Amino join units

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The genetic code

is the software that builds the protein

When the sidechain of each unit is known

and the join between each pair of units is known

the protein is defined

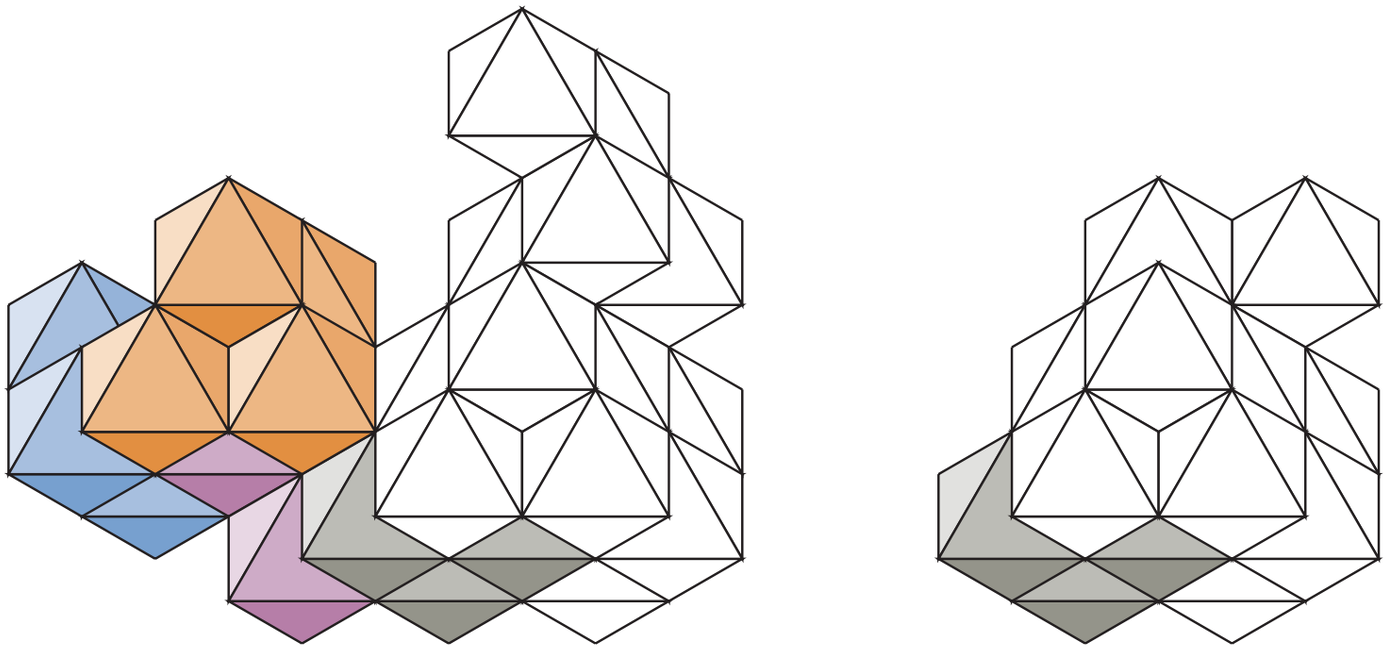
The sidechain defined by each codon is known

but the join defined by each codon is not

Six joins are possible between units

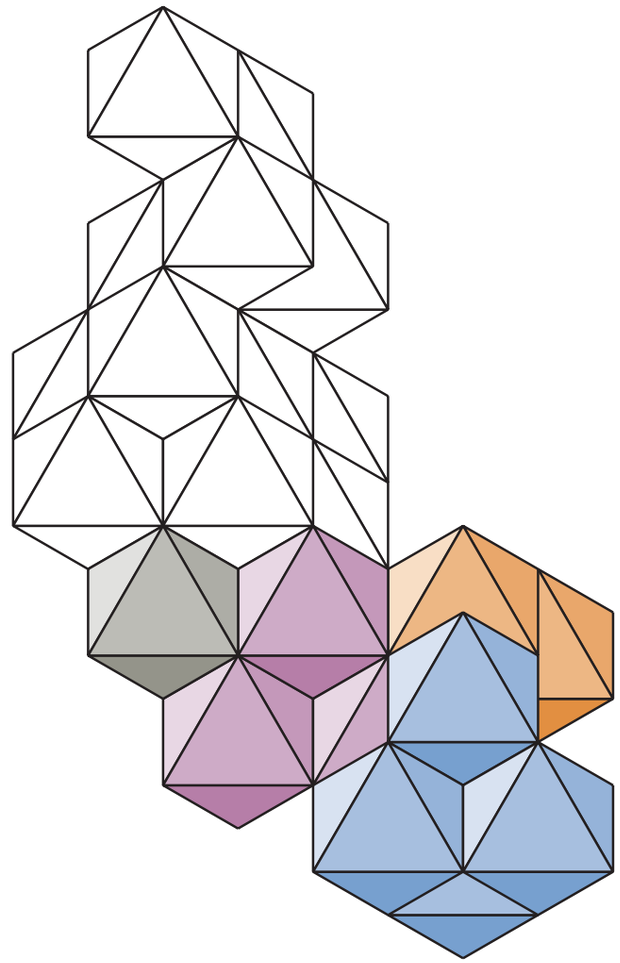
Each of these joins can be effected by a join unit

