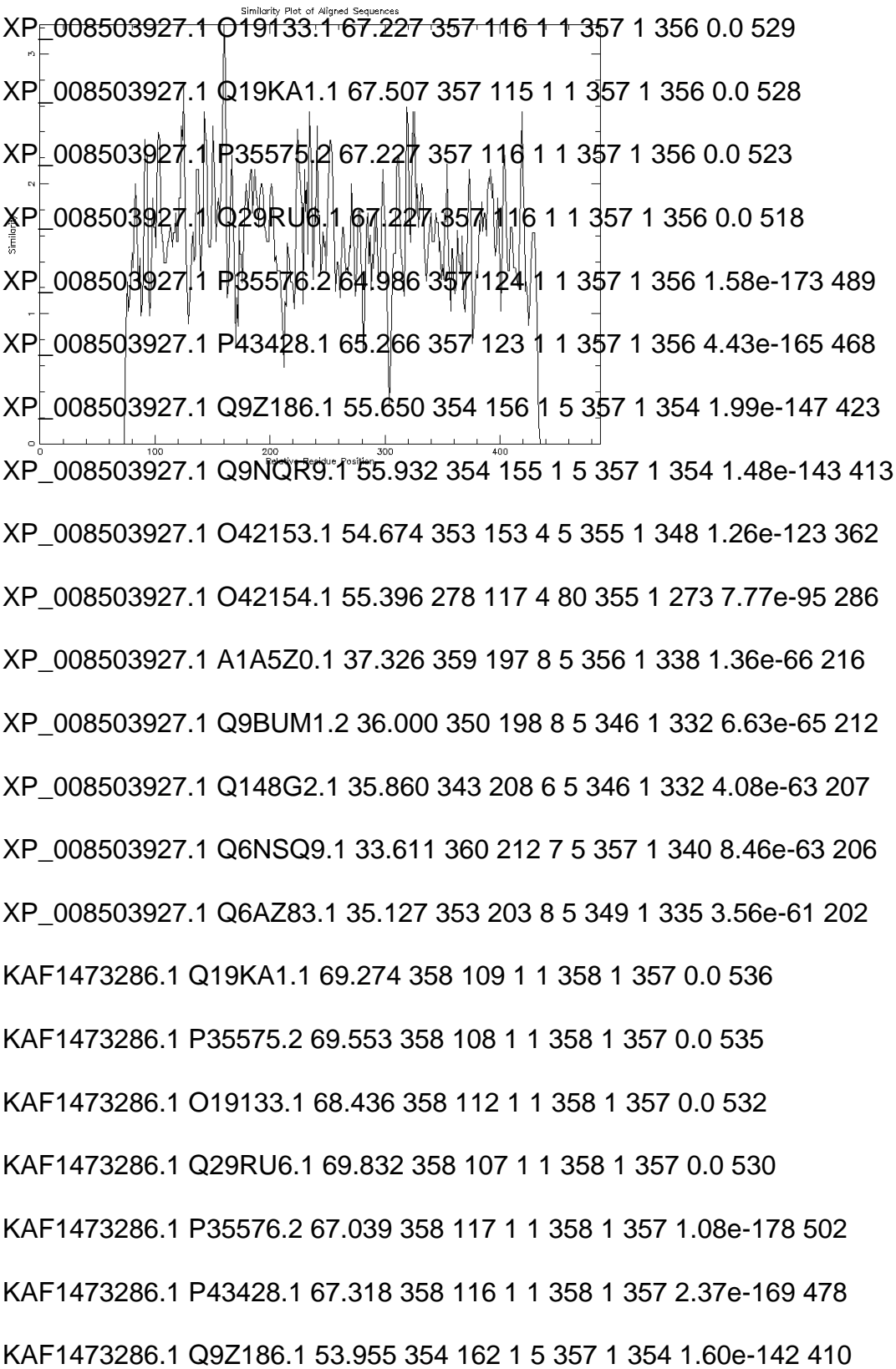query: glucose-6-phosphatase[protein] AND aves[Organism]

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:

