

Supporting Information

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DNA Modification under Mild Conditions by Suzuki–Miyaura Cross-Coupling for the Generation of Functional Probes**

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Contents

General considerations	3
Boronic esters used in this study.....	4
Synthesis of the short boronic ester amines for coupling.....	4
Synthesis of the long boronic ester amines for coupling	6
Amide couplings	8
Small molecule cross-couplings.....	11
Catalyst preparation.....	12
ODN crosscoupling	13
General reaction conditions.....	13
ODN1a	13
ODN1b	14
ODN1c.....	14
ODN1d	15
ODN1e	15
ODN1e reaction with 3-furane boronic acid	16
ODN1f.....	16
ODN1g	17
ODN1 Paladium adduct observed in PO4 buffer.....	17
ODN1 reaction intermediates by ESI-MS	18
ODN2 (no IdU control).....	18
ODN3b	19
ODN3c.....	19
ODN3d	20
ODN3f.....	20
ODN4 control reactions.....	21
ODN4 – Phosphate and Tris buffer comparison.....	22
ODN4d	23
ODN4f.....	23
ODN5f.....	24
ODN6f.....	24
dsDNA crosscoupling.....	25
PCR probe generation	27

Photocrosslinking	27
Streptavidin blot.....	28
Supplementary Results.....	28
Supplementary Table 2	31

General considerations

Proton nuclear magnetic resonance (^1H NMR) spectra were recorded on a Bruker DPX200 (200 MHz), a Bruker AV400 (400 MHz), or a Bruker AVII500 (500 MHz) spectrometer, as indicated. Carbon nuclear magnetic resonance (^{13}C NMR) spectra were recorded on a Bruker AV400 (100 MHz) or on a Bruker AVII500 (125 MHz) spectrometer, as indicated. NMR Spectra were assigned using COSY, HMQC, and DEPT 135. All chemical shifts are quoted on the δ scale in ppm using residual solvent as the internal standard (^1H NMR: $\text{CDCl}_3 = 7.26$, $\text{CD}_3\text{OD} = 3.31$; $\text{DMSO-d}_6 = 2.50$; $\text{CD}_3\text{CN} = 1.94$ and ^{13}C NMR: $\text{CDCl}_3 = 77.0$; $\text{CD}_3\text{OD} = 49.0$; $\text{DMSO-d}_6 = 39.5$; $\text{CD}_3\text{CN} = 1.94$). Coupling constants (J) are reported to the nearest 0.5 Hz with the following splitting abbreviations: s = singlet, d = doublet, t = triplet, q = quartet.

Infrared (IR) spectra were recorded on a Bruker Tensor 27 Fourier Transform spectrophotometer neat for both oils and solids. Absorption maxima (ν_{max}) are reported in wavenumbers (cm^{-1}). Low resolution mass spectra (LRMS) were recorded on a Waters Micromass LCT Premier TOF spectrometer Waters using electrospray ionization (ESI) and high resolution mass spectra (HRMS) were recorded on a Bruker MicroTOF ESI mass spectrometer. Nominal and exact m/z values are reported in Daltons.

Thin layer chromatography (TLC) was carried out using Merck aluminium backed sheets coated with 60F254 silica gel. Visualization of the silica plates was achieved using a UV lamp ($\lambda_{\text{max}} = 254$ nm), and/or ammonium molybdate (5% in 2 M H_2SO_4), and/or potassium permanganate (5% KMnO_4 in 1 M NaOH with 5% potassium carbonate).

Column chromatography was performed on a Biotage SP4 flash purification system using the indicated cartridges and solvent systems.

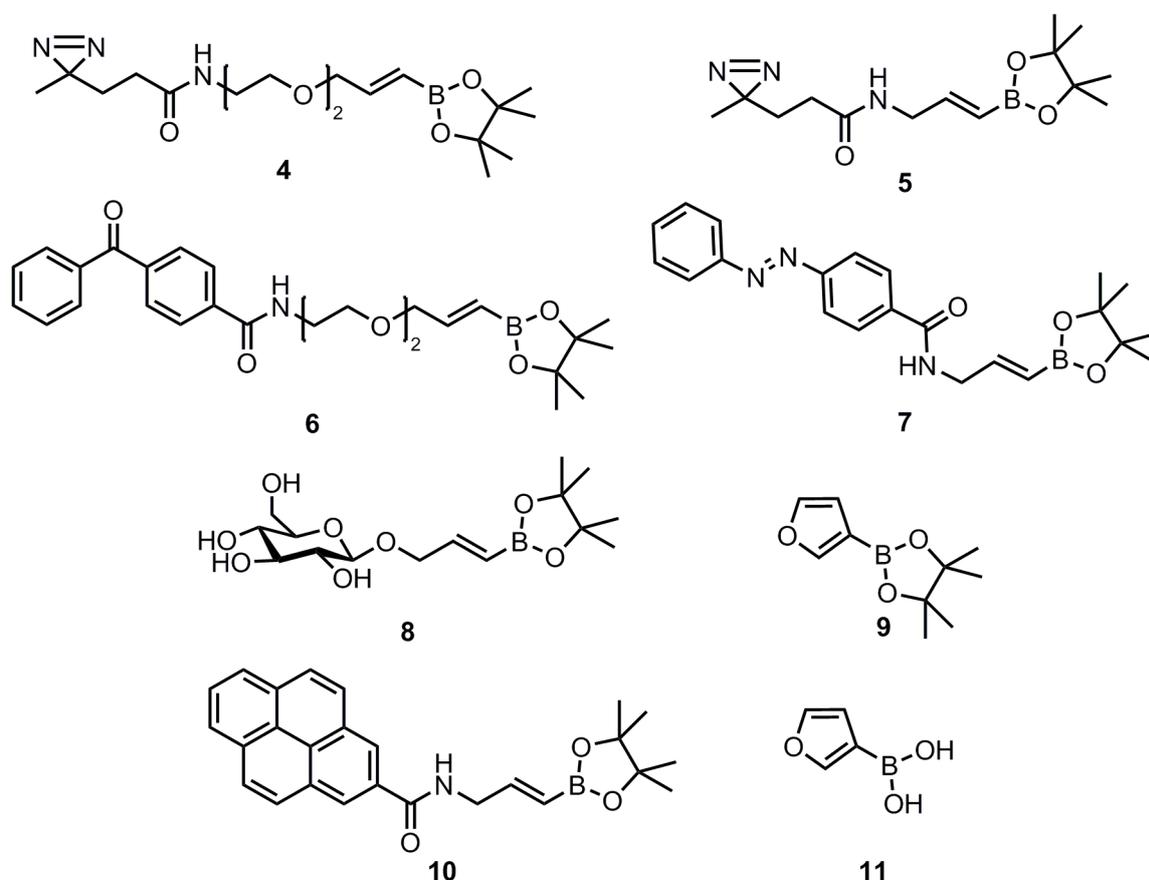
Anhydrous solvents were obtained from Fluka or Acros with the exception of CH_2Cl_2 and THF, which were dried in an alumina column under nitrogen. All other solvents were used as supplied (Analytical or HPLC grade), without prior purification. Deionized water was used for chemical reactions. Reagents were purchased from Sigma-Aldrich and used as supplied, unless otherwise indicated. All reactions using anhydrous conditions were performed using flame-dried apparatus under an atmosphere of argon or nitrogen.

Boronic ester **6** was prepared by Justin M. Chalker, as described previously^[1].

DNA analysis was performed on an Agilent 1260 Infinity system using an Agilent Eclipse Plus C18 column (4.6 x 100 mm, 3.5 μm). 0.1M triethylamine acetate (TEAA) in water (solvent A) and 0.1M TEAA in 80:20 acetonitrile:water (solvent B) were used as mobile phase. The mixtures were separated by a linear gradient as stated in the example. After this the column was washed and equilibrated (5

min – 40->100% B; 10 min – 100% B; 15 min – 100->0% B; 20 min 0% B). The run was monitored by UV absorption at 260nm. Collected fractions were freeze-dried and analyzed by MALDI-TOF using 3-hydroxypicolinic acid (hpa) as matrix or by ESI. The hpa stock was prepared as a saturated solution in water:acetonitrile 1:1 and mixed with the sample 1:1 on the MALDI target. MALDI analysis was performed on a Waters Micromass MALDI micro MX using the manufacturer's recommended settings. For ESI analysis, samples were dissolved in water and injected in a flow of 1:1 Water:Methanol with 0.1mM NH₄OAc. The analysis was performed on a Micromass LCT (ESI-TOF-MS). The data was processed using MassLynx.

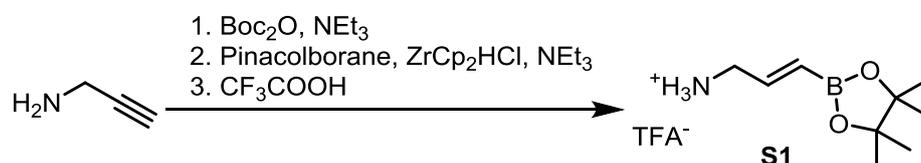
Boronic esters used in this study

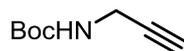


Supplemental Figure S1 Boronic acid pinacol esters used in this study.

For the synthesis of the different boronic esters, firstly two amine-containing boronic acid pinacol esters with different length linkers (see SI, with zero (**S1**) or two (**S2**) PEG units), starting from propargylamine or 2-(2-aminoethoxy)ethanol, were synthesized. The resulting amines were coupled to different carboxylic acids (mediated by carbodiimide), yielding the desired boronate esters.

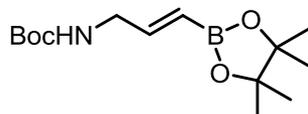
Synthesis of the short boronic ester amines for coupling



tert-Butyl prop-2-yn-1-ylcarbamate^[2]

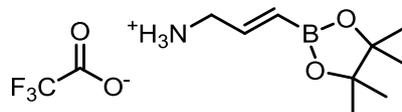
To a solution of di-*tert*-butyl dicarbonate (4.8 g, 22 mmol, 1.1 eq) in CH₂Cl₂ (20 mL) at 0°C was added dropwise propargylamine (1.3 mL, 1.1 g, 20 mmol, 1 eq) and subsequently triethylamine (5.6 mL, 4.05 g, 40 mmol, 2 eq). The resulting solution was warmed to rt and allowed to stir for 2 h. Then the reaction was quenched with sat. NH₄Cl (10 mL) and diluted with EtOAc (150 mL). The organic phase was washed with sat. NH₄Cl, sat. NaHCO₃ and brine; dried (MgSO₄), filtered and solvents were removed *in vacuo* yielding the title compound (2.68 g, 17 mmol, 85%) as a clear oil.

¹H NMR (400 MHz, CDCl₃) δ ppm 1.46 (s, 9 H, (CH₃)₃C) 2.22 (t, *J*=2.5 Hz, 1 H, CCH) 3.92 (m, 2 H, CH₂) 4.72 (br. s., 1 H, NH); ¹³C NMR (101 MHz, CDCl₃) δ ppm 28.3 ((CH₃)₃C) 30.4 (CH₂) 71.2 (CCH) 79.8 ((CH₃)₃C) 80.0 (C) 155.3 (OCONH); LRMS *m/z* (ESI⁺): 178.09 [M+Na]⁺; IR (neat): 3301, 2979, 2933, 1692, 1510, 1455 cm⁻¹.

(E)-tert-Butyl 3-(4,4,5,5-tetramethyl-1,3,2-dioxaborolan-2-yl)allylcarbamate^[3]

To neat *tert*-butyl prop-2-ynylcarbamate was added Pinacolborane (1.4 mL, 1.23 g, 9.6 mmol, 1.5 eq), NEt₃ (100 μL, 0.64 mmol, 0.1 eq) and ZrCp₂HCl (165 mg, 0.64 mmol, 0.1 eq). The solution was stirred at 65°C for 16 h. After completion the reaction was allowed to cool to rt and was diluted with EtOAc (25 mL) and quenched with sat. NH₄Cl. The mixture was further diluted with EtOAc (50 mL) and the organic layer was washed with sat. NH₄Cl, sat. NaHCO₃ and brine, dried (MgSO₄), filtered and solvents were removed *in vacuo*. The product was purified by automated column chromatography (Biotag SNAP 50g cartridge 0-40% over 10 CV EtOAc in petrol) yielding the title compound as a yellow oil (1.27g, 4.5 mmol, 70%).

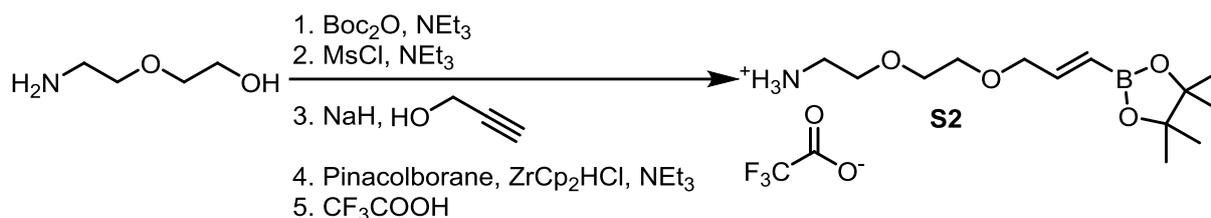
¹H NMR (400 MHz, CDCl₃) δ ppm 1.26 (s, 12 H, (CH₃)₂COB) 1.44 (s, 9 H, (CH₃)₃C) 3.84 (s, 2 H, CH₂) 4.67 (s, 1 H, NH) 5.57 (dd, *J*=18, 2 Hz, 1 H, CHB) 6.58 (d, *J*=18 Hz, 1 H, CHCH₂); ¹³C NMR (101 MHz, CDCl₃) δ ppm 24.7 (CH₂CCH₂) 28.4 ((CH₃)₃C) 44.0 (CNHCH₂) 79.4 (COB) 83.3 ((CH₃)₃C) 149.4 (CHB) 155.7 (OCONH); LRMS *m/z* (ESI⁺): 306.20 [M+Na]⁺; IR (neat): 3356, 2978, 2932, 2361, 2341, 1697, 1643, 1519 cm⁻¹.

(E)-3-(4,4,5,5-tetra-Methyl-1,3,2-dioxaborolan-2-yl)prop-2-en-1-amine TFA salt (S1)

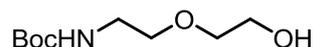
(E)-*tert*-Butyl 3-(4,4,5,5-tetramethyl-1,3,2-dioxaborolan-2-yl)allylcarbamate (250 mg, 0.88 mmol, 1 eq) was dissolved in 10 mL 9:1 CH₂Cl₂:CF₃COOH and stirred at rt for 1h. Then solvents were removed *in vacuo* and remaining CF₃COOH was removed by coevaporation (3x Toluene, 3x CH₂Cl₂) yielding **S1** (240 mg, 0.81 mmol, 92%) as a brown oil.

¹H NMR (400 MHz, CDCl₃) δ ppm 1.23 (s, 12 H, (CH₃)₂COB) 3.64 (br. s., 2 H, CH₂) 5.73 (d, *J*=18 Hz, 1 H, CHB) 6.46 - 6.60 (m, 1 H, CHCH₂) 8.21 (br. s., 3 H, NH); ¹³C NMR (101 MHz, CHLOROFORM-*d*) δ ppm 24.6 ((CH₃)₂COB) 42.8 (CH₂) 83.8 (COB) 116.1 (*J*=293 Hz, CF₃) 124.1 (CHCHB) 142.1 (CHB) 162.1 (*J*=36 Hz, CF₃COOH); LRMS *m/z* (ESI⁺): 184.16 [M+H]⁺ IR (neat): 2982, 1675, 1651, 1533 cm⁻¹ HRMS *m/z* (ESI⁺): Found 184.1503 (M+H)⁺; C₉H₁₉BNO₂ requires 184.1503

Synthesis of the long boronic ester amines for coupling



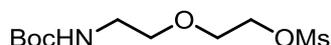
tert-Butyl 2-(2-hydroxyethoxy)ethylcarbamate



To a solution of di-*tert*-butyl dicarbonate (21.83 g, 100 mmol, 1 eq) in CH_2Cl_2 (70 mL) on ice was added 2-(2-aminoethoxy)ethanol (12.0 mL, 12.6 g, 120 mmol, 1.2 eq) dropwise, subsequently NEt_3 (27.8 mL, 20.24 g, 200 mM, 2 eq). The resulting mixture was stirred at rt for 3 h. The reaction was quenched with sat. NH_4Cl , diluted with EtOAc (400 mL), washed with sat. NH_4Cl (2x200 mL) and brine (200 mL), dried (MgSO_4), filtered and solvents were removed *in vacuo*. The title compound was obtained as a clear oil (18.2 g, 88.7 mmol, 89%) and was used in the next step without further purification.

^1H NMR (400 MHz, CDCl_3) d ppm 1.42 (s, 9 H, Boc-H) 3.01 (s, 1 H, OH) 3.28 (d, $J=5$ Hz, 2 H, CH_2) 3.52 (dt, $J=9.5, 5$ Hz, 4 H, CH_2) 3.65 - 3.73 (m, 2 H, CH_2) 5.24 (s, 1 H, NH); ^{13}C NMR (101 MHz, CDCl_3) d ppm 28.4 ($(\text{CH}_3)_3$) 40.3 (CH_2) 61.5 (CH_2) 70.3 (CH_2) 72.2 (CH_2) 79.3 ($\text{C}(\text{CH}_3)_3$) 156.2 (CONH); LRMS m/z (ESI^+): 228.13 [$\text{M}+\text{Na}$] $^+$; IR (neat): 3343, 2977, 2361, 1691, 1525 cm^{-1} .

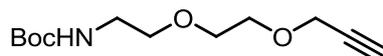
2-(2-(*tert*-Butoxycarbonylamino)ethoxy)ethyl methanesulfonate



To a solution of *tert*-butyl 2-(2-hydroxyethoxy)ethylcarbamate (17.8 g, 87 mmol, 1 eq) in 100 mL CH_2Cl_2 at 0°C was added NEt_3 (26.7 mL, 19.4 g, 191 mmol, 2.2 eq) and then dropwise $\text{CH}_3\text{SO}_2\text{Cl}$ (7.4 mL, 11 g, 96 mmol, 1.1 eq). The cloudy yellow solution was stirred on ice for 5 h and then quenched with sat. NH_4Cl . The reaction was then diluted with EtOAc (400 mL), washed with sat. NH_4Cl (200 mL), NaHCO_3 (200 mL) and brine (200 mL), dried (MgSO_4), filtered and solvents were removed *in vacuo*. The product was purified by column chromatography (Biotage KP-SIL SNAP 100 g cartridge 0-50% over 10CV EtOAc in petrol) yielding the title compound (18.35 g, 65 mmol, 75%) as an orange oil.

^1H NMR (400 MHz, CDCl_3) d ppm 1.42 (s, 9 H, Boc-H) 3.04 (s, 3 H, Ms-H) 3.30 (q, $J=5$ Hz, 2 H, CH_2) 3.54 (t, $J=5$ Hz, 2 H, CH_2) 3.68 - 3.75 (m, 2 H, CH_2) 4.30 - 4.38 (m, 2 H, CH_2) 4.92 (s, 1 H, NH); ^{13}C NMR (101 MHz, CDCl_3) d ppm 28.4 ($(\text{CH}_3)_3\text{C}$) 37.7 (CH_3S) 40.2, 68.6, 68.8, 70.3 (CH_2OS) 79.4 ($\text{C}(\text{CH}_3)_3$) 155.9 (OCCNH); LRMS m/z (ESI^+): 306.10 [$\text{M}+\text{Na}$] $^+$; IR (neat): 3402, 2978, 2936, 2874, 2361, 2342, 1701, 1512 cm^{-1} .

tert-Butyl 2-(2-(prop-2-ynoxy)ethoxy)ethylcarbamate

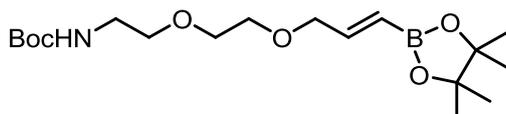


To a solution of propargylic alcohol (5.24 mL, 5.05 g, 90 mmol, 3 eq) in 100 mL THF on ice was added NaH (2.16 g, 90 mmol, 3 eq) portion wise. The resulting suspension was stirred on ice for 30 min then 2-(2-(*tert*-butoxycarbonylamino)ethoxy)ethyl methanesulfonate (8.5 g, 30 mmol, 1 eq) was added dropwise. The resulting suspension was stirred at rt for 19 h. The reaction was then quenched with sat. NH_4Cl (10 mL) and solvents were removed *in vacuo*. The resultant red liquid was partitioned between H_2O (50 mL) and EtOAc (350 mL). The organic phase was washed with sat. NH_4Cl (100

mL), sat. NaHCO₃ (100 mL) and brine (100 mL), dried (MgSO₄), filtered and solvents were removed *in vacuo*. The crude oil was purified by column chromatography (Biotage KP-SIL SNAP 100 g cartridge 0-50% over 10CV EtOAc in petrol) yielding the title compound (5.81 g, 24 mmol, 80%) as a clear oil.

¹H NMR (400 MHz, CDCl₃) d ppm 1.42 (s, 9 H, Boc-H) 2.44 (t, J=2.5 Hz, 1 H, CCH) 3.30 (q, J=5 Hz, 2 H, CH₂) 3.53 (t, J=5 Hz, 2 H, CH₂) 3.59 - 3.65 (m, 2 H, CH₂) 3.65 - 3.71 (m, 2 H, CH₂) 4.19 (d, J=2.5 Hz, 2 H, CH₂CCH) 4.99 (s, 1 H, NH); ¹³C NMR (101 MHz, CDCl₃) d ppm 28.4 ((CH₃)₃C) 40.3 (CH₂), 58.4 (CH₂CC) 69.0, 70.1, 70.3 (CH₂) 74.7 (CCH) 79.2 (CCH) 79.5 (C(CH₃)₃) 156 (OCCNH); LRMS m/z (ESI⁺): 266.14 [M+Na]⁺; IR (neat): 3296, 2870, 1698, 1512 cm⁻¹.

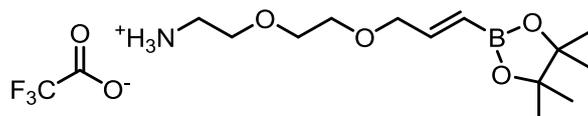
(E)-tert-Butyl 2-(2-(3-(4,4,5,5-tetramethyl-1,3,2-dioxaborolan-2-yl)allyloxy)ethoxy)ethylcarbamate^[3b]



To neat *tert*-butyl 2-(2-(prop-2-ynyloxy)ethoxy)ethylcarbamate (4.86 g, 20 mmol, 1 eq) was added pinacolborane (3.5 mL, 3.07 g, 22 mmol, 1.1 eq), NEt₃ (270 uL, 202 mg, 2 mmol, 0.1 eq) and ZrCp₂HCl (516 mg, 2 mmol, 0.1 eq). The solution was stirred at 65°C for 17 h. After completion the reaction was allowed to cool to rt and was diluted with EtOAc (25 mL) and quenched with sat. NH₄Cl. The mixture was further diluted with EtOAc (150 mL) and the organic layer was washed with sat. NH₄Cl (50 mL), sat. NaHCO₃ (50 mL) and brine (50 mL), dried (MgSO₄), filtered and solvents were removed *in vacuo*. The product was purified by automated column chromatography (Biotag SNAP 100g cartridge 5-50% over 10CV EtOAc in petrol) yielding the title compound as a yellow oil (6.5 g, 17.5 mmol, 88%).

¹H NMR (400 MHz, CDCl₃) d ppm 1.24 (s, 12 H, pinacol-H) 1.42 (s, 9 H, Boc-H) 3.29 (s, 2 H, CH₂) 3.52 (s, 2 H, CH₂) 3.55 - 3.62 (m, 4 H, CH₂) 4.04 - 4.12 (m, 2 H, CH₂) 5.05 (s, 1 H, NH) 5.67 (d, J=18 Hz, 1 H, CHB) 6.60 (dd, J=18, 2.5 Hz, 1 H, CHCH₂); ¹³C NMR (101 MHz, CDCl₃) d ppm 24.7 ((CH₃)₃C) 28.4 ((CH₂)₂C) 40.4, 69.7, 70.3, 72.8 (CH₂) 79.1 ((CH₃)₃C) 83.2 ((CH₂)₂C) 149.0 (CHB) 156.0 (OCONH); LRMS m/z (ESI⁺): 394.25 [M+Na]⁺ IR (neat): 3360, 2978, 2931, 2869, 1713, 1645, 1512 cm⁻¹; HRMS m/z (ESI⁺): Found 394.2367 (M+Na)⁺; C₁₈H₃₄BNO₃Na requires 394.2375.

(E)-2-(2-(3-(4,4,5,5-tetramethyl-1,3,2-dioxaborolan-2-yl)allyloxy)ethoxy)ethanamine (S2)

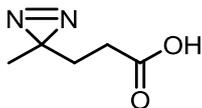


(E)-*tert*-Butyl-2-(2-(3-(4,4,5,5-tetramethyl-1,3,2-dioxaborolan-2-yl)allyloxy)ethoxy)ethylcarbamate (3.71 g, 10 mmol) was dissolved in 10% CF₃COOH in CH₂Cl₂ (50 mL total). The solution was then stirred for 3 h. The solvents were removed *in vacuo* and CF₃COOH was subsequently co-evaporated with toluene (2x30 mL) and CH₂Cl₂ (3x30 mL) yielding **S2** (3.41 g, 8.9 mmol, 89%) as a brown oil.

¹H NMR (400 MHz, CDCl₃) d ppm 1.26 (s, 12 H, pinacol-H) 3.22 (s, 2 H, CH₂) 3.61 (dd, J=6, 2.5 Hz, 2 H, CH₂) 3.67 (dd, J=6, 2.5 Hz, 2 H, CH₂) 3.70 - 3.79 (m, 2 H, CH₂) 4.10 (dd, J=5, 1.5 Hz, 2 H, CH₂) 5.61 - 5.73 (m, 1 H, CHB) 6.58 (dt, J=18, 5 Hz, 1 H, CHCH₂) 7.73 (s, 3 H, NH); ¹³C NMR (101 MHz, CDCl₃) d ppm 24.6 ((CH₃)₃C) 39.9, 66.4, 69.4, 70.1, 72.6 (CH₂) 83.6 ((CH₂)₂C) 118.4 (CHCHB) 148.1 (CHB); LRMS m/z (ESI⁺): 272.22 [M+H]⁺; IR (neat): 2984, 1783, 1673, 1646, 1519 cm⁻¹; HRMS m/z (ESI⁺): Found 272.2031 (M+H)⁺; C₁₃H₂₇BNO₄ requires 272.2030.

Amide couplings

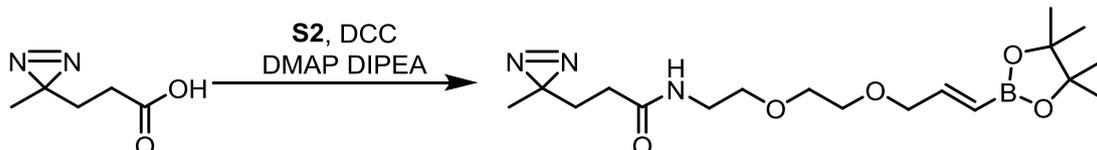
3-(3-Methyl-3H-diazirin-3-yl)propanoic acid (**S3**)^[4]



To NH₃ (150 mL) was added leuvenic acid (17.4 g, 150 mmol, 1 eq) at -78°C. The resulting clear solution was stirred at -50 to -40°C for 3.45 h. During this time a white precipitate was formed. The reaction mixture was then cooled to -78°C again and hydroxylamine-O-sulfonic acid (20.36 g, 180 mmol, 1.2 eq) in MeOH (150 mL) was added dropwise over 20 min. The reaction mixture was stirred at -78°C for 1.10 h and then let come to rt overnight. Most MeOH was removed *in vacuo* and the residue was taken up in MeOH (50 mL). NEt₃ was added and the resulting mixture was stirred at 0°C for 15 min. Solvents were removed *in vacuo* and the residue was taken up in MeOH (150 mL) and cooled to 0°C. NEt₃ (60 mL) was added and then I₂ was added in portions. The addition was continued until the colour of iodine persisted (total 33.2 g, 131 mmol). The reaction mixture was stirred at rt for 20 min. Subsequently, the solvents were removed and the residue was partitioned between Et₂O and water. The aqueous layer was acidified with 5M HCl and extracted with Et₂O (2x150 mL). The combined organic layers were washed with 20% NaHSO₃ and brine, dried (MgSO₄) filtered and solvents were removed *in vacuo* yielding sufficiently pure **S3** as a yellow oil (solidifies at -20°C; 7.82 g, 61 mmol, 40% yield).

¹H NMR (400 MHz, CDCl₃) δ ppm 1.02 (s, 3 H, CH₃) 1.69 (t, *J*=7.5 Hz, 2 H, CH₂) 2.21 (t, *J*=7.5 Hz, 2 H, CH₂) 11.11 (s, 1 H, CO₂H); ¹³C NMR (101 MHz, CDCl₃) δ ppm 19.6 (CCH₃), 25.0 (CH₃CN₂CH₂), 28.5, 29.3 (CH₂CH₂), 178.7 (COOH); LRMS *m/z* (ESI): 125.06 [M-H]⁻; IR (neat): 2960, 1709, 1586 cm⁻¹.

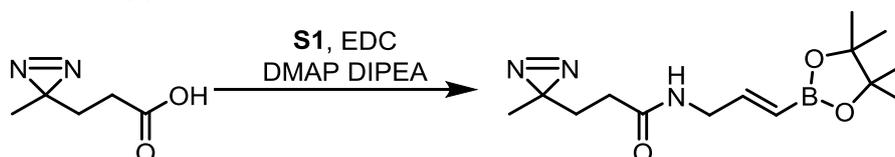
(*E*)-3-(3-Methyl-3H-diazirin-3-yl)-*N*-(2-(2-(3-(4,4,5,5-tetramethyl-1,3,2-dioxaborolan-2-yl)allyloxy)ethoxy)ethyl)propanamide (**4**)



To a solution of **S3** (769 mg, 6 mmol, 1.5 eq) in CH₂Cl₂ (20 mL) on ice was added *N,N'*-dicyclohexylcarbodiimide (DCC; 1.32 g, 6.4 mmol, 1.6 eq). The resulting solution was stirred on ice for 30 min and then 4-dimethylaminopyridine (DMAP; 244 mg, 2 mmol, 0.5 eq) and *N,N*-diisopropylethylamine (DIPEA; 1.4 mL; 1.03 g, 8 mmol, 2 eq) and **S2** (1.54 g, 4 mmol, 1 eq) were added. The reaction mixture was stirred at rt overnight and then filtered (wash with EtOAc or Et₂O) and diluted with EtOAc (100 mL). The organic phase was washed with sat. NH₄Cl (50 mL), sat. NaHCO₃ (50 mL) and brine (50 mL), dried (MgSO₄), filtered and solvents were removed *in vacuo*. The residue was purified by automated column chromatography (Biotag SNAP 25 g cartridge 0-10% over 10 CV MeOH in CH₂Cl₂) yielding **4** (738 mg, 2.1 mmol, 35%) as a brown oil.

¹H NMR (400 MHz, CDCl₃) δ ppm 1.02 (s, 3 H, CH₃CN₂) 1.26 (s, 12 H, Pinacol-CH₃) 1.73 (dd, *J*=9, 7 Hz, 2 H, CN₂CH₂CH₂) 2.01 (dd, *J*=9, 7 Hz, 2 H, CN₂CH₂CH₂) 3.44 (q, *J*=5 Hz, 2 H, CH₂) 3.54 (s, 2 H, CH₂) 3.58 - 3.62 (m, 4 H, CH₂) 4.10 (dd, *J*=5, 2 Hz, 2 H, CH₂) 5.71 (dt, *J*=18, 2 Hz, 1 H, CHB) 6.20 (br. s., 1 H, NH) 6.62 (dt, *J*=18, 5 Hz, 1 H, CHCHB); ¹³C NMR (101 MHz, CDCl₃) δ ppm 19.8 (CH₃) 24.7 ((CH₃)₂C) 25.4 (CH₃CNN) 30.1 (CH₂) 30.6 (CH₂) 39.3, 69.7, 69.8, 70.3 (CH₂) 72.7 (OCH₂CH), 83.3 ((CH₃)₂C) 148.8 (CHB) 171.4 (CH₂CONH); LRMS *m/z* (ESI⁺): 404.25 [M+Na]⁺; IR (neat): 3308, 2978, 2928, 2869, 1726, 1646, 1551 cm⁻¹; HRMS *m/z* (ESI⁺): Found 404.2318 (M+Na)⁺; C₁₈H₃₂BN₃O₅Na requires 404.2330.

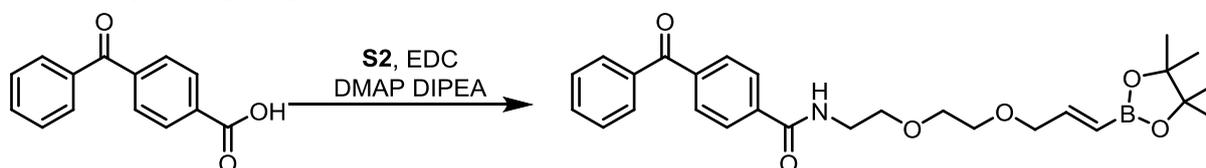
(E)-3-(3-Methyl-3H-diazirin-3-yl)-N-(3-(4,4,5,5-tetramethyl-1,3,2-dioxaborolan-2-yl)allyl)propanamide (5)



To a solution of *N*-(3-dimethylaminopropyl)-*N'*-ethylcarbodiimide hydrochloride (EDC.HCl; 422 mg, 2.2 mmol, 2.2 eq) in CH₂Cl₂ (15 mL) on ice was added **S3** (256 mg, 2 mmol, 2 eq). The resulting mixture was stirred on ice for 30 min and then 4-dimethylaminopyridine (DMAP; 49 mg, 0.4 mmol, 0.4 eq) and *N,N*-diisopropylethylamine (DIPEA; 435 μ L, 323 mg, 2.5 mmol, 2.5 eq) and **S1** (297 mg, 1 mmol, 1 eq) were added. The reaction mixture was stirred at rt overnight then quenched with NH₄Cl (sat., 20 mL) and diluted with EtOAc (80 mL). The organic phase was washed with sat. NH₄Cl (2x30 mL), sat. NaHCO₃ (30 mL) and brine (30 mL), dried (MgSO₄), filtered and solvents were removed *in vacuo*. The residue was purified by automated column chromatography (Biotag SNAP 25g cartridge 0-10% over 10 CV MeOH in CH₂Cl₂) yielding **5** (266 mg, 0.91 mmol, 91%) as a brown oil.

¹H NMR (400 MHz, CDCl₃) δ ppm 1.02 (s, 3 H, CH₃CN₂) 1.25 (s, 12 H, CH₂) 1.69 - 1.82 (m, 2 H, CH₂) 1.95 - 2.07 (m, 2 H, CH₂) 3.87 - 4.00 (m, 2 H, CH₂CH) 5.54 (dt, *J*=18, 2 Hz, 1 H, CHB) 5.69 (s, 1 H, NH) 6.55 (dt, *J*=18, 5 Hz, 1 H, CHCHB); ¹³C NMR (101 MHz, CDCl₃) δ ppm 19.9 (CH₃) 24.7 (Pinacol-CH₃), 25.6 (CN₂) 30.5 33.9 42.9 (CH₂) 83.4 ((CH₃)₂C) 148.2 (CHB) 171.1 (CONH); LRMS *m/z* (ESI+): 316.19 [M+Na]⁺; IR (neat): 3296, 3084, 2980, 2929, 2361, 2341, 1718, 1642, 1550 cm⁻¹; HRMS *m/z* (ESI+): Found 316.1806 (M+Na)⁺; C₁₄H₂₄BN₃NaO₃ requires 316.1803.

(E)-4-Benzoyl-N-(2-(2-((3-(4,4,5,5-tetramethyl-1,3,2-dioxaborolan-2-yl)allyl)oxy)ethoxy)ethyl)benzamide (6)

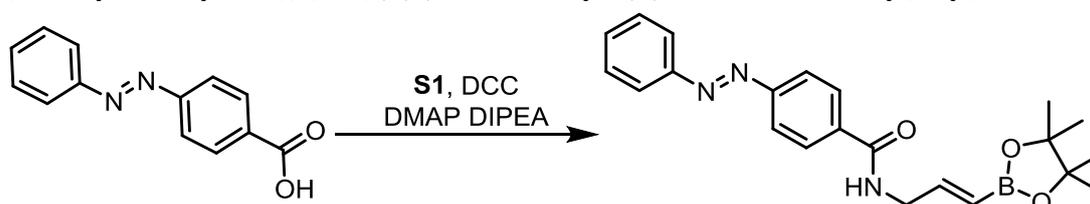


To a solution of *N*-(3-dimethylaminopropyl)-*N'*-ethylcarbodiimide hydrochloride (EDC.HCl; 211 mg, 1.1 mmol, 2.2 eq) in CH₂Cl₂ (10 mL) on ice was added 4-benzoylbenzoic acid (226 mg, 1 mmol, 2 eq). The resulting solution was stirred on ice for 30 min and then 4-dimethylaminopyridine (DMAP; 31 mg, 0.25 mmol, 0.5 eq) and *N,N*-diisopropylethylamine (DIPEA; 304 μ L, 226 mg, 1.75 mmol, 3.5 eq) and **S2** (192 mg, 0.5 mmol, 1 eq) were added. The reaction mixture was stirred at rt overnight then quenched with NH₄Cl (sat., 20 mL) and diluted with EtOAc (80 mL). The organic phase was washed with sat. NH₄Cl (2x30 mL), sat. NaHCO₃ (30 mL) and brine (30 mL), dried (MgSO₄), filtered and solvents were removed *in vacuo*. The residue was purified by automated column chromatography (Biotag SNAP 25g cartridge 0-5% over 10 CV MeOH in CH₂Cl₂) to give **6** (86 mg, 0.18 mmol, 36%)

¹H NMR (400 MHz, CDCl₃) δ ppm 1.22 (s, 12 H, CH₃) 3.58 - 3.74 (m, 8 H, CH₂) 4.10 (dd, *J*=5, 2 Hz, 2 H, CH₂CH) 5.72 (dt, *J*=18, 2 Hz, 1 H, CHB) 6.62 (dt, *J*=18, 5 Hz, 1 H, CHCHCB) 6.92 (br. s., 1 H, NH) 7.45 - 7.53 (m, 2 H, CHCHCCO) 7.56 - 7.64 (m, 1 H, CHCHCH) 7.76 - 7.81 (m, 2 H, CHCCO) 7.83 (m, *J*=8 Hz, 2 H, CHCHCONH) 7.90 (m, *J*=8 Hz, 2 H, CHCCONH); ¹³C NMR (101 MHz, CDCl₃) δ ppm 24.7 (CH₃) 39.8 (CH₂CH) 69.7 (CH₂) 69.7 (CH₂) 70.3 (CH₂) 72.7 (CH₂) 83.3 (CCH₃) 119.7 (CHCHB) 127.0 (CHCCONH) 128.4 (CHCHCCO) 130.1 (CHCHCCONH and CHCCO) 132.8 (CHCHCH) 137.1 (qAr-C) 137.8 (qAr-C) 139.9 (qAr-C) 148.8 (CHB) 166.6 (CONH) 196.0 (CO);

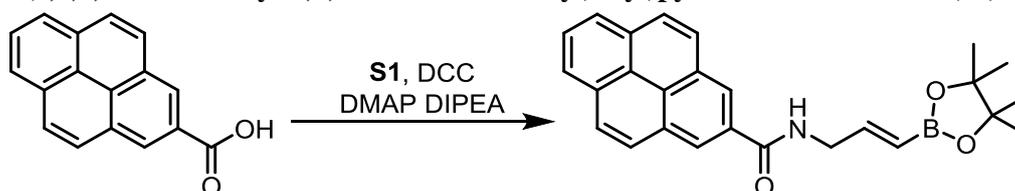
LRMS m/z (ESI⁺): 480.26 [M+H]⁺; HRMS m/z (ESI⁺): Found 502.2359 (M+Na)⁺; C₂₇H₃₄BNO₆Na requires 502.2376; IR (neat): 2978, 2361, 1645, 1538 cm⁻¹.

