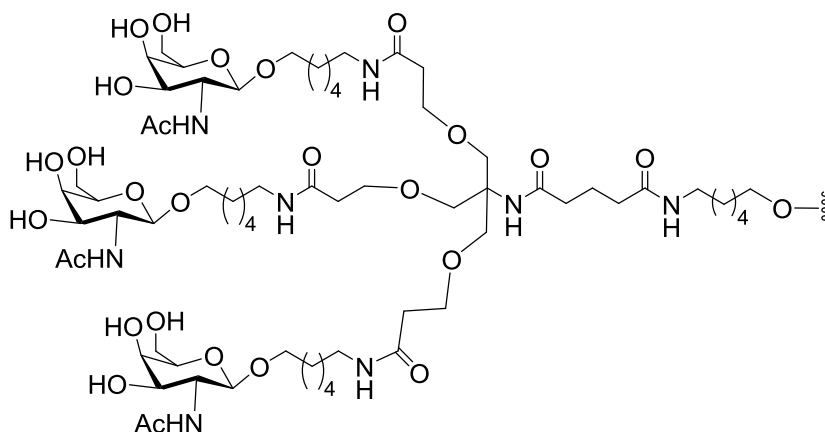


CLAIMS

1. A compound comprising a modified oligonucleotide and a conjugate group, wherein the modified oligonucleotide consists of 10 to 30 linked nucleosides and has a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 440, 198, 228, 237, 444, 448, 450, 453, 455, 549, 598, 6-197, 199-227, 229-236, 238-439, 441-443, 445-447, 449, 451, 452, 454, 456-548, 550-597, or 599-808 and wherein the conjugate group comprises:



2. The compound of claim 1, wherein the modified oligonucleotide consists of 10 to 30 linked nucleosides and has a nucleobase sequence comprising:

- a) at least 9 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 6-808;
- b) at least 10 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 6-808;
- c) at least 11 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 6-808;

or

- d) at least 12 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 6-808.

3. The compound of claim 1, wherein the modified oligonucleotide consists of 10 to 30 linked nucleosides and has a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 6-808.

4. The compound of claim 1, wherein the modified oligonucleotide consists of the nucleobase sequence of any one of SEQ ID NOs: 6-808.

5. The compound of claim 1, wherein the modified oligonucleotide has a nucleobase sequence comprising at least an 8 nucleobase portion of any one of SEQ ID NOs: 84, 238, 239, 317, 412, 413, 420, 421, 426, 434, 436, 437, 438, 439, 440, 442, 443, 444, 445, 446, 448, 451, 452, 453, 454, 455,

456, 457, 458, 459, 460, 461, 462, 464, 465, 472, 473, 514, 515, 542, 543, 544, 545, 546, 551, 553, 555, 556, 599, 600, 601, 602, 610, 616, 617, 618, 662, 666, 670, 676, 677, 678, 688, 689, 713, 723, 729, 730, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 755, 756, 768, 783, 793, 833, and 867.

6. The compound of claim 1, wherein the modified oligonucleotide consists of 10 to 30 linked nucleosides having a nucleobase sequence comprising any one of SEQ ID NOs: 198, 228, 237, 440, 444, 448, 450, 453, 455, 549, and 598, wherein the modified oligonucleotide comprises:

- a gap segment consisting of linked deoxynucleosides;
- a 5' wing segment consisting of linked nucleosides; and
- a 3' wing segment consisting of linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

7. The compound of claim 1, wherein the modified oligonucleotide consists of 20 linked nucleosides having a nucleobase sequence consisting of the sequence recited in SEQ ID NO: 198, 228, 237, 440, 444, 448, 450, 453, or 455, wherein the modified oligonucleotide comprises

- a gap segment consisting of ten linked deoxynucleosides;
- a 5' wing segment consisting of five linked nucleosides; and
- a 3' wing segment consisting of five linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, wherein each nucleoside of each wing segment comprises a 2'-O-methoxyethyl sugar; wherein each internucleoside linkage is a phosphorothioate linkage and wherein each cytosine is a 5-methylcytosine.

