

Processing doc. - non linear

DB 9948

②

2

①

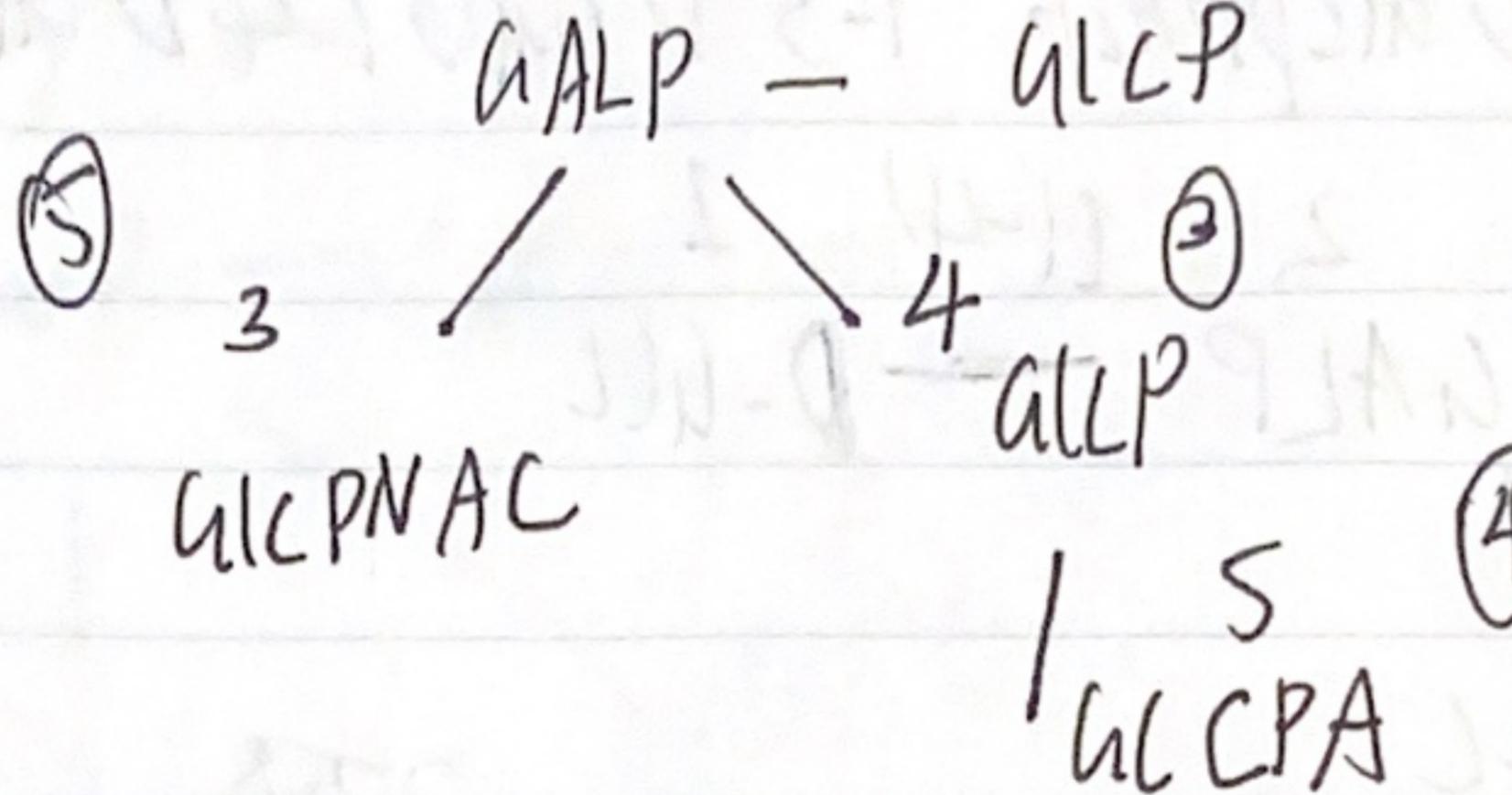
1

circle

① → Res

non-circle

② → PDB



Res.

PDB.

1

1

2

2

3

4

4

5

5

3

2.

DB26476

③

2

(1-2)

①

ARAF — ARAF

③

3

(1-3)

| (1-5)

④

⑤

5

(1-5)

⑦

⑧

4

ARAF

ARAF

ARAF

ARAF

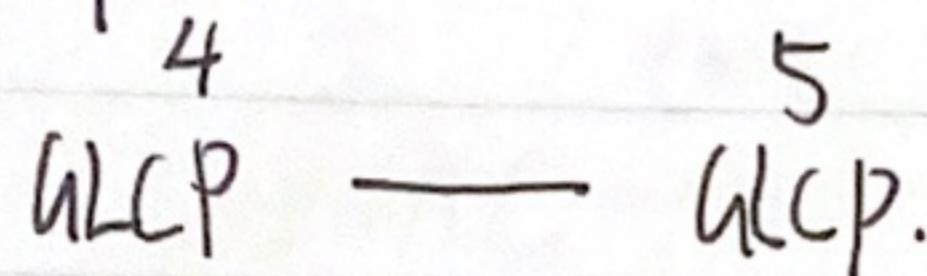
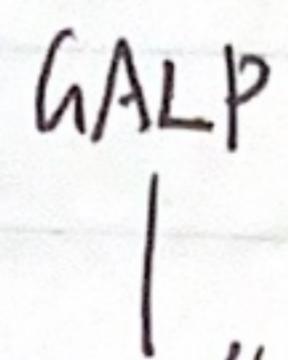
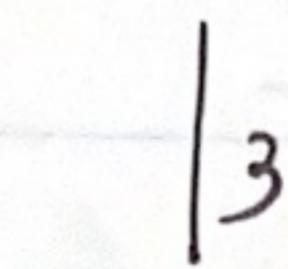
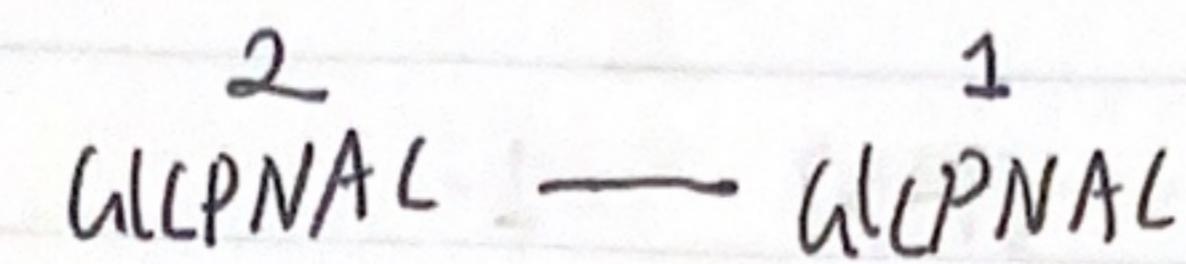
ARAF

