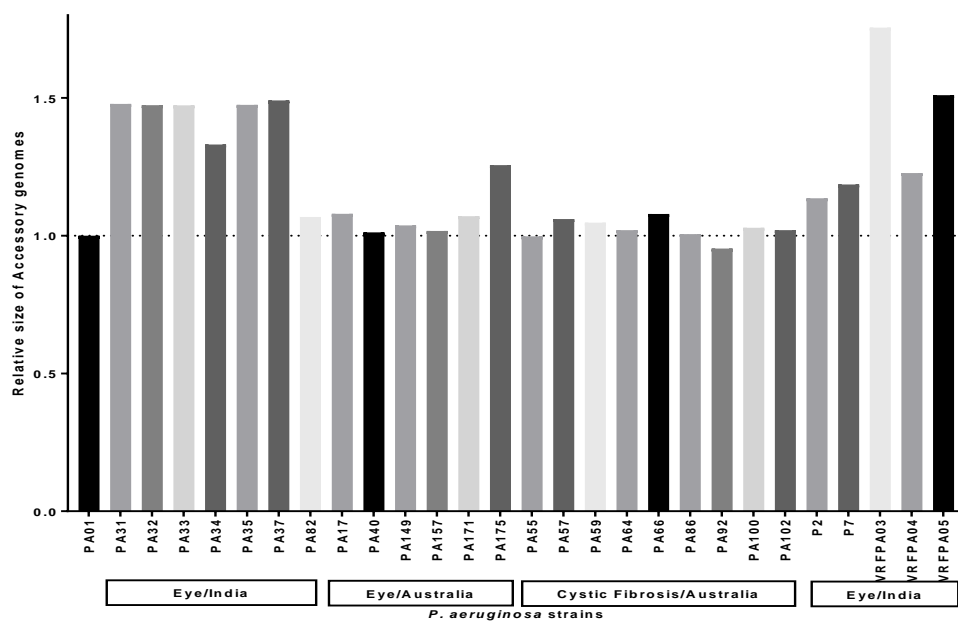


Supplementary information

Comparative genomics of clinical strains of *Pseudomonas aeruginosa* strains isolated from different geographic sites

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Supplementary Figure S1: Size of accessory genomes of 22 strains of this study and five published sequences of Indian *P. aeruginosa* isolates from eye infections relative to PAO1. Dotted line represents size of accessory genome of PAO1. The reference genomes Genbank[®] accession numbers *P. aeruginosa* VRFPA04 (CP008739.2) *P. aeruginosa* VRFPA03 (ATNK00000000.1), *P. aeruginosa* VRFPA05 (AXZJ00000000.1) *P. aeruginosa* P2-L230/9 (JMBS00000000) *P. aeruginosa* P7-L633/96 (JMBS02000000).

Supplementary Table S1: Strains of *Pseudomonas aeruginosa* used in the study downloaded from Pseudomonas genome database based on availability of complete genome

