FIGURE 1

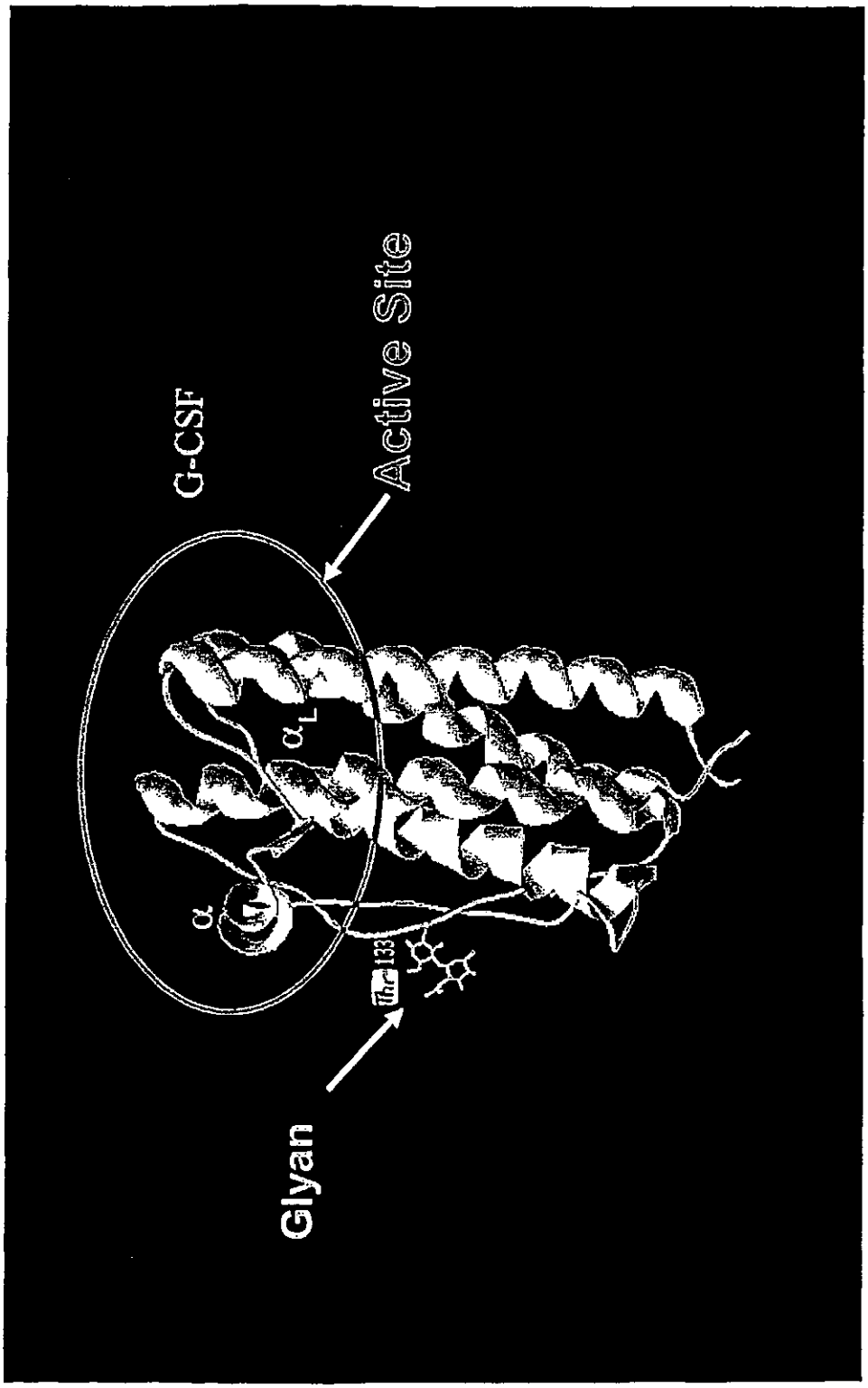


FIGURE 2

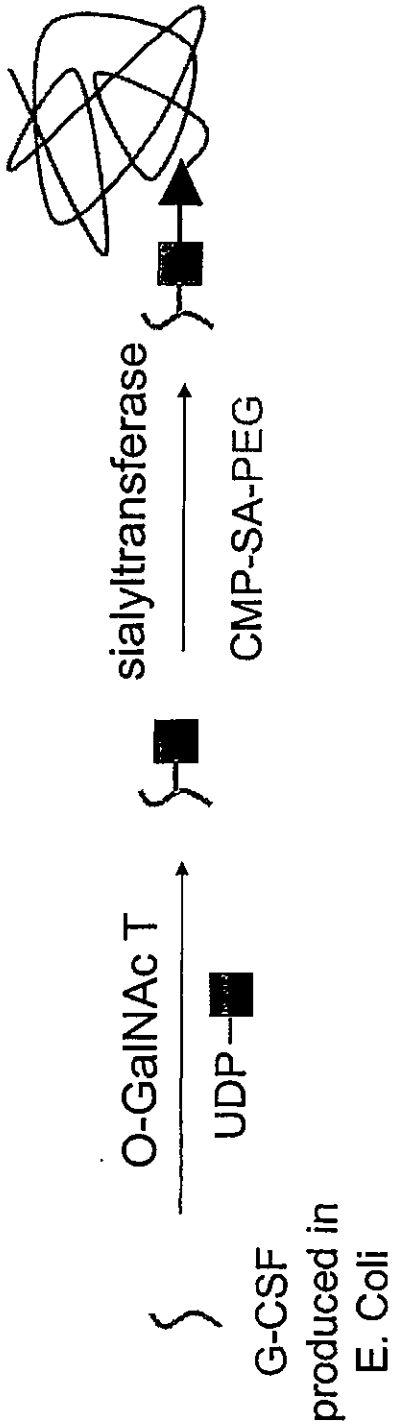

G-CSF
produced in
E. Coli
O-GalNAc T
UDP
sialyltransferase
CMP-SA-PEG

FIGURE 3

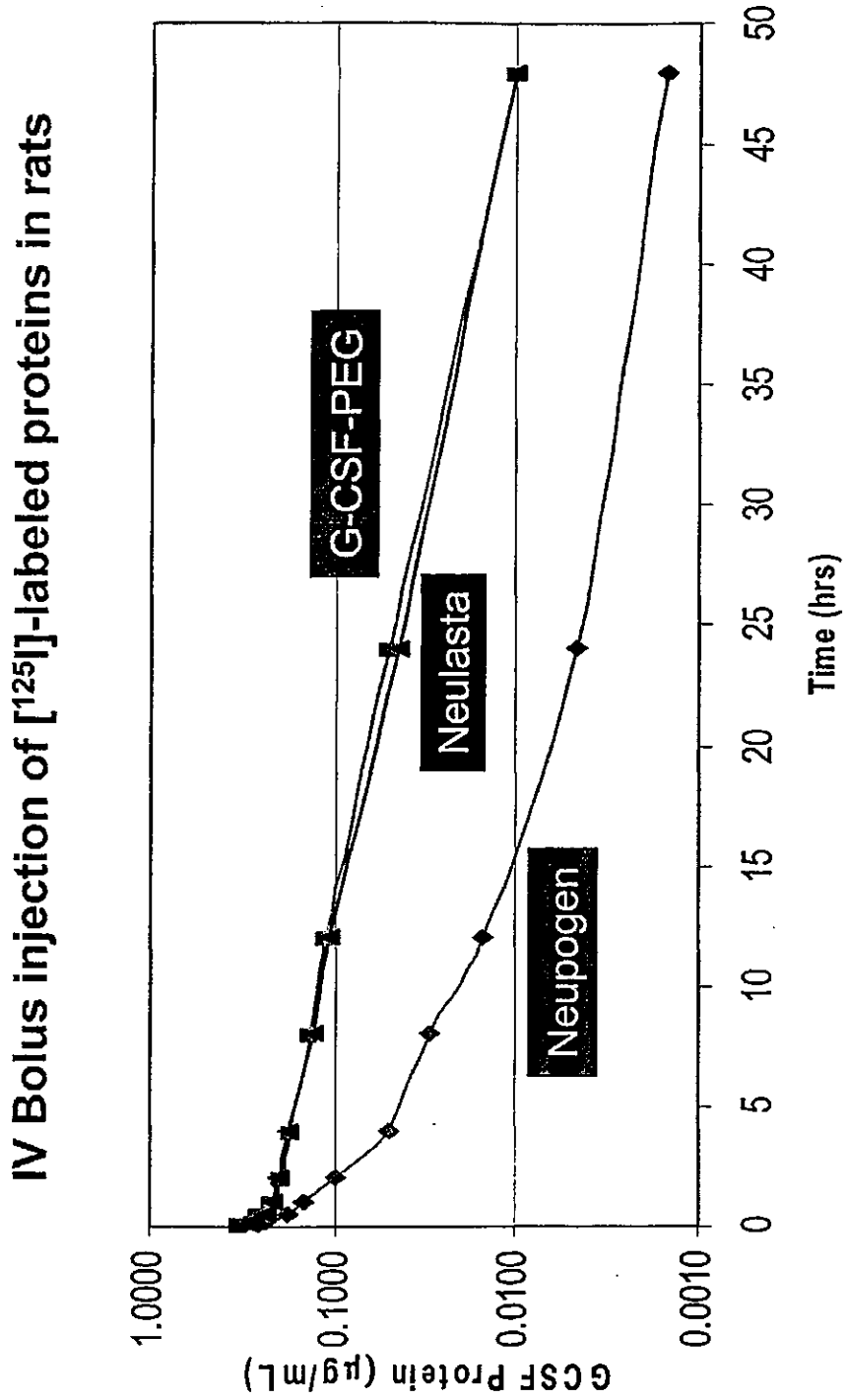

IV Bolus injection of [125I]-labeled proteins in rats
G-CSF-PEG
Neulasta
Neupogen
GCSF Protein (µg/mL)
1.0000
0.1000
0.0100
0.0010
0
5
10
15
20
25
30
35
40
45
50
Time (hrs)

