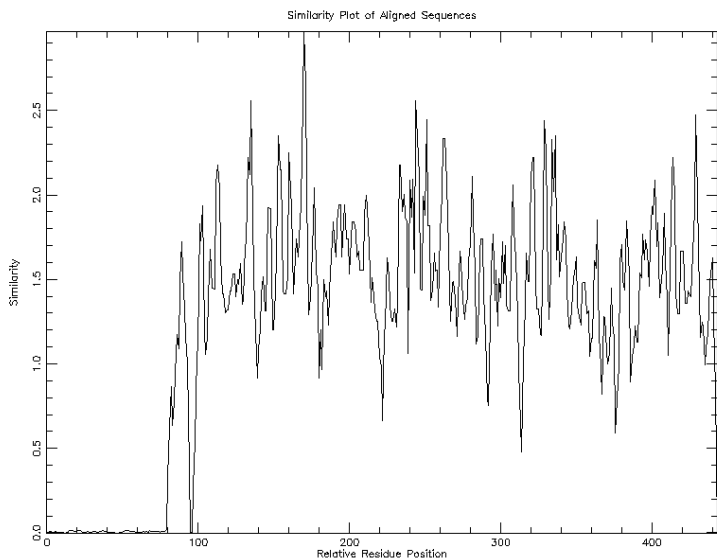


query: glucose-6-phosphatase[protein] AND aves[Organism]

96 sequences found96 sequences used for furter analysis. They are saved in con\_an\_seq\_out.fasta

Similarity plot of Aligned Sequences of glucose-6-phosphatase in aves



BlastP results:

QueryID	SubjectID	%Identity	Alignment_Len	Mismatches	GapOpenings	Q_start	Q_end	S_Start	S_end	E-val
XP_014740911.1	P35575.2	69.468	357	108	1	1	357	1	356	0.0 527
XP_014740911.1	Q19KA1.1	68.627	357	111	1	1	357	1	356	0.0 527
XP_014740911.1	Q29RU6.1	69.274	358	109	1	1	358	1	357	0.0 524
XP_014740911.1	O19133.1	67.507	357	115	1	1	357	1	356	0.0 520
XP_014740911.1	P35576.2	66.667	357	118	1	1	357	1	356	6.90e-175 493
XP_014740911.1	P43428.1	66.947	357	117	1	1	357	1	356	2.86e-167 473
XP_014740911.1	Q9Z186.1	52.260	354	168	1	5	357	1	354	1.53e-135 393
XP_014740911.1	Q9NQR9.1	53.803	355	161	2	5	357	1	354	2.68e-132 384
XP_014740911.1	O42153.1	55.241	353	151	4	5	355	1	348	1.89e-122 359
XP_014740911.1	O42154.1	55.755	278	116	4	80	355	1	273	7.66e-93 281

