

SEQUENCE LISTING

<110> Janssen Sciences Ireland Unlimited Company

<120> TREATMENT OR PREVENTION OF A DISEASE OR DISORDER

<130> T1P1134WOPCT1

<140> EPPCT/ 2021/ 082031

<141> 2021- 11- 17

<150> US63/ 115002

<151> 2020- 11- 17

<160> 5

<170> Bi SSAP 1. 3. 6

<210> 1

<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> rHuPH20

<400> 1

Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro	Phe	Leu	Trp
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Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe	Asp	Glu	Pro
			20					25					30		
Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg	Ile	Asn	Ala
		35					40					45			
Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu	Gly	Tyr	Tyr
	50					55				60					
Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly	Gly	Ile	Pro
65					70					75					80
Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys	Lys	Asp	Ile
				85					90					95	
Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val	Ile	Asp	Trp
			100					105					110		
Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro	Lys	Asp	Val
		115					120					125			
Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn	Val	Gln	Leu
	130					135					140				
Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe	Glu	Lys	Ala
145					150					155					160
Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys	Leu	Leu	Arg
				165					170					175	
Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr	Asn	His
			180					185					190		
His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn	Val	Glu	Ile
		195					200						205		

Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	G u	Ser	Thr	Al a	Leu
	210					215				220					
Tyr	Pro	Ser	I l e	Tyr	Leu	Asn	Thr	G n	G n	Ser	Pro	Val	Al a	Al a	Thr
225					230					235					240
Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	G u	Al a	I l e	Arg	Val	Ser	Lys	I l e
				245					250					255	
Pro	Asp	Al a	Lys	Ser	Pro	Leu	Pro	Val	Phe	Al a	Tyr	Thr	Arg	I l e	Val
			260					265					270		
Phe	Thr	Asp	G n	Val	Leu	Lys	Phe	Leu	Ser	G n	Asp	G u	Leu	Val	Tyr
		275					280					285			
Thr	Phe	G y	G u	Thr	Val	Al a	Leu	G y	Al a	Ser	G y	I l e	Val	I l e	Trp
	290					295					300				
G y	Thr	Leu	Ser	I l e	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu	Leu	Leu	Asp
305					310					315					320
Asn	Tyr	Met	G u	Thr	I l e	Leu	Asn	Pro	Tyr	I l e	I l e	Asn	Val	Thr	Leu
				325					330					335	
Al a	Al a	Lys	Met	Cys	Ser	G n	Val	Leu	Cys	G n	G u	G n	G y	Val	Cys
		340						345					350		
I l e	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	Hi s	Leu	Asn	Pro	Asp
	355					360					365				
Asn	Phe	Al a	I l e	G n	Leu	G u	Lys	G y	G y	Lys	Phe	Thr	Val	Arg	G y
	370					375					380				
Lys	Pro	Thr	Leu	G u	Asp	Leu	G u	G n	Phe	Ser	G u	Lys	Phe	Tyr	Cys
385					390					395					400
Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	G u	Lys	Al a	Asp	Val	Lys	Asp
				405					410					415	
Thr	Asp	Al a	Val	Asp	Val	Cys	I l e	Al a	Asp	G y	Val	Cys	I l e	Asp	Al a
		420						425					430		
Phe	Leu	Lys	Pro	Pro	Met	G u	Thr	G u	G u	Pro					
	435						440								

<210> 2

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> rHuPH20 variant 1

<400> 2

Leu	Asn	Phe	Arg	Al a	Pro	Pro	Val	I l e	Pro	Asn	Val	Pro	Phe	Leu	Trp
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Al a	Trp	Asn	Al a	Pro	Ser	G u	Phe	Cys	Leu	G y	Lys	Phe	Asp	G u	Pro
		20						25				30			
Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	I l e	G y	Ser	Pro	Arg	I l e	Asn	Al a
		35					40					45			
Thr	G y	G n	G y	Val	Thr	I l e	Phe	Tyr	Val	Asp	Arg	Leu	G y	Tyr	Tyr
	50					55				60					
Pro	Tyr	I l e	Asp	Ser	I l e	Thr	G y	Val	Thr	Val	Asn	G y	G y	I l e	Pro
65					70					75					80
G n	Lys	I l e	Ser	Leu	G n	Asp	Hi s	Leu	Asp	Lys	Al a	Lys	Lys	Asp	I l e
				85					90					95	
Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	G y	Met	Al a	Val	I l e	Asp	Trp

Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro	Phe	Leu	Trp
1				5					10					15	
Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe	Asp	Glu	Pro
			20					25					30		
Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg	Ile	Asn	Ala
		35					40					45			
Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu	Gly	Tyr	Tyr
	50					55				60					
Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly	Gly	Ile	Pro
65					70				75						80
Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys	Lys	Asp	Ile
				85					90					95	
Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val	Ile	Asp	Trp
			100					105					110		
Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro	Lys	Asp	Val
		115					120					125			
Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn	Val	Gln	Leu
	130					135					140				
Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe	Glu	Lys	Ala
145					150					155					160
Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys	Leu	Leu	Arg
				165					170					175	
Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr	Asn	His
			180					185					190		
His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn	Val	Glu	Ile
		195					200					205			
Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser	Thr	Ala	Leu
	210					215					220				
Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val	Ala	Ala	Thr
225					230					235					240
Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val	Ser	Lys	Ile
				245					250					255	
Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr	Arg	Ile	Val
			260					265					270		
Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu	Leu	Val	Tyr
		275					280					285			
Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile	Val	Ile	Trp
	290					295					300				
Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu	Leu	Leu	Asp
305					310					315					320
Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn	Val	Thr	Leu
				325					330					335	
Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln	Gly	Val	Cys
			340					345					350		
Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu	Asn	Pro	Asp
		355					360					365			
Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr	Val	Arg	Gly
	370					375					380				
Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys	Phe	Tyr	Cys
385					390					395					400
Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp	Val	Lys	Asp
				405					410					415	
Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys	Ile	Asp	Ala
			420					425						430	

Phe	Leu	Lys	Pro	Pro	Met	G u	Thr	G u	G u	Pro	G n	I l e	Phe
		435					440					445	

<210> 4

<211> 445

<212> PRT

<213> Artificial Sequence

<220>

<223> rHuPH20 variant 3

<400> 4

Leu	Asn	Phe	Arg	Al a	Pro	Pro	Val	I l e	Pro	Asn	Val	Pro	Phe	Leu	Trp
1				5					10					15	
Al a	Trp	Asn	Al a	Pro	Ser	G u	Phe	Cys	Leu	G y	Lys	Phe	Asp	G u	Pro
			20					25					30		
Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	I l e	G y	Ser	Pro	Arg	I l e	Asn	Al a
		35					40					45			
Thr	G y	G n	G y	Val	Thr	I l e	Phe	Tyr	Val	Asp	Arg	Leu	G y	Tyr	Tyr
	50					55				60					
Pro	Tyr	I l e	Asp	Ser	I l e	Thr	G y	Val	Thr	Val	Asn	G y	G y	I l e	Pro
65					70					75					80
G n	Lys	I l e	Ser	Leu	G n	Asp	H i s	Leu	Asp	Lys	Al a	Lys	Lys	Asp	I l e
			85					90						95	
Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	G y	Met	Al a	Val	I l e	Asp	Trp
			100					105						110	
G u	G u	Trp	Arg	Pro	Thr	Trp	Al a	Arg	Asn	Trp	Lys	Pro	Lys	Asp	Val
		115					120					125			
Tyr	Lys	Asn	Arg	Ser	I l e	G u	Leu	Val	G n	G n	G n	Asn	Val	G n	Leu
	130					135						140			
Ser	Leu	Thr	G u	Al a	Thr	G u	Lys	Al a	Lys	G n	G u	Phe	G u	Lys	Al a
145					150					155					160
G y	Lys	Asp	Phe	Leu	Val	G u	Thr	I l e	Lys	Leu	G y	Lys	Leu	Leu	Arg
			165						170					175	
Pro	Asn	H i s	Leu	Trp	G y	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr	Asn	H i s
			180					185						190	
H i s	Tyr	Lys	Lys	Pro	G y	Tyr	Asn	G y	Ser	Cys	Phe	Asn	Val	G u	I l e
	195						200					205			
Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	G u	Ser	Thr	Al a	Leu
	210					215					220				
Tyr	Pro	Ser	I l e	Tyr	Leu	Asn	Thr	G n	G n	Ser	Pro	Val	Al a	Al a	Thr
225					230					235					240
Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	G u	Al a	I l e	Arg	Val	Ser	Lys	I l e
			245						250					255	
Pro	Asp	Al a	Lys	Ser	Pro	Leu	Pro	Val	Phe	Al a	Tyr	Thr	Arg	I l e	Val
		260						265					270		
Phe	Thr	Asp	G n	Val	Leu	Lys	Phe	Leu	Ser	G n	Asp	G u	Leu	Val	Tyr
		275					280					285			
Thr	Phe	G y	G u	Thr	Val	Al a	Leu	G y	Al a	Ser	G y	I l e	Val	I l e	Trp
	290					295					300				
G y	Thr	Leu	Ser	I l e	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu	Leu	Leu	Asp
305					310					315					320
Asn	Tyr	Met	G u	Thr	I l e	Leu	Asn	Pro	Tyr	I l e	I l e	Asn	Val	Thr	Leu