4-((E)-Phenyldiazenyl)-N-((E)-3-(4,4,5,5-tetramethyl-1,3,2-dioxaborolan-2-yl)allyl)benzamide (7)



To a solution of 4-(phenyldiazenyl)benzoic acid (226 mg, 1 mmol, 2 eq) in dry Tetrahydrofuran (10 mL) was added *N*-(3-dimethylaminopropyl)-*N'*-ethylcarbodiimide hydrochloride (EDC.HCl; 211 mg, 1.1 mmol, 2.2 eq) at 0°C under N₂. The resulting solution was stirred for 30 min at 0°C and then **S1** (149 mg, 0.5 mmol, 1 eq), *N,N*-diisopropylethylamine (DIPEA; 325 μL, 1.75 mmol, 3.5 eq) and 4-dimethylaminopyridine (DMAP; 25 mg, 0.2 mmol, 0.4 eq) were added. The reaction mixture was allowed to warm to rt and stirred for 16 h. Solvents were removed *in vacuo* and the red oil was taken up in EtOAc (150 mL). The organic layer was washed with sat. NH₄Cl (2 x 50 mL), sat. NaHCO₃ (50 mL) and brine (50 mL); dried (MgSO₄), filtered and solvents were removed *in vacuo*. The red residue was purified by automated column chromatography (Biotage SNAP 10g; MeOH in CH₂Cl₂; 0% 5CV; 0-5% 10CV) yielding **7** a deep red solid (*trans:cis*; 7:1; 76 mg, 0.2 mmol, 39%). Values for the minor *cis* isomer are given in *italic*. ¹H NMR (400 MHz, CDCl₃) δ ppm 1.20 - 1.32 (m, (12+12x0.15)=14 H, CH₃) 4.10 - 4.17 (m, (2x0.15) H, CH₂) 4.18 - 4.25 (m, 2 H, CH₂) 5.61 (*dt*, *J*=18, 2 Hz, 1x0.15 H, CH) 5.68 (*dt*, *J*=18, 2 Hz, 1 H, CH) 6.35 (*t*, *J*=6 Hz, 1x0.15 H, NH) 6.48 (*t*, *J*=6 Hz, 1 H, NH) 6.62-6.67 (m, 1x0.15 H, CH) 6.65 - 6.76 (m, 1 H, CH) 6.81 - 6.89 (m, 4x0.15 H, ArH) 7.13 - 7.19 (m, 1x0.15 H, ArH) 7.22 - 7.29 (m, 2x0.15 H, ArH) 7.45 - 7.59 (m, 3 H, ArH) 7.68 (*d*, *J*=9 Hz, 2x0.15 H, ArH) 7.88 - 8.00 (m, 6 H, ArH); ¹³C NMR (101 MHz, CDCl₃) δ ppm 24.7 (CH₃) 43.4 (CH₂) 83.4 (CCH₃) 119.1 (CH) 120.2 (Ar-CH (minor)) 120.6 (Ar-CH (minor)) 122.9 (Ar-CH (major)) 123.0 (Ar-CH (major)) 127.7 (Ar-CH (minor)) 127.9 (Ar-CH (major)) 128.8 (Ar-CH (minor)) 129.1 (Ar-CH (major)) 131.5 (Ar-CH (major)) 136 (Ar-C) 148.1 (CH) 152.4 (Ar-C) 154.2 (Ar-C) 166.6 (CONH); LRMS m/z (ESI⁺): 414.18 [M+H]⁺; HRMS m/z (ESI⁺): Found 414.1960 (M+Na)⁺; C₂₂H₂₆BN₃ONa requires 414.1963; IR (neat): 3316, 2928, 2360, 2341, 1640, 1541 cm⁻¹.

(E)-N-(3-(4,4,5,5-tetra-Methyl-1,3,2-dioxaborolan-2-yl)allyl)pyrene-2-carboxamide (10)



To a solution of *N*-(3-dimethylaminopropyl)-*N'*-ethylcarbodiimide hydrochloride (EDC.HCl, 211 mg, 1.1 mmol, 2.2 eq) in CH₂Cl₂ (10 mL) on ice was added pyrene-2-carboxylic acid (246 mg, 1 mmol, 2 eq). The resulting solution was stirred on ice for 30 min and then 4-dimethylaminopyridine (DMAP; 25 mg, 0.2 mmol, 0.4 eq) and *N,N*-diisopropylethylamine (DIPEA; 304 μL, 226 mg, 1.75 mmol, 3.5 eq) and **S1** (150 mg, 0.5 mmol, 1 eq) were added. The reaction mixture was stirred at rt overnight, then quenched with NH₄Cl (sat., 20 mL) and diluted with EtOAc (80 mL). The organic phase was washed with sat. NH₄Cl (2x30 mL), sat. NaHCO₃ (30 mL) and brine (30 mL), dried (MgSO₄), filtered and solvents were removed *in vacuo*. The residue was purified by automated column chromatography (Biotag SNAP 25g cartridge 0-5% over 10 CV MeOH in CH₂Cl₂) yielding **10** (120 mg, 0.29 mmol, 58%) as a yellow foam.

^1H NMR (400 MHz, CDCl_3) δ ppm 1.29 (s, 12 H, CH_3) 4.24 - 4.34 (m, 2 H, CH_2) 5.76 (d, $J=18$ Hz, 1 H, CH_B) 6.53 (t, $J=6$ Hz, 1 H, NH) 6.78 (dt, $J=18, 5$ Hz, 1 H, CH_2CH) 7.82 - 8.01 (m, 6 H, Ar-H) 8.11 (t, $J=7$ Hz, 2 H, Ar-H) 8.44 (d, $J=9$ Hz, 1 H, Ar-H); ^{13}C NMR (101 MHz, CDCl_3) δ ppm 24.7 (CH_3) 43.5 (CH_2) 83.3 (CCH_3) 119.2 (CHB) 124.0 (Ar-C) 124.1 (Ar-C) 124.2 (Ar-C) 124.4 (Ar-C) 125.5 (Ar-C) 125.6 (Ar-C) 126.1 (Ar-C) 126.9 (Ar-C) 128.3 (Ar-C) 128.4 (Ar-C) 130.4 (Ar-C) 130.5 (Ar-C) 130.9 (Ar-C) 132.3 (Ar-C) 148.4 (CH_2CH) 169.7 (CONH); LRMS m/z (ESI $^+$): 434.20 $[\text{M}+\text{Na}]^+$; HRMS m/z (ESI $^+$): Found 434.1888 ($\text{M}+\text{Na}$) $^+$; $\text{C}_{26}\text{H}_{26}\text{BNNaO}_3$ requires 434.1903; IR (neat): 2977, 1637, 1534 cm^{-1} .

Small molecule cross-couplings

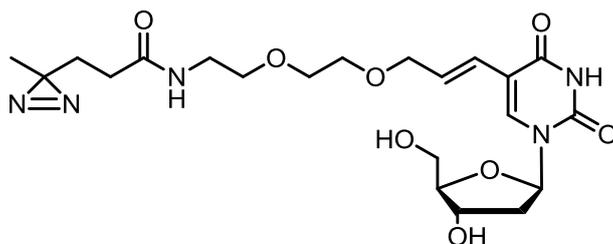
5-Phenyl-2'-deoxyuridine (**1**)^[5]



5-Iodo-2'-deoxyuridine (53 mg, 0.15 mmol, 1 eq), phenylboronic acid (28 mg, 0.23 mmol, 1.5 eq) and K_2CO_3 were assembled in a 15 mL vial. 2 mL ddH_2O , 0.5 mL MeCN and Pd*L1 (150 μL of a 0.05 M stock, 7.5 μmol , 5 mol%) were added. The vial was flushed with argon, closed and heated to 55°C for 5 h. The reaction mixture was allowed to cool down to rt, acidified with 2 M HCl (2 drops) and extracted with CH_2Cl_2 (3x10 mL). The combined organic phases were washed with brine, dried over MgSO_4 and the solvent was removed *in vacuo*. The crude product was purified by column chromatography (CH_2Cl_2 >9:1 CH_2Cl_2 :MeOH) yielding **1** as colorless oil (36 mg, 0.12 mmol, 80%).

^1H NMR (400 MHz, CD_3OD) δ ppm 2.97 (ddd, $J=13, 6, 4$ Hz, 1 H, C^2H) 3.06 (dt, $J=13, 7$ Hz, 1 H, C^2H) 4.33 - 4.47 (m, 2 H, C^5H_2) 4.63 (q, $J=3$ Hz, 1 H, C^4H) 5.06 - 5.13 (m, 1 H, C^3H) 5.94 (br. s., 1 H, 5'-OH) 6.08 (br. s., 1 H, 3'-OH) 7.05 (t, $J=7$ Hz, 1 H, C^1H) 8.07 - 8.14 (m, 1 H, Ph-H) 8.14 - 8.21 (m, 2 H, Ph-H) 8.32 - 8.40 (m, 2 H, Ph-H) 9.01 (s, 1 H, C^6H); ^{13}C NMR (101 MHz, CD_3OD) δ ppm 49.7 (C^1H) 70.6 (C^5H) 79.9 (C^3H) 94.1 (C^1H) 97.2 (C^4H) 123.1 (Ar-C) 136.8 (Ph-CH) 137.5 (Ph-CH) 137.8 (Ph-CH) 142.8 (Ar-C) 147.7 (C^6H) 159.6 (Ar-C) 171.7 (Ar-C) cm^{-1} ; LRMS m/z (ESI $^+$): 327.12 $[\text{M}+\text{Na}]^+$, 343.10 $[\text{M}+\text{K}]^+$; HRMS m/z (ESI $^+$): Found 327.0953 ($\text{M}+\text{Na}$) $^+$; $\text{C}_{15}\text{H}_{16}\text{N}_2\text{NaO}_5$ requires 327.0951.

N-(2-(2-((E)-3-(1-((2R,4S,5R)-4-hydroxy-5-(hydroxymethyl)tetrahydrofuran-2-yl)-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-5-yl)allyloxy)ethoxy)ethyl)-3-(3-methyl-3H-diazirin-3-yl)propanamide (**2**)

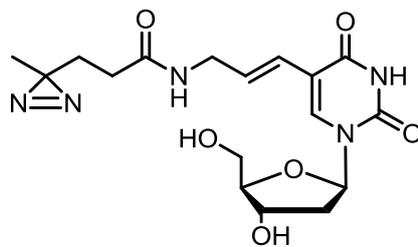


5-Iodo-2'-deoxyuridine (38 mg, 0.1 mmol, 1 eq) and K_2CO_3 (41 mg, 0.3 mmol, 3 eq) were dissolved in 4 mL 3:1 H_2O :MeCN in a 10 mL vial. To the stirred solution was added Pd*L1 (100 μL of a 0.05 M stock, 5 μmol , 5 mol%) and subsequent **4** (57 mg, 0.15 mmol, 1.5 eq). The reaction mixture was stirred at 55°C for 2h after which TLC indicated complete conversion. The solvents were removed *in*

vacuo and the residue was dissolved in MeOH (30 mL), filtered and purified by automated column chromatography (Biotag SNAP 10 g cartridge 0-20% over 20 CV MeOH in CH₂Cl₂) yielding **2** (41 mg, 85 μmol, 85%) as a yellow oil.

¹H NMR (400 MHz, CD₃OD) δ ppm 1.00 (s, 3 H, CH₃CN₂CH₂) 1.61 - 1.68 (m, 2 H, CN₂CH₂CH₂) 2.10 (dd, *J*=8, 7 Hz, 2 H, CN₂CH₂CH₂) 2.22 - 2.36 (m, 2 H, C^{2'}H₂) 3.37 (t, *J*=5 Hz, 2 H, NCH₂CH₂) 3.54 - 3.58 (m, 2 H, NCH₂CH₂) 3.63 (s, 4 H, OCH₂CH₂O) 3.77 (dd, *J*=12, 3 Hz, 1 H, C^{5'}H) 3.85 (dd, *J*=12, 3 Hz, 1 H, C^{5'}H) 3.95 (q, *J*=3 Hz, 1 H, C^{4'}H) 4.12 (dd, *J*=6, 1 Hz, 2 H, CH₂CHCH) 4.44 (dt, *J*=6, 4 Hz, 1 H, C^{3'}H) 6.30 (t, *J*=6 Hz, 1 H, C^{1'}H) 6.38 (d, *J*=16 Hz, 1 H, CH₂CHCH) 6.57 (dt, *J*=16, 6 Hz, 1 H, CH₂CH) 8.22 (s, 1 H, C⁶H); ¹³C NMR (101 MHz, CD₃OD) δ ppm 19.9 (CH₃CN₂) 26.5 (CN₂) 31.4 (CN₂CH₂CH₂) 31.7 (CN₂CH₂CH₂) 40.6 (NCH₂CH₂O) 41.8 (C^{2'}) 62.8 (C^{5'}) 70.7 (NCH₂CH₂O) 71.4 (OCH₂CH₂O) 72.1 (C^{4'}) 73.2 (CH₂CHCH) 86.9 (C^{1'}) 89.2 (C^{3'}) 112.6 (C⁵) 125.1 (CH₂CHCH) 127.9 (CH₂CHCH) 139.4 (C⁶) 151.7 (CO) 164.5 (CO) 174.8 (CO); LRMS *m/z* (ESI⁺): 504.24 [M+Na]⁺ IR (neat): 3400, 3062, 2926, 2871, 2493, 2429, 2361, 2342, 1683, 1644 cm⁻¹; HRMS *m/z* (ESI⁺): Found 504.2067 (M+Na)⁺; C₂₁H₃₁N₅NaO₈ requires 504.2065.

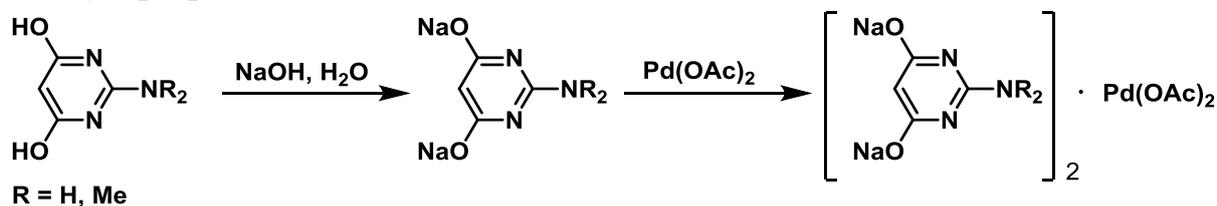
N-((E)-3-(1-((2R,4S,5R)-4-hydroxy-5-(hydroxymethyl)tetrahydrofuran-2-yl)-2,4-dioxo-1,2,3,4-tetrahydropyrimidin-5-yl)allyl)-3-(3-methyl-3H-diazirin-3-yl)propanamide (3)



5-Iodo-2'-deoxyuridine (28.3 mg, 0.08 mmol, 1 eq) and K₂CO₃ (33.2 mg, 0.24 mmol, 3 eq) were dissolved in 4 mL 3:1 H₂O:MeCN in a 10 mL vial. To the stirring solution was added Pd*L1 (80 μL of a 0.05 M stock, 4 μmol, 5 mol%) and subsequent **3** (35.2 mg, 0.12 mmol, 1.5 eq). The reaction mixture was stirred at 50°C for 4h. The solvents were removed *in vacuo* and the residue was dissolved in MeOH (30 mL), filtered and purified by automated column chromatography (Biotag SNAP 10 g cartridge 0-20% over 20 CV MeOH in CH₂Cl₂) yielding an inseparable mix of **5c** and starting material (30 mg, 76 μmol, 95%, 60% **3** as determined by NMR) as a yellow oil.

¹H NMR (400 MHz, CDCl₃) δ ppm 1.01 (s, 3 H, CH₃CN₂CH₂) 1.64 - 1.70 (m, 2 H, CN₂CH₂CH₂) 2.07 - 2.15 (m, 2 H, CN₂CH₂CH₂) 2.18 - 2.34 (m, 4 H, C^{2'}H₂) 3.35 (s, 1 H) 3.74 (ddd, *J*=12, 7, 3 Hz, 2 H, C^{5'}H₂) 3.79 - 3.85 (m, 2 H, C^{5'}H₂) 3.87 (d, *J*=6 Hz, 2 H, C^{4'}H) 3.93 (q, *J*=3 Hz, 2 H, CH₂CHCH) 4.38 - 4.44 (m, 2 H, C^{3'}H) 4.87 (s, 12 H) 6.20 - 6.31 (m, 3 H, C^{1'}H, CH₂CHCH) 6.39 - 6.52 (m, 1 H, CH₂CHCH) 8.15 (s, 1 H, C⁶H) 8.53 (s, 1 H, C⁶H); ¹³C NMR (101 MHz, CDCl₃) δ ppm 19.9 (CH₃CN₂) 31.4 (CN₂CH₂CH₂) 31.7 (CN₂CH₂CH₂) 41.8 (C^{2'}) 41.9 (C^{2'}) 42.9 (CH₂CHCH) 62.6 (C^{5'}) 62.8 (C^{5'}) 72.1 (C^{4'}) 72.2 (C^{4'}) 86.8 (C^{1'}) 87.1 (C^{1'}) 89.2 (C^{3'}) 89.2 (C^{3'}) 112.8 (C⁵) 124.0 (CH₂CHCH) 127.8 (CH₂CHCH) 139.0 (C⁶) 147.4 (C⁶) 151.7 (CO) 174.5 (CO); LRMS *m/z* (ESI⁺): 432.15 [M+K]⁺ IR (neat): 3727, 3325, 3068, 2928, 2261, 2341, 1680, 1638, 1548 cm⁻¹; HRMS *m/z* (ESI⁺): Found 416.1545 (M+Na)⁺; C₁₇H₂₃N₅NaO₆ requires 416.1541

Catalyst preparation



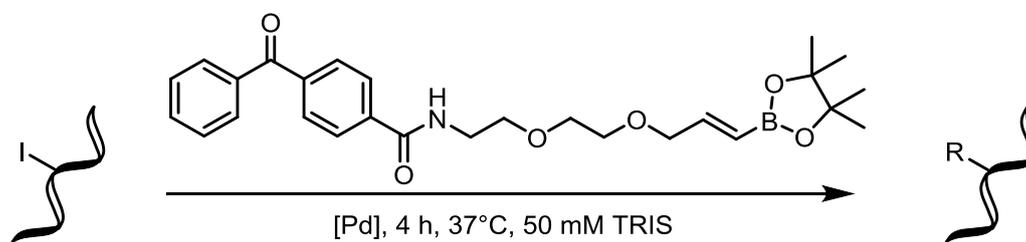
To 2-aminopyrimidine-4,6-diol (65 mg, 0.5 mmol, 2 eq, R = H) or 2-(dimethylamino)pyrimidine-4,6-diol (78 mg, 0.5 mmol, 2 eq, R = Me) in a 5 mL volumetric flask was added H₂O (3 mL) and NaOH (10 M stock, 100 μ L, 1 mmol, 4 eq). The solution was stirred for ~5 min at rt until all solids were dissolved. Then Pd(OAc)₂ (55 mg, 0.25 mmol, 1 eq) was added and the flask was stoppered and stirred at 65°C for 60 min. The stirring bar was removed and the solution was adjusted to 5 mL with H₂O to give a 50 mM stock solution.

ODN crosscoupling

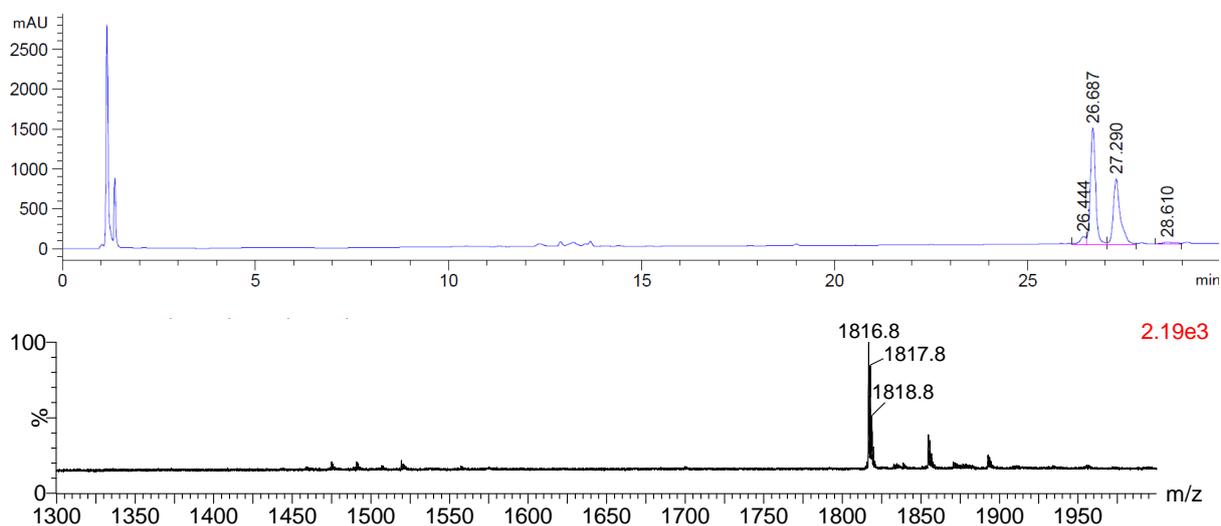
General reaction conditions

Unless otherwise noted, 100 μ M ODN1-4, 50 mM Tris pH 8.5, 10-50 μ M Pd(OAc)₂LX₂ and 10 mM boronic ester were combined in an eppendorf tube and shaken for 4h at 37°C in an incubator. Then the reaction was spun down (2 min, 16000 x g) and the supernatant was analyzed by HPLC and MS. Sometimes precipitation is observed after 24h in the catalyst stock solution. In these cases, probably due to lower actual concentration, the reaction proceeds better with 1 eq (100 μ M) Pd(OAc)₂LX₂.

ODN1a

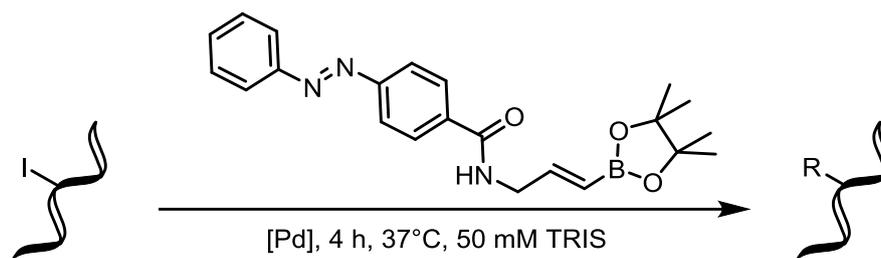


ODN1a elutes at 26.69 min. The peak at 27.29 is a small molecule impurity. Gradient is 5%-20% B in 30 min.

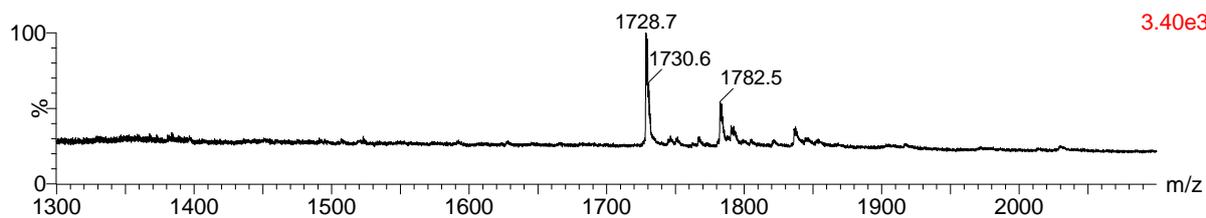
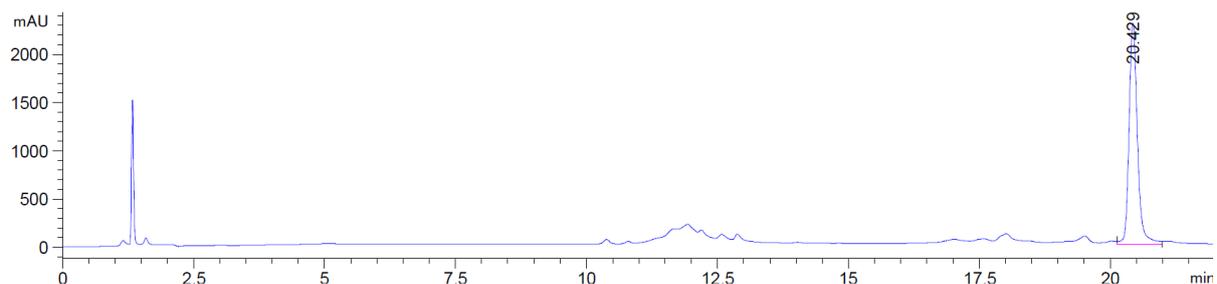


Calc 1816.3 found 1816.8

ODN1b

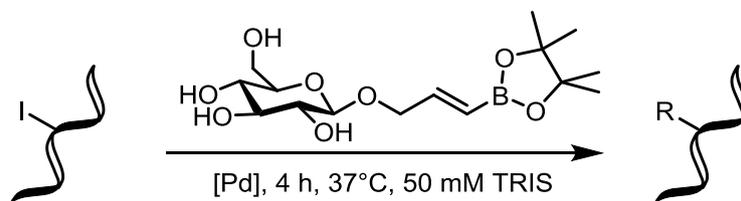


Product elutes at 20.4 min. Gradient is 5%-20% B in 20 min.

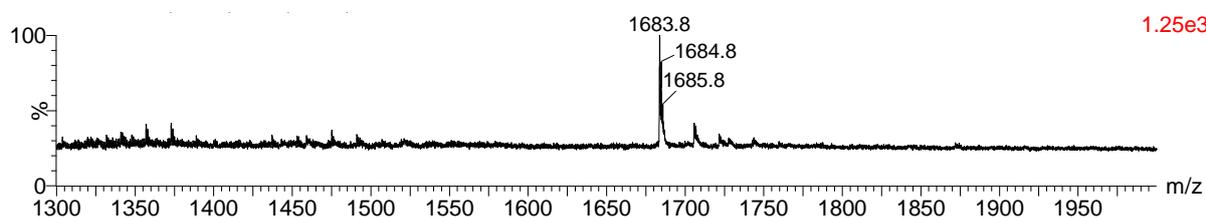
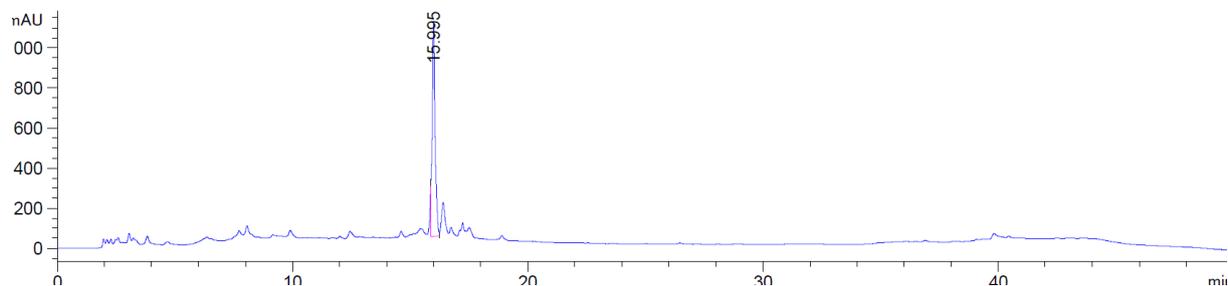


Calc 1728.2 found 1728.7

ODN1c

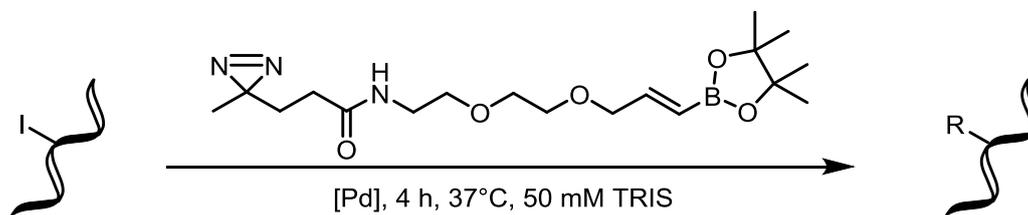


Product elutes at 16 min. Gradient is 0%-30% B in 30 min.

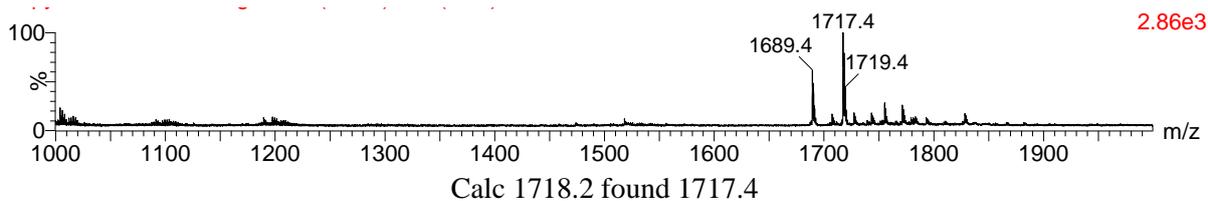
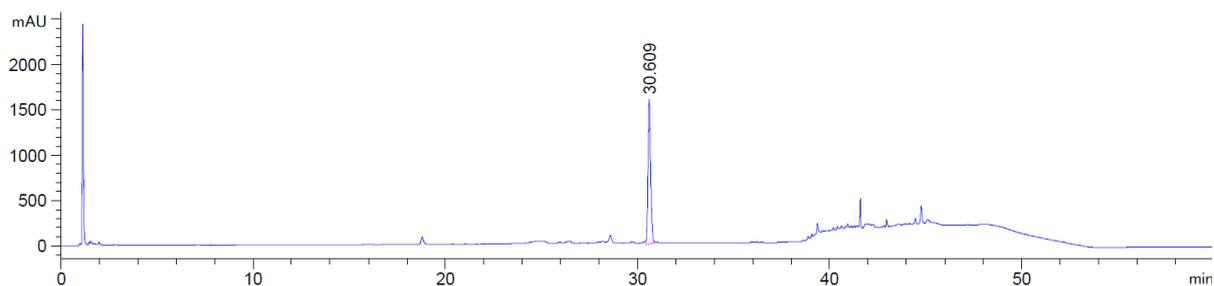


Calc 1683.2 found 1683.8

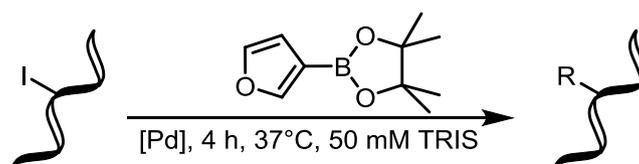
ODN1d



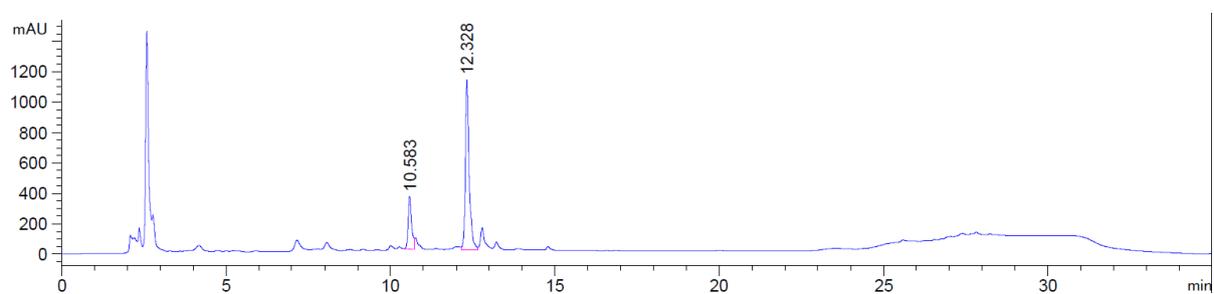
Product elutes at 30.6 min. Gradient is 5%-20% B in 35 min.

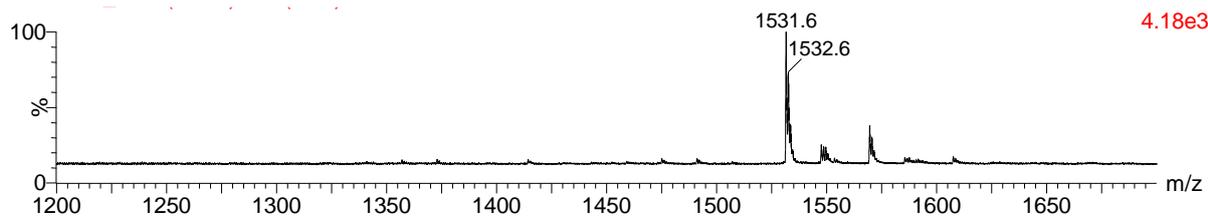


ODN1e

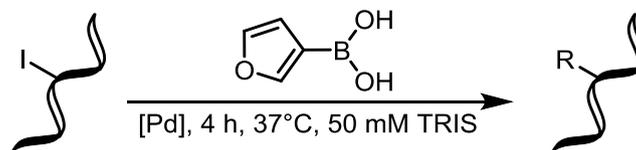


Product elutes at 12.3 min. Gradient is 5%-40% B in 20 min.

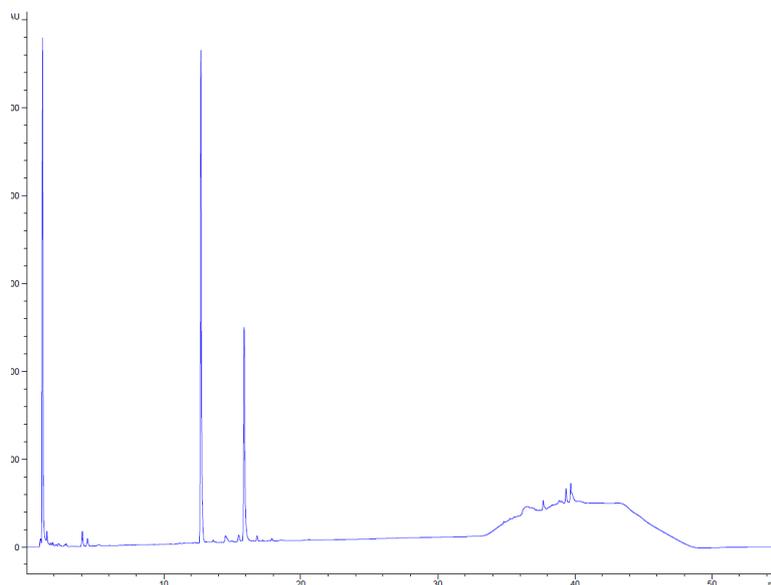




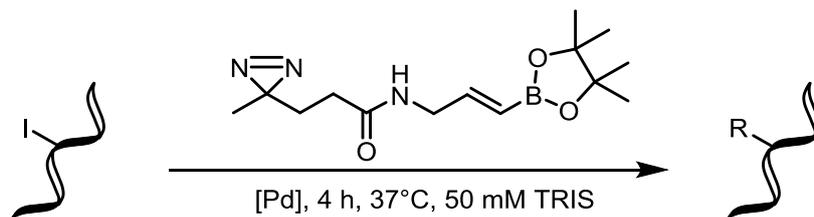
ODN1e reaction with 3-furane boronic acid



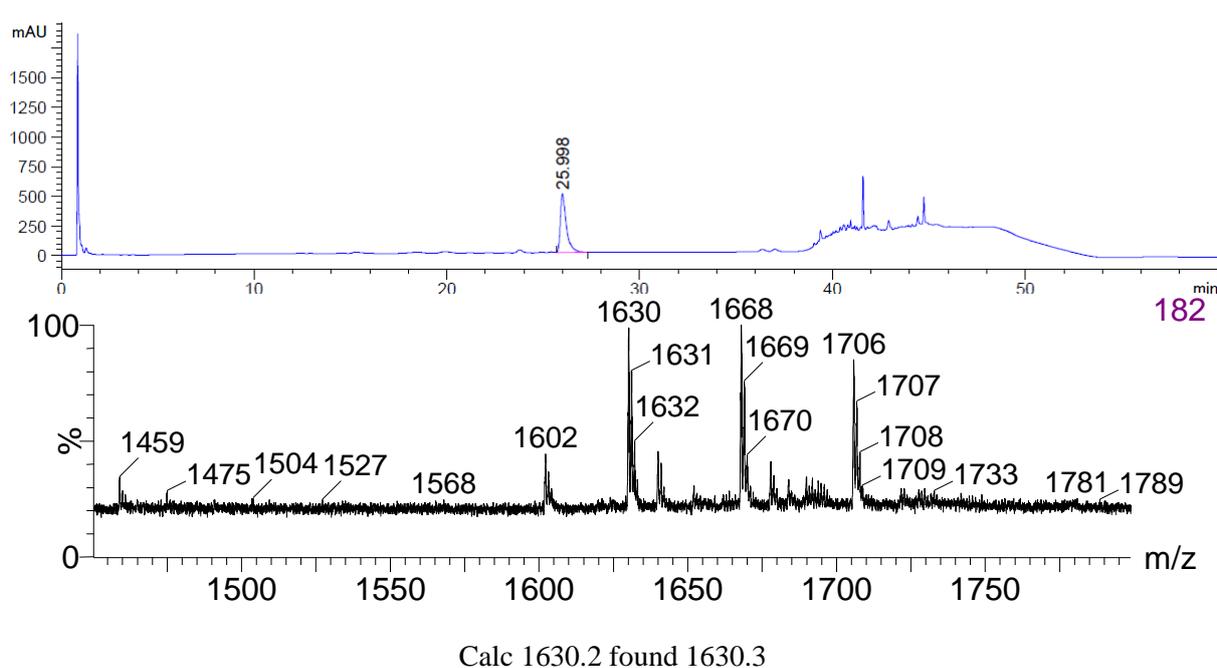
Product elutes at 15.8 min, the product of deiodination at 12.6 min. Gradient is 5%-20% B in 20 min.