XP\_014740911.1 A1A5Z0.1 38.701 354 199 7 5 356 1 338 1.97e-68 221

XP\_014740911.1 Q9BUM1.2 35.838 346 208 6 1 346 1 332 7.54e-65 212

XP\_014740911.1 Q6NSQ9.1 34.530 362 210 10 1 357 1 340 4.90e-63 207

XP\_014740911.1 Q6AZ83.1 35.143 350 211 7 1 349 1 335 5.11e-63 207

XP\_014740911.1 Q148G2.1 35.097 359 212 9 1 356 1 341 1.33e-62 206

KAF1561075.1 Q19KA1.1 68.994 358 110 1 1 358 1 357 0.0 534

KAF1561075.1 P35575.2 69.274 358 109 1 1 358 1 357 0.0 532

KAF1561075.1 O19133.1 68.156 358 113 1 1 358 1 357 0.0 529

KAF1561075.1 Q29RU6.1 69.553 358 108 1 1 358 1 357 0.0 527

KAF1561075.1 P35576.2 66.760 358 118 1 1 358 1 357 1.32e-177 499

KAF1561075.1 P43428.1 67.318 358 116 1 1 358 1 357 2.25e-169 479

KAF1561075.1 Q9Z186.1 53.955 354 162 1 5 357 1 354 2.22e-142 410

KAF1561075.1 Q9NQR9.1 55.085 354 158 1 5 357 1 354 3.57e-140 404

KAF1561075.1 O42153.1 54.391 353 154 4 5 355 1 348 3.24e-121 356

KAF1561075.1 O42154.1 55.036 278 118 4 80 355 1 273 5.14e-92 279

KAF1561075.1 A1A5Z0.1 38.418 354 201 5 5 356 1 339 1.38e-68 221

KAF1561075.1 Q9BUM1.2 36.313 358 213 8 1 358 1 343 1.70e-66 216

KAF1561075.1 Q148G2.1 35.754 358 215 7 1 358 1 343 1.40e-65 214

KAF1561075.1 Q6NSQ9.1 36.134 357 211 8 1 357 1 340 1.50e-64 211

KAF1561075.1 Q6AZ83.1 36.544 353 210 7 1 353 1 339 1.14e-63 209

PKU41280.1 Q19KA1.1 69.274 358 109 1 1 358 1 357 0.0 539

PKU41280.1 O19133.1 69.274 358 109 1 1 358 1 357 0.0 538

PKU41280.1 P35575.2 69.553 358 108 1 1 358 1 357 0.0 538

PKU41280.1 Q29RU6.1 69.832 358 107 1 1 358 1 357 0.0 534

PKU41280.1 P35576.2 67.039 358 117 1 1 358 1 357 1.16e-178 502

PKU41280.1 P43428.1 66.760 358 118 1 1 358 1 357 2.47e-168 476

PKU41280.1 Q9Z186.1 54.520 354 160 1 5 357 1 354 1.87e-145 418

PKU41280.1 Q9NQR9.1 55.650 354 156 1 5 357 1 354 1.21e-142 410

PKU41280.1 O42153.1 54.958 353 152 4 5 355 1 348 2.98e-122 359

PKU41280.1 O42154.1 55.396 278 117 4 80 355 1 273 2.08e-92 280

PKU41280.1 A1A5Z0.1 38.655 357 196 8 5 356 1 339 6.57e-68 219

PKU41280.1 Q9BUM1.2 36.901 355 211 9 5 358 1 343 1.76e-66 216

PKU41280.1 Q148G2.1 36.158 354 215 6 5 358 1 343 1.73e-65 213

PKU41280.1 Q6NSQ9.1 36.261 353 212 7 5 357 1 340 2.16e-64 211

PKU41280.1 Q6AZ83.1 36.857 350 209 7 5 353 1 339 6.11e-64 209

XP\_026720573.1 Q19KA1.1 67.507 357 115 1 62 417 1 357 0.0 523

XP\_026720573.1 P35575.2 67.507 357 115 1 62 417 1 357 0.0 519

XP\_026720573.1 Q29RU6.1 67.606 355 114 1 62 415 1 355 0.0 516

XP\_026720573.1 O19133.1 66.106 357 120 1 62 417 1 357 0.0 513

XP\_026720573.1 P35576.2 66.387 357 119 1 62 417 1 357 2.65e-175 496

XP\_026720573.1 P43428.1 66.667 357 118 1 62 417 1 357 3.05e-167 476

XP\_026720573.1 Q9Z186.1 54.391 353 158 1 66 415 1 353 1.56e-139 405

XP\_026720573.1 Q9NQR9.1 56.780 354 150 2 66 416 1 354 1.54e-138 403

XP\_026720573.1 O42153.1 55.056 356 152 5 66 417 1 352 8.84e-124 365

XP\_026720573.1 O42154.1 55.516 281 117 5 141 417 1 277 3.46e-93 284

XP\_026720573.1 Q9BUM1.2 37.960 353 205 8 62 413 1 340 4.35e-69 225

XP\_026720573.1 A1A5Z0.1 38.352 352 202 5 66 415 1 339 2.61e-68 223

XP\_026720573.1 Q148G2.1 37.784 352 207 6 62 413 1 340 5.75e-67 219

XP\_026720573.1 Q6NSQ9.1 37.249 349 203 8 62 408 1 335 1.67e-65 216

XP\_026720573.1 Q6AZ83.1 37.110 353 208 7 62 413 1 340 6.37e-65 214

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KAF1471003.1 O19133.1 68.436 358 112 1 1 358 1 357 0.0 532

