

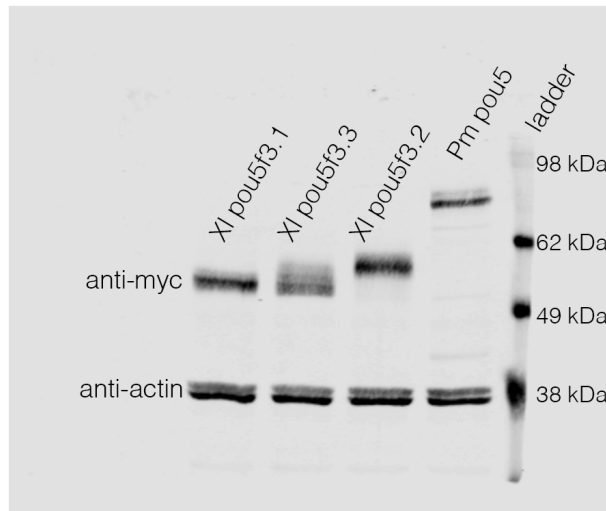
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# **Shared features of blastula and neural crest stem cells evolved at the base of vertebrates**

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In the format provided by the  
authors and unedited

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**Supplemental Data Fig. 1.** Uncropped Western blot for Extended Data Fig. 7a.

**Supplemental Data Fig. 2.** Multiple sequence alignment of vertebrate pou5 and chordate pou3 proteins.

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>Petromyzon_marinus_pou5_ncbi
METQSLQTSALDIP---QSG---PSLD--NRFRAYGP-----HQGVSVQRSPH
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SGLGD-----AGSPADDLAVA---GTSASFLASSVPCQPPPPHHHHHHGWQNLVPPPA
ASRYQESVVVIVDDDDDDDDDDSSGD---IVSVSDDECHGAMMQQQQQQQLL-----
-MHHLLQQQ---QQQQLPHQPHHGQRPGEWHGAMGEAGSDGKWGLPASSGGVESAAAS
PDP---WPAPSM---QQQQQQQHYQ-PHHQYHAGQHGLDADQTSPLQPTQRY-HYPP
QQQQQP---LQL---QQQQQEEQQEQQLNFQQHQQH--QQQLYQELRRQQEQHELLKR
RQQQELQRQLEDVVVVVSS-----PESDG-----AGSSCE-----
--PSTTTSWR-----
GRCDSSGGE-----DNLMSIDELARFAKELKVKRVNLGFTQAEMGLSIGSLCGRVFSQ
TTICRFEALQLSQRNLCQLPLFK---LVGSSG-GVG-----GVGGVGVSGGVD
AKEGKTPREVGYRM-RKKRTYFASYTRMQLEAYYNVCSPNMSAIAQQLKLENSDGD
GPLRVEL-----RSSAA-AVPEPLLMEKCRKASTSLADNN--VPQFHAN-----
-----GQNGPG--AAPVAVA-----RDNID--TDGSTGGVETVGA-
-AAAMAY-DGAFAACHAEGGVCKMETSASSCLRSAGAPRGADAHGFSGYGGGGDDGGRDG
NGDGSDLFPTAVHTCLRSFAGSGLNDT
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-----NVNKLRRRRRTTIENGVRDTLEAWYLVCSKPSAKEIARIAGELNLDKE---  
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-----VLGISPCPP-----

-----AY-EFCG

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-----TGTP-----FPGGAV-----SFPLPPGPHFGTPGYGSP---

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>Felis\_catus\_pou5f1\_ACY72350.1

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-----VWGIPPCPP-----

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ALGGTG-----STANCSP--GSAIPVPPG-----LYPSPLNQS----  
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---SG---AGAGFES-----S
RVEVKV-----ER-PDKEAGYGQ-----
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-----GAGG-----
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QMTSNG-----SS-----PLLS-SHAHSL-SGYS---
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PQH-HDNSD-----DDTPTSDDLEQFAKQFKQRRIKLGFTQADVGLALGTLYGNVFSQ
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--H-R-----SHLVHQP-----
-----TQNSHHG-SWA-----P-TTTH-HL-S
PLSPAS-----N-----GHQ--SL---VYSQ-TGYT---
-----ML---S-----PQ-----PSLH-HGLRD-----
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-----THHQWLPN-----
-----PASDWGS-----GSHLGA-----Q
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--HH-R-----SHLVHQQ-----
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PMSPGS-----N-----SHQ--PL---IYSQ-SSYT---
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-----VQ-----  
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-----VQ-----

>Xenopus\_tropicalis\_pou3f2\_NP\_001263306.1

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-----AH-QWITALSHG-----  
-----DGAPWASS-----PLGQ-----  
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--QHQR-----APHLVHPA-----  
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SMASSN-----G-----Q-GL---LYSQ-PSFT---  
-----VNGMI-----N-----PGSG-----QGMHH-HGLRD-----  
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-----SR-----DTPP-----HHGVQ--TS-----  
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-----VQ-----