Strain	Number of Genes	GenBank Accession	Phylogeny group	Isolation Source	Core genome SNPs
PAO1 (Reference)	5688	NC_002516.1	1	Wound	0
UCBPP-PA14	5977	NC_008463.1	2	burn wound	28500
PA7	6369	NC_009656.1	1	non-respiratory clinical isolate	176550
LESB58	6028	NC_011770.1	1	sputum	13325
VA-134	5804	CP013245.1	1	skin wound of burn human patient	13663
X78812	5782	CP008872.2	1	missing	13872
F9670	5987	CP008873.1	1	missing	13722
F22031	6077	CP007399.1	1	pubic bone	13687
NCTC10332	5704	LN831024.1	1	not known	13685
12-4-4(59)	5876	CP013696.1	1	Blood culture of burn human patient	13411
DSM50071	5803	CP012001.1	1	missing	13681
S86968	6360	CP008865.2	1	missing	13657
T38079	6137	CP008866.2	1	missing	13658
T52373	5643	CP008867.1	1	missing	13708
T63266	5880	CP008868.1	1	missing	13731
W16407	6181	CP008869.2	1	missing	11626
W36662	6237	CP008870.2	1	missing	13698
W45909	6225	CP008871.2	1	missing	13364
W60856	6333	CP008864.2	1	missing	13232
F23197	5905	CP008856.2	1	missing	14694
F30658	6622	CP008857.1	1	missing	14147
H5708	5804	CP008859.2	1	missing	14287
H27930	5964	CP008860.2	1	missing	13418
H47921	6249	CP008861.1	1	missing	18295
M1608	5887	CP008862.2	2	missing	27703
M37351	6322	CP008863.1	2	missing	27702
USDA-ARS-USMARC-41639	5814	CP013989.1	1	nasopharynx	13740
NCGM1984	6399	AP014646.1	2	catheter	27399
NCGM1900	6354	AP014622.1	2	catheter	27399
FRD1	6179	CP010555.1	1	sputum	14145
Carb01 63	7070	CP011317.1	1	environment	15254
DHS01	6608	CP013993.1	1	nose	13536
NCGM257	6628	AP014651.1	2	Midstream urine	28392
8380	6086	AP014839.2	1	environment	13960
IOMTU 133	6276	AP017302.1	2	Urinary catheter	28311
PACS2	5989	AAQW01000001.1	1	missing	14351
F9676	5827	CP012066.1	1	environment	13151
PA1088	6196	CP015001.1	1	urine	13860
213BR	6169	AFXK01000001.1	1	missing	13866
NHmuc	5795	CP013479.1	1	missing	13484
19BR	6189	AFXJ01000001.1	1	missing	13867
PA1RG	5994	CP012679.1	1	hospital sewage	15635
F63912	6149	CP008873.1	1	missing	13747
N17-1	5867	CP014948.1	1	soil	13451
PAER4_119	6083	CP013113.1	1	Lindberg collection	13806
ATCC 27853	6312	CP015117.1	1	missing	13649
BAMCPA07-48	6438	CP015377.1	2	combat injury wound	27990
PA121617	6303	CP016215.1	1	sputum	13407
PA_154197	6041	CP017306.1	1	missing	12908
PA_D1	6069	CP012585.1	2	sputum	27830
PA_D2	6066	CP012578.1	2	sputum	27833
PA_D9	6065	CP012580.1	2	sputum	27830
PA_D16	6086	CP012581.1	2	sputum	27831
PA_D22	6091	CP012583.1	2	sputum	27831
SCVJan	5794	CP013478.1	1	murine model	13483
PA_D25	6080	CP012584.1	2	sputum	27843
PA_D5	6087	CP012579.1	2	sputum	27830
PA_D21	6063	CP012582.1	2	sputum	27834
ATCC 15692	5744	CP017149.1	1	Infected wound	14
FA-HZ1	6147	CP017353.1	1	wastewater	13349
M18	5770	CP002496.1	1	missing	12888
NCGM2.S1	6274	AP012280.1	2	missing	27404
PA14Or_reads	5971	LT608330.1	2	missing	28430
PcyII-10	5847	LT673656.1	1	missing	13188
DK2	5959	CP003149.1	1	sputum	14269
B136-33	5904	CP004061.1	2	diarrhea	27981
RP73	5864	CP006245.1	1	missing	13795

Strain	Number of Genes	GenBank Accession	Phylogeny group	Isolation Source	Core genome SNPs
YL84	5908	CP007147.1	1	compost	13980
DN1	6626	CP017099.1	2	soil	27667
MTB-1	6186	CP006853.1	2	t-HCH contaminated soil	28100
SCV20265	6380	CP006931.1	1	lung	13980
VRFPA04	6308	CP008739.2	2	corneal button	27727
SCVFeb	5794	CP013477.1	1	murine model	13483
LES431	6091	CP006937.1	1	missing	13335
PA11803	6565	CP015003.1	1	bloodstream	13874
PA01_Orsay	5757	LN871187.1	1	missing	13
PA8281	6408	CP015002.1	1	tracheal aspirate	13873
PA1R	5689	CP004055.1	1	missing	15639
PA1	5987	CP004054.2	1	missing	15636
PA7790	6577	CP015000.1	1	tracheal aspirate	13875
B10W	6317	CP017969.1	2	wastewater	27524
Ocean_1155	6481	CP022526.1	2	Ocean	27659