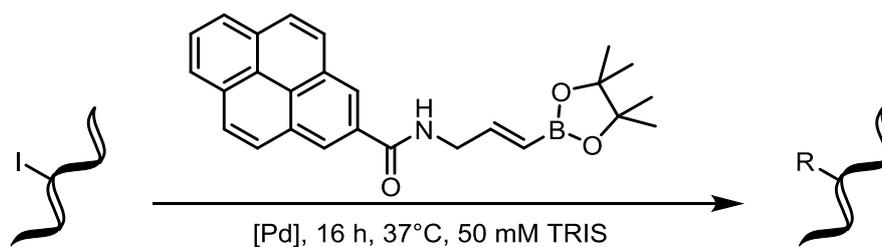
ODN1f



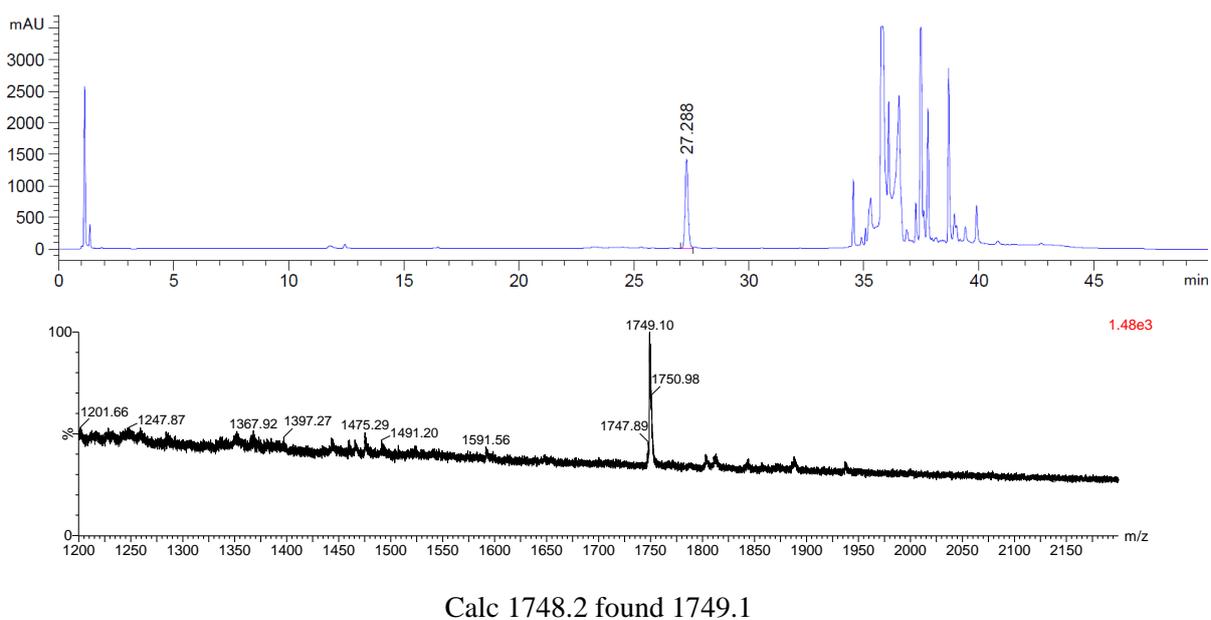
Product elutes after 26 min. Gradient is 5%-20% B in 30 min.



ODN1g

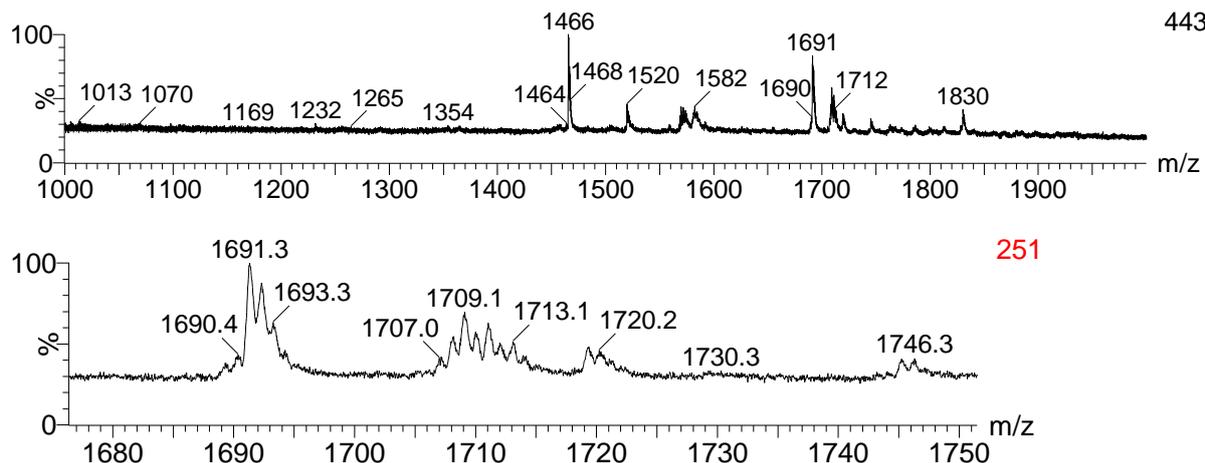


The reaction was performed in 40% MeCN. Product elutes at 27.3 min. Gradient is 5%-30% B in 30 min.



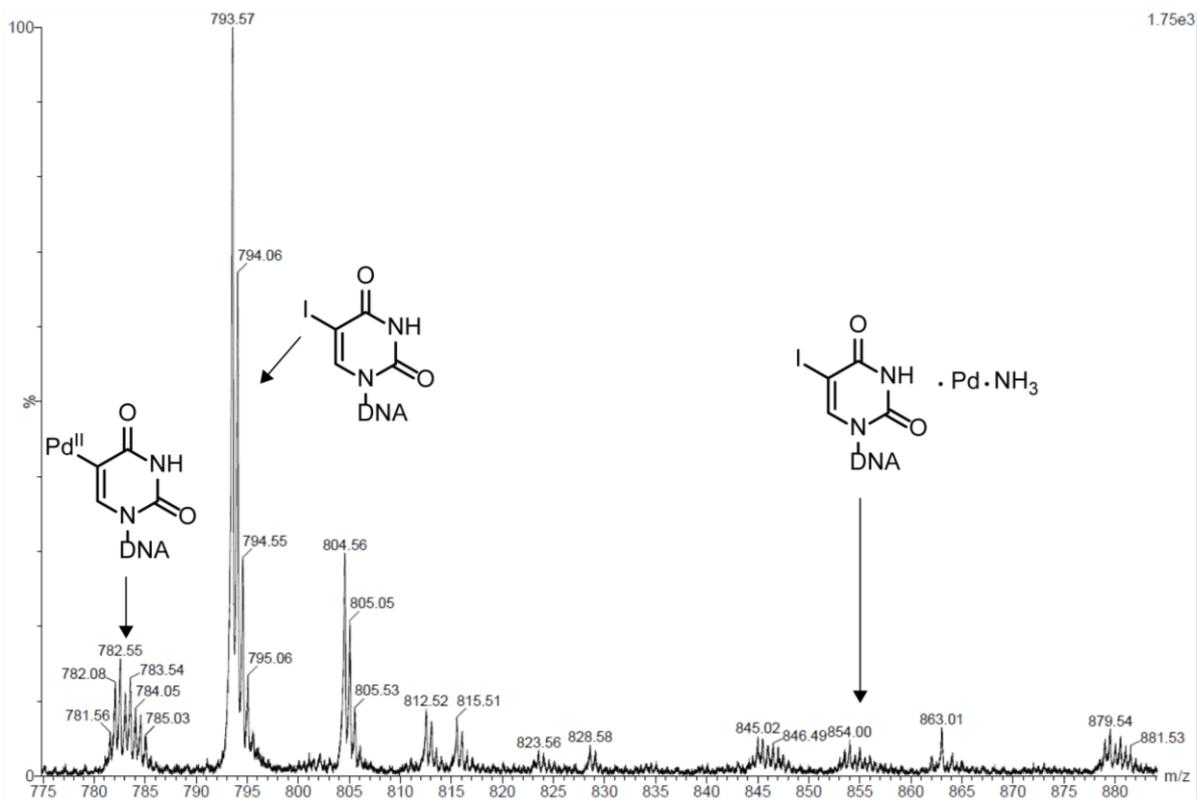
ODN1 Palladium adduct observed in PO4 buffer

When performing the cross-coupling of **5** to **ODN1d** in phosphate buffer the same species can be observed in the MALDI of the crude reaction mixture.



ODN1 reaction intermediates by ESI-MS

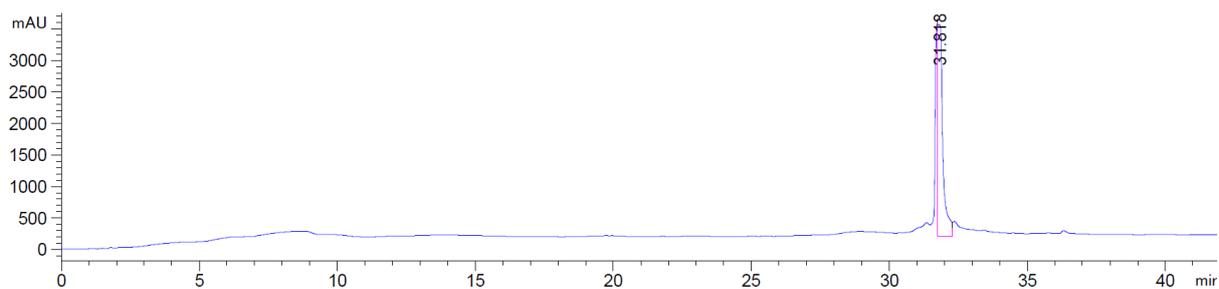
The PdOAc₂L1₂ species for this reaction was prepared as describe previously, but substituting NaOH with NH₄OH (33%). The reaction was conducted as described in the general reaction conditions, but using 10 mM NH₄OAc buffer (pH 8.5) and 100 μM Pd PdOAc₂L1₂ (1 eq relative to ODN1). The reaction was allowed to proceed for 30 min at 37°C. Then, particulates were removed by centrifugation (2 min, 16k x g) and 10 μL of the reaction mixture were injected into the LCT (ESI-) with the autosampler using a flow of 50:50 H₂O:MeOH (200 μL/min). While more Pd containing species can be observed, these could not be unambiguously identified.



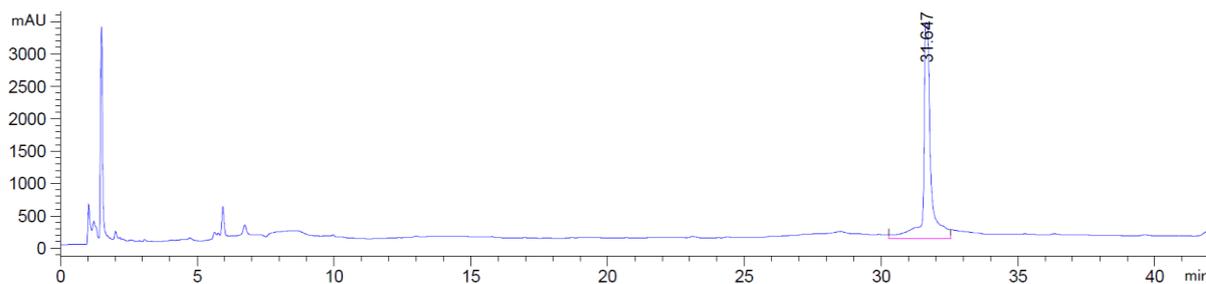
ODN2 (no IdU control)

ODN2 elutes at 31.8 min. Gradient is 0%-20% B in 40 min.

Before reaction:

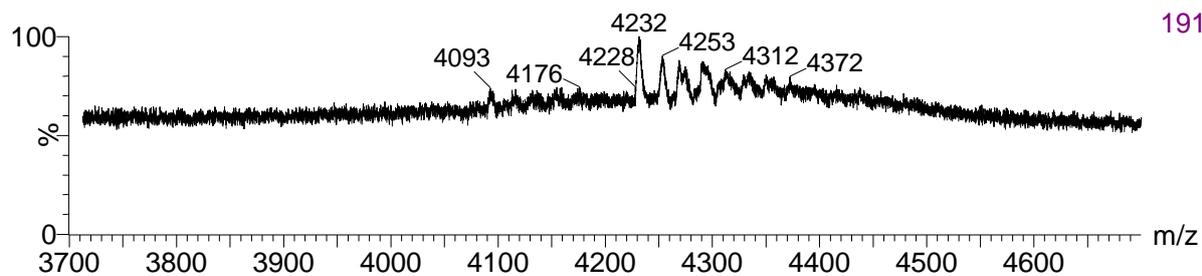
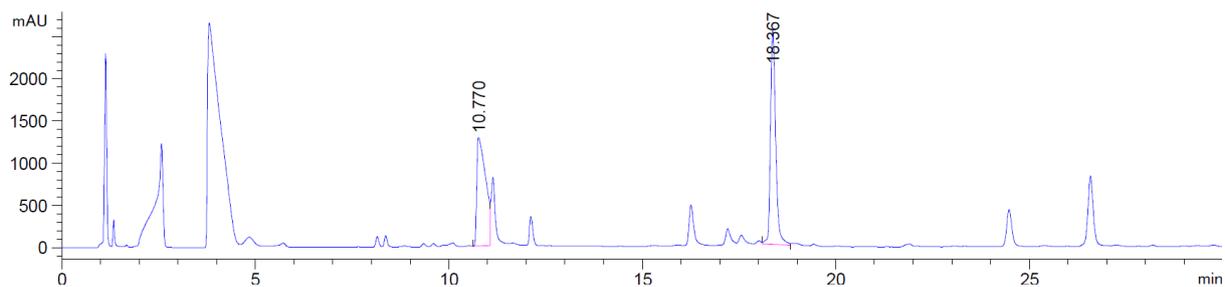


After the reaction:



ODN3b

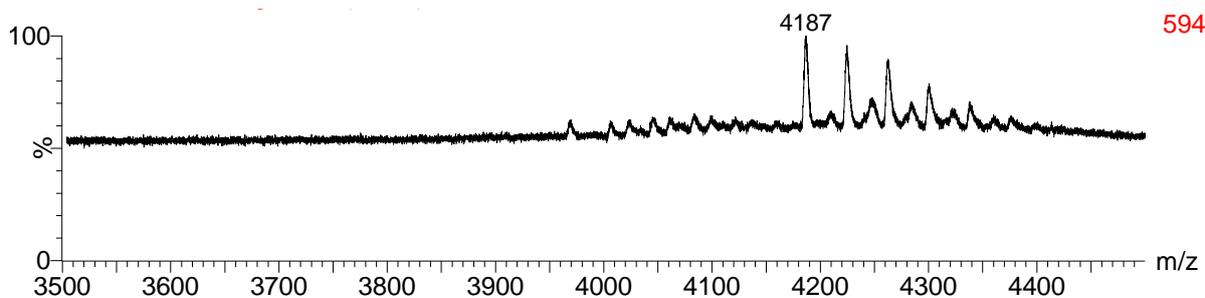
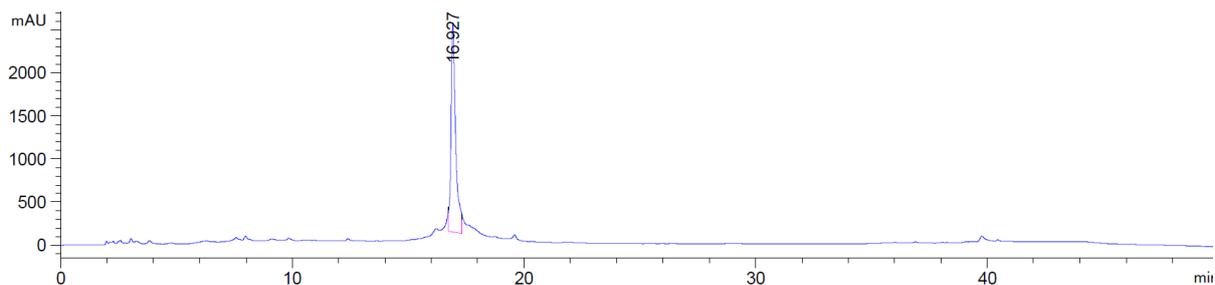
The Product elutes at 18.4 min. ODN was separated on a gradient of 5%-20% B in 20 min.



Calc. 4232 found 4232

ODN3c

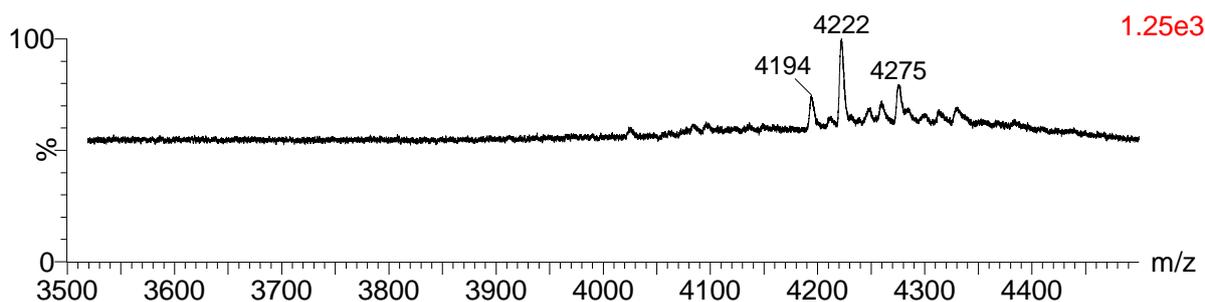
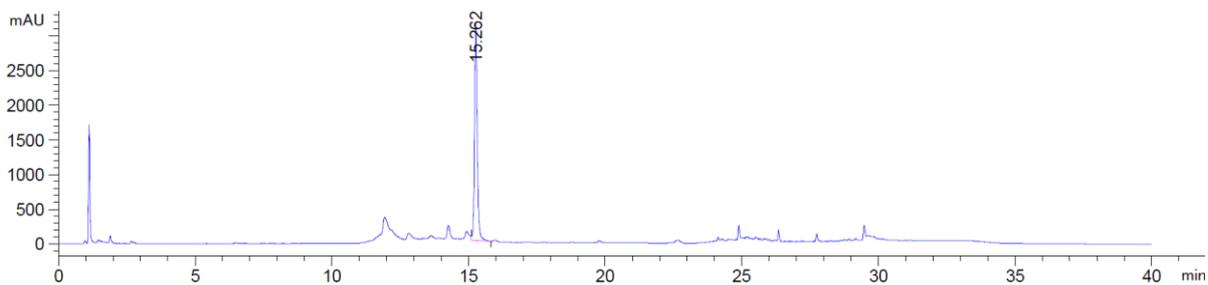
The Product elutes at 16.9 min. ODN was separated on a gradient of 0%-40% B in 30 min.



Calc. 4187 found 4187

ODN3d

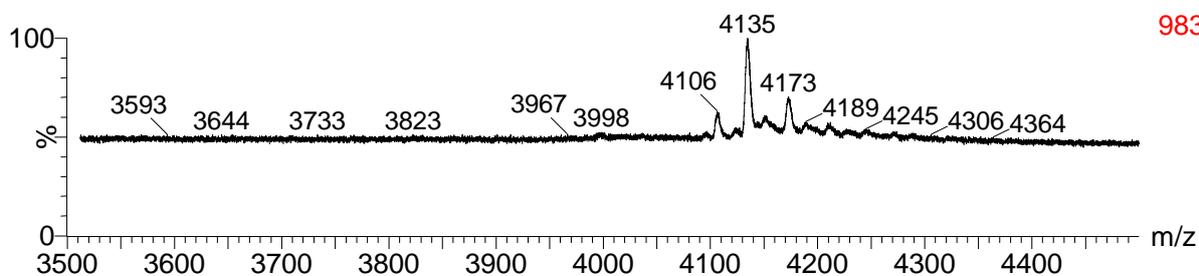
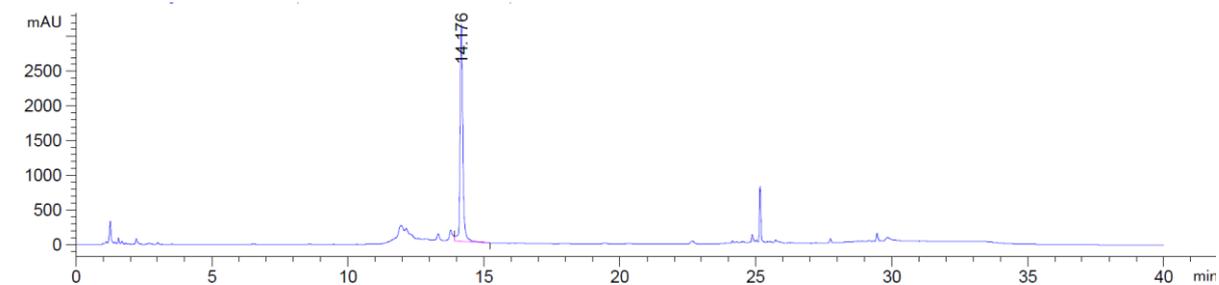
The Product elutes at 15.3 min. ODN was separated on a gradient of 5%-20% B in 20 min.



Calc. 4222 found 4222

ODN3f

The Product elutes at 14.2 min. ODN was separated on a gradient of 5%-20% B in 20 min.



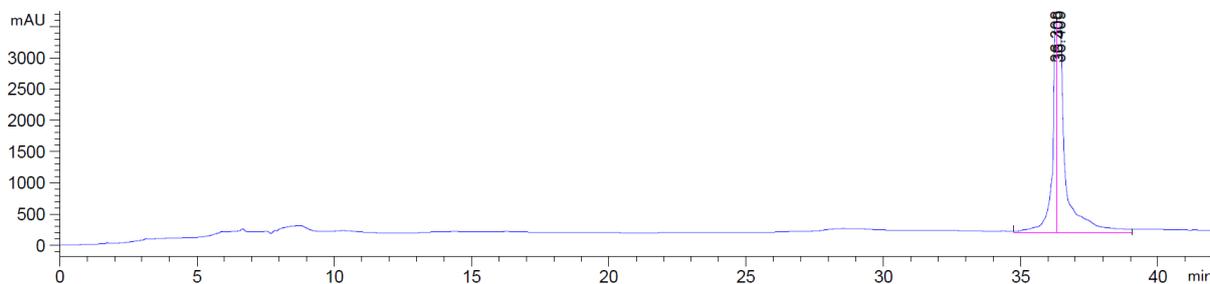
Calc. 4135 found 4135

ODN4 control reactions

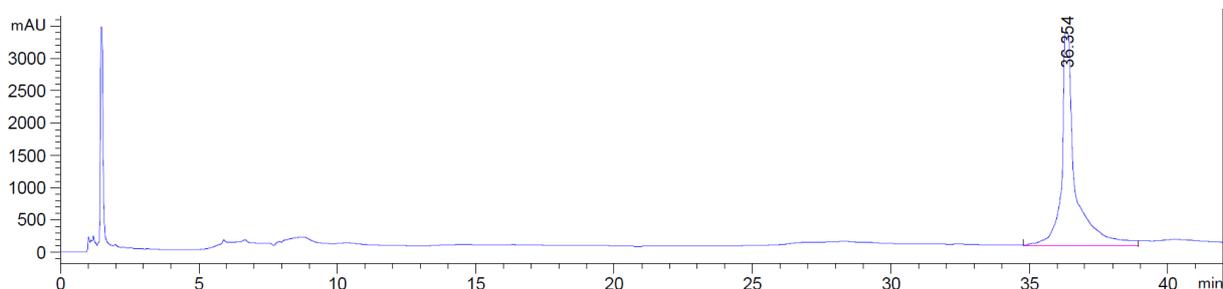
Control reactions were set up as described in the general procedure omitting one component where stated. Boronic ester **2** was used for these experiments.

ODN was separated on a gradient of 0%-20% B in 40 min. The starting material elutes at 36.4 min and the product at 40.5 min.

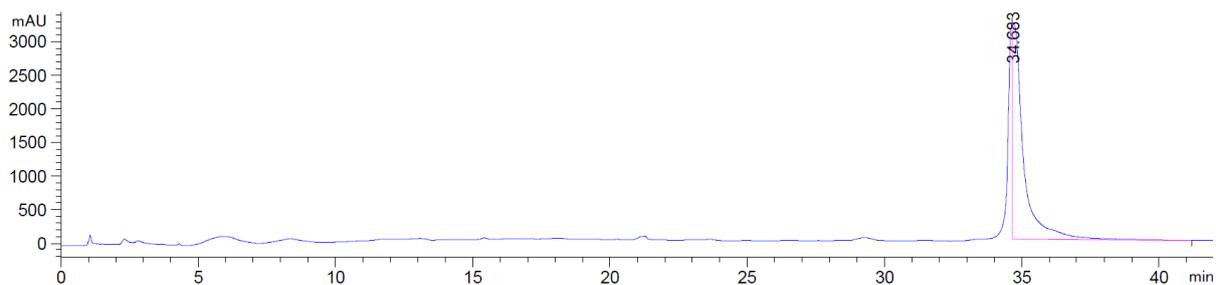
Starting material:



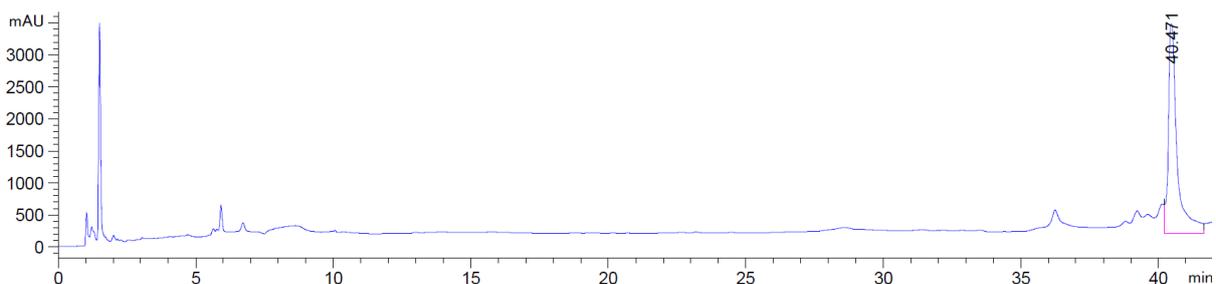
No Boronic ester:



No Palladium:



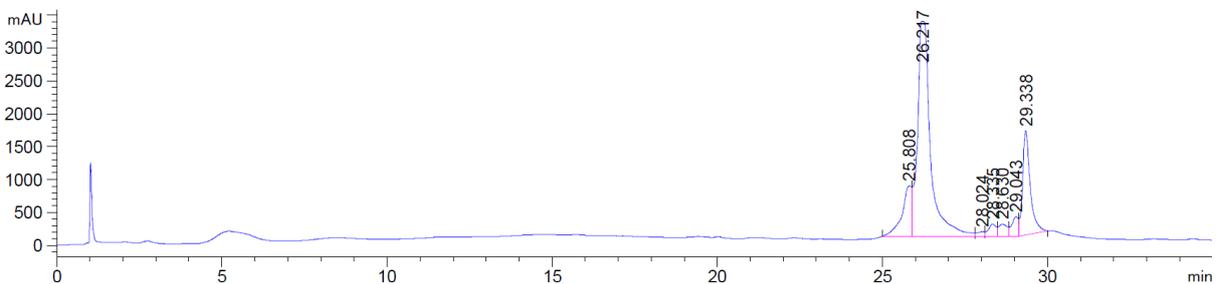
All components:



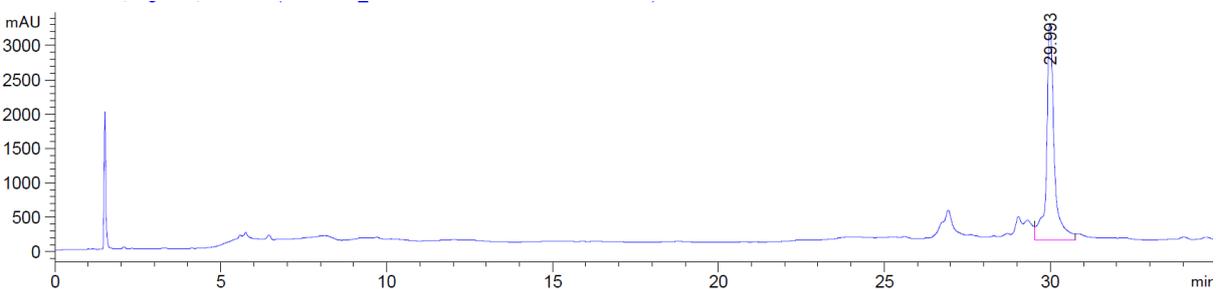
ODN4 – Phosphate and Tris buffer comparison

Reactions were conducted as described in the general procedure but in 100mM PO₄ pH 8.5 buffer with Boronic ester **2**. The starting material elutes at 26.2 min and the product at 29.3 min. ODN was separated on a gradient of 0%-30% B in 40 min.

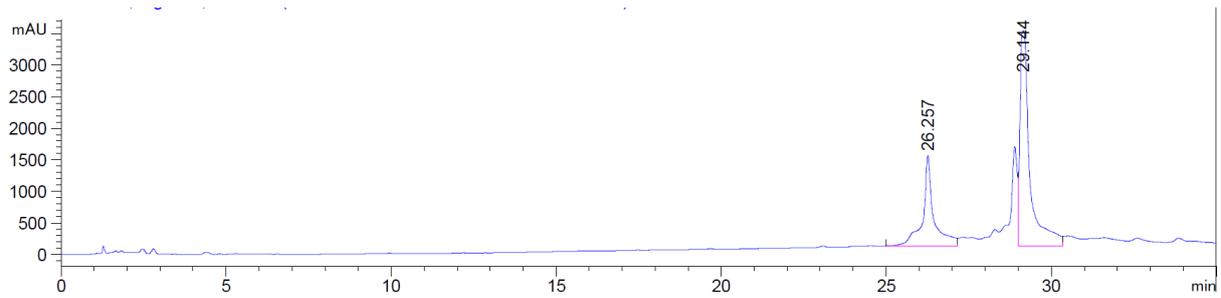
PO₄ after 3h:



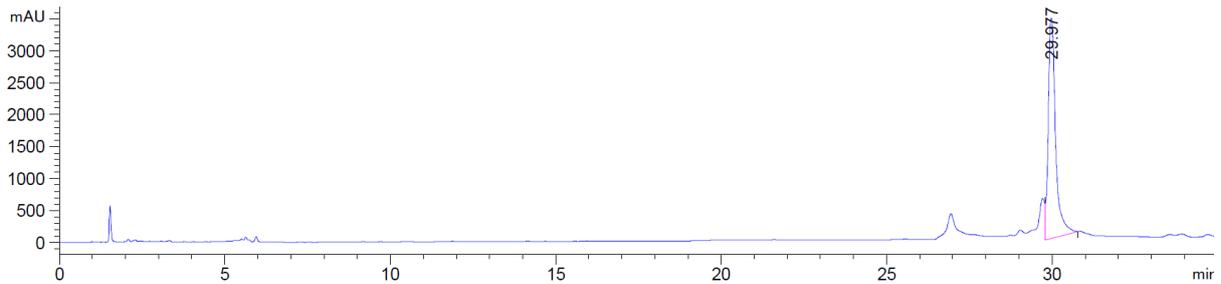
Tris after 3h:



PO₄ overnight:

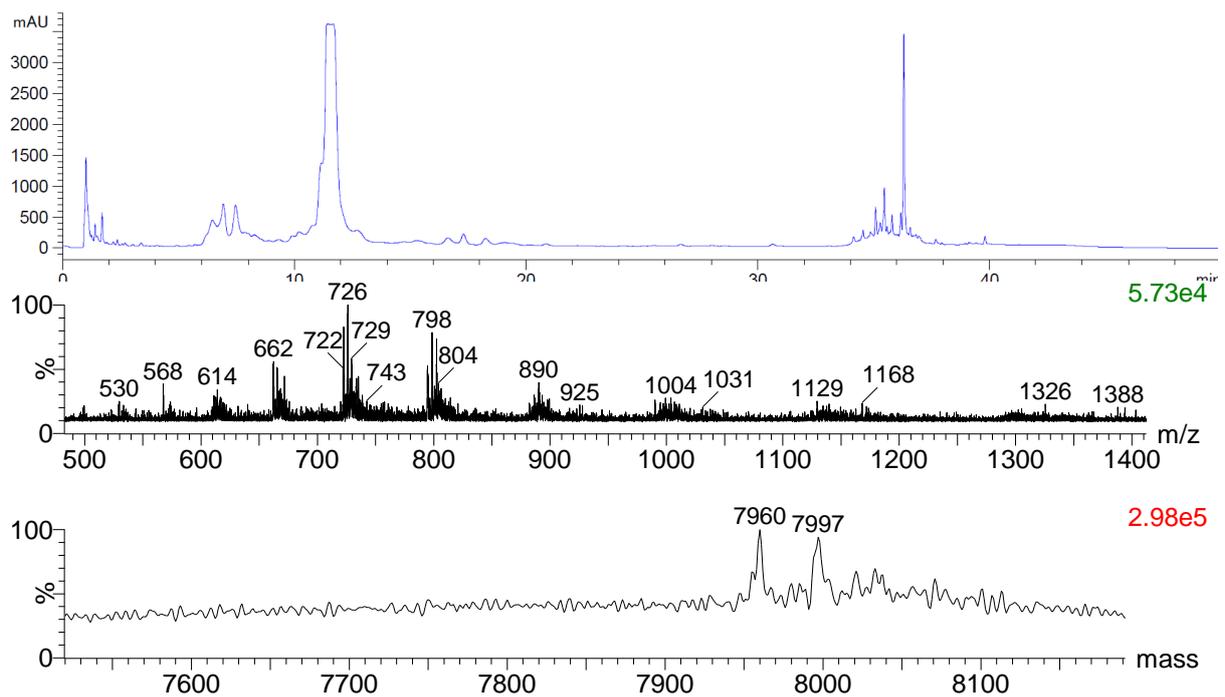


Tris overnight:



ODN4d

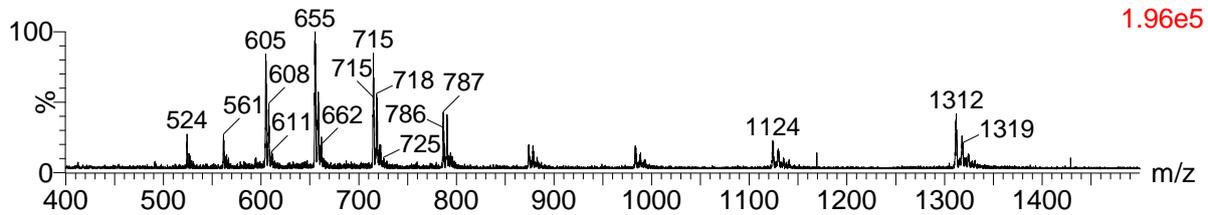
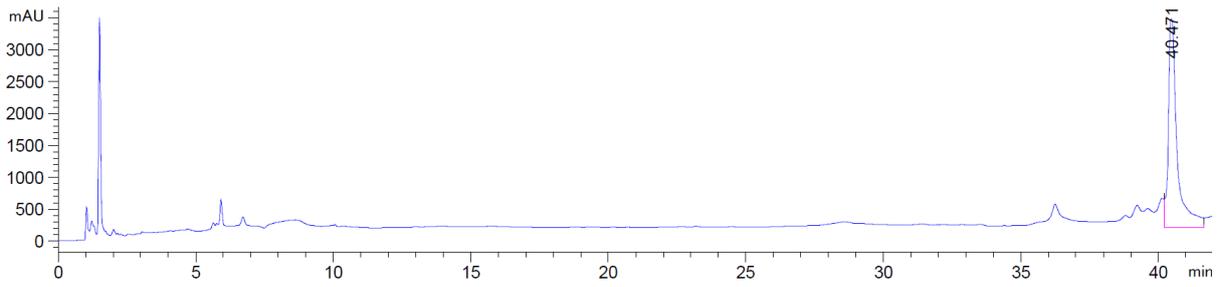
ODN was separated on a gradient of 15%-25% B in 30 min



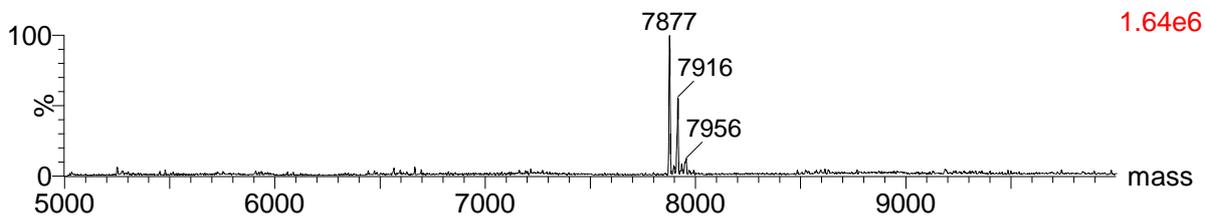
Calc. 7964 found 7960

ODN4f

ODN was separated on a gradient of 0%-20% B in 40 min



1.96e5

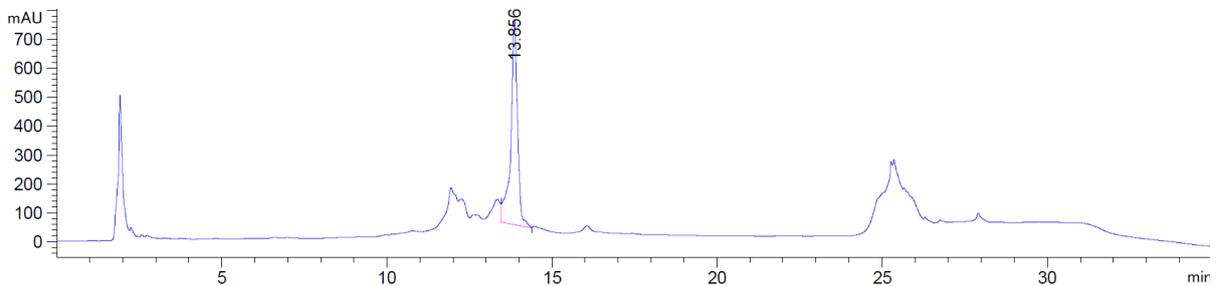


1.64e6

Calc. 7875 found 7877

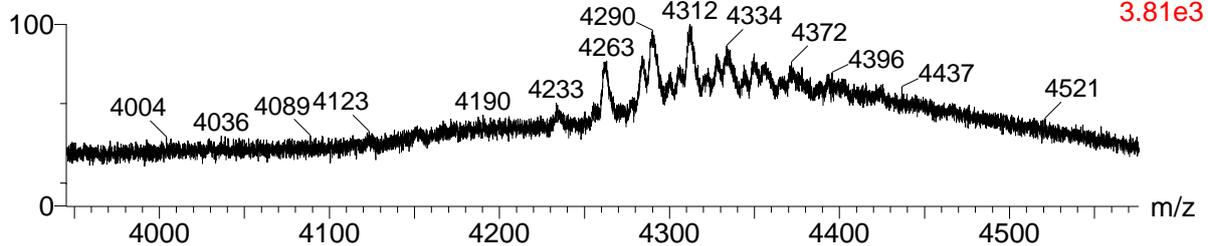
ODN5f

ODN was separated on a gradient of 10%-30% B in 20 min.



