571	3.11E-30	118
1645710	5.44E-29	114
2625816	7.94E-31	119
2.1E+07	1.34E-30	119
2.4E+07	3.80E-22	87
2.4E+07	3.80E-22	37.4
2.4E+07	2.26E-11	63.9
2.4E+07	8.14E-07	50.8
2.4E+07	0.014	38.5
2.1E+07	5.71E-30	117
2.2E+07	9.87E-18	82.4
3.8E+07	7.86E-30	117
1.3E+07	3.20E-25	103
1.3E+07	2.21E-24	101
1.5E+07	3.72E-14	72
1.5E+07	2.54E-09	58.2
1.5E+07	0.003	40
2E+07	0.096	35.8
1.5E+07	2.2	32
1.6E+07	2.82E-09	57.8
1.6E+07	9.93E-07	40.4
1.6E+07	9.93E-07	31.6
1.2E+07	7.4	30

] [protein_id=AAM74226.1] [location=66..539] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3040541	1.04E-26	107
3055218	1.67E-26	107
3046571	3.51E-26	106
3056575	4.47E-26	105
1645710	1.40E-25	104
2625816	1.15E-26	107
2.1E+07	2.98E-26	106
2.4E+07	5.00E-10	59.7
2.4E+07	2.28E-04	43.5
2.4E+07	0.001	41.6
2.1E+07	1.15E-25	104
2.2E+07	4.31E-15	74.3
3.8E+07	2.55E-25	103
1.3E+07	1.27E-22	95.9
1.3E+07	1.86E-21	92.8
1.5E+07	2.58E-12	66.6
1.5E+07	2.44E-09	57.8
1.5E+07	0.077	35.8
2E+07	3.5	31.2
1.6E+07	1.95E-09	58.2
1.6E+07	8.04E-04	35.8
1.6E+07	8.04E-04	25.8

one H3 isoform B] [protein_id=ADM18965.1] [location=1..534] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3040553	1.69E-26	108
3056563	3.05E-26	107
3055230	5.83E-26	106
3046583	1.27E-25	105
1645722	1.03E-24	102
3.8E+07	1.80E-26	107
2625828	3.92E-26	107
2.1E+07	4.67E-26	106
2.4E+07	4.32E-12	63.9
2.4E+07	4.32E-12	26.6
2.4E+07	1.7	32.3
2.1E+07	1.23E-25	105
2.2E+07	1.17E-15	77
1.3E+07	1.68E-22	96.7
1.3E+07	5.30E-21	92.4

1.5E+07	1.62E-11	64.7
1.5E+07	8.53E-08	53.9
1.5E+07	0.002	41.2
2E+07	2.1	32
1.6E+07	6.66E-08	54.3
1.6E+07	0.092	36.2
1.6E+07	9.8	30

iant] [protein_id=AYA72175.1] [location=11..475] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evalue, bit score

2625816	1.08E-36	136
3040541	1.19E-36	135
3055218	1.71E-36	135
3056575	1.97E-36	135
3046571	2.09E-35	132
1645710	4.68E-35	131
2.1E+07	3.39E-36	134
2.4E+07	9.78E-19	67.4
2.4E+07	9.78E-19	45.1
2.4E+07	0.003	40
2.1E+07	5.14E-36	134
2.2E+07	3.25E-25	103
3.8E+07	8.19E-36	133
1.3E+07	3.26E-32	123
1.3E+07	2.66E-30	117
1.5E+07	3.98E-23	97.4
1.5E+07	2.49E-19	73.2
1.5E+07	2.49E-19	41.6
2E+07	1.47E-04	36.2
2E+07	1.47E-04	27.7
1.6E+07	1.42E-22	72.8
1.6E+07	1.42E-22	41.2
1.6E+07	1.42E-22	31.2

iant] [protein_id=AYA72192.1] [location=15..479] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evalue, bit score

3040541	2.59E-35	132
3056575	3.57E-35	131
3055218	5.20E-35	131
3046571	3.79E-34	129
1645710	3.90E-34	129
2625816	2.77E-35	132

2.1E+07	7.67E-35	130
2.4E+07	3.49E-16	60.8
2.4E+07	3.49E-16	43.1
2.4E+07	0.004	39.7
2.1E+07	9.58E-35	130
2.2E+07	3.06E-24	100
3.8E+07	1.27E-34	130
1.3E+07	8.91E-32	122
1.3E+07	9.03E-29	113
1.5E+07	5.91E-23	97.1
1.5E+07	6.58E-19	73.6
1.5E+07	6.58E-19	39.7
2E+07	0.008	30.8
2E+07	0.008	26.9
1.5E+07	7.1	30
1.6E+07	1.23E-21	73.6
1.6E+07	1.23E-21	39.3
1.6E+07	1.23E-21	29.6

iant] [protein_id=AYA72176.1] [location=30..494] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

2625816	4.25E-39	143
3040541	6.32E-39	142
3055218	6.51E-39	142
3056575	1.93E-38	141
3046571	6.28E-38	139
1645710	6.94E-36	134
3154068	9.5	29.6
2.1E+07	1.78E-38	141
2.4E+07	1.52E-17	66.6
2.4E+07	1.52E-17	42.4
2.4E+07	0.003	40
2.1E+07	9.07E-38	139
2.2E+07	1.05E-26	107
3.8E+07	2.11E-37	138
1.3E+07	6.34E-33	125
1.3E+07	6.00E-31	119
1.5E+07	1.24E-21	93.2
1.5E+07	1.78E-14	72.4
1.5E+07	0.007	38.9
2E+07	0.23	34.7
1.5E+07	0.56	33.5
2E+07	3	31.2
1.6E+07	1.62E-14	72.8

