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FACA Panel Item #	ALM Item #	Code Type	Category	Code #	Final Code #	Long Code Descriptor	CDLT Panel Voting Results	CMS 2021 Preliminary Recommendation	Rationale	CMS 2021 Final Determination	Rationale
1	7		Proprietary Laboratory Analyses/ Immunology	0226U	0226U	Surrogate viral neutralization test (sVNT), severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]), ELISA, plasma, serum	1. Crosswalk to: 86769: 12	Gapfill	CMS disagrees with the recommendation of the CDLT Panel and recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).	Gapfill	Finalize as proposed. CMS continues to disagree with the recommendation of the CDLT Panel and recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
2	8	NEW	Immunology / Immunology	86413	86413	Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]) amibody.quantitative	1. Crosswalk to: 86769 x 1.25: 3 2. Crosswalk to 86769 x 2: 8 3. Abstain: 1	Gapfill	CMS disagrees with the recommendation of the CDLT Panel and recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).	Gapfill	Finalize as proposed. After reviewing public comments, CMS continues to believe gapfilling this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC) as the public health emergency continues.
3	63	NEW	Immunology / Immunology	863X4	86381	Mitochondrial antibody (cg, M2), each	1. Crosswalk to 86146: 12	Crosswalk to 86146	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 86146	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.
4	64	NEW	Immunology / Immunology	865X0	86596	Voltage-gated calcium channel antibody, each	1. Crosswalk to 84586: 12	Crosswalk to 83519	CMS disagrees with the Panel Recommendation and instead is recommending a different crosswalk. Currently a VGCC antibody panel is billed using 83519x2 and looks at 2 antibiodies. Therefore, CMS recommends that for each VGCC antibody, the crosswalk should be to 83519x1.	Crosswalk to 83519	Finalize as proposed. After reviewing public comments, CMS continues to believe a crosswalk to CPT 83519 is appropriate. CMS believes the methods are similar between the two codes.
5	65	NEW	Immunology / Immunology	86XX0	86015	Actin (smooth muscle) antibody (ASMA), each	1. Crosswalk to 86146: 2 2. Crosswalk to 83516: 10	Crosswalk to 83516	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 83516	Finalize as proposed. After reviewing public comments CMS continues to recommend a crosswalk to CPT 83516. We believe there are similar methods between the two codes.
6	66	NEW	Immunology / Immunology	86X00	86036	Antineutrophil cytoplasmic antibody (ANCA); screen, each antibody	1. Crosswalk to 86146: 2 2. Crosswalk to 86255: 10	Crosswalk to 86255	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 86255	Finalize as proposed. After reviewing public comments CMS continues to recommend a crosswalk to CPT 86255. We believe there are similar methods between the two codes.
7	67	NEW	Immunology / Immunology	86X01	86037	Antineutrophil cytoplasmic antibody (ANCA); titer, each antibody	1. Crosswalk to 86256: 12	Crosswalk to 86256	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 86256	Finalize as proposed. After reviewing public comments CMS continues to recommend a crosswalk to CPT 86256. We believe there are similar methods between the two codes.
8	79		Proprietary Laboratory Analyses: Immunology/ Immunology	0X65U	0275U	Hematology (heparin-induced thrombocytopenia) platelet antibody reactivity by flow cytometry, serum	1. Gapfill: 12	Crosswalk to 86022	CMS disagrees with the Panel Recommendation and instead is recommending a crosswalk. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 86022	CDLT Panel and recommends an alternate crosswalk. CMS believes the methods are similar between the two codes.
9	80	NEW	Proprietary Laboratory Analyses: Immunology/ Immunology	0X66U	0280U	Hematology (von Willebrand disease [VWD]), von Willebrand factor (VWF) and collagen IV binding by enzyme-linked immunosorbent assays (ELISA), plasma, report of collagen IV binding	1. Crosswalk to 83520: 11 2. Abstain: 1	Crosswalk to 83520	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 83520	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.
10	81	NEW	Proprietary Laboratory Analyses: Immunology/ Immunology	0X67U	0281U	Hematology (von Willebrand disease [VWD]), von Willebrand propeptide, enzyme- linked mmunosorbent assays (ELISA), plasma, diagnostic report of von Willebrand factor (VWF) propeptide antigen level	1. Crosswalk to 83520: 6 2. Crosswalk to 85246: 5 3. Abstain: 1	Crosswalk to 83520	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 83520	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.
11	82	NEW	Proprietary Laboratory Analyses: Immunology/ Immunology	0X68U	0283U	von Willebrand factor (VWF), type 2B, platelet-binding evaluation, radioimmunoassay, plasma	1. Crosswalk to 83519: 11 2. Abstain: 1	Crosswalk to 83519	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 83519	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.
12	83	NEW	Proprietary Laboratory Analyses: Immunology/ Immunology	0X69U	0284U	von Willebrand factor (VWD), type 2N, factor VIII and VWF binding evaluation, enzyme-linked immunosorbent assays (ELISA), plasma	1. Crosswalk to 83520: 1 2. Crosswalk to 85246 x 1.5: 4 3. Crosswalk to 85246 x 2: 6	Crosswalk to 83520	CMS agrees with the minority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 83520	Finalize as proposed. CMS agrees with the minority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.
13	40	NEW	Immunology / Immunology	860XX	86051	Aquaporin-4 (neuromyelitis optica [NMO]) antibody; enzyme-linked immunosorbent immunoassay (ELISA)	1. Crosswalk to 86146: 11 2. Abstain: 1	Crosswalk to 83516	CMS disagrees with the Panel Recommendation and instead is recommending a crosswalk. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 83516	Finalize as proposed. After reviewing public comments CMS continues to recommend a crosswalk to CPT 83516. We believe there are similar methods between the two codes.
14					86052	Aquaporin-4 (neuromyelitis optica [NMO]) antibody; cell-based immunofluorescence assay (CBA), each	2. Abstain: 1	Crosswalk to 86255	CMS disagrees with the Panel Recommendation and instead is recommending a crosswalk. The crosswalked code(s) appear to use similar methods and resource utilization.		Finalize as proposed. After reviewing public comments CMS continues to recommend a crosswalk to CPT 86255. We believe there are similar methods between the two codes.
15					86053	Aquaporin-4 (neuromyelitis optica [NMO]) antibody; flow cytometry (ie, fluorescence activated cell sorting [FACS]), each	2. Abstain: 1	Crosswalk to 86255	CMS disagrees with the Panel Recommendation and instead is recommending a crosswalk. The crosswalked code(s) appear to use similar methods and resource utilization.		Finalize as proposed. After reviewing public comments CMS continues to recommend a crosswalk to CPT 86255. We believe there are similar methods between the two codes.
16	43	NEW	Immunology / Immunology	863X2	86362	Myelin oligodendrocyte glycoprotein (MOG-IgGI) antibody; cell-based immunofluorescence assay (CBA), each	1. Crosswalk to 86357: 11 2. Abstain: 1	Crosswalk to 86255	CMS disagrees with the Panel Recommendation and instead is recommending a crosswalk. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 86255	Finalize as proposed. After reviewing public comments CMS continues to recommend a crosswalk to CPT 86255. We believe there are similar methods between the two codes.

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17	44	NEW	Immunology / Immunology	863X3	86363	Myelin oligodendrocyte glycoprotein (MOG-IgG1) antibody; flow cytometry (ie, fluorescence-activated cell sorting [FACS]), each	1. Crosswalk to 86367: 11 2. Abstain: 1	Crosswalk to 86255	CMS disagrees with the Panel Recommendation and instead is recommending a crosswalk. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 86255	Finalize as proposed. After reviewing public comments CMS continues to recommend a crosswalk to CPT 86255. We believe there are similar methods between the two codes.