⑥

16

ARAF

3. DB26405



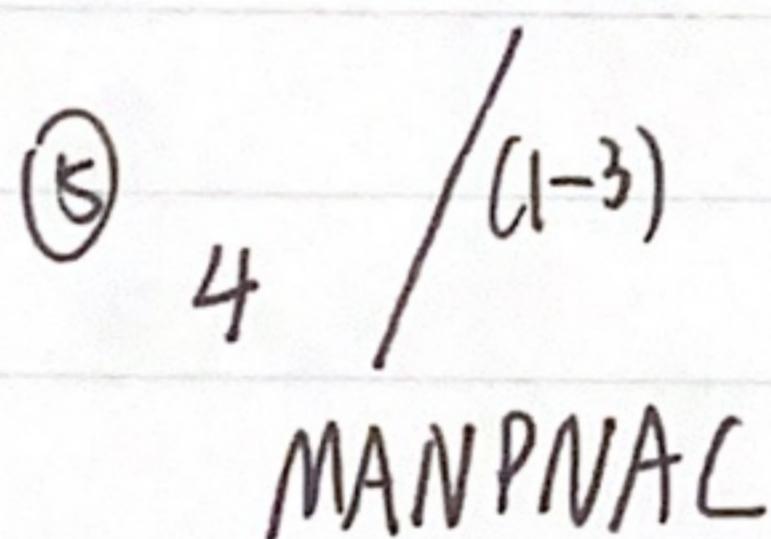
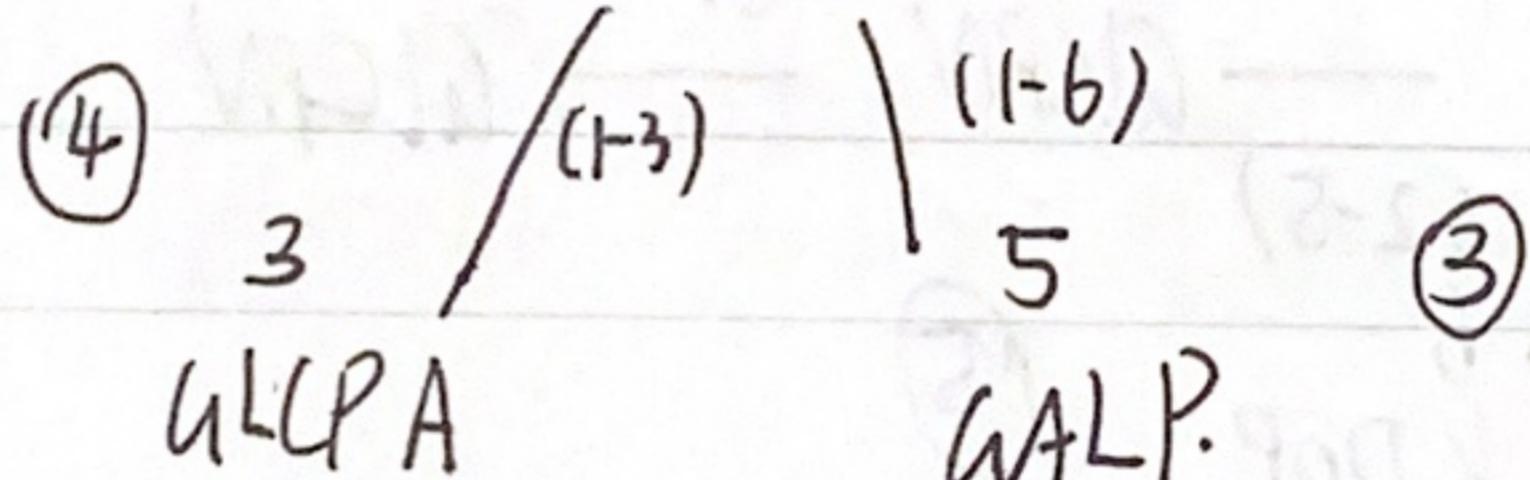
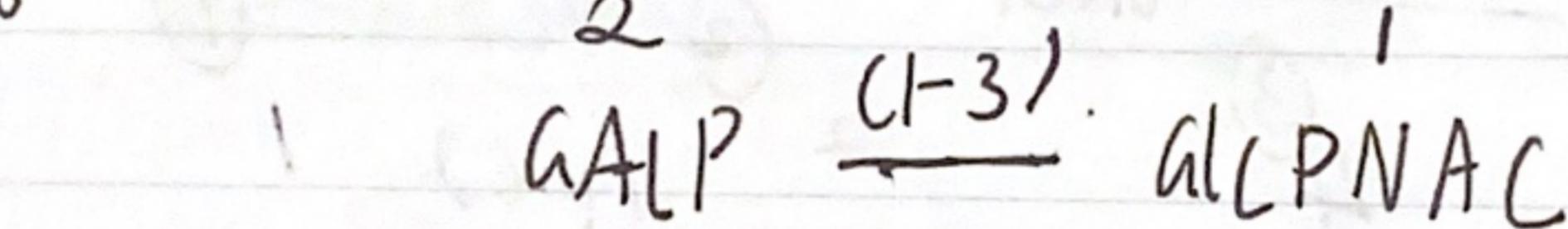
✓