1.6E+07	5.34E-07	38.9
1.6E+07	5.34E-07	33.5

stone H3] [protein_id=AUN88474.1] [location=1..456] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

2625816	8.86E-32	122
3040541	9.95E-32	121
3055218	1.52E-31	121
3046571	2.20E-31	120
3056575	2.89E-31	120
1645710	9.60E-31	119
2.1E+07	2.10E-31	120
2.4E+07	1.08E-10	59.7
2.4E+07	1.08E-10	25.8
2.4E+07	4.28E-07	51.2
2.4E+07	0.68	33.1
2.1E+07	7.83E-31	119
2.2E+07	6.26E-21	90.9
2E+07	1.1	32.3
3.8E+07	1.36E-30	118
1.3E+07	3.48E-29	114
1.3E+07	1.81E-27	109
1.5E+07	2.80E-20	89
1.5E+07	3.69E-17	69.7
1.5E+07	3.69E-17	37.4
2E+07	0.01	30
2E+07	0.01	27.3
1.6E+07	4.31E-20	71.2
1.6E+07	4.31E-20	40.8
1.6E+07	4.31E-20	24.6

ric histone H3] [protein_id=AUN88469.1] [location=1..456] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

3040541	6.96E-32	122
3055218	1.05E-31	121
3056575	1.60E-31	121
3046571	2.00E-31	120
1645710	1.02E-30	119
2625816	7.16E-32	122
2.1E+07	1.36E-31	121
2.4E+07	4.71E-11	59.7
2.4E+07	4.71E-11	26.9

2.4E+07	4.16E-07	51.2
2.4E+07	2.5	31.2
2.1E+07	4.92E-31	119
2.2E+07	8.22E-22	93.6
2E+07	6.6	30
3.8E+07	5.42E-31	119
1.3E+07	5.55E-29	114
1.3E+07	3.24E-27	108
1.5E+07	2.40E-20	89.4
1.5E+07	1.12E-16	68.2
1.5E+07	1.12E-16	37.4
2E+07	0.01	30
2E+07	0.01	27.3
1.6E+07	4.59E-20	71.2
1.6E+07	4.59E-20	40.8
1.6E+07	4.59E-20	24.6

eric histone H3] [protein_id=AUN88463.1] [location=1..462] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

2625816	7.96E-31	119
3040541	8.85E-31	119
3055218	1.28E-30	118
3056575	1.60E-30	118
3046571	2.10E-30	118
1645710	3.86E-30	117
2.1E+07	1.22E-30	119
2.4E+07	4.25E-10	56.2
2.4E+07	4.25E-10	26.9
2.4E+07	3.41E-08	54.3
2.4E+07	0.91	32.7
2.1E+07	4.55E-30	117
2.2E+07	1.22E-20	90.1
3.8E+07	8.29E-30	116
1.3E+07	1.18E-27	110
1.3E+07	5.28E-26	105
1.5E+07	1.34E-19	87
1.5E+07	2.48E-17	73.6
1.5E+07	2.48E-17	34.3
2E+07	0.008	30
2E+07	0.008	27.7
1.6E+07	2.56E-19	71.6
1.6E+07	2.56E-19	37.4
1.6E+07	2.56E-19	24.6

rotein_id=ALK04343.1] [location=103..633] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

2625819	1.88E-22	96.3
3040544	2.49E-22	95.9
3055221	2.51E-22	95.9
3046574	2.90E-22	95.9
3056572	4.79E-22	95.1
1645713	5.70E-22	95.1
2.1E+07	4.52E-22	95.1
2.4E+07	9.45E-09	57
2.4E+07	2.3	32
3.8E+07	6.28E-22	94.7
2.1E+07	1.10E-21	94.4
2.2E+07	4.84E-14	72
1.3E+07	1.96E-21	93.6
1.3E+07	1.76E-19	87.8
1.5E+07	4.40E-10	60.8
1.5E+07	1.06E-07	53.9
2E+07	0.65	33.5
1.5E+07	2.8	31.6
1.5E+07	8.4	30.4
1.6E+07	9.97E-08	53.9
1.6E+07	2.6	32

rotein_id=ALK04341.1] [location=59..583] [gbkey=CDS]

, q. start, q. end, s. start, s. end, eval, bit score

3.8E+07	1.99E-27	110
1645713	5.60E-27	109
3056572	5.87E-27	109
3040544	8.16E-27	108
3055221	1.12E-26	108
3046574	1.68E-26	107
1.3E+07	6.99E-27	108
1.3E+07	4.59E-24	100
2.1E+07	7.34E-27	108
2.2E+07	1.53E-18	85.1
2.1E+07	8.64E-27	108
2.4E+07	4.77E-10	55.5
2.4E+07	4.77E-10	28.1
2.4E+07	0.027	37.7
2625819	8.73E-27	108
1.6E+07	8.11E-17	71.2

1.6E+07	8.11E-17	28.1
1.6E+07	8.11E-17	26.6
1.5E+07	4.10E-15	71.2
1.5E+07	4.10E-15	29.6
1.5E+07	7.02E-15	74.3

ic histone H3] [protein_id=BAO51832.1] [location=1..459] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