18	45		Immunology / Immunology	862X0	86231	Endomysial antibody (EMA), each immunoglobulin (Ig) class	1. Crosswalk to 86038: 5 2. Crosswalk to 86038 x 2: 6 3. Abstain: 1	Crosswalk to 86038	CMS agrees with the minority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 86038	a crosswalk to CPT 86038. We believe there are similar methods between the two codes.
19	46	NEW	Immunology / Immunology	862XX	86258	Gliadin (deamidated) (DGP) antibody, each immunoglobulin (Ig) class	1. Crosswalk to 86147: 11 2. Abstain: 1	Crosswalk to 83516	CMS disagrees with the Panel Recommendation and instead is recommending a crosswalk. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 83516	Finalize as proposed. After reviewing public comments CMS continues to recommend a crosswalk to CPT 83516. We believe there are similar methods between the two codes.
20	47	NEW	Immunology / Immunology	862X1	86364	Tissue transglutaminase, each immunoglobulin (Ig) class	1. Crosswalk to 86147: 11 2. Abstain: 1	Crosswalk to 83516	CMS disagrees with the Panel Recommendation and instead is recommending a crosswalk. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 83516	Finalize as proposed. After reviewing public comments CMS continues to recommend a crosswalk to CPT 83516. We believe there are similar methods between the two codes.
21	98	NEW	Proprietary Laboratory Analyses: Immunology/ Immunology	0X85U	0279U	Hernatology (von Willebrand disease [VWD]), von Willebrand factor (VWF) and collagen III binding by enzyme-linked immunosorbent assays (ELISA), plasma, report of collagen III binding	1. Crosswalk to 83520: 4 2. Crosswalk to 85246: 7 3. Abstain: 1	Crosswalk to 83516	CMS disagrees with the Panel Recommendation and instead is recommending a crosswalk. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 83516	Finalize as proposed. CMS continues to disagrees with the recommendation of the CDLT Panel and recommends an alternate crosswalk. CMS believes the methods are similar between the two codes.
22	4	NEW	Immunology / Immunology	86408	86408	Neutralizing antibody, severe acute respiratory syndrome coronavirus 2 (SARS-CoV- 2) (Coronavirus disease [COVID-19]); sereen	1. Crosswalk to 86769: 1 2. Gapfill: 11	Gapfill	CMS agrees with the majority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).	Gapfill	Finalize as proposed. After reviewing public comments, CMS continues to believe gapfilling this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC)as the public health emergency continues.
23	5	NEW	Immunology / Immunology	86409	86409	Neutralizing antibody, severe acute respiratory syndrome coronavirus 2 (SARS-CoV- 2) (Coronavirus disease [COVID-19]); titer	1. Gapfill: 12	Gapfill	CMS agrees with the majority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).	Gapfill	Finalize as proposed. After reviewing public comments, CMS continues to believe gapfilling this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC)as the public health emergency continues.
24	1	NEW	Microbiology: Immunoassay/ Microbiology	87426	87426	Infectious agent antigen detection by immunoassay technique, (eg. enzyme immunoassay [EIA], enzyme-linked immunosorbent assay [ELISA], immunochemiluminometric assay [IMCA]) qualifative or semiquantitative, multiple- step method, severe acute respiratory syndrome coronavirus (eg. SARS-CoV, SARS- CoV-2 [COVID-19])	1. Crosswalk to 87430 x 2.5: 1 2. Crosswalk to 87430 x 2: 11	Gapfill	CMS disagrees with the recommendation of the CDLT Panel and recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).	Gapfill	Finalize as proposed. After reviewing public comments, CMS continues to believe gapfilling this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC)as the public health emergency continues.
25	2	NEW	Proprietary Laboratory Analyses: Microbiology/ Microbiology	0223U	0223U	Infectious disease (bacterial or viral respiratory tract infection), pathogen-specific nucleic acid (DNA or RNA), 22 targets including severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), qualitative RT-PCR, masopharyngeal swab, each pathogen reported as detected or not detected	1. Crosswalk to 87633: 12	Crosswalk to 87633	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 87633	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.
26	3	NEW	Proprietary Laboratory Analyses: Microbiology/ Microbiology	0224U	0224U	Antibody, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]), includes titer(s), when performed	1. Crosswalk to 86769: 11 2. Abstain: 1	Gapfill	CMS disagrees with the recommendation of the CDLT Panel and recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).	Gapfill	Finalize as proposed. CMS continues to disagree with the recommendation of the CDLT Panel and recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
27	9	NEW	Proprietary Laboratory Analyses: Microbiology/ Microbiology	0240U	0240U	Infectious disease (viral respiratory tract infection), pathogen-specific RNA, 3 targets (severe acute respiratory syndrome coronavirus 2 [SARS-CoV-2], influenza A, influenza B), upper respiratory specimen, each pathogen reported as detected detected	1. Crosswalk to 87631: 11 2. Abstain: 1	Crosswalk to 87631	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 87631	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.
28	10	NEW	Proprietary Laboratory Analyses: Microbiology/ Microbiology	0241U	0241U	Infectious disease (viral respiratory tract infection), pathogen-specific RNA, 4 targets (severe acute respiratory syndrome coronavirus 2 [SARS-CoV-2], influenza A, influenza B, respiratory snychial virus [RSV]), upper respiratory specimen, each pathogen reported as detected or not detected	1. Crosswalk to 87631:11 2. Abstain: 1	Crosswalk to 87631	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.		Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.
29			Microbiology/ Microbiology		87636	Infectious agent detection by nucleic acid (DNA or RNA); severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]) and influenza virus types A and B, multiplex amplified probe technique	1. Crosswalk to 87631: 11 2. Abstain: 1	Crosswalk to 87631	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.		Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.
30	58	NEW	Microbiology/ Microbiology	87637	87637	Infectious agent detection by nucleic acid (DNA or RNA); severe acute respiratory syndrome coronavinus 2 (SARS-CoV-2) (Coronavinus disease [COVID-19]), influenza virus types A and B, and respiratory syncytial virus, multiplex amplified probe technique	1. Crosswalk to 87631: 11 2. Abstain: 1	Crosswalk to 87631	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 87631	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.
31	60	NEW	Microbiology/ Microbiology	87811	87811	Infectious agent antigen detection by immunoassay with direct optical (ie, visual) observation; severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19])	1. Crosswalk to 87804 x 2.5: 1 2. Crosswalk to 87804 x 2: 11	Gapfill	CMS disagrees with the recommendation of the CDLT Panel and recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).	Gapfill	After reviewing public comments, CMS continues to believe gapfilling this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC)as the public health emergency continues.
32	68	NEW	Microbiology/ Microbiology	8715X	87154	Culture, typing; identification of blood pathogen and resistance typing, when performed, by nacleic acid (DNA or RNA) probe, multiplexed amplified probe technique including multiplex reverse transcription, when performed, per culture or isolate. 6 or more targets	1. Crosswalk to 87506: 11 2. Gapfill: 1	Crosswalk to 87632	CMS disagrees with the majority CDLT Panel recommended crosswalk for this code. Instead, CMS recommends a different crosswalk that appears to use similar methods and resource utilization.	Crosswalk to 87632	Finalize as proposed. CMS continues to disagree with the recommendation of the CDLT Panel and recommends an alternate crosswalk. CMS believes the methods are similar between the two codes.