FIGURE 4

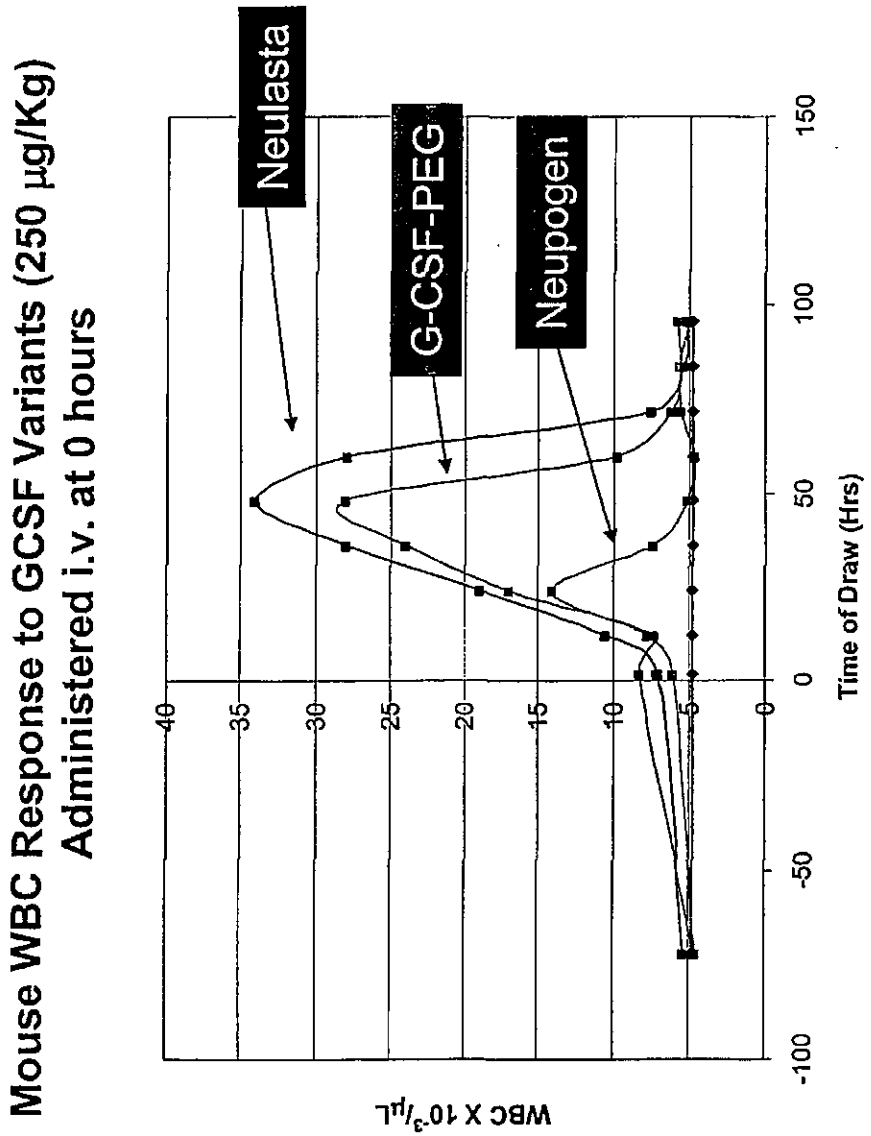

Mouse WBC Response to GCSF Variants (250 µg/Kg)
Administered i.v. at 0 hours
Neulasta
G-CSF-PEG
Neupogen
WBC X 10-3/µL
Time of Draw (Hrs)
40
35
30
25
20
15
10
5
0
150
100
50
0
-50
-100

FIGURE 5

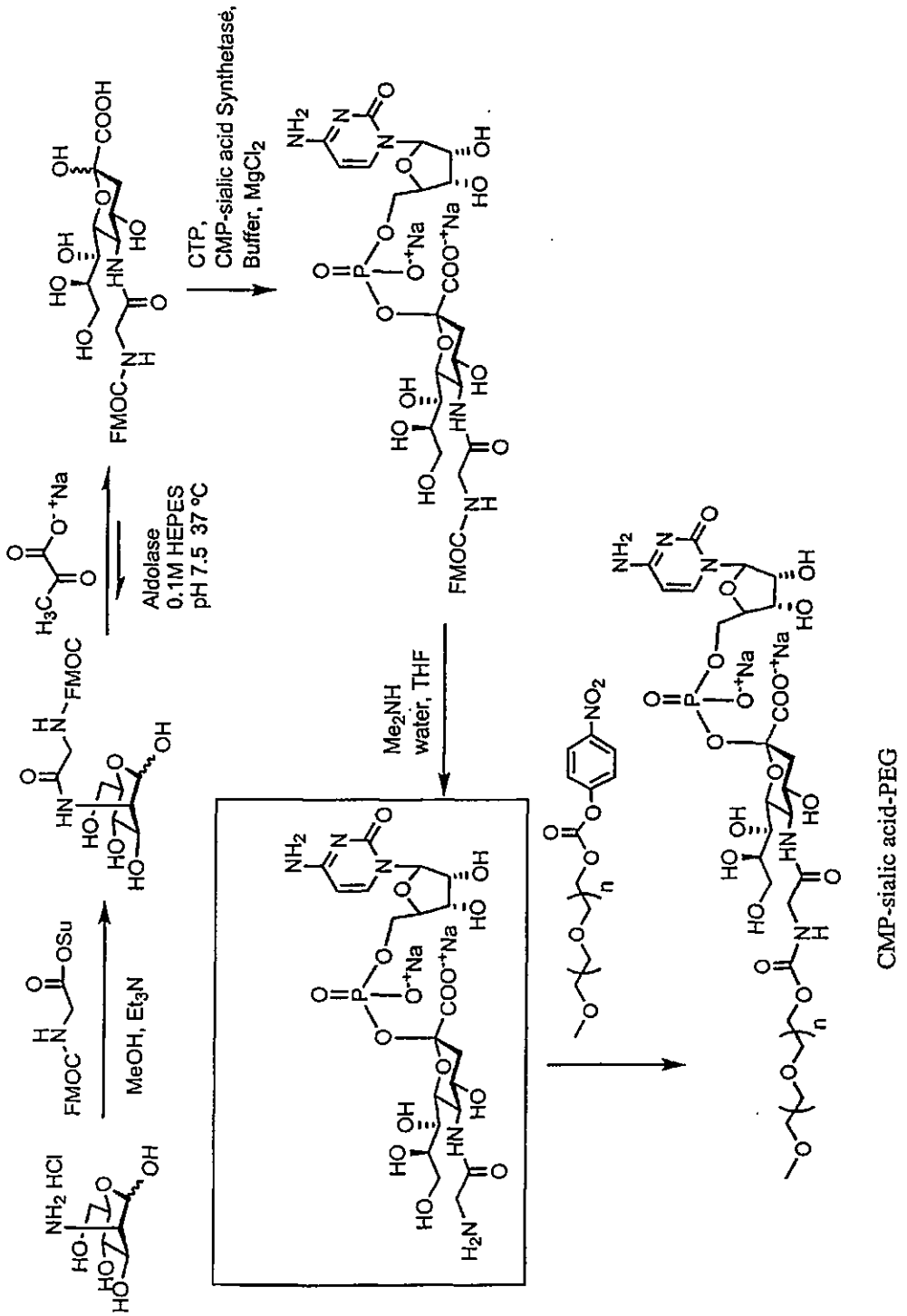

MeOH, Et3N
Aldolase
0.1M HEPES
pH 7.5 37 °C
CTP,
CMP-sialic acid Synthetase,
Buffer, MgCl2
Me2NH
water, THF
CMP-sialic acid-PEG

FIGURE 6

175 amino acid variant

MTPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCA
TYKLCHPEELVLLGHSLGIPWAPLSSCPSQALQLAGCLS
QLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFAT
TIWQQMEELGMAPALQPTQGAMPAFASAFQRRAGGVL
VASHLQSFLEVSYRVLRHLAQP **(SEQ ID NO: 1).**

174 amino acid variant

TPLGPASSLPQSFLLKCLEQVRKIQGDGAALQEKLCATY
KLCHPEELVLLGHSLGIPWAPLSSCPSQALQLAGCLSQL
HSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTI
WQQMEELGMAPALQPTQGAMPAFASAFQRRAGGVLV
ASHLQSFLEVSYRVLRHLAQP **(SEQ ID NO: 2).**

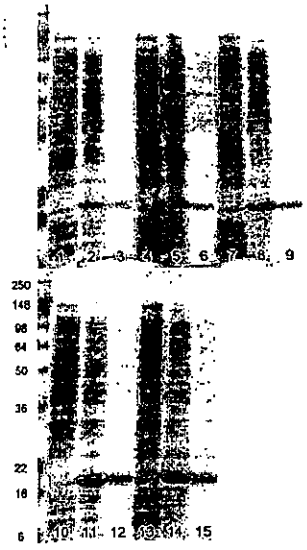
FIGURE 7

Testing growth conditions – washing IBs

	37°C, 1mM (final) IPTG			IB yields (~0.7-1g/L)
	Media	Buffered pH	Time	wet IB pellet (mg)
1.	LB	n/a	5hr	120
2.	TB	7.4 ($K\text{-}PO_4$)	5hr	230
3.	TB	6 (MES)	5hr	170
4.	LB	n/a	o/n	190
5.	TB	7.4 ($K\text{-}PO_4$)	o/n	250

Cell samples, loaded equally by ug
(better expression of overnights more apparent)

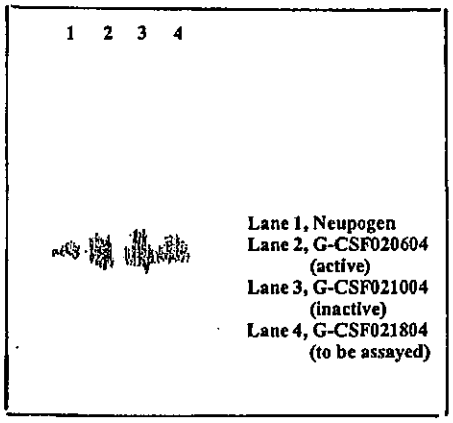
1. #1 lysate, supe
2. #1 lysate, pellet
3. #1 final IB
4. #2 lysate, supe
5. #2 lysate, pellet
6. #2 final IB
7. #3 lysate, supe
8. #3 lysate, pellet
9. #3 final IB
10. #4 lysate, supe
11. #4 lysate, pellet
12. #4 final IB
13. #5 lysate, supe
14. #5 lysate, pellet
15. #5 final IB



Purified IB's are shown in lanes 3, 6, 9, 12 and 15. Note IB lanes loaded at approximately ½ the amount of the preceding lane (based on predicted pellet weight).