2625819	3.58E-30	117
3055221	4.92E-30	117
3040544	5.16E-30	117
3056572	2.08E-29	115
3046574	9.92E-27	107
1645713	1.94E-25	103
2.1E+07	1.07E-29	115
2.4E+07	3.57E-07	51.6
2.4E+07	0.22	34.7
2.1E+07	1.26E-28	113
2.2E+07	3.80E-16	77.4
3.8E+07	1.43E-28	112
1.3E+07	1.72E-21	92.4
1.3E+07	1.20E-19	87.4
1.5E+07	1.90E-11	63.9
1.5E+07	2.21E-07	52
1.5E+07	0.003	39.7
1.5E+07	0.71	33.1
1.6E+07	2.39E-07	52
1.6E+07	0.023	37.4
1.6E+07	0.61	33.1
4666601	0.66	33.1

13 HTR12] [protein_id=AAL86777.1] [location=1..531] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

2625819	1.21E-22	97.1
3040544	1.64E-22	96.7
3055221	1.90E-22	96.3
3046574	2.30E-22	96.3
3056572	2.64E-22	95.9
1645713	2.54E-21	93.2
3.8E+07	2.69E-22	95.9
2.1E+07	2.93E-22	95.9
2.4E+07	1.98E-08	55.8

2.4E+07	1.2	32.7
2.1E+07	5.38E-22	95.1
2.2E+07	3.39E-13	69.7
1.3E+07	2.26E-21	93.2
1.3E+07	1.48E-19	88.2
1.5E+07	6.21E-10	60.1
1.5E+07	2.90E-08	55.5
2E+07	0.35	34.3
1.6E+07	2.16E-08	55.8
1.6E+07	0.028	29.3
1.6E+07	0.028	26.9

i3 HTR12] [protein_id=AAL86775.1] [location=1..537] [gbkey=CDS]

, q. start, q. end, s. start, s. end, evaluate, bit score

3040544	1.99E-21	93.6
3055221	2.66E-21	93.2
3056572	2.79E-21	93.2
3046574	5.69E-21	92
1645713	6.90E-21	92
2625819	2.19E-21	93.6
3.8E+07	2.24E-21	93.2
2.1E+07	2.90E-21	93.2
2.4E+07	6.03E-07	51.6
2.4E+07	1.2	32.7
2.1E+07	5.80E-21	92
2.2E+07	3.87E-13	69.7
1.3E+07	2.29E-18	84.7
1.3E+07	5.57E-17	80.9
1.5E+07	1.97E-09	58.9
1.5E+07	3.20E-08	55.5
2E+07	0.74	33.5
1.6E+07	2.59E-08	55.5

i3 HTR12] [protein_id=AAL86776.1] [location=join(1..52,166..206,306..351,447..481,552..585]

, q. start, q. end, s. start, s. end, evaluate, bit score

2625819	1.20E-22	97.1
3040544	1.66E-22	96.7
3055221	1.74E-22	96.7
3046574	2.24E-22	96.3
3056572	2.35E-22	96.3
1645713	2.56E-21	93.2
3.8E+07	2.54E-22	95.9

2.1E+07	2.77E-22	95.9
2.4E+07	1.82E-08	55.8
2.4E+07	1.2	32.7
2.1E+07	5.33E-22	95.1
2.2E+07	5.16E-13	69.3
1.3E+07	2.11E-21	93.2
1.3E+07	1.42E-19	88.2
1.5E+07	8.58E-10	59.7
1.5E+07	2.85E-08	55.5
2E+07	0.34	34.7
1.6E+07	2.06E-08	55.8
1.6E+07	0.027	29.3
1.6E+07	0.027	26.9

OX=37682 GN=alphaCENH3 PE=2 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

2625816	1.34E-36	135
1.8E+07	0.62	32.7
1.4E+07	5.8	30
2.4E+07	7.1	29.6
3040541	2.12E-36	134
3055218	2.16E-36	134
3056575	2.51E-35	131
3046571	7.16E-32	121
1645710	5.22E-31	119
2.8E+07	3.5	30.8
1.6E+07	9.7	29.3
2.1E+07	6.22E-36	133
2.4E+07	1.47E-16	66.2
2.4E+07	1.47E-16	38.5
2.4E+07	3.01E-06	48.5
2.4E+07	0.007	38.5
2.4E+07	0.19	34.3
8282384	1.3	32
8334114	6.4	30
7739703	7.2	29.6
7092007	7.4	29.6
1.2E+07	7.8	29.6
2.1E+07	9.19E-35	130
2.2E+07	2.82E-21	91.7
6034982	2	31.6
1.6E+07	5.9	30
1.6E+07	5.9	30
3.8E+07	6.77E-34	127

1E+07	1	32.3
1.3E+07	8.15E-31	118
1.3E+07	2.49E-29	114
2.7E+07	6.4	30
1.6E+07	2.69E-18	70.1
1.6E+07	2.69E-18	32
1.6E+07	2.69E-18	28.5
2E+07	4	30.4
1.9E+07	7.2	29.6
1.5E+07	4.17E-17	79.7
1.5E+07	1.69E-15	67
1.5E+07	1.69E-15	34.3
2E+07	1.96E-05	36.6
2E+07	1.96E-05	30
1.5E+07	9.7	29.3
4633661	3.3	30.8
1.1E+07	3.8	30.4
1.2E+07	5	30.4
1.3E+07	6.6	30
7580759	9	29.6
1.3E+07	9.6	29.3
9325304	10	29.3

IS=Avena sativa OX=4498 GN=AsCENH3-2 PE=2 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