33	59		Microbiology/ Microbiology		87428	Infectious agent antigen detection by immunoassay technique, (eg, enzyme immunoassay [EIA], enzyme-linked immunosorbent assay [ELSA], fluorescence immunoassay [FIA], immunochemiluminometric assay [IMCA]) qualitative or semiquarifiative; severe acute respiratory syndrome coronavirus (eg, SARS-CoV,	1. Crosswalk to 87430 x2.5 + 87400 x 2: 2 2. Crosswalk to 87430 x 2 + 87400 x 2: 10	Crosswalk to 87400+87449	CMS agrees with the recommended crosswalk codes for this test, but disagrees with the use of multipliers.	Crosswalk to 87430+87400	After additional review and further consideration, CMS agrees with the majority recommendation of the CDLT Panel to crosswalk this code, but without the use of the multipliers. The crosswalked code(s) appear to use similar methods and resource utilization.
34	11	NEW	Proprietary Laboratory Analyses Chemistry / Drug Testing, Metabolism and Therapeutic monitoring	0227U	0227U	Drug assay, presumptive, 30 or more drugs or metabolites, urine, liquid chromatography with tandem mass spectrometry (LC-MS/MS) using multiple reaction monitoring (MRM), with drug or metabolite description, includes sample validation	1. Crosswalk to 80307: 12	Crosswalk to 80307	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.	Crosswalk to 80307	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.

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Panel	Item #		Category	Couc #	r mai coue #	Long Code Descriptor	CDET Tallet voting Results	Preliminary	Rational	Determination	Rationale
	Item #	Туре								Determination	
Item #								Recommendation			
35	53	Reconsi	Other Methods of	81338	81338	MPL (MPL proto-oncogene, thrombopoietin receptor) (eg, myeloproliferative	1. Crosswalk to 81120: 12	Crosswalk to 81402	CMS disagrees with the recommendation of the CDLT Panel and commenters to	Crosswalk to 81402	Finalize as proposed. CMS continues to disagree with the recommendation of the
		dered	Sequencing: Common			disorder) gene analysis; common variants (eg, W515A, W515K, W515L, W515R)			crosswalk molecular pathology tests to different gene analysis tests. In the most recent		CDLT Panel and recommends an alternate crosswalk. CMS believes the methods are
			variants / Other Methods of						years, CMS utilized codes known as "Tier 2 molecular pathology" test codes as		similar between the two codes.
			Sequencing/ Reconsidered						crosswalks for these types of tests. Tier 2 molecular pathology test codes are based on		
26	54	Reconsi	Other Methods of	81339	81339	MPL (MPL proto-oncogene, thrombopoietin receptor) (eg, myeloproliferative	1. Crosswalk to 81310: 12	Crosswalk to 81403	CMS disagrees with the recommendation of the CDLT Panel and commenters to	Creaseruslly to \$1402	Finalize as proposed. CMS continues to disagree with the recommendation of the
50	54			81339	01559		1. Closswaik to 81310. 12	Closswalk to 81405	crosswalk molecular pathology tests to different gene analysis tests. In the most recent	Closswalk to 81405	
		dered	Sequencing: Targeted			disorder) gene analysis; sequence analysis, exon 10					CDLT Panel and recommends an alternate crosswalk. CMS believes the methods are
			sequence analysis / Other						years, CMS utilized codes known as "Tier 2 molecular pathology" test codes as		similar between the two codes.
			Methods of Sequencing /						crosswalks for these types of tests. Tier 2 molecular pathology test codes are based on		
37	61	NEW	Therapeutic Drug Assay /	801XX	80220	Hydroxychloroquine	1. Crosswalk to 80204: 12	Crosswalk to 80299	CMS disagrees with the majority CDLT Panel recommended crosswalk for this code.	Crosswalk to 80299	Finalize as proposed. CMS continues to disagree with the recommendation of the
			Drug testing, Metabolism and						Instead, CMS recommends a different crosswalk that appears to use similar methods		CDLT Panel and recommends an alternate crosswalk. CMS believes the methods are
			Therapeutic monitoring						and resource utilization.		similar between the two codes.
38	32	NEW	Proprietary Laboratory	0248U	0248U	Oncology (brain), spheroid cell culture in a 3D microenvironment, 12 drug panel,	1. Gapfill: 12	Gapfill	CMS agrees with the majority recommendation of the CDLT Panel to gapfill this code	Ganfill	Finalize as proposed. CMS agrees with the majority recommendation of the CDLT
50	22		Analyses Oncology	02100	02100	tumor-response prediction for each drug	1. Ouplin: 12	Cupin	so that the resources used in this code can be better estimated by a Medicare	oupini	Panel to gapfill this code so that the resources used in this code can be better estimated
			therapeutic response / Drug			ranor-response prediction for each drug			Administrative Contractor (MAC).		by a Medicare Administrative Contractor (MAC).
									Administrative Contractor (MAC).		by a Medicare Administrative Contractor (MAC).
			Testing, Metabolism and								
39	48	Reconsi	Chemistry: Drug Testing,	80151	80151	Amiodarone	1. Crosswalk to 80155: 12	Crosswalk to 80299	CMS disagrees with the majority CDLT Panel recommended crosswalk for this code.	Crosswalk to 80299	Finalize as proposed. CMS continues to disagree with the recommendation of the
		dered	Monitoring / Drug Testing,						CMS continues to believe the original crosswalk recommendation is appropriate for this		CDLT Panel and recommends an alternate crosswalk. CMS believes the methods are
			Metabolism and Therapeutic						test.		similar between the two codes.
			monitoring / Reconsidered								
40	49	Reconsi	Chemistry: Drug Testing,	80161	80161	Carbamazepine; 10,11-epoxide	1. Crosswalk to 80155: 12	Crosswalk to 80299	CMS disagrees with the majority CDLT Panel recommended crosswalk for this code.	Crosswalk to 80299	Finalize as proposed. CMS continues to disagree with the recommendation of the
		dered	Monitoring / Drug Testing,						CMS continues to believe the original crosswalk recommendation is appropriate for this		CDLT Panel and recommends an alternate crosswalk. CMS believes the methods are
			Metabolism and Therapeutic						test		similar between the two codes.
			monitoring / Reconsidered								sinnan between nie two codes.
41	50	n		80167	80167	Felbamate	1. Crosswalk to 80199: 12	Crosswalk to 80299	CMC I I I C I I C I I C I I C I I C I I C I I C I	Crosswalk to 80299	E E E E E E E E E E E E E E E E E E E
41	50	Reconsi	Chemistry: Drug Testing,	80107	80107	reibamate	1. Crosswaik to 80199: 12	Crosswaik to 80299	CMS disagrees with the majority CDLT Panel recommended crosswalk for this code.	Crosswalk to 80299	Finalize as proposed. CMS continues to disagree with the recommendation of the
		dered	Monitoring / Drug Testing,						CMS continues to believe the original crosswalk recommendation is appropriate for this		CDLT Panel and recommends an alternate crosswalk. CMS believes the methods are
			Metabolism and Therapeutic						test.		similar between the two codes.
			monitoring / Reconsidered								
42	51	Reconsi	Chemistry: Drug Testing,	80181	80181	Flecainide	1. Crosswalk to 80193: 2	Crosswalk to 80299	CMS disagrees with the majority CDLT Panel recommended crosswalk for this code.	Crosswalk to 80299	Finalize as proposed. CMS continues to disagree with the recommendation of the
		dered	Monitoring / Drug Testing,				2. Crosswalk to 80155: 10		CMS continues to believe the original crosswalk recommendation is appropriate for this		CDLT Panel and recommends an alternate crosswalk. CMS believes the methods are
			Metabolism and Therapeutic						test		similar between the two codes.
			monitoring / Reconsidered								
43	52	Reconsi	Other Methods of	81279	81279	JAK2 (Janus kinase 2) (eg, myeloproliferative disorder) targeted sequence analysis	1. Crosswalk to 81272: 11	Crosswalk to 81403	CMS disagrees with the majority CDLT Panel recommended crosswalk for this code.	Crosswalk to 81403	Finalize as proposed. CMS continues to disagree with the recommendation of the
7.5	52	dered	Sequencing: Targeted	01277	01277	(eg, exons 12 and 13)	2. Crosswalk to 81403: 1	Closswalk to 01405	CMS onsugrees while majorky CDET Faller recommendation is appropriate for this	C1055walk to 01405	CDLT Panel and recommends an alternate crosswalk. CMS believes the methods are
		dered				(eg, exons 12 and 15)	2. Crosswaik to 81405: 1		CNIS continues to believe the original crosswalk recommendation is appropriate for this		
			sequence analysis / Other						test.		similar between the two codes.