FIGURE 8

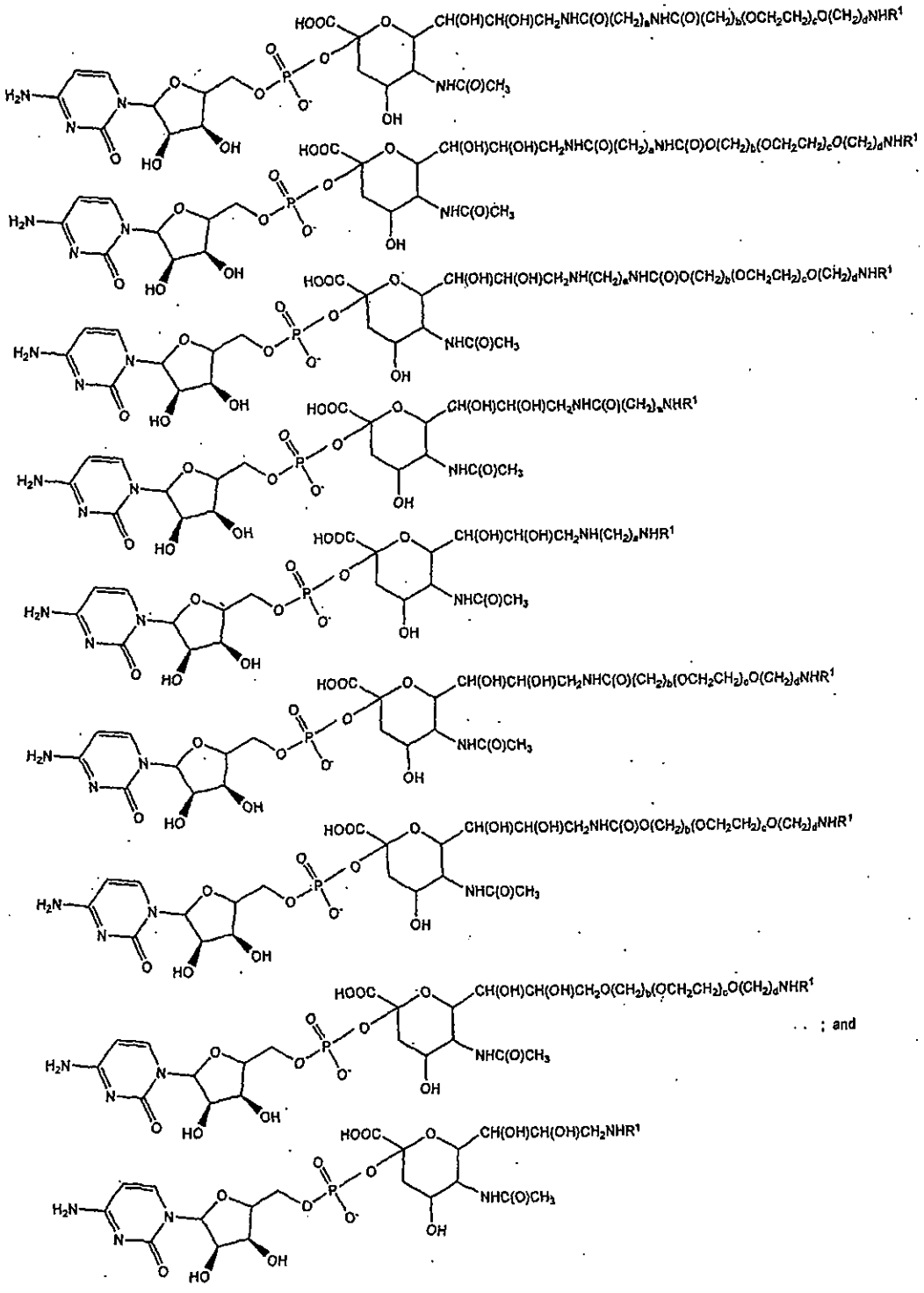
Western Blot Analysis of Refolded G-CSF
Native Polyacrylamide Gel Electrophoresis



G-CSF020604 and G-CSF021004 came from the same batch of refolding reaction. The only difference was that G-CSF021004 was saved from the flowthough of G-CSF020604 by adjusting pH and reloading onto SP Sepharose. G-CSF021804 was a separate refolding batch.

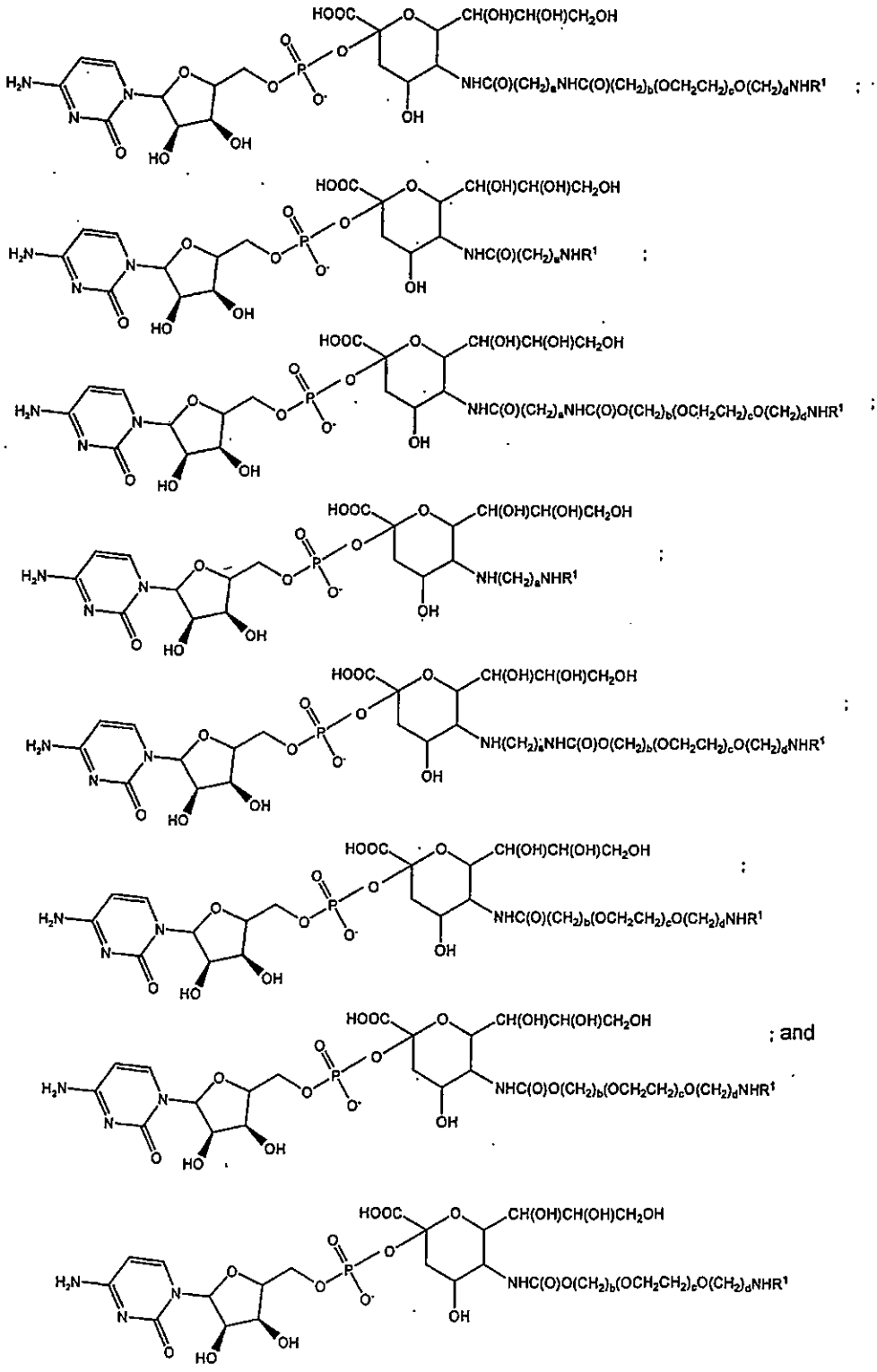
After SP-sepharose you see only one band by Coomassie stain or Western.

FIGURE 9


HOOC
CH(OH)CH(OH)CH2NHC(O)(CH2)aNHC(O)(CH2)b(OCH2CH2)cO(CH2)dNHR1
NHC(O)CH3
OH
H2N
N
O
HO
CH(OH)CH(OH)CH2NHC(O)(CH2)aNHC(O)O(CH2)b(OCH2CH2)cO(CH2)dNHR1
CH(OH)CH(OH)CH2NH(CH2)aNHC(O)O(CH2)b(OCH2CH2)cO(CH2)dNHR1
CH(OH)CH(OH)CH2NHC(O)(CH2)aNHR1
CH(OH)CH(OH)CH2NH(CH2)aNHR1
CH(OH)CH(OH)CH2NHC(O)(CH2)b(OCH2CH2)cO(CH2)dNHR1
CH(OH)CH(OH)CH2NHC(O)O(CH2)b(OCH2CH2)cO(CH2)dNHR1
CH(OH)CH(OH)CH2O(CH2)b(OCH2CH2)cO(CH2)dNHR1
CH(OH)CH(OH)CH2NHR1