2625828	1.52E-32	124
3040553	1.84E-32	124
3055230	2.03E-32	124
3046583	4.52E-32	123
3056563	5.93E-32	122
1645722	3.69E-31	120
2.1E+07	4.70E-32	123
2.4E+07	1.13E-15	67.4
2.4E+07	1.13E-15	35
2.4E+07	7.03E-06	47.8
2.4E+07	3.11E-04	43.1
3.8E+07	1.13E-31	122
2.1E+07	3.19E-31	120
2.2E+07	3.73E-22	94.7
1.3E+07	3.42E-31	120
1.3E+07	2.09E-27	109
1.5E+07	8.46E-19	85.1
1.5E+07	4.96E-17	67.4
1.5E+07	4.96E-17	39.3

2E+07	0.17	35
1.5E+07	7	30
1.6E+07	8.84E-17	67.4
1.6E+07	8.84E-17	38.9
1.6E+07	5.6	30.4
1018019	1.1	32.7

OS=Avena sativa OX=4498 GN=AsCENH3-3 PE=2 SV=1

, q. start, q. end, s. start, s. end, evalue, bit score

2625828	1.21E-32	124
3040553	1.41E-32	124
3055230	1.66E-32	124
3046583	4.17E-32	123
3056563	4.77E-32	123
1645722	2.20E-31	121
2.1E+07	4.64E-32	123
2.4E+07	7.09E-17	71.6
2.4E+07	7.09E-17	34.7
2.4E+07	1.07E-05	47.4
2.4E+07	0.99	32.7
3.8E+07	9.04E-32	122
1.3E+07	1.98E-31	121
1.3E+07	1.78E-27	110
2.1E+07	2.81E-31	120
2.2E+07	5.10E-22	94.4
1.5E+07	2.55E-19	86.7
1.5E+07	6.45E-17	67.4
1.5E+07	6.45E-17	38.9
2E+07	0.037	37
1.5E+07	4.2	30.8
1.6E+07	1.16E-16	67
1.6E+07	1.16E-16	38.5
1.6E+07	3	31.2
1018019	0.82	33.1

les OX=4573 GN=betaCENH3 PE=2 SV=1

, q. start, q. end, s. start, s. end, evalue, bit score

2625816	2.08E-28	112
3040541	2.08E-28	112
3055218	2.84E-28	112
3056575	3.22E-28	112
1645710	4.43E-28	111

3046571	4.60E-28	111
2.1E+07	3.44E-28	111
2.4E+07	3.44E-10	60.1
2.4E+07	2.11E-08	55.1
2.4E+07	0.8	32.7
2.1E+07	1.02E-27	110
2.2E+07	1.69E-18	84
3.8E+07	1.59E-27	109
1.3E+07	8.08E-26	105
1.3E+07	2.46E-24	100
1.6E+07	8.50E-18	68.9
1.6E+07	8.50E-18	33.9
1.6E+07	8.50E-18	26.2
1.5E+07	6.45E-17	79.7
1.5E+07	1.31E-15	70.9
1.5E+07	1.31E-15	31.2
2E+07	0.019	31.6
2E+07	0.019	25

OS=Avena sativa OX=4498 GN=AsCENH3-1 PE=2 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

2625828	2.06E-34	129
8742463	3.2	31.2
3040553	2.65E-34	129
3055230	3.10E-34	129
3046583	6.28E-34	128
3056563	7.19E-34	128
1645722	3.38E-33	126
2.1E+07	5.43E-34	128
2.4E+07	1.06E-15	63.9
2.4E+07	1.06E-15	38.5
2.4E+07	7.03E-06	47.8
2.4E+07	3.27E-04	43.1
3.8E+07	7.47E-34	128
2.1E+07	1.37E-33	127
2.2E+07	5.63E-24	100
1.3E+07	1.30E-32	124
1.3E+07	3.23E-29	115
1.5E+07	1.71E-18	84.3
1.5E+07	3.06E-18	69.7
1.5E+07	3.06E-18	41.2
2E+07	1.87E-05	35
2E+07	1.87E-05	32
1.5E+07	5.6	30.4

1.6E+07	2.62E-18	69.7
1.6E+07	2.62E-18	41.6
1.6E+07	4.3	30.8

ent) OS=Luzula pilosa OX=223700 PE=2 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

3040553	2.63E-27	109
3056563	5.69E-27	108
3055230	8.70E-27	108
3046583	9.14E-27	108
1645722	6.31E-26	105
2625828	4.43E-27	109
2.1E+07	6.97E-27	108
2.4E+07	1.13E-11	62.4
2.4E+07	1.13E-11	26.6
2.4E+07	0.7	33.5
3.8E+07	7.46E-27	108
2.1E+07	3.06E-26	107
2.2E+07	6.97E-16	77
1.3E+07	5.10E-23	97.8
1.3E+07	4.02E-22	95.1
1.5E+07	1.65E-12	67.4
1.5E+07	8.05E-08	53.9
1.5E+07	0.001	41.6
2E+07	1.7	32.3
1.5E+07	9.1	30
1.6E+07	4.63E-08	54.7
1.6E+07	0.073	36.2
1.6E+07	7.3	30.4

ent) OS=Luzula pilosa OX=223700 PE=3 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

3056563	2.21E-30	118
1645722	2.39E-30	118
3040553	3.28E-30	118
3055230	1.18E-29	116
3046583	3.44E-29	115
3.8E+07	2.25E-30	118
1.3E+07	3.98E-30	117
1.3E+07	1.09E-26	108
2.1E+07	4.34E-30	117
2.2E+07	9.95E-20	88.2

2.1E+07	5.48E-30	117
2.4E+07	6.89E-15	63.5
2.4E+07	6.89E-15	36.2
2.4E+07	0.2	35
2625828	6.34E-30	117
1.5E+07	2.42E-18	84
1.5E+07	2.70E-16	68.6
1.5E+07	2.70E-16	36.2
2E+07	3.07E-04	35.8
2E+07	3.07E-04	27.3
1.6E+07	1.23E-15	69.7
1.6E+07	1.23E-15	32.7
1.6E+07	1.3	32.3
2.5E+07	4.7	30.8

ent) OS=Luzula sylvatica OX=59018 PE=2 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