			Methods of Sequencing/								
44	6	NEW	Proprietary Laboratory	0225U	0225U	Infectious disease (bacterial or viral respiratory tract infection) pathogen-specific	1. Crosswalk to 87633: 12	Crosswalk to 87633	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code.	Crosswalk to 87633	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to
			Analyses: Molecular			DNA and RNA, 21 targets, including severe acute respiratory syndrome coronavirus 2			The crosswalked code(s) appear to use similar methods and resource utilization.		crosswalk the code. The crosswalked code(s) appear to use similar methods and
			Pathology (Other than GSP			(SARS-CoV-2), amplified probe technique, including multiplex reverse transcription					resource utilization.
			or MAAA)			for RNA targets, each analyte reported as detected or not detected					
45	12	NEW	Proprietary Laboratory	0228U	0228U	Oncology (prostate), multianalyte molecular profile by photometric detection of	1. Gapfill: 11	Gapfill	CMS agrees with the majority recommendation of the CDLT Panel to gapfill this code	Ganfill	Finalize as proposed. CMS agrees with the majority recommendation of the CDLT
			Analyses: Molecular			macromolecules adsorbed on nanosponge array slides with machine learning, utilizing			so that the resources used in this code can be better estimated by a Medicare		Panel to gapfill this code so that the resources used in this code can be better estimated
			Pathology (Other than GSP			first morning voided urine, algorithm reported as likelihood of prostate cancer			Administrative Contractor (MAC).		by a Medicare Administrative Contractor (MAC).
			or MAAA)			hist morning volded unite, algorithm reported as intermode of prostate cancer			Administrative Contractor (MAC).		by a wednare Administrative Constactor (wirke).
16		NEW		815X0	81560		1. Gapfill: 11	C CII	CMC	C CII	E L CMC de CDLT
40	22	INE W	Multi-Analyte Assay with	815A0	81500	Transplantation medicine (allograft rejection, pediatric liver and small bowel),	1. Gaphii: 11	Gapfill	CMS agrees with the majority recommendation of the CDLT Panel to gapfill this code	Gapfill	Finalize as proposed. CMS agrees with the majority recommendation of the CDLT
			Algorithmic Analyses:			measurement of donor and third-party-induced CD154+T-cytotoxic memory cells,			so that the resources used in this code can be better estimated by a Medicare		Panel to gapfill this code so that the resources used in this code can be better estimated
			Transplantation / Tests with			utilizing whole peripheral blood, algorithm reported as a rejection risk score			Administrative Contractor (MAC).		by a Medicare Administrative Contractor (MAC).
			algorithm in code descriptor								
47	56	NEW	Multi-Analyte Assay with	815X1	81523	Oncology (breast), mRNA, next-generation sequencing gene expression profiling of	1. Crosswalk to 81521: 11	Crosswalk to 81521	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code.	Crosswalk to 81521	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to
1		1	Algorithmic Analyses:	1		70 content genes and 31 housekeeping genes, utilizing formalin-fixed paraffin-			The crosswalked code(s) appear to use similar methods and resource utilization.		crosswalk the code. The crosswalked code(s) appear to use similar methods and
			Oncology breast / Tests with			embedded tissue, algorithm reported as index related to risk to distant metastasis					resource utilization.
1	l	1	algorithm in code descriptor	I	1	/ e 1		1		1	
48	25	NEW		0017M	0017M	Oncology (diffuse large B-cell lymphoma [DLBCL]), mRNA, gene expression	1. Crosswalk to 0120U: 11	Crosswlk to 0120U	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code.	Crosswlk to 0120U	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to
10	~~		Algorithmic Analyses:	001/141	001/141	profiling by fluorescent probe hybridization of 20 genes, formalin-fixed paraffin-	1. Crosswark to 01200. 11	C1055WIK 10 01200	The crosswalked code(s) appear to use similar methods and resource utilization.	C1008WIK 10 01200	crosswalk the code. The crosswalked code(s) appear to use similar methods and
1	l	1		I	1	proming by nubrescent prote nyoralization of 20 genes, formalin-fixed parallin-		1	The crosswarked code(s) appear to use similar methods and resource utilization.	1	crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.
1		1	Oncology lymphoma/ Tests		1	embedded tissue, algorithm reported as cell of origin					resource utilization.
<u> </u>		l	with algorithm in code		1						
49	26	NEW	Proprietary Laboratory	0243U	0243U	Obstetrics (preeclampsia), biochemical assay of placental-growth factor, time-	1. Crosswalk to 82731:11	Crosswalk to 82731	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code.	Crosswalk to 82731	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to
1		1	Analyses: Molecular		1	resolved fluorescence immunoassay, maternal serum, predictive algorithm reported as			The crosswalked code(s) appear to use similar methods and resource utilization.		crosswalk the code. The crosswalked code(s) appear to use similar methods and
1		1	Pathology (Other than GSP	1		a risk score for preeclampsia					resource utilization.
			or MAAA)								
50	69	NEW	Multi-Analyte Assay with	002XM	0018M	Transplantation medicine (allograft rejection, renal), measurement of donor and third-	1. Gapfill: 11	Gapfill	CMS agrees with the majority recommendation of the CDLT Panel to gapfill this code	Gapfill	Finalize as proposed. CMS agrees with the majority recommendation of the CDLT
1		1	Algorithmic Analyses / Tests		1	party-induced CD154+T-cytotoxic memory cells, utilizing whole peripheral blood,			so that the resources used in this code can be better estimated by a Medicare	*	Panel to gapfill this code so that the resources used in this code can be better estimated
			with algorithm in code			algorithm reported as a rejection risk score			Administrative Contractor (MAC).		by a Medicare Administrative Contractor (MAC).
1		1	descriptor to report	1		angoriana reported as a rejection risk score			annanana conditor (mac).		oy a measure ramansulative contractor (wrec).
61	70	NEW		0X56U	0255U	A dealers (Colored to a) and the second s	1. Gapfill: 11	Gapfill	CMC	C 61	Enterna 1 CMC solution in the second state of the CMC
51	/0	INEW	Proprietary Laboratory	0A30U	02550	Andrology (infertility), sperm-capacitation assessment of ganglioside GM1	i. Gaptili: 11	Gaprin	CMS agrees with the majority recommendation of the CDLT Panel to gapfill this code	Gaptill	Finalize as proposed. CMS agrees with the majority recommendation of the CDLT
1		1	Analyses: Molecular		1	distribution patterns, fluorescence microscopy, fresh or frozen specimen, reported as			so that the resources used in this code can be better estimated by a Medicare		Panel to gapfill this code so that the resources used in this code can be better estimated
1		1	Pathology (Other than GSP		1	percentage of capacitated sperm and probability of generating a pregnancy score			Administrative Contractor (MAC).		by a Medicare Administrative Contractor (MAC).
