HP-2014-000037

IN THE HIGH COURT OF JUSTICE CHANCERY DIVISION PATENTS COURT

BETWEEN:

HOSPIRA UK LIMITED

Claimant

-v-

CUBIST PHARMACEUTICALS INC

Defendant

AMENDED CLAIMS AS REFERRED TO IN STATEMENT OF REASONS IN SUPPORT OF APPLICATION TO CONDITIONALLY AMEND EUROPEAN PATENT (UK) NO. 1 252 179

1. A method to purify daptomycin, <u>wherein daptomycin is selected from the group</u> <u>consisting of essentially pure daptomycin, daptomycin that is at least 98% pure,</u> <u>daptomycin that is substantially free of anhydro-daptomycin and substantially free of</u> <u>beta-isomer of daptomycin, daptomycin that is essentially free of anhydro-daptomycin</u> <u>and substantially free of beta-isomer of daptomycin, daptomycin that is free of</u> <u>anhydro-daptomycin and substantially free of beta-isomer of daptomycin, daptomycin, daptomycin, daptomycin, daptomycin, that is essentially free of <u>that is substantially free of impurities 1 to 14 and daptomycin that is essentially free of</u> <u>impurities 1 to 14, wherein impurities 1 to 14 are as follows:</u></u>

Impurity	Retention	Molecular	Structure
	time	weight	per la presenta de la constante
	(minutes)		
1	<u>7.96</u>	<u>1638</u>	HO_2C HO_2C HO_3C HO_4C
2	<u>9.11</u>	<u>1638</u>	$\begin{array}{c} HO_{2}C \\ HO_{2}C \\ HN \\ HO \\ HN \\ HO \\ HN \\ HN \\ HN \\ HN$
3	<u>11.54</u>	<u>745</u>	HO = HO = O = O = O = O = O = O = O = O
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Impurity	Retention	Molecular	Structure
	time	weight	
	(minutes)		
<u>4</u>	12.28	1624	$HO_{2}C$
5	13.10	<u>1618</u>	
<u>6</u>	<u>14.43</u>	<u>587</u>	HO H H H (CH2)8CH3
2	14.43	1606	$HO_{2}C$ HN $HO_{2}C$ HN $HO_{2}C$ HN HN HN HN HN $HO_{2}C$ HN HN HN HN HN HN HN HN

Impurity	Retention	Molecular	Structure
	time	weight	
	(minutes)		
<u>8</u>	15.10	1620	$HO_{2}C + HN + HV + HV + HV + HV + HV + HV + HV$
9	17.92	<u>874</u>	a .
<u>10</u>	<u>19.57</u>	<u>1810</u>	
11	19.57	<u>1635</u>	Ξ
12	20.93	<u>859</u>	HO =
13	23.11	<u>1602</u>	

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Impurity	Retention time (minutes)	<u>Molecular</u> weight	Structure
14	24.53	<u>1634</u>	$\begin{array}{c} HO_{2}C\\ HO_{2}C\\ HN\\ HO\\ HO\\ HO\\ HO\\ HO\\ C\\ HN\\ H\\ HO\\ H\\ H\\ HO\\ H\\ H\\ HO\\ H\\ H\\ HO\\ H\\ H\\$

comprising the steps of:

- a) supplying a daptomycin preparation that contains at least 2.5% of a combined amount of anhydro-daptomycin and β-isomer of daptomycin;
- b) binding the daptomycin preparation to an anion exchange resin in the presence of a modified buffer under conditions in which daptomycin binds to the anion exchange resin in a monomeric and non-micellar state, wherein the modified buffer comprises a buffering agent selected from acetate, phosphate, citrate and Tris-HCI and one or more chaotropic agents selected from ammonia, urea, benzoate and ascorbate;
- c) washing the anion exchange resin in the presence of the modified buffer under conditions that elutes anhydro-daptomycin but retains daptomycin;
- eluting daptomycin in the presence of the modified buffer under conditions that separate the purified daptomycin from the β-isomer of daptomycin; and
- e) obtaining purified daptomycin.
- The method according to claim 1, further comprising the step of filtering and concentrating the eluted daptomycin.
- 3. A method to purify daptomycin, wherein daptomycin is selected from the group consisting of essentially pure daptomycin, daptomycin that is at least 98% pure, daptomycin that is substantially free of anhydro-daptomycin and substantially free of beta-isomer of daptomycin, daptomycin that is essentially free of anhydro-daptomycin and substantially free of beta-isomer of daptomycin, daptomycin that is free of anhydrodaptomycin and substantially free of beta-isomer of daptomycin, daptomycin that is

substantially free of impurities 1 to 14 and aptomycin that is essentially free of impurities 1 to 14, wherein impurities 1 to 14 are as follows:

Impurity	Retention	Molecular	Structure
	time	weight	1 Na ZilioStrag
	(minutes)		
	7.96	<u>1638</u>	$HO_{2}C$
2	9.11	1638	$HO_{2}C$ HN $HO_{2}C$ HN HN HN HO HO HO HO HO HO HO HO
3	<u>11.54</u>	745	HO = H = O $HO = H = O$ $HO = O$