3.8E+07	2.45E-28	112
4816907	8.5	30
3056563	4.86E-28	111
1645722	5.96E-28	111
3040553	6.56E-28	111
3055230	1.25E-27	110
3046583	2.31E-27	109
2.1E+07	5.36E-28	111
2.2E+07	8.13E-19	85.5
2625828	1.01E-27	110
2.1E+07	1.09E-27	110
2.4E+07	2.49E-13	63.5
2.4E+07	2.49E-13	31.2
2.4E+07	0.042	37
1.3E+07	2.44E-26	107
1.3E+07	1.75E-23	98.6
1.6E+07	4.27E-17	65.1
1.6E+07	4.27E-17	33.5
1.6E+07	4.27E-17	28.1
1.5E+07	5.67E-17	80.1
1.5E+07	7.53E-15	63.9
1.5E+07	7.53E-15	35.8
2E+07	0.19	35
7595156	9.6	29.6

ent) OS=Luzula alpinopilosa OX=630085 PE=3 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

3.8E+07	5.08E-31	120
1645722	6.22E-31	120
3056563	6.40E-31	120
3040553	8.98E-31	119
3055230	2.21E-30	118
3046583	5.75E-30	117
2.1E+07	1.27E-30	119
2.4E+07	1.80E-15	63.5
2.4E+07	1.80E-15	38.5
2.4E+07	0.076	36.2
2.1E+07	1.36E-30	119
2.2E+07	4.37E-21	92
2625828	2.14E-30	118
1.3E+07	9.51E-30	116
1.3E+07	3.26E-26	106
1.5E+07	8.31E-19	85.5
1.5E+07	1.21E-16	69.3
1.5E+07	1.21E-16	36.6
2E+07	0.77	33.1
1.6E+07	2.26E-16	70.5
1.6E+07	2.26E-16	34.3
1.6E+07	4.1	30.8

it) OS=Luzula luzuloides OX=318444 PE=3 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

3056563	1.93E-31	121
3040553	2.36E-31	121
1645722	4.14E-31	120
3055230	9.80E-31	119
3046583	5.53E-30	117
3.8E+07	2.71E-31	121
2.1E+07	7.12E-31	120
2.4E+07	2.03E-15	65.5
2.4E+07	2.03E-15	36.2
2.4E+07	0.2	35
2.1E+07	7.47E-31	120
2.2E+07	1.91E-20	90.1
2625828	7.92E-31	119
1.3E+07	9.61E-31	119
1.3E+07	2.67E-27	109
1.6E+07	2.52E-19	70.1
1.6E+07	2.52E-19	34.3

1.6E+07	2.52E-19	30
2.5E+07	3	31.6
2.3E+07	3.5	31.2
1.5E+07	4.11E-19	86.3
1.5E+07	5.88E-17	68.9
1.5E+07	5.88E-17	38.1
2E+07	1.01E-04	37.4
2E+07	1.01E-04	27.3

ent) OS=Luzula lutea OX=630107 PE=3 SV=1

, q. start, q. end, s. start, s. end, evaluate, bit score

3.8E+07	1.37E-30	119
1645722	2.89E-30	118
3056563	3.01E-30	118
3040553	3.10E-30	118
3055230	9.70E-30	116
3046583	2.81E-29	115
2.1E+07	4.18E-30	117
2.2E+07	7.64E-21	91.3
2.1E+07	4.97E-30	117
2.4E+07	4.48E-15	63.5
2.4E+07	4.48E-15	37
2.4E+07	0.14	35.4
2625828	8.97E-30	117
1.3E+07	3.25E-29	115
1.3E+07	7.71E-26	105
1.5E+07	3.03E-18	84
1.5E+07	4.71E-16	67.4
1.5E+07	4.71E-16	36.6
2E+07	0.003	33.5
2E+07	0.003	25.8
7595156	9	30
1.6E+07	1.03E-15	68.2
1.6E+07	1.03E-15	34.3
2.5E+07	3	31.6
1.6E+07	5.6	30.4

it) OS=Luzula arcuata OX=223686 PE=3 SV=1

, q. start, q. end, s. start, s. end, evaluate, bit score

3.8E+07	8.97E-30	117
1645722	1.27E-29	116
3056563	1.30E-29	116

3040553	1.59E-29	116
3055230	4.30E-29	115
3046583	9.41E-29	114
2.1E+07	2.29E-29	115
2.2E+07	8.29E-20	88.2
2.1E+07	2.63E-29	115
2.4E+07	1.32E-16	67.4
2.4E+07	1.32E-16	38.1
2.4E+07	0.25	34.7
2625828	3.61E-29	115
1.3E+07	3.50E-28	112
1.3E+07	8.31E-25	102
1.5E+07	1.43E-17	82
1.5E+07	1.46E-15	65.9
1.5E+07	1.46E-15	36.6
2E+07	1.4	32.3
7595156	8.3	30
1.6E+07	2.85E-15	66.6
1.6E+07	2.85E-15	34.3
1.6E+07	5.4	30.8

it) OS=Luzula wahlenbergii OX=223707 PE=3 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