KAF1471003.1 Q29RU6.1 69.832 358 107 1 1 358 1 357 0.0 530

KAF1471003.1 P35576.2 67.039 358 117 1 1 358 1 357 1.08e-178 502  
KAF1471003.1 P43428.1 67.318 358 116 1 1 358 1 357 2.37e-169 478  
KAF1471003.1 Q9Z186.1 53.955 354 162 1 5 357 1 354 1.60e-142 410  
KAF1471003.1 Q9NQR9.1 55.085 354 158 1 5 357 1 354 2.21e-140 405  
KAF1471003.1 O42153.1 54.391 353 154 4 5 355 1 348 2.91e-121 356  
KAF1471003.1 O42154.1 55.036 278 118 4 80 355 1 273 4.51e-92 279  
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KAF1471003.1 Q9BUM1.2 36.888 347 208 7 12 358 8 343 3.53e-66 215  
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OWK54800.1 Q19KA1.1 63.713 237 85 1 1 237 121 356 8.08e-109 320  
OWK54800.1 P35575.2 65.401 237 81 1 1 237 121 356 3.16e-108 318  
OWK54800.1 O19133.1 63.291 237 86 1 1 237 121 356 6.35e-108 318  
OWK54800.1 Q29RU6.1 63.713 237 85 1 1 237 121 356 2.22e-105 311  
OWK54800.1 P35576.2 61.603 237 90 1 1 237 121 356 7.44e-96 287  
OWK54800.1 P43428.1 62.869 237 87 1 1 237 121 356 4.99e-89 270  
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OWK54800.1 Q9NQR9.1 52.301 239 111 2 1 237 117 354 2.24e-78 242  
OWK54800.1 O42154.1 51.899 237 107 4 1 235 42 273 3.01e-66 209  
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OWK54800.1 Q9BUM1.2 33.051 236 143 8 1 233 116 339 1.68e-27 110  
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KFQ16131.1 Q9Z186.1 53.541 353 163 1 2 353 1 353 1.17e-143 413

KFQ16131.1 Q9NQR9.1 55.241 353 157 1 2 353 1 353 8.25e-141 406

KFQ16131.1 O42153.1 55.241 353 151 4 2 352 1 348 7.18e-124 363

KFQ16131.1 O42154.1 56.115 278 115 4 77 352 1 273 2.38e-95 287

KFQ16131.1 A1A5Z0.1 39.548 354 197 6 2 353 1 339 1.51e-72 231

KFQ16131.1 Q9BUM1.2 38.192 343 202 6 8 350 7 339 3.27e-68 220

KFQ16131.1 Q148G2.1 37.609 343 204 5 8 350 7 339 2.03e-66 216

KFQ16131.1 Q6NSQ9.1 37.647 340 202 6 7 346 6 335 8.40e-66 214

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XP\_021233644.1 P43428.1 67.598 358 115 1 75 432 1 357 1.05e-166 475

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XP\_021233644.1 O42153.1 55.807 353 149 4 79 429 1 348 4.59e-122 361

XP\_021233644.1 O42154.1 56.115 278 115 4 154 429 1 273 1.40e-91 281

XP\_021233644.1 A1A5Z0.1 38.920 352 202 5 79 430 1 339 2.81e-68 223

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XP\_021233644.1 Q148G2.1 36.443 343 208 6 85 427 7 339 6.13e-63 209

XP\_021233644.1 Q6NSQ9.1 35.312 337 208 5 84 420 6 332 1.45e-60 203

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XP\_005059732.1 P35576.2 67.598 358 114 2 1 358 1 356 1.08e-175 494