		1	or MAAA)		L			<u> </u>	<u> </u>		
52	73	NEW	Proprietary Laboratory	0X59U	0258U	Autoimmune (psoriasis), mRNA, next-generation sequencing, gene expression	1. Crosswalk to 0019U: 6	Gapfill	CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code	Crosswalk to 0019U	After additional review and further consideration, CMS agrees with the majority
1	l	1	Analyses: Molecular	I	1	profiling of 50-100 genes, skin- surface collection using adhesive patch, algorithm	2. Gapfill: 5	1	so that the resources used in this code can be better estimated by a Medicare	1	recommendation of the CDLT Panel to crosswalk this code. The crosswalked code(s)
1		1	Pathology (Other than GSP		1	reported as likelihood of response to psoriasis biologics			Administrative Contractor (MAC).		appear to use similar methods and resource utilization.
1	l	1	or MAAA)	I	1			1	` ´	1	**
53	28	NEW	Proprietary Laboratory	0245U	0245U	Oncology (thyroid), mutation analysis of 10 genes and 37 RNA fusions and expression	1. Crosswalk to 81455: 9	Gapfill	CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code	Ganfill	After reviewing public comments CMS still feels gapfill is the most appropriate. This
22	20	1912 W	Analyses: Molecular	02700	02400		2. Gapfill: 2	Saprin		capin	
1		1			1	of 4 mRNA markers using next-generation sequencing, fine needle aspirate, report	2. Gapini: 2		so that the resources used in this code can be better estimated by a Medicare		will allow the MACs to review the code more closely and particularly look at other
1		1	Pathology (Other than GSP		1	includes associated risk of malignancy expressed as a percentage			Administrative Contractor (MAC).		codes similar.
			or MAAA)								

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We welcome reconsideration requests on our final determinations for the basis of payment. All comments must be submitted electronically by January 24, 2022 to the following CMS mailbox: CLFS_Annual_Public_Meeting@ems.hhs.gov. When submitting reconsideration requests, please refer to the specific code and its rationale.

FACA Panel Item #	ALM Item #	Code Type	Category	Code #	Final Code #	Long Code Descriptor	CDLT Panel Voting Results	CMS 2021 Preliminary Recommendation	Rationale	CMS 2021 Final Determination	Rationale
54	30	NEW	Proprietary Laboratory Analyses: Molecular Pathology (Other than GSP or MAAA)	0247U	0247U	Obstetrics (preterm birth), insulin-like growth factor-binding protein 4 (IBP4), sex hormone-binding globulin (SHBG), quantitative measurement by LC-MS/MS, utilizing maternal serum, combined with clinical data, reported as predictive-risk stratification for spontaneous preterm birth	1. Crosswalk to 0080U X 0.2: 10 2. Gapfill: 1	Gapfill	CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).		0063U. The crosswalked code(s) appear to use similar methods and resource utilization.
55	31	NEW	Proprietary Laboratory Analyses: Molecular Pathology (Other than GSP or MAAA)	0252U	0252U	Fetal aneuploidy short tandem-repeat comparative analysis, fetal DNA from products of conception, reported as normal (euploidy), monosomy, trisomy, or partial deletion/duplications, mosaicism, and segmental aneuploidy	1. Gapfill: 11	Gapfill	CMS agrees with the majority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).		Finalize as proposed. CMS agrees with the majority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
56	33	NEW	Proprietary Laboratory Analyses: Molecular Pathology (Other than GSP or MAAA)	0249U	0249U	Oncology (breast), semiquantitative analysis of 32 phosphoproteins and protein analytes, includes laser capture microdissection, with algorithmic analysis and interpretative report	1. Crosswalk to 0037U: 2 2. Gapfill: 9	Gapfill	CMS agrees with the majority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).	Gapfill	Finalize as proposed. CMS agrees with the majority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
57	36	NEW	Proprietary Laboratory Analyses: Molecular Pathology (Other than GSP or MAAA)	0253U	0253U	Reproductive medicine (endometrial receptivity analysis), RNA gene expression profile, 238 genes by next-generation sequencing, endometrial tissue, predictive algorithm reported as endometrial window of implantation (eg, pre-receptive, receptive, post-receptive)	1. Gapfill: 11	Gapfill	CMS agrees with the majority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).	Gapfill	Finalize as proposed. CMS agrees with the majority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
58	37	NEW	Proprietary Laboratory Analyses: MAAA NGS Reproductive medicine	0254U	0254U	Reproductive medicine (preimplantation genetic assessment), analysis of 24 ehromosomes using embryonic DNA genomic sequence analysis for aneuploidy, and a mitochondrial DNA score in euploid embryos, results reported as normal (euploidy), monosomy, trisomy, or partial deletion/duplications, mosaicism, and segmental	1. Gapfill: 11	Gapfill	CMS agrees with the majority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).	Gapfill	Finalize as proposed. CMS agrees with the majority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
59	84	NEW	Proprietary Laboratory Analyses: MAAA Oncology	0X71U	0262U	Oncology (solid tumor), gene expression profiling by real-time RT-PCR of 7 gene pathways (ER, AR, PI3K, MAPK, HH, TGFB, Notch), formalin-fixed paraffin- embedded (FFPE), algorithm reported as gene pathway activity score	1. Crosswalk to 0011M: 8 2. Gapfill: 3	Gapfill	CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).	Gapfill	Finalize as proposed. CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
60	100	NEW	Proprietary Laboratory Analyses	0X70U	0261U	Oncology (colorectal cancer), image analysis with artificial intelligence assessment of 4 histologic and immunohistochemical features (CD3 and CD8 within tumor-stroma border and tumor core), tissue, reported as immune response and recurrence-risk score	1. Crosswalk to 0108U: 3 2. Crosswalk to 0108U x 1.2: 4 3. Gapfill: 3 4. Abstain: 1	Gapfill	CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).	Crosswalk to 0108U	After additional review and further consideration, CMS agrees with the majority recommendation of the CDLT Panel to crosswalk this code. The crosswalked code(s) appear to use similar methods and resource utilization.
61	62	NEW	Chemistry	826X0	82653	Elastase, pancreatic (EL-1), fecal; quantitative	1. Crosswalk to 82715: 10	Crosswalk to 82715	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. Both codes appear to use similar methods and resource utilization.	Crosswalk to 82715	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.
62	71	NEW	Proprietary Laboratory Analyses: Chemistry	0X57U	0256U	Trimethylamine/trimethylamine N-oxide (TMA/TMAO) profile, tandem mass spectrometry (MS/MS), urine, with algorithmic analysis and interpretive report	1. Gapfill: 11	Gapfill	CMS agrees with the majority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).	Gapfill	Finalize as proposed. CMS agrees with the majority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
63	72	NEW	Proprietary Laboratory Analyses: Chemistry	0X58U	0257U	Very long chain acyl- coenzyme A (CoA) dehydrogenase (VLCAD), leukocyte enzyme activity, whole blood	1. Gapfill: 11	Gapfill	CMS agrees with the majority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).	Gapfill	Finalize as proposed. CMS agrees with the majority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
64	74	NEW	Proprietary Laboratory Analyses: Chemistry	0X60U	0259U	Nephrology (chronic kidney disease), nuclear magnetic resonance spectroscopy measurement of myo-inositol, valine, and creatinine, algorithmically combined with cystatin C (by immunoassay) and demographic data to determine estimated glomerular filtration rate (GFR), serum, quantitative	1. Crosswalk to (83704 x2) + (82610): 2 2. Crosswalk to 83704 + 82610: 6 3. Gapfill: 1	Crosswalk to 83704 + 82610	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. Both codes appear to use similar methods and resource utilization.	Crosswalk to 83704 + 82610	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.