Supplementary Table S2: Single Nucleotide Polymorphisms (SNPs) observed in core genome of 22 strains of *P. aeruginosa*

<i>P. aeruginosa</i> strains	Core genome SNPs (reference to PAO1)
PA31	27547
PA32	27607
PA33	27607
PA34	28502
PA35	27608
PA37	27609
PA82	27990
PA17	13484
PA40	14442
PA149	13898
PA157	14248
PA171	13345
PA175	27411
PA55	14
PA57	46459
PA59	13844
PA64	14133
PA66	13856
PA86	13851
PA92	14129
PA100	15067
PA102	13381

Supplementary Table S3: List of resistome and associated functions

Locus tag (PA01)	Gene	Product/Function
PA0004	<i>gyrB</i>	DNA gyrase subunit B
PA0156	<i>triA</i>	Resistance-Nodulation-Cell Division (RND) triclosan efflux membrane fusion protein, TriA
PA0157	<i>triB</i>	Resistance-Nodulation-Cell Division (RND) triclosan efflux membrane fusion protein, TriB
PA0158	<i>triC</i>	Resistance-Nodulation-Cell Division (RND) triclosan efflux transporter, TriC
PA0424	<i>mexR</i>	multidrug resistance operon repressor
PA0425	<i>mexA</i>	Resistance-Nodulation-Cell Division (RND) multidrug efflux membrane fusion protein MexA precursor
PA0426	<i>mexB</i>	Resistance-Nodulation-Cell Division (RND) multidrug efflux transporter MexB
PA0427	<i>oprM</i>	Major intrinsic multiple antibiotic resistance efflux outer membrane protein OprM precursor
PA0706	<i>catB7</i>	chloramphenicol acetyltransferase
PA0903	<i>alaS</i>	alanyl-tRNA synthetase
PA0920	<i>mprF</i>	alanyl-phosphatidylglycerol synthase
PA1129	<i>fosA</i>	fosfomycin resistance protein, FosA
PA1236	<i>farB</i>	probable major facilitator superfamily (MFS) transporter
PA1282	<i>lrfA</i>	probable major facilitator superfamily (MFS) transporter
PA1316	<i>lrfA</i>	probable major facilitator superfamily (MFS) transporter
PA1435	<i>mexM</i>	probable Resistance-Nodulation-Cell Division (RND) efflux membrane fusion protein precursor
PA1436	<i>mdtC</i>	probable Resistance-Nodulation-Cell Division (RND) efflux transporter
PA1754	<i>cysB</i>	transcriptional regulator CysB
PA1972	<i>pmrC</i>	conserved hypothetical protein
PA2018	<i>mexY</i>	Resistance-Nodulation-Cell Division (RND) multidrug efflux transporter MexY
PA2019	<i>mexX</i>	Resistance-Nodulation-Cell Division (RND) multidrug efflux membrane fusion protein MexX precursor
PA2389	<i>macA</i>	Membrane fusion protein that forms an antibiotic efflux complex with MacB and TolC.
PA2390	<i>macB</i>	ATP-binding cassette (ABC) transporter
PA2391	<i>opmQ</i>	probable outer membrane protein precursor
PA2491	<i>mexS</i>	suppressor of MexT
PA2493	<i>mexE</i>	Resistance-Nodulation-Cell Division (RND) multidrug efflux membrane fusion protein MexE precursor
PA2494	<i>mexF</i>	Resistance-Nodulation-Cell Division (RND) multidrug efflux transporter MexF
PA2495	<i>oprN</i>	Multidrug efflux outer membrane protein OprN precursor
PA2525	<i>adeC</i>	outer membrane factor of the AdeABC multidrug efflux complex

