

1 UproC

1.1 UproC Ausgabe

1	2,>gi 62288991 ref NC_006932.1 ,103,5,2,33,PF01926,4.196
2	15,>gi 62288991 ref NC_006932.1 ,103,6,3,32,PF03734,1.415
3	16,>gi 62288991 ref NC_006932.1 ,103,4,1,33,PF00702,4.437
4	25,>gi 62288991 ref NC_006932.1 ,103,6,3,32,PF02092,3.647
5	36,>gi 62288991 ref NC_006932.1 ,103,4,1,33,PF06325,4.669
6	44,>gi 62288991 ref NC_006932.1 ,103,3,3,33,PF01546,1.606
7	47,>gi 62288991 ref NC_006932.1 ,103,1,1,33,PF01464,2.918
8	53,>gi 62288991 ref NC_006932.1 ,103,6,3,32,PF02784,4.455
9	55,>gi 62288991 ref NC_006932.1 ,103,2,2,33,PF00639,4.550
10	69,>gi 62288991 ref NC_006932.1 ,103,5,2,33,PF00581,4.535
11	70,>gi 62288991 ref NC_006932.1 ,103,6,3,32,PF00005,4.076
12	75,>gi 62288991 ref NC_006932.1 ,103,6,3,32,PF01502,4.345
13	77,>gi 62288991 ref NC_006932.1 ,103,3,3,33,PF02021,4.339
14	102,>gi 62288991 ref NC_006932.1 ,103,3,3,33,PF00290,4.621
15	112,>gi 62288991 ref NC_006932.1 ,103,2,2,33,PF01553,3.695
16	125,>gi 62288991 ref NC_006932.1 ,103,1,1,33,PF05698,3.765
17	144,>gi 62288991 ref NC_006932.1 ,103,1,1,33,PF02463,4.570
18	145,>gi 62288991 ref NC_006932.1 ,103,3,3,32,PF00326,4.299
19	154,>gi 62288991 ref NC_006932.1 ,103,1,1,33,PF01923,4.310
20	155,>gi 62288991 ref NC_006932.1 ,103,4,1,33,PF06516,3.395
21	170,>gi 62288991 ref NC_006932.1 ,103,6,3,32,PF01653,4.314
22	174,>gi 62288991 ref NC_006932.1 ,103,1,1,33,PF00562,3.479
23	175,>gi 62288991 ref NC_006932.1 ,103,2,2,33,PF02852,4.501
24	179,>gi 62288991 ref NC_006932.1 ,103,1,1,33,PF02705,4.365
25	191,>gi 62288991 ref NC_006932.1 ,103,5,2,33,PF05187,4.556
26	195,>gi 62288991 ref NC_006932.1 ,103,3,3,32,PF00009,0.576
27	196,>gi 62288991 ref NC_006932.1 ,103,6,3,32,PF00291,4.257
28	216,>gi 62288991 ref NC_006932.1 ,103,1,1,33,PF00892,2.937
29	220,>gi 62288991 ref NC_006932.1 ,103,1,1,33,PF00501,3.530

1.2 Beschreibung der Ausgabe

1. sequence number
2. sequence header up to the first white space
3. sequence length
4. ORF-frame (1-6)
5. ORF index in the sequence (starting with 1)
6. ORF length
7. predicted protein family
8. classification score

