

Assignment of *emm* type, subtype, predicted pattern and predicted cluster:

1. *emm* types and *emm* subtypes

Beginning in March 2015, all new isolate submissions will require an *emm* type.

The ***emm* type** needs to be in the new "numeric" format.

A number should be entered into the isolate template xls file. The only exception to a numerical value is for *emm* types derived from another streptococcal species (e.g., stG6).

***emm* subtype** assignments are optional, but most welcome. They should be listed in the isolate template xls file in the following format: *emm*##

E.g., *emm*5.32 or *emm*103.1

Please examine the "isolates database" if you are unsure of the proper formats.

A guide for conversion of old *emm* sequence types (st) into numerals can be found here: <http://www.cdc.gov/streplab/types-emm103-124.html>

Queries on *emm* types and *emm* subtypes can be made through the C.D.C. BLAST server. Assignments requires 100% sequence identity (over 150 nt):

<http://www2a.cdc.gov/ncidod/biotech/strepblast.asp>

2. Predicted *emm* pattern

The "isolates database" allows for entry of "predicted *emm* pattern" based on:

[Multilocus sequence typing of *Streptococcus pyogenes* representing most known *emm* types and distinctions among subpopulation genetic structures.](#) McGregor KF, Spratt BG, Kalia A, Bennett A, Bilek N, Beall B, Bessen DE. J Bacteriol. 2004 Jul;186(13):4285-94.

[Updated model of group A *Streptococcus M* proteins based on a comprehensive worldwide study.](#) McMillan DJ, Drèze PA, Vu T, Bessen DE, Guglielmini J, Steer AC, Carapetis JR, Van Melder L, Sriprakash KS, Smeesters PR. Clin Microbiol Infect. 2013 May;19(5):E222-9.

This field is optional, but most welcome.

There are 4 choices: A-C, D, E, REA (rearranged)

Predicted <i>emm</i> patterns based on <i>emm</i> types								
A-C		D			E			REA
1	51	32	86	172	2	76	114	170
3	55	33	91	179	4	77	117	174
5	57	34	93	181	8	78	118	
6	137	36	95	182	9	79	124	
12	139	41	97	184	11	82	144	
14	142	42	98	185	13	84	164	
17	157	43	99	186	15	87	165	
18	163	52	100	186	22	88	166	
19	193	53	101	191	25	89	168	
23	197	56	105	192	27	90	169	
24	222	56	108	194	28	92	175	
26	226	59	111	205	44	96	176	
29	228	64	115	207	48	102	177	
30	229	65	116	208	49	103	180	
37	233	67	119	213	50	104	183	
38	233	70	120	217	58	106	209	
39	238	71	121	221	60	107	211	
46	239	72	122	223	63	109	215	
47		74	123	224	66	110	231	
		80	134	225	68	112	232	
		81	140	230	73	113	236	
		83	158	242	75			
		85						

3. Predicted *emm* cluster

The "isolates database" allows for entry of "predicted *emm* cluster" based on:

[A systematic and functional classification of *Streptococcus pyogenes* that serves as a new tool for molecular typing and vaccine development.](#) Sanderson-Smith M, De Oliveira DM, Guglielmini J, McMillan DJ, Vu T, Holien JK, Henningham A, Steer AC, Bessen DE, Dale JB, Curtis N, Beall BW, Walker MJ, Parker MW, Carapetis JR, Van Melder L, Sriprakash KS, Smeesters PR; M Protein Study Group. J Infect Dis. 2014 Oct 15;210(8):1325-38

This field is optional, but most welcome.

Singletons and outliers should be listed in the isolate template xls file in the format exemplified by: "clade_Y_M6" and "outlier_M55"

Please examine the "isolates database" if you are unsure of the proper formats.

clade	<i>emm</i> cluster	<i>emm</i> types represented
X	E1	4, 60, 78, 165, 176
X	E2	13, 27, 50, 66, 68, 76, 90, 92, 96, 104, 106, 110, 117, 166, 168
X	E3	9, 15, 25, 44, 49, 58, 79, 82, 87, 103, 107, 113, 118, 144, 180, 183, 209, 219, 231
X	E4	2, 8, 22, 28, 73, 77, 84, 88, 89, 102, 109, 112, 114, 124, 169, 175, 232
X	E5	34, 51, 134, 137, 170, 174, 205
X	E6	11, 42, 48, 59, 63, 65, 67, 75, 81, 85, 94, 99, 139, 158, 172, 177, 182, 191
X	Singletons	164, 185, 211, 236
Y	D1	36, 54, 207
Y	D2	32, 71, 100, 115, 213
Y	D3	123, 217
Y	D4	33, 41, 43, 52, 53, 56, 56, 64, 70, 72, 80, 83, 86, 91, 93, 98, 101, 108, 116, 119, 120, 121, 178, 186, 192, 194, 208, 223, 224, 225, 230, 242
Y	D5	97, 157, 184
Y	A-C1	46, 142
Y	A-C2	30, 197
Y	A-C3	1, 163, 227, 238, 239
Y	A-C4	12, 39, 193, 228, 229
Y	A-C5	3, 31, 133
Y	Singletons	5, 6, 14, 17, 18, 19, 23, 24, 26, 29, 37, 38, 47, 57, 74, 105, 122, 140, 179, 218, 233, 234
Outliers	Outliers	55, 95, 111, 215, 221, 222