Locus tag (PAO1)	Gene	Product/Function
PA2526	<i>muxC</i>	transporter that forms a heteromultimer complex with MdtB to form a multidrug transporter
PA2527	<i>muxB</i>	transporter that forms a heteromultimer complex with MdtB to form a multidrug transporter
PA2837	<i>opmA</i>	probable outer membrane protein precursor
PA3002	<i>mfd</i>	transcription-repair coupling protein Mfd
PA3019	<i>taeA</i>	probable ATP-binding component of ABC transporter
PA3137	<i>farB</i>	probable major facilitator superfamily (MFS) transporter
PA3168	<i>gyrA</i>	DNA gyrase subunit A
PA3521	<i>opmE</i>	outer membrane factor protein that is part of the multidrug efflux pump MexPQ-OpmE
PA3522	<i>mexQ</i>	inner membrane transporter of the AdeFGH multidrug efflux complex
PA3523	<i>mexP</i>	membrane fusion protein of the MexPQ-OpmE multidrug efflux complex
PA3553	<i>PmrF</i>	required for the synthesis and transfer of 4-amino-4-deoxy-L-arabinose (Ara4N) to Lipid A for resistance to polymyxin
PA3554	<i>arnA</i>	modifies lipid A with 4-amino-4-deoxy-L-arabinose (Ara4N)
PA3574	<i>nalD</i>	repressor of MexAB-OprM
PA3676	<i>mexK</i>	inner membrane resistance-nodulation-cell division (RND) transporter in the MexJK multidrug efflux protein
PA3677	<i>mexJ</i>	membrane fusion protein of the MexJK multidrug efflux protein
PA3678	<i>mexL</i>	specific repressor of mexJK transcription and autoregulates its own expression
PA3894	<i>adeC</i>	probable outer membrane protein precursor
PA3946	<i>rosC</i>	two-component sensor RocS1
PA4109	<i>ampR</i>	Transcriptional Regulator
PA4110	<i>ampC</i>	beta-lactamase precursor
PA4119	<i>APH(3')-IIb</i>	aminoglycoside 3'-phosphotransferase type IIb
PA4205	<i>mexG</i>	hypothetical protein
PA4206	<i>mexH</i>	probable Resistance-Nodulation-Cell Division (RND) efflux membrane fusion protein precursor
PA4207	<i>mexI</i>	probable Resistance-Nodulation-Cell Division (RND) efflux transporter
PA4208	<i>opmD</i>	probable outer membrane protein precursor
PA4265	<i>tufA</i>	elongation factor Tu
PA4277	<i>tufB</i>	elongation factor Tu
PA4374	<i>mexV</i>	Resistance-Nodulation-Cell Division (RND) multidrug efflux membrane fusion protein MexV
PA4375	<i>mexW</i>	Resistance-Nodulation-Cell Division (RND) multidrug efflux transporter MexW
PA4560	<i>ileS</i>	isoleucyl-tRNA synthetase
PA4595	<i>yjjk</i>	probable ATP-binding component of ABC transporter
PA4597	<i>oprJ</i>	Multidrug efflux outer membrane protein OprJ precursor