20130617_2ldU_P1 7 (0.234)

TOF LD+
3.81e3

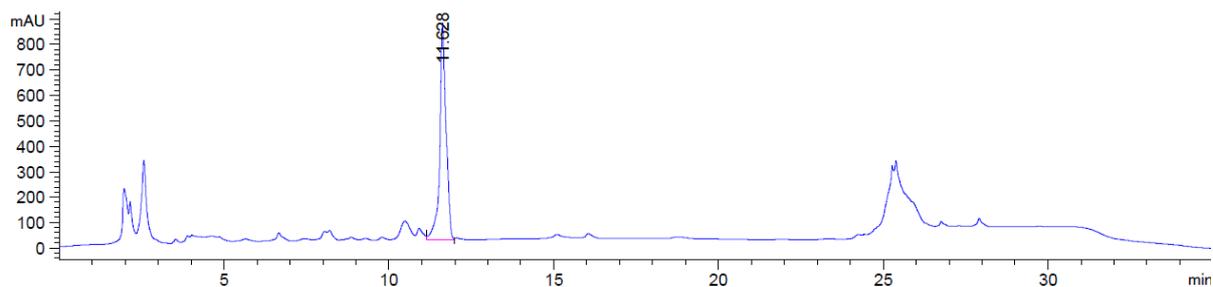


Calc. 4291 found 4290

(other peaks correspond to a Na^+ adduct (4321) or loss of N_2 (4263) and the corresponding Na^+ adduct (4286))

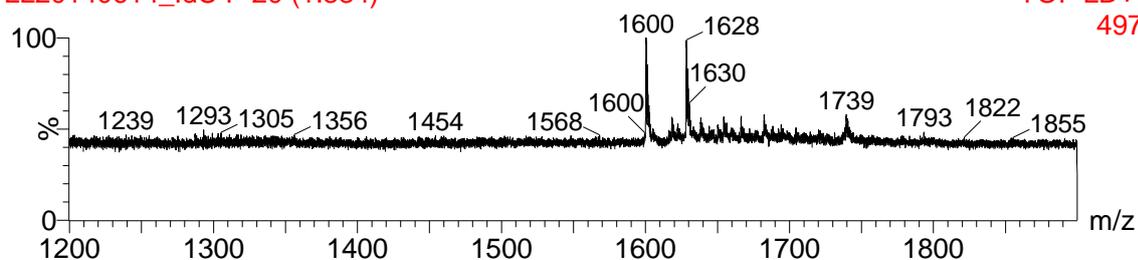
ODN6f

ODN was separated on a gradient of 10%-30% B in 20 min.



LL20140614_IdC P 20 (1.334)

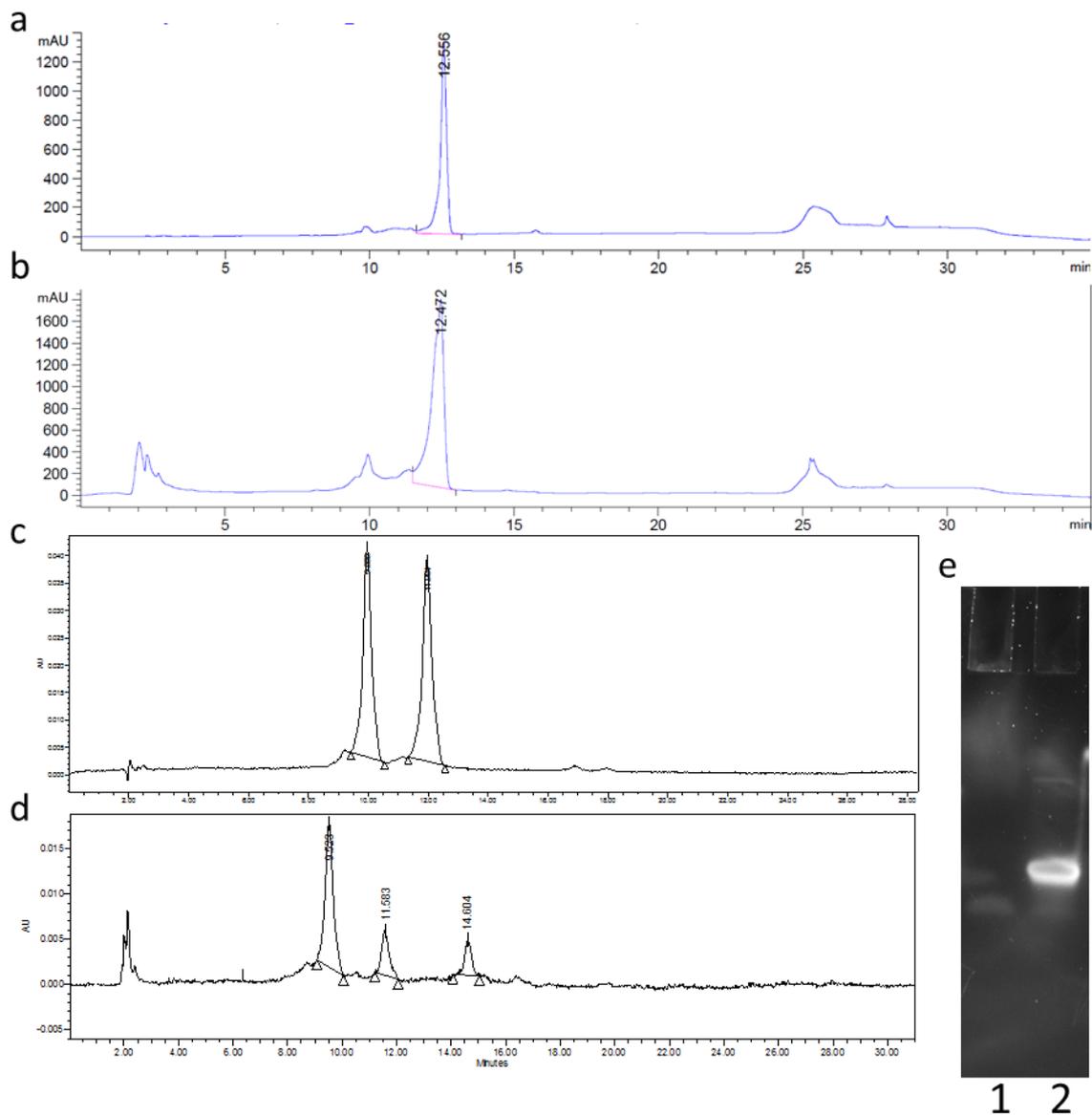
TOF LD+
497



Calc. 1628 found 1628

dsDNA crosscoupling

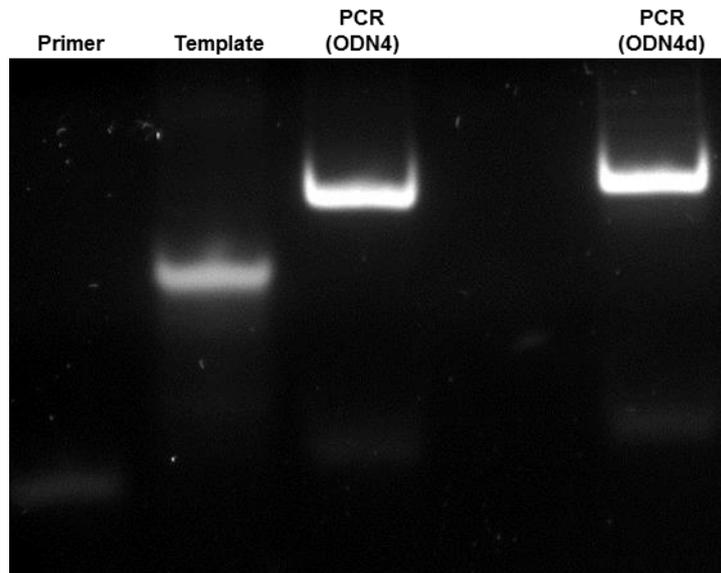
ODN3 was annealed with the appropriate complementary strand (CTACTGCATCGGT; predicted melting temperature 43°C) by cooling a 150 μ M solution of each ODN in annealing buffer (10 mM TRIS pH 7.5, 100 mM NaCl) from 90°C to 4°C at 1°C per minute in a PCR block. The resulting dsODN was used as substrate for the crosscoupling reaction under the standard conditions (100 μ M dsODN, 100 μ M PdOAc₂L₂, 10 mM **5**, 50 mM TRIS pH 8.5) and was shaken at 37°C for 16h. The resulting mixture was analyzed by PAGE (15%, 0.5x TBE; stained with Sybr safe), HPLC (10%-30% buffer B in 20 min) or denaturing HPLC (column was heated at 50°C; 10%-20% B in 30 min). Chromatograms and gel are shown below.



Supplemental Figure S 2. a. HPLC chromatogram of dsODN3 after annealing (retention time: 12.6 min). **b.** HPLC chromatogram of the crosscoupling reaction on dsODN3. Main peak retention time is 12.5 min, but the peak is broad and a smaller peak with smaller retention time can be observed. **c.** Denaturing HPLC chromatogram of the dsODN3. 2 Peaks with almost identical area can be observed at retention times of 10 min and 12 min, representing the two ssODN. **d.** Denaturing HPLC chromatogram of the crosscoupling reaction of dsODN3. 3 main peaks are observed at 9.5 min, 11.5 min and 14.6 min. The peak at 9.5 corresponds to the unreactive ODN, while 11.5 is the IdU containing ODN and 14.6 the crosscoupling product. Yield of the crosscoupling product, when comparing to the unmodified ODN is 21%. **e.** PAGE gel showing the ssODN3 in lane 1 and dsODN3 after the crosscoupling reaction. The dsODN is largely still hybridized, but a faint band at the height of the ssODN can be seen, indicating some melting during the reaction.

PCR probe generation

Following template (T1: GCT GCC TGG ACT GAC CTC ACA TGA CCT TAC GCG CAG AGA CCT AGA CAG TGC TTC AGG) and Primers (ODN4d and P2: GCT GCC TGG ACT GAC CTC ACA TGA CC) were used. The PCR was performed with Vent exo⁻ (NEB, M0257S) using the manufacturers recommended buffers and dNTP concentrations. Temperature cycle for the PCR was as follows (55°C, 20 sec; 72°C, 30 sec; 95°C, 15 sec) and was repeated 40x. The PCR product was purified by phenol extraction and ethanol precipitation.



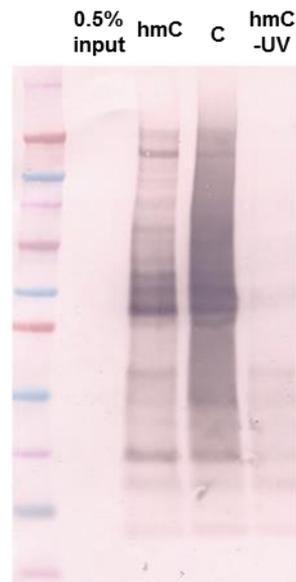
Supplemental Figure S3 PAGE (15%, 0.5% TBE) analysis of the PCR. Primer (lane 1) and template (lane 2; ssDNA) are shown as control. The obtained product molecular weight and yield are not affected by the presence of primer modification (compare lane 3 (IdU; ODN4 as primer) and lane 4 (ODN4d as primer)).

Photocrosslinking

Nuclear extract was prepared using the NE-PER kit (Pierce, 78833) from two confluent 145 mm petri-dishes HeLa cells using the manufacture recommended procedure. Obtained nuclear extract was dialyzed into cross linking buffer (25 mM TRIS pH 7.5, 100 mM NaCl, 1 mM EDTA, 2 mM MgCl₂, 0.5 mM DTT, 20% glycerol and one Complete Protease Inhibitor (Pierce, without EDTA) per 50 mL) for 3h. The obtained extract was pre-cleared with Captavidin beads (50 µL, life technology, C-21386), by incubation for 1:30 h at 4°C. The beads were removed by centrifugation and Probes were added (3 nmol, purified from PCR). The mixture was incubated for 20 min on ice and then irradiated for 30 min at 311 nm (caprobox; Caprotec) for silac experiments or at 365 nm using a handheld UV lamp (8W). The solution was adjusted to 1M NaCl and Dynabeads® MyOne™ Streptavidin T1 (200 µL, life technology, 65601) were added. Binding was performed on at room temperature for 1.30 h under constant agitation. The beads were immobilized on DynaMag™- Spin Magnet (life technology, 12320D), and washed with wash buffer (10 mM TRIS, 1 mM EDTA, 1 M NaCl) three times and with wash buffer + 6 M Urea two times. The proteins were released by boiling in Laemli loading buffer for 10 min and separated on a 4-12% gradient gel (NuPAGE® Novex® 4-12% Bis-Tris Gel, Invitrogen). The gel was either visualized by silver stain (Pierce Silver Stain Kit, Thermo Scientific, 24612) or transferred to PVDF membrane using the iBlot (Invitrogen). The membrane was then blocked (3% BSA in TBS-T) for 30 min at room temperature, washed 5 times with TBS-T and then incubated with ExtrAvidin® –Alkaline Phosphatase (Sigma, E2636) for 1h at room temperature. The membrane was then again washed with TBS-T (5x) and water (3x) before visualizing with the BCIP/NBT Liquid Substrate System (Sigma, B1911).

For SILAC experiments the hmC containing probe was incubated and cross-linked with unlabeled cell lysate and the C containing probe with isotope labeled cell lysate (Arg10 and Lys8) for the forward experiment. For the reverse experiment, heavy and light cells were switched. After crosslinking the mixtures were pooled and processed together as described above. After SDS-PAGE the gel was stained with coomassie blue, cut in slices and tryptic digest was performed as described elsewhere (<http://www.ccmp.ox.ac.uk/protocols-and-tools>).

Streptavidin blot



Supplemental Figure S4 Biotin western blot of the photo-crosslinking reaction in HeLa nuclear extract using hmC or C containing probes (lane 2 and 3) and the control without UV irradiation (lane 4). Only upon irradiation covalent DNA-Protein conjugates are observed.

Supplementary Results

SILAC experiments were carried out twice, the first time where the DNA probe containing CTP was incubated with extracts prepared from cells labeled with heavy amino acid isotopes (heavy), whereas extracts from unlabeled cells (light) were incubated with the dhmCTP containing DNA probe. In the second experiment, extracts prepared from heavy labeled cells were incubated with the hmCTP DNA probe and unlabeled cell extracts with the CTP DNA probe. This allowed the SILAC mass spectrometry analysis to be performed in forward and reverse ratios, and proteins differentially present would be expected to exert inverted abundance ratios between the two SILAC experiments (Supplementary Tables 2 A and B). This strategy allowed the elimination of potential “false positives”, and led to the selection of DNA interacting proteins identified and quantified with complementary abundance ratios (Supplementary Table 1). A number of DNA-binding proteins were identified including p20-CGGBP, p52/p100, DHX 9, DDX3X and LIG3 (Supplementary Table 1). CGG triplet repeat-binding protein 1 (P20-CGGBP) binds sequence-specifically to the double-stranded trinucleotide repeat 5'-d(CGG)-3'.^[6] Interestingly, the binding is inhibited by complete or partial cytosine-specific DNA methylation of the binding motif in the promoter of the fragile X mental retardation 1 (FMR1) gene,^[7] whilst we observed enrichment of p20-CGGBP in hmC versus C containing DNA probes (Supplementary Table 1).

Supplementary Table 1: DNA interacting proteins enriched by either C or hmC DNA probes

Protein Names	Uniprot	PEP	Ratio H/L Normalized	Ratio Variability [%]	H/L Ratio H/L Count	hmC	Ref
54 kDa nuclear RNA- and DNA-binding protein	Q15233	0.00	1.6	110	166	Heavy	[8]
		0.00	0.7	115	44	Light	
100 kDa DNA-pairing protein	P23246-1	0.00	1.8	112	116	Heavy	[8a]
		0.00	0.3	97	23	Light	
ATP-dependent RNA helicase A	Q08211	0.00	2.0	81	41	Heavy	[9]
		0.00	0.2	238	8	Light	
ATP-dependent RNA helicase DDX3X	O00571	0.00	1.5	111	18	Heavy	[10]
		0.00	0.5	133	10	Light	
DNA ligase 3	P49916-1	0.00	1.3	54	3	Heavy	[11]
		0.00	0.6	90	15	Light	
20 kDa CGG-binding protein	Q9UFW	0.01	1.9	-	1	Heavy	[6]
		0.00	0.4	174	2	Light	

DNA ligase 3 (LIG3) is involved in mitochondrial DNA maintenance, interacts with DNA-repair protein XRCC1 and can correct defective DNA strand-break repair and sister chromatid exchange following treatment with ionizing radiation and alkylating agents.^[11a, 11d] We observed enriched LIG3 in the presence of hmCTP DNA, indicating a preference for modified nucleotides (Supplementary Table 2).

The ATP-dependent helicases DHX9 and DDX3X were also found to be enriched with hmC containing DNA probes (Supplementary Table 2). Both enzymes unwind DNA and are part of mRNP complexes involved in target gene activation.^[9-10, 12]

In addition, we found the two components of the SFPQ-NONO complex, which is a heterotetramer of two 52 kDa (NONO) and two 100 kDa (SFPQ) subunits. NONO is a component of spliceosome and U5.4/6 snRNP complexes. The SFPQ-NONO heteromer may be involved in DNA unwinding by modulating the function of topoisomerase I/TOPI1, but also in DNA nonhomologous end joining

(NHEJ) required for double-strand break repair and V(D)J recombination and may stabilize paired DNA ends.^[8]

Nothing is known for these proteins identified in our SILAC screen in terms of specific recognition of hmC modifications, but our results indicate potential functional connections that warrant further investigation in hmC associated DNA modification biology, in particular in CpG islands.

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Supplementary Table 2

ODN-to-protein conjugates identified by tandem mass spectrometry and quantified using SILAC. (A) hmC=light; C=heavy; (B) hmC=light; C=heavy. Protein accession numbers are given for the Uniprot database; PEP: posterior error propability; H: heavy; L: light.

See associated excel update spreadsheet.

Supplementary Table 2 A: ODN-to-protein conjugates identified by tandem mass spectrometry and quantified using SILAC (hmC=light; C=heavy)

Protein Names	Gene Names	Protein Descriptions	Uniprot	PEP	Ratio H/L	Ratio H/L Normalized	Ratio H/L Variability [%]	Ratio H/L Count	log2(H/L)
Androgen receptor coactivator 160 kDa protein;Androgen receptor-associated protein of 160 kDa;TATA elem ARA160;TMF1 Isoform 2 of TATA elem P82094-2;P82094;f				0.069813	0.0077013	0.0058149		1	-7.42603
Putative zinc finger protein		Putative zinc finger prc Q9P0K0		0.0088382	0.0066263	0.0093325	93.038	2	-6.74352
Coiled-coil domain-containing protein 72	CCDC72;HSPC	Coiled-coil domain-cor Q9Y2S6		0.006873	0.01286	0.018093		1	-5.78842
60S ribosomal protein L24;60S ribosomal protein L30;Putative uncharacterized protein RPL24;Ribosomal prc RPL24;hCG_21 19 kDa protein;60S ribo P83731;C9JNWS;C				2.20E-08	0.011647	0.018333	258.07	4	-5.76941
cDNA FLJ54752, highly similar to Poly(rC)-binding protein 2		cDNA FLJ54752, highly B4DRD7		7.27E-106	0.020091	0.028473		1	-5.13426
Kinesin-like protein KIF14	KIAA0042;KIF	Kinesin-like protein KIF Q15058		0.089053	0.024161	0.030588		1	-5.03089
		similar to hCG1652800		0.00062443	0.023462	0.039512	10.311	2	-4.79927
Zinc finger protein 646;cDNA FLJ61089, highly similar to Zinc finger protein 646	KIAA0296;ZNF	Isoform 2 of Zinc finger O15015-2;O15015;		0.088792	0.028676	0.039728	43.717	2	-4.6537
Glyceraldehyde-3-phosphate dehydrogenase, testis-specific;Spermatogenic cell-specific glyceraldehyde 3-ph	GAPD2;GAPDI	Glyceraldehyde-3-phos O14556		6.19E-05	0.031398	0.04366	5.6678	2	-4.51754
High density lipoprotein-binding protein;Vigilin;cDNA, FLJ92652, highly similar to Homo sapiens high density HBP;HDLBP;V		Vigilin;cDNA FLJ56889, Q00341;B2R5V9;B		0.0053285	0.033592	0.048823		1	-4.3563
Coding region determinant-binding protein;IGF-II mRNA-binding protein 1;Insulin-like growth factor 2 mRNA	CRDBP;IGF2BI	Insulin-like growth fact Q9NZI8;D3DTW3		0.0018885	0.037391	0.050814		1	-4.29863
Insulin-like growth factor-binding protein 3;Insulin-like growth factor binding protein 3;Insulin-like growth fa	IBP3;IGFBP3;I	insulin-like growth fact P17936;A6XND0;A		1.28E-07	0.037068	0.052608	121.56	6	-4.24857
Enaptin;Mycocyte nuclear envelope protein 1;Nesprin-1;Nuclear envelope spectrin repeat protein 1;Synaptic	C6orf98;KIAA	Isoform 1 of Nesprin-1 Q8NF91-1;Q8NF91		0.010116	0.034683	0.055904	18.598	2	-4.1609
High mobility group protein 2;High mobility group protein B2;High-mobility group box 2	HMG2;HMGB	High mobility group pr P26583;Q5U071;D		2.18E-14	0.0424	0.067693	192.31	4	-3.88485
High mobility group nucleosome-binding domain-containing protein 1;Non-histone chromosomal protein H	HMG14;HMG1	Non-histone chromoso P05114;Q3B790;A		5.57E-15	0.04643	0.069726		1	-3.84216
AU-rich element RNA-binding protein 1;Heterogeneous nuclear ribonucleoprotein D0;cDNA FLJ54150, highl	AUF1;HNRNP1	Isoform 2 of Heteroger Q14103-2;Q14103;		5.37E-118	0.044941	0.070552		1	-3.82517
Dystrophin;DMD protein;Duchenne muscular dystrophy gene;Duchenne muscular dystrophy protein;Dystro	DMD;GS1-19C	Isoform 4 of Dystrophii P11532-1;P11532;f		0.0089536	0.055105	0.07077		1	-3.82072
AU-rich element RNA-binding protein 1;Heterogeneous nuclear ribonucleoprotein D0	AUF1;HNRNP1	Isoform 1 of Heteroger Q14103-1;Q14103;		7.97E-175	0.05491	0.079821	144.31	69	-3.64709
BT;lg mu heavy chain disease protein;lg mu chain C region;Full-length cDNA clone CSDD006YL02 of Neurr	IGHM	52 kDa protein;Protein P04220;P01871-1;f		1.31E-09	0.067675	0.083606		1	-3.58025
Putative uncharacterized protein RAN;RAN, member RAS oncogene family, isoform CRA_c;Androgen recept	hCG_1744585	26 kDa protein;27 kDa B5MDF5;P62826;A		0.0094139	0.06453	0.088324		1	-3.50105
cGMP-binding cGMP-specific phosphodiesterase; cGMP-specific 3',5'-cyclic phosphodiesterase;CGMP-specifi	PDE5;PDE5A	Isoform PDE5A1 of cG O76074-1;O76074;		0.0042421	0.055282	0.089074		1	-3.48885
Signal recognition particle 9 kDa protein;cDNA FLJ76514, highly similar to Homo sapiens signal recognition	SRP9;hCG_17	Signal recognition part P49458;A8K0N0;Q		2.29E-11	0.067365	0.093878	153.31	3	-3.41307
cDNA FLJ78093, highly similar to Homo sapiens ribosomal protein L29 (RPL29), mRNA;60S ribosomal protei	RPL29;RP11-6	27 kDa protein;26 kDa A8K0H3;P47914;Q		8.04E-05	0.069116	0.098074	58.325	2	-3.34999
Dermcidin isoform 2;DCD-1;Dermcidin;Preproteolysin;Survival-promoting peptide;Proteolysin inducing	DCD;AIDD;DSI	Dermcidin isoform 2;D A5JHP3;P81605;Q5		0.00021482	0.075223	0.10238		1	-3.28799
Nucleolysin TIA-1 isoform p15;Nucleolysin TIA-1 isoform p40;p15-TIA-1;p40-TIA-1;RNA-binding protein	TIA-1	Isoform Short of Nucle P31483-2;P31483;		9.60E-46	0.065824	0.10291	11.281	2	-3.28054
DEAD box protein 49;Probable ATP-dependent RNA helicase DDX49;cDNA FLJ77346, highly similar to Homo	DDX49	Probable ATP-depende Q9Y6V7;A8K7A1;Q		0.0012823	0.07964	0.10591		1	-3.23909
Activated RNA polymerase II transcriptional coactivator p15;p14;Positive cofactor 4;SUB1 homolog;cDNA FL	PC4;RPO2TC1	Activated RNA polyme P53999;B72120;Q5		1.37E-37	0.073206	0.10635	129.01	3	-3.23311
Elongation factor 1-alpha 1;Elongation factor Tu;Eukaryotic elongation factor 1 A-1;Leukocyte receptor	EEF1A;EEF1A3	Elongation factor 1-alp P68104;A8K9C4;A9		6.02E-27	0.067829	0.10828	139.08	3	-3.20716
Axonemal beta dynein heavy chain 10;Ciliary dynein heavy chain 10;Dynein heavy chain 10, axonemal;DNA	DNAH10;KIAA	Isoform 1 of Dynein he Q8IVF4-1;Q8IVF4;B		0.087971	0.078248	0.11224		1	-3.15534
CLL-associated antigen KW-7;Dense fine speckles 70 kDa protein;Lens epithelium-derived growth factor;	PC4 DFS70;LEDGF;	Isoform 1 of PC4 and S O75475-1;O75475;		1.79E-115	0.082223	0.11709	120.76	28	-3.09431
Histone H1.3;Histone H1c;Histone H1.4;Histone H1b;Liver histone H1e;Histone 1, H1e;Histone H1e;cDNA, FI	H1F3;HIST1H3	Histone H1.3;Histone P16402;P10412;A3		3.68E-10	0.076807	0.11802	137.53	4	-3.0829
UPF0688 protein C1orf174	C1orf174	UPF0688 protein C1orf Q8IYL3		0.00041138	0.093767	0.12966		1	-2.94719
ATP-dependent RNA helicase #46;DEAH box protein 15;Putative pre-mRNA-splicing factor ATP-dependent	R DBP1;DDX15;	Putative pre-mRNA-spl O43143;B4E056		0.0050922	0.09722	0.13023	90.035	2	-2.94087
Nucleolar phosphoprotein B23;Nucleolar protein N038;Nucleophosmin;Numatrin;Truncated nucleolar phos	NPM1;NPM1	Isoform 1 of Nucleophi P06748-1;P06748;f		0.012239	0.095961	0.13528		1	-2.88598
Forkhead box protein A1;Hepatocyte nuclear factor 3-alpha;Transcription factor 3A;cDNA FLJ50362, highl	s FOXA1;HNF3A	Hepatocyte nuclear fac P55317;B4E257;B7		2.51E-06	0.10571	0.13708	106.53	3	-2.86691
Ubiquitin-like protein FUBI;40S ribosomal protein S30	FAU	ubiquitin-like protein fi P35544;P62861		0.012101	0.099286	0.13928		1	-2.84394
Protein DEK;cDNA FLJ51914, highly similar to Protein DEK;cDNA FLJ53031, highly similar to Protein DEK;	cDN DEK	Protein DEK;cDNA FLJ5 P35659;B4DNW3;B		2.16E-123	0.12934	0.14215	137.84	45	-2.81451
Heterogeneous nuclear ribonucleoproteins A2/B1;Putative uncharacterized protein HNRNPA2B1	HNRNPA2B1;f	Isoform B1 of Heteroge P22626-1;P22626;f		5.13E-193	0.10804	0.14315	89.552	72	-2.8044
Importin subunit alpha-2;Karyopherin subunit alpha-2;RAG cohort protein 1;SRP1-alpha;cDNA FLJ78270, h	ig kPNA2;RCH1;	Importin subunit alpha P52292;A8K7D9;Q		0.010612	0.11086	0.14373		1	-2.79857
86 kDa subunit of Ku antigen;ATP-dependent DNA helicase 2 subunit 2;ATP-dependent DNA helicase II 80	kL G22P2;XRCC5	X-ray repair cross-com;P13010;Q53T09;Q		1.58E-63	0.099512	0.14462	118.9	30	-2.78966
Replication factor A protein 1;Replication protein A 70 kDa DNA-binding subunit;Single-stranded DNA-b	indir REPA1;RPA1;R	Replication protein A 7 P27694		4.77E-125	0.10462	0.14601	124.26	33	-2.77586
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0;HNI	Heterogeneous nuclea Q13151		7.03E-109	0.10881	0.14629	152.89	27	-2.7731
cDNA FLJ56389, highly similar to Elongation factor 1-gamma;eEF-1B gamma;Elongation factor 1-gamma;	Euk EEF1G;EF1G;P	cDNA FLJ56389, highly B4DTG2;P26641;Q		7.47E-24	0.11408	0.14683	141.27	3	-2.76778
Brain trypsinogen;Mesotrypsinogen;Serine protease 3;Serine protease 4;Trypsin III;Trypsin IV;Trypsin-3;	Prot PRSS3;PRSS4;	Isoform A of Trypsin-3; P35030-1;P35030;f		0.002293	0.10796	0.14859		1	-2.75059
Lamina-associated polypeptide 2, isoform alpha;Splenin;Thymopentin;Thymopoietin;Thymopoietin isoform	LAP2;TMPO	Lamina-associated poly P42166		5.73E-49	0.11296	0.1491	10.908	2	-2.74565
Glutathione S-transferase kappa 1;Glutathione S-transferase subunit 13;GST 13-13;GST class-kappa;	GSTK1-1	GSTK1-1 HDOM1 Isoform 2 of Glutathior Q9Y2Q3-2;Q9Y2Q3		2.28E-19	0.10584	0.15258	21.528	3	-2.71236
40S ribosomal protein S2;40S ribosomal protein S4;Protein LLRep3;Similar to 40S ribosomal protein	S2;Ribo RPS2;RPS4;LO	40S ribosomal protein P15880;A4D0Y7;O		0.00017114	0.10956	0.15468	30.855	2	-2.69264
Nuclear factor 1;CCAAT-box-binding transcription factor;Nuclear factor 1 C-type;Nuclear factor I/C;	TGGCA-bi NFIC;NFI	Uncharacterized protei B5MDB4;B7Z4U5;P		6.83E-07	0.1059	0.16149	127.55	3	-2.63048
Putative RNA-binding protein 3;RNA-binding motif protein 3;RNPL	RBM3;RNPL	Putative RNA-binding f P98179		2.18E-15	0.13145	0.16281	29.412	3	-2.61874
Helix-destabilizing protein;Heterogeneous nuclear ribonucleoprotein A1;hnRNP core protein A1;Single-str	an HNRNPA1;HNI	Isoform A1-B of Heterc P09651-1;P09651;f		2.01E-206	0.12628	0.16694	89.536	63	-2.5826
Histone H1.5;Histone H1a	H1F5;HIST1H1	Histone H1.5 P16401		1.26E-09	0.11325	0.16733	128.84	4	-2.57923
NTEF-1;Protein GT-1IC;TEA domain family member 1;Transcription factor 13;Transcriptional enhancer	factor TCF13;TEAD1;	Transcriptional enhanc P28347;Q59EF3		5.66E-05	0.12275	0.16862	1	1	-2.56815
Nucleolin;Protein C23;cDNA FLJ10452 fis, clone NT2RP1000966, highly similar to NUCLEOLIN;Nucleolin, isof	NCL;hCG_339	Nucleolin;cDNA FLJ457 P19338;B3KM80;B		2.47E-50	0.12268	0.17227	137.73	20	-2.53726
cDNA FLJ7718;Cellular nucleic acid binding protein alpha variant 1;Zinc finger protein 9 (A cellular retrov	CNBP;RNF163	cellular nucleic acid b A8K7V4;Q5U0E9;P		8.10E-10	0.14176	0.17444	75.157	3	-2.5192
ATP-dependent helicase SMARCA2;BRG1-associated factor 190B;Probable global transcription activator	SNF BAF190B;BRM	Isoform Long of Probal P51531-1;P51531;f		9.75E-11	0.18271	0.17456	1	1	-2.51821
50 kDa nuclear polyadenylated RNA-binding protein;Bruno-like protein 2;CUG triplet repeat RNA-binding	pr BRUNOL2;CEL	Isoform 4 of CUGBP El Q92879-4;Q92879;		3.19E-38	0.123	0.17905	102.05	21	-2.48157
High mobility group nucleosome-binding domain-containing protein 3;Thyroid receptor-interacting	protein HMGN3;PNAS	Isoform 1 of High mobi Q15651-1;Q15651;f		2.95E-28	0.12038	0.18049	181.68	2	-2.47001
Heterogeneous nuclear ribonucleoprotein L;cDNA, FLJ94229, highly similar to Homo sapiens heterogeneo	HNRNPL;HNRI	Heterogeneous nuclea P14866;B2R959;Q		4.81E-113	0.14368	0.18559	144.68	42	-2.42981