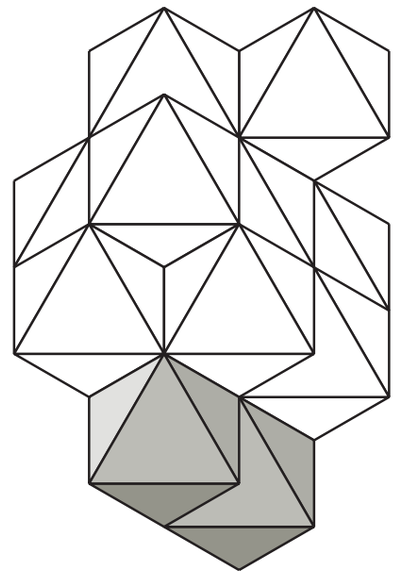
alpha



The alpha helical join and its join unit

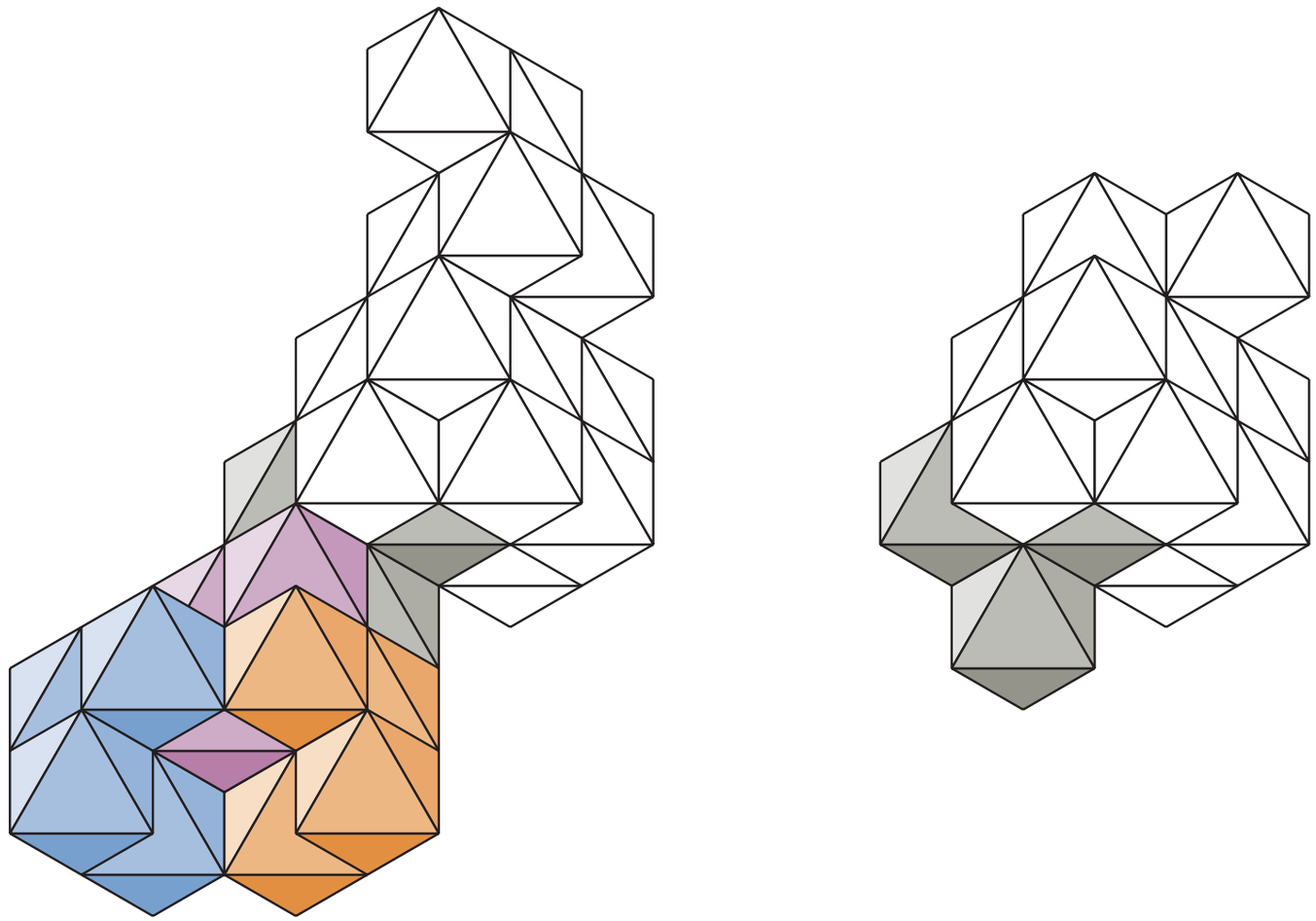
32-chain