XP_008503927.1 O19133.1 67.227 357 116 1 1 357 1 356 0.0 529

XP_008503927.1 Q19KA1.1 67.507 357 115 1 1 357 1 356 0.0 528

XP_008503927.1 P35575.2 67.227 357 116 1 1 357 1 356 0.0 523

XP_008503927.1 Q29RU6.1 67.227 357 116 1 1 357 1 356 0.0 518

XP_008503927.1 P35576.2 64.986 357 124 1 1 357 1 356 1.58e-173 489

XP_008503927.1 P43428.1 65.266 357 123 1 1 357 1 356 4.43e-165 468

XP_008503927.1 Q9Z186.1 55.650 354 156 1 5 357 1 354 1.99e-147 423

XP_008503927.1 Q9NQR9.1 55.932 354 155 1 5 357 1 354 1.48e-143 413

XP_008503927.1 O42153.1 54.674 353 153 4 5 355 1 348 1.26e-123 362

XP_008503927.1 O42154.1 55.396 278 117 4 80 355 1 273 7.77e-95 286

XP_008503927.1 A1A5Z0.1 37.326 359 197 8 5 356 1 338 1.36e-66 216

XP_008503927.1 Q9BUM1.2 36.000 350 198 8 5 346 1 332 6.63e-65 212

XP_008503927.1 Q148G2.1 35.860 343 208 6 5 346 1 332 4.08e-63 207

XP_008503927.1 Q6NSQ9.1 33.611 360 212 7 5 357 1 340 8.46e-63 206

XP_008503927.1 Q6AZ83.1 35.127 353 203 8 5 349 1 335 3.56e-61 202

KAF1473286.1 Q19KA1.1 69.274 358 109 1 1 358 1 357 0.0 536

KAF1473286.1 P35575.2 69.553 358 108 1 1 358 1 357 0.0 535

KAF1473286.1 O19133.1 68.436 358 112 1 1 358 1 357 0.0 532

KAF1473286.1 Q29RU6.1 69.832 358 107 1 1 358 1 357 0.0 530

KAF1473286.1 P35576.2 67.039 358 117 1 1 358 1 357 1.08e-178 502

KAF1473286.1 P43428.1 67.318 358 116 1 1 358 1 357 2.37e-169 478

KAF1473286.1 Q9Z186.1 53.955 354 162 1 5 357 1 354 1.60e-142 410

KAF1473286.1 Q9NQR9.1 55.085 354 158 1 5 357 1 354 2.21e-140 405

KAF1473286.1 O42153.1 54.391 353 154 4 5 355 1 348 2.91e-121 356

KAF1473286.1 O42154.1 55.036 278 118 4 80 355 1 273 4.51e-92 279

KAF1473286.1 A1A5Z0.1 38.701 354 200 6 5 356 1 339 9.89e-69 222

KAF1473286.1 Q9BUM1.2 36.888 347 208 7 12 358 8 343 3.53e-66 215

KAF1473286.1 Q148G2.1 36.311 347 210 6 12 358 8 343 3.52e-65 213

KAF1473286.1 Q6NSQ9.1 36.494 348 208 7 10 357 6 340 3.77e-64 210

KAF1473286.1 Q6AZ83.1 36.919 344 207 6 10 353 6 339 2.34e-63 208

KFO97556.1 Q19KA1.1 67.705 353 113 1 1 353 4 355 0.0 523

KFO97556.1 O19133.1 67.422 353 114 1 1 353 4 355 0.0 522

KFO97556.1 P35575.2 67.422 353 114 1 1 353 4 355 0.0 518

KFO97556.1 Q29RU6.1 67.614 352 113 1 2 353 5 355 0.0 514

KFO97556.1 P35576.2 65.156 353 122 1 1 353 4 355 1.30e-171 484

KFO97556.1 P43428.1 65.439 353 121 1 1 353 4 355 7.29e-163 462