3.8E+07	2.95E-30	118
3056563	3.87E-30	117
3040553	4.22E-30	117
1645722	4.65E-30	117
3055230	9.98E-30	116
3046583	1.70E-29	116
2.1E+07	7.69E-30	117
2.2E+07	3.22E-20	89.4
2625828	8.07E-30	117
2.1E+07	8.72E-30	117
2.4E+07	4.77E-16	65.5
2.4E+07	4.77E-16	38.1
2.4E+07	0.27	34.7
1.3E+07	6.09E-29	114
1.3E+07	1.65E-25	104
1.5E+07	5.72E-18	83.2
1.5E+07	6.47E-16	67
1.5E+07	6.47E-16	36.6
2E+07	0.002	33.1
2E+07	0.002	26.9
1.6E+07	1.19E-15	68.2

1.6E+07	1.19E-15	34.7
2.5E+07	2.8	31.6
1.6E+07	5.4	30.8
2.3E+07	7.5	30
1.9E+07	9.6	30

nt) OS=Luzula abyssinica OX=630083 PE=3 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

3.8E+07	8.72E-30	117
1645722	1.04E-29	116
3040553	1.72E-29	115
3056563	1.89E-29	115
3055230	5.97E-29	114
3046583	2.94E-28	112
2.1E+07	1.54E-29	116
2.2E+07	7.53E-20	88.6
2.1E+07	3.34E-29	115
2.4E+07	7.05E-14	63.9
2.4E+07	7.05E-14	32.7
2.4E+07	0.018	38.1
1.2E+07	8.7	30
2625828	4.38E-29	114
1.3E+07	5.31E-28	111
1.3E+07	6.40E-25	102
1.6E+07	2.69E-18	67.4
1.6E+07	2.69E-18	33.9
1.6E+07	2.69E-18	30
1.5E+07	1.04E-17	82.4
1.5E+07	1.71E-15	66.2
1.5E+07	1.71E-15	35.8
2E+07	0.049	36.6
7595156	7	30.4

ent) OS=Luzula abyssinica OX=630083 PE=2 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

3.8E+07	5.75E-34	128
3040553	1.30E-33	127
3056563	1.31E-33	127
3055230	3.65E-33	126
3046583	8.32E-33	125
1645722	2.46E-32	124
2625828	2.30E-33	127

2.1E+07	2.55E-33	126
2.4E+07	1.59E-16	65.1
2.4E+07	1.59E-16	40
2.4E+07	0.01	38.5
2.1E+07	8.00E-33	125
2.2E+07	7.27E-22	94
1.3E+07	7.13E-31	119
1.3E+07	3.99E-28	112
1.5E+07	5.46E-20	88.6
1.5E+07	5.32E-19	72.8
1.5E+07	5.32E-19	40.8
2E+07	0.66	33.1
2E+07	1.1	32.7
2.6E+07	1.8	32
1.6E+07	7.16E-18	72.8
1.6E+07	7.16E-18	37
1.7E+07	0.39	33.9

nt) OS=Luzula multiflora OX=178423 PE=2 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

3.8E+07	8.80E-34	128
3040553	1.75E-33	127
3056563	1.78E-33	127
3055230	5.42E-33	126
3046583	1.22E-32	125
1645722	3.15E-32	124
2625828	3.54E-33	126
2.1E+07	3.54E-33	126
2.4E+07	1.45E-16	65.1
2.4E+07	1.45E-16	40.4
2.4E+07	0.011	38.5
2.1E+07	9.88E-33	125
2.2E+07	1.33E-21	93.6
1.3E+07	2.75E-29	115
1.3E+07	3.20E-27	109
1.5E+07	7.63E-20	88.6
1.5E+07	5.64E-19	72.8
1.5E+07	5.64E-19	41.2
2E+07	0.9	33.1
2E+07	1.9	32
2.6E+07	2.2	32
1.6E+07	8.10E-18	72.8
1.6E+07	8.10E-18	37
1.7E+07	0.45	33.9

ent) OS=Luzula luzuloides OX=318444 PE=2 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

3.8E+07	7.84E-34	128
3056563	1.36E-33	127
3040553	1.60E-33	127
3055230	4.60E-33	126
3046583	1.21E-32	125
1645722	2.50E-32	124
2.1E+07	2.84E-33	127
2.4E+07	1.16E-16	65.5
2.4E+07	1.16E-16	40.4
2.4E+07	0.011	38.5
2625828	2.92E-33	127
2.1E+07	8.46E-33	125
2.2E+07	1.67E-21	93.2
1.3E+07	2.31E-29	115
1.3E+07	2.69E-27	109
1.5E+07	8.40E-20	88.2
1.5E+07	6.02E-19	72.4
1.5E+07	6.02E-19	41.2
2E+07	0.63	33.5
2E+07	1.6	32.3
2.6E+07	2.1	32
1.6E+07	7.65E-18	72.8
1.6E+07	7.65E-18	37
1.7E+07	0.5	33.9

ent) OS=Luzula canariensis OX=223688 PE=2 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

3.8E+07	4.21E-29	114
4816907	7.4	30
3056563	8.13E-29	114
1645722	8.87E-29	114
3040553	9.77E-29	114
3055230	1.81E-28	113
3046583	4.33E-28	112
2.1E+07	8.37E-29	114
2.2E+07	5.12E-19	85.9
2625828	1.54E-28	113
2.1E+07	1.63E-28	113
2.4E+07	1.02E-13	63.5

2.4E+07	1.02E-13	32.3
2.4E+07	0.023	37.7
1.2E+07	7.4	30
2715423	7.9	30
1.3E+07	1.04E-26	107
1.3E+07	5.70E-24	100
1.6E+07	1.25E-17	67
1.6E+07	1.25E-17	33.5
1.6E+07	1.25E-17	28.1
1.5E+07	1.27E-17	82
1.5E+07	2.12E-15	65.9
1.5E+07	2.12E-15	35.4
2E+07	0.21	34.7

ent) OS=Luzula canariensis OX=223688 PE=2 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