8. The compound of claim 1, wherein the modified oligonucleotide consists of 16 linked nucleosides having a nucleobase sequence consisting of the sequence recited in SEQ ID NO: 598, wherein the modified oligonucleotide comprises

- a gap segment consisting of ten linked deoxynucleosides;
- a 5' wing segment consisting of three linked nucleosides; and
- a 3' wing segment consisting of three linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein the 5' wing segment comprises a 2'-O-methoxyethyl sugar, 2'-O-methoxyethyl sugar, and cEt sugar in the 5' to 3' direction; wherein the 3' wing segment comprises a cEt sugar, cEt sugar, and 2'-O-methoxyethyl sugar in the 5' to 3' direction; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine.

9. The compound of claim 1, wherein the modified oligonucleotide consists of 16 linked nucleosides having a nucleobase sequence consisting of the sequence recited in SEQ ID NO: 549, wherein the modified oligonucleotide comprises

- a gap segment consisting of ten linked deoxynucleosides;
- a 5' wing segment consisting of three linked nucleosides; and
- a 3' wing segment consisting of three linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of each wing segment comprises a cEt sugar; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine.

10. The compound of any one of claims 1-9, wherein the oligonucleotide is at least 80%, 85%, 90%, 95% or 100% complementary to SEQ ID NO: 1 or 2.

11. The compound of any one of claims 1-10, wherein the modified oligonucleotide comprises at least one modified internucleoside linkage, at least one modified sugar, or at least one modified nucleobase.

12. The compound of claim 11, wherein the modified internucleoside linkage is a phosphorothioate internucleoside linkage.

13. The compound of claim 12, wherein the modified oligonucleotide comprises:

- a) at least 1 phosphodiester internucleoside linkage;
- b) at least 2 phosphodiester internucleoside linkages;
- c) at least 3 phosphodiester internucleoside linkages;
- d) at least 4 phosphodiester internucleoside linkages;
- e) at least 5 phosphodiester internucleoside linkages;
- f) at least 6 phosphodiester internucleoside linkages; or
- g) at least 7 phosphodiester internucleoside linkages.

14. The compound of claim 13, wherein each internucleoside linkage of the modified oligonucleotide is selected from a phosphodiester internucleoside linkage and a phosphorothioate internucleoside linkage.

15. The compound of claim 12, wherein each internucleoside linkage of the modified oligonucleotide comprises a phosphorothioate internucleoside linkage.

16. The compound of any one of claims 11-15, wherein the modified sugar is:

a) a bicyclic sugar, optionally wherein the bicyclic sugar is selected from the group consisting of: 4'-(CH₂)-O-2' (LNA); 4'-(CH₂)₂-O-2' (ENA); and 4'-CH(CH₃)-O-2' (cEt); or

b) the modified sugar is 2'-O-methoxyethyl.

17. The compound of any one of claims 11-16, wherein the modified nucleobase is a 5-methylcytosine.

18. The compound of any one of claims 1-17, wherein the modified oligonucleotide comprises:

(a) a gap segment consisting of linked deoxynucleosides;

(b) a 5' wing segment consisting of linked nucleosides; and

(c) a 3' wing segment consisting of linked nucleosides;

wherein the gap segment is positioned immediately adjacent to and between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

19. The compound of any one of claims 1-18, wherein the compound is:

a) single-stranded; or

b) double-stranded.

20. The compound of any one of claims 1-19, wherein the compound comprises:

a) ribonucleotides; or

b) deoxyribonucleotides.