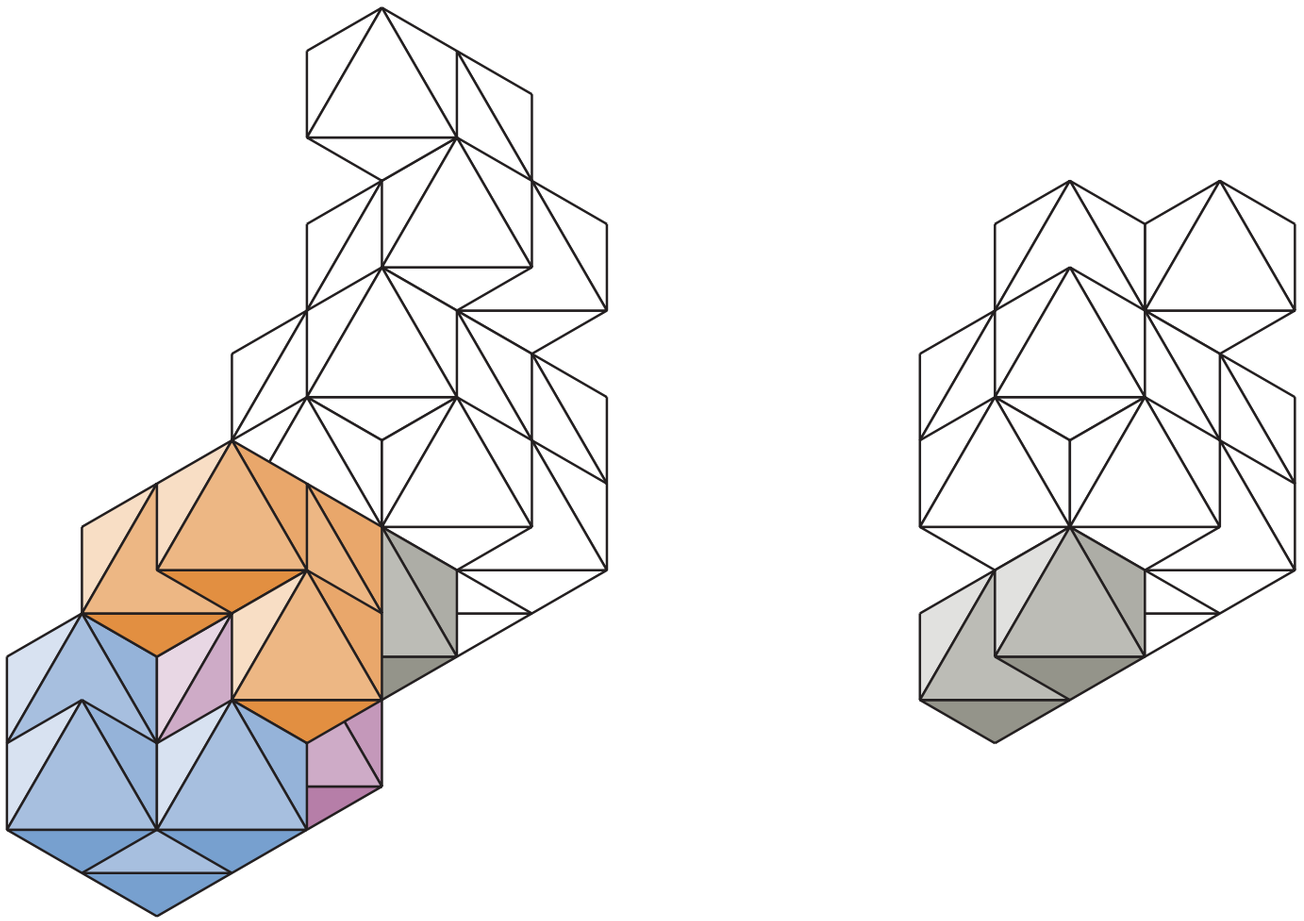
The 32-chain join and its join unit

epsilon



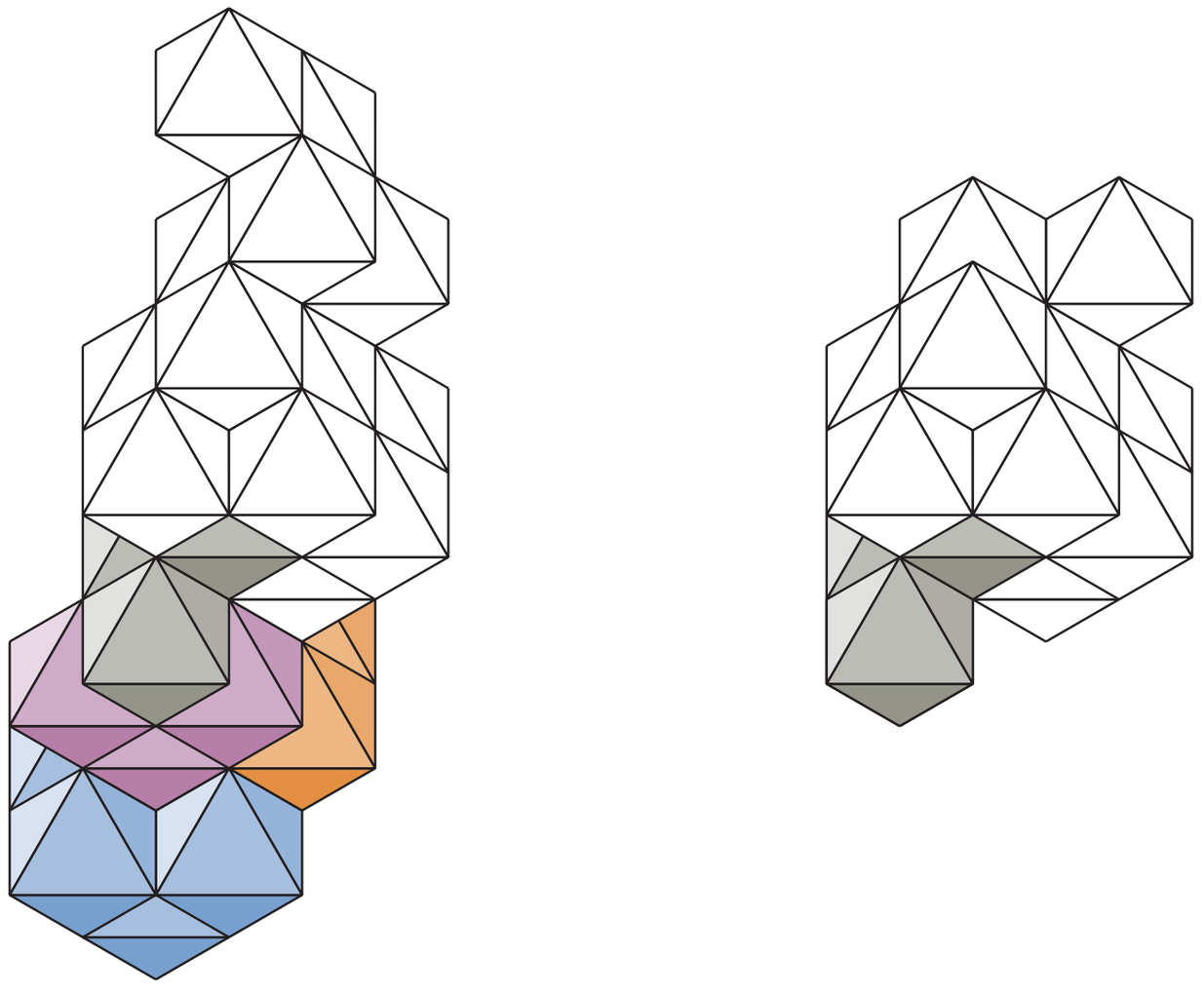
The epsilon helical join and its join unit