4 DB26521

✓ ②

5 DB4858

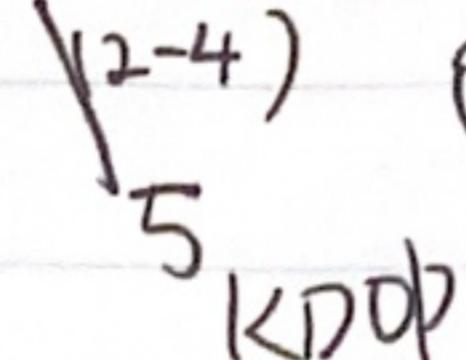
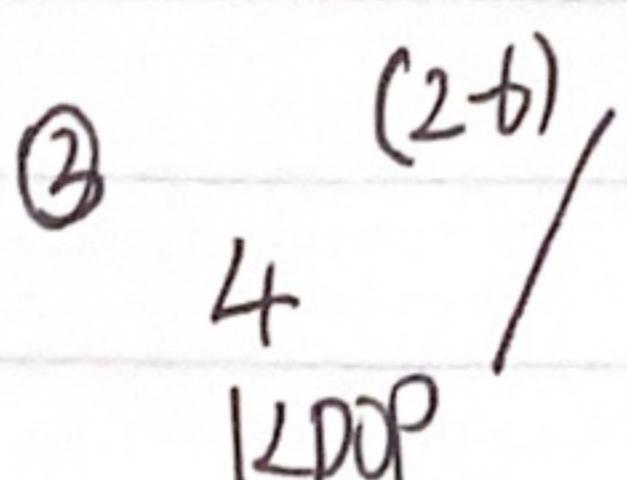
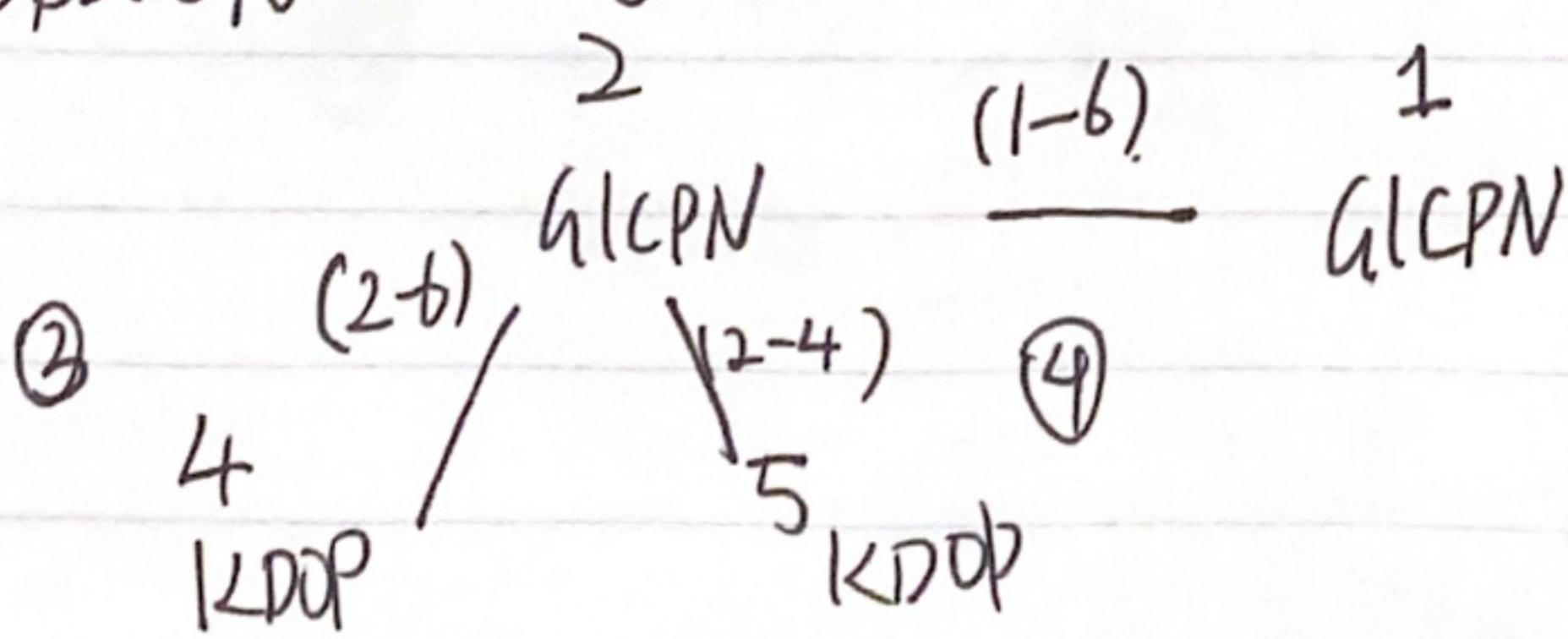
2 ①



Res	PDB
1	1
2	2
3	5
4	3
5	4

6 DB26370

② ①



Res	PDB
1	1
2	2
3	4
4	5

7. DB26404.

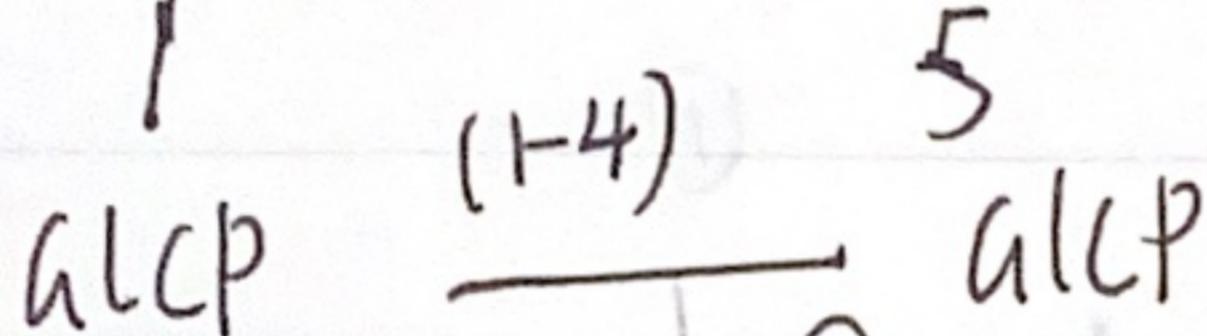
2 (1-3) 1



3 / (1-3)

GALP

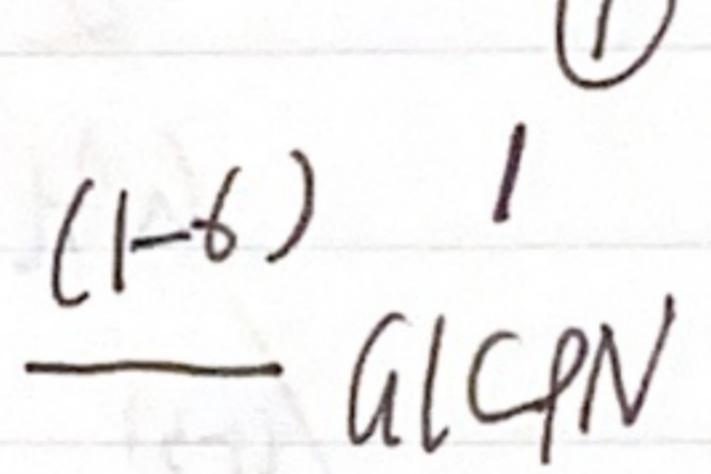
4 | (1-3)



③ 4



② 2

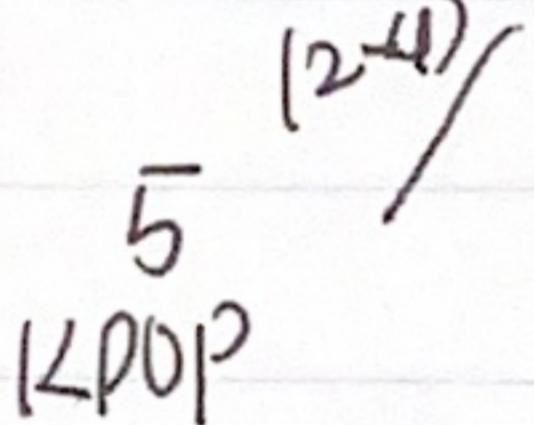


① 1

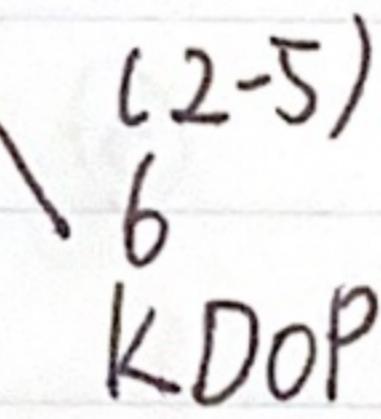
8.

DB26379.