>Mus\_musculus\_pou3f2\_NP\_032925.1

MATAASNH-----Y-----SLLTSSASIVH  
AEP-----PGGMQQA-----GGYRE-----AQ---  
-----SLV-QGDY-----G--ALQSNHGHLPLSH-----  
-----AH-QWITALSHGGGGGGGGGG-----G  
GGGGGGGGGGGGDGSPWSTS-----PLGQ-----  
-PDIKPSVV-VQQGGRGDELHGPGALQQQH-----QQQQQQQQQQQQQQQQQ  
QQQQQQR-----PPHLVHHA-----  
-----ANHHPGP-AWR-----SAAAAA-HLPP  
SMGASN-----G-----GL---LYSQ-PSFT---  
-----VNGML-----G-----AGGQP-----AGLHH-HGLRD-----  
--AHDE-----PHHADHHPHPHSHPHQQPPPPPPPPQGP PGHPG-----  
AHH-DPHSD-----EDTPTSDDLEQFAKQFKQRRIKLGFTQADVGLALGTLYGNVFSQ  
TTICRFEALQLSFKNMCKLKPLLKNWLEEADSSSG-SPT-----SIDKIAA-----  
-----QGRK-RKKRTSIEVSVKGALESHFLKCPKPSAQEITSLADSLQLEKE---  
-VVRVWFCNRRQKEK--RMTPP-GGTLP-----AEDVYGG-----  
-----SR-----DTPP-----HHGVQ--TP-----  
-----

-----VQ-----  
>Gallus\_gallus\_pou3f2\_XP\_015140157.1  
MATAASNH-----Y-----SLLASGSPMVH  
AEP-----PGGMQPG-----GGYRD-----AG----  
-----ALV-QADY-----ALQSNHGHLPLSH-----  
-----AH-QWIAALSHGGPPGGGGGG-----G  
GGGGGGGGGG-GEAPWAAA-----GALGP-----  
-PDIKPAA--VQAAPRGDELPPQHP-----  
--PPPGR-----APHLVHHG-----  
-----GGGGGHHA-AWR-----A-GGAA-HLPP  
GMAAAN-----GA-----AQA-GL----LYPQPPGFT---  
-----VNGML----G-----AAQ-----PALHH-HGLRD-----  
--AHDEAPG-----PPAPPHHGAEHPP--GPHPAGGGGGPGGGGAAAAGG-----  
PHH-EAHS-----EDTPTSDDLEQFAKQFKQRRIKLGFTQADVGLALGTLYGNVFSQ  
TTICRFEALQLSFKNMCKLKPLLKNWLEEADSSSG-SPT-----SIDKIAA-----  
-----QGRK-RKKRTSIEVSVKGALESHFLKCPKPSAQEITSLADSLQLEKE---  
-VVRVWFCNRRQKEK--RMTTP-GGTLPG-----AEDVYGP-----  
-----SR-----DTPP-----HHGVQ--TP-----  
-----

-----VQ-----  
>Danio\_rerio\_pou3f3\_NP\_571225.2  
MATAASNP-----YLAS-----STILSSASLVH  
SES-----GGGGMQPGSGAVTSVSGGYRG-----DPTV---  
-----KMV-QSDFM-----QGAMAASNGGHMLSH-----  
-----AH-QWVTSPLPAAAAAAAAA-----A  
AAAAE-----AGSPWSSSPV---GMAGSPQQ-----  
-QDVKSSS-----NR-EDLHSGTAL-----  
--HH--R-----PSHLG-----  
-----AHQSHQS-AWG-----GTTAS-HI-S  
TITGG-----QQSQSQ--SL----IYSQPGGFT---  
-----VNGML----N-----PPG-----SLVH-PGLMR-----  
--GES-----PEM-DHHHHHHHHHQQQHPHHHHHH--QHHA-----GV  
NSH-DSHSD-----EDTPTSDDLEQFAKQFKQRRIKLGFTQADVGLALGTLYGNVFSQ  
TTICRFEALQLSFKNMCKLKPLLKNWLEEADSTTG-SPT-----SIDKIAA-----  
-----QGRK-RKKRTSIEVSVKGALESHFLKCPKPSAQEITSLADNLQLEKE---  
-VVRVWFCNRRQKEK--RMTTP-GV-PQT-----PEDVYTHAGNGS  
FVVDYLKGASLKD-----EPDS-----NHNVT--TASS-----  
-----Y-----