65	35	NEW	Proprietary Laboratory Analyses: Chemistry	0251U	0251U	Hepcidin-25, enzyme-linked immunosorbent assay (ELISA), serum or plasma	1. Crosswalk to 83520: 11	Crosswalk to 83520	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. Both codes appear to use similar methods and resource utilization.	Crosswalk to 83520	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.
66	38	NEW	Chemistry/ Chemistry	835X1	83529	Interleukin-6 (IL-6)	1. Crosswalk to 83006: 10 2. Abstain: 1	Crosswalk to 83520	CMS disagrees with the Panel Recommendation and instead is recommending a different crosswalk that is consistent with other similar tests	Crosswalk to 83520	After reviewing public comments CMS continues to recommend a crosswalk to CPT 83520. We believe there are similar methods between the two codes.
67	39	NEW	Chemistry/ Chemistry	8352X	83521	Immunoglobulin light chains (ie, kappa, lambda), free, each	1.Crosswalk to 83520: 11	Crosswalk to 83520	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. Both codes appear to use similar methods and resource utilization.	Crosswalk to 83520	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.
68	90	NEW	Proprietary Laboratory Analyses: Chemistry / Chemistry	0X77U	0263U	Neurology (autism spectrum disorder [ASD]), quantitative measurements of 16 central carbon metabolites (ie, a-ketog lutrante, alanine, lactate, phenylalanine, pyruvate, succinate, carnitine, citrate, fumarate, hypoxanthine, inosine, malate, S- sulfocysteine, uturine, urate, and xanthine), liquid chromatography tandem mass	1. Crosswalk to 0063U: 10	Crosswalk to 0063U	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. Both codes appear to use similar methods and resource utilization.	Crosswalk to 0063U	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.
69	13	NEW	Proprietary Laboratory Analyses: Oncology colorectal / Genomic Sequencing Related Tests	0229U	0229U	BCAT1 (Branched chain amino acid transaminase 1) or IKZF1 (IKAROS family zinc finger 1) (eg, colorectal cancer) promoter methylation analysis	1. Crosswalk to 81327 x 2: 9	Crosswalk to 81287	CMS disagrees with the Panel Recommendation and instead is recommending a different crosswalk that is consistent with other similar tests	Crosswalk to 81327	After reviewing comments CMS agrees that CPT 81327 is the more appropriate crosswalk for 0229U. However, CMS does not feel a multiplier of 2 is appropriate, given the CPT descriptor stipulates 1 gene OR the other.
70	14	NEW	Proprietary Laboratory Analyses: Oncology colorectal / Genomic Sequencing Related Tests	0230U	0230U	AR (androgen receptor) (eg, spinal and bulbar muscular atrophy, Kernedy disease, X chromosome inactivation), full sequence analysis, including small sequence changes in exonic and intronic regions, deletions, duplications, short tandem repeat (STR) expansions, mobile element insertions, and variants in non-uniquely mappable regions	1. Crosswalk to 81173 + 81204: 9	Crosswalk to 81173	CMS agrees with part of the recommended crosswalk. CMS considers the 'full gene sequence' to include all components described in new code	Crosswalk to 81173	Finalize as proposed. CMS continues to agree with part of the CDLT Panel recommendation to crosswalk recommended by the CDLT Panel. CMS considers the full gene sequence' to include all components described in new code
71	15	NEW	Proprietary Laboratory Analyses: GSP neuromuscular disorders / Genomic Sequencing Related	0231U	0231U	CACNA1A (calcium voltage-gated channel subunit alpha 1A) (eg, spinocerebellar ataxia), full gene analysis, including small sequence changes in exonic and intronic regions, duelications, short tandem repeat (STR) gene expansions, mobile element insertions, and variants in non-uniquely mappable regions	1. Crosswalk to 81184 + 81185: 9	Crosswalk to 81185	CMS agrees with part of the recommended crosswalk. CMS considers the 'full gene sequence' to include all components described in new code	Crosswalk to 81185	Finalize as proposed. CMS continues to agree with part of the CDLT Panel recommendation to crosswalk recommended by the CDLT Panel. CMS considers the full gene sequence' to include all components described in new code
72	16	NEW	Proprietary Laboratory Analyses: GSP neuromuscular disorders / Genomic Sequencing Related	0232U	0232U	CENTR (systain lactators and variants in the variated variance regions GSTB (systain B) (eg. progressive myclosine eiphesy type 1A, Unverricht-Lundborg disease), full gene analysis, including small sequence changes in exonic and intronic regions, deletions, aduptications, short tandem repeat (STR) expansions, mobile element insertions, and variants in non-uniquely mappable regions	1. Crosswalk to 81188 + 81189: 9	Crosswalk to 81189	CMS agrees with part of the recommended crosswalk. CMS considers the 'full gene sequence' to include all components described in new code	Crosswalk to 81189	Finalize as proposed. CMS continues to agree with part of the CDLT Panel recommendation to crosswalk recommended by the CDLT Panel. CMS considers the full gene sequence' to include all components described in new code

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We welcome reconsideration requests on our final determinations for the basis of payment. All comments must be submitted electronically by January 24, 2022 to the following CMS mailbox: CLFS_Annual_Public_Meeting@ems.hhs.gov. When submitting reconsideration requests, please refer to the specific code and its rationale.

FACA Panel Item #	ALM Item #	Code Type	Category	Code #	Final Code #	Long Code Descriptor	CDLT Panel Voting Results	CMS 2021 Preliminary Recommendation	Rationale	CMS 2021 Final Determination	Rationale
73	17	NEW	Proprietary Laboratory Analyses: GSP neuromuscular disorders / Genomic Sequencing Related	0233U	0233U	FXN (frataxin) (eg, Friedreich ataxia), gene analysis, including small sequence changes in exonic and intronic regions, deletions, duplications, short tandem repeat (STR) expansions, mobile element insertions, and variants in non-uniquely mappable revions	1. Crosswalk to 81285 + 81286: 9	Crosswalk to 81286	CMS agrees with part of the recommended crosswalk. CMS considers the 'full gene sequence' to include all components described in new code	Crosswalk to 81286	Finalize as proposed. CMS continues to agree with part of the CDLT Panel recommendation to crosswalk recommended by the CDLT Panel. CMS considers the full gene sequence to include all components described in new code
74	18	NEW	Proprietary Laboratory Analyses: GSP neurodevelopmental disorder / Genomic Sequencing	0234U	0234U	MECP2 (methyl CpG binding protein 2) (eg, Rett syndrome), full gene analysis, including small sequence changes in exonic and intronic regions, deletions, duplications, mobile element insertions, and variants in non-uniquely mappable regions	1. Crosswalk to 81302 + 81304: 9	Crosswalk to 81302	CMS agrees with part of the recommended crosswalk. CMS considers the 'full gene sequence' to include all components described in new code	Crosswalk to 81302	Finalize as proposed. CMS continues to agree with part of the CDLT Panel recommendation to crosswalk recommended by the CDLT Panel. CMS considers the 'full gene sequence' to include all components described in new code
75	19	NEW	Proprietary Laboratory Analyses: GSP Inherited disorders / Genomic Sequencing Related Tests	0235U	0235U	PTEN (phosphatase and tensin homolog) (eg. Cowden syndrome, PTEN hamartoma tumor syndrome), full gene analysis, including small sequence changes in exonic and intronic regions, deletions, duplications, mobile element insertions, and variants in non- uniquely mappable regions	1. Crosswalk to 81321 + 81323: 9	Crosswalk to 81321	CMS agrees with part of the recommended crosswalk. CMS considers the 'full gene sequence' to include all components described in new code	Crosswalk to 81321	Finalize as proposed. CMS continues to agree with part of the CDLT Panel recommendation to crosswalk recommended by the CDLT Panel. CMS considers the 'full gene sequence' to include all components described in new code
76	20	NEW	Proprietary Laboratory Analyses: GSP neuromuscular disorders / Genomic Sequencing Related	0236U	0236U	SMN1 (survival of motor neuron 1, telomeric) and SMN2 (survival of motor neuron 2, centromeric) (eg, spinal muscular atrophy) full gene analysis, including small sequence changes in exonic and intronic regions, duplications and deletions, and mobile element insertions	1. Crosswalk to 81329 + 81337: 9	Crosswalk to 81336+81405	CMS disagrees with the recommended crosswalk and instead recommends a crosswalk that represents both genes sequenced in this code.	Crosswalk to 81336+81405	Finalize as proposed. CMS continues to disagree with the recommendation of the CDLT Panel and recommends an alternate crosswalk. CMS believes the methods are similar between the two codes.