KFO97556.1 Q9Z186.1 55.807 353 155 1 2 353 1 353 1.74e-147 423

KFO97556.1 Q9NQR9.1 56.091 353 154 1 2 353 1 353 3.62e-143 412

KFO97556.1 O42153.1 54.674 353 153 4 2 352 1 348 1.46e-123 362

KFO97556.1 O42154.1 55.396 278 117 4 77 352 1 273 7.07e-95 286

KFO97556.1 A1A5Z0.1 37.326 359 197 8 2 353 1 338 1.43e-66 216

KFO97556.1 Q9BUM1.2 36.000 350 198 8 2 343 1 332 7.85e-65 212

KFO97556.1 Q148G2.1 35.860 343 208 6 2 343 1 332 5.16e-63 207

KFO97556.1 Q6NSQ9.1 33.807 352 209 6 2 346 1 335 1.33e-62 206

KFO97556.1 Q6AZ83.1 35.127 353 203 8 2 346 1 335 4.01e-61 202

XP_027751872.1 Q19KA1.1 69.748 357 107 1 1 357 1 356 0.0 536

XP_027751872.1 O19133.1 68.908 357 110 1 1 357 1 356 0.0 532

XP_027751872.1 P35575.2 70.028 357 106 1 1 357 1 356 0.0 531

XP_027751872.1 Q29RU6.1 70.112 358 106 1 1 358 1 357 0.0 531

XP_027751872.1 P35576.2 68.067 357 113 1 1 357 1 356 0.0 508

XP_027751872.1 P43428.1 68.347 357 112 1 1 357 1 356 7.58e-174 490

XP_027751872.1 Q9NQR9.1 54.930 355 157 2 5 357 1 354 6.10e-139 401

XP_027751872.1 Q9Z186.1 51.977 354 169 1 5 357 1 354 7.27e-139 401

XP_027751872.1 O42153.1 54.674 353 153 4 5 355 1 348 6.50e-125 365

XP_027751872.1 O42154.1 55.036 278 118 4 80 355 1 273 1.37e-94 286

XP_027751872.1 A1A5Z0.1 39.548 354 196 7 5 356 1 338 3.15e-70 226

XP_027751872.1 Q9BUM1.2 36.522 345 208 7 12 356 8 341 9.73e-67 217

XP_027751872.1 Q148G2.1 36.232 345 209 7 12 356 8 341 4.15e-64 210

XP_027751872.1 Q6NSQ9.1 35.260 346 211 7 12 357 8 340 1.85e-63 208

XP_027751872.1 Q6AZ83.1 36.311 347 206 9 12 356 8 341 1.91e-63 208

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KAF1459431.1 P35575.2 69.832 358 107 1 1 358 1 357 0.0 537

KAF1459431.1 O19133.1 68.715 358 111 1 1 358 1 357 0.0 534

KAF1459431.1 Q29RU6.1 70.112 358 106 1 1 358 1 357 0.0 532

KAF1459431.1 P35576.2 67.318 358 116 1 1 358 1 357 1.95e-179 504

KAF1459431.1 P43428.1 67.598 358 115 1 1 358 1 357 5.07e-170 480

KAF1459431.1 Q9Z186.1 53.955 354 162 1 5 357 1 354 1.13e-142 411

KAF1459431.1 Q9NQR9.1 55.085 354 158 1 5 357 1 354 1.72e-140 405

KAF1459431.1 O42153.1 54.391 353 154 4 5 355 1 348 1.80e-121 357

KAF1459431.1 O42154.1 55.036 278 118 4 80 355 1 273 2.82e-92 280

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KAF1459431.1 Q9BUM1.2 37.176 347 207 7 12 358 8 343 8.46e-67 217