21. The compound of any one of claims 1-20, wherein the modified oligonucleotide:

a) consists of 15 to 20 linked nucleosides;

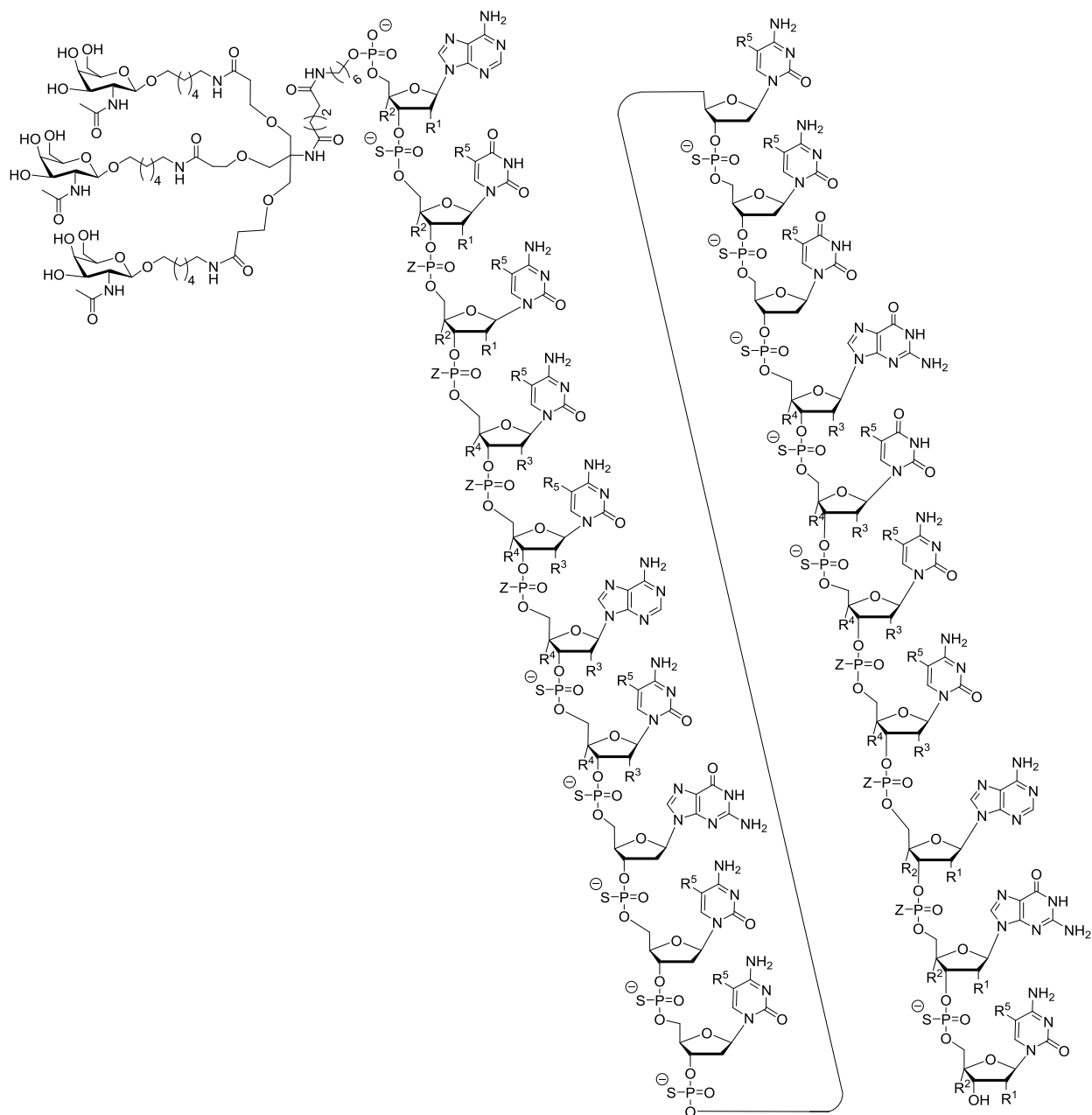
b) consists of 12 to 30 linked nucleosides; or

c) consists of 15 to 30 linked nucleosides.