ORF = open reading frame

2 Diamond

2.1 Diamond Ausgabe

1	-q1 62288991 ref NC_006932.1	sp B25676 RL2_BRUA1 100.0	33	0	0	100	2	120	152	2.3e-12	71.2
2	-q1 62288991 ref NC_006932.1	sp Q2YM06 RL2_BRUA2 100.0	33	0	0	100	2	120	152	2.3e-12	71.2
3	-q1 62288991 ref NC_006932.1	sp Q57CR1 RL2_BRUA3 100.0	33	0	0	100	2	120	152	2.3e-12	71.2
4	-q1 62288991 ref NC_006932.1	sp A9M5P7 RL2_BRUC2 100.0	33	0	0	100	2	120	152	2.3e-12	71.2
5	-q1 62288991 ref NC_006932.1	sp CORJ18 RL2_BRUMB 100.0	33	0	0	100	2	120	152	2.3e-12	71.2
6	-q1 62288991 ref NC_006932.1	sp BOCH29 RL2_BRUST 100.0	33	0	0	100	2	120	152	2.3e-12	71.2
7	-q1 62288991 ref NC_006932.1	sp Q6G079 RL2_BRUSJ 100.0	33	0	0	100	2	120	152	2.3e-12	71.2
8	-q1 62288991 ref NC_006932.1	sp A6XOC1 RL2_OCHA4 93.9	33	2	0	100	2	120	152	6.7e-12	69.7
9	-q1 62288991 ref NC_006932.1	sp Q8YH7 RL2_BRUME 97.0	33	1	0	100	2	120	152	1.1e-11	68.9
10	-q1 62288991 ref NC_006932.1	sp A5VR03 RL2_BRUJ2 97.0	33	1	0	100	2	120	152	1.1e-11	68.9
11	-q1 62288991 ref NC_006932.1	sp Q11HQ5 RL2_CHESE 90.6	32	3	0	97	2	122	153	7.4e-11	66.2
12	-q1 62288991 ref NC_006932.1	sp Q98V54 RL2_RHIL0 87.5	32	4	0	97	2	121	152	9.7e-11	65.9
13	-q1 62288991 ref NC_006932.1	sp Q6FZC5 RL2_BAROU 84.8	33	5	0	100	2	120	152	2.2e-10	64.7
14	-q1 62288991 ref NC_006932.1	sp A9IW24 RL2_BART1 84.8	33	5	0	100	2	120	152	2.2e-10	64.7
15	-q1 62288991 ref NC_006932.1	sp Q6G2W8 RL2_BARHE 81.8	33	6	0	100	2	120	152	2.8e-10	64.3
16	-q1 62288991 ref NC_006932.1	sp A1B030 RL2_PARDP 87.1	31	4	0	94	2	122	152	4.8e-10	63.5
17	-q1 62288991 ref NC_006932.1	sp A1U5L7 RL2_BARKK 84.4	32	5	0	97	2	121	152	6.3e-10	63.2
18	-q1 62288991 ref NC_006932.1	sp A7HWR4 RL2_PARL1 83.9	31	5	0	94	2	122	152	1.1e-09	62.4
19	-q1 62288991 ref NC_006932.1	sp B6IRQ9 RL2_RHOCS 87.1	31	4	0	94	2	123	153	1.1e-09	62.4
20	-q1 62288991 ref NC_006932.1	sp AOL5X6 RL2_MAGMM 81.8	33	6	0	100	2	123	155	1.4e-09	62.0
21	-q1 62288991 ref NC_006932.1	sp Q2RQW3 RL2_RHORI 86.7	30	4	0	91	2	123	152	1.4e-09	62.0
22	-q1 62288991 ref NC_006932.1	sp A3PGL4 RL2_RHOS1 86.7	30	4	0	91	2	123	152	1.4e-09	62.0
23	-q1 62288991 ref NC_006932.1	sp Q3J5R9 RL2_RHOS4 86.7	30	4	0	91	2	123	152	1.4e-09	62.0
24	-q1 62288991 ref NC_006932.1	sp A4WVK5 RL2_RHOSS 86.7	30	4	0	91	2	123	152	1.4e-09	62.0
25	-q1 62288991 ref NC_006932.1	sp B9KL94 RL2_RHOSK 86.7	30	4	0	91	2	123	152	1.4e-09	62.0
26	-q1 62288991 ref NC_006932.1	sp Q9K9H0 ACEA_BACHD 78.8	33	7	0	2	100	344	376	2.2e-07	54.7
27	-q1 62288991 ref NC_006932.1	sp PQASH4 ACEA1_MYCB0 68.8	32	10	0	2	97	347	378	9.4e-06	49.3
28	-q1 62288991 ref NC_006932.1	sp H8EVV4 ACEA1_MYCTE 68.8	32	10	0	2	97	347	378	9.4e-06	49.3
29	-q1 62288991 ref NC_006932.1	sp P9WKK6 ACEA1_MYCTO 68.8	32	10	0	2	97	347	378	9.4e-06	49.3
30	-q1 62288991 ref NC_006932.1	sp P9WKK7 ACEA1_MYCTU 68.8	32	10	0	2	97	347	378	9.4e-06	49.3
31	-q1 62288991 ref NC_006932.1	sp P41554 ACEA1_PROK-A 62.5	32	12	0	2	97	347	378	7.9e-05	46.2
32	-q1 62288991 ref NC_006932.1	sp Q8RQW6 ACEA1_COREF 64.5	31	11	0	2	94	349	379	3.0e-04	44.3
33	-q1 62288991 ref NC_006932.1	sp P42449 ACEA1_COREL 61.3	31	12	0	2	94	349	379	5.2e-04	43.5
34	-q1 62288991 ref NC_006932.1	sp B25877 0001_BRUA1 100.0	32	0	0	98	3	325	356	1.7e-12	71.6

2.2 Beschreibung der Ausgabe

1. query seq-ID
2. subject seq-ID
3. percentage of identical matches
4. length of alignment
5. number of mismatches
6. number of gap openings
7. start of alignment in query
8. end of alignment in query
9. start of alignment in subject
10. end of alignment in subject
11. e-value
12. bit-score