4-helix



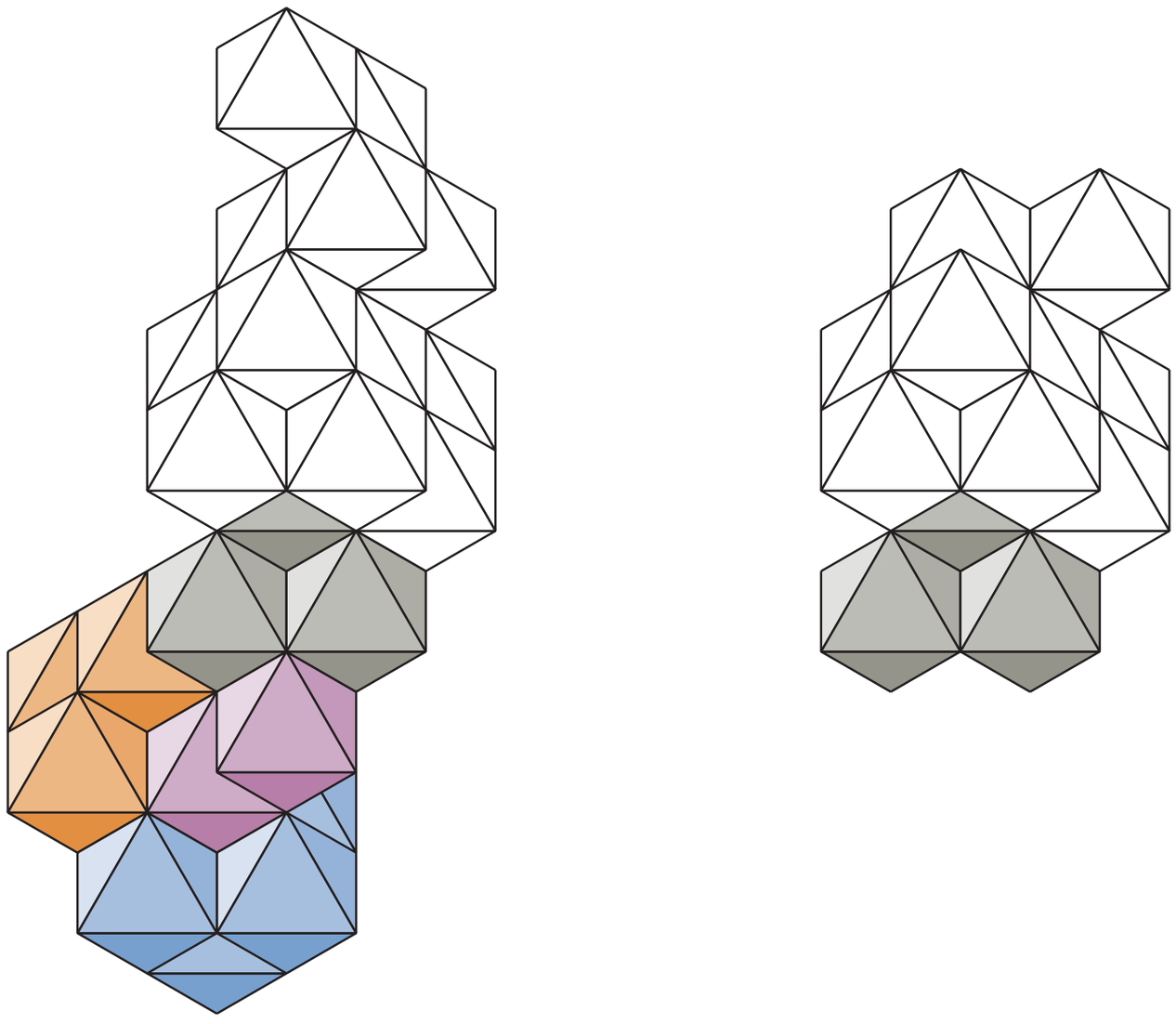
The 4-helix join and its join unit

beta180

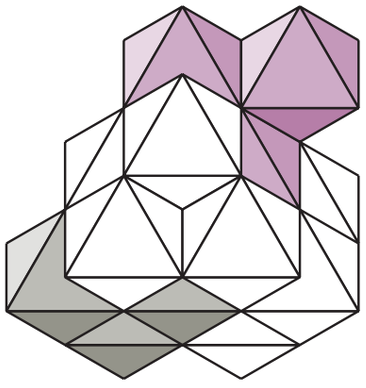


The beta180 join and its join unit

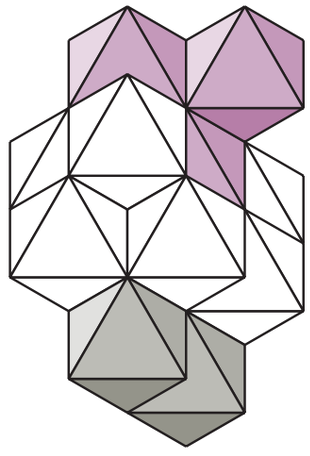
beta90



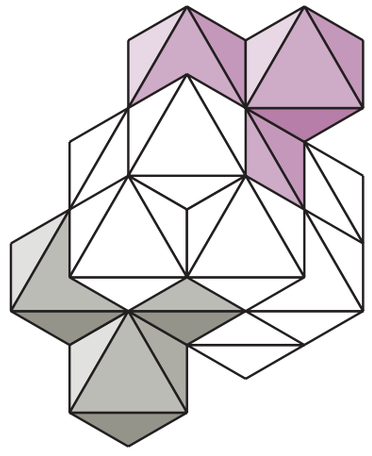
The beta90 join and its join unit



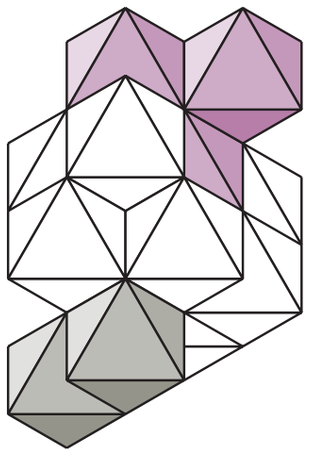
alpha



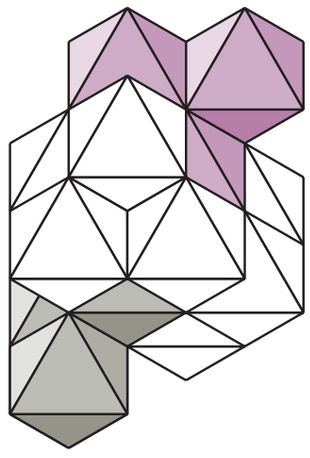
32-chain



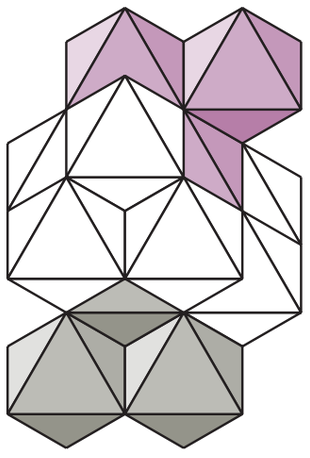
epsilon



4-helix

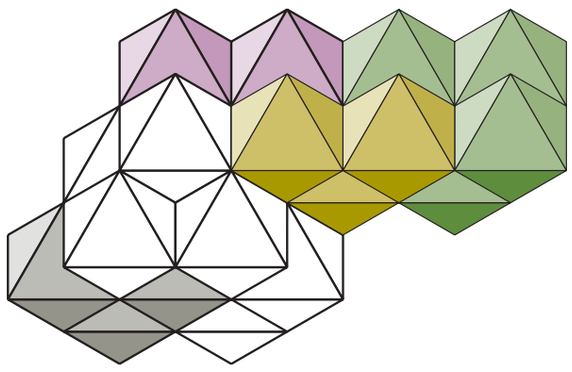


beta180

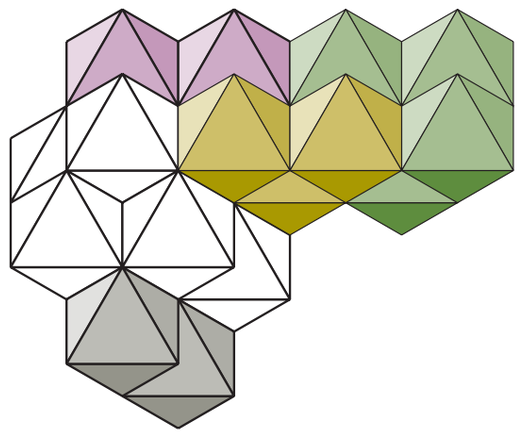