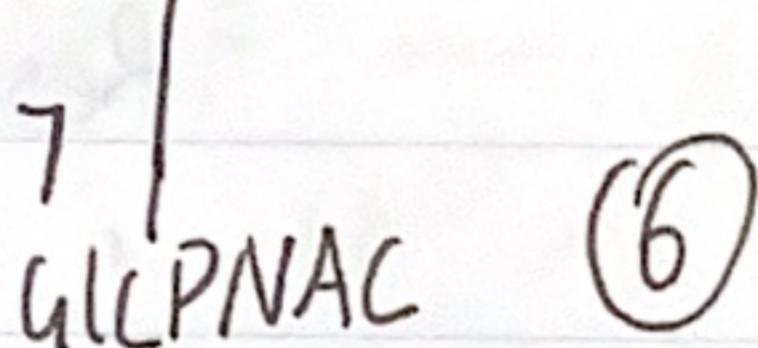
④



5



⑤



⑥

Res

PDB

1

2

3

4

5

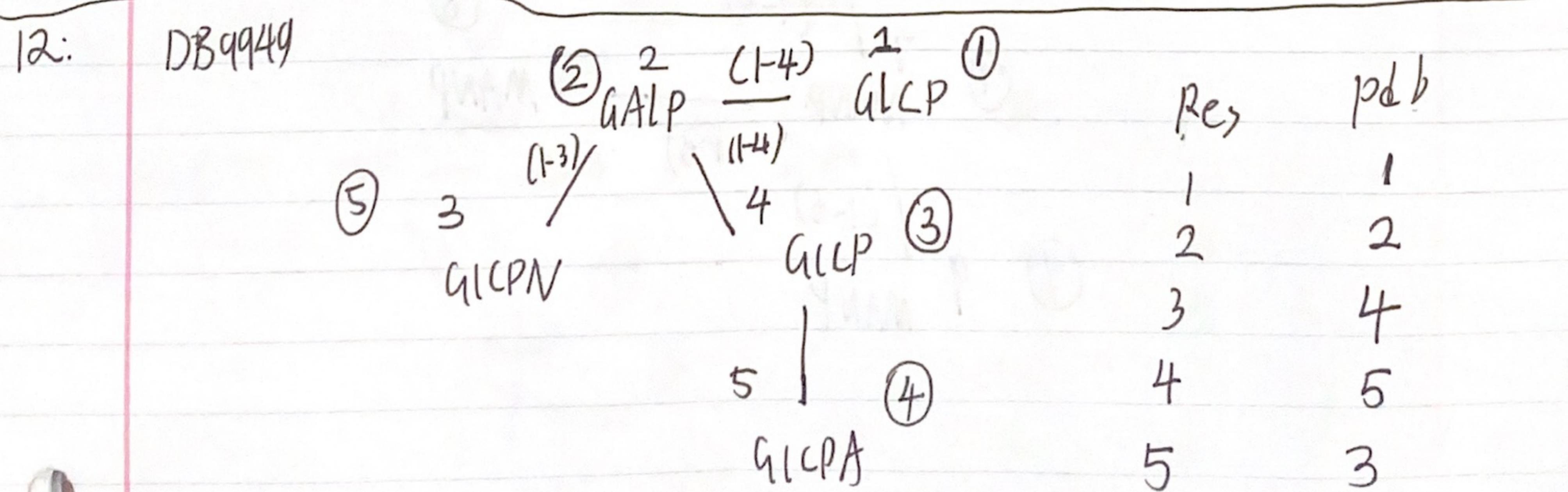
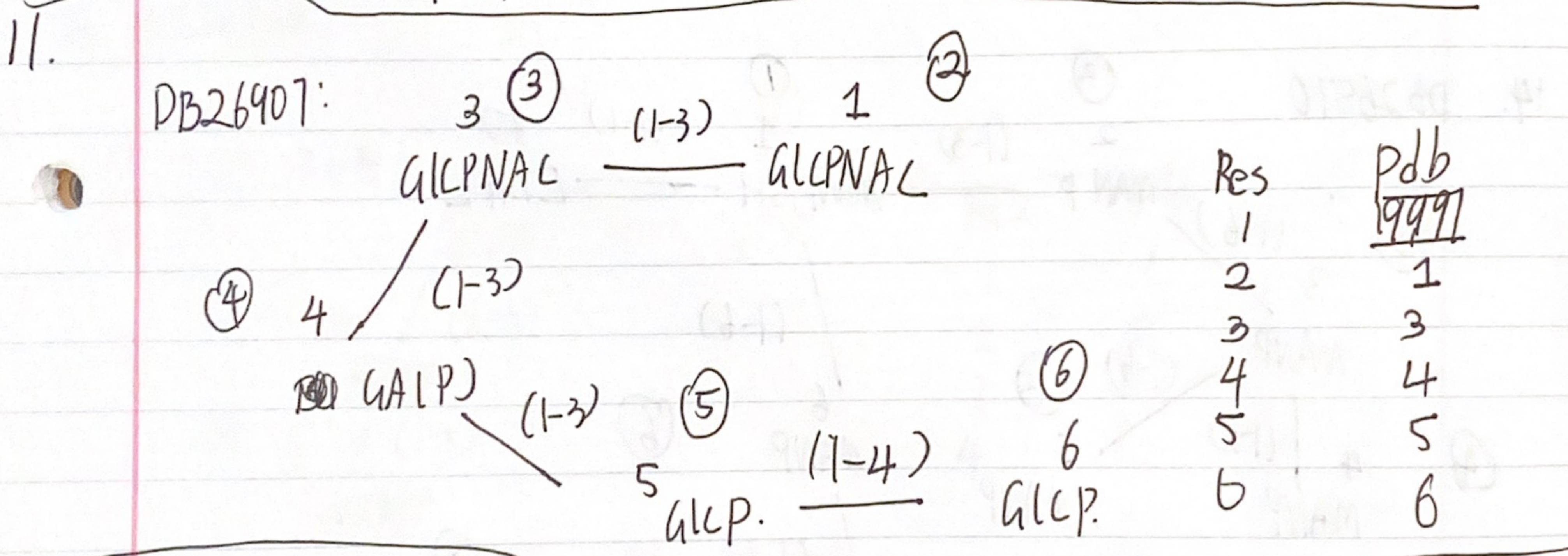
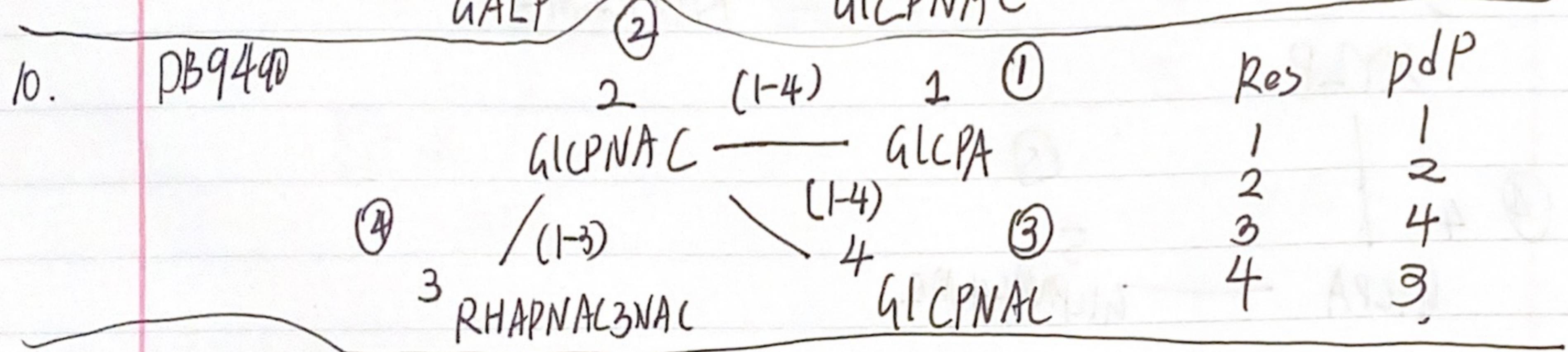
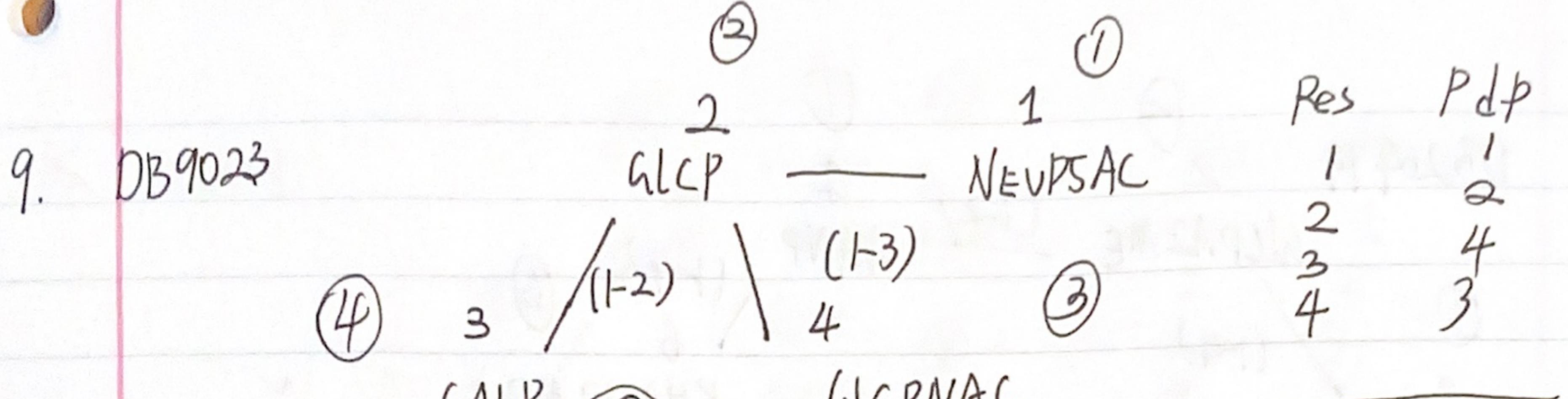
6