77	21	NEW	Proprietary Laboratory Analyses: GSP cardiovascular disorders / Genomic Sequencing Related	0237U	0237U	Cardiae ion channelopathies (eg, Brugada syndrome, long QT syndrome, short QT syndrome, catecholaminergie polymorphic ventricular tachycardia), genomic sequence analysis panel including ANK2, CASQ2, CAV3, KCNE1, KCNE2, KCNH2, KCNJ2, KCNO1, RYR2, and SCNSA, including small sequence changes in exonic and intronic	1. Crosswalk to 81413 + 81414: 9	Crosswalk to 81413	CMS agrees with part of the recommended crosswalk. CMS considers the 'full gene sequence' to include all components described in new code	Crosswalk to 81413	Finalize as proposed. CMS continues to agree with part of the CDLT Panel recommendation to crosswalk recommended by the CDLT Panel. CMS considers the 'full gene sequence' to include all components described in new code
78	22	NEW	Proprietary Laboratory Analyses: GSP Oncology / Genomic Sequencing Related Tests	0238U	0238U	Oncology (Lynch syndrome), genomic DNA sequence analysis of MLH1, MSH2, MSH6, PMS2, and EPCAM, including small sequence changes in exonic and intronic regions, deletions, duplications, mobile element insertions, and variants in non-uniquely mappable regions	1. Crosswalk to 81435 + 81436: 9	Crosswalk to 81435	CMS agrees with part of the recommended crosswalk. CMS considers the 'full gene sequence' to include all components described in new code	Crosswalk to 81435	Finalize as proposed. CMS continues to agree with part of the CDLT Panel recommendation to crosswalk recommended by the CDLT Panel. CMS considers the 'full gene sequence' to include all components described in new code
80	76	NEW	Proprietary Laboratory Analyses: GSP constitutional or other heritable disorders or syndromes / Genomic	0X62U	0265U	Rare constitutional and other heritable disorders, whole- genome and mitochondrial DNA sequence analysis, blood, frozen and formalin-fixed paraffin-embedded (FFPE) tissue, saliva, buccal swabs or cell lines, identification of single nucleotide and copy number variants	1. Crosswalk to 81425+81460: 5 2. Gapfill: 4	Gapfill	CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).	Gapfill	Finalize as proposed. CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
81	34	NEW	Proprietary Laboratory Analyses: GSP Oncology solid organ / Genomic Sequencing Related Tests	0250U	0250U	Oncology (solid organ neoplasm), targeted genomic sequence DNA analysis of 505 genes, interrogation for somatic alterations (SNVs [single nucleotide variant], small insertions and deletions, one amplification, and four translocations), microsatellite instability and tumor-mutation burden	1. Crosswalk to 81455: 11	Crosswalk to 81455	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. Both codes appear to use similar methods and resource utilization.	Crosswalk to 81455	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.
82	77	NEW	Proprietary Laboratory Analyses: GSP constitutional or other heritable disorders or syndromes / Genomic	0X63U	0266U	Unexplained constitutional or other heritable disorders or syndromes, tissue-specific gene expression by whole-transcriptome and next-generation sequencing, blood, formalin-fixed paraffin-embedded (FFPE) tissue or fresh frozen tissue, reported as presence or absence of splicing or expression changes	1. Crosswalk to 81425: 1 2. Crosswalk to 81415: 6 3. Gapfill: 1	Gapfill	CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).	Gapfill	Finalize as proposed. CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
83	78	NEW	Proprietary Laboratory Analyses: GSP constitutional or other heritable disorders or syndromes / Genomic	0X64U	0267U	Rare constitutional and other heritable disorders, identification of copy number variations, inversions, insertions, translocations, and other structural variants by optical genome mapping and whole-genome sequencing	1. Crosswalk to 81425 + 81229: 7 2. Gapfill: 1	Gapfill	CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC). In particular, gapfilling this code will help to understand the resources involved in optical genome mapping, which does not have a	Gapfill	Finalize as proposed. CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
84	86	NEW	Proprietary Laboratory Analyses: GSP hematology / Genomic Sequencing Related Tests	0X73U	0268U	Hematology (atypical hemolytic uremic syndrome [aHUS]), genomic sequence analysis of 15 genes, blood, buccal swab, or amniotic fluid	1. Crosswalk to 81432: 5 2. Crosswalk to 81443: 5	Gapfill	CMS disagrees with the recommendations to crosswalk this code and instead recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC). CMS welcomes comments that would help to better identify potential crosswalks for the genetic	Gapfill	Finalize as proposed. CMS continues to disagree with the recommendation of the CDLT Panel and recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
85	87	NEW	Proprietary Laboratory Analyses: GSP hematology / Genomic Sequencing Related Tests	0X74U	0269U	Hematology (autosomal dominant congenital thrombocytopenia), genomic sequence analysis of 14 genes, blood, buccal swab, or amniotic fluid	1. Crosswalk to 81432 + 81433: 2 2. Crosswalk to 81443: 8	Gapfill	CMS disagrees with the recommendations to crosswalk this code and instead recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC). CMS welcomes comments that would help to better identify potential crosswalks for the genetic	Gapfill	Finalize as proposed. CMS continues to disagree with the recommendation of the CDLT Panel and recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
86	88	NEW	Proprietary Laboratory Analyses: GSP hematology / Genomic Sequencing Related Tests	0X75U	0270U	Hematology (congenital coagulation disorders), genomic sequence analysis of 20 genes, blood, buccal swab, or amniotic fluid	1. Crosswalk to 81432: 2 2. Crosswalk to 81443: 8	Gapfill	CMS disagrees with the recommendations to crosswalk this code and instead recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC). CMS welcomes comments that would help to better identify potential crosswalks for the genetic	Gapfill	Finalize as proposed. CMS continues to disagree with the recommendation of the CDLT Panel and recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
87	89	NEW	Proprietary Laboratory Analyses: GSP hematology / Genomic Sequencing Related Tests	0X76U	0272U	Hematology (genetic bleeding disorders), genomic sequence analysis of 51 genes, blood, buccal swab, or amniotic fluid, comprehensive	1. Crosswalk to 81430: 10	Gapfill	CMS disagrees with the recommendations to crosswalk this code and instead recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC). CMS welcomes comments that would help to better identify potential crosswalks for the genetic	Gapfill	Finalize as proposed. CMS continues to disagree with the recommendation of the CDLT Panel and recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
88	91	NEW	Proprietary Laboratory Analyses: GSP hematology / Genomic Sequencing Related Tests	0X78U	0274U	Hematology (genetic platelet disorders), genomic sequence analysis of 43 genes, blood, buccal swab, or amniotic fluid	1. Crosswalk to 81443: 2 2. Crosswalk to 81430: 7	Gapfill	CMS disagrees with the recommendations to crosswalk this code and instead recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC). CMS welcomes comments that would help to better identify potential crosswalks for the genetic	Gapfill	Finalize as proposed. CMS continues to disagree with the recommendation of the CDLT Panel and recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