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XP\_032566992.1 P43428.1 67.787 357 114 1 1 357 1 356 1.25e-174 492

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XP\_032566992.1 O42153.1 54.674 353 153 4 5 355 1 348 1.96e-124 364

XP\_032566992.1 O42154.1 55.396 278 117 4 80 355 1 273 1.25e-95 288

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XP\_032566992.1 Q6AZ83.1 35.754 358 211 10 1 356 1 341 2.90e-63 207

XP\_032566992.1 Q148G2.1 35.112 356 216 8 1 356 1 341 4.04e-63 207

XP\_032566992.1 Q6NSQ9.1 34.648 355 215 9 1 354 1 339 1.97e-62 206

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KAF1584371.1 Q29RU6.1 70.112 358 106 1 1 358 1 357 0.0 530

KAF1584371.1 P35576.2 67.318 358 116 1 1 358 1 357 1.12e-178 502

KAF1584371.1 P43428.1 67.598 358 115 1 1 358 1 357 2.43e-169 478

KAF1584371.1 Q9Z186.1 53.955 354 162 1 5 357 1 354 2.92e-142 410

KAF1584371.1 Q9NQR9.1 55.085 354 158 1 5 357 1 354 4.25e-140 404

KAF1584371.1 O42153.1 54.391 353 154 4 5 355 1 348 4.60e-121 356

KAF1584371.1 O42154.1 55.036 278 118 4 80 355 1 273 7.27e-92 279

KAF1584371.1 A1A5Z0.1 38.418 354 201 5 5 356 1 339 1.60e-68 221

KAF1584371.1 Q9BUM1.2 36.888 347 208 7 12 358 8 343 2.82e-66 216

KAF1584371.1 Q148G2.1 36.311 347 210 6 12 358 8 343 2.96e-65 213

KAF1584371.1 Q6NSQ9.1 36.494 348 208 7 10 357 6 340 2.88e-64 210

KAF1584371.1 Q6AZ83.1 36.919 344 207 6 10 353 6 339 1.75e-63 208

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XP\_030321679.1 Q19KA1.1 67.507 357 115 1 1 357 1 356 0.0 528

XP\_030321679.1 P35575.2 67.227 357 116 1 1 357 1 356 0.0 523

XP\_030321679.1 Q29RU6.1 67.227 357 116 1 1 357 1 356 0.0 518

XP\_030321679.1 P35576.2 64.986 357 124 1 1 357 1 356 1.58e-173 489

XP\_030321679.1 P43428.1 65.266 357 123 1 1 357 1 356 4.43e-165 468

XP\_030321679.1 Q9Z186.1 55.650 354 156 1 5 357 1 354 1.99e-147 423

XP\_030321679.1 Q9NQR9.1 55.932 354 155 1 5 357 1 354 1.48e-143 413

XP\_030321679.1 O42153.1 54.674 353 153 4 5 355 1 348 1.26e-123 362

XP\_030321679.1 O42154.1 55.396 278 117 4 80 355 1 273 7.77e-95 286

XP\_030321679.1 A1A5Z0.1 37.326 359 197 8 5 356 1 338 1.36e-66 216

XP\_030321679.1 Q9BUM1.2 36.000 350 198 8 5 346 1 332 6.63e-65 212

XP\_030321679.1 Q148G2.1 35.860 343 208 6 5 346 1 332 4.08e-63 207

XP\_030321679.1 Q6NSQ9.1 33.611 360 212 7 5 357 1 340 8.46e-63 206

XP\_030321679.1 Q6AZ83.1 35.127 353 203 8 5 349 1 335 3.56e-61 202

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KFQ94573.1 P35575.2 70.170 352 104 1 2 353 5 355 0.0 529

KFQ94573.1 O19133.1 69.034 352 108 1 2 353 5 355 0.0 526

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KFQ94573.1 P35576.2 68.466 352 110 1 2 353 5 355 1.88e-178 501