beta90

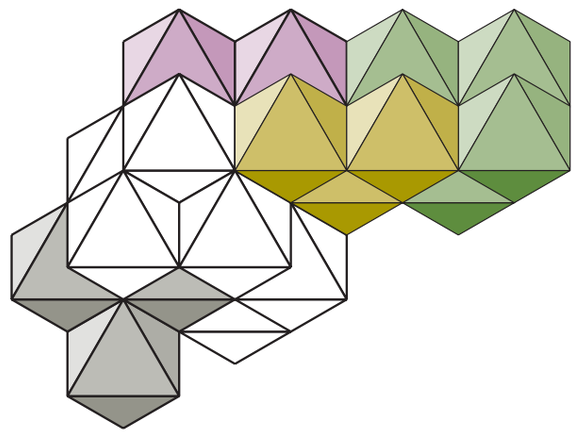
The join units



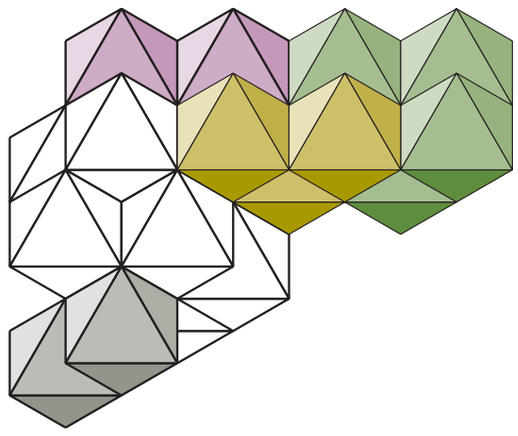
alpha



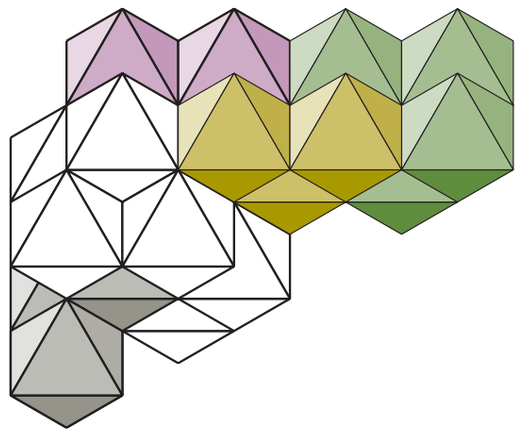
32-chain



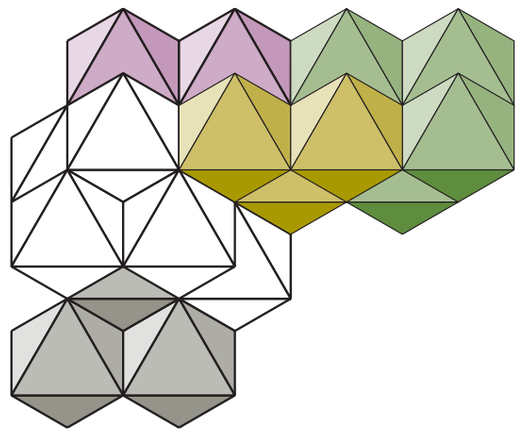
epsilon



4-helix



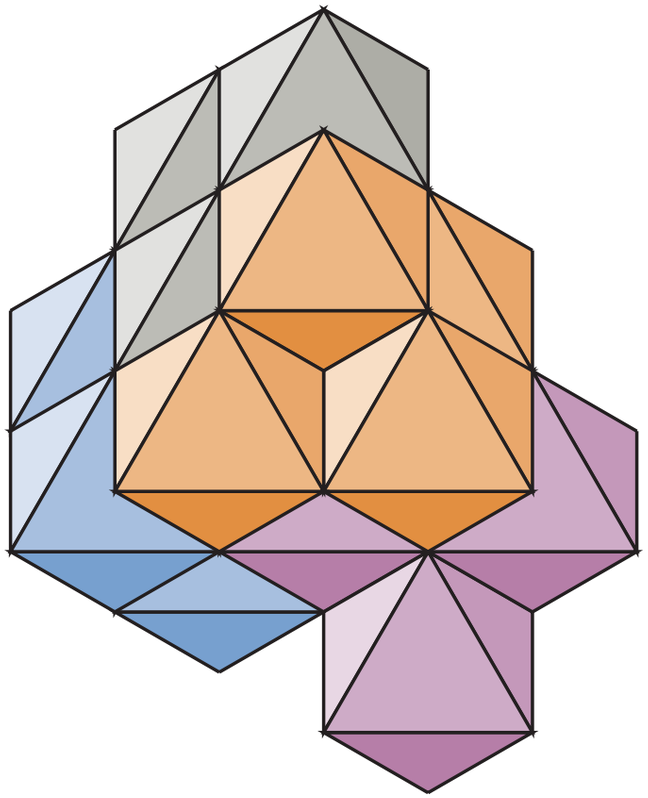
beta180

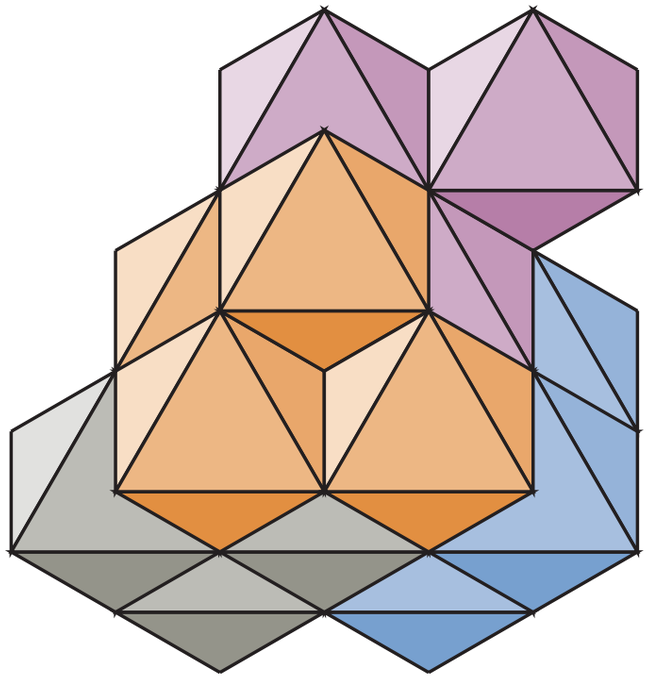


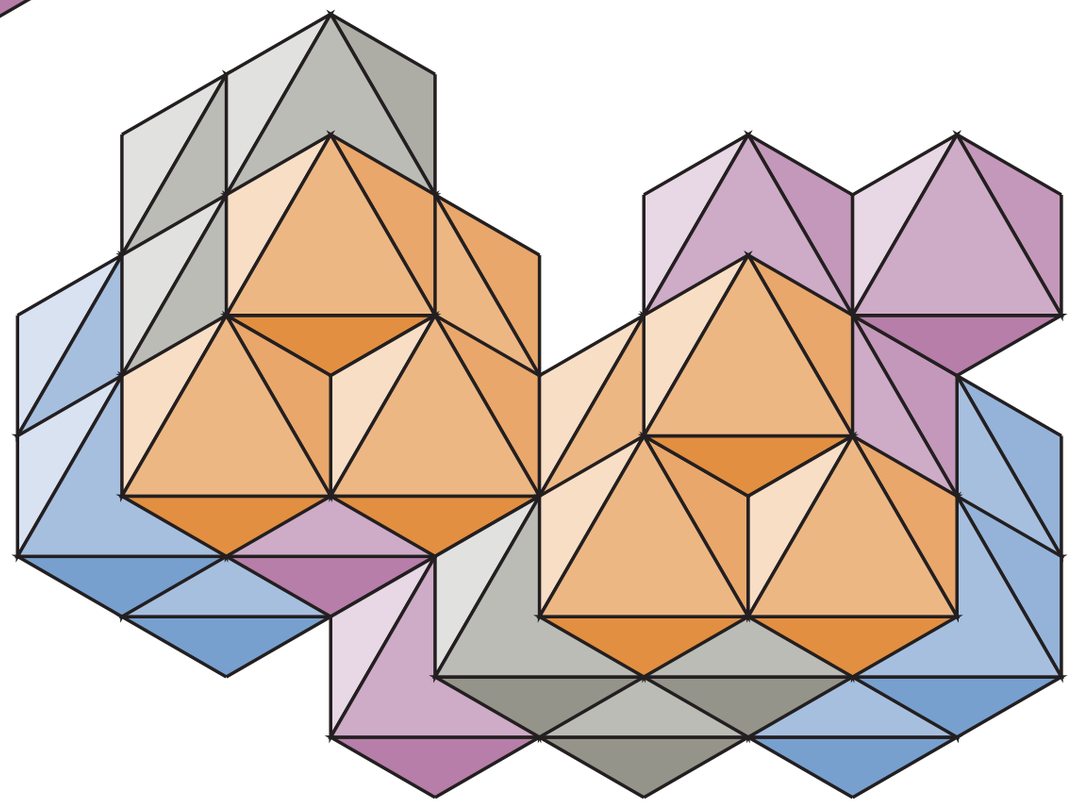
beta90

The serine join units

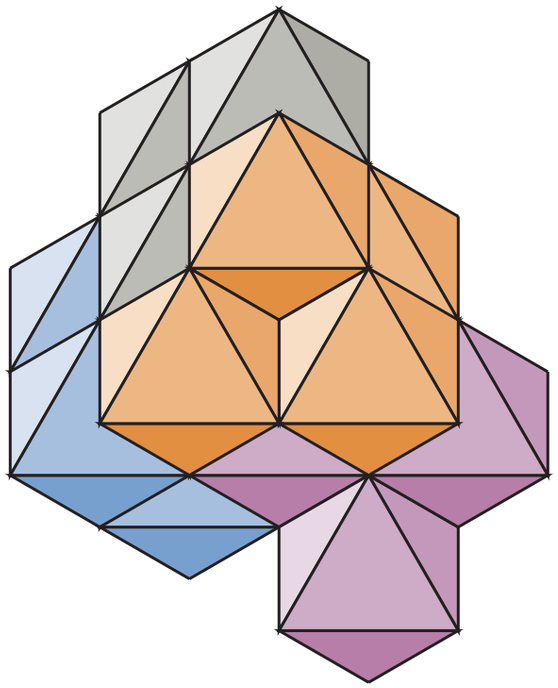
The joining of join units

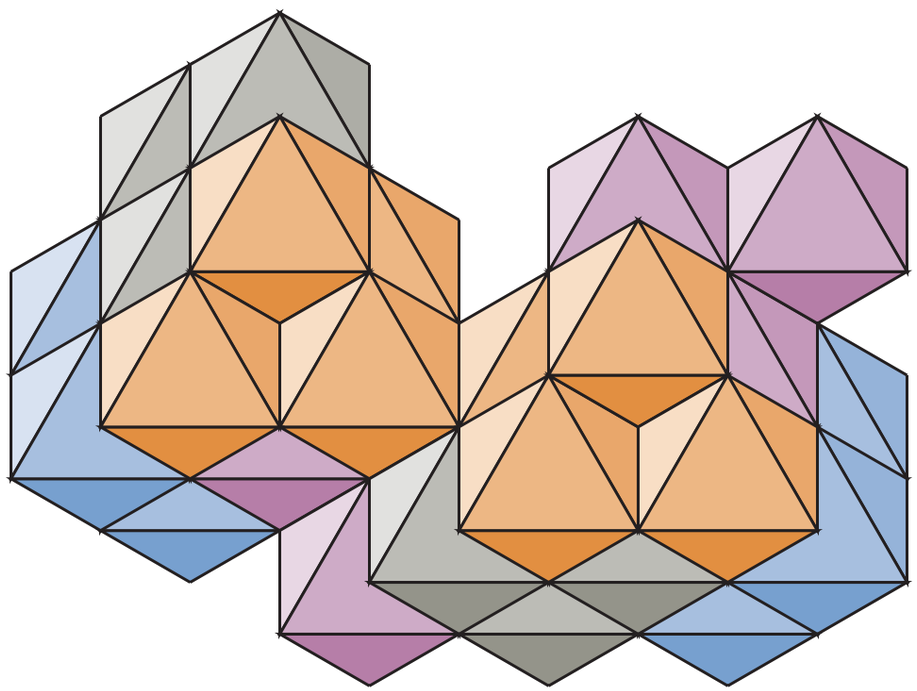


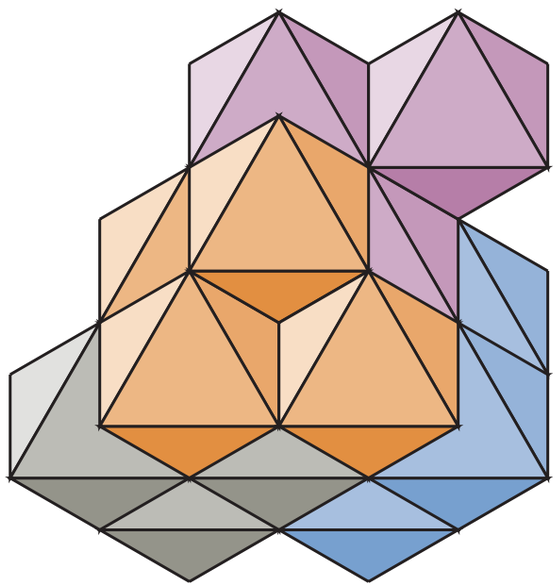