22. The compound of any of claims 1 to 21, wherein the conjugate group is linked to the modified oligonucleotide:

- a) at the 5' end of the modified oligonucleotide; or
- b) at the 3' end of the modified oligonucleotide.

23. A compound having the formula:



wherein either R^1 is $-\text{OCH}_2\text{CH}_2\text{OCH}_3$ (MOE) and R^2 is H; or R^1 and R^2 together form a bridge, wherein R^1 is $-\text{O}-$ and R^2 is $-\text{CH}_2-$, $-\text{CH}(\text{CH}_3)-$, or $-\text{CH}_2\text{CH}_2-$, and R^1 and R^2 are directly connected such that the resulting bridge is selected from: $-\text{O}-\text{CH}_2-$, $-\text{O}-\text{CH}(\text{CH}_3)-$, and $-\text{O}-\text{CH}_2\text{CH}_2-$;

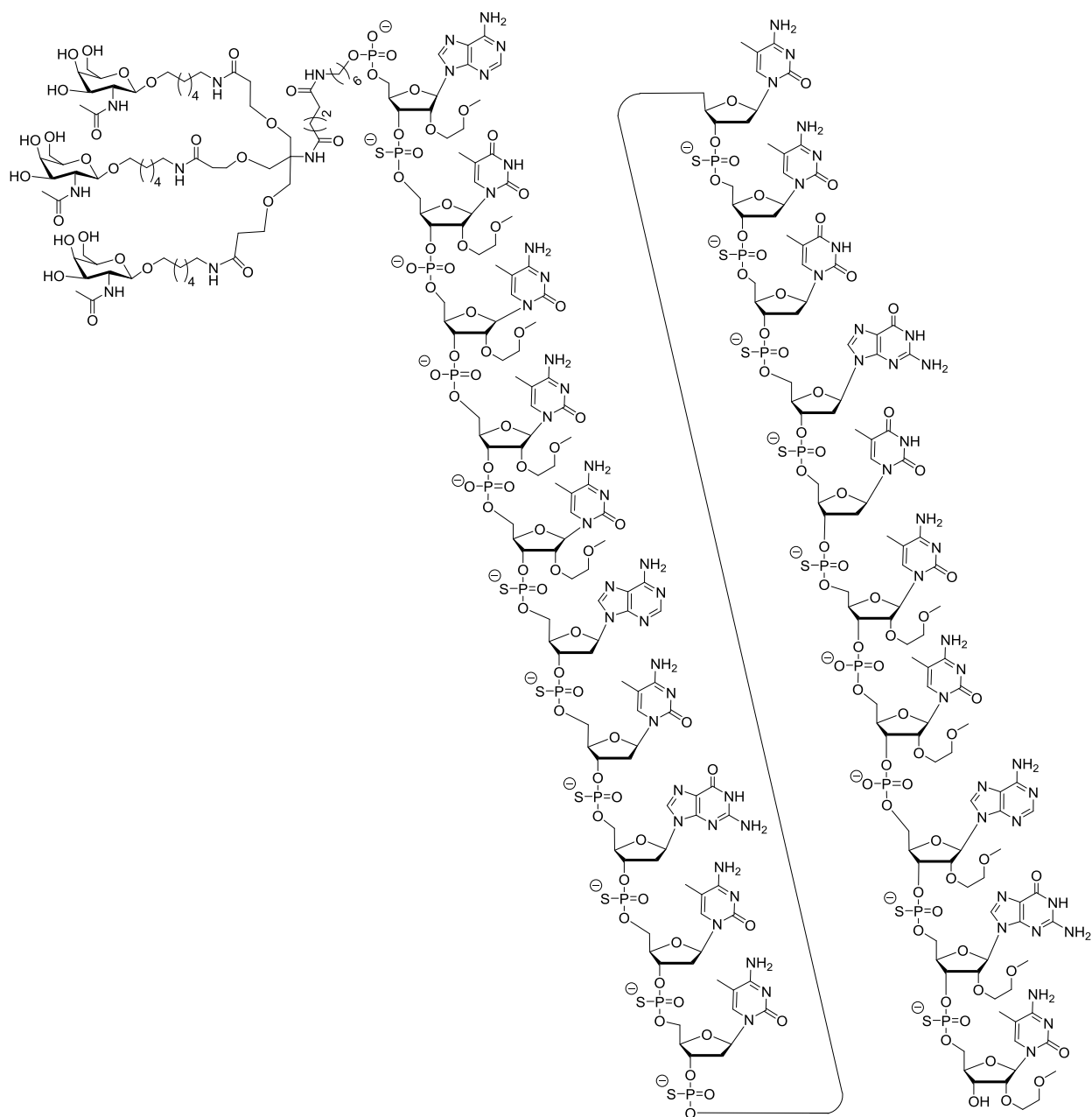
and for each pair of R^3 and R^4 on the same ring, independently for each ring: either R^3 is selected from H and $-\text{OCH}_2\text{CH}_2\text{OCH}_3$ and R^4 is H; or R^3 and R^4 together form a bridge, wherein R^3 is $-\text{O}-$, and R^4 is $-\text{CH}_2-$, $-\text{CH}(\text{CH}_3)-$, or $-\text{CH}_2\text{CH}_2-$ and R^3 and R^4 are directly connected such that the resulting bridge is selected from: $-\text{O}-\text{CH}_2-$, $-\text{O}-\text{CH}(\text{CH}_3)-$, and $-\text{O}-\text{CH}_2\text{CH}_2-$;