. . ; and

FIGURE 10



; and

FIGURE 11A

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
At1g08280	*Arabidopsis thaliana*	n.d.	AC011438 AAF18241.1 BT004583 AAO42829.1 NC_003070 NP_172305.1	Q84W00 Q9SGD2	
At1g08660/F22O13.14	*Arabidopsis thaliana*	n.d.	AC003981 AAF99778.1 AY064135 AAL36042.1 AY124807 AAM70516.1 NC_003070 NP_172342.1 NM_180609 NP_850940.1	Q8VZJ0 Q9FRR9	
At3g48820/T21J18_90	*Arabidopsis thaliana*	n.d.	AY080589 AAL86966.1 AY133816 AAM91750.1 AL132963 CAB87910.1 NM_114741 NP_190457.1	Q8RY00 Q9M301	
α-2,3-sialyltransferase (ST3GAL-IV)	*Bos taurus*	n.d.	AJ584673 CAE48298.1		
α-2,3-sialyltransferase (St3Gal-V)	*Bos taurus*	n.d.	AJ585768 CAE51392.1		
α-2,6-sialyltransferase (Siat7b)	*Bos taurus*	n.d.	AJ620651 CAF05850.1		
α-2,8-sialyltransferase (SIAT8A)	*Bos taurus*	2.4.99.8	AJ699418 CAG27880.1		
α-2,8-sialyltransferase (Siat8D)	*Bos taurus*	n.d.	AJ699421 CAG27883.1		
α-2,8-sialyltransferase ST8Sia-III (Siat8C)	*Bos taurus*	n.d.	AJ704563 CAG28696.1		
CMP α-2,6-sialyltransferase (ST6Gal I)	*Bos taurus*	2.4.99.1	Y15111 CAA75385.1 NM_177517 NP_803483.1	O18974	
sialyltransferase 8 (fragment)	*Bos taurus*	n.d.	AF450088 AAL47018.1	Q8WN13	
sialyltransferase ST3Gal-II (Siat4B)	*Bos taurus*	n.d.	AJ748841 CAG44450.1		
sialyltransferase ST3Gal-III (Siat6)	*Bos taurus*	n.d.	AJ748842 CAG44451.1		
sialyltransferase ST3Gal-VI (Siat10)	*Bos taurus*	n.d.	AJ748843 CAG44452.1		
ST3Gal I	*Bos taurus*	n.d.	AJ305086 CAC24698.1	Q9BEG4	
St6GalNAc-VI	*Bos taurus*	n.d.	AJ620949 CAF06586.1		
CDS4	*Branchiostoma floridae*	n.d.	AF391289 AAM18873.1	Q8T771	
polysialyltransferase (PST) (fragment) ST8Sia IV	*Cercopithecus aethiops*	2.4.99.-	AF210729 AAF17105.1	Q9TT09	
polysialyltransferase (STX) (fragment) ST8Sia II	*Cercopithecus aethiops*	2.4.99.-	AF210318 AAF17104.1	Q9TT10	
α-2,3-sialyltransferase ST3Gal I (Siat4)	*Ciona intestinalis*	n.d.	AJ626815 CAF25173.1		
α-2,3-sialyltransferase ST3Gal I (Siat4)	*Ciona savignyi*	n.d.	AJ626814 CAF25172.1		
α-2,8-polysialyltransferase ST8Sia IV	*Cricetulus griseus*	2.4.99.-	AAE28634 Z46801 CAA86822.1	Q64690	
Gal β-1,3/4-GlcNAc α-2,3-sialyltransferase St3Gal I	*Cricetulus griseus*	n.d.	AY266675 AAP22942.1	Q80WL0	
Gal β-1,3/4-GlcNAc α-2,3-sialyltransferase St3Gal II (fragment)	*Cricetulus griseus*	n.d.	AY266676 AAP22943.1	Q80WK9	
α-2,3-sialyltransferase ST3Gal I (Siat4)	*Danio rerio*	n.d.	AJ783740 CAH04017.1		
α-2,3-sialyltransferase ST3Gal II (Siat5)	*Danio rerio*	n.d.	AJ783741 CAH04018.1		
α-2,3-sialyltransferase ST3Gal III (Siat6)	*Danio rerio*	n.d.	AJ626821 CAF25179.1		
α-2,3-sialyltransferase ST3Gal IV (Siat4c)	*Danio rerio*	n.d.	AJ744809 CAG32845.1		

FIGURE 11B

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
α-2,3-sialyltransferase ST3Gal V (Siat5-related)	*Danio rerio*	n.d.	AJ783742 CAH04019.1		
α-2,6-sialyltransferase ST6Gal I (Siat1)	*Danio rerio*	n.d.	AJ744801 CAG32837.1		
α-2,6-sialyltransferase ST6GalNAc II (Siat7B)	*Danio rerio*	n.d.	AJ634459 CAG25680.1		
α-2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	*Danio rerio*	n.d.	AJ646874 CAG26703.1		
α-2,6-sialyltransferase ST6GalNAc VI (Siat7F) (fragment)	*Danio rerio*	n.d.	AJ646883 CAG26712.1		
α-2,8-sialyltransferase ST8Sia I (Siat 8A) (fragment)	*Danio rerio*	n.d.	AJ715535 CAG29374.1		
α-2,8-sialyltransferase ST8Sia III (Siat 8C) (fragment)	*Danio rerio*	n.d.	AJ715543 CAG29382.1		
α-2,8-sialyltransferase ST8Sia IV (Siat 8D) (fragment)	*Danio rerio*	n.d.	AJ715545 CAG29384.1		
α-2,8-sialyltransferase ST8Sia V (Siat 8E) (fragment)	*Danio rerio*	n.d.	AJ715546 CAG29385.1		
α-2,8-sialyltransferase ST8Sia VI (Siat 8F) (fragment)	*Danio rerio*	n.d.	AJ715551 CAG29390.1		
β-galactosamide α-2,6-sialyltransferase II (ST6Gal II)	*Danio rerio*	n.d.	AJ627627 CAF29495.1		
N-glycan α-2,8-sialyltransferase	*Danio rerio*	n.d.	BC050483 AAH50483.1 AY055462 AAL17875.1 NM_153662 NP_705948.1	Q7ZU51 Q8QH83	
ST3Gal III-related (siat6r)	*Danio rerio*	n.d.	BC053179 AAH53179.1 AJ626820 CAF25178.1 NM_200355 NP_956649.1	Q7T3B9	
St3Gal-V	*Danio rerio*	n.d.	AJ619960 CAF04061.1		
st6GalNAc-VI	*Danio rerio*	n.d.	BC060932 AAH60932.1 AJ620947 CAF06584.1		
α-2,6-sialyltransferase (CG4871) ST6Gal I	*Drosophila melanogaster*	2.4.99.1	AE003465 AAF47256.1 AF218237 AAG13185.1 AF397532 AAK92126.1 AE003465 AAM70791.1 NM_079129 NP_523853.1 NM_166684 NP_726474.1	Q9GU23 Q9W121	
α-2,3-sialyltransferase (ST3Gal VII)	*Gallus gallus*	n.d.	AJ585767 CAE51391.1 AJ627204 CAF25503.1		
α-2,3-sialyltransferase ST3Gal I	*Gallus gallus*	2.4.99.4	X80503 CAA56666.1 NM_205217 NP_990548.1	Q11200	
α-2,3-sialyltransferase ST3Gal IV (fragment)	*Gallus gallus*	2.4.99.-	AF035250 AAC14163.1	O73724	
α-2,3-sialytransferase (ST3GAL-II)	*Gallus gallus*	n.d.	AJ585761 CAE51385.2		
α-2,6-sialyltransferase (Siat7b)	*Gallus gallus*	n.d.	AJ620653 CAF05852.1		
α-2,6-sialyltransferase ST6Gal I	*Gallus gallus*	2.4.99.1	X75558 CAA53235.1 NM_205241 NP_990572.1	Q92182	
α-2,6-sialyltransferase ST6GalNAc I	*Gallus gallus*	2.4.99.3	AAE68028.1 AAE68029.1 X74946 CAA52902.1 NM_205240 NP_990571.1	Q92183	
α-2,6-sialyltransferase ST6GalNAc II	*Gallus gallus*	2.4.99.-	X77775 AAE68030.1 NM_205233 CAA54813.1 NP_990564.1	Q92184	
α-2,6-sialyltransferase ST6GalNAc III (SIAT7C)	*Gallus gallus*	n.d.	AJ634455 CAG25677.1		

FIGURE 11C

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
(fragment)					
α-2,6-sialyltransferase ST6GalNAc V (SIAT7E) (fragment)	*Gallus gallus*	n.d.	AJ646877 CAG26706.1		
α-2,8-sialyltransferase (GD3 Synthase), ST8Sia I	*Gallus gallus*	2.4.99.-	U73176 AAC28888.1	P79783	
α-2,8-sialyltransferase (SIAT8B)	*Gallus gallus*	n.d.	AJ699419 CAG27881.1		
α-2,8-sialyltransferase (SIAT8C)	*Gallus gallus*	n.d.	AJ699420 CAG27882.1		
α-2,8-sialyltransferase (SIAT8F)	*Gallus gallus*	n.d.	AJ699424 CAG27886.1		
α-2,8-syalyltransferase ST8Siα-V (SIAT8C)	*Gallus gallus*	n.d.	AJ704564 CAG28697.1		
β-galactosamide α-2,6-sialyltransferase II (ST6Gal II)	*Gallus gallus*	n.d.	AJ627629 CAF29497.1		
GM3 synthase (SIAT9)	*Gallus gallus*	2.4.99.9	AY515255 AAS83519.1		
polysialyltransferase ST8Sia IV	*Gallus gallus*	2.4.99.-	AF008194 AAB95120.1	O42399	
α-2,3-sialyltransferase ST3Gal I	*Homo sapiens*	2.4.99.4	L29555 AAA36612.1	Q11201	
			AF059321 AAC17874.1	O60677	
			L13972 AAC37574.1	Q9UN51	
			AF155238 AAD39238.1		
			AF186191 AAG29876.1		
			BC018357 AAH18357.1		
			NM_003033 NP_003024.1		
			NM_173344 NP_775479.1		
α-2,3-sialyltransferase ST3Gal II	*Homo sapiens*	2.4.99.4	U63090 AAB40389.1	Q16842	
			BC036777 AAH36777.1	O00654	
			X96667 CAA65447.1		
			NM_006927 NP_008858.1		
α-2,3-sialyltransferase ST3Gal III (SiaT6)	*Homo sapiens*	2.4.99.6	L23768 AAA35778.1	Q11203	
			BC050380 AAH50380.1	Q86UR6	
			AF425851 AAO13859.1	Q86UR7	
			AF425852 AAO13860.1	Q86UR8	
			AF425853 AAO13861.1	Q86UR9	
			AF425854 AAO13862.1	Q86US0	
			AF425855 AAO13863.1	Q86US1	
			AF425856 AAO13864.1	Q86US2	
			AF425857 AAO13865.1	Q8IX43	
			AF425858 AAO13866.1	Q8IX44	
			AF425859 AAO13867.1	Q8IX45	
			AF425860 AAO13868.1	Q8IX46	
			AF425861 AAO13869.1	Q8IX47	
			AF425862 AAO13870.1	Q8IX48	
			AF425863 AAO13871.1	Q8IX49	
			AF425864 AAO13872.1	Q8IX50	
			AF425865 AAO13873.1	Q8IX51	
			AF425866 AAO13874.1	Q8IX52	
			AF425867 AAO13875.1	Q8IX53	
			AY167992 AAO38806.1	Q8IX54	
			AY167993 AAO38807.1	Q8IX55	
			AY167994 AAO38808.1	Q8IX56	
			AY167995 AAO38809.1	Q8IX57	
			AY167996 AAO38810.1	Q8IX58	
			AY167997 AAO38811.1		
			AY167998 AAO38812.1		
			NM_006279 NP_006270.1		
			NM_174964 NP_777624.1		
			NM_174965 NP_777625.1		
			NM_174966 NP_777626.1		
			NM_174967 NP_777627.1		
			NM_174969 NP_777629.1		
			NM_174970 NP_777630.1		
			NM_174972 NP_777632.1		