Dimethyladenosine transferase 2, mitochondrial;Hepatitis C virus NS5A-transactivated protein 5;Mitochondrial NS5A-ATP5;TFB; Dimethyladenosine tra	Q9H5Q4;B4DTJ4	0.00020666	0.13654	0.18564	1	-2.42942
Chromatin assembly factor 1 subunit A;Chromatin assembly factor 1 p150 subunit	CAF;CAF1P15 Isoform 1 of Chromatin	2.45E-10	0.12428	0.18722	1	-2.41719
APOBEC1-binding protein 1;Heterogeneous nuclear ribonucleoprotein A/B;cDNA FLJ60713, highly similar to ABBP1;HNRN1 Isoform 3 of Heteroger	Q99729-3;Q99729;	9.47E-60	0.14826	0.18958	17	-2.39912
CAAT box DNA-binding protein subunit C;Nuclear transcription factor Y subunit C;Nuclear transcription factor NFYC;DKFZp61 Isoform 3 of Nuclear tr	Q13952-1;Q13952;	2.16E-11	0.13223	0.18981	1	-2.39737
Ribosomal protein S27;40S ribosomal protein S27;Metallopan-stimulin 1;40S ribosomal protein S27-like;Put LOC392748;tc Similar to ribosomal pr	A4D1G5;C9JL16;P4;	0.0036727	0.1373	0.19091	1	-2.38904
DEAD box protein 21;Gu-alpha;Nucleolar RNA helicase 2;Nucleolar RNA helicase Q;Nucleolar RNA helicase DDX21;OK/SW Isoform 1 of Nucleolar	Q9NR30-1;Q9NR3C	0.0025836	0.14483	0.19613	4	-2.35012
A18 hnRNP;Cold-inducible RNA-binding protein;Glycine-rich RNA-binding protein C1RP;Cold inducible RNA b A18HNRNP;Cl Cold-inducible RNA-bir	Q14011;Q53X5;B;	5.97E-27	0.13937	0.19773	1	-2.3384
PAI1 RNA-binding protein 1;Plasminogen activator inhibitor 1 RNA-binding protein;SERPINE1 mRNA-binding CGI-55;PAIRBF SERPINE1 mRNA bindir	Q8NC51-1;Q8NC51	1.28E-63	0.14067	0.19968	7	-2.32424
Bardet-Biedl syndrome 14 protein;Cancer/testis antigen 87;Centrosomal protein of 290 kDa;Nephrocystin 6 BBS14;CEP290 Isoform 1 of Centroso	O15078-1;O15078;	0.13248	0.15069	0.20244	1	-2.30443
Microtubule-associated protein 4;cDNA FLJ58263, highly similar to Microtubule-associated protein 4;MAP4 MAP4	245 kDa protein;Isofori	7.17E-58	0.1332	0.20435	17	-2.29089
ATP-dependent DNA helicase Q1;DNA helicase, RecQ-like type 1;DNA-dependent ATPase Q1;RecQ protein-li RECQ1;RECQL ATP-dependent DNA h	P46063	2.58E-80	0.14322	0.20587	26	-2.28019
ATP-dependent RNA helicase A;DEAH box protein 9;Nuclear DNA helicase II;cDNA FLJ39263 fis, clone OCBFF DDX9;DHX9;LI ATP-dependent RNA h	Q08211;B3KU66;Q;	1.08E-11	0.15393	0.20758	8	-2.26826
TAR DNA-binding protein 43;cDNA FLJ57180, highly similar to TAR DNA-binding protein 43;TAR DNA binding TARDBP;TDP4	Isoform 2 of TAR DNA-I	3.85E-78	0.1746	0.2091	11	-2.25774
DNA topoisomerase 1;DNA topoisomerase I;Topoisomerase (DNA) I;TOP1 protein;Putative uncharacterized I TOP1	DNA topoisomerase 1	5.71E-58	0.17106	0.21015	28	-2.25051
75 kDa DNA-pairing protein;Oncogene FUS;Oncogene TLS;POMP75;RNA-binding protein FUS;Translocated in FUS;TLS	Fus-like protein (Fragm	2.66E-33	0.189	0.21386	24	-2.22526
Zinc fingers and homeobox protein 1;cDNA FLJ78425, highly similar to Homo sapiens zinc fingers and hom ZHX1	Zinc fingers and home	6.29E-17	0.14876	0.22018	1	-2.18324
High mobility group protein 1;High mobility group protein B1;High-mobility group box 1;Putative high mobil HMG1;HMGB	High mobility group pr	3.79E-17	0.14739	0.22414	6	-2.15753
RNA-binding motif protein 47;RNA-binding protein 47;RNA binding motif protein 47;cDNA FLJ51456, moder RBM47	Isoform 1 of RNA-bindi	0.00029068	0.17408	0.22696	2	-2.13949
Activating transcription factor 1;Cyclic AMP-dependent transcription factor ATF-1;Protein TREB36;cDNA, FLJ ATF1	Cyclic AMP-dependent	6.87E-13	0.16627	0.23314	8	-2.10073
Serine/threonine-protein kinase VRK1;Vaccinia-related kinase 1;cDNA FLJ75441, highly similar to Homo sapi VRK1	Serine/threonine-prote	3.42E-05	0.1878	0.2339	2	-2.09604
PWP1-interacting protein 17;Single-stranded DNA-binding protein, mitochondrial;cDNA, FLJ93504, Homo sa SSBP;SSBP1;h Single-stranded DNA-b	Q04837;A4DU3;Q;	1.03E-38	0.16666	0.23459	11	-2.09179
Far upstream element-binding protein 3;cDNA FLJ58115, highly similar to Far upstream element-binding prc FBP3;FUBP3;h Isoform 1 of Far upstre	Q96124-1;Q96124;A	8.31E-181	0.19578	0.24453	69	-2.03192
Heterogeneous nuclear ribonucleoprotein A3;cDNA FLJ52659, highly similar to Heterogeneous nuclear ribonucleoprotein A3;HNRNPA3;HNI	Isoform 1 of Heteroger	2.28E-60	0.17397	0.24969	18	-2.00179
DNA helicase V;Far upstream element-binding protein 1;cDNA FLJ59240, highly similar to Far upstream elen FUBP1	Isoform 1 of Far upstre	5.38E-133	0.19398	0.25681	39	-1.96123
Glycine- and tyrosine-rich RNA-binding protein;Heterogeneous nuclear ribonucleoprotein Q;NS1-associated HNRPQ;NSAP	Isoform 3 of Heteroger	1.42E-127	0.21155	0.25756	30	-1.95702
Far upstream element-binding protein 2;KH type-splicing regulatory protein;p75;cDNA FLJ51330, highly simi FUBP2;KHSRP	Isoform 1 of Far upstre	2.17E-157	0.2016	0.25896	34	-1.9492
Splicing factor 9G8;Splicing factor, arginine/serine-rich 7;Putative uncharacterized protein SFRS7;cDNA FLJ5 SFRS7	Isoform 1 of Serine/arg	5.88E-06	0.18703	0.26497	4	-1.9161
CTD-associated SR protein 11;Renal carcinoma antigen NY-REN-40;SC35-interacting protein 1;SFRS2-interact CASP11;SFRS2	Isoform 1 of SRSF2-inte	2.69E-05	0.2249	0.26548	2	-1.91332
UPF0361 protein C3orf37;cDNA FLJ57398	C3orf37;DC12 UPF0361	1.32E-79	0.18986	0.2688	16	-1.89539
Polypyrimidine tract binding protein 1;Polypyrimidine tract binding protein 1, isoform CRA_c;57 kDa RNA-bi hCG_20560;P' polypyrimidine tract-bi	Q9BUQ0;P26599-2	6.90E-210	0.17972	0.27122	69	-1.88246
Heterogeneous nuclear ribonucleoprotein U;p120;pp120;Scaffold attachment factor A;cDNA FLJ44920 fis, cl HNRNPU;HNR	Isoform Long of Heterc	3.26E-137	0.19912	0.2717	34	-1.87991
DEAH box protein 36;MLE-like protein 1;Probable ATP-dependent RNA helicase DHX36;RNA helicase associa DDX36;DHX36	Isoform 1 of Probable	5.86E-118	0.19905	0.27283	14	-1.87393
Heterogeneous nuclear ribonucleoprotein K;Transformation up-regulated nuclear protein;cDNA FLJ53312, h HNRNPK;HNR	Isoform 2 of Heteroger	4.29E-233	0.21745	0.27505	65	-1.86223
Cold shock domain-containing protein A;DNA-binding protein A;Single-strand DNA-binding protein NF-GMB CSDA;DBPA	Isoform 1 of DNA-bindi	4.16E-20	0.21785	0.27786	5	-1.84757
Kinesin-like protein 2;Kinesin-like protein KIFC1;Kinesin-related protein HSET;cDNA FLJ53841, highly similar HSET;KIFC1;Kt	Kinesin-like protein KIF	3.41E-21	0.20576	0.28124	2	-1.83013
Death-associated transcription factor 1;Death-inducer obliterator 1	C20orf158;DA	5.41E-08	0.19746	0.28484	3	-1.81178
CCT-gamma;hTRIC5;T-complex protein 1 subunit gamma;cDNA FLJ57603, highly similar to T-complex protein CCT3;CCTG;Tf T-complex protein 1 su	P49368;B4DUR8;Q;	1.52E-10	0.21061	0.28655	2	-1.80314
NAD(+) ADP-ribosyltransferase 1;Poly [ADP-ribose] polymerase 1;Poly[ADP-ribose] synthase 1;cDNA, FLJ926 ADPRT;PARP1	Poly [ADP-ribose] poly	0	0.23292	0.29369	176	-1.76763
cDNA FLJ56904, highly similar to RNA-binding protein Musashi homolog 2;RNA-binding protein Musashi hom MS12	cDNA FLJ56904, highl	2.06E-08	0.22156	0.29521	182	-1.76019
Lark homolog;RNA-binding motif protein 4;RNA-binding motif protein 4a;RNA-binding protein 4;cDNA FLJ78 RBM4;RBM4A	Isoform 1 of RNA-bindi	8.25E-128	0.22967	0.3017	42	-1.72881
RNA-binding motif, single-stranded-interacting protein 1;Single-stranded DNA-binding protein MSSP-1;Supp C2orf12;MSSF	Isoform 1 of RNA-bindi	8.58E-13	0.20884	0.30363	2	-1.71961
Pre-mRNA-splicing factor SRP20;Splicing factor, arginine/serine-rich 3;cDNA, FLJ92926, Homo sapiens splicir SFRS3;SRP20;I	Serine/arginine-rich sp	5.42E-05	0.22952	0.30679	2	-1.70468
Heterogeneous nuclear ribonucleoprotein R;cDNA, FLJ93632, highly similar to Homo sapiens heterogeneou: HNRNPR;HNR	71 kDa protein;Isoform	1.32E-24	0.22256	0.30712	9	-1.70313
ATP-dependent RNA helicase DDX48;ATP-dependent RNA helicase eIF4A-3;DEAD box protein 48;Eukaryotic i DDX48;EIF4A3	Eukaryotic initiation fa	0.0090536	0.2198	0.30755	1	-1.70111
130 kDa leucine-rich protein;GP130;Leucine-rich PPR motif-containing protein, mitochondrial;cDNA FLJ600E LRP130;LRPPF	Leucine-rich PPR motif	4.20E-48	0.24797	0.30974	15	-1.69087
60S ribosomal protein L3;HIV-1 TAR RNA-binding protein B;Ribosomal protein L3;cDNA FLJ35376 fis, clone S OK/SW-cl.32;f	60S ribosomal protein	0.00014215	0.22227	0.31654	102	-1.65954
60S ribosomal protein L10;Laminin receptor homolog;Protein QM;Tumor suppressor QM;Ribosomal protein DXS648E;QM; 60S ribosomal protein	P27635;Q5HY50;Q;	0.014478	0.24474	0.3169	2	-1.6579
Hepatoma-derived growth factor;High mobility group protein 1-like 2;cDNA, FLJ96580, highly similar to Hon HDGF;HMG1L	Hepatoma-derived gro	1.26E-38	0.22528	0.31868	5	-1.64982
cDNA FLJ75056, highly similar to Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICACALM);PICAL	Uncharacterized protei	1.99E-22	0.24046	0.31868	9	-1.64982
cDNA FLJ60076, highly similar to ELAV-like protein 1;ELAV-like protein 1;Hu-antigen R	ELAVL1;HUR	6.07E-53	0.2493	0.32873	10	-1.60502
Dr1-associated corepressor;Dr1-associated protein 1;Negative co-factor 2-alpha;Putative uncharacterized pi DRAP1	Uncharacterized protei	7.08E-06	0.23868	0.32982	4	-1.60025
Poly(RC)-binding protein 2 isoform b variant;Poly(RC) binding protein 2, isoform (c HCG_2017557	poly(RC)-binding protei	5.33E-123	0.23347	0.33282	126	-1.58719
Heterogeneous nuclear ribonucleoprotein 2H9;Heterogeneous nuclear ribonucleoprotein H3;Heterogeneous HNRNPH3;HN	Isoform 1 of Heteroger	1.12E-18	0.25647	0.33337	4	-1.5848
UPF0534 protein C4orf43	C4orf43	7.42E-51	0.25504	0.33745	7	-1.56725
High mobility group protein 2a;High mobility group protein 4;High mobility group protein B3;Non-histone cl	HMG2A;HMG	1.02E-27	0.22013	0.33875	8	-1.56171
100 kDa DNA-pairing protein;DNA-binding p52/p100 complex, 100 kDa subunit;Polypyrimidine tract-binding PSF;SFPQ	Isoform Long of Splicin	4.96E-69	0.2388	0.33924	23	-1.55962
Cullin-1;cDNA FLJ38844 fis, clone MESAN2003662, highly similar to Cullin-1;cDNA FLJ39186 fis, clone OCBFF CUL1	Cullin-1;cDNA FLJ5850	0.10854	0.2542	0.33962	1	-1.55801
cDNA FLJ75459;cDNA FLJ76290, highly similar to Homo sapiens TIA1 cytotoxic granule-associated RNA bindi TIAL1;hCG_40	nucleolysin TIAR isofor	1.40E-51	0.25481	0.35613	3	-1.48952
Alpha-CP1;Heterogeneous nuclear ribonucleoprotein E1;Nucleic acid-binding protein SUB2.3;Poly(RC)-bindir PCBP1;hCG_1	Poly(RC)-binding protei	2.46E-111	0.2759	0.36033	25	-1.47261
Beta-II spectrin;Fodrin beta chain;Spectrin beta chain, brain 1;Spectrin, non-erythroid beta chain 1;Spectrin SPTB2;SPTBN	Isoform Long of Spectr	0.0024362	0.25301	0.36142	1	-1.46825
AU-rich element RNA-binding factor;Heterogeneous nuclear ribonucleoprotein D-like;JKT41-binding protein HNRPDL;JKTBI	Isoform 1 of Heteroger	1.09E-10	0.29097	0.36322	3	-1.46108

Nucleolysin TIA-1 isoform p15;Nucleolysin TIA-1 isoform p40;p15-TIA-1;p40-TIA-1;RNA-binding protein TIA-1: TIA1;hCG_405 Isoform Long of Nucleol	P31483-1;P31483;C	3.34E-45	0.28083	0.37092	72.947	15	-1.43082
cDNA FLJ53554	cDNA FLJ53554 B4DGK4	0.0036811	0.30004	0.37271	113.13	4	-1.42387
cDNA FLJ75516, highly similar to Xenopus tropicalis ubiquitin C, mRNA;Ubiquitin C variant;Ubiquitin C splice UBC;DKFZp343 Polyubiquitin-C;39 kDa	POCG48;A8K674;Q	1.14E-25	0.26443	0.37426	198.31	11	-1.41789
Zinc finger and SCAN domain-containing protein 2;Zinc finger protein 29 homolog;cDNA FLJ77532, highly similar to ZFP29;ZSCAN; Isoform 1 of Zinc finger Q727L9-1;Q727L9;	Isoform 1 of Zinc finger Q727L9-1;Q727L9;	0.32681	0.30043	0.37549	1	1	-1.41315
70 kDa subunit of Ku antigen;ATP-dependent DNA helicase 2 subunit 1;ATP-dependent DNA helicase II 70 kT G22P1;XRCC6 X-ray repair cross-com; P12956;B2RDN9;B:	1.84E-94	0.33118	0.37882	123.56	28	1	-1.40042
Ribosomal protein S10 variant;Ribosomal protein S10;40S ribosomal protein S10	RP11-375E1_ Ribosomal protein S10 Q59GE4;Q5T2B9;P:	6.07E-05	0.25964	0.37971	1	1	-1.39703
Putative uncharacterized protein DKFZp779B0247;Cold shock domain-containing protein E1;N-ras upstream DKFZp779B02 94 kDa protein;cold sh Q68DF1;O75534-1;	1.75E-24	0.31478	0.38135	135.98	11	1	-1.39081
Heterogeneous nuclear ribonucleoprotein M;Heterogeneous nuclear ribonucleoprotein M isoform a variant HNRNPM;HNF	Isoform 1 of Heteroger P52272-1;P52272;C	2.14E-75	0.31263	0.38213	85.947	24	-1.38786
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit;Dolichyl-diphosphooligosac RP N1	Dolichyl-diphosphoolig P04843;Q53EP4;Q	0.010782	0.28979	0.39116	1	1	-1.35417
ATP-dependent RNA helicase eIF4A-2;Eukaryotic initiation factor 4A-II;Eukaryotic translation initiation factor DDX2B;EIF4A2; Isoform 2 of Eukaryotic Q14240-2;Q14240;	3.59E-06	0.29707	0.39207	155.24	2	1	-1.35082
Protein PR264;Splicing component, 35 kDa;Splicing factor SC35;Splicing factor, arginine/serine-rich 2;cDNA I SFRS2;hCG_2; Serine/arginine-rich sp	Q01130;B3KUY1;Q	5.01E-25	0.31358	0.39317	29.142	6	-1.34677
Basic transcription element-binding protein 4;Krueppel-like factor 16;Novel Sp1-like zinc finger transcription BTEB4;KLF16;I	Krueppel-like factor 16 Q9BXK1;D6W5Z8	1.53E-31	0.31828	0.39555	1	1	-1.33807
60 kDa poly(U)-binding-splicing factor;FUSE-binding protein-interacting repressor;Poly(U)-binding-splicing fe FIR;PUF60;RO	Isoform 1 of Poly(U)-bi Q9UHX1-1;Q9UHX1;	3.51E-21	0.29121	0.39939	65.145	6	-1.32413
Heterogeneous nuclear ribonucleoprotein L-like;Stromal RNA-regulating factor;cDNA FLJ77927;Heterogener BLOCK24;HNR	Isoform 1 of Heteroger Q8WVV9-1;Q8WVV	0.00020195	0.31742	0.40056	55.911	2	-1.31991
p195;Ras GTPase-activating protein IQGAP1;IQ motif containing GTPase activating protein 1;cDNA FLJ5: IQGAP1;KIAA Ras GTPase-activating-	P46940;A4QP80;B:	2.41E-16	0.27648	0.40131	104.86	3	-1.31721
Adenovirus early region 1B-associated protein 5;E1B-55 kDa-associated protein 5;Heterogeneous nuclear ril E1BAP5;HNRN	Isoform 1 of Heteroger Q9BUJ2-1;Q9BUJ2;	1.70E-19	0.27648	0.40131	120.17	3	-1.31721
20 kDa CGG-binding protein;CGG triplet repeat-binding protein 1;p20-CGGBP DNA-binding protein;Putative CGGBP;CGGBI CGG triplet repeat-binc	Q9UFW8;C9JUJO	1.33E-06	0.2955	0.40248	173.7	2	-1.31301
Cellular apoptosis susceptibility protein;Chromosome segregation 1-like protein;Exportin-2;Importin-alpha CAS;CSE1L;XP	Isoform 1 of Exportin-2 P55060-1;P55060;I	0.014654	0.27639	0.4147	278.71	1	-1.26986
Hepatocellular carcinoma protein 1;RNA-binding motif protein 39;RNA-binding protein 39;RNA-binding regii HCC1;RBM39; Isoform 1 of RNA-binding Q14498-1;Q14498;	3.73E-59	0.33697	0.41564	68.689	9	2	-1.26659
DAZ-associated protein 1;Deleted in azoospermia-associated protein 1;cDNA FLJ35575 fis, clone SPLEN2006 DAZAP1	Isoform 1 of DAZ-assoc Q96EP5-1;Q96EP5;	6.31E-94	0.31466	0.42046	84.474	16	-1.24996
IGF-II mRNA-binding protein 3;Insulin-like growth factor 2 mRNA-binding protein 3;KH domain-containing pi IGF2BP3;IMP3; Isoform 1 of insulin-like	O00425-1;O00425	6.47E-11	0.33465	0.42077	87.704	7	-1.2489
CCAAT-binding transcription factor I subunit A;DNA-binding protein B;Enhancer factor 1 subunit A;Nuclease--NSEP1;Y81;YB Protein;Nuclease-sensi	P67809;A01LU4;Q	2.65E-91	0.25598	0.43396	149.46	19	-1.20437
Neural polypyrimidine tract-binding protein;Neurally-enriched homolog of PTB;Polypyrimidine tract-binding NPTB;PTB;PTE	Isoform 2 of Polypyrim Q9UKA9-2;Q9UKA	7.81E-17	0.32231	0.43725	11.35	2	-1.19347
cDNA FLJ31747 fis, clone NT2R12007377, highly similar to RNA-BINDING PROTEIN EWS;Ewing sarcoma breal EWSR1;hCG_2 RNA-binding protein E	Q96MX4;Q01844-I	1.28E-24	0.34603	0.4402	60.348	3	-1.18377
Thymocyte nuclear protein 1;Thymocyte protein Thy28	HSPC144;MDS; Isoform 1 of Thymocyt Q9P016-1;Q9P016	6.47E-12	0.32384	0.44086	133.08	5	-1.18161
Activator 1 140 kDa subunit;Activator 1 large subunit;Activator 1 subunit 1;DNA-binding protein PO-GA;Repl	RFC1;RFC140; Isoform 1 of Replicatio P35251-1;P35251;f	0.003283	0.3151	0.44467	1	1	-1.16919
Methyl-CpG-binding protein 2;cDNA FLJ75240, highly similar to Homo sapiens methyl CpG binding protein 2	MCP2;hCG_3 Isoform B of Methyl-Cp P51608-2;P51608;H	1.47E-38	0.3528	0.46218	191.03	2	-1.1347
Heterogeneous nuclear ribonucleoprotein H;Heterogeneous nuclear ribonucleoprotein H, N-terminally proc HNRNPH1;HN	51 kDa protein;Hetero; P31943;B4DP51;Q	1.95E-79	0.37484	0.46626	72.011	15	-1.10079
ATP-dependent RNA helicase DDX3X;DEAD box protein 3, X-chromosomal;DEAD box, X isoform;Helicase-like DBX;DDX3;DD	ATP-dependent RNA he O00571;B4E3E8;B5	1.60E-31	0.38143	0.47004	133.36	10	-1.08914
40S ribosomal protein S3;Ribosomal protein S3 variant;Ribosomal protein S3	OK/SW-cl.26;f 28 kDa protein;40S ribi P23396;Q53G83;Q:	8.67E-07	0.33187	0.47354	72.584	5	-1.07844
Brunton tyrosine kinase-associated protein 135;General transcription factor II-1;SRF-Phox1-interacting proteir	BAP135;GTF2I Isoform 1 of General tr P78347-1;P78347;f	1.73E-17	0.32284	0.47694	98.937	7	-1.06812
Histone H4	H4/A;H4/B;H4 Histone H4 P62805;B2R4R0;Q:	9.67E-16	0.38387	0.47877	129.47	10	-1.0626
60S ribosomal protein L30	RPL30 60S ribosomal protein P62888;E5R199;E5F	3.85E-23	0.37144	0.48455	116.23	4	-1.04528
Gamma-interferon-inducible protein 16;Interferon-inducible myeloid differentiation transcriptional activato	IF16;IFNGP1. Interferon, gamma-ind Q16666-2;Q16666;	6.66E-103	0.33879	0.48556	124.89	25	-1.04228
Glycylpeptide N-tetradecanoyltransferase 1;Myristoyl-CoA:protein N-myristoyltransferase 1;Peptide N-myris	NMT;NMT1 Isoform Long of Glycyl; P30419-1;P30419;C	0.00012716	0.349	0.48848	6.4037	2	-1.03363
Replication factor A protein 2;Replication protein A 32 kDa subunit;Replication protein A 34 kDa subunit;cdI	REPA2;RPA2;R Isoform 3 of Replicatio P15927-3;P15927;f	6.85E-23	0.40183	0.50021	155.12	6	-0.99939
DEAD box polypeptide 17 isoform p82 variant;DEAD box protein 17;DEAD box protein p72;Probable ATP-de; DDX17;RP3-4; probable ATP-dep	DDX17;RP3-4; probable ATP-dep Q59F66;Q92841-4;	5.66E-32	0.41146	0.50126	59.592	7	-0.99637
Glycoprotein p43;Heterogeneous nuclear ribonucleoprotein G;Heterogeneous nuclear ribonucleoprotein G, HNRPG;RBMX	Heterogeneous nuclea P38159;B4E352;Q2	1.52E-13	0.37601	0.51458	122.16	3	-0.95853
Nonsense mRNA reducing factor 3B;Regulator of nonsense transcripts 3B;Up-frameshift suppressor 3 homo	RENT3B;UPF3 Isoform 1 of Regulator Q9BZ17-1;Q9BZ17;C	0.00058423	0.40252	0.51777	117.67	2	-0.94962
Nucleolar and spindle-associated protein 1;cDNA FLJ78441, highly similar to Homo sapiens nucleolar and sp	ANKT;BM-037 Isoform 1 of Nucleolar Q9BX56-1;Q9BX56;	6.22E-23	0.44778	0.54006	117.63	9	-0.88881
Pre-rRNA-processing protein TSR1 homolog	KIAA1401;TSR Pre-rRNA-processing p Q2NL82	5.70E-11	0.37939	0.54125	90.668	3	-0.88563
Target of EGR1 protein 1;cDNA FLJ36001 fis, clone TESTI2015213, highly similar to Homo sapiens target of E	TOE1 Target of EGR1 protein Q96GM8;B3KSC7;B	0.0010216	0.40255	0.54137	1	1	-0.88531
eNOS-interacting protein;Nitric oxide synthase-interacting protein;cDNA FLJ75703, highly similar to Homo s	CGI-25;NOSIP Nitric oxide synthase-ir Q9Y314;A8K670;B4	0.0060592	0.43633	0.54873	1	1	-0.86583
DNA mismatch repair protein Msh6;G/T mismatch-binding protein;MutS-alpha 160 kDa subunit;cDNA FLJ55 GTBP;MSH6	Isoform GTBP-N of DN P52701-1;P52701;f	1.54E-81	0.38163	0.54939	113.91	24	-0.8641
60S ribosomal protein L11;CLL-associated antigen KW-12;Cell growth-inhibiting protein 34;cDNA, FLJ92077, RPL11;hCG_1	Isoform 1 of 60S ribosc P62913-1;P62913;C	1.73E-33	0.41962	0.55078	131.73	10	-0.86045
68 kDa TATA-binding protein-associated factor;RNA-binding protein 56;TATA-binding protein-associated fact	RBP56;TAF15; Isoform Long of TATA-b Q92804-1;Q92804;	8.65E-37	0.47177	0.58201	16.195	4	-0.78088
DNA ligase 3;DNA ligase III;Polydeoxyribonucleotide synthase [ATP] 3;DNA ligase;Ligase III, DNA, ATP-depen	LIG3 Isoform Alpha of DNA I P49916-1;P49916;f	1.60E-57	0.47197	0.5973	90.387	15	-0.74347
Mitochondrial transcription factor 1;Transcription factor 6;Transcription factor 6-like 2;Transcription factor A	TCF6;TCF6L2; Transcription factor A, Q00059;E5KSU5;E5	5.98E-57	0.48656	0.59961	132.67	20	-0.7379
DNA topoisomerase 2;DNA topoisomerase 2-alpha;DNA topoisomerase II, alpha isozyme	TOP2A;TOP2 Uncharacterized protei C9J4C3;P11388-4;F	6.39E-14	0.44586	0.60089	90.401	4	-0.73483
40S ribosomal protein S5;40S ribosomal protein S5, N-terminally processed;Ribosomal protein S5 variant	RP55 40S ribosomal protein P46782;Q53G25	1.69E-07	0.46927	0.60462	97.642	6	-0.7259
Inactive ubiquitin-specific peptidase 39;SAD1 homolog;U4/U6.U5 tri-snRNP-associated 65 kDa protein;U4/L	CGI-21;HSPC3 U4/U6.U5 tri-snRNP-as Q53GS9;B7Z179;B9	2.71E-26	0.45748	0.60779	94.209	7	-0.71836
Bromodomain-containing protein 4;Protein HUNK1;Similar to bromodomain-containing 4;BRD4 protein;Bro	BRD4;HUNK1; Isoform 1 of Bromodor O60885-1;O60885;	0.0081511	0.41333	0.61217	1	1	-0.708
PHD finger protein 6;PHD finger protein 6, isoform CRA_d;PHD-like zinc finger protein;cDNA FLJ60207, highl	AC004383.6-0 PHD finger protein 6, is Q5JRC6;Q8IWS0-1;	2.93E-10	0.48427	0.62059	105.87	8	-0.68829
cDNA FLJ56786, moderately similar to 40S ribosomal protein S16;40S ribosomal protein S16;RPS16 protein	RPS16 cDNA FLJ56786, mode: B4DP32;P62249;Q:	8.92E-07	0.47022	0.62463	98.554	5	-0.67893
Mortality factor 4 like 1;cDNA FLJ38504 fis, clone HCHON2000156, highly similar to Mortality factor 4-like pi	MORF4L1;FW cDNA FLJ38504 fis, cloi A5D8W6;B3KTM8;f	0.00073968	0.46242	0.63161	35.846	2	-0.66289
MORF-related gene X protein;Mortality factor 4-like protein 2;Protein MSL3-2;Transcription factor-like prote	KIAA0026;MO Mortality factor 4-like j Q15014;B3KWX6;B	0.0089338	0.50423	0.63739	1	1	-0.64975
NOL1/NOP2/Sun domain family member 2;Substrate of AIM1/Aurora kinase B;tRNA (cytosine-5--methyltra	NSUN2;SAKI;tRNA (cytosine-5--mei Q08J23;A8K529;B3	1.88E-62	0.47584	0.64108	89.08	20	-0.64142
DEAD box protein 5;Probable ATP-dependent RNA helicase DDX5;RNA helicase p68;cDNA FLJ53366, highly s	DDX5;G17P1; Probable ATP-depnde P17844;B4DN41;B:	1.06E-11	0.52831	0.66007	1	1	-0.59793
DNA-directed RNA polymerase, mitochondrial;DNA-directed RNA polymerase;cDNA FLJ58806, highly similar	POLRMT DNA-directed RNA pol Q00411;Q4G0F4;Q	3.47E-10	0.5319	0.67628	7.5559	3	-0.56431
54 kDa nuclear RNA- and DNA-binding protein;55 kDa nuclear protein;DNA-binding p52/p100 complex, 52 k	NONO;NRB54 Non-POU domain-cont Q15233;A8K525;B:	5.16E-97	0.55701	0.68159	115.12	44	-0.55302
Chromokinesin-A;Chromosome-associated kinesin KIF4A;cDNA FLJ14204 fis, clone NT2RP3003138, highly si	KIF4;KIF4A Isoform 1 of Bromosc Q95239-1;Q95239;	9.75E-55	0.54367	0.68959	97.985	17	-0.53619

DNase IV;Flap endonuclease 1;Flap structure-specific endonuclease 1;Maturation factor 1;cDNA FLJ51365, f FEN1;RAD2;h4 Flap endonuclease 1	P39748;B4DWZ4;Q	7.53E-101	0.50395	0.6927	150.98	18	-0.5297	
DNA topoisomerase 2-beta;DNA topoisomerase II, beta isozyme;Topoisomerase IIb;DNA topoisomerase 2;c1 TOP2B;topIIb; Isoform Beta-2 of DNA	Q02880-1;Q02880;	6.85E-11	0.51796	0.70427		1	-0.5058	
MutY homolog (E. coli);A/G-specific adenine DNA glycosylase;MutY homolog;MYHbeta;MutY homolog (E. coli);MUTYH;RP4-5 a/G-specific adenine D	E5K2P5;E5K30;E5	0.001055	0.55805	0.70667	51.827	2	-0.50089	
Nuclear envelope pore membrane protein POM 121;Nuclear envelope pore membrane protein POM 121A; KIAA0618;NU1 Isoform 1 of Nuclear e	Q96HA1-1;Q96HA1	0.0062477	0.5638	0.70747		1	-0.49926	
Nuclear factor 1;Putative uncharacterized protein NFIA;CCAAT-box-binding transcription factor;Nuclear fact	NFIA;RPS-902 nuclear factor 1 A-type	B4DS53;E2QR17;B1	2.12E-21	0.54265	0.7153	143.27	8	-0.48338
DNA-binding protein/plasminogen activator inhibitor 1 regulator;Helicase-like transcription factor;HIP116;R HIP116A;HLTF Isoform 1 of Helicase-li	Q14527-1;Q14527;	4.94E-289	0.57942	0.73174	140.57	89	-0.4506	
Activator 1 40 kDa subunit;Activator 1 subunit 2;Replication factor C 40 kDa subunit;Replication factor C sub RFC2;hCG_38 Isoform 1 of Replicatio	P35250-1;P35250;f	0.00036469	0.52913	0.73468		1	-0.44481	
ATP-dependent helicase SKIV2L2;Superkiller viralicidic activity 2-like 2;cDNA FLJ76877, highly similar to Hom	KIAA0052;SK1 Superkiller viralicidic ac	P42285;A8K614;B4I	0.011265	0.58588	0.74895	1	-0.41706	
Forkhead box protein K1;Myocyte nuclear factor;cDNA FLJ16099 fis, clone TESTI2008278, highly similar to H FOXK1;MNF;K Isoform 1 of Forkhead	P85037-1;P85037;f	7.14E-18	0.59275	0.75091	52.038	10	-0.41329	
NF-A1;Octamer-binding protein 1;Octamer-binding transcription factor 1;POU domain, class 2, transcription OCT1;OTF1;P	POU domain, class 2, ti P14859-1;P14859;f	5.62E-07	0.59826	0.75288		1	-0.40951	
RNA-binding motif protein 42;RNA-binding protein 42;cDNA FLJ60187	RBM42 Isoform 1 of RNA-bind	Q9BTD8-1;Q9BTD8	2.47E-19	0.5586	0.76968	12.154	2	-0.37767
96 kDa nucleoporin;98 kDa nucleoporin;Nuclear pore complex protein Nup96;Nuclear pore complex protei	ADAR2;NUP98 Isoform 1 of Nuclear p	P52948-1;P52948;f	4.67E-32	0.59973	0.77259	170.25	4	-0.37223
60S ribosomal protein L7;Similar to 60S ribosomal protein L7; similar to P18124 (PID:d133021);Putative unc	RPL7;WUGSC: 32 kDa protein;30 kDa	P18124;O95036;AE	2.98E-24	0.62479	0.77447	105.9	7	-0.36872
Leucine-rich repeat-containing protein 47	KIAA1185;LRR Leucine-rich repeat-co	Q8N1G4	9.93E-30	0.63456	0.77533	17.165	5	-0.36712
CAAT box DNA-binding protein subunit B;Nuclear transcription factor Y subunit B;Nuclear transcription fact	HAP3;NFYB Nuclear transcription f	P25208	0.012304	0.52126	0.7787		1	-0.36086
Suppressor of hairy wing homolog 4;Zinc finger protein 280D;cDNA FLJ76213, highly similar to Homo sapien	KIAA1584;SUH Isoform 1 of Zinc finger	Q6N043-1;Q6N043	6.15E-05	0.58553	0.78153	216.72	2	-0.35563
40S ribosomal protein S19;cDNA, FLJ92047, Homo sapiens ribosomal protein S19 (RPS19), mRNA;Ribosoma	RPS19;hCG_1 40S ribosomal protein	P39019;B0ZBD0;Q	0.00033165	0.63315	0.78357		1	-0.35187
cDNA FLJ60565, highly similar to Nuclear pore complex protein Nup153;Nucleoporin 153kDa;153 kDa nucle	NUP153;NUP: cDNA FLJ60565, highly	B4DIK2;Q72743;P4	2.30E-118	0.62235	0.78413	99.288	16	-0.35084
Membrane-organizing extension spike protein;Moesin;MSN protein	MSN Moesin	P26038;Q6PI7A	1.32E-12	0.61129	0.78628	186.35	4	-0.34688
Histone H2B;Histone H2B type 1-N;Histone H2B.d;Histone H2B type 1-C/E/F/G/I;Histone H2B.1 A;Histone H	H2BFD;HIST1H cDNA FLJ56787, highly	B4DR52;Q99877;B	2.03E-32	0.64428	0.78798	148.75	9	-0.34377
Double-stranded RNA-binding protein 76;Interleukin enhancer-binding factor 3;M-phase phosphoprotein 4;	DRBF;ILF3;MP interleukin enhancer-b	Q12906-4;Q12906;	2.50E-26	0.63184	0.79158	97.566	6	-0.33719
T-box transcription factor TBX3;Putative uncharacterized protein TBX3	TBX3 Isoform 1 of T-box tran	O15119-1;O15119;	1.21E-85	0.61289	0.79197	62.996	10	-0.33648
Cellular transcription factor ILF-1;Forkhead box protein K2;FOXK1;Interleukin enhancer-binding factor 1	FOXK2;ILF;ILF: Isoform 1 of Forkhead	Q01167-1;Q01167;	3.07E-14	0.65303	0.79363	11.594	2	-0.33346
Nucleolar protein EMG1 homolog;Probable ribosome biogenesis protein NEP1;Protein C2f;cDNA FLJ76620, C2f;EMG1	Probable ribosome bio	Q92979;A8K6D2;B	3.10E-06	0.62091	0.79744	18.969	3	-0.32655
Deletion target in pancreatic carcinoma 4;Mothers against decapentaplegic homolog 4;SMAD family memb	DPCA;MAD4 Mothers against decap	Q13485;Q9BYG6;B	2.72E-08	0.6275	0.80033		1	-0.32133
LDH heart subunit;L-lactate dehydrogenase B chain;Renal carcinoma antigen NY-REN-46;L-lactate dehydrog	LDHB;hCG_24 L-lactate dehydrogena:	P07195;Q5U077;A	8.16E-17	0.61436	0.80374	101.16	4	-0.3152
NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae);High mobility group-like nuclear protein 2 ho	CTA-216E10.8 NHP2 non-histone chr	B1AHD1;P55769;Q	1.93E-07	0.66665	0.82214		1	-0.28254
Pescadillo homolog;cDNA, FLJ96584, Homo sapiens pescadillo homolog 1, containing BRCT domain(zebrafis	PE51;hCG_20: Isoform 1 of Pescadillo	Q00541-1;Q00541;	4.90E-18	0.60845	0.82551	57.269	7	-0.27664
FLYWCH family member 2	FLYWCH2 FLYWCH family membe	Q96CP2	0.016053	0.61261	0.83259		1	-0.26432
ATP-binding cassette 50;ATP-binding cassette sub-family F member 1;TNF-alpha-stimulated ABC protein;ATP	ABCS0;ABCF1 Isoform 1 of ATP-bindir	Q8NE71-1;Q8NE71	3.30E-131	0.55943	0.83481	111.71	29	-0.26048
Radixin isoform b;Radixin isoform e;Radixin isoform f;Radixin, isoform d;Radixin; isoform CRA_	hCG_39182;R Radixin, isoform CRA_	z A7YU8;A7YIK3;P35:	4.12E-13	0.63428	0.84468		1	-0.24352
Eukaryotic translation initiation factor 5B;Translation initiation factor IF-2;EIF5B protein;cDNA FLJ10524 fis, c	EIF5B;IF2;KIA/ Eukaryotic translation i	O60841;A0JLR8;B3	1.58E-10	0.66702	0.84802	221.19	3	-0.23783
CBF-1;J kappa-recombination signal-binding protein;RBP-J kappa;Recombining binding protein suppressor o	IGKJRB;IGKJRE Isoform APCR-2 of Rec	Q06330-1;Q06330;	0.0015342	0.70902	0.85491		1	-0.22616
L-lactate dehydrogenase;Cell proliferation-inducing gene 19 protein;LDH muscle subunit;L-lactate dehydrog	LDHA;PIG19;h L-lactate dehydrogena:	B7Z5E3;P00338-1;f	4.30E-09	0.69554	0.86299		1	-0.21258
Activator 1 38 kDa subunit;Activator 1 subunit 3;Replication factor C 38 kDa subunit;Replication factor C sub	RFC3 Replication factor C sul	P40938;B4DK6E;Q	2.73E-11	0.69231	0.86519		1	-0.20891
TTF-I-interacting peptide 20;Zinc finger protein 787	ZNF787 Zinc finger protein 787	Q6DD87	2.26E-06	0.72167	0.87537		1	-0.19204
Paraspeckle protein 2;RNA-binding motif protein 14;RNA-binding protein 14;RRM-containing coactivator act	RBM14;SIP Isoform 1 of RNA-bind	Q96PK6-1;Q96PK6;	2.34E-113	0.72993	0.87744	35.171	39	-0.18863
DNA-binding factor KBF2;H2TF1;Lymphocyte translocation chromosome 10 protein;Nuclear factor NF-kapp	LYT10;NFKB2; Isoform 1 of Nuclear fa	Q00653-1;Q00653;	0.0058312	0.62763	0.89003		1	-0.16807
40S ribosomal protein S9;Ribosomal protein S9;Ribosomal protein S9, isoform CRA_a;cDNA FLJ61636, high	RPS9;hCG_20 40S ribosomal protein	P46781;A9C4C1;B7	0.0023886	0.69696	0.89809		1	-0.15507
Cyclophilin B;CYP-51;Peptidyl-prolyl cis-trans isomerase B;Rotamase B;S-cyclophilin	CYPB;PPIB Peptidyl-prolyl cis-tran	P23284	8.36E-28	0.70893	0.89904	131.21	20	-0.15354
Cell division control protein 2 homolog;Cyclin-dependent kinase 1;p34 protein kinase;Putative uncharacte	CDC2;DKFZp6 Putative uncharacteriz	P06493-1;P06493;f	1.57E-09	0.72593	0.89991	7.1124	3	-0.15215
Sucrose nonfermenting protein 2 homolog;SWI/SNF-related matrix-associated actin-dependent regulator of	SMARCA5;SNI SWI/SNF-related matri	O60264;B4DZC0;B;	2.30E-22	0.71575	0.90112	90.789	11	-0.15021
S1 RNA-binding domain-containing protein 1;cDNA FLJ31974 fis, clone NT2RP7008167, weakly similar to 85	SRB01 Isoform 1 of S1 RNA-bi	Q8N5C6-1;Q8N5C6	4.98E-17	0.72445	0.9095	1.6967	2	-0.13685
Cytovillin;Ezrin;p81;Villin-2;cDNA, FLJ92973, highly similar to Homo sapiens villin 2 (ezrin) (VIL2), mRNA;cD	EZR;VIL2 Ezrin;69 kDa protein	P15311;B2R612;B7:	9.21E-19	0.70123	0.91062	89.403	9	-0.13508
cDNA FLJ78091, highly similar to Homo sapiens ubiquitin-like, containing PHD and RING finger domains, 1 (l	UHRF1;ICBP9E3 ubiquitin-protein lig	A8K024;B2RBA9;Q:	8.34E-303	0.69597	0.91119	101.83	61	-0.13418
cDNA FLJ58953, highly similar to 40S ribosomal protein S20;40S ribosomal protein S20	RPS20 40S ribosomal protein	B4DW28;P60866;E:	5.71E-10	0.73884	0.91348	110.32	7	-0.13055
C-2K;Cell division cycle 2-like protein kinase 4;Cell division protein kinase 9;Cyclin-dependent kinase 9;Serin	CDC2L4;CDK9 Isoform 2 of Cyclin-dep	P50750-2;P50750;f	3.21E-05	0.7221	0.91834		1	-0.1229
Glutaminyl-peptide cyclotransferase-like protein	QPCTL Glutaminyl-peptide cyc	Q9NXS2	0.0010763	0.73942	0.91973		1	-0.12072
Down-regulator of transcription 1;Negative cofactor 2-beta;Protein Dr1;TATA-binding protein-associated ph	DR1;DKFZp66 Protein Dr1	Q01658;Q53F47;Q:	0.00015648	0.74286	0.91993		1	-0.1204
Androgen-induced proliferation inhibitor;Androgen-induced prostate proliferative shutoff-associated protei	APRIN;AS3;KI/ 165 kDa protein;Isofo	Q9NT15-1;Q9NT15;f	1.23E-14	0.73323	0.92028	23.603	2	-0.11986
40S ribosomal protein S19-binding protein 1;Active regulator of SIRT1	AROS;RPS19B Active regulator of SIR	Q86WX3	2.51E-05	0.74651	0.92824		1	-0.10743
18 kDa Alu RNA-binding protein;Signal recognition particle 14 kDa protein	SRP14 Signal recognition part	P37108	1.39E-11	0.74794	0.9314	37.186	3	-0.10253
23 kDa highly basic protein;60S ribosomal protein L13a;RPL13A protein;Ribosomal protein L13a variant;FWI	RPL13a;hCG_ 60S ribosomal protein	P40429;Q0VGL3;Q:	0.087812	0.72747	0.93494	5.5781	2	-0.09705
Kinesin-like DNA-binding protein;Kinesin-like protein 4;Kinesin-like protein KIF22;cDNA FLJ53835, highly sim	KIF;KIF22;KNS Kinesin-like protein KIF	Q14807;B7Z265;B7	6.29E-127	0.78155	0.94994	117.79	29	-0.07409
Protein RCC2;RCC1-like protein TD-60;Telophase disk protein of 60 kDa;RCC2 protein	KIAA1470;RCC Protein RCC2	Q9P258;A5PLK7	2.64E-50	0.73193	0.95118	122.23	2	-0.07221
SMARCA4 protein;SMARCA4 isoform 2;SWI/SNF related, matrix associated, actin dependent regulator of ch	SMARCA4;hCC SMARCA4 protein;tran	B9EGQ8;Q9HBD4;E	1.26E-28	0.75978	0.95689	11.214	9	-0.06358
ESRRB protein;Estrogen receptor-related receptor beta2-delta-10;ERR beta-2;Estrogen receptor-like 2;Estr	ESRRB;ERRB2; steroid hormone recep	A2VDJ2;Q5F0P7;O:	0.0075667	0.72634	0.95795	1.825	2	-0.06198
60S ribosomal protein L13;Breast basic conserved protein 1;Ribosomal protein L13	BBC1;OK/SW- 60S ribosomal protein	P26373;A8K4C8;B4	4.13E-17	0.75668	0.97157	1.54	6	-0.04161
DNA mismatch repair protein Msh2;MutS protein homolog 2;cDNA FLJ57316, highly similar to DNA mismatr	MSH2 DNA mismatch repair f	P43246;B4DL39;B4	7.97E-27	0.75626	0.97247	63.057	10	-0.04027
DNA-dependent protein kinase catalytic subunit;DNPK1;p460;cDNA FLJ57825, highly similar to DNA-depenc	HYRC;HYRC1; Isoform 1 of DNA-depe	P78527-1;P78527;f	4.65E-16	0.78394	0.97739	68.77	6	-0.03299
Importin subunit beta-1;Importin-90;Karyopherin subunit beta-1;Nuclear factor p97;Pore targeting complex	KPNB1;NTF97 Importin subunit beta-	Q14974;B2RBR9;B:	7.12E-08	0.77766	0.98508	11.236	3	-0.02169