			(25)
Impurity	Retention	Molecular	Structure
	time	weight	
y y	(minutes)	Troopens	9
<u> </u>	14 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1604	
4	12.28	<u>1624</u>	
4 1			
<u>5</u>	<u>13.10</u> 14.43	<u>1618</u> <u>587</u>	=
<u>D</u>	19,93	<u>501</u>	HO H H H (CH2)6CH3
7	14.43	1606	$ \begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} \end{array} \\ \end{array} \\ \end{array} \\ \end{array} \\ \end{array} \\ \end{array} \\ \begin{array}{c} \end{array} \\ \end{array} \\ \end{array} \\ \begin{array}{c} \end{array} \\ \end{array} \\ \end{array} \\ \begin{array}{c} \end{array} \\ \end{array} \\ \begin{array}{c} \end{array} \\ \end{array} \\ \end{array} \\ \begin{array}{c} \end{array} \\ \end{array} \\ \end{array} \\ \begin{array}{c} \end{array} \\ \end{array} \\ \begin{array}{c} \end{array} \\ \end{array} \\ \end{array} \\ \end{array} \\ \begin{array}{c} \end{array} \\ \end{array} \\ \end{array} \\ \end{array} \\ \begin{array}{c} \end{array} \\ \end{array} \\ \end{array} \\ \end{array} \\ \begin{array}{c} \end{array} \\ \end{array} \\ \end{array} \\ \end{array} \\ \end{array} \\ \end{array} \\ \begin{array}{c} \end{array} \\ \end{array} $

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Impurity	Retention	Molecular	Structure
	time	weight	
	(minutes)		
8	15.10	1620	$HO_{2}C + HN + HV + HV + HV + HV + HV + HV + HV$
9	<u>17.92</u>	<u>874</u>	=
10	<u>19.57</u>	<u>1810</u>	
11	<u>19.57</u>	1635	- · · · · · · · · · · · · · · · · · · ·
12	20.93	<u>859</u>	HO =
13	23.11	1602	

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Impurity	Retention time (minutes)	<u>Molecular</u> weight	Structure
	24.53	1634	$\begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} \\ \end{array} \\ \end{array} \\ \end{array} \\ \end{array} \\ \end{array} \\ \begin{array}{c} \end{array} \\ \end{array} \\ \begin{array}{c} \end{array} \\ \end{array} \\ \end{array} \\ \begin{array}{c} \end{array} \\ \end{array} \\ \begin{array}{c} \end{array} \\ \end{array} \\ \end{array} \\ \end{array} \\ \end{array} \\ \end{array} \\ \begin{array}{c} \end{array} \\ \end{array} \\ \end{array} \\ \end{array} \\ \end{array} \\ \end{array} \\ \begin{array}{c} \end{array} \\ \end{array} $

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comprising the step of:

- a) fermenting Streptomyces reseosporus with a feed of n-decanoic acid to produce daptomycin in a fermentation broth;
- b) clarifying the fermentation broth;
- subjecting the fermentation broth to anion exchange chromatography to obtain an enriched daptomycin preparation;
- d) subjecting the enriched daptomycin preparation to hydrophobic interaction chromatography to obtain a semi-purified daptomycin preparation; and
- e) subjecting the semi-purified daptomycin preparation to modified buffer enhanced anion chromatography, wherein the modified buffer comprises a buffering agent selected from acetate, phosphate, citrate and Tris-HCI and one or more chaotropic agents selected from ammonia urea, benzoate and ascorbate to obtain purified daptomycin.
- 4. The method according to claim 3, wherein the feed of n-decanoic acid in step a) is regulated to achieve a residual concentration of n-decanoic acid of no more than 50 parts per million (ppm) during fermentation; said clarifying in step b) comprises extracting the fermentation broth with a buffer comprising butanol; the anion exchange chromatography in step c) is performed on FP-DA 13 resin; or either or both steps c) or e) comprises the use of a continuous salt gradient or step salt gradient.
- 5. The method according to claim 3, wherein the modified buffer enhanced anion exchange chromatography in step e) comprises the step of:
 - i. supplying the semi-purified daptomycin preparation form step d) in a buffer appropriate for modified buffer enhanced anion exchange chromatography;
 - binding the daptomycin preparation to an anion exchange resin in the presence of the modified buffer under conditions in which daptomycin binds to the anion exchange resin in a monomeric and non-micellar state;
 - iii. washing the anion exchange resin in the presence of the modified buffer under conditions that elutes anhydro-daptomycin but retains daptomycin; and
 - iv. eluting daptomycin in the presence of the modified buffer under conditions that permit the separation of daptomycin from β-isomer.
- The method according to claim 3, further comprising: the step of anion exchange chromatography prior to step e); or the step of filtering and/or concentrating daptomycin.

- 7. The method according to claim 3, further comprising the step of depyrogenating daptomycin.
- 8. The method according to claim 7, further comprising the step of lyophilizing daptomycin.