FIGURE 11D

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
α-2,3-sialyltransferase ST3Gal IV	*Homo sapiens*	2.4.99.-	L23767 AAA16460.1 AF035249 AAC14162.1 BC010645 **AAH10645.1** AY040826 AAK93790.1 AF516602 AAM66431.1 AF516603 AAM66432.1 AF516604 AAM66433.1 AF525084 AAM81378.1 X74570 CAA52662.1 CR456858 CAG33139.1 NM_006278 NP_006269.1	Q11206 O60497 Q96QQ9 Q8N6A6 Q8N6A7 Q8NFD3 Q8NFG7	
α-2,3-sialyltransferase ST3Gal VI	*Homo sapiens*	2.4.99.4	AF119901 AAD39131.1 BC023312 AAH23312.1 AB022918 BAA77609.1 AX877828 CAE89895.1 AX886023 CAF00161.1 NM_006100 NP_006091.1	Q9Y274	
α-2,6-sialyltransferase (ST6Gal II ; KIAA1877)	*Homo sapiens*	n.d.	BC008680 AAH08680.1 AB058780 **BAB47506.1** AB059555 BAC24793.1 AJ512141 CAD54408.1 AX795193 CAE48260.1 AX795193 CAE48261.1 NM_032528 NP_115917.1	Q86Y44 Q8IUG7 Q96HE4 Q96JF0	
α-2,6-sialyltransferase (ST6GALNAC III)	*Homo sapiens*	n.d.	BC059363 AAH59363.1 AY358540 AAQ88904.1 AK091215 BAC03611.1 AJ507291 CAD45371.1 NM_152996 NP_694541.1	Q8N259 Q8NDV1	
α-2,6-sialyltransferase (ST6GalNAc V)	*Homo sapiens*	n.d.	BC001201 **AAH01201.1** AK056241 BAB71127.1 AL035409 CAB72344.1 AJ507292 CAD45372.1 NM_030965 NP_112227.1	Q9BVH7	
α-2,6-sialyltransferase (SThM) ST6GalNAc II	*Homo sapiens*	2.4.99.-	U14550 AAA52228.1 BC040455 **AAH40455.1** AJ251053 CAB61434.1 NM_006456 NP_006447.1	Q9UJ37 Q12971	
α-2,6-sialyltransferase ST6Gal I	*Homo sapiens*	2.4.99.1	BC031476 AAH31476.1 BC040009 AAH40009.1 A17362 **CAA01327.1** A23699 CAA01686.1 X17247 CAA35111.1 X54363 CAA38246.1 X62822 CAA44634.1 NM_003032 NP_003023.1 NM_173216 NP_775323.1	P15907	
α-2,6-sialyltransferase ST6GalNAc I	*Homo sapiens*	2.4.99.3	BC022462 AAH22462.1 AY096001 AAM22800.1 AY858918 AAQ89277.1 AK000113 BAA90953.1 Y11339 CAA72179.2 NM_018414 NP_060884.1	Q8TB16 Q9NSC7 Q9NXQ7	
α-2,8-polysialyltransferase ST8Sia IV	*Homo sapiens*	2.4.99.-	L41680 AAC41775.1 BC027866 AAH27866.1 BC053657 **AAH53657.1** NM_005668 NP_005659.1	Q8N1F4 Q92187 Q92693	
α-2,8-sialyltransferase (GD3 synthase) ST8Sia I	*Homo sapiens*	2.4.99.8	L32867 AAA62366.1 L43494 AAC37586.1 BC046158 AAH46158.1 AAQ53140.1 AY569975 AAS75783.1 D26360 BAA05391.1 X77922 CAA54891.1 NM_003034 NP_003025.1	Q86X74 Q92185 Q93064	
α-2,8-sialyltransferase	*Homo sapiens*	2.4.99.-	L29556 AAA36613.1	Q92186	

FIGURE 11E

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
ST8Sia II			U82762 AAB51242.1 U33551 **AAC24458.1** BC069584 AAH69584.1 NM_006011 NP_006002.1	Q92470 Q92746	
α-2,8-sialyltransferase ST8Sia III	*Homo sapiens*	2.4.99.-	AF004668 AAB87642.1 AF003092 AAC15901.2 NM_015879 NP_056963.1	O43173 Q9NS41	
α-2,8-sialyltransferase ST8Sia V	*Homo sapiens*	2.4.99.-	U91641 **AAC51727.1** CR457037 CAG33318.1 NM_013305 NP_037437.1	O15466	
ENSP00000020221 (fragment)		n.d.	AC023295		
lactosylceramide α-2,3-sialyltransferase (ST3Gal V)	*Homo sapiens*	2.4.99.9	AF105026 **AAD14634.1** AF119415 AAF66146.1 BC065936 AAH65936.1 AY152815 AAO16866.1 AAP65066 AAP65066.1 AY359105 AAQ89463.1 AB018356 BAA33950.1 AX876536 CAE89320.1 NM_003896 NP_003887.2	Q9UNP4 O94902	
N-acetylgalactosaminide α-2,6-sialyltransferase (ST6GalNAc VI)	*Homo sapiens*	2.4.99.-	BC006564 AAH06564.1 BC007802 AAH07802.1 BC016299 AAH16299.1 AY358672 AAQ89035.1 AB035173 BAA87035.1 AK023900 BAB14715.1 AJ507293 CAD45373.1 AX880950 CAE91115.1 CR457418 CAG33599.1 NM_013443 NP_038471.2	Q969X2 Q9H8A2 Q9ULB8	
N-acetylgalactosaminide α-2,6-sialyltransferase IV (ST6GalNAc IV)	*Homo sapiens*	2.4.99.-	AF127142 AAF00102.1 BC036705 AAH36705.1 -AAP63349.1 AB035172 **BAA87034.1** AK000600 BAA91281.1 Y17461 CAB44354.1 AJ271734 CAC07404.1 AX061620 CAC24981.1 AX068265 CAC27250.1 AX969252 CAF14360.1 NM_014403 NP_055218.3 NM_175039 NP_778204.1	Q9H4F1 Q9NWU6 Q9UKU1 Q9ULB9 Q9Y3G3 Q9Y3G4	
ST8SIA-VI (fragment)	*Homo sapiens*	n.d.	AJ621583 CAF21722.1 XM_291725 XP_291725.2		
unnamed protein product	*Homo sapiens*	n.d.	AK021929 **BAB13940.1** AX881696 CAE91353.1	Q9HAA9	
Gal β-1,3/4-GlcNAc α-2,3-sialyltransferase (ST3Gal III)	*Mesocricetus auratus*	2.4.99.6	AJ245699 **CAB53394.1**	Q9QXF6	

FIGURE 11F

Protein		Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
Gal β-1,3/4-GlcNAc α-2,3-sialyltransferase (ST3Gal IV)		*Mesocricetus auratus*	2.4.99.6	AJ245700 **CAB53395.1**	Q9QXF5	
GD3 synthase (fragment) ST8Sia I		*Mesocricetus auratus*	n.d.	AF141657 **AAD33879.1**	Q9WUL1	
polysialyltransferase (ST8Sia IV)		*Mesocricetus auratus*	2.4.99.-	AJ245701 **CAB53396.1**	Q9QXF4	
α-2,3-sialyltransferase ST3Gal I	*St3gal1*	*Mus musculus*	2.4.99.4	AF214028 AAF60973.1 AK031344 BAC27356.1 AK078469 BAC37290.1 X73523 CAA51919.1 NM_009177 NP_033203.1	P54751 Q11202 Q9JL30	
α-2,3-sialyltransferase ST3Gal II	*St3gal2*	*Mus musculus*	2.4.99.4	BC015264 **AAH15264.1** BC066064 AAH66064.1 AK034554 BAC28752.1 AK034863 BAC28859.1 AK053827 BAC35543.1 X76989 CAA54294.1 NM_009179 NP_033205.1 NM_178048 NP_835149.1	Q11204 Q8BPL0 Q8BSA0 Q8BSE9 Q91WH6	
α-2,3-sialyltransferase ST3Gal III	*St3gal3*	*Mus musculus*	2.4.99.-	BC006710 AAH06710.1 AK005053 **BAB23779.1** AK013016 BAB28598.1 X84234 CAA59013.1 NM_009176 NP_033202.2	P97325 Q922X5 Q9CZ48 Q9DBB6	
α-2,3-sialyltransferase ST3Gal IV	*St3gal4*	*Mus musculus*	2.4.99.4	BC011121 AAH11121.1 BC050773 **AAH50773.1** D28941 BAA06068.1 AK008543 BAB25732.1 AB061305 BAB47508.1 X95809 CAA65076.1 NM_009178 NP_033204.2	P97354 Q61325 Q91Y74 Q921R5 Q9CVE8	
α-2,3-sialyltransferase ST3Gal VI	*St3gal6*	*Mus musculus*	2.4.99.4	AF119390 AAD39130.1 BC052338 AAH52338.1 AB063326 **BAB79494.1** AK033562 BAC28360.1 AK041173 BAC30851.1 NM_018784 NP_061254	Q80UR7 Q8BLV1 Q8VIB3 Q9WVG2	
α-2,6-sialyltransferase ST6GalNAc II	*St6galnac2*	*Mus musculus*	2.4.99.-	NM_009180 6677963 BC010208 AAH10208.1 AB027198 BAB00637.1 AK004613 BAB23410.1 X93999 CAA63821.1 X94000 CAA63822.1 NM_009180 NP_033206.2	**P70277** Q9DC24 Q9JJM5	
α-2,6-sialyltransferase ST6Gal I	*St6gal1*	*Mus musculus*	2.4.99.1	[redacted] AAE68031.1 BC027833 AAH27833.1 D16106 BAA03680.1 AK034768 BAC28828.1 AK084124 BAC39120.1 NM_145933 NP_666045.1	Q64685 Q8BM62 Q8K1L1	
α-2,6-sialyltransferase ST6Gal II	*St6gal2*	*Mus musculus*	n.d.	AK082566 BAC38534.1 AB095093 **BAC87752.1** AK129462 BAC98272.1 NM_172829 NP_766417.1	Q8BUU4	
α-2,6-sialyltransferase ST6GalNAc I	*St6galnac1*	*Mus musculus*	2.4.99.3	Y11274 CAA72137.1 NM_011371 NP_035501.1	Q9QZ39 Q9JJP5	
α-2,6-sialyltransferase ST6GalNAc III	*St6galnac3*	*Mus musculus*	n.d.	BC058387 AAH58387.1 AK034804 BAC28836.1 Y11342 CAA72181.2 Y11343 **CAB95031.1** NM_011372 NP_035502	Q9WUV2 Q9JHP5	
α-2,6-sialyltransferase ST6GalNAc IV	*St6galnac4*	*Mus musculus*	2.4.99.7	BC056451 AAH56451.1 AK085730 BAC39523.1 AJ007310 CAA07446.1 Y15779 CAB43507.1	Q8C3J2 Q9JHP2 Q9R2B6 O88725	