89	92	NEW	Proprietary Laboratory Analyses: GSP hematology / Genomic Sequencing Related Tests	0X79U	0271U	Hematology (congenital neutropenia), genomic sequence analysis of 23 genes, blood, buccal swab, or amniotic fluid	1. Crosswalk to 81443: 8 2. Gapfill: 1	Gapfill	CMS disagrees with the recommendations to crosswalk this code and instead recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC). CMS welcomes comments that would help to better identify potential crosswalks for the genetic	Gapfill	Finalize as proposed. CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
90	93	NEW	Proprietary Laboratory Analyses: GSP hematology / Genomic Sequencing Related Tests	0X80U	0273U	Hematology (genetic hyperfibrinolysis, delayed bleeding), genomic sequence analysis of 8 genes (F13A1, F13B, FGA, FGB, FGG, SERPINA1, SERPINE1, SERPINF2, PLAU) blood, buccal swab, or amniotic fluid	1. Crosswalk to 81443: 4 2. Crosswalk to 81432: 6	Gapfill	CMS disagrees with the recommendations to crosswalk this code and instead recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC). CMS welcomes comments that would help to better identify potential crosswalks for the genetic	Gapfill	Finalize as proposed. CMS continues to disagree with the recommendation of the CDLT Panel and recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
91	94	NEW	Proprietary Laboratory Analyses: GSP hematology / Genomic Sequencing Related Tests	0X81U	0276U	Hematology (inherited thrombocytopenia), genomic sequence analysis of 23 genes, blood, buccal swab, or amniotic fluid	1. Crosswalk to 81443: 9 2.Gapfill: 1	Gapfill	CMS disagrees with the recommendations to crosswalk this code and instead recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC). CMS welcomes comments that would help to better identify potential crosswalks for the genetic	Gapfill	Finalize as proposed. CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
92	95	NEW	Proprietary Laboratory Analyses: GSP hematology / Genomic Sequencing Related Tests	0X82U	0277U	Hematology (genetic platelet function disorder), genomic sequence analysis of 31 genes, blood, buccal swab, or amniotic fluid	1. Crosswalk to 81443: 3 2. Crosswalk to 81430: 7	Gapfill	Commission and would help to better identify powerant closes with this code and instead recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC). CMS welcomes comments that would help to better identify potential crosswalks for the genetic	Gapfill	Finalize as proposed. CMS continues to disagree with the recommendation of the CDLT Panel and recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).

This first worksheet "A. Final Determinations" of this Excel workbook contains all of the new CLFS codes and CMS final payment determinations. The second worksheet "B. Edits or Corrections" contains any edits/corrections to the original CMS final payment determinations excel workbook that was displayed on the CMS website on November 24, 2021.

We welcome reconsideration requests on our final determinations for the basis of payment. All comments must be submitted electronically by January 24, 2022 to the following CMS mailbox: CLFS_Annual_Public_Meeting@ems.hhs.gov. When submitting reconsideration requests, please refer to the specific code and its rationale.

	ALM Item #		Category	Code #	Final Code #	Long Code Descriptor	CDLT Panel Voting Results	CMS 2021 Preliminary Recommendation	Rationale	CMS 2021 Final Determination	Rationale
93	96	NEW	Proprietary Laboratory Analyses: GSP hematology / Genomic Sequencing Related Tests	0X83U	0278U	Hematology (genetic thrombosis), genomic sequence analysis of 12 genes, blood, buccal swab, or amniotic fluid	1. Crosswalk to 81443: 9 2. Gapfill: 1	Gapfill	CMS disagrees with the recommendations to crosswalk this code and instead recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC). CMS welcomes comments that would help to better identify potential crosswalks for the genetic	Gapfill	Finalize as proposed. CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
94	97	NEW	Proprietary Laboratory Analyses: GSP hematology / Genomic Sequencing Related Tests	0X84U	0282U	Red blood cell antigen typing, DNA, genotyping of 12 blood group system genes to predict 44 red blood cell antigen phenotypes	1. Crosswalk to 0001U: 10	Crosswalk to 0001U	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. Both codes appear to use similar methods and resource utilization.	Crosswalk to 0001U	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.
95	75	NEW	Proprietary Laboratory Analyses: Molecular Pathology (Other than GSP / Other Genomic Sequencing	0X61U	0264U	Rare diseases (constitutional/heritable disorders), identification of copy number variations, inversions, insertions, translocations, and other structural variants by optical genome mapping	1. Crosswalk to 81229: 9 2. Gapfill: 1 3. Abstain: 1	Gapfill	CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC). In particular, gapfilling this code will help to understand the resources involved in optical genome mapping, which does not have a	Gapfill	Finalize as proposed. CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
96	27		Proprietary Laboratory Analyses: GSP Oncology solid organ / Other Genomic Sequencing Related Tests	0244U	0244U	Oncology (solid organ), DNA, comprehensive genomic profiling, 257 genes, interrogation for single-nucleotide variants, insertions/deletions, copy number alterations, gene rearrangements, tumor-mutational burden and microsatellite instability, utilizing formalin-fixed parafilm-embedded tumor tissue	1. Crosswalk to 0037U: 8 2. Gapfill: 1	Gapfill	CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC). In particular, gapfilling this code will help to understand the resources involved in optical genome mapping, which does not have a	Crosswalk to 0037U	After additional review and further consideration, CMS agrees with the majority recommendation of the CDLT Panel to crosswalk this code. The crosswalked code(s) appear to use similar methods and resource utilization.
97	29		Proprietary Laboratory Analyses: GSP RBC antigens / Other Genomic Sequencing Related Tests	0246U	0246U	Red blood cell antigen typing, DNA, genotyping of at least 16 blood groups with phenotype prediction of at least 51 red blood cell antigens	1. Crosswalk to 0001U: 10	Crosswalk to 0001U	CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. Both codes appear to use similar methods and resource utilization.	Crosswalk to 0001U	Finalize as proposed. CMS agrees with the majority CDLT Panel recommendation to crosswalk the code. The crosswalked code(s) appear to use similar methods and resource utilization.
98	85		Proprietary Laboratory Analyses: Molecular Pathology (Other than GSP / Other Genomic Sequencing	0X72U	0260U	Rare diseases (constitutional/heritable disorders), identification of copy number variations, inversions, insertions, translocations, and other structural variants by optical genome mapping	1. Crosswalk to 81229: 9 2. Gapfill: 1 3. Abstain: 1	Gapfill	CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC). In particular, gapfilling this code will help to understand the resources involved in optical genome mapping, which does not have a	Gapfill	Finalize as proposed. CMS agrees with the minority recommendation of the CDLT Panel to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC).
99	99		Molecular Pathology chromosomal abnormalities / Other Genomic Sequencing Related Tests	812X0	81349	Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number and loss-of-heterozygosity variants, low-pass sequencing analysis	1. Crosswalk to 81277: 4 2. Crosswalk to 81229: 6	Gapfill	CMS disagrees with the recommendations to crosswalk this code and instead recommends to gapfill this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC). CMS welcomes comments that would help to understand the difference in resources for low-pass	Gapfill	After reviewing public comments, CMS continues to believe gapfilling this code so that the resources used in this code can be better estimated by a Medicare Administrative Contractor (MAC)