---GQEIL--VH-----  
>Gallus\_gallus\_pou3f3\_XP\_040518115.1  
MAAATSNP-----YLPG-----NGILAAGSIVH  
ADS-----GGGGGGGGGGGGMQPGGVAVTSVAGGYRG-----DPAA----  
-----KMV-QSDFM-----PGAMAASNGGHMLSH-----  
-----AH-QWVTALPAAAAAAAAA-----A  
AAAAE-----AGSPWSGSPV---GMTGSPQQPP--PPPP-----  
-PDVKGGG-----GR-EELHAGAAL-----  
--HH--R-----PPHLG-----  
-----PPHQHQA-AWG-----AAAAA-HL-P  
AMAGG-----QQ-QQQ--SL----LYSQPGGFT---  
-----VNGML----S-----PAGGG-----QSLVH-PGLVR-----  
--GGET-----AELGEHPGHHHHHHHPHP--GHHA---PHHG-----AV

NSH-EAHS-----EDTPTSDDLEQFAKQFKQRRRIKLGFTQADVGLALGTLYGNVFSQ  
TTICRFEALQLSFKNMCKLKPLLKNWLEEADSSTG-SPT-----SIDKIAA-----  
-----QGRK-RKKRTSIEVSVKGALESHFLKCPKPSAQEITNLADSLQLEKE---  
-VVRVWFCNRRQKEK---RMTTP-GIQQQT-----PDDVYSQVGAVS  
-----SD-----TPPP-----HHGLQ--SG-----  
-----

-----VQ-----

>Mus\_musculus\_pou3f3\_NP\_032926.2

MATAASNP-----YLP-----NSLLTAGSIVH  
SDAAGAGGGGGGGGGGGGGAGGGGGGMQPGSAAVTS--GAYRG-----DPSS---  
-----VKMV-QSDFM-----QGAMAASNGGHMLSH-----  
-----AH-QWVTALPH-AAAAAAAA-----A  
AAAVE-----ASSPWGSAV---GMAGSPQQPP--QPPPP-----PPQ  
GPDVKGGA-----GR-EDLHAGTAL-----  
--HH-R-----GPPHLGPPP-----