FIGURE 11G

Protein		Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
				Y15780 CAB43514.1	Q9JHP0	
				Y19055 CAB93946.1	Q9QUP9	
				Y19057 CAB93948.1	Q9R2B5	
				NM_011373 NP_035503.1		
α-2,8-sialyltransferase (GD3 synthase) ST8Sia I	*St8sia1*	*Mus musculus*	2.4.99.8	L38677 AAA91869.1	Q64468	
				BC024821 **AAH24821.1**	Q64687	
				AK046188 BAC32625.1	Q8BL76	
				AK052444 BAC34994.1	Q8BWI0	
				X84235 CAA59014.1	Q8K1C1	
				AJ401102 CAC20706.1	Q9EPK0	
				NM_011374 NP_035504.1		
α-2,8-sialyltransferase (ST8Sia VI)	*St8sia6*	*Mus musculus*	n.d.	AB059554 **BAC01265.1**	Q8BI43	
				AK085105 BAC39367.1	Q8K4T1	
				NM_145838 NP_665837.1		
α-2,8-sialyltransferase ST8Sia II	*St8sia2*	*Mus musculus*	2.4.99.-	X83562 CAA58548.1	**O35696**	
				X99646 CAA67965.1		
				X99647 CAA67965.1		
				X99648 CAA67965.1		
				X99649 CAA67965.1		
				X99650 CAA67965.1		
				X99651 CAA67965.1		
				NM_009181 NP_033207.1		
α-2,8-sialyltransferase ST8Sia IV	*St8sia4*	*Mus musculus*	2.4.99.8	BC060112 AAH60112.1	Q64692	
				AK003690 BAB22941.1	Q8BY70	
				AK041723 BAC31044.1		
				AJ223956 **CAA11685.1**		
				X86000 CAA59992.1		
				Y09484 CAA70692.1		
				NM_009183 NP_033209.1		
α-2,8-sialyltransferase ST8Sia V	*St8sia5*	*Mus musculus*	2.4.99.-	BC034855 AAH34855.1	P70126	
				AK078670 BAC37354.1	P70127	
				X98014 **CAA66642.1**	P70128	
				X98014 CAA66643.1	Q8BJW0	
				X98014 CAA66644.1	Q8JZQ3	
				NM_013666 NP_038694.1		
				NM_153124 NP_694764.1		
				NM_177416 NP_803135.1		
α-2,8-sialytransferase ST8Sia III	*St8sia3*	*Mus musculus*	2.4.99.-	BC075645 AAH75645.1	Q64689	
				AK015874 BAB30012.1	Q9CUJ6	
				X80502 CAA56665.1		
				NM_009182 NP_033208.1		
GD1 synthase (ST6GalNAc V)	*St6galnac5*	*Mus musculus*	n.d.	BC055737 **AAH55737.1**	Q8CAM7	
				AB030836 BAA85747.1	Q8CBX1	
				AB028840 BAA89292.1	Q9QYJ1	
				AK034387 BAC28693.1	Q9R0K6	
				AK038434 BAC29997.1		
				AK042683 BAC31331.1		
				NM_012028 NP_036158.2		
GM3 synthase (α-2,3-sialyltransferase) ST3Gal V	*St3gal5*	*Mus musculus*	2.4.99.9	AF119416 **AAF66147.1**	O88829	
				AAP65063.1	Q9CZ65	
				AB018048 BAA33491.1	Q9QWF9	
				AB013302 BAA76467.1		
				AK012961 BAB28571.1		
				CAA75235.1		
				NM_011375 NP_035505.1		
N-acetylgalactosaminide α-2,6-sialyltransferase (ST6GalNAc VI)	*St6galnac6*	*Mus musculus*	2.4.99.-	BC036985 **AAH36985.1**	Q8CDC3	
				AB035174 BAA87036.1	Q8JZW3	
				AB035123 BAA95940.1	Q9JM95	
				AK030648 BAC27064.1	Q9R0G9	
				NM_016973 NP_058669.1		
M138L		*Myxoma virus*	n.d.	U46578 AAD00069.1		
				AF170726 AAE61323.1		
				NC_001132 AAE61326.1		
				AAF15026.1		
				NP_051852.1		
α-2,3-sialyltransferase		*Oncorhynchus*	n.d.	AJ585760 **CAE51384.1**		

FIGURE 11H

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
(St3Gal-I)	*mykiss*				
α-2,6-sialyltransferase (Siat1)	*Oncorhynchus mykiss*	n.d.	AJ620649 CAF05848.1		
α-2,8-polysialyltransferase IV (ST8Sia IV)	*Oncorhynchus mykiss*	n.d.	AB094402 BAC77411.1	Q7T2X5	
GalNAc α-2,6-sialyltransferase (RtST6GalNAc)	*Oncorhynchus mykiss*	n.d.	AB097943 BAC77520.1	Q7T2X4	
α-2,3-sialyltransferase ST3Gal IV	*Oryctolagus cuniculus*	2.4.99.-	AF121967 AAF28871.1	Q9N257	
OJ1217_F02.7	*Oryza sativa (japonica cultivar-group)*	n.d.	AP004084 BAD07616.1		
OSJNBa0043L24.2 or OSJNBb0002J11.9	*Oryza sativa (japonica cultivar-group)*	n.d.	AL731626 CAD41185.1 AL662969 CAE04714.1		
P0683f02.18 or P0489B03.1	*Oryza sativa (japonica cultivar-group)*	n.d.	AP003289 BAB63715.1 AP003794 BAB90552.1		
α-2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	*Oryzias latipes*	n.d.	AJ646876 CAG26705.1		
α-2,3-sialyltransferase ST3Gal I (Siat4)	*Pan troglodytes*	n.d.	AJ744803 CAG32839.1		
α-2,3-sialyltransferase ST3Gal II (Siat5)	*Pan troglodytes*	n.d.	AJ744804 CAG32840.1		
α-2,3-sialyltransferase ST3Gal III (Siat6)	*Pan troglodytes*	n.d.	AJ626819 CAF25177.1		
α-2,3-sialyltransferase ST3Gal IV (Siat4c)	*Pan troglodytes*	n.d.	AJ626824 CAF25182.1		
α-2,3-sialyltransferase ST3Gal VI (Siat10)	*Pan troglodytes*	n.d.	AJ744808 CAG32844.1		
α-2,6-sialyltransferase (Sia7A)	*Pan troglodytes*	n.d.	AJ748740 CAG38615.1		
α-2,6-sialyltransferase (Sia7B)	*Pan troglodytes*	n.d.	AJ748741 CAG38616.1		
α-2,6-sialyltransferase ST6GalNAc III (Siat7C)	*Pan troglodytes*	n.d.	AJ634454 CAG25676.1		
α-2,6-sialyltransferase ST6GalNAc IV (Siat7D) (fragment)	*Pan troglodytes*	n.d.	AJ646870 CAG26699.1		
α-2,6-sialyltransferase ST6GalNAc V (Siat7E)	*Pan troglodytes*	n.d.	AJ646875 CAG26704.1		
α-2,6-sialyltransferase ST6GalNAc VI (Siat7F) (fragment)	*Pan troglodytes*	n.d.	AJ646882 CAG26711.1		
α-2,8-sialyltransferase 8A (Siat8A)	*Pan troglodytes*	2.4.99.8	AJ697658 CAG26896.1		
α-2,8-sialyltransferase 8B (Siat8B)	*Pan troglodytes*	n.d.	AJ697659 CAG26897.1		
α-2,8-sialyltransferase 8C (Siat8C)	*Pan troglodytes*	n.d.	AJ697660 CAG26898.1		
α-2,8-sialyltransferase 8D (Siat8D)	*Pan troglodytes*	n.d.	AJ697661 CAG26899.1		
α-2,8-sialyltransferase 8E (Siat8E)	*Pan troglodytes*	n.d.	AJ697662 CAG26900.1		
α-2,8-sialyltransferase 8F (Siat8F)	*Pan troglodytes*	n.d.	AJ697663 CAG26901.1		
β-galactosamide α-2,6-sialyltransferase I (ST6Gal I; Siat1)	*Pan troglodytes*	2.4.99.1	AJ627624 CAF29492.1		
β-galactosamide α-2,6-sialyltransferase II (ST6Gal II)	*Pan troglodytes*	n.d.	AJ627625 CAF29493.1		
GM3 synthase ST3Gal V	*Pan troglodytes*	n.d.	AJ744807 CAG32843.1		