Valyl-tRNA synthetase;Protein G7a;Valine--tRNA ligase	DAAP-21F2.2- Valyl-tRNA synthetase; B0V043;P26640	1.56E-06	1.1979	1.5348	12.906	4	0.618051
UPF0609 protein C4orf27	C4orf27 UPF0609 protein C4orf Q9NWWY4	2.86E-16	1.226	1.6361	142.54	11	0.710261
BPY2-interacting protein 1;MAP1S heavy chain;MAP1S light chain;Microtubule-associated protein 1S;Microt	BPY2IP1;C19o Microtubule-associated protein 1S;Q66K74;A8K940;B4	0.00066442	0.98408	1.6426		1	0.715981
40S ribosomal protein S7;cDNA, FLJ92055, Homo sapiens ribosomal protein S7 (RPS7), mRNA;Putative unch	RPS7;hCG_17: 40S ribosomal protein P62081;Q57Z92;B5	1.67E-05	1.2999	1.8254	84.113	2	0.868213
cDNA FLJ51656, highly similar to Actin-like protein 2;Actin-like protein 2;Actin-related protein 2;ACTR2	actin-related protein 2 B4DHK9;P61160;Q	0.016945	1.3077	1.8801		1	0.910809
Transcription factor jun-D	JUND Transcription factor jur P17535	6.62E-15	1.5638	1.9391	108.23	4	0.955387
Rap1-interacting factor 1 homolog;Telomere-associated protein RIF1	RIF1 Isoform 1 of Telomere- Q5UIP0-1;Q5UIP0;I	0.0061568	1.4995	2.1479		1	1.102927
62 kDa nucleoporin;Nuclear pore glycoprotein p62;Nucleoporin Nup62;Putative uncharacterized protein pp	NUP62;pp705 Nuclear pore glycoprot P37198;Q8WYU3	0.004906	1.8031	2.58		1	1.367371
Transcription factor jun-B;Jun B proto-oncogene variant;cDNA, FLJ94337, Homo sapiens jun B proto-oncoge	JUNB;hCG_17 Transcription factor jur P17275;Q53HP8;Q	4.29E-18	2.1192	2.6232	84.736	3	1.391328
18S rRNA dimethylase;DIM1 dimethyladenosine transferase 1-like;Probable dimethyladenosine transferase;	DIMT1;DIMT1 Probable dimethylader Q9UNQ2;A8K9K8;E	0.002424	2.0672	3.0832		1	1.624428
Cyclic AMP-responsive element-binding protein 1;cAMP responsive element binding protein 1;CAMP respor	CREB1;hCG_1 Isoform CREB-A of Cycl P16220-1;P16220;C	4.17E-14	2.7056	3.3213	19.383	3	1.731748
cDNA FLJ54188, moderately similar to High mobility group protein HMG-I/HMG-Y;Putative uncharacterized	HMG1;HMG cDNA FLJ54188, modei B4DWA0;C9J292;P:	0.0058359	2.7178	3.9783		1	1.992152
Probable tumor suppressor protein MN1;Meningioma (Disrupted in balanced translocation) 1	MN1 Meningioma (Disrupte: Q10571;A5HML1	0.12914	3.5346	4.441	289.97	2	2.150885
Outer mitochondrial membrane protein porin 2;Voltage-dependent anion-selective channel protein 2;cDNA	VDAC2;RP11-: Isoform 1 of Voltage-de P45880-1;P45880;f	0.025034	4.2551	6.0233		1	2.590554

Supplementary Table 2 B: ODN-to-protein conjugates identified by tandem mass spectrometry and quantified using SILAC (hmC=heavy; C=light)

Protein Names	Gene Names	Protein Descriptions	Uniprot	Mol. Weight [kDa]	PEP	Ratio H/L	Ratio H/L Normalized	Ratio H/L Variability [%]	Ratio H/L Cou Log2(H/L)
Arginine/proline-rich coiled-coil domain-containing protein 1;MAP7 domain-containing protein 1; KIAA1187;MAAP7D1;PARCC1;PP2464;RPRC1		Isoform 1 of MAP7 domain-containing protein 1;Isoform Q3KQU3-1;Q3KQU3		92.819	0.0050669	16.103	22.347	95.012	2
cDNA FLJ58590, highly similar to YLP motif-containing protein 1;YLPM1 protein;FLJ00353 protein;N YLPM1;FLJ00353;C4orf170;ZAP3		YLP motif-containing protein 1;Isoform 1 of YLP motif-cc B4DMQ9;Q86YA8		241.64	1.21E-07	5.1737	5.0139	30.67	3
Bcl-2-associated transcription factor 1;BCLAF1 protein;cDNA, FLJ79533, highly similar to Bcl-2-asso BCLAF1;BTF;KIAA0164		Isoform 1 of Bcl-2-associated transcription factor 1;Isof. Q9NYF8-1;Q9NYF1		106.12	0.024252	5.0929	4.3068	40.879	2
Testis-expressed sequence 10 protein;cDNA FLJ54377;cDNA FLJ57815;cDNA FLJ50343;cDNA FLJ50118;Nbla10363;TEX10		Testis-expressed sequence 10 protein;testis-expressed s Q9NFX1;B4DQK0;		105.67	2.34E-05	3.0351	3.4481	23.068	3
Scaffold attachment factor B2;SAFB2 protein KIAA0138;SAFB2		Scaffold attachment factor B2 Q14151;A0PJQ7		107.47	0.0030361	3.4403	3.1023	1	1.5989845
RRP12-like protein;cDNA FLJ12434 fis, clone NTR2RM1000037, highly similar to Homo sapiens KIAA0202B;toplib;TOP2A;TOP2;top2beta		Isoform Beta-2 of DNA topoisomerase 2-beta;Isoform B Q02880-1;Q0288C		183.26	1.60E-12	2.9181	2.8733	39.254	2
Cleavage and polyadenylation specificity factor 100 kDa subunit;Cleavage and polyadenylation spe: CP5F100;CP5F2;KIAA1367		Cleavage and polyadenylation specificity factor subunit Q9P210;B3KN45		88.486	6.35E-05	2.6873	2.8419	1	1.5068786
cDNA FLJ32832 fis, clone TESTI2003196;Embryonic large molecule derived from yolk sac;Protein EL AHCT1;ELYS;MSTP108;TMB562		protein ELYS;Isoform 2 of Protein ELYS;Isoform 1 of Prot Q96M44;Q8WYPS		256.24	4.33E-08	3.6765	2.8287	1	1.5001392
60S ribosomal protein L15;Ribosomal protein L15 EC45;RPL15;TCBAPO781;hCG_1996483		60S ribosomal protein L15;21 kDa protein;cDNA FLJ5147: P61313;Q5UOCC;E		24.146	0.00019599	3.5637	2.7977	1	1.4842413
60S ribosomal protein L10;Laminin receptor homolog;Protein QM;Tumor suppressor QM;Ribosom; DXS648E;Q;RPL10;XX-FW8356389.1-011;F		60S ribosomal protein L10;60S ribosomal protein L10-h1 P27635;Q5HY0;C		24.604	0.26025	2.8193	2.7556	1	1.4623665
One-twenty two protein 1;Putative RNA-binding protein 15;RNA-binding motif protein 15;RNA binc OTT;OTT1;RBM15		Isoform 1 of Putative RNA-binding protein 15;Isoform 3 Q96T37-1;Q96T37		107.19	0.0010035	3.3142	2.7486	55.228	2
68 kDa TATA-binding protein-associated factor;RNA-binding protein 56;TATA-binding protein-associ RBP56;TAF15;TAF2N;hCG_1992163		Isoform Long of TATA-binding protein-associated factor Q92804-1;Q92804		61.829	3.29E-35	4.2848	2.6415	1	1.4013574
ATP-dependent RNA helicase DDX42;DEAD box protein 42;RNA helicase-like protein;RNA helicase-r DDX42		Isoform 1 of ATP-dependent RNA helicase DDX42;Isofo Q86XP3-1;Q86XP3		102.97	9.65E-07	2.8963	2.6245	1	1.3920426
Zinc finger protein 326 ZNF326		Isoform 1 of Zinc finger protein 326 Q5XK21-1;Q5XK21		65.653	3.03E-06	2.7956	2.6177	37.191	3
Modulator of estrogen-induced transcription;SAFB-like transcription modulator;cDNA FLJ30633 fis, MET;SLTM		SAFB-like transcription modulator;SAFB-like transcriptio Q9NWH9;A8K5V8		117.15	0.14794	3.1228	2.6002	1	1.3786226
Coilin;p80 COLN8;COL		Coilin P38432		62.608	6.18E-07	2.4354	2.5992	25.358	3
Cell proliferation-inducing gene 4/52 protein;Mitochondrial inner membrane protein;Mitofilin;p87, HMP;JMPT;PIG4;PIG52		Isoform 1 of Mitochondrial inner membrane protein;Iso Q16891-1;Q16891		83.677	0.022615	2.3239	2.5898	51.17	2
Apoptotic chromatin condensation inducer in the nucleus;ACIN1 protein;cDNA FLJ50838, highly sim ACIN1;ACINUS;KIAA0670;DKFZp667N107		Isoform 1 of Apoptotic chromatin condensation inducer Q9YKUV3-1;Q9YKUV		151.86	5.52E-44	3.3541	2.5737	36.863	6
Emerin;EMD protein;Emerin (Emery-Dreifuss muscular dystrophy), isoform CRA_a;Emerin (Emery- EDMD;EMD;STA;hCG_41343;XX-FW88778H2		Emerin;Emerin (Emery-Dreifuss muscular dystrophy), is P50402;Q6F102;Q		28.994	6.91E-08	3.2088	2.5342	6.3089	2
Thyroid hormone receptor-associated protein 3;Thyroid hormone receptor-associated protein com THRAP3;TRAP150		Thyroid hormone receptor-associated protein 3 Q9Y2W1;Q5D020		108.66	2.14E-05	2.6093	2.484	33.808	2
Cleavage and polyadenylation specificity factor 160 kDa subunit;Cleavage and polyadenylation spe: CP5F1;CP5F160;hCG_2039719;P/c.18		Cleavage and polyadenylation specificity factor subunit Q10570;B4DEF4;E		160.88	7.08E-08	2.6146	2.4789	1	1.3097001
60S ribosomal protein L18;Ribosomal protein L18 RPL18		60S ribosomal protein L18;cDNA FLJ59178, moderately Q07020;Q0QEW2		21.634	2.30E-21	2.5148	2.3512	6.7436	4
Modulator of non-genomic activity of estrogen receptor;Proline-, glutamic acid- and leucine-rich p HMX3;MNAR;PELP1		Isoform 2 of Proline-, glutamic acid- and leucine-rich pr Q8I2L2-2;Q8I2L8;C		135.49	4.16E-07	2.1986	2.3059	12.623	4
40 kDa SR-repressor protein;FUS-interacting serine-arginine-rich protein 1;Splicing factor SRp38;Sp FUSIP1;FUSIP2;SFR513A;TASR;RP11-4M23.6		Isoform 1 of Serine/arginine-rich splicing factor 10;Isofo Q75494-1;Q75494		31.3	2.16E-18	2.6556	2.3047	9.5842	5
NUMA1 variant protein;Nuclear mitotic apparatus protein 1;SP-H antigen;cDNA FLJ76708, highly si NUMA1 variant protein;NUMA;NUMA1;Nul		NUMA1 variant protein (Fragment);Isoform 1 of Nuclea Q4LE64;Q14980-1		238.86	6.08E-65	2.9051	2.3027	16.086	8
Activating enhancer-binding protein 2-delta;Transcription factor AP-2-beta-like 1;Transcription fact TFAP2B1;TFAP2D		Transcription factor AP-2-delta Q726R9		49.577	0.004079	2.4548	2.2633	1	1.1784278
Outer mitochondrial membrane protein porin 2;Voltage-dependent anion-selective channel protei VDACC2;RP11-375G3.1-010;RP11-375G3.1-0C		Isoform 1 of Voltage-dependent anion-selective channe P45880-1;P45880		33.371	0.014099	2.8908	2.2433	1	1.1662226
220 kDa uS snRNP-specific protein;p220;Pre-mRNA-processing-splicing factor 8;PRP8 homolog;Spli PRPC8;PRP8F		Pre-mRNA-processing-splicing factor 8 Q6P2Q9;B4DKC15		273.6	2.30E-17	3.0826	2.2168	21.213	9
AIR carboxylase;Multifunctional protein ADE2;Phosphoribosylaminoimidazole carboxylase;Phosph: ADE2;ACIRC;PAICS;PAIS;DKFZp781N1372		Multifunctional protein ADE2;multifunctional protei AI P22234;Q68CQ5;E		49.679	1.56E-15	2.44	2.2138	1.1524	2
Transformer-2 protein homolog A;Transformer-2 protein homolog alpha;cDNA FLJ50614, highly sim TRAA2A;hCG_37979;HSU53209		Isoform Long of Transformer-2 protein homolog alpha;I Q13595-1;Q13595		32.688	0.0017494	2.4739	2.2015	1	1.1384868
cDNA FLJ76836, highly similar to Homo sapiens splicing factor, arginine/serine-rich 14 (SFRS14), tra KIAA0365;SFRS14		cDNA FLJ76836, highly similar to Homo sapiens splicing al P18359;Q8X100-1		121.31	0.016807	2.2552	2.1466	1	1.1020344
300 kDa nuclear matrix antigen;Serine/arginine repetitive matrix protein 2;Serine/arginine-rich spli HSPC075;KIAA0343;SRL300;SRM300;SRM		Isoform 1 of Serine/arginine repetitive matrix protein 2 Q9UQ35-1;Q9UQ3		299.61	0.0022308	2.498	2.1354	1	1.0945063
EPB72-like protein 2;Stomatin-like protein 2;cDNA FLJ61039, highly similar to Stomatin-like protein HSPC108;SLP2;STOML2		Stomatin-like protein 2;cDNA FLJ61039, highly similar t Q9H1U2;B4E1K7		38.534	0.021587	2.0046	2.1276	1	1.0892269
ATP-dependent RNA helicase p54;DEAD box protein 6;Oncogene RCK;Probable ATP-dependent RN DDX6;HLR2;RCK		Probable ATP-dependent RNA helicase DDX6 P26196;B2R858;Q		54.416	0.0049494	2.4675	2.1181	1	1.0827707
RRP12-like protein;cDNA FLJ12434 fis, clone NTR2RM1000037, highly similar to Homo sapiens KIAA KIAA0690;RRP12		Isoform 1 of RRP12-like protein;RRP12-like protein isofo Q5JTH9-1;Q5JTH9		143.7	1.98E-08	2.2805	2.1031	1	1.0521575
100 kDa coated vesicle protein A;Adapter-related protein complex 2 alpha-1 subunit;Adapter protein ADTAA;APA2A1;CLAPA1		Isoform A of AP-2 complex subunit alpha-1;108 kDa pr Q95782-1;Q95782		107.54	0.005984	2.2419	2.0987	1.2092	2
Nucleoporin NUP188 homolog KIAA0169;NUP188		Isoform 1 of Nucleoporin NUP188 homolog;Isoform 2 o Q5SRES-1;Q5SRES		196.04	0.0010557	2.0086	2.0874	1	1.0617071
Glycoprotein p43;Heterogeneous nuclear ribonucleoprotein G;Heterogeneous nuclear ribonucleo HNRPG;RBMX;RBMXP1;CCBL2;DKFZp547N1		Heterogeneous nuclear ribonucleoprotein G;cDNA FLJ3 P8159;B4E352;B		42.331	3.71E-20	2.4543	2.0745	57.462	18
G patch domain-containing protein 9;RNA-binding motif protein 10;RNA-binding protein 10;RNA-bi DXS8237E;GPATC3;GPATC9;KIAA0122;RBM		Putative uncharacterized protein DKFZp686E2459;Isofo P98175-1;P98175		110.34	1.40E-05	3.1403	2.0527	25.434	3
U1 small nuclear ribonucleoprotein 70 kDa;cDNA FLJ77404, highly similar to Homo sapiens small n RNPU12;RPU1;SNRNP70;SNRP70;U1AP1;DKI		Isoform 1 of U1 small nuclear ribonucleoprotein 70 kDa P08621-1;P08621		115.556	1.29E-15	2.3944	2.0519	13.374	7
ATP-dependent RNA helicase A;DEAH box protein 9;Nuclear DNA helicase II;cDNA FLJ39263 fis, clor DDX9;DHX9;LKP;NDH2		ATP-dependent RNA helicase A Q08211;B3KU66;C		140.96	8.68E-147	2.9925	2.0429	81.264	41
Cytochrome c oxidase polypeptide II;Cytochrome c oxidase subunit 2;Cytochrome c oxidase subuni COII;COXII;MTCO2;MT-CO2;COX2;CO2		Cytochrome c oxidase subunit 2 P00403;A0S0W7;C		25.565	1.99E-05	2.5888	2.0251	1	1.0250997
Hemidesmosomal protein 1;Plectin-1;HCG1994702;Plectin isoform 1b;Plectin 1, intermediate filam PLEC1;hCG_1994702;hCG_1994701		Isoform 1 of Plectin;Isoform 2 of Plectin;Isoform 3 of Plc Q15149-1;Q15145		531.78	0.0042976	1.7844	2.0309	1	1.0221192
Oculospasin;Tetraspanin-10;TSPAN10 protein QCS;TSPAN10		Tetraspanin-10 Q9H129;Q6PI65		36.498	0.0037661	2.8974	2.0235	11.164	2
Small nuclear ribonucleoprotein Sm D1;Sm-D autoantigen;snRNP core protein D1 SNRPD1		Small nuclear ribonucleoprotein Sm D1;Small nuclear rl P62314;Q7Z5A3		13.281	4.54E-09	1.6183	2.0203	131.03	3
Heterogeneous nuclear ribonucleoprotein M;Heterogeneous nuclear ribonucleoprotein M isoform HNRNPM;HNRPM;NAGR1;ORF;DKFZp547H1		Isoform 1 of Heterogeneous nuclear ribonucleoprotein P52272-1;P52272		77.515	2.05E-121	2.741	2.0114	55.273	75
Dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit;Dolichol-phosphate man DPM1;RPS-914P20.2-003;RPS-914P20.2-005		Isoform 1 of THO complex subunit 1;Isoform 2 of THO c Q96FV9-1;Q96FV9		33.349	0.019022	2.4447	2.0082	1	1.005903
HTREX84;Nuclear matrix protein p84;THO complex subunit 1 HPR1;THOC1		Isoform 1 of THO complex subunit 1;Isoform 2 of THO c Q96FV9-1;Q96FV9		75.665	2.16E-29	2.2217	2.0012	35.225	8
D-3-phosphoglycerate dehydrogenase;cDNA FLJ35987 fis, clone TESTI2014269, highly similar to D-3 PGDH3;PHGDH;RP4-683H9.1-002		D-3-phosphoglycerate dehydrogenase;Phosphoglycerat Q43175;B3KSC3;C		56.65	0.0094531	2.0143	1.9994	31.34	4
40S ribosomal protein S9;Ribosomal protein S9;Ribosomal protein S9, isoform CRA_a;cDNA FLJ616 RPS9;hCG_2009111;XXbac-BCX105G6.6-001		40S ribosomal protein S9;Similar to 40S ribosomal prot P46781;A9C4C1		22.591	2.08E-05	2.0912	1.9956	28.729	4
60S ribosomal protein L27a;Ribosomal protein L27a RPL27A;L27a		60S ribosomal protein L27a P46776;Q6N252;C		16.561	3.15E-06	2.6582	2.0303	3	0.9871025
cDNA FLJ5484, highly similar to ATP-dependent RNA helicase DDX39 (EC 3.6.1.-);ATP-dependent R DDX39;DKFZp547B159;hCG_1776331		cDNA FLJ5484, highly similar to ATP-dependent RNA h B4DX78;Q00148;C		53.696	5.61E-26	2.1766	1.9696	1	0.9779027
Zinc finger CCH domain-containing protein 11A;cDNA FLJ58196, highly similar to Zinc finger CCH KIAA0663;ZC3H11A;ZC3HDC11A		Zinc finger CCH domain-containing protein 11A;ZC3H1 Q75152;B4DLG2;C		89.13	3.11E-19	2.554	1.9681	7.9014	7
DNA repair protein XRCC1;X-ray repair cross-complementing protein 1;cDNA, FLJ96373, highly simi XRCC1		DNA repair protein XRCC1;cDNA FLJ56491, highly similia P18887;B2RCY5;B		69.476	0.0015455	2.0582	1.9553	1	0.96739
20 kDa CGG-binding protein 1;p20-CGGBP DNA-binding protein;CGGBP1;CGGBP1		CGG triplet repeat-binding protein 1;Uncharacterized pr Q9UFW8;C9JU10		18.82	0.007001	2.3836	1.9349	1	0.9525259
60S ribosomal protein L8;cDNA FLJ53750, highly similar to 60S ribosomal protein L8 RPL8		32 kDa protein;60S ribosomal protein L8;26 kDa protein P62917;B4DVG7		31.75	1.65E-05	2.443	1.9303	65.765	3
Sm protein B/B';Small nuclear ribonucleoprotein-associated proteins B and B';Putative uncharacte COD;SNRPB;SNRPB1;hCG_2039421;HCERN3		Isoform SM-B1 of Small nuclear ribonucleoprotein-asso P14678-3;P14678		30.032	0.00020308	2.2389	1.9011	7.9344	7
E3 ubiquitin-protein ligase MIB2;Mind bomb homolog 2;Novel zinc finger protein;Putative NF-kapp MIB2;SKD;ZZANK1		E3 ubiquitin-protein ligase MIB2 isoform 1;E3 ubiquitin- Q96AX9-9;Q96AX		115.86	0.0065087	2.1871	1.8857	39.563	3
Functional spliceosome-associated protein 79;hTREX90;NF2/meningioma region protein pK1.3;Plac C22orf19;KIAA0983;THOCS		THO complex subunit 5 homolog;40 kDa protein;Protein Q13769;C9JXG5		78.507	0.0016864	2.0989	1.8748	2.6464	2
Cleavage and polyadenylation specificity factor 59 kDa subunit;Cleavage and polyadenylation spei CP5F7		Isoform 3 of Cleavage and polyadenylation specificity fa Q8N684-3;Q8N68		56.374	2.46E-13	2.4365	1.8709	10.151	3
Alternative-splicing factor 1;pre-mRNA-splicing factor SF2, P33 subunit;Splicing factor, arginine/seri ASF;OK/SW-cl-3;SF2;SF2P33;SFRS1		Isoform ASF-1 of Serine/arginine-rich splicing factor 1;Is Q07955-1;Q07955		27.744	5.27E-14	2.0715	1.8709	23.011	9
Importin subunit beta-1;importin-90;Karyopherin subunit beta-1;Nuclear factor p97;Pore targeting KPNB1;NTPF9		Importin subunit beta-1 Q14974;B2RBR9;E		97.169	6.40E-12	2.1626	1.861	51.364	9
Arsenite-resistance protein 2;Serrate RNA effector molecule homolog ARS2;ARS2;SRRT		Isoform 1 of Serrate RNA effector molecule homolog;Is Q9BXP5-1;Q9BXP		100.67	0.00011906	2.2699	1.8588	1	0.8947315
60S ribosomal protein L19;Ribosomal protein L19 RPL19		60S ribosomal protein L19 P84098;Q53G49;C		23.466	2.80E-36	2.3923	1.8538	12.724	3
T-cell activation WD repeat-containing protein;WD repeat-containing protein 36;Putative uncharac WDR36;DKFZp6861650		Uncharacterized protein;WD repeat-containing protei D6RAY5;Q8N136;C		105.28	0.0015502	1.7963	1.853	23.72	3
Epidermal surface antigen;Flotillin-2;Membrane component chromosome 17 surface marker 1;FLO ESA1;FLOT2;M17S1;hCG_1998851		53 kDa protein;Flotillin-2;FLOT2 protein Q14254;Q6FG43;C		53.137	2.21E-22	2.1963	1.8367	14.757	3
ATP-dependent RNA helicase DHX8;DEAH box protein 8;RNA helicase HRH1;cDNA FLJ76879, highly DDX8;DHX8		ATP-dependent RNA helicase DHX8 Q14562;A8K619;B		139.31	0.40917	1.908	1.8413	1	0.8807427
Heterogeneous nuclear ribonucleoprotein F;Heterogeneous nuclear ribonucleoprotein F, N-termi HNRNPF;HNRPF;OK/SW-cl.23		Heterogeneous nuclear ribonucleoprotein F P52597;B4DKS8;Q		45.671	1.46E-97	2.3718	1.841	92.803	6
Gamma-1-tubulin;Gamma-tubulin complex component 1;Tubulin gamma-1 chain;Gamma-2-tubuli TUBG;TUBG1;TUBG2		Tubulin gamma-1 chain;Tubulin gamma-2 chain;34 kDa P23258;Q9NRH3		51.169	0.0031104	1.8531	1.791	1	0.8407653
Nuclear envelope pore membrane protein POM 210;Nuclear pore membrane glycoprotein 210;Nu KIAA0906;NUP210;PSEC0245		Isoform 1 of Nuclear pore membrane glycoprotein 210 Q8TEM1-1;Q8TEM		205.11	1.03E-35	2.2599	1.79	47.416	10
100 kDa DNA-pairing protein;DNA-binding p52/p100 complex, 100 kDa subunit;Polypyrimidine tra SF;SFPQ		Isoform Long of Splicing factor, proline- and glutamine- P23246-1;P23246		76.149	7.84E-170	2.5104	1.7871	112.45	116
Protein FAM195A C16orf14;FAM									

