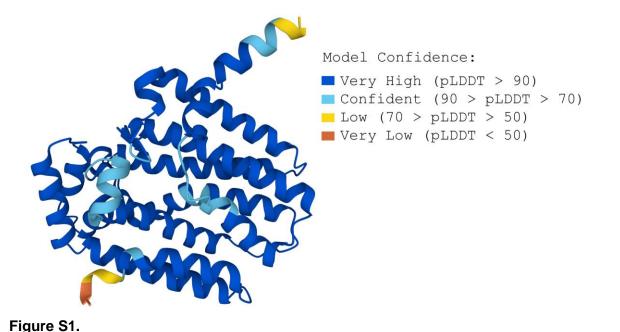
SUPPLEMENTARY DATA

Structural insight into geranylgeranyl diphosphate synthase (GGDPS) for cancer therapy Andrew C. Pham¹, Sarah A. Holstein², Gloria E. O. Borgstahl^{1,3*}

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AlphaFold model of an hGGDPS monomer (1). Regions are colored based on the perresidue confidence scores (pLDDT) ranging from 0 - 100 with higher scores reflecting welldefined parts of the structure. Residues which show a "very high" confidence score have been determined with supporting crystal structures. These residues include those at the active site. Disordered loops that have not been structurally established are shown to have "confident" scores (His194-Phe204, Leu22-Thr29). The N-terminal (Met1-Lys3) and Cterminal ends (Glu297-Glu300) are very disordered and are shown to have "low" and "very low" confidence scores.

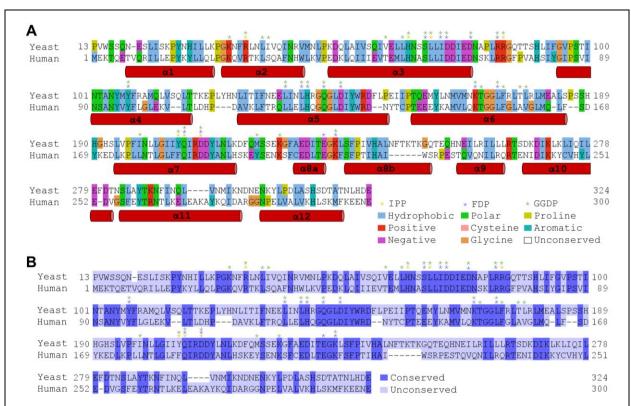


Figure S2.

Sequence alignment of hGGDPS and yGGDPS reveals similarity in residue properties and overall conservation. **A.** Sequence alignment highlighting the conservation of residue properties. Helices are shown as red cylinders and are numbered sequentially. Residues contributing to IPP, FDP, and GGDP binding are shown as colored asterisks. **B.** A sequence alignment of the conservation of residues between yGGDPS and hGGDPS. Conserved residues are colored in a dark blue while unconserved residues are colored a light blue. A pairwise alignment calculation found yGGDPS and hGGDPS to be 39.2% similar. Asterisks represent binding sites for the respective ligands as indicated in the legend. Allignment was performed with the Jalview software of *Saccharomyces cerevisiae* GGDPS (yGGDPS Uniprot: Q12051, top) and *Homo sapiens* GGDPS (hGGDPS Uniprot: O95749, bottom).

Dimer Interface ^a				Trimer Interf	Trimer Interface ^b		
α4	α5	α1	α6	α3	Region 1	Region 2	
Y83	V112	Q5	Q150	163	R10	E226	
G84	K113	V8		166	E14	S227	
185	F115	111		E65	Y18	T228	
P86	T116	L12			Q21	Q229	
S87	L119	E14			K71	N232	
189	L120				L72	1233	
N90	H123				F76	R235	
N93	Q124				P77	Q236	
Y94	Q126				S81	N240	
Y96	G127				182	1243	
F97	L126				Y83	Y246	
L98	L128					Y250	
L100	1130						
E101	Y131						
L104	R133						
	D134						

Table S1. Residues involved in the hGGDPS oligomerization

^a Dimer interface residues were determined utilizing the *InterfaceResidues* command in PyMOL ^b Trimer interface residues were described by Kavanaugh *et al.* (2)

Yeast (IPP) a	Human (IPP) ^a	Yeast (FDP) ^b	Human (FDP) ^b
R39	R28	S71	S60
H68	H57	L72	L61
L72	L61	174	163
R85	R74	D75	D64
Y205	F184	D79	D68
Q206	Q185	R84	R73
D209	D188	Y107	Y96
		L135	L119
		L138	L122
		H139	H123
		Q142	Q126
		D145	D129
		K169	K151
		L173	L155
		Q206	Q185
		D209	D188
		E231	E210
		K233	K212
		1	

Table S2. Residues involved in IPP and FDP binding

^a Residues found to have sidechains within 4 Å of the IPP substrate in 2E8T and AF 2Q80 ^b Residues found to have sidechains within 4 Å of the FDP substrate in 2E8T and AF 2Q80