FIGURE 11I

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
(Siat9) S138	Rabbit fibroma virus Kasza	n.d.	NC_001266 NP_052025		
α-2,3-sialyltransferase ST3Gal III	*Rattus norvegicus*	2.4.99.6	M97754 AAA42146.1 NM_031697 NP_113885.1	Q02734	
α-2,3-sialyltransferase ST3Gal IV (Siat4c)	*Rattus norvegicus*	n.d.	AJ626825 CAF25183.1		
α-2,3-sialyltransferase ST3Gal VI	*Rattus norvegicus*	n.d.	AJ626743 CAF25053.1		
α-2,6-sialyltransferase ST3Gal II	*Rattus norvegicus*	2.4.99.-	X76988 CAA54293.1 NM_031695 NP_113883.1	Q11205	
α-2,6-sialyltransferase ST6Gal I	*Rattus norvegicus*	2.4.99.1	M18769 AAA41196.1 M83143 AAB07233.1	P13721	
α-2,6-sialyltransferase ST6GalNAc I (Siat7A)	*Rattus norvegicus*	n.d.	AJ634458 CAG25684.1		
α-2,6-sialyltransferase ST6GalNAc II (Siat7B)	*Rattus norvegicus*	n.d.	AJ634457 CAG25679.1		
α-2,6-sialyltransferase ST6GalNAc III	*Rattus norvegicus*	2.4.99.-	L29554 AAC42086.1 BC072501 AAH72501.1 NM_019123 NP_061996.1	Q64686	
α-2,6-sialyltransferase ST6GalNAc IV (Siat7D) (fragment)	*Rattus norvegicus*	n.d.	AJ646871 CAG26700.1		
α-2,6-sialyltransferase ST6GalNAc V (Siat7E)	*Rattus norvegicus*	n.d.	AJ646872 CAG26701.1		
α-2,6-sialyltransferase ST6GalNAc VI (Siat7F) (fragment)	*Rattus norvegicus*	n.d.	AJ646881 CAG26710.1		
α-2,8-sialyltransferase (GD3 synthase) ST8Sia I	*Rattus norvegicus*	2.4.99.-	U53883 AAC27541.1 D45255 BAA08213.1	P70554 P97713	
α-2,8-sialyltransferase (SIAT8E)	*Rattus norvegicus*	n.d.	AJ699422 CAG27884.1		
α-2,8-sialyltransferase (SIAT8F)	*Rattus norvegicus*	n.d.	AJ699423 CAG27885.1		
α-2,8-sialyltransferase ST8Sia II	*Rattus norvegicus*	2.4.99.-	L13445 AAA42147.1 NM_057156 NP_476497.1	Q07977 Q64688	
α-2,8-sialyltransferase ST8Sia III	*Rattus norvegicus*	2.4.99.-	U55938 AAB50061.1 NM_013029 NP_037161.1	P97877	
α-2,8-sialyltransferase ST8Sia IV	*Rattus norvegicus*	2.4.99.-	U90215 AAB49989.1	O08563	
β-galactosamide α-2,6-sialyltransferase II (ST6Gal II)	*Rattus norvegicus*	n.d.	AJ627626 CAF29494.1		
GM3 synthase ST3Gal V	*Rattus norvegicus*	n.d.	AB018049 BAA33492.1 NM_031337 NP_112627.1	O88830	
sialyltransferase ST3Gal-I (Siat4A)	*Rattus norvegicus*	n.d.	AJ748840 CAG44449.1		
α-2,3-sialyltransferase (St3Gal-II)	*Silurana tropicalis*	n.d.	AJ585763 CAE51387.1		
α-2,6-sialyltransferase (Siat7b)	*Silurana tropicalis*	n.d.	AJ620650 CAF05849.1		
α-2,6-sialyltransferase (St6galnac)	*Strongylocentrotus purpuratus*	n.d.	AJ699425 CAG27887.1		
α-2,3-sialyltransferase (ST3GAL-III)	*Sus scrofa*	n.d.	AJ585765 CAE51389.1		
α-2,3-sialyltransferase (ST3GAL-IV)	*Sus scrofa*	n.d.	AJ584674 CAE48299.1		
α-2,3-sialyltransferase ST3Gal I	*Sus scrofa*	2.4.99.4	M97753 AAA31125.1	Q02745	
α-2,6-sialyltransferase (fragment) ST6Gal I	*Sus scrofa*	2.4.99.1	AF136746 AAD33059.1	Q9XSG8	
β-galactosamide α-2,6-sialyltransferase (ST6GalNAc-V)	*Sus scrofa*	n.d.	AJ620948 CAF06585.2		
sialyltransferase (fragment) ST6Gal I	*sus scrofa*	n.d.	AF041031 AAC15633.1	O62717	

FIGURE 11J

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
ST6GALNAC-V	*Sus scrofa*	n.d.	AJ620948 CAF06585.1		
α-2,3-sialyltransferase (Siat5-r)	*Takifugu rubripes*	n.d.	AJ744805 CAG32841.1		
α-2,3-sialyltransferase ST3Gal I (Siat4)	*Takifugu rubripes*	n.d.	AJ626816 CAF25174.1		
α-2,3-sialyltransferase ST3Gal II (Siat5) (fragment)	*Takifugu rubripes*	n.d.	AJ626817 CAF25175.1		
α-2,3-sialyltransferase ST3Gal III (Siat6)	*Takifugu rubripes*	n.d.	AJ626818 CAF25176.1		
α-2,6-sialyltransferase ST6Gal I (Siat1)	*Takifugu rubripes*	n.d.	AJ744800 CAG32836.1		
α-2,6-sialyltransferase ST6GalNAc II (Siat7B)	*Takifugu rubripes*	n.d.	AJ634460 CAG25681.1		
α-2,6-sialyltransferase ST6GalNAc II B (Siat7B-related)	*Takifugu rubripes*	n.d.	AJ634461 CAG25682.1		
α-2,6-sialyltransferase ST6GalNAc III (Siat7C) (fragment)	*Takifugu rubripes*	n.d.	AJ634456 CAG25678.1		
α-2,6-sialyltransferase ST6GalNAc IV (siat7D) (fragment)	*Takifugu rubripes*	2.4.99.3	Y17466 CAB44338.1 AJ646869 CAG26698.1	Q9W6U6	
α-2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	*Takifugu rubripes*	n.d.	AJ646873 CAG26702.1		
α-2,6-sialyltransferase ST6GalNAc VI (Siat7F) (fragment)	*Takifugu rubripes*	n.d.	AJ646880 CAG26709.1		
α-2,8-sialyltransferase ST8Sia I (Siat 8A) (fragment)	*Takifugu rubripes*	n.d.	AJ715534 CAG29373.1		
α-2,8-sialyltransferase ST8Sia II (Siat 8B) (fragment)	*Takifugu rubripes*	n.d.	AJ715538 CAG29377.1		
α-2,8-sialyltransferase ST8Sia III (Siat 8C) (fragment)	*Takifugu rubripes*	n.d.	AJ715541 CAG29380.1		
α-2,8-sialyltransferase ST8Sia IIIr (Siat 8Cr)	*Takifugu rubripes*	n.d.	AJ715542 CAG29381.1		
α-2,8-sialyltransferase ST8Sia V (Siat 8E) (fragment)	*Takifugu rubripes*	n.d.	AJ715547 CAG29386.1		
α-2,8-sialyltransferase ST8Sia VI (Siat 8F) (fragment)	*Takifugu rubripes*	n.d.	AJ715549 CAG29388.1		
α-2,8-sialyltransferase ST8Sia VIr (Siat 8Fr)	*Takifugu rubripes*	n.d.	AJ715550 CAG29389.1		
α-2,3-sialyltransferase (Siat5-r)	*Tetraodon nigroviridis*	n.d.	AJ744806 CAG32842.1		
α-2,3-sialyltransferase ST3Gal I (Siat4)	*Tetraodon nigroviridis*	n.d.	AJ744802 CAG32838.1		
α-2,3-sialyltransferase ST3Gal III (Siat6)	*Tetraodon nigroviridis*	n.d.	AJ626822 CAF25180.1		
α-2,6-sialyltransferase ST6GalNAc II (Siat7B)	*Tetraodon nigroviridis*	n.d.	AJ634462 CAG25683.1		
α-2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	*Tetraodon nigroviridis*	n.d.	AJ646879 CAG26708.1		
α-2,8-sialyltransferase ST8Sia I (Siat 8A) (fragment)	*Tetraodon nigroviridis*	n.d.	AJ715536 CAG29375.1		
α-2,8-sialyltransferase ST8Sia II (Siat 8B) (fragment)	*Tetraodon nigroviridis*	n.d.	AJ715537 CAG29376.1		
α-2,8-sialyltransferase	*Tetraodon*	n.d.	AJ715539 CAG29378.1		

FIGURE 11K

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
ST8Sia III (Siat8C) (fragment)	*nigroviridis*				
α-2,8-sialyltransferase ST8Sia IIIr (Siat 8Cr) (fragment)	*Tetraodon nigroviridis*	n.d.	AJ715540 CAG29379.1		
α-2,8-sialyltransferase ST8Sia V (Siat 8E) (fragment)	*Tetraodon nigroviridis*	n.d.	AJ715548 CAG29387.1		
α-2,3-sialyltransferase (St3Gal-II)	*Xenopus laevis*	n.d.	AJ585762 CAE51386.1		
α-2,3-sialyltransferase (St3Gal-VI)	*Xenopus laevis*	n.d.	AJ585766 CAE51390.1		
α-2,3-sialyltransferase St3Gal-III (Siat6)	*Xenopus laevis*	n.d.	AJ585764 CAE51388.1 AJ626823 CAF25181.1		
α-2,8-polysialyltransferase	*Xenopus laevis*	2.4.99.-	AB007468 BAA32617.1	O93234	
α-2,8-sialyltransferase ST8Siα-I (Siat8A;GD3 synthase)	*Xenopus laevis*	n.d.	AY272056 AAQ16162.1 AY272057 AAQ16163.1 AJ704562 CAG28695.1		
Unknown (protein for MGC:81265)	*Xenopus laevis*	n.d.	BC068760 AAH68760.1		
α-2,3-sialyltransferase (3Gal-VI)	*Xenopus tropicalis*	n.d.	AJ626744 CAF25054.1		
α-2,3-sialyltransferase (Siat4c)	*Xenopus tropicalis*	n.d.	AJ622908 CAF22058.1		
α-2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	*Xenopus tropicalis*	n.d.	AJ646878 CAG26707.1		
α-2,8-sialyltransferase ST8Sia III (Siat 8C) (fragment)	*Xenopus tropicalis*	n.d.	AJ715544 CAG29383.1		
β-galactosamide α-2,6-sialyltransferase II (ST6Gal II)	*Xenopus tropicalis*	n.d.	AJ627628 CAF29496.1		
sialytransferase St8Sial	*Xenopus tropicalis*	n.d.	AY652775 AAT67042		
poly-α-2;8-sialosyl sialyltransferase (NeuS)	*Escherichia coli K1*	2.4.-.-	M76370 AAA24213.1 X60598 CAA43053.1	Q57269	
polysialyltransferase	*Escherichia coli K92*	2.4.-.-	M88479 AAA24215.1	Q47404	
α-2,8 polysialyltransferase SiaD	*Neisseria meningitidis B1940;*	2.4.-.-	M95053 AAA20478.1 X76068 CAA54985.1	Q51281 Q51145	
SynE	*Neisseria meningitidis FAM18*	n.d.	U75650 AAB53842.1	O06435	
polysialyltransferase (SiaD)(fragment)	*Neisseria meningitidis M1019*	n.d.	AY234192 AAO85290.1		
SiaD (fragment)	*Neisseria meningitidis M209*	n.d.	AY281046 AAP34769.1		
SiaD (fragment)	*Neisseria meningitidis M3045*	n.d.	AY281044 AAP34767.1		
polysialyltransferase (SiaD)(fragment)	*Neisseria meningitidis M3315*	n.d.	AY234191 AAO85289.1		
SiaD (fragment)	*Neisseria meningitidis M3515*	n.d.	AY281047 AAP34770.1		
polysialyltransferase (SiaD)(fragment)	*Neisseria meningitidis M4211*	n.d.	AY234190 AAO85288.1		
SiaD (fragment)	*Neisseria meningitidis M4642*	n.d.	AY281048 AAP34771.1		
polysialyltransferase (SiaD)(fragment)	*Neisseria meningitidis M5177*	n.d.	AY234193 AAO85291.1		
SiaD	*Neisseria meningitidis M5178*	n.d.	AY281043 AAP34766.1		
SiaD (fragment)	*Neisseria meningitidis M980*	n.d.	AY281045 AAP34768.1		
NMB0067	*Neisseria meningitidis MC58*	n.d.	NC_003112 NP_273131		