-----PPPHQGHPG-GWGAAAAAAAA-----AAAAAAAA-HL-P

SMAGG-----QQPPPQ--SL----LYSQPGGFT---

-----VNGML-----S---APPGPGGGGGGAGGGAQSLVH-PGLVR-----

---GDT-----PELAHHHHHHHHHAHPHPHPHHAQGP-PHHGGGGAGPGL

NSH-DPHSD-----EDTPTSDDLEQFAKQFKQRRRIKLGFTQADVGLALGTLYGNVFSQ

TTICRFEALQLSFKNMCKLKPLLKNWLEEADSSTG-SPT-----SIDKIAA-----

-----QGRK-RKKRTSIEVSVKGALESHFLKCPKPSAQEITNLADSLQLEKE---  
-VVRVWFCNRRQKEK---RMTTP-GIQQQT-----PDDVYSQVGTVS

-----AD-----TPPP-----HHGLQ--TS-----  
-----

-----

-----VQ-----

>Xenopus\_tropicalis\_pou3f3\_XP\_017947125.1

MATAASNP-----YLAS-----NSILSPGSIVH

SDS-----GIGMQPGSAAVTSVAGGYRG-----DPTV---

-----KMV-QSDFM-----QGAMAASNGGHMLSH-----

-----AH-QWVTALPH-AAAAAAAA-----A

AAAAE-----AGSPWSSSPV---GMTGSPQHPQ--Q-----Q

QQDVKGGA-----GR-DELHPGAAL-----

--HH-R-----PPHLG-----

-----PHQGHPG-GWG-----AAAAS-HI-Q

SMAAGT-P-----QQQQQQ-----QQQQQQQ--AL----LYAQPGAFT---

-----VNGML-----S-----PPPGS-----QNLVH-PGLVR-----

---GDT-----PELGDHPGHHHHHHHHQHQQHHQQQQQQQHHG-----GV

NSH-DPHSD-----EDTPTSDDLEQFAKQFKQRRRIKLGFTQADVGLALGTLYGNVFSQ

TTICRFEALQLSFKNMCKLKPLLKNWLEEADSSTG-SPT-----SIDKIAA-----

-----QGRK-RKKRTSIEVSVKGALESHFLKCPKPSAQEITNLADSLQLEKE---  
-VVRVWFCNRRQKEK---RMTTP-GIQQQT-----PDDVYSQVGNVG

-----AD-----TPPP-----HHGMQ--TS-----  
-----

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-----VQ-----

>Gallus\_gallus\_pou3f4\_XP\_003641125.3

MATAASNP-----Y-----GLLGSGSLAH

AD-----GAGMQQG-----SPFRN-----PQ---

-----KLL-QSEYL-----QG--VPGNGHPL-----

-----GH-HWVTSL-----

-----DAAPWPSA-----LAGGPLEQ-----

-PDVKP-----GR-EDLQLGALL-----  
--HH--R-----SPHVSHHS-----  
-----PHANHPG-AWG-----ASPA-HG-G  
SLGPAG-----QPPPLG---VYPQ-AGFA---  
-----VGGVL----EHGGLTPP-PAAAA-----QPPPP--PQGLH-----  
--PGEH-----GELG-----  
GHHQCQDHS-----EETPTSDELEQFAKQFKQRRRIKLGFTQADVGLALGTLYGNVFSQ  
TTICRFEALQLSFKNMCKLKPLLKNWLEEADSSTG-SPT-----SIDKIAA-----  
-----QGRK-RKKRTSIEVSVKGVLETHFLKCPKPAAQEISSLADSLQLEKE---  
-VVRVWFCNRRQKEK--RMTPP-GEQQ-----QHEVYA-----  
-----HGVK--TD-----  
-----

-----SAC-----HDL  
>Mus\_musculus\_pou3f4\_NP\_032927.1  
MATAASN-----Y-----SILSSSSLVH  
AD-----SAGMQQG-----SPFRN-----PQ---  
-----KLL-QSDYL-----QG---VPSNGHPL-----  
-----GH-HWVTSL-----  
-----DGGPWSST-----LATSPLDQ-----  
-QDVKP-----GR-EDLQLGAIL-----  
--HH--R-----SPHVAHHS-----  
-----PHTNHPN-AWG-----ASPA-PN-S  
SITSSG-----Q--PLN---VYSQ-PGFT---  
-----VSGML----EHGGLTPP-PAAAS-----TQSLH--PVLRE-----  
--PPDH-----GELG-----  
SHHCQDHS-----EETPTSDELEQFAKQFKQRRRIKLGFTQADVGLALGTLYGNVFSQ  
TTICRFEALQLSFKNMCKLKPLLKNWLEEADSSTG-SPT-----SIDKIAA-----  
-----QGRK-RKKRTSIEVSVKGVLETHFLKCPKPAAQEISSLADSLQLEKE---  
-VVRVWFCNRRQKEK--RMTPP-GDQQ-----PHEVYS-----  
-----HTVK--TD-----  
-----

-----ASC-----HDL  
>Xenopus\_tropicalis\_pou3f4\_NP\_001090728.1  
MATAASN-----Y-----SILSSSSLVH  
-D-----SAIMQQG-----SPFRN-----PQ---  
-----KLL-QSDYL-----QG---VPSNGHPL-----  
-----GH-HWVTSL-----  
-----DANPWSTS-----LGSSPLDQ-----  
-QDIKP-----GR-EDLQLGAIL-----  
--HH--R-----SPHVTHHS-----  
-----PHTNHPN-AWG-----ASPA-HN-S  
SLTSNG-----Q--PIN---VYSQ-SGFT---  
-----VSGML----DHGGLTPP-PPSGT-----TQSLH--PVLRE-----  
--PVDH-----GDLG-----  
SHHCQDHS-----EETPTSDELEQFAKQFKQRRRIKLGFTQADVGLALGTLYGNVFSQ  
ATICRFEALQLSFKNMCKLKPLLKNWLEEADSSTG-SPT-----SIDKIAA-----  
-----QGRK-RKKRTSIEVSVKGVLETHFLKCPKPAAQEISSLADSLQLEKE---  
-VVRVWFCNRRQKEK--RMTPP-GDPQ-----QHEVYS-----  
-----HSV-K--TD-----  
-----  
-----TSC-----NEL

>Petromyzon\_marinus\_pou3f2-like\_XP\_032828582.1

MSGAEQTH-----  
-----PAYREHA-----  
-----KLLPAAEYL-----GTNGHLPPF-----  
-----SP-QWLTALQHHAASESMGHHHHHHHHH-----PPS  
QGVGS-----SHHSWAG-----GSPLAH-----  
-----QDTPKVEDMQQQQQQ-----QQQ-----  
-NHHQQQ-----HQQQQQ-----  
-----QQDQQRHSPHGVWG-----PNPTAA-----  
-----TLLQ--SPPGQQPHHHQQQQQHHHHHH--HHQSALAYSPPPYGHA----  
-----GASGLL-----P-----LGLSPLHGGSPQ-----  
--PGQDGPGVGGGGGG-----GGGG-----  
SISDTELEE-----PAPPTSDDLEQFAKEFKQRRIKLGFTQADVGLALGTLYGNVFSQ  
TTICRFEALQLSFKNMCKLKPLLSKWLEEADSANGCAGGAC-----GLDKMAA-----  
-----QGRK-RKKRTSIEVAVKGALEKHFLQSPKPSAQEITAIAEALQLEKE---  
-VVRVWFCNRRQKEK---RMTVQ-GVGGPE-----DQG--LQGSMAG-----  
-----GC-----NSPS-----HHAHH--AL-----  
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