Yeast (GGDP) ^a	Human (GGDP) ^a	Yeast (GGDPi) ^b	Human (GGDPi) ^b
K36	K25	R39	R28
R39	R28	L42	L31
L67	L56	143	S32
H68	H57	V64	T53
S71	S60	H68	D64
L72	L61	L72	D68
174	163	D75	R73
D75	D64	D79	D129
R85	R74	R84	K151
Y107	Y96	L138	T152
L135	L119	Q142	L155
L138	L122	K169	F156
H139	H123	L173	A159
Q142	Q126	F174	V160
K169	K151	T177	Q185
Y205	F184	1198	D188
Q206	Q185	Y205	Y198
		Q206	K202
		D209	K212
		K233	

Table S3. Residues involved in GGDP binding

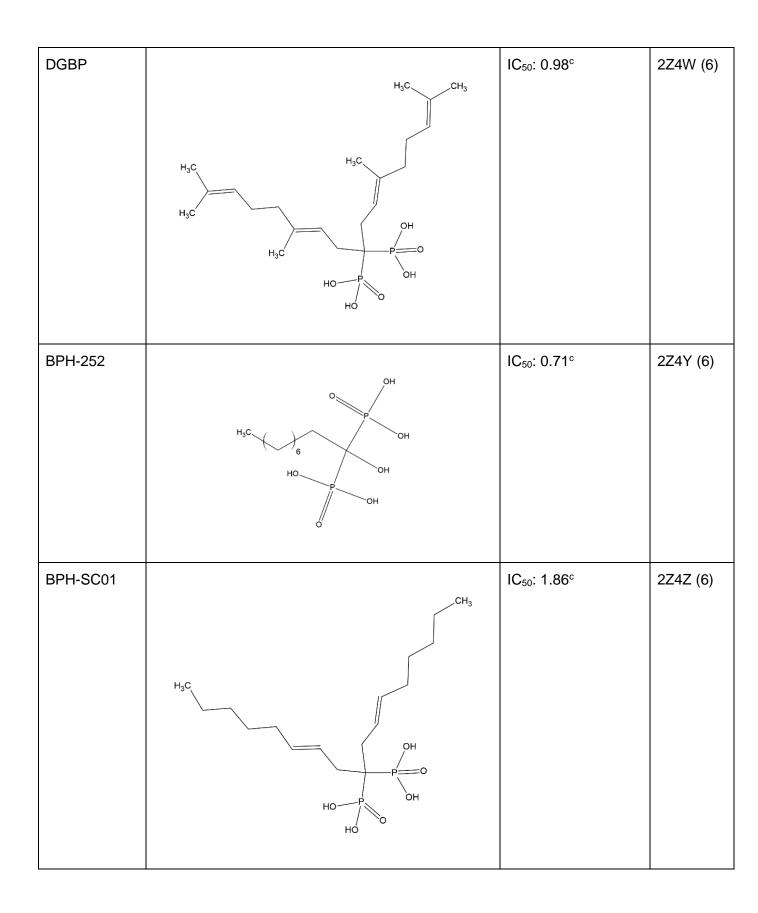
^a Residues found to have sidechains within 4 Å of the GGDP product in 2E8V and AF 2Q80 ^b Residues found to have sidechains within 4 Å of the GGDP product in 2Z4V and AF 2Q80