Locus tag (PAO1)	Gene	Product/Function
PA4598	<i>mexD</i>	Resistance-Nodulation-Cell Division (RND) multidrug efflux transporter MexD
PA4599	<i>mexC</i>	Resistance-Nodulation-Cell Division (RND) multidrug efflux membrane fusion protein MexC precursor
PA4600	<i>nfxB</i>	transcriptional regulator NfxB
PA4964	<i>parC</i>	topoisomerase IV subunit A
PA4967	<i>parE</i>	topoisomerase IV subunit B
PA4974	<i>opmH</i>	probable outer membrane protein precursor
PA4990	<i>emrE</i>	SMR multidrug efflux transporter
PA4997	<i>msbA</i>	transport protein MsbA
PA5158	<i>adeC</i>	probable outer membrane protein precursor
PA5160	<i>farB</i>	drug efflux transporter
PA5514	<i>OXA-50</i>	probable beta-lactamase
PA5518	<i>rosB</i>	probable potassium efflux transporter

Supplementary Table S4: List of virulence genes used in the study

Virulence genes	Functions
<i>alg44</i>	Type 4 fimbrial precursor
<i>alg8</i>	Alginate biosynthesis protein
<i>algA</i>	Alginate-c5-mannuronan-epimerase
<i>algB</i>	Phosphomannose isomerase/guanosine 5'-diphospho-D-mannose pyrophosphorylase
<i>algC</i>	Two-component response regulator
<i>algD</i>	Phosphomannomutase
<i>algE</i>	GDP-mannose 6-dehydrogenase
<i>algF</i>	Alginate biosynthetic protein AlgK precursor
<i>algG</i>	Alginate o-acetyltransferase
<i>algI</i>	Outer membrane protein
<i>algJ</i>	Alginate o-acetyltransferase
<i>algK</i>	Alginate o-acetyltransferase
<i>algL</i>	Alginate biosynthesis protein
<i>algP/algR3</i>	Poly(beta-d-mannuronate) lyase precursor
<i>algQ</i>	Alginate regulatory protein
<i>algR</i>	Alginate regulatory protein
<i>algU</i>	Alginate biosynthesis regulatory protein
<i>algW</i>	Alginate biosynthesis protein
<i>algX</i>	AlgW protein [Alginate regulation (CVF523)]
<i>algZ</i>	Alginate biosynthesis protein
<i>aprA</i>	Sigma factor
<i>aprA</i>	Sigma factor
<i>exoS</i>	Hypothetical protein
<i>exoT</i>	Type III secretion system effector
<i>exoU*</i>	Type III secretion system effector
<i>exoY</i>	Type III secretion system effector
<i>exsA</i>	Type III secretion system effector
<i>exsB</i>	Type III secretion system regulatory protein
<i>exsC</i>	Type III secretion system pilotin
<i>exsD</i>	Type III secretion system regulatory protein
<i>exsE</i>	Type III secretion system regulatory protein
<i>fleI/flag</i>	FimX [type IV pili (AI097)]
<i>fleN</i>	Flagellar protein FlaG [Deoxyhexose linking sugar]
<i>fleP</i>	Flagellar synthesis regulator
<i>fleQ</i>	Flagellar protein
<i>fleR</i>	Transcriptional regulatore
<i>fleS</i>	Two-component response regulator
<i>flgA</i>	Two-component sensor [Deoxyhexose linking sugar, 209 linking sugar, island]
<i>flgB</i>	Flagellar basal body P-ring biosynthesis protein linking Da
<i>flgC</i>	Flagellar basal body rod protein