KAF1459431.1 Q148G2.1 36.599 347 209 6 12 358 8 343 7.10e-66 214

KAF1459431.1 Q6NSQ9.1 36.494 348 208 7 10 357 6 340 1.63e-64 211

KAF1459431.1 Q6AZ83.1 36.919 344 207 6 10 353 6 339 1.16e-63 209

XP_005429668.1 P35575.2 68.994 358 109 2 1 358 1 356 0.0 517

XP_005429668.1 Q19KA1.1 67.039 358 116 2 1 358 1 356 0.0 511

XP_005429668.1 Q29RU6.1 67.967 359 113 2 1 359 1 357 0.0 509

XP_005429668.1 O19133.1 66.480 358 118 2 1 358 1 356 9.82e-180 507

XP_005429668.1 P35576.2 66.760 358 117 2 1 358 1 356 2.51e-173 491

XP_005429668.1 P43428.1 66.480 358 118 2 1 358 1 356 4.83e-165 470

XP_005429668.1 Q9Z186.1 51.966 356 167 3 5 358 1 354 1.74e-130 382

XP_005429668.1 Q9NQR9.1 52.809 356 164 3 5 358 1 354 4.96e-128 376

XP_005429668.1 O42153.1 56.322 348 144 4 5 350 1 342 1.23e-120 357

XP_005429668.1 O42154.1 57.143 273 109 4 80 350 1 267 4.72e-91 279

XP_005429668.1 A1A5Z0.1 37.960 353 205 5 5 357 1 339 6.87e-66 216

XP_005429668.1 Q9BUM1.2 35.277 343 211 6 12 354 8 339 8.13e-61 203

XP_005429668.1 Q6AZ83.1 35.393 356 211 9 1 354 1 339 1.06e-60 203

XP_005429668.1 Q6NSQ9.1 34.795 365 216 10 1 362 1 346 6.16e-60 201

XP_005429668.1 Q148G2.1 34.844 353 214 8 12 362 8 346 7.68e-59 198

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XP_021233644.1 Q29RU6.1 70.950 358 103 1 75 432 1 357 0.0 531

XP_021233644.1 O19133.1 69.274 358 109 1 75 432 1 357 0.0 530

XP_021233644.1 P35576.2 67.877 358 114 1 75 432 1 357 5.56e-176 498

XP_021233644.1 P43428.1 67.598 358 115 1 75 432 1 357 1.05e-166 475

XP_021233644.1 Q9Z186.1 54.958 353 158 1 79 430 1 353 1.57e-145 421

XP_021233644.1 Q9NQR9.1 55.085 354 158 1 79 431 1 354 2.08e-140 408

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

XP_021233644.1 Q9BUM1.2 36.599 347 202 8 85 427 7 339 7.24e-65 214

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

XP_021233644.1 Q6AZ83.1 35.756 344 211 6 84 427 6 339 1.38e-59 201

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XP_005531541.2 Q29RU6.1 68.908 357 111 0 1 357 1 357 0.0 528

XP_005531541.2 O19133.1 67.416 356 116 0 1 356 1 356 0.0 525

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XP_005531541.2 Q9Z186.1 52.825 354 165 1 5 356 1 354 4.20e-137 397

XP_005531541.2 Q9NQR9.1 52.825 354 165 1 5 356 1 354 9.36e-132 383

XP_005531541.2 O42153.1 54.545 352 154 3 5 354 1 348 8.57e-123 360

XP_005531541.2 O42154.1 54.874 277 119 3 80 354 1 273 4.84e-93 281

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XP_005531541.2 Q6AZ83.1 36.158 354 209 10 1 352 1 339 5.70e-63 207

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XP_010583936.1 O19133.1 69.553 358 108 1 1 358 1 357 0.0 538

XP_010583936.1 P35575.2 70.112 358 106 1 1 358 1 357 0.0 537

XP_010583936.1 Q29RU6.1 70.670 358 104 1 1 358 1 357 0.0 536

XP_010583936.1 P35576.2 67.877 358 114 1 1 358 1 357 5.36e-180 505

XP_010583936.1 P43428.1 67.598 358 115 1 1 358 1 357 1.60e-169 479

XP_010583936.1 Q9Z186.1 54.802 354 159 1 5 357 1 354 9.13e-145 416

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XP_010583936.1 O42153.1 55.807 353 149 4 5 355 1 348 3.94e-126 369

XP_010583936.1 O42154.1 56.475 278 114 4 80 355 1 273 1.32e-95 288

XP_010583936.1 A1A5Z0.1 38.701 354 199 7 5 356 1 338 8.60e-69 222

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XP_010583936.1 Q148G2.1 36.311 347 210 6 12 358 8 343 3.46e-66 215

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XP_010411101.1 P35575.2 70.028 357 106 1 1 357 1 356 0.0 531

XP_010411101.1 O19133.1 68.908 357 110 1 1 357 1 356 0.0 530

XP_010411101.1 Q29RU6.1 69.832 358 107 1 1 358 1 357 0.0 528

XP_010411101.1 P35576.2 67.507 357 115 1 1 357 1 356 8.11e-177 497

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XP_010411101.1 O42154.1 55.755 278 116 4 80 355 1 273 2.92e-95 287

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XP_010411101.1 Q9BUM1.2 36.901 355 206 8 1 353 1 339 4.29e-66 215

XP_010411101.1 Q6NSQ9.1 34.444 360 213 9 1 357 1 340 1.58e-62 206

XP_010411101.1 Q6AZ83.1 35.112 356 211 8 1 353 1 339 1.63e-62 206

XP_010411101.1 Q148G2.1 35.475 358 212 9 1 356 1 341 4.55e-62 204