FIGURE 11L

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
Lst	*Aeromonas punctata Sch3*	n.d.	AF126256 **AAS66624.1**		
ORF2	*Haemophilus influenzae A2*	n.d.	M94855 **AAA24979.1**		
HI1699	*Haemophilus influenzae Rd*	n.d.	U32842 **AAC23345.1** NC_000907 NP_439841.1	Q4821.1	
α-2,3-sialyltransferase	*Neisseria gonorrhoeae F62*	2.4.99.4	U60664 **AAC44539.1** AAE67205.1	P72074	
α-2,3-sialyltransferase	*Neisseria meningitidis 126E, NRCC 4010*	2.4.99.4	U60662 **AAC44544.2**		
α-2,3-sialyltransferase	*Neisseria meningitidis 406Y, NRCC 4030*	2.4.99.4	U60661 **AAC44543.1**		
α-2,3-sialyltransferase (NMB0922)	*Neisseria meningitidis MC58*	2.4.99.4	U60660 AAC44541.1 AE002443 AAF41330.1 NC_003112 NP_273962.1	P72097	
NMA1118	*Neisseria meningitidis Z2491*	n.d.	AL162755 CAB84380.1 NC_003116 NP_283887.1	**Q9JUV5**	
PM0508	*Pasteurella multocida PM70*	n.d.	AE006086 **AAK02592.1** NC_002663 NP_245445.1	Q9CNC4	
WaaH	*Salmonella enterica SARB25*	n.d.	AF519787 **AAM82550.1**	Q8KS93	
WaaH	*Salmonella enterica SARB3*	n.d.	AF519788 **AAM82551.1**	Q8KS92	
WaaH	*Salmonella enterica SARB39*	n.d.	AF519789 **AAM82552.1**		
WaaH	*Salmonella enterica SARB53*	n.d.	AF519790 **AAM82553.1**		
WaaH	*Salmonella enterica SARB57*	n.d.	AF519791 **AAM82554.1**	Q8KS91	
WaaH	*Salmonella enterica SARB71*	n.d.	AF519793 **AAM82556.1**	Q8KS89	
WaaH	*Salmonella enterica SARB8*	n.d.	AF519792 **AAM82555.1**	Q8KS90	
WaaH	*Salmonella enterica SARC10V*	n.d.	AF519779 **AAM88840.1**	Q8KS99	
WaaH (fragment)	*Salmonella enterica SARC12*	n.d.	AF519781 **AAM88842.1**		
WaaH (fragment)	*Salmonella enterica SARC13I*	n.d.	AF519782 **AAM88843.1**	Q8KS98	
WaaH (fragment)	*Salmonella enterica SARC14I*	n.d.	AF519783 **AAM88844.1**	Q8KS97	
WaaH	*Salmonella enterica SARC15II*	n.d.	AF519784 **AAM88845.1**	Q8KS96	
WaaH	*Salmonella enterica SARC16II*	n.d.	AF519785 **AAM88846.1**	Q8KS95	

FIGURE 11M

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
WaaH (fragment)	*Salmonella enterica SARC3l*	n.d.	AF519772 AAM88834.1	Q8KSA4	
WaaH (fragment)	*Salmonella enterica SARC4l*	n.d.	AF519773 AAM88835.1	Q8KSA3	
WaaH	*Salmonella enterica SARC5lla*	n.d.	AF519774 AAM88836.1		
WaaH	*Salmonella enterica SARC6lla*	n.d.	AF519775 AAM88837.1	Q8KSA2	
WaaH	*Salmonella enterica SARC8*	n.d.	AF519777 AAM88838.1	Q8KSA1	
WaaH	*Salmonella enterica SARC9V*	n.d.	AF519778 AAM88839.1	Q8KSA0	
UDP-glucose: α-1,2-glucosyltransferase (WaaH)	*Salmonella enterica subsp. arizonae SARC-5*	2.4.1.-	AF511116 AAM48166.1		
bifunctional α-2,3/-2,8-sialyltransferase (Cst-II)	*Campylobacter jejuni ATCC 43449*	n.d.	AF401529 AAL06004.1	Q93CZ5	
Cst	*Campylobacter jejuni 81-176*	n.d.	AF305571 AAL09368.1		
α-2,3-sialyltransferase (Cst-III)	*Campylobacter jejuni ATCC 43429*	2.4.99.-	AY044156 AAK73183.1		
α-2,3-sialyltransferase (Cst-III)	*Campylobacter jejuni ATCC 43430*	2.4.99.-	AF400047 AAK85419.1		
α-2,3-sialyltransferase (Cst-II)	*Campylobacter jejuni ATCC 43432*	2.4.99.-	AF215659 AAG43979.1	Q9F0M9	
α-2,3/8-sialyltransferase (CstII)	*Campylobacter jejuni ATCC 43438*	n.d.	AF400048 AAK91725.1	Q93MQ0	
α-2,3-sialyltransferase cst-II	*Campylobacter jejuni ATCC 43446*	2.4.99.-	AF167344 AAF34137.1		
α-2,3-sialyltransferase (Cst-II)	*Campylobacter jejuni ATCC 43456*	2.4.99.-	AF401528 AAL05990.1	Q93D05	
α-2,3-/α-2,8-sialyltransferase (CstII)	*Campylobacter jejuni ATCC 43460*	2.4.99.-	AY044868 AAK96001.1	Q938X6	
α-2,3/8-sialyltransferase (Cst-II)	*Campylobacter jejuni ATCC 700297*	n.d.	AF216647 AAL36462.1		
ORF	*Campylobacter jejuni GB11*	n.d.	AY422197 AAR82875.1		
α-2,3-sialyltransferase cstIII	*Campylobacter jejuni MSC57360*	2.4.99.-	AF195055 AAG29922.1		
α-2,3-sialyltransferase cstIII Cj1140	*Campylobacter jejuni NCTC 11168*	2.4.99	AL139077 CAB73395.1 NC_002163 NP_282288.1	Q9PNF4	
α-2,3/α-2,8-sialyltransferase II (cstII)	*Campylobacter jejuni O:10*	n.d.	-AAO96669.1 AX934427 CAF04167.1		
α-2,3/α-2,8-sialyltransferase II (CstII)	*Campylobacter jejuni O:19*	n.d.	AX934431 CAF04169.1		
α-2,3/α-2,8-sialyltransferase II (CstII)	*Campylobacter jejuni O:36*	n.d.	AX934436 CAF04171.1		
α-2,3/α-2,8-sialyltransferase II (CstII)	*Campylobacter jejuni O:4*	n.d.	AX934434 CAF04170.1		
α-2,3/α-2,8-sialyltransferase II (CstII)	*Campylobacter jejuni O:41*	n.d.	-AAO96670.1 -AAT17967.1 AX934429 CAF04168.1		
α-2,3-sialyltransferase cst-I	*Campylobacter jejuni OH4384*	2.4.99.-	AF130466 AAF13495.1 AAS36261.1	Q9RGF1	
bifunctional α-2,3/-2,8-sialyltransferase (Cst-II)	*Campylobacter jejuni OH4384*	2.4.99.-	AF130984 AAF31771.1 AX934425 CAF04166.1		1RO7 C 1RO8 A

FIGURE 11N

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
HI0352 (fragment)	*Haemophilus influenzae Rd*	n.d.	U32720 AAC22013.1 X57315 CAA40567.1 NC_000907 NP_438516.1	P24324	
PM1174	*Pasteurella multocida PM70*	n.d.	AE006157 AAK03258.1 NC_002663 NP_246111.1	Q9CLP3	
Sequence 10 from patent US 6503744	*Unknown.*	n.d.	-AAO96672.1		
Sequence 10 from patent US 6699705	*Unknown.*	n.d.	-AAT17969.1		
Sequence 12 from patent US 6699705	*Unknown.*	n.d.	-AAT17970.1		
Sequence 2 from patent US 6709834	*Unknown.*	n.d.	-AAT23232.1		
Sequence 3 from patent US 6503744	*Unknown.*	n.d.	-AAO96668.1		
Sequence 3 from patent US 6699705	*Unknown.*	n.d.	-AAT17965.1		
Sequence 34 from patent US 6503744	*Unknown.*	n.d.	-AAO96684.1		
Sequence 35 from patent US 6503744 (fragment)	*Unknown.*	n.d.	-AAO96685.1 -AAS36262.1		
Sequence 48 from patent US 6699705	*Unknown.*	n.d.	-AAT17988.1		
Sequence 5 from patent US 6699705	*Unknown.*	n.d.	-AAT17966.1		
Sequence 9 from patent US 6503744	*Unknown.*	n.d.	-AAO96671.1		