3 Lambda

3.1 Lambda Ausgabe

1	>gl 62288991 ref NC_006932.1	sp Q8FYF7 0001_BRUSU	100.00	32	0	0	98	3	325	356	1e-12	71.6
2	>gl 62288991 ref NC_006932.1	sp B0CIS7 0001_BRUSI	100.00	32	0	0	98	3	325	356	1e-12	71.6
3	>gl 62288991 ref NC_006932.1	sp A5V5Q0 0001_BRU02	100.00	32	0	0	98	3	325	356	1e-12	71.6
4	>gl 62288991 ref NC_006932.1	sp Q9VJE4 0001_BRUME	100.00	32	0	0	98	3	325	356	1e-12	71.6
5	>gl 62288991 ref NC_006932.1	sp C0RF58 0001_BRUMB	100.00	32	0	0	98	3	325	356	1e-12	71.6
6	>gl 62288991 ref NC_006932.1	sp A9M8Q9 0001_BRUC2	100.00	32	0	0	98	3	325	356	1e-12	71.6
7	>gl 62288991 ref NC_006932.1	sp Q57AX5 0001_BRUAB	100.00	32	0	0	98	3	325	356	1e-12	71.6
8	>gl 62288991 ref NC_006932.1	sp Q2YLS2 0001_BRUA2	100.00	32	0	0	98	3	325	356	1e-12	71.6
9	>gl 62288991 ref NC_006932.1	sp S2S877 0001_BRUA1	100.00	32	0	0	98	3	325	356	1e-12	71.6
10	>gl 62288991 ref NC_006932.1	sp A6WPF0 0001_OCHM4	96.88	32	1	0	98	3	321	352	5e-12	69.7
11	>gl 62288991 ref NC_006932.1	sp Q4UK18 0001_RICFE	63.33	30	11	0	95	6	323	352	0.002	41.2
12	>gl 62288991 ref NC_006932.1	sp Q92J42 0001_RICCN	58.06	31	13	0	98	6	273	303	0.003	40.4
13	>gl 62288991 ref NC_006932.1	sp P20967 0001_YEAST	67.86	28	8	1	98	15	326	352	0.006	39.7
14	>gl 62288991 ref NC_006932.1	sp Q1RH14 0001_RICBR	66.67	27	9	0	95	15	272	298	0.007	39.3
15	>gl 62288991 ref NC_006932.1	sp Q68X17 0001_RICTY	59.26	27	11	0	95	15	275	301	0.048	36.6
16	>gl 62288991 ref NC_006932.1	sp Q9ZD73 Y47L_RICPR	62.07	29	11	0	91	5	104	132	4e-05	47.0
17	>gl 62288991 ref NC_006932.1	sp M4MR97 RNJ_S1NM2	75.76	33	8	0	2	100	236	268	8e-07	52.4
18	>gl 62288991 ref NC_006932.1	sp Q34992 OPUCA_BACSU	58.62	29	12	0	96	10	208	236	0.003	40.8
19	>gl 62288991 ref NC_006932.1	sp Q45460 OPUBA_BACSU	51.72	29	14	0	96	10	208	236	0.021	37.7
20	>gl 62288991 ref NC_006932.1	sp Q5L705 POTA_RUEPO	50.00	30	15	0	99	10	218	247	0.048	36.6
21	>gl 62288991 ref NC_006932.1	sp Q8ZTL6 POTA_NITEU	46.67	30	16	0	99	10	205	234	0.048	36.6
22	>gl 62288991 ref NC_006932.1	sp Q8RI39 POTA_FUSNN	46.67	30	16	0	99	10	207	236	0.062	36.2
23	>gl 62288991 ref NC_006932.1	sp P47433 Y187_MYCGE	53.57	28	13	0	93	10	441	468	0.081	35.8
24	>gl 62288991 ref NC_006932.1	sp Q83658 POTA_TREPA	50.00	30	15	0	99	10	211	240	0.081	35.8
25	>gl 62288991 ref NC_006932.1	sp Q9X5X3 ATCU_S1NMW	87.88	33	4	0	99	1	656	688	3e-09	60.5
26	>gl 62288991 ref NC_006932.1	sp P58342 ATCU2_RHIME	90.91	33	3	0	99	1	656	688	4e-09	60.1
27	>gl 62288991 ref NC_006932.1	sp P58341 ATCU1_RHIME	87.88	33	4	0	99	1	655	687	3e-08	57.4
28	>gl 62288991 ref NC_006932.1	sp Q8NUQ9 COPA_STAAM	63.64	33	12	0	99	1	632	664	9e-06	48.9

3.2 Beschreibung der Ausgabe

1. query seq-ID
2. subject seq-ID
3. percentage of identical matches
4. length of alignment
5. number of mismatches
6. number of gap openings
7. start of alignment in query
8. end of alignment in query
9. start of alignment in subject
10. end of alignment in subject
11. e-value
12. bit-score

4 Vergleich

Lambda und Diamond stimmen in Ausgaben ueberein. UproC unterscheidet sich deutlich in dem was ausgegeben wird -> kein Bezug auf die Vergleichssequenz.