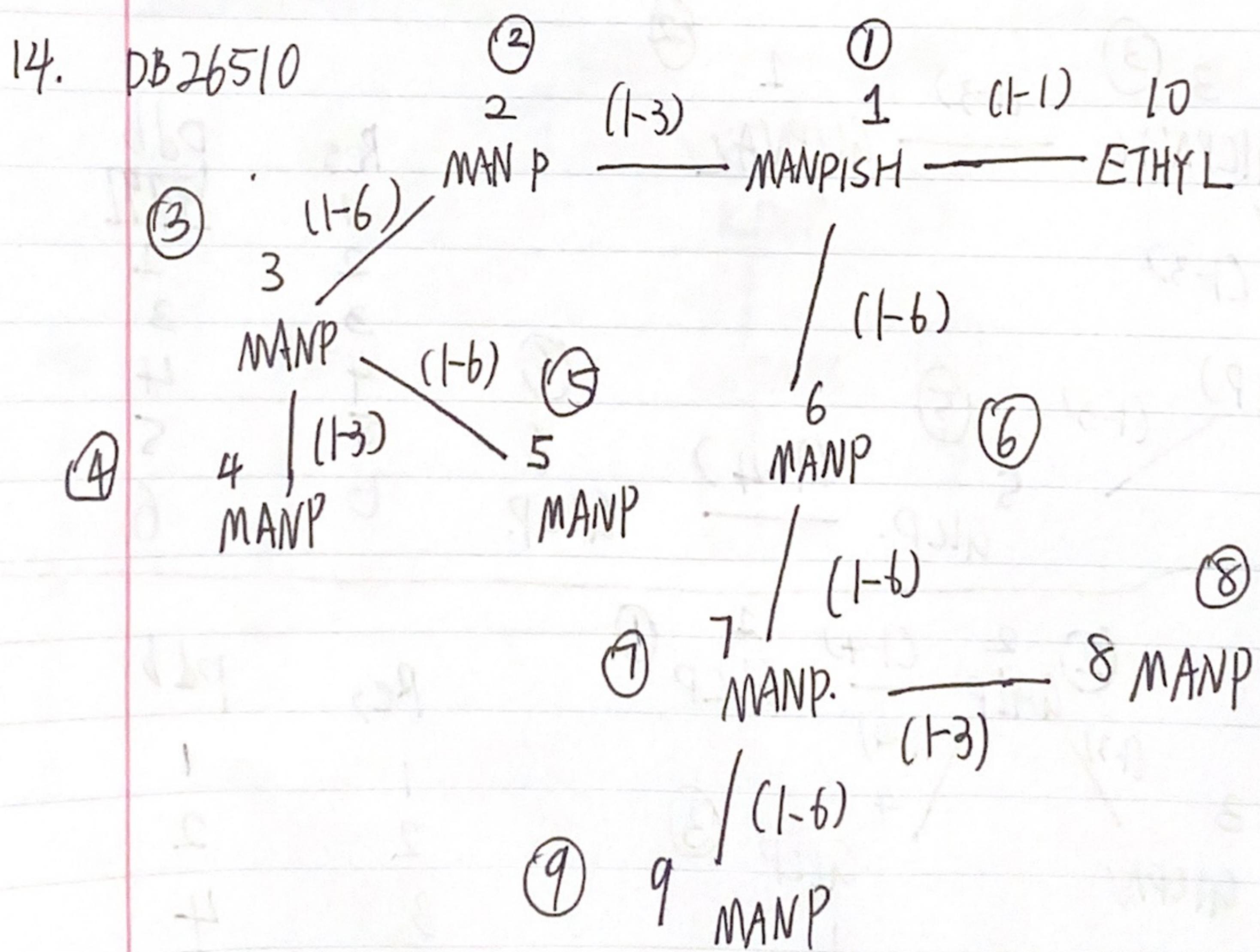
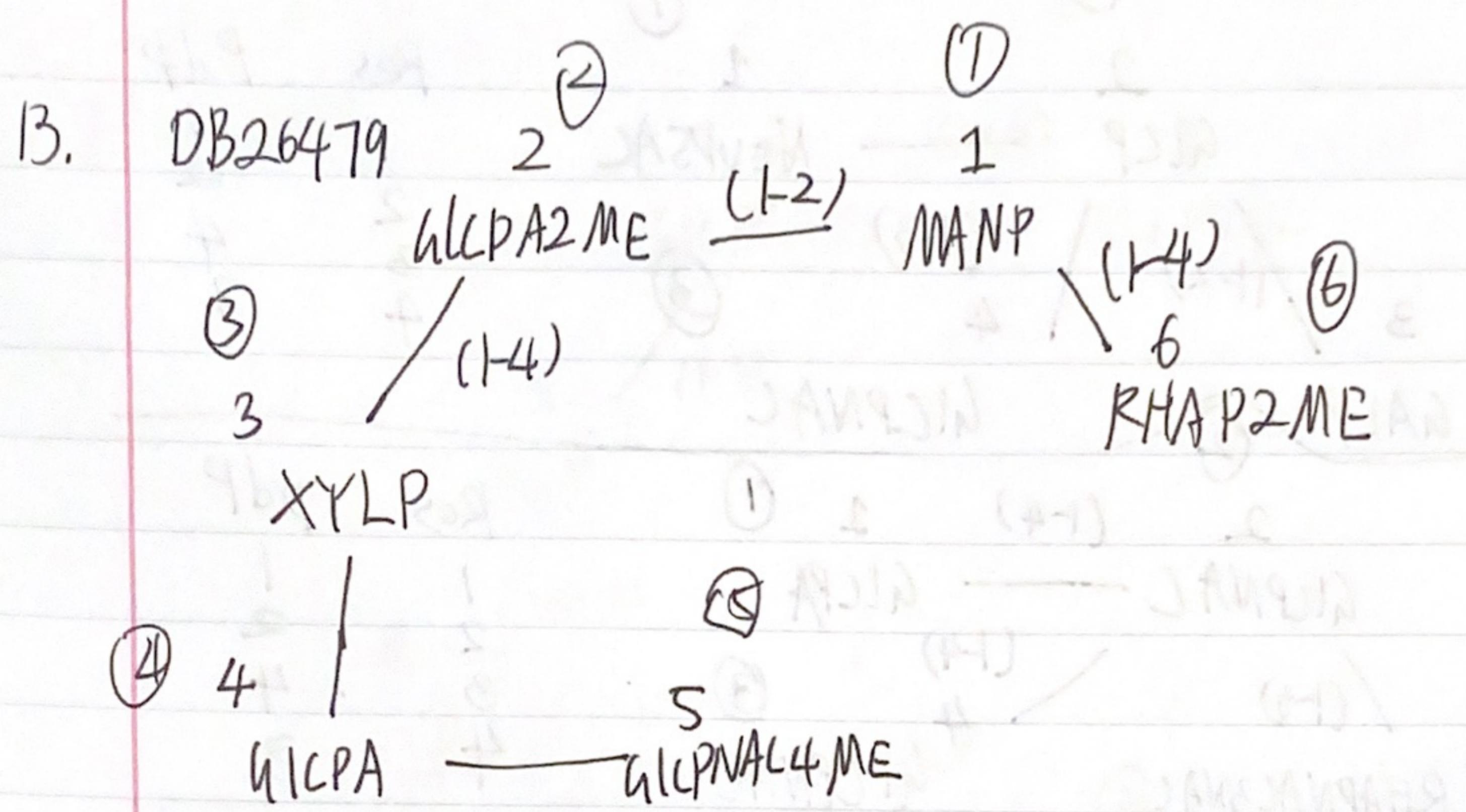
6