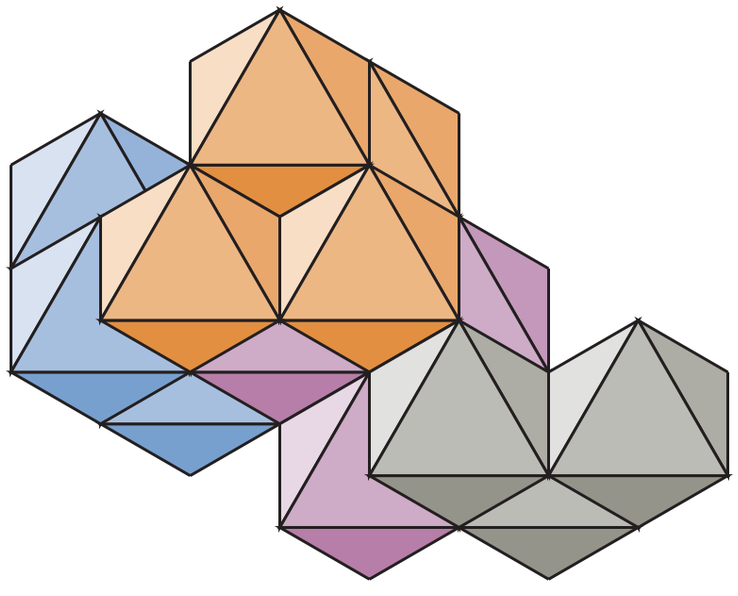


Joining two alpha join units

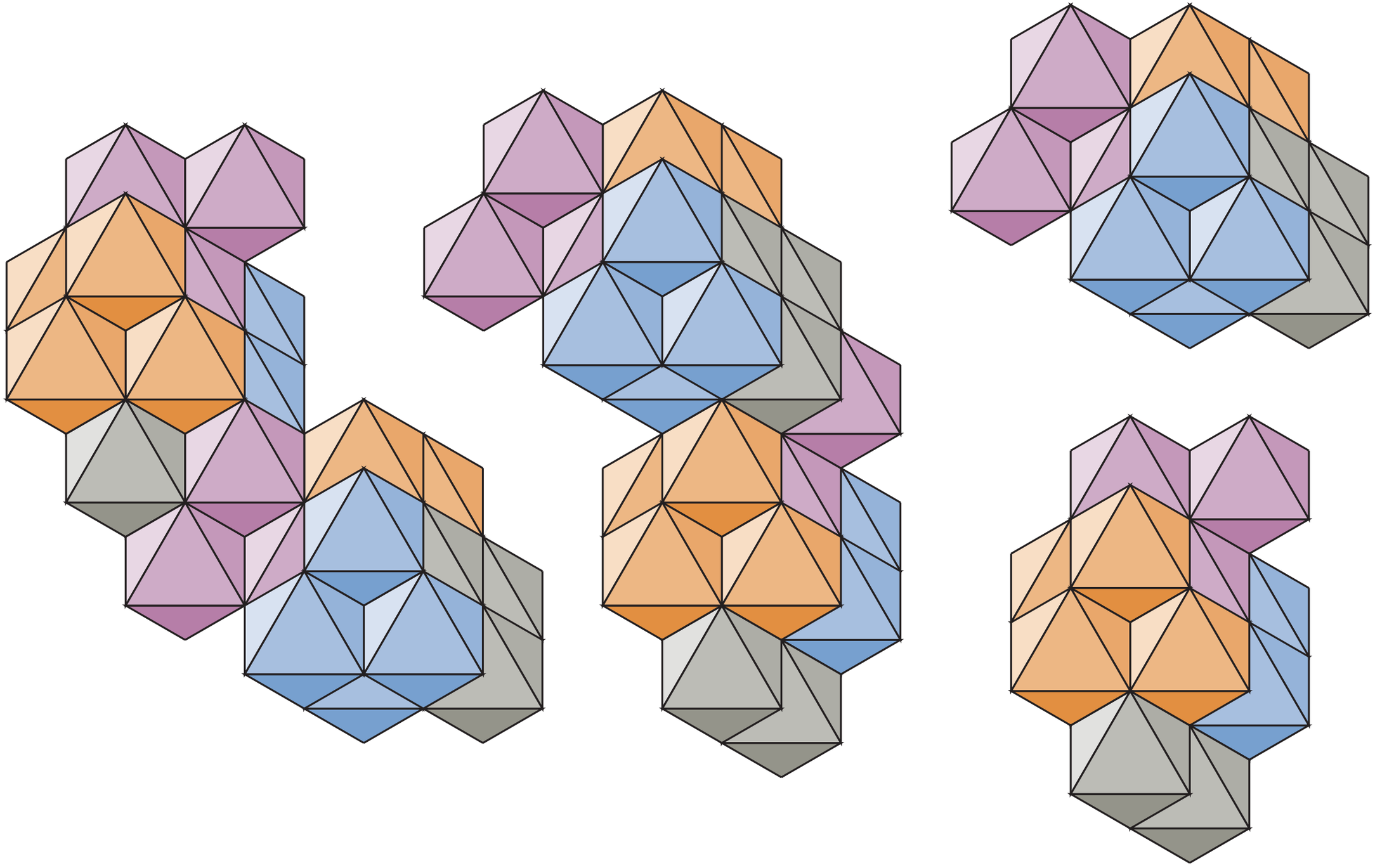








Joining completes the amino



Joining two 32-chain join units

Facial planes of the genetic cube

X = U		Y			
		U	C	A	G
Z	U	phe	ser	tyr	cys
	C	phe	ser	tyr	cys
	A	leu	ser		
	G	leu	ser		trp

X = C		Y			
		U	C	A	G
Z	U	leu	pro	his	arg
	C	leu	pro	his	arg
	A	leu	pro	gln	arg
	G	leu	pro	gln	arg

X = A		Y			
		U	C	A	G
Z	U	ile	thr	asn	ser
	C	ile	thr	asn	ser
	A	ile	thr	lys	arg
	G	met	thr	lys	arg

X = G		Y			
		U	C	A	G
Z	U	val	ala	asp	gly