60S ribosomal protein L6;Neoplasm-related protein C140;Tax-responsive enhancer element-binding RPL6;TXREB1	DNA-binding protein TAXREB107;60S ribosomal protein B2R4K7;Q9HBB3;	32.872	3.55E-09	1.9854	1.7846	18.906	8	0.8356007
Novel nuclear protein 1;Nucleolar protein Nop52;Ribosomal RNA processing protein 1 homolog A; D2152056;ENP1;NOP52;RRP1;RRP1A	Ribosomal RNA processing protein 1 homolog A; cDNA F P56182;Q53FR7;C	52.839	9.88E-05	1.8708	1.7773	9.8643	2	0.8296872
Myb-binding protein 1A; cDNA FLJ60422, highly similar to Myb-binding protein 1A; cDNA FLJ57836, MYBBP1A; P160	Isoform 2 of Myb-binding protein 1A; Isoform 1 of Myb-1	149.37	0.001988	2.1051	1.7768	27.423	3	0.8292830
Sm protein E; Small nuclear ribonucleoprotein E; Putative small nuclear ribonucleoprotein polypepti SNRPE; SNRPE1	Small nuclear ribonucleoprotein E; Putative small nuclea	10.803	2.81E-10	2.2616	1.7694	12.863	6	0.8232602
Phosphoinositide lipid phosphatase; Protein-tyrosine phosphatase mitochondrial 1; PTEN-like phospho MOSP; PLIP; PNAS-129; PTPMT1	Isoform 1 of Protein-tyrosine phosphatase mitochondri	22.843	0.00016931	2.0657	1.7689		1	0.8228525
DEAD box protein 5; Probable ATP-dependent RNA helicase DDX5; RNA helicase p68; cDNA FLJ53366 DDX5; G17P1; HELR; HLR1; DKFZp686J01190	Probable ATP-dependent RNA helicase DDX5; cDNA FLJ5	69.147	3.58E-49	2.5056	1.7615	22.431	10	0.8168045
Intron-binding protein aquarius; Intron-binding protein of 160 kDa; cDNA FLJ75449, highly similar to AQR; KIAA00560	Q60306; A8K6F0; B	171.38	0.018615	1.8473	1.7584		1	0.8142633
Leucine-rich repeat-containing protein 47	Leucine-rich repeat-containing protein 47	63.472	1.68E-16	1.9279	1.7542	56.949	2	0.8108132
DEAD box polypeptide 17 isoform p82 variant; DEAD box protein 17; DEAD box protein p72; Probabli DDX17; RP3-434P1.4-009; RP3-434P1.4-005	probable ATP-dependent RNA helicase DDX17 isoform 3	80.457	1.36E-105	2.5744	1.754	84.063	42	0.8106487
Putative uncharacterized protein CHCHD3; Coiled-coil-helix-coiled-coil-helix domain-containing prot CHCHD3; hCG_2014841; tcag7.1158	28 kDa protein; Uncharacterized protein; Coiled-coil-heli	27.735	0.0030977	1.9305	1.7533		1	0.8100729
Putative uncharacterized protein MATR3; Matrin-3; cDNA FLJ53172, highly similar to Matrin-3; Putat MATR3; KIAA0723; DKFZp686K23100	Uncharacterized protein; Matrin-3; Uncharacterized prot	99.966	1.44E-117	2.4205	1.7499	88.471	28	0.8072725
Tubulin beta-2A chain; TUBB2A protein; Tubulin beta-2B chain; TUBB2B protein; Homo sapiens clone TUBB2; TUBB2A; TUBB2B; DKFZp566F223; Ok	Tubulin beta-2A chain; Tubulin beta-2B chain; cDNA, FLJ	49.906	4.48E-21	2.1804	1.7433	42.386	11	0.8018209
Acetoacetyl-CoA thiolase; Acetyl-CoA acetyltransferase, mitochondrial; T2; ACAT1 protein	ACAT; ACAT1; MAT	45.199	0.00080164	1.4699	1.7313		1	0.7918557
FTP-3; Heterogeneous nuclear ribonucleoprotein H'; Heterogeneous nuclear ribonucleoprotein H2; cFTP3; HNRNPH2; HNRHP3	Heterogeneous nuclear ribonucleoprotein H2; cDNA FLJ	49.263	2.21E-116	2.0971	1.7292	24.142	9	0.7901047
Paraspeckle protein 2; RNA-binding motif protein 14; RNA-binding protein 14; RRM-containing coat RBM14; SIP	Isoform 1 of RNA-binding protein 14; RNA binding motif	69.491	4.94E-37	2.2599	1.7184	19.648	21	0.7810659
Nucleolar phosphoprotein B23; Nucleolar protein NO38; Nucleophosmin; Numatrin; Truncated nucle NPM1; NPM1	Isoform 1 of Nucleophosmin; Isoform 2 of Nucleophosm	32.575	5.67E-123	2.134	1.7157	104.89	28	0.7787973
Clathrin heavy chain 1; Clathrin heavy chain on chromosome 17	Isoform 1 of Clathrin heavy chain 1; Isoform 2 of Clathri	191.61	7.52E-15	2.123	1.7147	79.603	6	0.7779562
Functional spliceosome-associated protein 35; THO complex subunit 6 homolog; WD repeat-contain PSEC0006; THOCC; WDR58	Isoform 1 of THO complex subunit 6 homolog; Isoform 3	37.535	3.21E-48	2.1631	1.7137	111.68	8	0.7771446
Nucleoprotein TPR; TPR protein; Tpr protein; Tpr	Nucleoprotein TPR	267.29	0.00180763	1.7546	1.7117		1	0.7754299
Activating signal co-receptor 1 complex subunit 3-like 1; BRR2 homolog; U5 small nuclear ribonucleo ASSC3L1; HELIC2; KIAA0788; SNRPN200	Isoform 1 of U5 small nuclear ribonucleoprotein 200 k	244.5	5.02E-14	1.8746	1.7099	31.759	7	0.773912
Female-lethal(2)D homolog; Pre-mRNA-splicing regulator WTAP; Wilms tumor 1-associating protein; KIAA0105; WTAP; DKFZp686F20131	Isoform 1 of Pre-mRNA-splicing regulator WTAP	44.243	0.15007-1	Q15007	1.7088	103.87	3	0.7729836
PABPC4 protein; Poly(A) binding protein, cytoplasmic 4 (Inducible form); Poly(A) binding protein, cyt hCG_2031827; PABPC4; RP11-69E11.6-002; Al	polyadenylate-binding protein 4 isoform 1; Isoform 1 of	72.39	1.02E-30	2.0756	1.6992	101	1	0.7648557
Uncharacterized protein C3orf26; cDNA FLJ42396 fs, clone ASTRO2001107; cDNA FLJ58983; hCG20; C3orf26; hCG_2023567	Uncharacterized protein C3orf26; hypothetical protein L	31.884	0.0087477	1.9236	1.6992		1	0.7608557
Splicing factor 9G8; Splicing factor, arginine/serine-rich 7; Putative uncharacterized protein SFRS7; c; SFRS7	Isoform 1 of Serine/arginine-rich splicing factor 7; Unch	27.366	1.92E-12	1.8778	1.6891	32.111	4	0.7562547
cDNA FLJ31747 fs, clone NT2R12007377, highly similar to RNA-BINDING PROTEIN EWS; Ewing sarco EVWSR1; hCG_2010995; EWS; AC002059.7-002	RNA-binding protein EWS isoform 1; Isoform EWS of RN	68.965	8.43E-75	2.7168	1.678	111.49	11	0.7467427
Symplekin; cDNA FLJ61705, highly similar to Symplekin	Isoform 1 of Symplekin	141.15	9.79E-07	1.891	1.6766		1	0.7455385
Docking protein alpha; Signal recognition particle receptor subunit alpha; cDNA FLJ53386, highly simi SRP	Signal recognition particle receptor subunit alpha; signal	69.81	1.70E-05	1.8378	1.6751	30.582	2	0.7442472
cDNA FLJ43948 fs, clone TEST14014924, highly similar to Homo sapiens cytoplasmic FMR1 interact CYFIP1; KIAA0068; CYFIP2; KIAA1168; PIR1211	cDNA FLJ43948 fs, clone TEST14014924, highly similar t	145.52	0.0001222	1.5885	1.6673	6.114	3	0.7375137
Npw38-binding protein; SH3 domain-binding protein SNP70; Splicing factor that interacts with PQB NPWPBP; SIPP1; SNP70; WBP11	WW domain-binding protein 11; cDNA FLJ60194, highly	69.997	0.05776	1.6757	1.6584		1	0.729792
Elongation factor Tu, mitochondrial; P43	Tu translation elongation factor, mitochondrial precurs	49.874	7.90E-11	2.0493	1.6436	2.6195	2	0.7168592
DEAD box protein 46; Probable ATP-dependent RNA helicase DDX46; PRP5 homolog; cDNA FLJ78679; DDX46; KIAA0801; hCG_16595	cDNA FLJ78679, highly similar to Homo sapiens DEAD (117.47	0.00016125	1.5349	1.6381	34.222	3	0.7120234
54 kDa nuclear RNA- and DNA-binding protein; 55 kDa nuclear protein; DNA-binding p52/p100 comi NONO; NRB54	Non-POU domain-containing octamer-binding protein; r	54.231	1.16E-258	2.5096	1.6368	110.05	166	0.7108781
60S ribosomal protein L3; HIV-1 TAR RNA-binding protein B; Ribosomal protein L3; cDNA FLJ53376 fs; OK/SW-cl.32; RPL3; hCG_2015191; rpl3	60S ribosomal protein L3; 60S ribosomal protein L3 iso	46.108	3.09E-09	1.9243	1.6358	98.548	5	0.7099644
ATP-dependent RNA helicase EIF4A-1; Eukaryotic initiation factor 4A-1; cDNA FLJ78614, highly simila DDX2A; EIF4A1; DD2X2B; EIF4A2; EIF4F; hi	Eukaryotic initiation factor 4A-1; Isoform 2 of Eukaryo	46.153	2.07E-18	2.0777	1.6334	29.357	6	0.7078781
Flotillin-1; Flotillin 1 variant; FLOT1; protein; Flotillin 1; Flotillin 1, isoform CRA_b; cDNA FLJ54943, highly FLOT1; DADB-118P11.2-001; DAQB-47P19.1-1	Flotillin-1; cDNA FLJ54943, highly similar to Flotillin-1	47.355	1.15E-70	2.0741	1.6328	95.925	8	0.7073481
CF-1 50 kDa subunit; Cleavage stimulation factor 50 kDa subunit; Cleavage stimulation factor subunit CSTF1; hCG_39097; RPS-1167HA-1-001	Cleavage stimulation factor subunit 1; 38 kDa protein	48.357	0.00015	1.857	1.6316	43.42	4	0.7062784
Lark homolog; RNA-binding motif protein 4a; RNA-binding motif protein 4a; RNA-binding protein 4a; c; RBM4; RBM4A; RBM30; RBM4B; RBM14/RBM	Isoform 1 of RNA-binding protein 4; RNA-binding protei	40.313	1.08E-62	2.0421	1.6274	16.093	3	0.7025689
U2 small nuclear ribonucleoprotein A'; Small nuclear ribonucleoprotein polypeptide A' variant	U2 small nuclear ribonucleoprotein A'	28.415	2.89E-11	2.0909	1.6204	1.3957	2	0.69635
cDNA FLJ59630, highly similar to Growth hormone-inducible transmembrane protein; GHITM prote GHITM; DERP2; My021; TMBM15; UNQ244/PR	cDNA FLJ59630, highly similar to Growth hormone-indu	37.535	0.011299	2.0623	1.6197		1	0.6957266
4F2 cell-surface antigen heavy chain; 4F2 heavy chain antigen; Lymphocyte activation antigen 4F2 Ia MDU1; SLCSA2	Isoform 4 of 4F2 cell-surface antigen heavy chain; 4F2 c	71.122	5.47E-24	1.8635	1.6048	74.766	8	0.6823935
cDNA FLJ56786, moderately similar to 40S ribosomal protein S16; RP516 RPS16	cDNA FLJ56786, moderately similar to 40S ribosomal pr	16.412	2.90E-209	2.0324	1.6011	103.89	4	0.6829634
Zinc finger protein 207 variant; Zinc finger protein 207; Putative uncharacterized protein ZNF207; Pui ZNF207; DKFZp761N202	53 kDa protein; zinc finger protein 207 isoform 3; ciso	53.008	2.61E-05	2.0754	1.5974	31.37	3	0.6757256
Nuclear matrix protein 200; Pre-mRNA-processing factor 19; PRP19/PSO4 homolog; Senescence eva NMP200; PRP19; PRP19; SNEV	Pre-mRNA-processing factor 19	55.18	1.57E-12	2.1149	1.5906	17.693	5	0.6695711
155 kDa nucleoporin; Nucleolar pore complex protein Nup155; Nucleoporin Nup155; cDNA FLJ56637, KIAA0791; NUP155	Isoform 1 of Nucleolar pore complex protein Nup155; iso	155.2	1.63E-06	1.7551	1.5899	40.916	3	0.668936
GCN1-like protein 1; Translational activator GCN1; cDNA FLJ54481, highly similar to GCN1-like protei KIAA0111; KIAA0219	Translational activator GCN1	292.75	0.00011067	1.6082	1.5896	22.817	4	0.6686638
93 kDa nucleoporin; Nuclear pore complex protein Nup93; Nucleoporin Nup93; cDNA FLJ78686, high KIAA0095; NUP93	Nuclear pore complex protein Nup93; cDNA FLJ58756, h	93.487	8.13E-09	2.0237	1.5877	50.021	2	0.6669383
18S rRNA dimethylase; DIM1 dimethyladenosine transferase 1-like; Probable dimethyladenosine tra DIMT1; DIMT1L; HUSSY-05	Probable dimethyladenosine transferase; cDNA FLJ5671	35.236	0.008216	1.8833	1.5653		1	0.6464392
ATP-dependent RNA helicase DDX48; ATP-dependent RNA helicase EIF4A-3; DEAD box protein 48; E; DDX48; EIF4A3; KIAA0111	Eukaryotic initiation factor 4A-III	46.871	6.57E-18	1.994	1.5646	117.92	5	0.6457939
Nuclear poly(A)-binding protein 1; Poly(A)-binding protein II; Polyadenylate-binding nuclear protein	Isoform 1 of Polyadenylate-binding protein 2; Isoform 2	32.749	3.88E-06	1.8114	1.558	24.451	2	0.6396952
Integral nuclear envelope inner membrane protein; Lamin-B receptor; LMN2R	Lamin-B receptor	70.702	7.24E-28	1.825	1.5571	29.692	6	0.6388616
Phosphate carrier protein, mitochondrial; Phosphate transport protein; Solute carrier family 25 mem OK/SW-cl.48; PHC; SLC25A3	Isoform A of Phosphate carrier protein, mitochondria;	40.094	1.21E-25	1.9453	1.554	32.606	8	0.6359865
Cytoplasmic dynein 1 intermediate chain 2; Cytoplasmic dynein intermediate chain 2; Dynein interm DNC12; DNC12; DYNC12	Isoform 2A of Cytoplasmic dynein 1 intermediate chain	71.456	4.21E-12	1.842	1.5489		1	0.631244
G(i) alpha-3; Guanine nucleotide-binding protein G(i) subunit alpha; cDNA, FLJ92547, Homo sapien; GNAI3; hCG_1997731; RPS-1160K1.2-001	Guanine nucleotide-binding protein G(i) subunit alpha	40.532	2.24E-05	1.9237	1.5386		1	0.6216182
Pre-mRNA-splicing factor SRp30C; Splicing factor, arginine/serine-rich 9; cDNA FLJ76387, highly simi SFRS9; SRP30C	Serine/arginine-rich splicing factor 9; cDNA FLJ56571, hi	25.542	2.80E-08	1.9758	1.5294	9.5941	2	0.6129658
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit; Dolichyl-diphospho RPN1	Dolichyl-diphosphooligosaccharide--protein glycosyltr	72.777	4.45E-21	1.6892	1.5281	25.3	6	0.611739
Cutaneous T-cell lymphoma-associated antigen se33-1; Nuclear protein 220; Zinc finger matrin-like 1; NP220; ZFML; ZNF638	Isoform 1 of Zinc finger protein 638; Isoform 3 of Zinc f	220.62	5.37E-06	1.9673	1.5179	57.412	2	0.6027067
Cellular apoptosis susceptibility protein; Chromosome segregation 1-like protein; Exportin-2; Import CAS; CSE1L; XP02; CSE1L-2	Isoform 1 of Exportin-2; Isoform 3 of Exportin-2; cDNA FL	110.42	0.0021881	1.6525	1.5123	176.82	4	0.5967444
DEAD box protein 47; Probable ATP-dependent RNA helicase DDX47; DEAD (Asp-Glu-Ala-Asp) box p DDX47; hCG_27698; MIST162; E4-DBP	Probable ATP-dependent RNA helicase DDX47; probabl	50.646	7.83E-16	1.3476	1.5063	14.714	9	0.5910091
Vimentin; Vimentin variant 3; Vimentin variant 4; cDNA FLJ34494 fs, clone HLUNG2005030, highly si VIM	Vimentin	53.651	4.57E-105	1.8797	1.5048	87.327	26	0.5895718
60S ribosomal protein L7; Similar to 60S ribosomal protein L7; similar to P18124 (PID:d133021); Put; RPL7; WUGSCH_RG054D04.1	32 kDa protein; 30 kDa protein; 60S ribosomal protein L	32.275	1.30E-16	1.7368	1.489	112.58	6	0.5743438
U1 small nuclear ribonucleoprotein C	U1 small nuclear ribonucleoprotein C; U1 small nuclear	19.687	1.32E-11	1.9398	1.4886		1	0.5739561
Cytoplasmic dynein 1 heavy chain 1; Cytoplasmic dynein heavy chain 1; Dynein heavy chain, cytosol DHCI; DNCN1; DNCN2; DNCN3; DYHC; DYNC1H1	Cytoplasmic dynein 1 heavy chain 1	53.2	6.90E-23	2.0465	1.487	20.512	5	0.5724046
5'-3' exoribonuclease 2; DHM1-like protein; cDNA FLJ10711 fs, clone NTZRP300917, highly similar XRN2	Isoform 1 of 5'-3' exoribonuclease 2; Isoform 2 of 5'-3'	108.507	3.42E-07	1.5978	1.4867	10.692	5	0.5712136
116 kDa U5 small nuclear ribonucleoprotein component; Elongation factor Tu GTP-binding domain- EFTUD2; KIAA0031; SNRP116; US-116KD	116 kDa U5 small nuclear ribonucleoprotein componen	109.43	1.13E-19	1.8424	1.4848	62.925	8	0.5702686
CD2 antigen cytoplasmic tail-binding protein 2; FWP010	CD2 antigen cytoplasmic tail-binding protein 2	37.646	0.0060661	1.7798	1.482		1	0.5675454
Heterogeneous nuclear ribonucleoprotein H; Heterogeneous nuclear ribonucleoprotein H, N-termin HNRNPH1; HNRHP; HNRPH1; DKFZp686A1517	51 kDa protein; Heterogeneous nuclear ribonucleoprote	51.229	1.85E-182	2.1446	1.4729	95.173	46	0.5586595
Adenovirus early region 1B-associated protein 5; E1B-55 kDa-associated protein 5; Heterogeneous n E1BAP5; HNRNPU1; HNRPU1	Isoform 1 of Heterogeneous nuclear ribonucleoprotein	95.737	8.83E-51	1.8814	1.4721	95.514	13	0.5578757
75 kDa DNA-pairing protein; Oncogene FUS; Oncogene TLS; POMp75; RNA-binding protein FUS; Trans FUS; TLS	Fus-like protein (Fragment); Isoform Short of RNA-bindir	53.376	2.63E-44	1.8649	1.4705	99.61	17	0.5563606
ATP-dependent RNA helicase DDX3X; DEAD box protein 3, X-chromosomal; DEAD box, X isoform; Heli DBX; DDX3; DDX3X; DBY; DDX3Y	ATP-dependent RNA helicase DDX3X; cDNA FLJ60675, hi	73.243	4.52E-40	1.7795	1.4484	111.11	18	0.5344061
Activator 1 40 kDa subunit; Activator 1 subunit 2; Replication factor 40 kDa subunit; Replication fac RFC2; hCG_18034	Isoform 1 of Replication factor C subunit 2; Isoform 2	39.157	0.00059871	1.6179	1.4477	17.699	2	0.5337627
160 kDa neurofilament protein; Neurofilament 3; Neurofilament medium polypeptide; Neurofilamer NEF3; NEFM; NFM	Neurofilament medium polypeptide; NEFM protein; DN	102.47	0.014178	1.9324	1.4465		1	0.5323620
DNA mismatch repair protein Msh2; MutS protein homolog 2; cDNA FLJ57316, highly similar to DNA MSH2	DNA mismatch repair protein Msh2; MutS homolog 2 va	104.74	0.0011005	1.3117	1.4435	4.7158	1	0.5295711
Kinesin-like DNA-binding protein; Kinesin-like protein 4; Kinesin-like protein KIF22; cDNA FLJ53835, h KID; KIF22; KNSL4; hCG_2039829; A-328A3.5; C	Kinesin-like protein KIF22	73.261	0.00067663	1.7699	1.4421		1	0.5281712
Heterogeneous nuclear ribonucleoprotein U-like protein 2; Scaffold-attachment factor A2	HNRNPUL2; HNRPU2	85.104	6.62E-14	1.5466	1.4338	49.874	3	0.5198438
Polyadenylate-binding protein 1; cDNA FLJ57246, highly similar to Poly(A)-binding protein 1; cDNA F PAB1; PABP1; PABPC1; PABPC2; PABP3; PABPC3	Isoform 1 of Polyadenylate-binding protein 1; cDNA FLJ3	70.67	1.66E-30	1.8059	1.4314	40.283	3	0.5174269

214 kDa nucleoporin;Nuclear pore complex protein Nup214;Nucleoporin Nup214;Protein CAN;CDN CAIN;CAN;KIAA0023;NUP214;RP11-5444A12	Isoform 5 of Nuclear pore complex protein Nup214;Isof	P35658-5;P35658	215.4	1.27E-06	1.6152	1.4312	68.791	3	0.5172253
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit;Dolichyl-diphospho	RNP2;hCG_37142;RP3-343K2-2-003;RP3-34	P04844;B2RE46;Q	69.283	5.10E-07	1.4623	1.4292	22.593	2	0.5152078
Sm protein F.Small nuclear ribonucleoprotein F	PN2C;SNRPF	P62306	9.7251	0.0022352	1.6507	1.4282	1	0.514198	
Heterogeneous nuclear ribonucleoprotein 2H9;Heterogeneous nuclear ribonucleoprotein H3;Hete	HNRNP3;HNRNP3	P31942-1;P31942	36.926	9.13E-29	1.8634	1.4251	18.213	12	0.5110632
Sex comb on midleg-like protein 2;cDNA FLJ54781, highly similar to Sex comb on midleg-like protei	SCML2;RP5-1129A6.3-002	Q19UQR0-1;Q9UQ4	77.256	0.0044503	1.6925	1.4113	1	0.4987615	
Pre-mRNA-splicing factor SF3b 155 kDa subunit;Spliceosome-associated protein 155;Splicing fac	SAP155;SF3B1;DKFZp434M052	O79553;A0ULT9;A1	145.83	5.01E-13	2.1988	1.4129	73.047	9	0.4986594
Mannosyl-oligosaccharide glucosidase;Processing A-glucosidase I;Glucosidase I;cDNA FLJ75504, h	GC313;MOGS	Q13724;Q58F09;P	91.916	1.29E-05	1.3395	1.3993	1	0.4847055	
Serine/threonine-protein phosphatase PP1-beta catalytic subunit;Serine/threonine-protein phosp	PPP1C8	P62140;B4D75;B	37.186	1.78E-23	1.7782	1.3651	1	0.4808855	
Transmembrane and coiled-coil domain-containing protein 2;Transmembrane and coiled-coil doma	PNAS-120;PNAS-136;TMCC4;TMCO1;UNC151	Q9UM00-1;Q9UMU	21.175	1.85E-08	1.7475	1.3943	1	0.479541	
Lamin-B1;cDNA FLJ50934, highly similar to Lamin-B1;LMNB1 protein	LMNB2;LMNB;LMNB1	P20700;B4DZT3;Q	66.408	4.07E-28	1.8999	1.3931	73.648	13	0.4782898
Heterogeneous nuclear ribonucleoproteins C1/C2;cDNA FLJ75154, highly similar to Homo sapiens I	HNRNPC;HNRPC;hCG_1641229	P07910-1;P07910	33.67	8.97E-46	1.7235	1.3918	108.44	17	0.4769519
Pre-mRNA-splicing factor SRP75;Splicing factor, arginine/serine-rich 4;SRP001L8;cDNA FLJ76859, h	SFRS4;SRP75;hCG_23483;SFR56;SRP55;HRS	P07910-1;Q08170;A8K644;C	56.678	0.0029898	1.7655	1.3906	6.8785	3	0.4757075
ATP synthase subunit alpha, mitochondrial;ATP synthase subunit alpha;cDNA FLJ54625, highly simi	ATP5A;ATP5A1;ATP5AL2;ATPM	P25705;A8K092;B	59.75	3.22E-20	1.6426	1.3879	21.678	5	0.4729036
Splicing factor U2AF 35 kDa subunit;U2 auxiliary factor 35 kDa subunit;U2 snRNP auxiliary fact	U2AF1;U2AF55;U2AF6P;DKFZp3131J172;hC	Q92927;Q92927	27.872	4.57E-35	1.5846	1.3775	24.523	6	0.4620523
78 kDa gastrin-binding protein;Long chain 3-hydroxyacyl-CoA dehydrogenase;Long-chain enoyl-Co	HADH;HADHA	P40939;B4DDZ5;B	82.999	0.00066885	1.5632	1.375	1	0.4594316	
Lamina-associated polypeptide 2, isoforms beta/gamma;Spleenin;Thymopoietin;Thymopoietin;Thym	LAP2;TMPO	P42167-1;P42167	50.67	1.30E-163	1.8283	1.3748	66.687	36	0.4592218
Signal sequence receptor subunit delta;Translocon-associated protein subunit delta;Putative uncha	SSRA;TRAPD	P51571;A6NLML8	20.213	1.53E-09	1.4751	1.3701	16.733	4	0.4547023
40S ribosomal protein S14	PRO2640;RPS14	P62263;E5RH77	16.273	0.00028311	1.762	1.3684	1	0.45249	
cDNA FLJ59809, highly similar to Bone marrow stromal antigen 2;Bone marrow stromal antigen 2;	BST2	B4E02E;Q10589	23.537	0.00022268	1.7413	1.3616	6.471	2	0.4453029
60S ribosomal protein L13;Breast basic conserved protein 1;Ribosomal protein L13	BBC1;OK/SW-cl.46;RPL13;hCG_1723872	P26373;A8K4C8;B	24.261	9.08E-16	1.7104	1.3508	69.138	5	0.4338141
Complex 1-PDSW;NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10;NADH-ubiquin	NBDFB10;hCG_42700	O96000;A8K76;B	20.776	0.90E-162	1.6489	1.3471	1	0.429857	
Heat shock 70 kDa protein 1/2;Heat shock 70 kDa protein 1A/1B;cDNA FLJ75127, highly similar t	HSPA1;HSPA1A;HSPA1B;DAAP-21F2.7-001;C	P08107;A8K510;B	70.051	1.53E-27	1.7395	1.3371	2.452	4	0.4191074
136 kDa double-stranded RNA-binding protein;Double-stranded RNA-specific adenosine deaminas	ADAR;ADAR1;DSRAD;G1P1;JF14;hCG_18813	P55265-4;P55265	140.84	2.42E-41	1.1523	1.3361	1	0.418028	
Basement membrane-associated chondroitin proteoglycan;Chondroitin sulfate proteoglycan 6;Ch	CRBAM;BMH;CSP66;SMC3;SMC3L1	Q9UQE7;B0AZQ4;	141.54	0.043309	1.4384	1.3349	12.142	2	0.4167317
ATP-dependent helicase SKI2V2L2;Superkiller viralicidic activity 2-like 2;cDNA FLJ76877, highl	SKI2V2L2	P118.2	117.8	3.67E-05	1.3961	1.3306	47.751	3	0.4120769
B-cell receptor-associated protein 31, isoform CRA_b;cDNA FLJ33051 fis, clone TRACH1000063, h	BACP31;hCG_2004982;BAP31;DXS1357E	Q92927;Q92927	34.752	0.14934	1.5605	1.3301	1	0.4115347	
Cell proliferation-inducing gene 46 protein;Cytokeratin-18;Keratin, type I cytoskeletal 18;Kera	18	Q95783;B2RA03	48.057	4.95E-86	1.6096	1.3274	50.843	38	0.4088205
40S ribosomal protein S4, X isoform;SCR10;Single copy abundant mRNA protein;cDNA FLJ40595 fis	CCG2;RPS4;RPS4X;SCAR;hCG_18634;RPS4Y2	P62701;B2R491;Q	29.597	0.00010633	1.7119	1.3214	51.277	4	0.4020672
CD44 antigen;Cdw44;Epican;Extracellular matrix receptor III;Gp90 lymphocyte homing/adhesion r	CD44;LHR;MDU2;MDU3;MIC3;AL133330.1-C	P16070-1;P16070	81.537	3.26E-14	1.6842	1.3202	14.33	3	0.4007665
IGF-1I mRNA-binding protein 3;insulin-like growth factor 2 mRNA-binding protein 3;KH domain-con	IGF2BP3;IMP3;KDCU;VIC2	P00425-1;O00425	63.704	5.53E-21	1.5343	1.3167	131.29	2	0.3969267
Chromokinesin-B;Chromosome-associated kinesin KIF4B;highly similar to Chromo: KIF4B;KIF4A	KIF4B	Q2V1Q3;B4DYE2;C	140.03	8.74E-06	1.3168	1.3158	1	0.3959402	
38 kDa nuclear protein containing a WW domain;Polyglutamine tract-binding protein 1;Polyglutam	JM26;NPW38;PQB81	P060828-1;O60828	30.472	0.012481	1.5014	1.3049	42.577	2	0.3893993
Sucrose nonfermenting protein 2 homolog;SWI/SNF-related matrix-associated actin-dependent reg	SMARCA5;SNF2H;WCRF135;SMARCA1;SNF2	P06026;B4DZC0;B	121.9	2.99E-09	1.5516	1.3024	43.82	7	0.3811726
hTREC120;THO complex subunit 2;cDNA FLJ61096, highly similar to THO complex subunit 2;THO	cc Xor3f3;THOC2;RP5-1189B24.5-003	Q8M27-1;Q8M27	182.77	3.10E-25	1.8292	1.2994	127.79	5	0.3778456
Aldehyde dehydrogenase 10;Aldehyde dehydrogenase family 3 member A2;Fatty aldehyde dehyd	ALDH10;ALDH3A2;FALDH;DKFZp686E23276;	P51648-2;P51648	57.669	0.020632	1.4499	1.2922	1	0.3698294	
Putative uncharacterized protein SPTAN1;Alpha-II spectrin;Fodrin alpha chain;Spectrin alpha	chain;ALPH2;DKFZp646P0562	Q13813-3	284.94	2.52E-07	1.2884	1.2796	2.8414	2	0.3556929
107 kDa nucleoporin;Nuclear pore complex protein Nup107;Nucleoporin Nup107;cDNA FLJ11217 f	NUP107	P57740;B3KMK0;I	106.37	0.0037	1.4215	1.2763	1	0.3519675	
96 kDa nucleoporin;98 kDa nucleoporin;Nuclear pore complex protein Nup96;Nuclear pore comple	ADAR2;NUP98	P52948-1;P52948	197.58	3.06E-22	1.6034	1.2762	68.2	3	0.3518544
56 kDa U2AF65-associated protein;ATP-dependent RNA helicase p47;DEAD box protein UAP56;HLA	BAT1;UAP56;Xbbac-BCX270M.2-2-006;DADB	Q13838-2;Q13838	50.679	2.30E-39	1.8752	1.2752	65.671	20	0.3507235
40S ribosomal protein S18;Ke-3 ribosomal protein S18;Ribosomal protein S18, isoform CRA_b	DS6218E;RPS18;DADB-159G18.1-001;DAMC	P62MVS5;QSUJ3	17.718	2.38E-05	1.3552	1.2674	29.101	4	0.3418719
Putative uncharacterized protein DBN1;Developmentally-regulated brain protein;Drebrin;cDNA FLJ	DBN1;DOS117;hCG_1039393	P88275;Q16643	76.299	9.23E-06	1.5626	1.2658	1	0.3400495	
Heat shock 70 kDa protein 6;Heat shock 70 kDa protein 6;cDNA, FLJ93166, highly similar to	Homo SGP70B;HSPA6;HSP70B;HSPA7;HSPA1B	P17066;B2R6X5;B	71.027	8.11E-30	1.6735	1.2656	1	0.3398215	
DNA ligase 3;DNA ligase III;Polydeoxyribonucleotide synthase [ATP] 3;DNA ligase;Ligase III, D	NA, AT LIG3	P49916-1;P49916	112.91	2.11E-08	1.2747	1.2636	53.995	3	0.3375398
Double-stranded RNA-binding protein 76;Interleukin enhancer-binding factor 3;M-phase phosph	DRBF1;ILF3;MPHOSPH4;NF90	Q12906-4;Q12906	95.807	9.66E-61	1.7135	1.2549	86.728	22	0.3275274
Isoleucyl-tRNA ligase;Isoleucyl-tRNA synthetase, cytoplasmic;cDNA FLJ55373, highly similar	to Isr IARS;DKFZp686L17145;DKFZp686L0869;RP1	P41252-9;B4DXV2;C	144.5	0.0063994	1.3469	1.2529	1	0.3252713	
Heterogeneous nuclear ribonucleoprotein A3;cDNA FLJ52659, highly similar to Heterogeneous	nuclear HNRNP3;HNRNP3;hCG_2005824	P51991-1;P51991	39.594	7.90E-53	1.7326	1.2405	35.122	12	0.3109217
Mitsugumin-23;Transmembrane protein 109;cDNA, FLJ94551;cDNA FLJ57860, highly similar to	Trar TMEM109	P098V6;B2R9T9;E	26.21	1.80E-11	1.642	1.233	1	0.3021728	
205 kDa nucleoporin;Nuclear pore complex protein Nup205;Nucleoporin Nup205;cDNA FLJ50078,	C7orf14;KIAA0225;NUP205	Q92621;B4DE72;C	227.92	6.15E-06	1.2086	1.2314	1	0.3002995	
Pre-mRNA-splicing factor SRP20;Splicing factor, arginine/serine-rich 3;cDNA, FLJ92926, Homo	sapie SFRS3;SRP20;hCG_14802	P51571;B2RE63;B	19.329	5.14E-17	1.582	1.2271	23.899	10	0.2952528
Leucine-rich repeat-containing protein 59;cDNA, FLJ59555	LRRCS9;PRO1855	Q96AG4;B2RE83;I	34.93	5.74E-11	1.5766	1.2238	129.19	6	0.2913678
Basic leucine zipper and W2 domain-containing protein 2;cDNA FLJ10398 fis, clone NT2RM400034	BZW2;HSPC028;MSTP017;hCG_19293	Q9Y6E2;B3KM68;I	48.162	0.005815	1.3288	1.2236	1	0.291132	
Chromobox protein homolog 8;Polycomb 3 homolog;Rectachrome 1;Putative uncharacterized prot	CBX8;PC3;RC1	Q9H652;C9JMS4;I	43.395	0.0033459	1.4639	1.2184	127.07	2	0.2849878
Heterogeneous nuclear ribonucleoprotein K;Transformation up-regulated nuclear protein;cDNA FLJ	HNRNPK;HNRPK;hCG_1985922;RP11-575L7	P16978-2;P61978	51.028	9.11E-273	1.5037	1.2071	117.96	82	0.2715452
mRNA export factor;mRNA-associated protein mrnp 41;Rae1 protein homolog;cDNA FLJ75499, hig	MRNP41;RAE1;hCG_2018215;RP4-800J21.2-	mRNA export factor	40.968	0.050575	1.479	1.2065	1	0.2708729	
GAP-associated tyrosine phosphoprotein p62;KH domain-containing, RNA-binding, signal transdu	CHDRB51;SAM68;hCG_41606	Q07666-1;Q07666	48.227	1.26E-14	1.6143	1.2031	74.997	16	0.2667566
MORF-related gene X protein;Mortality factor 4-like protein 2;Protein MSL3-2;Transcription fac	KIAA0026;MORF4L2;MRGX;RP5-1055C14.2-H	Q15014;B39KWX;P	32.307	0.0061761	1.2321	1.1937	1	0.2629142	
Foocen;Neurite outgrowth inhibitor;Neuroendocrine-specific protein;Neuroendocrine-specific	proteins KIAA0886;MYO43;NOGO;RTL4;SP1507;hCG	Q9NQC4-1;Q9NQNI	129.93	0.0075044	1.4804	1.1991	1	0.261952	
91 kDa synaptoosomal-associated protein 109;Cathrin coat assembly protein AP180;Cathrin coat	assembly protein AP180;Cathrin coat assembly protein AP180;PICALM;PICALM variant f	Q9Y4W6;D3DUJ0;	92.501	0.012683	1.274	1.1959	1	0.2580968	
AFG3-like protein 2;Paralepin-like protein;AFG3 ATPase family gene 3-like 2 (Yeast), isoform	CRA_1 AFG3L2;hCG_38275	Q9Y4W6;D3DUJ0;	88.583	0.0081591	1.3403	1.1932	1	0.2548359	
Cap2 alpha-2-F-actin-capping protein subunit alpha-2;Capping protein (Actin filament) muscle 2-	lin CAP2A2;hCG_37884;tcag7.31;CAPZA1	P05141;B2RCV1;C	32.949	0.00051536	1.5132	1.1929	1	0.2547331	
Adenine nucleotide translocator 2;ADP/ATP carrier protein 2;ADP/ATP carrier protein, fibrobl	ast isoform ANT2;SLC25A5;ANT3;CDABP0051;SLC25A6;I	ADP/ATP translocase 2;ADP/ATP translocase 3;ADP/ATP	32.852	2.62E-20	1.4665	1.1918	98.726	11	0.2531422
Cytokine-induced protein of 29 kDa;Nuclear protein Hcc-1;Proliferation-associated cytokine-indu	ctil HCC1;HSPC316;SARNP;CIP29;LOC402290;tc	52 kDa protein;SAP domain-containing ribonucleoprotein	51.782	6.31E-11	1.474	1.1907	25.472	6	0.25181
Vasodilator-stimulated phosphoprotein	VASP	P05052	39.829	9.89E-09	1.3008	1.1882	18.731	2	0.2487777
Protein APMFC1;Signal recognition particle receptor subunit beta;Signal recognition particle rec	PSEC0230;SRPRB;hCG_2023361	Q9Y5M8;Q549N5;	29.702	4.16E-31	1.5373	1.1843	1.0967	2	0.2440346
Protein phosphatase 1C catalytic subunit;Serine/threonine-protein phosphatase PP1-gamma catal	PPP1C1;PPP1C1;hCG_16123	P36873-2;P36873	38.518	2.76E-33	1.4564	1.1824	85.639	4	0.2417182
Lamina-associated polypeptide 2, isoform alpha;Spleenin;Thymopoietin;Thymopoietin;Thymopoi	et;TMPO	P42166	75.491	1.14E-127	1.4268	1.1778	19.957	3	0.2360946
Zinc finger protein 91 homolog;cDNA FLJ57065, highly similar to Zinc finger protein 91	FKSG11;ZF9P1	Q961P5-1;Q961P5;	63.444	0.0015587	1.1947	1.1735	32.364	2	0.2308178
Pre-mRNA-splicing factor SF3b 130 kDa subunit;Spliceosome-associated protein 130;Splicing	factor KIAA0017;SAP130;SF3B3	Q15393-1;Q15393	135.58	8.04E-23	1.3965	1.1618	21.25	4	0.2163617
Cullin-associated and neddylation-dissociated protein 1;Cullin-associated NEDD8-dissociated	proteins CAND1;KIAA0829;TIP120	Q96V6-1;Q96V6	136.37	2.43E-09	1.1163	1.1538	45.859	4	0.2063932
40S ribosomal protein S3;Ribosomal protein S3 variant	OK/SW-cl.26;RPS3	P23396;Q53C83	28.486	6.24E-36	1.5027	1.1529	61.225	7	0.2052674
Heat shock 84 kDa;Heat shock protein HSP 90-beta;cDNA FLJ77842;cDNA FLJ53619, highly simi	lar t HSP90A81;HSP90B;HSP90C	P08238;A8K3W9;I	83.263	1.60E-14	1.3354	1.1508	91.013	6	0.2026371
CCAAT displacement protein;Homeobox protein cut-like 1;Homeobox protein cut-like 1;Protein	CASP;cutL1;CUX1;Nbla10317	P39880-3;P39880	165.69	8.59E-06	1.2275	1.1417	7.2062	2	0.1911836
Actinin alpha 1 isoform 3;ACTN1 protein;cDNA FLJ59209, highly similar to Alpha-actinin-1;Actin	in alpha 1;ACTN1;ACTN1;hCG_22243	Q9Y5M8;Q549N5;	107.14	2.84E-05	1.0655	1.1406	11.095	3	0.1891297
Heat shock 70 kDa protein 8;Heat shock cognate 71 kDa protein;cDNA FLJ38781 fis HSC70;HSP	70;HSPA10;HSPA8;HSPA2	P11142-1;P11142	70.897	3.35E-69	1.4101	1.138			