KFQ94573.1 P43428.1 68.466 352 110 1 2 353 5 355 3.94e-169 478

KFQ94573.1 Q9Z186.1 55.241 353 157 1 2 353 1 353 3.00e-144 414

KFQ94573.1 Q9NQR9.1 56.091 353 154 1 2 353 1 353 7.80e-142 409

KFQ94573.1 O42153.1 54.674 353 153 4 2 352 1 348 2.16e-123 362

KFQ94573.1 O42154.1 55.755 278 116 4 77 352 1 273 1.01e-94 286

KFQ94573.1 A1A5Z0.1 39.266 354 198 5 2 353 1 339 3.63e-71 228

KFQ94573.1 Q9BUM1.2 37.536 349 208 6 2 350 1 339 1.93e-68 221

KFQ94573.1 Q148G2.1 37.822 349 207 6 2 350 1 339 2.78e-67 218

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KAF1487788.1 P35576.2 67.598 358 115 1 1 358 1 357 4.65e-180 506

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KAF1487788.1 Q9Z186.1 54.237 354 161 1 5 357 1 354 5.43e-143 412

KAF1487788.1 Q9NQR9.1 55.367 354 157 1 5 357 1 354 7.09e-141 406

KAF1487788.1 O42153.1 54.674 353 153 4 5 355 1 348 1.36e-122 360

KAF1487788.1 O42154.1 55.396 278 117 4 80 355 1 273 2.32e-93 283

KAF1487788.1 A1A5Z0.1 38.701 354 200 5 5 356 1 339 3.67e-69 223

KAF1487788.1 Q9BUM1.2 37.356 348 207 7 11 358 7 343 6.34e-68 220

KAF1487788.1 Q148G2.1 36.494 348 210 6 11 358 7 343 2.45e-66 216

KAF1487788.1 Q6NSQ9.1 36.782 348 207 7 10 357 6 340 1.38e-65 214

KAF1487788.1 Q6AZ83.1 37.209 344 206 6 10 353 6 339 9.65e-65 211

KFV54932.1 Q19KA1.1 70.201 349 103 1 1 349 8 355 0.0 532

KFV54932.1 O19133.1 69.628 349 105 1 1 349 8 355 0.0 529

KFV54932.1 P35575.2 69.914 349 104 1 1 349 8 355 0.0 526

KFV54932.1 Q29RU6.1 70.487 349 102 1 1 349 8 355 0.0 526

KFV54932.1 P35576.2 68.195 349 110 1 1 349 8 355 2.64e-178 501

KFV54932.1 P43428.1 68.195 349 110 1 1 349 8 355 1.29e-169 479

KFV54932.1 Q9NQR9.1 56.857 350 150 1 1 349 4 353 1.75e-142 410

KFV54932.1 Q9Z186.1 54.571 350 158 1 1 349 4 353 2.27e-142 410

KFV54932.1 O42153.1 54.000 350 154 4 1 348 4 348 8.37e-121 355

KFV54932.1 O42154.1 54.676 278 119 4 73 348 1 273 2.81e-93 282

KFV54932.1 Q9BUM1.2 37.901 343 203 6 4 346 7 339 2.62e-69 223

KFV54932.1 A1A5Z0.1 38.177 351 200 6 1 349 4 339 7.00e-68 219

KFV54932.1 Q148G2.1 38.192 343 202 6 4 346 7 339 1.26e-67 219

KFV54932.1 Q6NSQ9.1 37.647 340 202 6 3 342 6 335 3.54e-67 218

KFV54932.1 Q6AZ83.1 37.500 344 205 6 3 346 6 339 2.67e-66 215

XP\_025900367.1 Q19KA1.1 60.894 358 116 2 1 335 1 357 3.68e-165 467

XP\_025900367.1 O19133.1 60.615 358 117 2 1 335 1 357 1.35e-163 463  
XP\_025900367.1 P35576.2 60.615 358 117 2 1 335 1 357 2.38e-163 462  
XP\_025900367.1 Q29RU6.1 60.335 358 118 2 1 335 1 357 1.46e-161 458  
XP\_025900367.1 P35575.2 59.218 358 122 2 1 335 1 357 1.94e-159 452  
XP\_025900367.1 P43428.1 59.777 358 120 2 1 335 1 357 6.00e-154 439  
XP\_025900367.1 Q9Z186.1 50.425 353 151 2 5 333 1 353 3.97e-128 373  
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XP\_025900367.1 O42153.1 53.353 343 138 3 5 326 1 342 2.69e-120 353  