	C	val	ala	asp	gly
	A	val	ala	glu	gly
	G	val	ala	glu	gly

Y = U		X			
		U	C	A	G
Z	U	phe	leu	ile	val
	C	phe	leu	ile	val
	A	leu	leu	ile	val
	G	leu	leu	met	val

Y = C		X			
		U	C	A	G
Z	U	ser	pro	thr	ala
	C	ser	pro	thr	ala
	A	ser	pro	thr	ala
	G	ser	pro	thr	ala

Y = A		X			
		U	C	A	G
Z	U	tyr	his	asn	asp
	C	tyr	his	asn	asp
	A		gln	lys	glu
	G		gln	lys	glu

Y = G		X			
		U	C	A	G
Z	U	cys	arg	ser	gly
	C	cys	arg	ser	gly
	A		arg	arg	gly
	G	trp	arg	arg	gly

Z = U		Y			
		U	C	A	G
X	U	phe	ser	tyr	cys
	C	leu	pro	his	arg
	A	ile	thr	asn	ser
	G	val	ala	asp	gly

Z = C		Y			
		U	C	A	G
X	U	phe	ser	tyr	cys
	C	leu	pro	his	arg
	A	ile	thr	asn	ser
	G	val	ala	asp	gly

Z = A		Y			
		U	C	A	G
X	U	leu	ser		
	C	leu	pro	gln	arg
	A	ile	thr	lys	arg
	G	val	ala	glu	gly

Z = G		Y			
		U	C	A	G
X	U	leu	ser		trp
	C	leu	pro	gln	arg
	A	met	thr	lys	arg
	G	val	ala	glu	gly

Codons per residue

codons	sidechain				
6	ser	arg	leu		
4	pro	thr	val	ala	gly
3	ile				
2	phe	tyr	cys	his	gln
	asn	lys	asp	glu	
1	met	trp			

Each codon specifies a join unit and its sidechain.

There are no duplicates.

References

www.robertwilliamwhitby.com/

The end