Virulence genes	Functions
<i>flgD</i>	Flagellar basal-body rod protein
<i>flgE</i>	Flagellar basal-body rod modification protein
<i>flgF</i>	Flagellar hook protein
<i>flgG</i>	Flagellar basal-body rod protein
<i>flgH</i>	Flagellar basal-body rod protein
<i>flgI</i>	Flagellar L-ring protein precursor
<i>flgJ</i>	Flagellar P-ring protein precursor
<i>flgK</i>	Flagellar rod assembly protein/muramidase
<i>flgL</i>	Flagellar hook-associated protein 1
<i>flgM</i>	Flagellar hook-associated protein 3
<i>flgN</i>	Negative regulator of flagellin synthesis
<i>flhA</i>	Flagella synthesis protein
<i>flhB</i>	Flagellar biosynthesis protein
<i>flhF</i>	Flagellar biosynthetic protein
<i>fliA</i>	Flagellar biosynthesis protein
<i>fliC</i>	Flagellar biosynthesis sigma factor
<i>fliD</i>	B-type flagellin
<i>fliE</i>	Flagellar capping protein
<i>fliF</i>	Flagellar hook-basal body complex protein
<i>fliG</i>	Flagellar M-ring protein
<i>fliH</i>	Flagellar motor switch protein G
<i>fliI</i>	Flagellar assembly protein H
<i>fliJ</i>	Flagellum-specific ATP synthase
<i>fliK</i>	Flagellar protein
<i>fliL</i>	Flagellar hook-length control protein
<i>fliM</i>	Flagellar basal body protein
<i>fliN</i>	Flagellar motor switch protein
<i>fliO</i>	Flagellar motor switch protein
<i>fliP</i>	Flagellar protein
<i>fliQ</i>	Flagellar biosynthetic protein
<i>fliR</i>	Flagellar biosynthetic protein
<i>fliS</i>	Flagellar biosynthetic protein
<i>fliT</i>	Flagellar biosynthetic protein
<i>gacA</i>	Response regulator
<i>gacS</i>	Sensor/response regulator hybrid
<i>hdtS</i>	Hypothetical protein
<i>lasA</i>	Hypothetical protein
<i>lasB</i>	LasA protease precursor
<i>lasI</i>	Elastase
<i>lasR</i>	Autoinducer synthesis protein
<i>lepA</i>	<i>Pseudomonas aeruginosa</i> -derived large extracellular protease

Virulence genes	Functions
<i>motA</i>	MbtH-like protein from the pyoverdine cluster
<i>motB</i>	Flagellar motor protein
<i>motC</i>	Flagellar motor protein
<i>motD</i>	Flagellar motor protein
<i>motY</i>	Flagellar motor protein
<i>mucA</i>	Probable outer membrane protein precursor
<i>mucB</i>	Alkaline metalloproteinase precursor
<i>mucC</i>	Anti-sigma factor MucA, inhibitor of alg gene activity
<i>mucD</i>	Negative regulator for alginate biosynthesis
<i>mucE</i>	Serine protease MucD precursor
<i>mucP</i>	Small envelope protein
<i>mvfR</i>	Transcriptional regulator
<i>ndVB</i>	Required for the synthesis of periplasmic glucans, and involved in biofilm-specific resistance to a subset of antibiotics
<i>pasP</i>	Small protease
<i>pcr1</i>	Transcriptional regulator
<i>pcr2</i>	Type III secretion system protein
<i>pcr3</i>	Type III secretion system protein
<i>pcr4</i>	Type III secretion system protein
<i>pcrD</i>	Type III secretion system protein
<i>pcrG</i>	Type III secretion system protein
<i>pcrH</i>	Type III secretion system cytoplasmic regulator
<i>pcrR</i>	Type III secretion system regulatory protein
<i>pcrV</i>	Type III secretion system regulatory protein
<i>phnA</i>	Anthranilate synthase component I
<i>phnB</i>	Anthranilate synthase component II
<i>phzM</i>	Phenazine-modifying enzyme
<i>phzS</i>	Phenazine-specific methyltransferase
<i>plcB</i>	Phospholipase C,
<i>plcH</i>	Hemolytic phospholipase C precursor
<i>plcN</i>	Non-hemolytic phospholipase C precursor
<i>pldA</i>	Phospholipase D
<i>popB</i>	Type III secretion system hydrophobic translocator, pore
<i>popD</i>	Type III secretion system hydrophobic translocator, pore
<i>popN</i>	Type III secretion system outer membrane protein
<i>pqsA</i>	Pseudomonas quinolone signal response
<i>pqsB</i>	Pseudomonas quinolone signal response
<i>pqsC</i>	Quinolone signal biosynthesis
<i>pqsD</i>	Quinolone signal biosynthesis
<i>pqsE</i>	Pseudomonas quinolone signal response
<i>pqsH</i>	FAD-dependent monooxygenase
<i>pqsL</i>	Putative monooxygenase