XP\_025900367.1 O42154.1 53.358 268 103 3 80 326 1 267 2.82e-91 276  
XP\_025900367.1 A1A5Z0.1 38.177 351 184 6 5 334 1 339 2.26e-67 217  
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XP\_025900367.1 Q148G2.1 35.608 337 188 5 5 320 1 329 1.07e-57 192  
XP\_025900367.1 Q6AZ83.1 34.957 349 196 6 5 331 1 340 3.43e-57 191  
XP\_025900367.1 Q6NSQ9.1 34.911 338 189 7 5 320 1 329 4.88e-57 191  
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XP\_031456423.1 Q19KA1.1 69.832 358 107 1 75 432 1 357 0.0 533  
XP\_031456423.1 Q29RU6.1 71.229 358 102 1 75 432 1 357 0.0 533  
XP\_031456423.1 O19133.1 69.553 358 108 1 75 432 1 357 0.0 531  
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XP\_031456423.1 Q9Z186.1 54.674 353 159 1 79 430 1 353 2.51e-144 418  
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XP\_031456423.1 O42153.1 55.807 353 149 3 79 429 1 348 2.43e-123 364  
XP\_031456423.1 O42154.1 56.115 278 115 3 154 429 1 273 2.32e-93 285  
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KFP28446.1 O42154.1 57.194 278 112 4 77 352 1 273 4.41e-98 294

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KAF4787459.1 O42154.1 56.115 278 115 4 80 355 1 273 1.50e-93 283

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KAF4787459.1 Q6AZ83.1 35.714 350 209 7 1 349 1 335 4.50e-65 213

KAF4787459.1 Q6NSQ9.1 35.180 361 209 10 1 357 1 340 1.56e-64 211

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KAF1604860.1 O42154.1 55.396 278 117 4 80 355 1 273 3.25e-92 280

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KAF1604860.1 Q6AZ83.1 36.919 344 207 6 10 353 6 339 2.19e-63 208

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XP\_009870532.1 P35576.2 66.935 248 77 2 1 248 1 243 1.49e-120 352

XP\_009870532.1 P35576.2 59.184 49 20 0 250 298 309 357 2.52e-11 67.0

XP\_009870532.1 P43428.1 66.129 248 79 2 1 248 1 243 1.02e-110 327

XP\_009870532.1 P43428.1 59.184 49 20 0 250 298 309 357 6.94e-11 65.5

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XP\_009870532.1 Q9NQR9.1 50.000 42 21 0 256 297 313 354 7.78e-06 50.1

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XP\_009870532.1 Q148G2.1 38.053 226 133 3 23 248 15 233 3.91e-43 153

XP\_009870532.1 Q6NSQ9.1 38.496 226 132 4 23 248 15 233 3.28e-42 151

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KFQ28029.1 Q9NQR9.1 55.807 353 155 1 2 353 1 353 1.95e-141 407

KFQ28029.1 O42153.1 56.091 353 148 4 2 352 1 348 9.06e-127 370

KFQ28029.1 O42154.1 56.475 278 114 4 77 352 1 273 4.41e-96 289

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KFQ28029.1 Q6AZ83.1 36.676 349 211 6 2 350 1 339 2.11e-64 211

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KAF1671963.1 O42153.1 54.674 353 153 4 5 355 1 348 1.36e-122 360

KAF1671963.1 O42154.1 55.396 278 117 4 80 355 1 273 2.32e-93 283

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