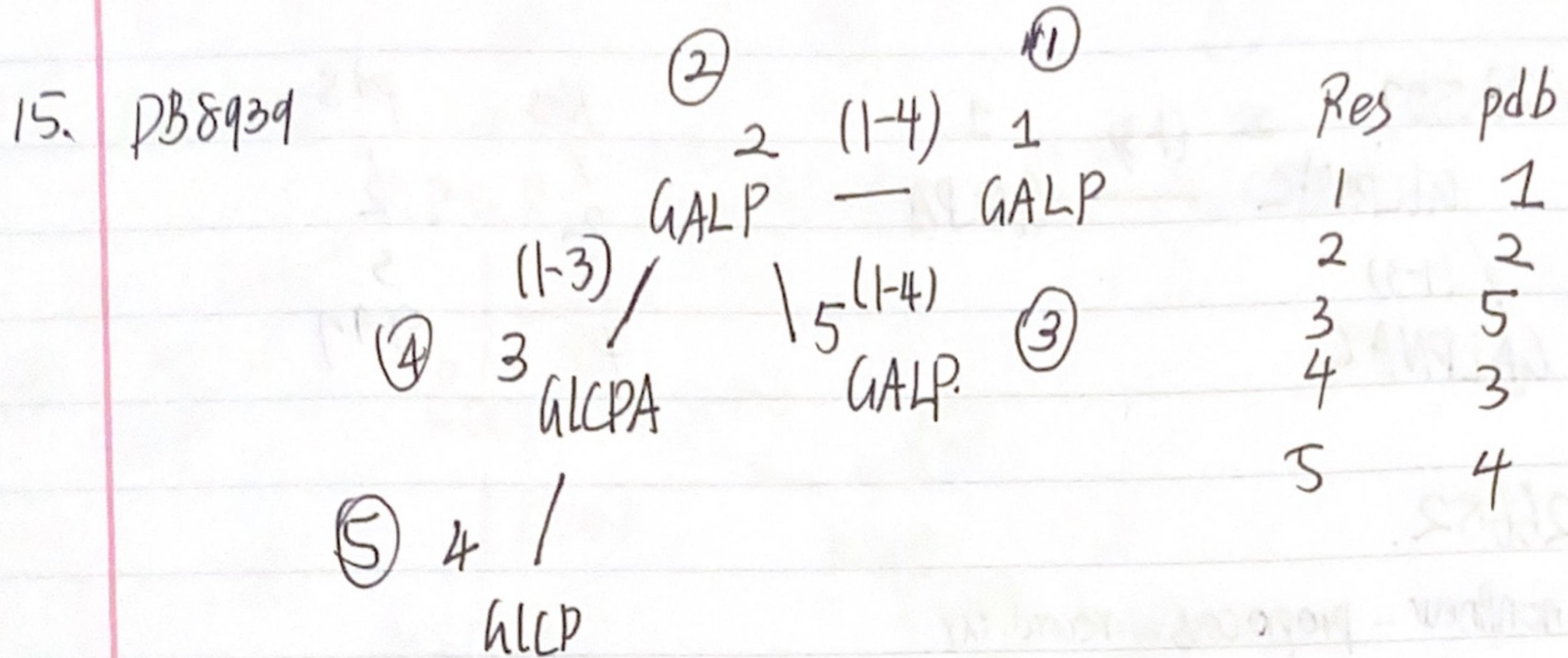
7

7

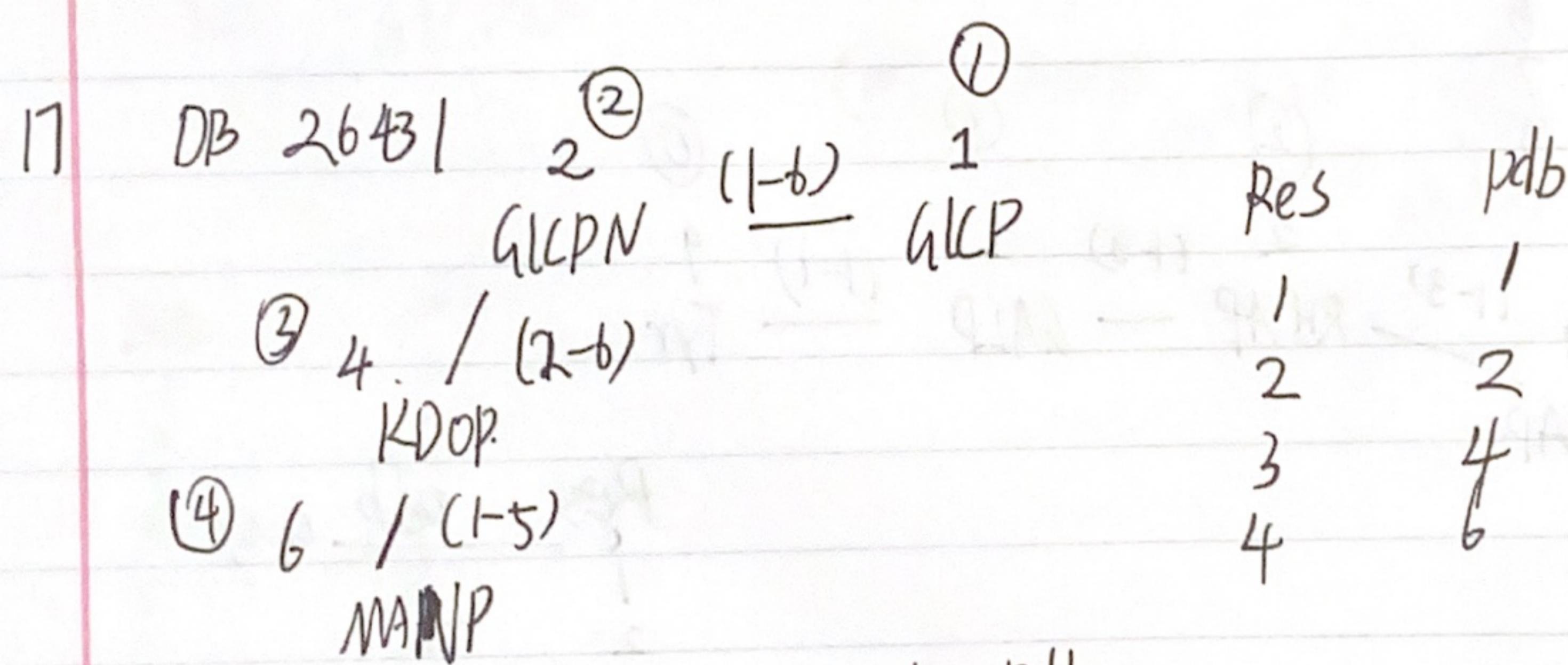
8



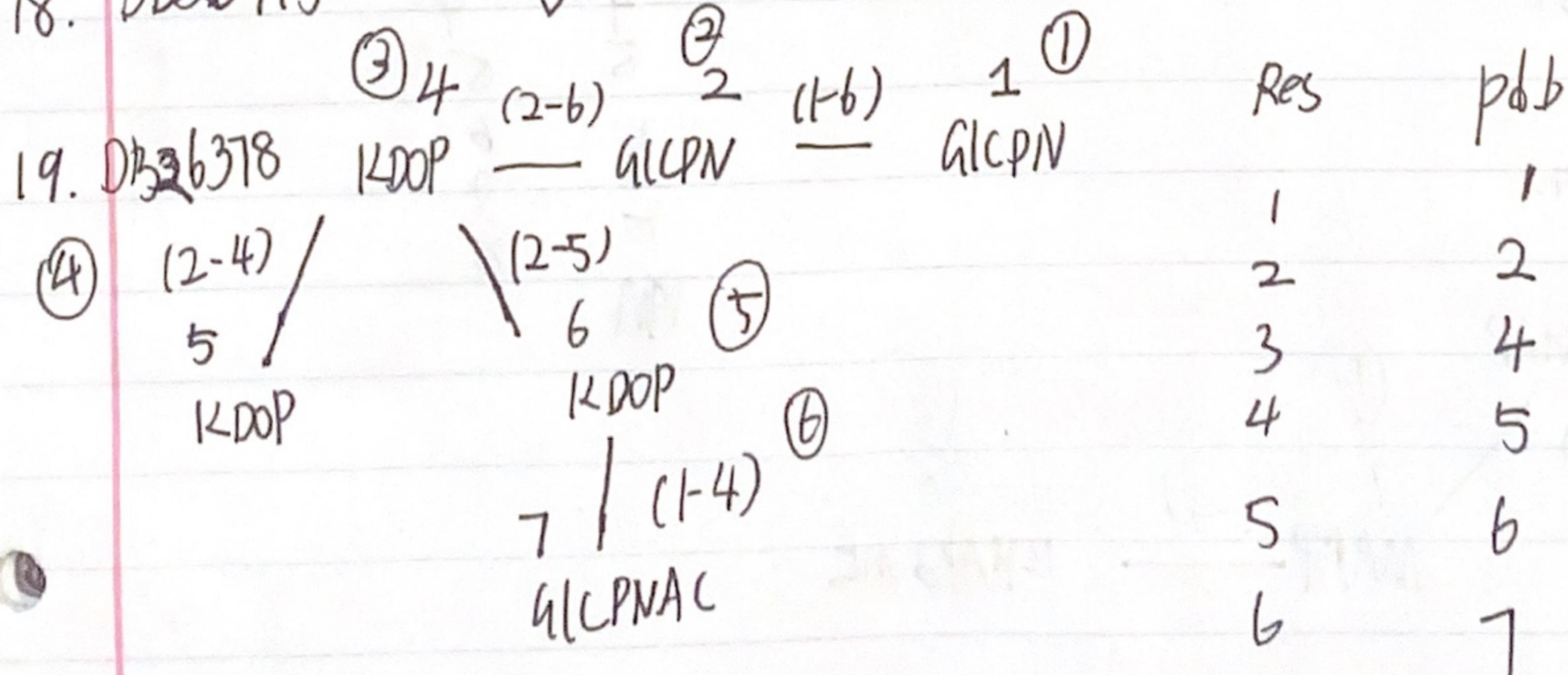


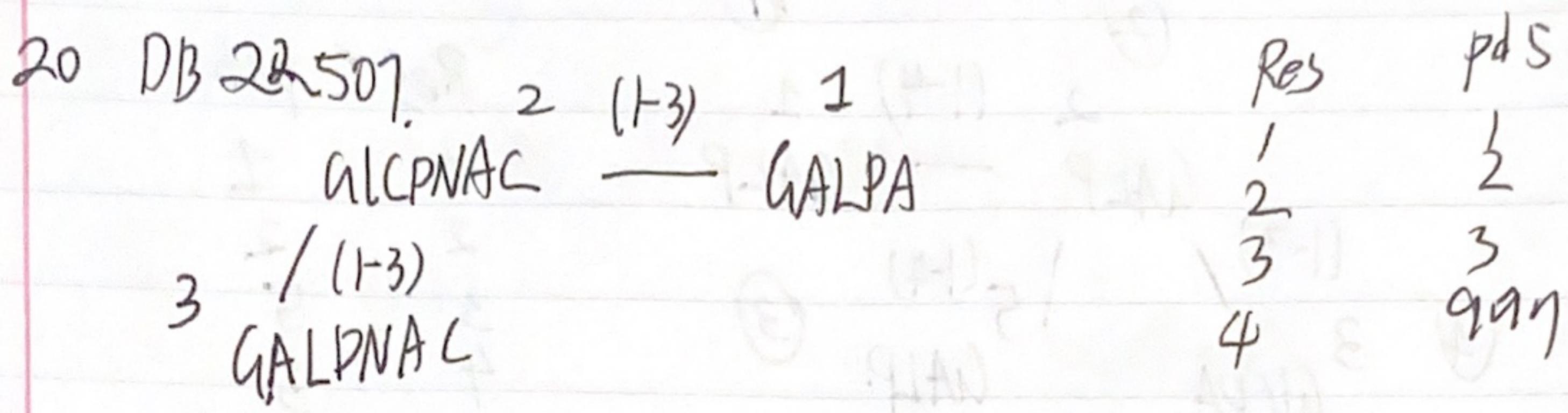