				325					330					335		
Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln	Gly	Val	Cys	
			340					345					350			
Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu	Asn	Pro	Asp	
		355					360					365				
Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr	Val	Arg	Gly	
	370					375					380					
Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys	Phe	Tyr	Cys	
385					390					395					400	
Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp	Val	Lys	Asp	
			405					410						415		
Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys	Ile	Asp	Ala	
		420					425					430				
Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu	Pro	Gln	Ile				
	435						440					445				

<210> 5

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> rHuPH20 variant 4

<400> 5

Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro	Phe	Leu	Trp	
1				5					10					15		
Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe	Asp	Glu	Pro	
		20						25					30			
Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg	Ile	Asn	Ala	
	35						40					45				
Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu	Gly	Tyr	Tyr	
	50					55				60						
Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly	Gly	Ile	Pro	
65					70					75					80	
Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys	Lys	Asp	Ile	
			85						90					95		
Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val	Ile	Asp	Trp	
	100							105					110			
Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro	Lys	Asp	Val	
	115						120					125				
Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn	Val	Gln	Leu	
	130					135					140					
Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe	Glu	Lys	Ala	
	145				150					155					160	
Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys	Leu	Leu	Arg	
			165					170						175		
Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr	Asn	His	
		180						185					190			
His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn	Val	Glu	Ile	
	195						200					205				
Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser	Thr	Ala	Leu	
	210					215					220					

Tyr 225	Pro	Ser	Ile	Tyr 230	Leu	Asn	Thr	Gln	Gln	Ser 235	Pro	Val	Ala	Ala	Thr 240
Leu	Tyr	Val	Arg	Asn 245	Arg	Val	Arg	Glu	Ala	Ile 250	Arg	Val	Ser	Lys	Ile 255
Pro	Asp	Ala	Lys 260	Ser	Pro	Leu	Pro	Val 265	Phe	Ala	Tyr	Thr	Arg 270	Ile	Val
Phe	Thr	Asp 275	Gln	Val	Leu	Lys	Phe 280	Leu	Ser	Gln	Asp	Glu 285	Leu	Val	Tyr
Thr	Phe 290	Gly	Glu	Thr	Val	Ala 295	Leu	Gly	Ala	Ser	Gly 300	Ile	Val	Ile	Trp
Gly 305	Thr	Leu	Ser	Ile	Met 310	Arg	Ser	Met	Lys	Ser 315	Oys	Leu	Leu	Leu	Asp 320
Asn	Tyr	Met	Glu	Thr 325	Ile	Leu	Asn	Pro	Tyr 330	Ile	Ile	Asn	Val	Thr	Leu
Ala	Ala	Lys	Met 340	Oys	Ser	Gln	Val	Leu 345	Oys	Gln	Glu	Gln	Gly 350	Val	Oys
Ile	Arg	Lys 355	Asn	Trp	Asn	Ser	Ser 360	Asp	Tyr	Leu	His 365	Leu	Asn	Pro	Asp
Asn	Phe 370	Ala	Ile	Gln	Leu	Glu 375	Lys	Gly	Gly	Lys	Phe 380	Thr	Val	Arg	Gly
Lys 385	Pro	Thr	Leu	Glu	Asp 390	Leu	Glu	Gln	Phe	Ser 395	Glu	Lys	Phe	Tyr	Oys 400
Ser	Oys	Tyr	Ser	Thr 405	Leu	Ser	Oys	Lys	Glu 410	Lys	Ala	Asp	Val	Lys	Asp
Thr	Asp	Ala	Val 420	Asp	Val	Oys	Ile	Ala 425	Asp	Gly	Val	Oys	Ile 430	Asp	Ala
Phe	Leu	Lys 435	Pro	Pro	Met	Glu	Thr 440	Glu	Glu	Pro	Gln				