And R^5 is selected from H and $-\text{CH}_3$;

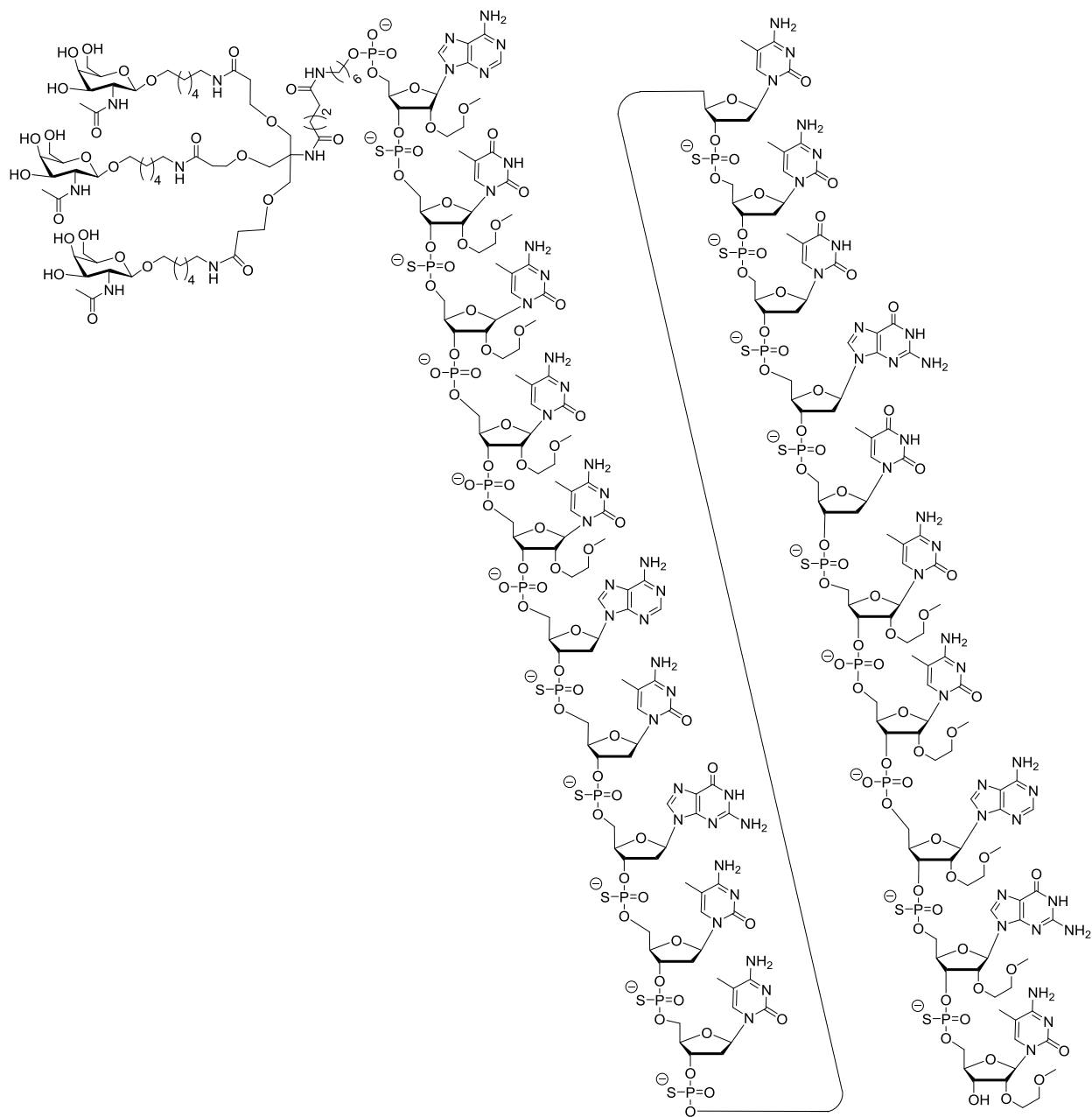
And Z is selected from S^- and O^- .