16. PB26122. ✓



18. DB26715 ✓ PO3 in Pdb

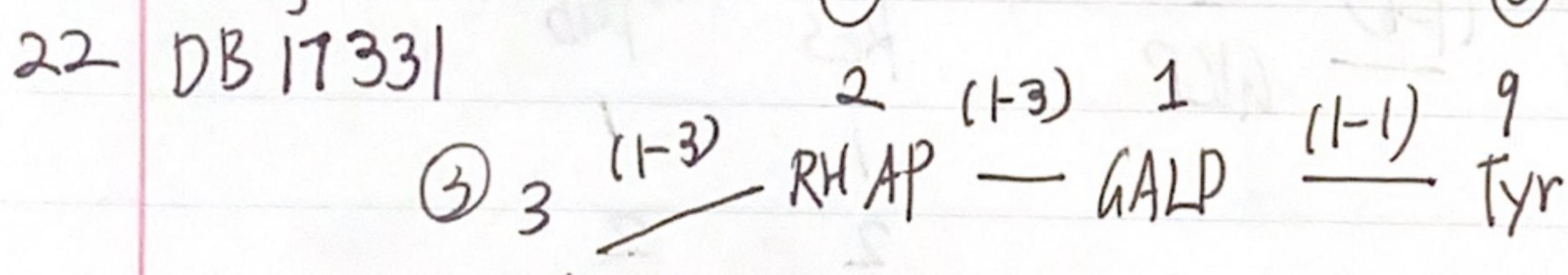




21. DB 26682.

In nonlinear - preprocess - record.txt.