3.8E+07	9.41E-34	128
3040553	1.41E-33	128
3056563	1.66E-33	127
3055230	5.21E-33	126
3046583	1.29E-32	125
1645722	2.91E-32	124
2625828	3.47E-33	127
2.1E+07	3.64E-33	127
2.4E+07	1.34E-16	65.5
2.4E+07	1.34E-16	40.4
2.4E+07	0.012	38.5
2.1E+07	1.05E-32	125
2.2E+07	6.10E-21	91.7
1.3E+07	4.94E-30	117
1.3E+07	9.30E-28	111
1.5E+07	8.57E-20	88.6
1.5E+07	7.27E-19	72.8
1.5E+07	7.27E-19	40.8
2E+07	0.48	33.9
2E+07	2.5	31.6
2.6E+07	2.7	31.6
1.6E+07	1.17E-17	72.8
1.6E+07	1.17E-17	36.6
1.7E+07	2.4	32

it) OS=Luzula divulgata OX=223689 PE=2 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

3.8E+07	6.21E-34	129
3056563	1.27E-33	127
3040553	1.44E-33	127
3055230	4.92E-33	126
3046583	1.07E-32	125
1645722	3.61E-32	124
2.1E+07	2.55E-33	127
2.4E+07	2.15E-16	65.5
2.4E+07	2.15E-16	39.7
2.4E+07	0.011	38.5
2625828	2.68E-33	127
2.1E+07	7.61E-33	125
2.2E+07	3.51E-21	92.4
1.3E+07	1.10E-29	116
1.3E+07	7.64E-28	111
1.5E+07	3.23E-20	89.7
1.5E+07	6.43E-19	72.8
1.5E+07	6.43E-19	40.8
2E+07	1.33E-04	32.7
2E+07	1.33E-04	31.6
2.6E+07	3.3	31.2
1.6E+07	8.50E-18	72.8
1.6E+07	8.50E-18	37
1.7E+07	0.24	34.7

DX=4572 GN=betaCENH3 PE=2 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

3040541	2.81E-30	117
3055218	4.22E-30	117
3056575	7.85E-30	116
3046571	8.90E-30	116
1645710	1.52E-29	115
2625816	3.25E-30	117
2.1E+07	6.34E-30	116
2.4E+07	5.88E-10	55.5
2.4E+07	5.88E-10	26.9
2.4E+07	2.24E-08	55.1
2.4E+07	0.056	36.2
2.1E+07	1.50E-29	115
2.2E+07	2.47E-20	89.4
3.8E+07	3.38E-29	114
3E+07	7.8	30
1.3E+07	2.72E-27	108

1.3E+07	9.39E-26	104
1.6E+07	5.13E-19	71.2
1.6E+07	5.13E-19	37.7
1.6E+07	5.13E-19	24.3
1.5E+07	1.13E-17	81.6
1.5E+07	7.56E-17	71.6
1.5E+07	7.56E-17	34.3
2E+07	0.026	29.6
2E+07	0.026	26.2
1.8E+07	9.5	29.6

n marinum subsp. marinum OX=112516 GN=CENH3 PE=3 SV=1

, q. start, q. end, s. start, s. end, evalule, bit score

3040541	2.20E-28	109
3056575	2.57E-28	109
3055218	4.21E-28	108
3046571	6.21E-28	108
1645710	6.71E-28	108
2625816	2.86E-28	108
2.1E+07	3.54E-28	108
2.4E+07	4.06E-07	48.9
2.4E+07	6.70E-07	47
2.4E+07	6.70E-07	24.3
2.4E+07	0.78	31.2
2.1E+07	9.53E-28	107
2.2E+07	2.67E-21	89.4
3.8E+07	2.10E-26	103
3E+07	9.9	28.1
1.3E+07	6.66E-26	102
1.3E+07	1.39E-25	101
1.5E+07	1.39E-21	90.1
1.5E+07	1.52E-18	73.6
1.5E+07	1.52E-18	37.7
2E+07	7.1	28.5
1.6E+07	5.69E-19	71.2
1.6E+07	5.69E-19	41.2

V=1

, q. start, q. end, s. start, s. end, evalule, bit score

1645737	8.42E-16	75.5
3040568	9.45E-16	75.5
3046598	1.34E-15	75.1

3055245	1.49E-15	74.7
3056548	3.60E-15	73.6
2.1E+07	8.58E-16	75.5
2.4E+07	9.15E-14	63.2
2.4E+07	9.15E-14	32
2.1E+07	2.9	30.8
2625843	1.09E-15	75.1
1.4E+07	6.4	29.6
2.5E+07	9.9	29.3
2.1E+07	4.91E-15	73.2
2.2E+07	3.76E-08	53.5
3.8E+07	5.51E-15	73.2
1.3E+07	2.62E-14	71.2
1.3E+07	1.28E-12	66.2
1.6E+07	3.37E-07	34.7
1.6E+07	3.37E-07	28.9
1.6E+07	3.37E-07	27.7
2879986	0.45	33.1
2E+07	0.4	33.1