The image displays a complex chemical structure of a long-chain nucleoside phosphate derivative. The structure is highly branched and complex, featuring a central sugar-phosphate backbone. The sugar is a ribose derivative, and the phosphate groups are linked by phosphodiester bonds. The nucleobases include adenine, guanine, cytosine, and uracil. The structure is highly branched and complex, with multiple phosphate groups and sugar units. The structure is highly branched and complex, with multiple phosphate groups and sugar units.

26. A compound having the formula:



27. A compound having the formula:



28. A composition comprising the compound of any of claims 1-27 or salt thereof and at least one of a pharmaceutically acceptable carrier or diluent.

29. The compound of any one of claims 1-27 or the composition of claim 28 for use in a method of treating, preventing, or ameliorating a disease associated with dysregulation of the complement alternative pathway.

30. The compound or composition for use of claim 29, wherein the disease is macular degeneration, age related macular degeneration (AMD), wet AMD, dry AMD or Geographic Atrophy.

31. The compound or composition for use of claim 29, wherein the disease is a kidney disease.

32. The compound or composition for use of claim 31, wherein the kidney disease is lupus nephritis, dense deposit disease (DDD), C3 glomerulonephritis (C3GN), CFHR5 nephropathy, or atypical hemolytic uremic syndrome (aHUS).

33. Use of the compound of any one of claims 1-27 or the composition of claim 28 in the manufacture of a medicament for treating, preventing, or ameliorating a disease associated with dysregulation of the complement alternative pathway.

34. Use of the compound or composition in the manufacture of a medicament of claim 33, wherein the disease is macular degeneration, age related macular degeneration (AMD), wet AMD, dry AMD or Geographic Atrophy.

35. Use of the compound or composition in the manufacture of a medicament of claim 33, wherein the disease is a kidney disease.

36. Use of the compound or composition in the manufacture of a medicament of claim 35, wherein the kidney disease is lupus nephritis, dense deposit disease (DDD), C3 glomerulonephritis (C3GN), CFHR5 nephropathy, or atypical hemolytic uremic syndrome (aHUS).