Virulence genes	Functions
<i>pscB</i>	Type III secretion system protein
<i>pscC</i>	Type III secretion system secretin
<i>pscD</i>	Type III secretion system basal body protein
<i>pscE</i>	Type III secretion system cochaperone
<i>pscF</i>	Type III secretion system needle filament protein
<i>pscG</i>	Type III secretion system chaperone
<i>pscH</i>	Type III secretion system protein
<i>pscI</i>	Type III secretion system inner rod protein
<i>pscJ</i>	Type III secretion system inner MS ring IV
<i>pscK</i>	Type III secretion system protein
<i>pscL</i>	Type III secretion system protein
<i>pscN</i>	Type III secretion system ATPase
<i>pscO</i>	Type III secretion system protein
<i>pscP</i>	Type III secretion system protein
<i>pscQ</i>	Type III secretion system protein
<i>pscR</i>	Type III secretion system protein
<i>pscS</i>	Type III secretion system protein
<i>pscT</i>	Type III secretion system protein
<i>pscU</i>	Translocation protein in type III secretion
<i>pvdE</i>	Pyoverdine biosynthesis protein
<i>rhlI</i>	Autoinducer synthesis protein
<i>rhlR</i>	Transcriptional regulator
<i>toxA</i>	Exotoxin A precursor
<i>tssC1</i>	Type VI secretion protein
<i>vgrG3</i>	Hypothetical protein

*All the genes are from *P. aeruginosa* PAO1 except for *exoU* for which *P. aeruginosa* UCBPP-PA14 is taken as reference.

Supplementary Table S5: Multi-locus sequence typing (MLST) allelic profiles and sequence type of *P. aeruginosa* strains

<i>P. aeruginosa</i> strain	Strain group	Allelic type							Sequence type (ST)
		<i>acsA</i>	<i>aroE</i>	<i>guaA</i>	<i>mutL</i>	<i>nuoD</i>	<i>ppsA</i>	<i>trpE</i>	
PA17	Eye/Australia	16	5	11	1	2	7	2	New
PA31	Eye/India	13	4	5	5	12	7	15	308
PA32	Eye/India	13	4	5	5	12	7	15	308
PA33	Eye/India	13	4	5	5	12	7	15	308
PA34	Eye/India	32	8	5	3	5	6	26	1284
PA35	Eye/India	13	4	5	5	12	7	15	308
PA37	Eye/India	13	4	5	5	12	7	15	308
PA40	Eye/Australia	15	5	36	72	1	42	19	New
PA55	Cystic fibrosis/Australia	7	5	12	3	4	1	7	549
PA57	Cystic fibrosis/Australia	111	30	31	26	48	59	32	New
PA59	Cystic fibrosis/Australia	11/151	84	11	3	4	4	7	New (59)
PA64	Cystic fibrosis/Australia	28	5	11	5	4	4	7	775
PA66	Cystic fibrosis/Australia	11/151	84	11	3	4	4	7	New (59)
PA82	Eye/India	32	5	61	13	1	6	54	1027
PA86	Cystic fibrosis/Australia	11/151	84	11	3	4	4	7	New (59)
PA92	Cystic fibrosis/Australia	28	5	11	5	4	4	7	775
PA100	Cystic fibrosis/Australia	116	5	6	5	3	12	68	483
PA102	Cystic fibrosis/Australia	28	24	91	5	4	4	14	1717
PA149	Eye/Australia	28	New	12	3	4	12	3	New
PA157	Eye/Australia	17	5	11	18	4	10	3	386
PA171	Eye/Australia	17	5	11	5	4	4	2	471
PA175	Eye/Australia	13	8	9	3	1	17	15	309

(59) new but like PA59