$v=1$

, q. start, q. end, s. start, s. end, eval, bit score

1.7E+07	4.25E-16	84
2.1E+07	7.32E-13	73.9
2.2E+07	8.91E-05	48.1
1.7E+07	0.027	40.4
2.2E+07	4.3	33.1
1.2E+07	9.2	32
2.6E+07	9.4	32
3.8E+07	2.18E-13	75.5
4E+07	3.7	33.5
2.5E+07	5	33.1
2625861	3.30E-13	75.1
1480291	5	33.1
3046616	3.42E-13	75.1
1645755	4.54E-13	74.7
3040586	4.92E-13	74.7
3055263	5.00E-13	74.7
3056530	6.88E-13	73.9
2.1E+07	7.86E-13	73.9
2.4E+07	2.11E-09	48.5
2.4E+07	2.11E-09	34.7
2.4E+07	0.003	43.1
1.3E+07	8.83E-10	64.3

1.3E+07	3.01E-08	59.3
1.6E+07	1.10E-05	41.2
1.6E+07	1.10E-05	24.3
1.6E+07	1.10E-05	23.5
30571	1.7	34.7
2.7E+07	2.5	33.9
1.5E+07	4.13E-04	39.7
1.5E+07	4.13E-04	25.4
1.5E+07	0.004	43.1
1.7E+07	4	33.1
1.8E+07	1.4	34.7
1103744	6.4	32.7

4522 GN=CenH3 PE=4 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

3040787	2.70E-04	40.4
3055464	3.55E-04	40
3046817	3.69E-04	40
3056329	4.96E-04	39.7
1645956	0.001	38.5
2626062	2.92E-04	40
1.3E+07	3.03E-04	40
1.3E+07	0.032	34.3
2.1E+07	3.62E-04	40
2.4E+07	0.009	35.8
2.4E+07	1.4	29.6
3.8E+07	5.05E-04	39.7
2.1E+07	6.15E-04	39.3
2.2E+07	0.12	32.7
2E+07	0.014	35.4
1.5E+07	0.091	33.1
1.6E+07	0.088	33.1

388680 GN=CenH3 PE=4 SV=1

OX=1104334 GN=CenH3 PE=4 SV=1

OX=1104331 GN=CenH3 PE=4 SV=1

DX=860324 GN=CenH3.M2 PE=4 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

2.4E+07	5	27.3
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:1104336 GN=CenH3 PE=4 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

2626062	0.24	30
3055464	0.26	29.6
3046817	0.29	29.6
1645956	1.2	28.1
3056329	2.3	27.3
3040787	4	26.6
3.8E+07	0.49	28.9
2.4E+07	0.66	28.5
2.1E+07	0.71	28.5
2E+07	1.7	27.7
1.3E+07	2.5	26.9
2.1E+07	2.9	26.9

/=1

, q. start, q. end, s. start, s. end, eval, bit score

1.6E+07	3.4	27.3
5339458	5.5	26.6
1.5E+07	7.3	26.2
1.3E+07	7.5	26.2
1.9E+07	8.6	26.2
5362919	9.8	26.2

254778 GN=CenH3 PE=4 SV=1

=860324 GN=CenH3 PE=4 SV=1

, q. start, q. end, s. start, s. end, eval, bit score

2.4E+07	0.007	35
2.1E+07	0.022	33.5
3.8E+07	0.018	33.5

7848467	1.6	28.1
6071617	7.4	26.2
3040787	0.022	33.5
3056329	0.023	33.5
3046817	0.027	33.1
3055464	0.03	33.1
1645956	0.062	32
2626062	0.027	33.1
2.1E+07	0.042	32.7
2.2E+07	3.6	27.3
1.3E+07	0.086	31.6
2E+07	0.19	30.8
1.5E+07	3.2	27.3
2.3E+07	5.6	26.6
2.1E+07	6.6	26.6
1.6E+07	7.7	26.2
4467769	8.6	26.2

i OX=669780 GN=CenH3 PE=4 SV=1

=1

, q. start, q. end, s. start, s. end, evalue, bit score

2.4E+07	1.4	28.9
1.4E+07	2.3	28.1
1.8E+07	5.4	27.3

SV=1

, q. start, q. end, s. start, s. end, evalue, bit score

2.2E+07	0.17	32.3
2973054	1.9	29.3
2.6E+07	3.2	28.9
8612549	7.7	27.7
2.9E+07	4.4	28.5
5183134	7.2	27.7

iV=1

SV=1

, q. start, q. end, s. start, s. end, evaluate, bit score

1.3E+07	0.56	30.4
1.6E+07	4.4	28.1
2.1E+07	5.2	27.7
7780327	6.3	27.7
1.2E+07	9.1	26.9
2815256	9.3	26.9

¡V=1

, q. start, q. end, s. start, s. end, evaluate, bit score

3056443	2.20E-06	44.3
3040649	0.008	34.3
3046679	0.009	34.3
3055326	0.055	32
1645812	0.24	30.4
2.4E+07	3.35E-05	41.2
2.1E+07	0.73	28.9
1.6E+07	0.001	37
1.3E+07	0.002	36.2
1.3E+07	0.011	33.9
2.2E+07	0.005	35
2.1E+07	0.12	31.2
1.5E+07	0.13	30.8
1.5E+07	0.34	29.6
3.8E+07	0.56	29.3
3.3E+07	8	25.8
2625921	0.83	28.9

¡V=1

√=1

¡V=1

, q. start, q. end, s. start, s. end, evaluate, bit score

1.2E+07	1.3	27.7
2.1E+07	1.4	27.3

1.7E+07	6.3	25.8
2.1E+07	4.4	26.2
2.8E+07	5	25.8
1.8E+07	5.2	25.8
5525657	5.6	25.8

595,665..780,920..997,1099..1174,1255..1310)] [gbkey=CDS]

5,675..787,1207..1284,1416..1491,1632..1687)) [gbkey=CDS]