cDNA FLJ59683, highly similar to Homo sapiens malignant T cell amplified sequence 1 (MCTS1), mF MCT1;MCTS1	malignant T cell-amplified sequence 1 isoform 2;isoform	20.55	0.0013696	0.88895	0.86004	12.177	2	-0.2175243
C1 factor;CFF;HCF C-terminal chain 1;HCF C-terminal chain 2;HCF C-terminal chain 3;HCF C-terminal chain 4;HCF1;HCF1C1	Isoform 1 of Host cell factor 1;Isoform 2 of Host cell factor	208.73	4.97E-08	1.0959	0.85192	33.69	2	-0.2312101
Heat shock 70 kDa protein 14;Heat shock protein HSP60;HSP70-like protein 1;cDNA FLJ77376, high HSP60;HSP70L1;HSPA14;hCG_25570	Heat shock 70 kDa protein 14;Heat shock 70kDa protein	54.794	1.62E-06	1.0753	0.84947	7.4048	2	-0.2353651
M-phase phosphoprotein homolog;Zinc finger RNA-binding protein;cDNA FLJ75527, highly similar 1 ZFR	Zinc finger RNA binding protein;Uncharacterized protein	117.69	2.82E-07	0.85344	0.84814	125.05	2	-0.2376257
Protein PR264;Splicing component, 35 kDa;Splicing factor SC35;Splicing factor, arginine/serine-rich SFRS2;hCG_27842;LOC392896;tcag7.956;LO	Serine/arginine-rich splicing factor 2;cDNA FLJ52570, hq	25.476	1.27E-23	0.87492	0.84208	16.868	6	-0.2479708
Mammalian branch point-binding protein;Splicing factor 1;Transcription factor ZFM1;Zinc finger gene SF1;ZFM1;ZNF162	Isoform 5 of Splicing factor 1;Isoform 1 of Splicing factor	80.62	2.28E-05	0.7631	0.84165	52.875	2	-0.2487077
Bromodomain adjacent to zinc finger domain protein 1B;hWALP2;Tyrosine protein kinase BAZ1B;h BAZ1B;WBSCR10;WBSCR9;WSTF	Isoform 1 of Tyrosine-protein kinase BAZ1B;Isoform 2 of	170.9	0.0078575	1.0819	0.84063		1	-0.2504572
Cell division control protein 2 homolog;Cyclin-dependent kinase 1;p34 protein kinase;Putative uncl C0622;DKFZp686L22022	Putative uncharacterized protein DKFZp686L22022;cell	34.778	5.36E-05	1.0403	0.83814	43.026	3	-0.2543688
40S ribosomal protein S7;cDNA, AF192055, Homo sapiens ribosomal protein S7 (RP57), mRNA;Putat RP57;hCG_1784266	40S ribosomal protein S7;22 kDa protein;19 kDa protein	22.127	5.19E-11	0.83042	0.83291	108.34	5	-0.2637675
cDNA FLJ78091, highly similar to Homo sapiens ubiquitin-like, containing PHD and NHR9 finger dom UHRF1;ICBP90;NRP5;RNF106;hCG_23497;h	E3 ubiquitin-protein ligase UHRF1;E3 ubiquitin	91.099	1.48E-10	0.8691	0.83218	57.67	9	-0.2626218
BRG1-associated factor 57;SWI/SNF-related matrix-associated actin-dependent regulator of chrom;BAF57;SMARCE1	Isoform 1 of SWI/SNF-related matrix-associated actin-d	46.649	0.0005753	1.0695	0.82238		1	-0.2821229
Metastasis-associated 1-like 1;Metastasis-associated protein MTA2;p53 target protein in deacetyla: MTA1L1;MTA2;PID;DKFZp686F2281	Metastasis-associated protein MTA2	75.022	2.24E-57	1.1221	0.82202	74.002	15	-0.2827546
Heterogeneous nuclear ribonucleoproteins A2/B1;Putative uncharacterized protein HNRNPA2B1	Isoform B1 of Heterogeneous nuclear ribonucleoprotein	37.429	1.07E-155	1.0891	0.81883	91.267	74	-0.2883641
Protein DB83;Transmembrane protein 33;SHINC3	Transmembrane protein 33;Uncharacterized protein	27.978	0.035671	1.0143	0.81808	17.72	2	-0.2896862
cDNA FLJ75459;cDNA FLJ76290, highly similar to Homo sapiens TIA1 cytotoxic granule-associated f TIA1L1;hCG_40603	nucleolysin TIAR isoform 2;Nucleolysin TIAR;TIA1 cytot	43.448	1.42E-53	0.97722	0.81681	95.642	14	-0.2919276
Small nuclear ribonucleoprotein Sm D3;snRNP core protein D3;cDNA FLJ51872, highly similar to Sr SNRPD3	19 kDa protein;Small nuclear ribonucleoprotein Sm D3;	18.829	1.11E-07	0.856	0.81587	10.621	2	-0.2935888
Protein RCC2;RCC1-like protein TD-60;Telophase disk protein of 60 kDa;RCC2 protein	Protein RCC2	56.084	4.91E-27	1.1108	0.81569	82.307	18	-0.2939071
Mitochondrial transcription factor 1;Transcription factor 6;Transcription factor 6-like 2;Transcriptio TCF6;TCF6L2;TFAM	Transcription factor A, mitochondrial;Protein;Uncharact	29.096	7.05E-20	1.0276	0.81305	41.942	13	-0.298584
SMARCA4 protein;SMARCA4 isoform 2;SWI/SNF related, matrix associated, actin dependent regula SMARCA4;hCG_29955;BAF190A;BRG1;SNF2	SMARCA4 protein;transcription activator BRG1 isoform	189.45	1.14E-12	1.1157	0.80929	13.685	4	-0.3053605
Poly(RC)-binding protein 2 isoform b variant;Poly(RC) binding protein 2;Poly(RC) binding protein 2, hCG_201257;PCBP2	poly(rC)-binding protein 2 isoform a;Poly(rC)-binding pr	38.651	1.21E-103	1.0032	0.80506	113.59	27	-0.3128318
DNA-directed RNA polymerase II subunit A;DNA-directed RNA polymerase II subunit RPB1;DNA-dir POLR2;POLR2A	DNA-directed RNA polymerase II subunit RPB1	217.17	1.287E-08	1.2281	0.80243		1	-0.3175526
Nucleolysin TIA-1 isoform p15;Nucleolysin TIA-1 isoform p40;p15-TIA-1;p40-TIA-1;RNA-binding pro TIA1	Isoform Short of Nucleolysin TIA-1 isoform p40;Unchar	41.8	1.66E-36	0.89041	0.79249		1	-0.3355354
DNA polymerase;DNA polymerase delta catalytic subunit;DNA polymerase subunit delta p125	DNA-directed polymerase delta 1;DNA polymerase del	126.34	4.37E-05	0.91047	0.79053	52.182	5	-0.3391079
Far upstream element-binding protein 3;cDNA FLJ58115, highly similar to Far upstream element-bi FBP3;FUBP3;hCG_31253;RP11-57C19.3-002	Isoform 1 of Far upstream element-binding protein 3;U	61.64	1.22E-45	0.98549	0.79047	62.396	13	-0.3392174
cDNA FLJ56389, highly similar to Elongation factor 1-gamma;EF1B gamma;Elongation factor 1-ga EEF1G;EF1G;PR01608;hCG_2039458	cDNA FLJ56389, highly similar to Elongation factor 1-ga	56.149	0.935E-37	1.0574	0.78943	99.459	24	-0.3411167
Membrane-organizing extension spike protein;Moesin;MSN protein;Radixin isoform b;Radixin isofo MSN;hCG_39182;RDX;DKFZp434O1812	Moesin;Radixin, isoform CRA_a;Radixin	67.819	1.67E-22	0.87406	0.78809	48.829	8	-0.3435677
cDNA FLJ58953, highly similar to 40S ribosomal protein S20;40S ribosomal protein S20	40S ribosomal protein S20 isoform 1;40S ribosomal pr	16.005	0.001059	0.90418	0.7878		1	-0.3440987
AC40;DNA-directed RNA polymerases I and III 40 kDa polypeptide;DNA-directed RNA polymerase	Isoform 1 of DNA-directed RNA polymerases I and III sul	39.249	0.0016019	0.8268	0.78559	11.233	1	-0.3481515
ATP-dependent helicase CHD3;Chromodomain-helicase-DNA-binding protein 3;Mi-2 autoantigen 2 CHD3	chromodomain-helicase-DNA-binding protein 3 isoform	233.03	4.83E-14	0.83662	0.78441		1	-0.3503202
Coronin-1C_12 protein;Coronin-1C_13 protein;cDNA FLJ13143 fs, clone NT2RP3003230, highly simil CORO1C;CRNN4	Coronin-1C_13 protein;Coronin-1C;cDNA FLJ50992, high	58.947	2.85E-11	0.91023	0.78287	189.08	3	-0.3523263
ATP-dependent helicase CHD4;Chromodomain-helicase-DNA-binding protein 4;Mi-2 autoantigen 2 CHD4	Isoform 2 of Chromodomain-helicase-DNA-binding prot	220.85	4.30E-40	1.1288	0.77179	80.026	15	-0.3737197
Hepatocellular carcinoma protein 1;RNA-binding motif protein 39;RNA-binding protein 39;RNA-bi RBM39;RNPC2;DKFZp781C0423;DKFZ	Isoform 1 of RNA-binding protein 39;Isoform 2 of RNA-l	59.379	1.88E-54	0.97677	0.77132	90.292	16	-0.3745986
Eukaryotic translation initiation factor 2 subunit 3;Eukaryotic translation initiation factor 2 subunit, EIF2G;EIF2S3;EIF2S3L	Eukaryotic translation initiation factor 2 subunit 3;Isof	51.109	1.61E-06	0.88596	0.76044	193.53	3	-0.3950739
3'-5' exonuclease TREX1;DNase III;Three prime repair exonuclease 1;TREX1 protein;Three prime rei TREX1;hCG_1997849	Isoform 1 of Three prime repair exonuclease 1;Isoform	38.923	1.79E-05	0.98496	0.75853	1	1	-0.3987219
cDNA FLJ55039, moderately similar to Hepatoma-derived growth factor;Hepatoma-derived growth HDGF;HMG1L2;RP11-66D17.10-003;hCG_17	cDNA FLJ55039, moderately similar to Hepatoma-deriv	28.819	1.84E-27	0.67013	0.75538	99.394	10	-0.4047255
L-lactate dehydrogenase;Cell proliferation-inducing gene 19 protein;LDH muscle subunit;L-lactate c LDHA;PG119;hCG_96677;LDHAL6;LDHAL6B;L	L-lactate dehydrogenase A chain isoform 3;Isoform 1 of	39.837	0.011863	0.93782	0.75003	1	1	-0.4091824
cDNA FLJ53464, highly similar to Threonyl-tRNA synthetase, cytoplasmic [EC 6.1.1.3];Threonyl-tRNA TARS;TARSL2	cDNA FLJ53464, highly similar to Threonyl-tRNA synthet	86.86	2.51E-06	0.923	0.75192	41.139	2	-0.4113489
Paraspeckle component 1;Paraspeckle protein 1;cDNA FLJ57805, highly similar to Homo sapiens pa PSp1;PSPC1	Isoform 1 of Paraspeckle component 1;Isoform 2 of Par	58.743	1.14E-08	1.0421	0.74518	28.423	2	-0.4121392
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit;cDNA FLJ55714, hig DDO5T;XIA00115;OK/SW-cl-45;OST48	Dolichyl-diphosphooligosaccharide--protein glycosyltr	50.8	3.34E-22	0.94139	0.74203	156.19	4	-0.4304506
DNA-binding protein/plasminogen activator inhibitor 1 regulator;Helicase-like transcription factor; HPI1;6A;HTF;RNF80;SMARCA3;SNF2L3;ZBL	Isoform 1 of Helicase-like transcription factor;HTF prot	113.93	5.78E-06	0.96405	0.74037	10.243	3	-0.4336817
Cavin-1;Polymerase I and transcript release factor;cDNA FLJ35087 fs, clone PLACE6005546, highly FPG113;PTRF	Isoform 1 of Polymerase I and transcript release factor;G	43.476	2.14E-08	0.87654	0.73995	9.8889	2	-0.4345003
CF-1 77 kDa subunit;Cleavage stimulation factor 77 kDa subunit;Cleavage stimulation factor subu	Cleavage stimulation factor subunit 3;cleavage stimuli	82.921	7.30E-07	0.7574	0.73738	116.96	2	-0.4395198
ATP-binding cassette 50;ATP-binding cassette sub-family F member 1;TNF-alpha-stimulated ABC pr ABC50;ABCF1;DADB-129D20.7-001;DTAMA-1	Isoform 1 of ATP-binding cassette sub-family F member	95.925	2.80E-42	0.914	0.73121	133.88	10	-0.4516423
RCC1L1;Regulator of chromosome condensation 1;Putative uncharacterized protein RCC1;Cell cycle RCC1;CHC1;hCG_27809;RP4-669K10.2-001	regulator of chromosome condensation isoform a;regul	48.145	7.29E-144	0.90155	0.72128	86.582	26	-0.4713687
A34.5;Antisense to ERCC-1 protein;CD3-epsilon-associated protein;DNA-directed RNA polymerase I	Isoform 2 of DNA-directed RNA polymerase I subunit RF	55.171	3.19E-13	0.93814	0.72026	1	1	-0.4734103
FSCN1 protein;55 kDa actin-bundling protein;Fascin;p55;Singed-like protein;cDNA FLJ37935 fs, cloi FSCN1;FAN1;HSN;SNL	FSCN1 protein (Fragmin);Fascin	55.135	0.0038352	0.9269	0.71949		1	-0.4749535
Histone deacetylase 2;cDNA FLJ40057 fs, clone TCERX200431, highly similar to HISTONE DEACET	Histone deacetylase 2;Histone deacetylase 1;cDNA FLJ3	65.537	3.76E-06	0.91989	0.71871	99.755	3	-0.4765183
Putative RNA-binding protein 3;RNA-binding motif protein 3;RNPL	Putative RNA-binding protein 3	17.17	2.80E-16	0.87801	0.71852	14.762	8	-0.4768998
Cyclophilin B;CYP-51;Peptidyl-prolyl cis-trans isomerase B;Rotamase B;S-cyclophilin	Peptidyl-prolyl cis-trans isomerase B;20 kDa protein	23.742	1.82E-55	0.91546	0.71274	108.41	29	-0.4885522
Cell proliferation-inducing gene 21 protein;Guanine nucleotide-binding protein subunit beta-2-like	Guanine nucleotide-binding protein subunit beta-2-like	35.076	2.23E-24	0.92148	0.71098	57.587	5	-0.4921191
DNA mismatch repair protein Msh6;G/T mismatch-binding protein;MutS-alpha 160 kDa subunit;cD	Isoform GTBP-N of DNA mismatch repair protein Msh6;	152.78	7.81E-32	1.0456	0.68474	95.948	13	-0.5463718
40S ribosomal protein S19;cDNA, FLJ92047, Homo sapiens ribosomal protein S19 (RPS19), mRNA;R	40S ribosomal protein S19	16.06	4.09E-08	0.86388	0.68252	94.793	4	-0.5510568
APEX nuclease;Aprurinic-apryrimidinic endonuclease 1;DNA-(apurinic or apyrimidinic site) lyase;Prot	DNA-(apurinic or apyrimidinic site) lyase	35.554	1.47E-159	0.87753	0.68106	72.509	42	-0.5541462
Microtubule-associated protein 4;MAP4 protein;Microtubule-associated protein;cDNA FLJ58263, h	245 kDa protein;Isoform 1 of Microtubule-associated pr	245.44	9.08E-19	1.0712	0.67236	70.339	6	-0.5726942
2'(3')-polynucleotidease;Bifunctional polynucleotide phosphatase/kinase;DNA 5'-kinase/3'-phos	Bifunctional polynucleotide phosphatase/kinase;PNKP	57.076	0.0030099	0.80973	0.66834		1	-0.5813459
Ribosome-recycling factor, mitochondrial;Ribosome-recycling factor;Novel protein S MRRF;RP1-57A12.2;RP1-57A13.2-001	Isoform 1 of Ribosome-recycling factor, mitochondrial;	29.277	0.00024268	0.79096	0.66519	130.17	3	-0.5881616
Bcl-XL domain protein v68;Phosphoglycerate mutase family member 5;Serine/threonine-protein p	Isoform 1 of Serine/threonine-protein phosphatase P6a	32.004	0.0012435	0.68963	0.66443	111.83	10	-0.5898109
Coiled-coil domain-containing protein 124	Coiled-coil domain-containing protein 124	25.835	7.49E-06	0.74343	0.65793	17.365	7	-0.6441042
Damage-specific DNA-binding protein 1;DDB p127 subunit;DNA damage-binding protein 1;DNA da	DNA damage-binding protein 1;cDNA FLJ51067, highly s	126.97	0.00024638	0.84163	0.65378	6.4049	2	-0.6131229
60S ribosomal protein L22;EBER-associated protein;Epstein-Barr virus small RNA-associated protei	60S ribosomal protein L22;11 kDa protein;9 kDa protein	14.787	0.0036503	0.75948	0.65315	1	1	-0.6145137
CXXC-type zinc finger protein 9;DNA (cytosine-5)-methyltransferase 1;DNA methyltransferase	Isoform 1 of DNA (cytosine-5)-methyltransferase 1;Isof	189.56	1.81E-35	0.9343	0.64864	52.558	22	-0.6245101
Histone H2B;Histone H2B type 1-N;Histone H2B.d;Histone H2B type 1-C/E/F/G/I;Histone H2B.1 A;H	cDNA FLJ56787, highly similar to Histone H2B type 2-F;	18.041	2.02E-31	0.8638	0.6484	90.766	11	-0.625044
3-alkyladenine DNA glycosylase;3-methyladenine DNA glycosylase;ADPG;DNA 3-methyladenine g	Isoform 1 of DNA-3-methyladenine glycosylase;Isoform	32.868	2.01E-52	0.8563	0.64729	24.33	25	-0.6275159
Histone H2A type 1;Histone H2A/p;Histone H2A;Histone H2A type 1-D;Histone H2A.3;Histone H2A	Isoform 1 of Serine/threonine-protein phosphatase P6a	14.091	1.03E-38	0.79852	0.64455	142.48	10	-0.6336358
Cleavage and polyadenylation specificity factor 68 kDa subunit;Cleavage and polyadenylation	Isoform 2 of Cleavage and polyadenylation specifi	63.47	2.79E-06	0.53762	0.63989	1	1	-0.6441042
AU-rich element RNA-binding factor;Heterogeneous nuclear ribonucleoprotein D-like;JKT41-b	Isoform 1 of Heterogeneous nuclear ribonucleoprotein	46.437	4.86E-10	0.79847	0.63578	55.131	4	-0.6534005
cDNA FLJ54030, highly similar to Polymerase delta-interacting protein 3;46 kDa DNA polymerase	cDNA FLJ54030, highly similar to Polymerase delta-inter	48.101	1.12E-13	0.66639	0.62456	176.38	2	-0.6790879
Chromatin assembly factor 1 subunit B;Chromatin assembly factor I p60 subunit;M-phase phospho	Chromatin assembly factor 1 subunit B	61.492	0.0074106	0.70755	0.62091	1	1	-0.6875438
Mitotic checkpoint protein BUB3;cDNA FLJ57899, highly similar to Mitotic checkpoint protein	Isoform 1 of Mitotic checkpoint protein BUB3;Isoform	37.154	1.16E-11	0.63775	0.61795	138.7	8	-0.6944539
Histone H3.3;Histone H3;Histone H3.1;Histone H3/a;Histone H3/b;Histone H3/c;Histone H3/d;Hist	Histone H3.3;cDNA FLJ93172, highly similar to Homo s	15.328	0.00026702	0.6889	0.61715	27.25	6	-0.6963069
UPF0361 protein C3orf37;cDNA FLJ57398	UPF0361 protein C3orf37;cDNA FLJ57398;Uncharacteri	40.574	3.14E-07	0.64101	0.61448	7.7988	2	-0.702562
DAZ-associated protein 1;Deleted in azoospermia-associated protein 1;cDNA FLJ35575 fs, clone	Isoform 1 of DAZ-associated protein 1;Isoform 2 of DAZ	43.383	4.14E-57	0.81341	0.6076	60.756	15	-0.7188062
Bruton tyrosine kinase-associated protein 135;General transcription factor II-1;SRF;Phox1-interac	Isoform 1 of General transcription factor II-1;Isoform	112.42	3.64E-61	0.78771	0.60587	73.985	21	-0.7229198
cDNA FLJ51656, highly similar to Actin-like protein 2;Actin-like protein 2;Actin-related protei	actin-related protein 2 isoform a;Actin-related protei	45.376	1.57E-08	0.74191	0.60538	5.1545	3	-0.7240871
Dermal papilla-derived protein 9;ELL-associated protein of 20 kDa;ESCR-T II complex subunit	Vacuolar protein-sorting-associated protein 25	20.747	0.015056	0.73561	0.60223	1	1	-0.7316135

Treacher Collins syndrome protein;Treacle protein;TCOF1 protein variant;Putative uncharacterized	TCOF1;DKFZp434G1035	Isoform 4 of Treacle protein;Isoform 3 of Treacle protei	Q13428-4;Q13428	156.06	3.84E-95	0.89118	0.59577	108.57	17	-0.7471726
Polypyrimidine tract binding protein 1;Polypyrimidine tract binding protein 1, isoform CRA_c57 kd	hCG_20560;PTB1;PTB	polypyrimidine tract-binding protein 1 isoform a;Isoform	Q9BU00;Q26599-	59.632	8.80E-191	0.67182	0.59485	117.98	59	-0.7494022
WD repeat-containing protein 18	WDR18	WD repeat-containing protein 18	Q9BVS3	47.405	0.00081502	0.51722	0.59031	1	1	-0.7604553
Imporin subunit alpha-2;Karyopherin alpha 2;RAG cohort protein 1;SRP1-alpha;cDNA FLJ7	KPNA2;RCR1;SRP1	Imporin subunit alpha-2;Karyopherin alpha 2	P52292;A8K7D9;C	57.861	3.71E-05	0.6219	0.58655	91.373	4	-0.7659674
ATP-dependent DNA helicase VIII;GAP 5H3 domain-binding protein 1;Ras GTPase-activating protein	G3BP1;DKFZp313K0921;DKFPz686L11	Ras GTPase-activating protein binding protein 1;CDNA F	Q13283;B7Z8K4;E	52.164	0.00013748	0.58954	0.58197	73.127	2	-0.7809833
Tubulin beta-2 chain;Tubulin beta-2C chain;Class IVb beta tubulin;Tubulin, beta 2C;TUBB2C protein	TUBB2C;XTP3TPTATP1;DAAP-285E11.4-002;	Tubulin beta-2C chain;cDNA FLJ11352 fis, clone HEMBA	P68371;Q8HW6;C	49.83	9.85E-18	0.62187	0.57144	187	2	-0.8074271
Natural killer cell-enhancing factor B;Peroxiredoxin-2;PRP;Thiol-specific antioxidant protein;Thiore	NKEIFB;PRDX2;TPDX1;hCG_172488	Peroxiredoxin-2;cDNA FLJ06461, highly similar to Peroxi	P32119;B4DF07;A	21.892	5.67E-06	0.58939	0.56646		1	-0.819954
60 kDa poly(U)-binding-splicing factor;FUSE-binding protein-interacting repressor;Poly(U)-bindi	FIR;PUF60;ROBP;SIAHBP1	Isoform 2 of Poly(U)-binding-splicing factor PUF60;Isofo	Q9UHX1;Z;Q9UHX	58.171	3.80E-26	0.60914	0.5573	54.317	12	-0.8434753
NOL1/NOP2/Sun domain family member 2;Substrate of AIMP1/Aurora kinase B;tRNA (cytosine-5-)	NSUN2;SAKI;TRNA4;hCG_18368	tRNA (cytosine-5-)-methyltransferase NSUN2;cDNA FLJ5	Q082J3;A8K529;B	86.47	7.19E-32	0.62343	0.55577	43.548	6	-0.8474401
Telomeric repeat-binding factor 2-interacting protein Rap1	PR8000;RAP1;TERF2IP	Telomeric repeat-binding factor 2-interacting protein 1	Q9NYB0	44.259	5.86E-05	0.49467	0.54059	1	1	-0.8873933
Arginine-rich 54 kDa nuclear protein;Splicing factor, arginine/serine-rich 11;Splicing factor, arg	SFRS11;hCG_22837;RP4-677H15.3-002;DKF1	Serine/arginine-rich splicing factor 11;Splicing factor, ar	Q05519;Q8IWE6;C	53.542	7.15E-06	0.49277	0.53997	54.5	2	-0.8890488
28 kDa heat- and acid-stable phosphoprotein;PDGFA-associated protein 1;PDGF-associated protein	HASPP28;PDP1	28 kDa heat- and acid-stable phosphoprotein;4 kDa pro	Q13442	20.63	0.0026033	0.44782	0.5372	1	1	-0.8964688
Interleukin enhancer-binding factor 2;Nuclear factor of activated T-cells 45 kDa;cDNA FLJ51660,	hig ILF2;NF45;P303063	Interleukin enhancer-binding factor 2;12 kDa protein	Q12905;B4DY09;C	43.062	3.65E-77	0.53447	0.53326	110.73	12	-0.907089
Splicing factor U2AF 65 kDa subunit;U2 auxiliary factor 65 kDa subunit;U2 snRNP auxiliary fac	U2AF2;U2AF65	Isoform 1 of Splicing factor U2AF 65 kDa subunit;Isofor	P26368-1;P26368,	53.5	6.43E-19	0.58749	0.52334	157.64	4	-0.9341796
Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0;HNRNP0	Heterogeneous nuclear ribonucleoprotein A0	Q13151	30.84	2.92E-104	0.63754	0.51974	133.46	42	-0.9441338
Heterogeneous nuclear ribonucleoprotein U;p120;pp120;Scaffold attachment factor A;cDNA FLJ44	HNRNP0;HNRPU;SAFA;U21.1;RP11-11N7.3-4	Isoform Long of Heterogeneous nuclear ribonucleopro	Q00839-1;Q0083	90.583	2.58E-222	0.75189	0.51852	136.5	82	-0.9475285
Adenylate cyclase-stimulating G alpha protein;Extra large alpha protein;Guanine nucleotide-bindin	GNAS;GNAS1;GSP;hCG_1788380;GNAL;hCG	Isoform XLas-1 of Guanine nucleotide-binding protein G	Q5JWF2-1;Q5JWF	111.02	3.06E-10	0.52874	0.50413	152.59	2	-0.9881323
DNA helicase V;Far upstream element-binding protein 1;cDNA FLJ59240, highly similar to Far upstr	FUBP1	Isoform 1 of Far upstream element-binding protein 1;c	Q96AE4-1;Q96AE-	67.56	1.61E-126	0.56546	0.49544	97.354	17	-1.0132177
RNA-binding protein Musashi homolog 2;cDNA FLJ56904, highly similar to RNA-binding protein Mu	MS12	Isoform 1 of RNA-binding protein Musashi homolog 2;Cl	Q96DH6-1;Q96DH	35.196	5.53E-12	0.42093	0.48468	42.971	2	-1.0448955
Cytovillin;Ezrin;p81;Villin-2;cDNA, FLJ92973, highly similar to Homo sapiens villin 2 (ezrin)	(VIL2), m EZR;VIL2	Ezrin;69 kDa protein	P15311;B2R6J2;B;	69.412	3.39E-16	0.48971	0.45547	77.121	2	-1.1345721
Eukaryotic translation initiation factor 5B	EIF5B;hCG_38421	Eukaryotic translation initiation factor 5B	Q60841;A0L1R8;B;	138.83	2.68E-23	0.66345	0.45474	70.38	7	-1.1359347
40S ribosomal protein S5;40S ribosomal protein S5, N-terminally processed;Ribosomal protein	S5 v RP55	40S ribosomal protein S5	P46782;Q5G25	22.876	0.038659	0.55759	0.43149	76.043	3	-1.2126101
33 kDa VAMP-associated protein;Vesicle-associated membrane protein-associated protein A;cDNA	VAPB3;VAPA;UNQ484/PRO983;VAPB;hCG_2	Isoform 2 of Vesicle-associated membrane protein-asso	Q9P0L0-2;Q9P0L0	32.613	3.80E-12	0.4286	0.42944	95.805	2	-1.1914725
Beta-II spectrin;Fodrin beta chain;Spectrin beta chain, brain 1;Spectrin, non-erythroid beta	chain 1; SPTB2;SPTBN1;hCG_17370	Isoform Long of Spectrin beta chain, brain 1;Isoform Sh	Q01082-1;Q0108	274.61	3.99E-12	0.47514	0.42508	73.037	2	-1.2341937
cDNA FLJ56425, highly similar to Very-long-chain specific acyl-CoA dehydrogenase, mitochondria	[E ACADVL;VLCAH];hCG_42007	cDNA FLJ56425, highly similar to Very-long-chain specifi	B4DEA8;B2RH02;I	75.209	7.11E-09	0.35939	0.42141	43.061	2	-1.2467035
Caprin-1;Cell cycle-associated protein 1;Cytoplasmic activation- and proliferation-associated	protein CAPRIN1;GPIAP1;GPII137;M1151	Isoform 1 of Caprin-1;Isoform 2 of Caprin-1;cDNA FLJ57	Q14444-1;Q1444	78.365	1.65E-05	0.33876	0.41681	1	1	-1.2625382
Heterogeneous nuclear ribonucleoprotein L;cDNA, FLJ94229, highly similar to Homo sapiens heter	HNRNPL;HNRPLP;QOk1.14	Heterogeneous nuclear ribonucleoprotein L;heterogen	P14866;B2R959;C	64.132	4.54E-43	0.38536	0.41379	113.82	32	-1.2730293
cDNA FLJ57954, highly similar to 60S ribosomal protein L28;60S ribosomal protein L28;Ribosomal	r RPL28;hCG_38234	60S ribosomal protein L28 isoform 3;60S ribosomal prot	B4DEP9;P46779;C	19.148	0.010927	0.34496	0.41334	1	1	-1.2745991
[Acyl-carrier-protein] S-acyltransferase;[Acyl-carrier-protein] S-malonyltransferase;3-hydroxy	palmit FAS;FASN	Fatty acyl synthase	P49327;Q13587;C	273.42	4.68E-19	0.45552	0.40696	115.46	2	-1.2970441
Helix-destabilizing protein;Heterogeneous nuclear ribonucleoprotein A1;hRNP core protein A1;	hRNP1;HNRPA1;HNRPA1L3;HNRNP1A1;H	Isoform A1-B of Heterogeneous nuclear ribonucleopro	Q09651-1;P09651	38.746	5.91E-166	0.51734	0.40337	101.02	64	-1.3098243
APOBEC1-binding protein 1;Heterogeneous nuclear ribonucleoprotein A/B;cDNA FLJ0713, highly	: ABBP1;HNRNPAB;HNRPAB	Isoform 3 of Heterogeneous nuclear ribonucleoprotein.	Q99729-3;Q9972	30.588	3.70E-66	0.31851	0.39065	149.22	17	-1.3565105
Epidermal Langerhans cell protein LCP1;TOX high mobility group box family member 4;cDNA FLJ	C140f992;KIAA0737;TOX4	TOX high mobility group box family member 4;cDNA FLJ	Q94842;B4DPY8;E	66.194	0.0051205	0.30792	0.38212	1	1	-1.3879023
Autoantigen p542;Heterogeneous nuclear ribonucleoprotein C-like 2;hRNP associated with leth	HNRPCL2;P542;RALY;hCG_37136;RP1-64K7.	cDNA FLJ77422, highly similar to Homo sapiens RNA bir	Q9UKM9-1;Q9UKI	32.55	0.0067281	0.31645	0.38023	1	1	-1.3950557
DNase IV;Flap endonuclease 1;Flap structure-specific endonuclease 1;Maturation factor 1;cDNA	FL FEN1;RAD2;hCG_40848	Flap endonuclease 1	P39748;B4DWZ4;I	42.592	1.13E-197	0.35446	0.36909	134.47	46	-1.4379554
Chromatin-specific transcription elongation factor 80 kDa subunit;Facilitates chromatin tran	script FCT80;SSRP1	FACT complex subunit SSRP1	Q08945	81.074	6.74E-05	0.3076	0.36887	20.259	2	-1.4388156
Natural killer cell-enhancing factor A;Peroxiredoxin-1;Proliferation-associated gene protein;	Thioredoxin;PAGA;PAGB;PRDX1;TPDX2	Peroxiredoxin-1;19 kDa protein	Q06803;B2R4P2	22.11	1.05E-07	0.46435	0.35447	162.32	2	-1.4962646
Cyclophilin A;Cyclosporin A-binding protein;Peptidyl-prolyl cis-trans isomerase A;Rotamase	A;Pepti CYP;PPIA	Peptidyl-prolyl cis-trans isomerase A;cDNA FLJ53060, m	P62937;A8K220;A	18.012	1.29E-10	0.35069	0.3527	157.57	2	-1.5034865
Death-associated transcription factor 1;Death-inducer obliterator 1	C20orf158;DATF1;DIDO1;KIAA0333	Isoform 4 of Death-inducer obliterator 1	Q98TCC-4;Q98TCC	243.87	2.03E-08	0.29722	0.34661	1	1	-1.5297665
PWP1-interacting protein 17;Single-stranded DNA-binding protein, mitochondrial;cDNA, FLJ93504,	SSBP;SSBP1;hCG_2014251;tcag7.401	Single-stranded DNA-binding protein, mitochondrial;c	Q04837;A4D1U3;I	17.259	3.13E-162	0.4605	0.34642	100.52	24	-1.5294059
Glutathione S-transferase kappa 1;Glutathione S-transferase subunit 13;GST 13-13;GST class-	kappa GSTK1;HDCM047P;hCG_20682;LOC51064;L	Isoform 2 of Glutathione S-transferase kappa 1;Isoform	Q9Y2Q3-2;Q9Y2Q	31.566	1.07E-12	0.28612	0.34453	1	1	-1.5372985
Long-chain acyl-CoA synthetase 3;Long-chain-fatty-acid-CoA ligase 3;cDNA, FLJ95462, highly	similar to ACAC3;ACLS3;FACL3;LACS3;ACS4;ACSL4;FACL4	Long-chain-fatty-acid-CoA ligase 3;Isoform Long of Lon	Q92588	80.419	0.001214	0.27122	0.32588	114.37	2	-1.6175873
cDNA FLJ32471 fis, clone SKNCM200322, highly similar to Peptidyl-rRNA hydrolase 2, mitochon	dri B1T1;CG1-147;PTH2;PTRH2	cDNA FLJ32471 fis, clone SKNCM200322, highly simila	Q96ME4;Q9Y3E5	19.325	0.018848	0.26459	0.31638	1	1	-1.6602697
Cleavage and polyadenylation specificity factor 25 kDa subunit;Cleavage and polyadenylation	specific CFIM25;CFPS25;CFPS5;NUDT21;DKFZp3130	Cleavage and polyadenylation specificity factor subunit	Q43892;B2R6U8;C	26.227	2.64E-09	0.26189	0.31496	203	3	-1.6667595
Eukaryotic translation initiation factor 2 subunit 2;Eukaryotic translation initiation factor 2	subunit EIF2B;EIF2S2;hCG_2018881	Eukaryotic translation initiation factor 2 subunit 2;Euk	P20042;B5BU01;C	38.388	8.66E-33	0.31223	0.31474	54.83	3	-1.6677676
ATP-dependent DNA helicase Q1;DNA helicase, RecQ-like type 1;DNA-dependent ATPase Q1;RecQ	1;RECQ1;RECQL1;RECQL1	ATP-dependent DNA helicase Q1;73 kDa protein	P46063	73.457	8.04E-104	0.27272	0.30971	119.84	38	-1.6907888
Sb1.8;Structural maintenance of chromosomes protein 1A;cDNA FLJ71762, highly similar to Ho	mo DSX423E;KIAA0178;SB1.8;SMC1;SMC1A;SM	Structural maintenance of chromosomes protein 1A;c	Q14683;A8K7A6;C	143.23	0.0031608	0.2449	0.30716	77.189	3	-1.7029377
BRG1-associated factor 170;SWI/SNF complex 170 kDa subunit;SWI/SNF complex subunit	SMARCC2;BAF150;SMARCC2;BAF155;SMARCC1	Isoform 1 of SWI/SNF complex subunit SMARCC2;Isofor	Q8TQA0;Q8TQA	132.88	1.33E-09	0.26332	0.30397	51.399	3	-1.7179991
60S acidic ribosomal protein P0;60S ribosomal protein L10E;cDNA FLJ75549, highly similar to	Homo RPLP0	60S acidic ribosomal protein P0;60S acidic ribosomal pr	P05388;A8K4Z4;Q	34.273	3.82E-05	0.25213	0.30304	87.084	2	-1.7224199
Activating transcription factor 1;Cyclic AMP-dependent transcription factor ATF-1;Protein TREM3	6;ATF1;CREM;CREB1;hCG_15208;hCREM-1;hC	Cyclic AMP-dependent transcription factor ATF-1;Isofor	P18846;B2R8K4;Q	29.232	0.0024591	0.26584	0.29415	154.01	2	-1.7653761
Caspase recruitment domain-containing protein 6;Caspase recruitment domain family, member 6	v CARD6	Caspase recruitment domain-containing protein 6	Q9B869;Q59EG7	116.47	0.0048408	0.38958	0.29064	250.25	3	-1.7826948
40S ribosomal protein S25	RPS25	40S ribosomal protein S25	P62851	13.742	2.76E-08	0.29876	0.28709	139.47	6	-1.8004225
22 kDa neuronal tissue-enriched acidic protein;Brain acid soluble protein 1;Neuronal axonal memb	BASP1;NAP22	Isoform 1 of Brain acid soluble protein 1;Isoform 2 of Br	P80723-1;P80723;	22.693	0.018686	0.23749	0.28703	1	1	-1.8007266
86 kDa subunit of Ku antigen;ATP-dependent DNA helicase 2 subunit 2;ATP-dependent DNA heli	c G22P2;XRCC5	X-ray repair cross-complementing protein 5	P13010;Q53T09;C	82.704	8.04E-41	0.25111	0.28687	115.83	19	-1.801351
Ribosomal protein S10;40S ribosomal protein S10;Ribosomal protein S10 variant	RP11-375E11_A-4.005;RPS10	Ribosomal protein S10;40S ribosomal protein S10;15 k	Q5T2B9;P46783;C	19.868	0.00026313	0.23271	0.2786	100.76	7	-1.8437328
cDNA FLJ61295, highly similar to Gamma-interferon-inducible protein IFI16;IFNGIP1;hCG_1995098		cDNA FLJ61295, highly similar to Gamma-interferon-ind	B4DJTR;Q16666-2	82.875	6.34E-33	0.22553	0.27685	72.553	7	-1.8528236
Heterogeneous nuclear ribonucleoprotein R;cDNA, FLJ93632, highly similar to Homo sapiens heter	HNRNPR;HNRPR;hCG_38907;DKFZp686A132	71 kDa protein;Isoform 2 of Heterogeneous nuclear rib	Q43390-2;Q4339	71.313	6.23E-62	0.23732	0.26451	95.313	12	-1.9186058
50 kDa nuclear polyadenylated RNA-binding protein;Bruno-like protein 2;CUG triplet repeat	RNA-B BRUNO12;CELFI1;CUGBP;CUGBP1;NAB50	Isoform 4 of CUGBP Elav-like family member 1;Isoform	Q92879-4;Q9287	55	5.03E-06	0.25981	0.26393	149.61	4	-1.9217727
70 kDa subunit of Ku antigen;ATP-dependent DNA helicase 2 subunit 1;ATP-dependent DNA heli	c G22P1;XRCC6;TGA-216E10-7.002;hCG_2013	X-ray repair cross-complementing protein 6;cDNA FLJ31	P12956;B2RD9N;E	69.842	8.75E-58	0.22931	0.2613	86.259	16	-1.936221
Nucleolin;Protein C23;cDNA FLJ10452 fis, clone NT2RP1000966, highly similar to NUCLEOLIN;Nucle	NCL;hCG_33980	Nucleolin;cDNA FLJ45706 fis, clone FEBRA2028457, higl	P19338;B3KM80;I	76.613	1.22E-48	0.22633	0.26042	90.301	15	-1.9410878
Dr1-associated corepressor;Dr1-associated protein 1;Negative co-factor 2-alpha;Putative unchara	cterized DRAP1	Uncharacterized protein;Isoform 1 of Dr1-associated co	Q14919-2;Q1491	23.205	0.061773	0.20173	0.24156	1	1	-2.0495465
Pre-rRNA-processing protein TSR1 homolog	KIAA1401;TSR1	Pre-rRNA-processing protein TSR1 homolog	Q2NL82	91.809	1.63E-08	0.23616	0.23375	168.79	2	-2.0969617
NAD(+) ADP-ribosyltransferase 1;Poly[ADP-ribose] polymerase 1;Poly[ADP-ribose] synthase 1;	cdNI ADPRT;PARP1;PPOL	Poly[ADP-ribose] polymerase 1	P09874;B2R5W3;I	113.08	0	0.19651	0.23088	111.85	210	-2.1147849
Macrophage myristoylated alanine-rich C kinase substrate;MARCKS-related	MARCKS1;MLP;MRP	similar to hCG2040253;similar to hCG2040253;MARCKS	P49006	22.922	0.02024	0.18989	0.22705	1	1	-2.1389181
PA1 RNA-binding protein 1;Plasminogen activator inhibitor 1 RNA-binding protein;SERPINE1 mRN	E CGI-55;PAIRBP1;SERBP1;hCG_2032021;DKFZ	SERPINE1 mRNA binding protein 1, isoform CRA_d;Isof	Q8NC51-1;Q8NC5	50.92	7.01E-119	0.17971	0.21972	101.77	19	-2.2029094
Protein DEK;cDNA FLJ51914, highly similar to Protein DEK;cDNA FLJ53031, highly similar to	Protein DEK	Protein DEK;cDNA FLJ53031, highly similar to Protein D	E P35659;B4DNW3;C	42.674	2.16E-44	0.18542	0.20997	85.923	13	-2.2517449
Cold shock domain-containing protein A;DNA-binding protein A;Single-strand DNA-binding	protein A;hCG;DBPA	Isoform 1 of DNA-binding protein A;Isoform 2 of DNA-B	E P16989-1;P16989;	40.089	3.49E-65	0.20746	0.20964	81.159	5	-2.2540141
Desmoykin;Neuroblast differentiation-associated protein AHNAK;cDNA FLJ57801, highly similar	to HNAK;PM227									