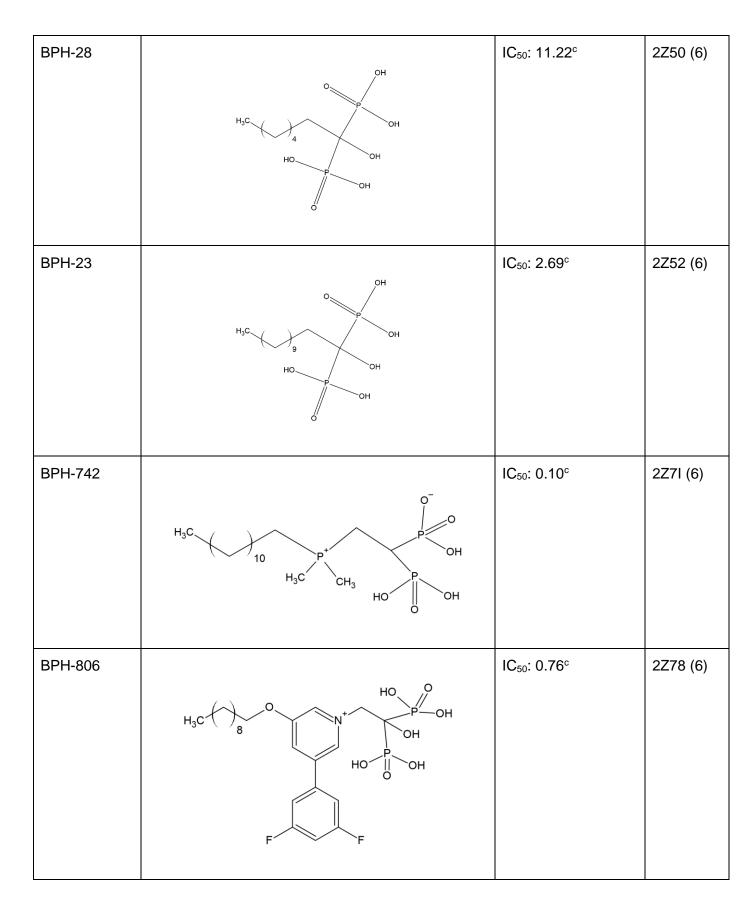
Species	PDB	Compound	Reference
Human	6G31	Zoledronic Acid	Lisnyansky et al. 2018 (3)
Human	6R4V	Ibandronate	Lisnyansky et al. 2019 (4)
Human	6C57	FV0109	Lacbay et al. 2018 (5)
Yeast	2Z4W	BPH-749 (DGBP)	Chen et al. 2008 (6)
Yeast	2Z4Y	BPH-252	Chen et al. 2008 (6)
Yeast	2Z4Z	BPH-SC01	Chen et al. 2008 (6)
Yeast	2Z50	BPH-28	Chen et al. 2008 (6)
Yeast	2Z52	BPH-23	Chen et al. 2008 (6)
Yeast	2Z7I	BPH-742	Chen et al. 2008 (6)
Yeast	2Z78	BPH-806	Chen et al. 2008 (6)
Yeast	2E95	BPH-675	Guo et al. 2007 (7)
Yeast	2E94	BPH-364	Guo et al. 2007 (7)
Yeast	2E93	BPH-629	Guo et al. 2007 (7)
Yeast	2E92	Minodronate	Guo et al. 2007 (7)
Yeast	2E91	BPH-91	Guo et al. 2007 (7)
Yeast	2ZEU	BPH-715	Zhang et al. 2009 (8)

Table S4. Drug-bound PDB structures

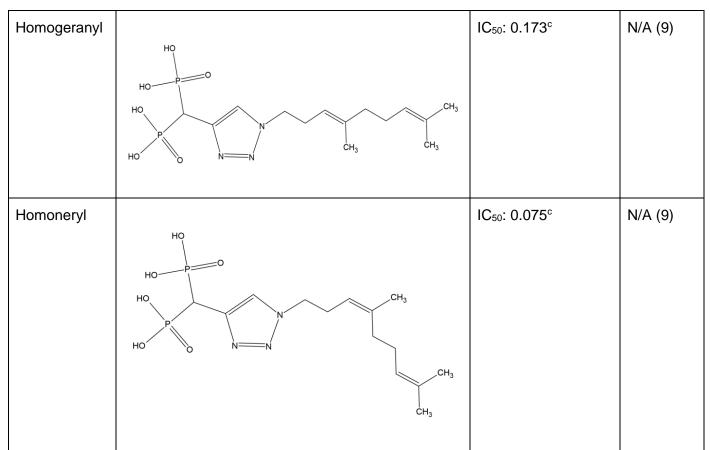
Compound	Structure	IC50 (μM)*	PDB
Zoledronic Acid		K _i : 2.1 ^a yGGDPS IC ₅₀ : 0.66 ^b hGGDPS IC ₅₀ : 97 ^c	6G31 (3) 2E91 (7)
Ibandronate	H ₃ C H ₃ C HO HO HO HO HO HO HO HO HO HO HO HO HO	N/A	6R4V (4)
FV0109		IC ₅₀ : 0.042 ^c EC ₅₀ : 0.70 ^d	6C57 (5)

Table S5. Drug-bound PDB structures





BPH-675	O O O P OH S NH OH O OH O OH OH OH	yGGDPS IC ₅₀ : 0.20 ^b hGGDPS IC ₅₀ : 2.6 ^c	2E95 (7)
BPH-364		yGGDPS IC ₅₀ : 0.03 ^b hGGDPS IC ₅₀ : 8.2 ^c	2E94 (7)
BPH-629	OH OH OH OH OH OH	yGGDPS IC ₅₀ : 0.28 ^b hGGDPS IC ₅₀ : 4.0 ^c	2E93 (7)
Minodronate		yGGDPS IC ₅₀ : 0.34 ^b hGGDPS IC ₅₀ : 65 ^c	2E92 (7)
BPH-715		IC ₅₀ : 2.9 ^e	2ZEU (8)



* Unless stated, IC⁵⁰ refers to inhibition of hGGDPS

^a Determined from differential scanning fluorimetry of wild-type GGDPS with zoledronate

^b Determined from *in vitro* enzyme assay of yGGDPS with the corresponding compound

^c Determined from *in vitro* enzyme assay of hGGDPS with the corresponding compound

^d Determined through MTT after 72h incubation of cells with and without compound

^e Determined through a mouse fetal metatarsal ⁴³Ca²⁺ release inhibition assay

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