Res	pdS
1	3
2	4
3	6
4	7
5	8



RHAP.

④ 4 / (1-3)

RHAP

⑤ 5 / (1-3)

MANP

(1-4)

6 RHAP

(1-3)

7

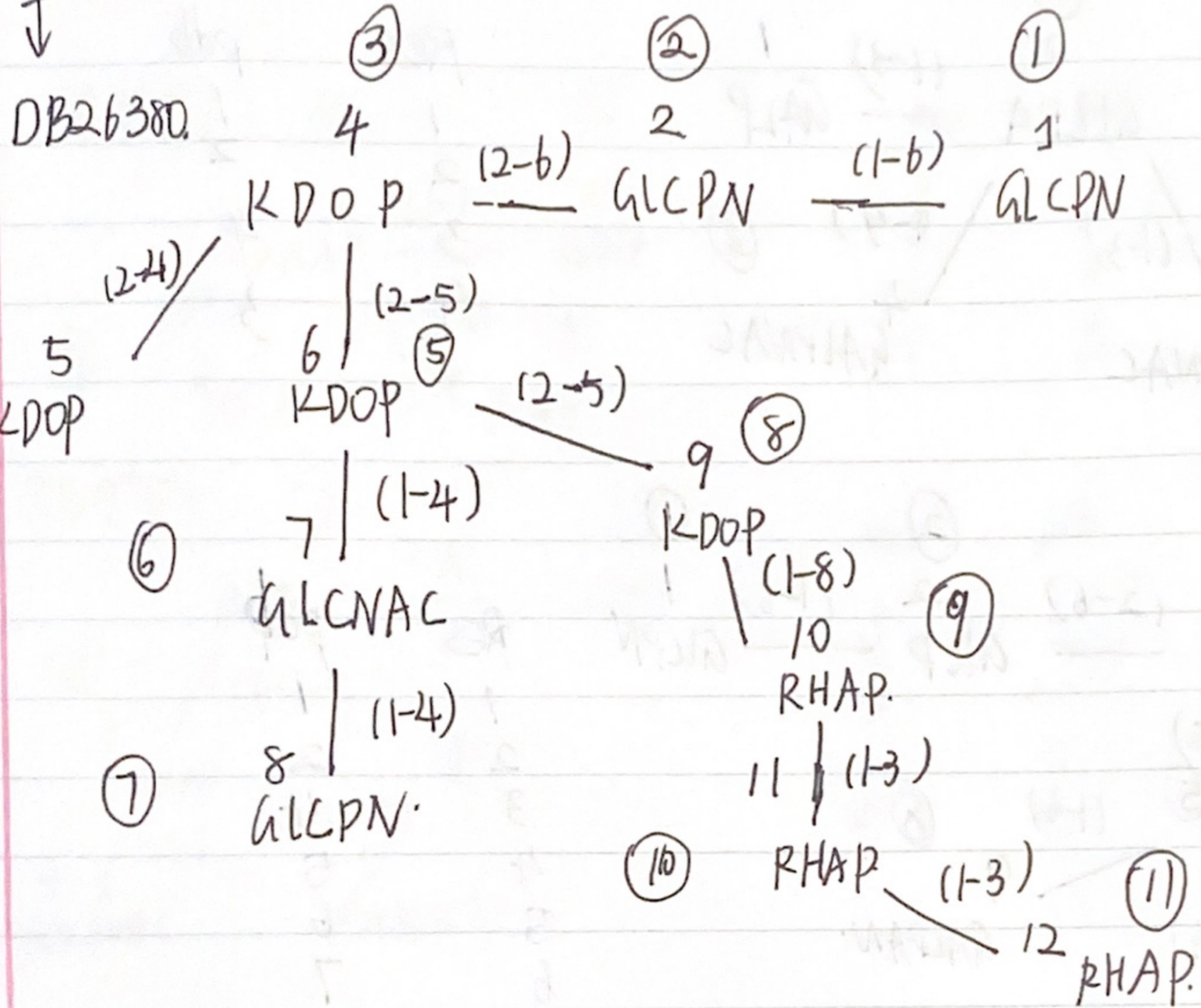
MANP (1-4)

RHAP3ME

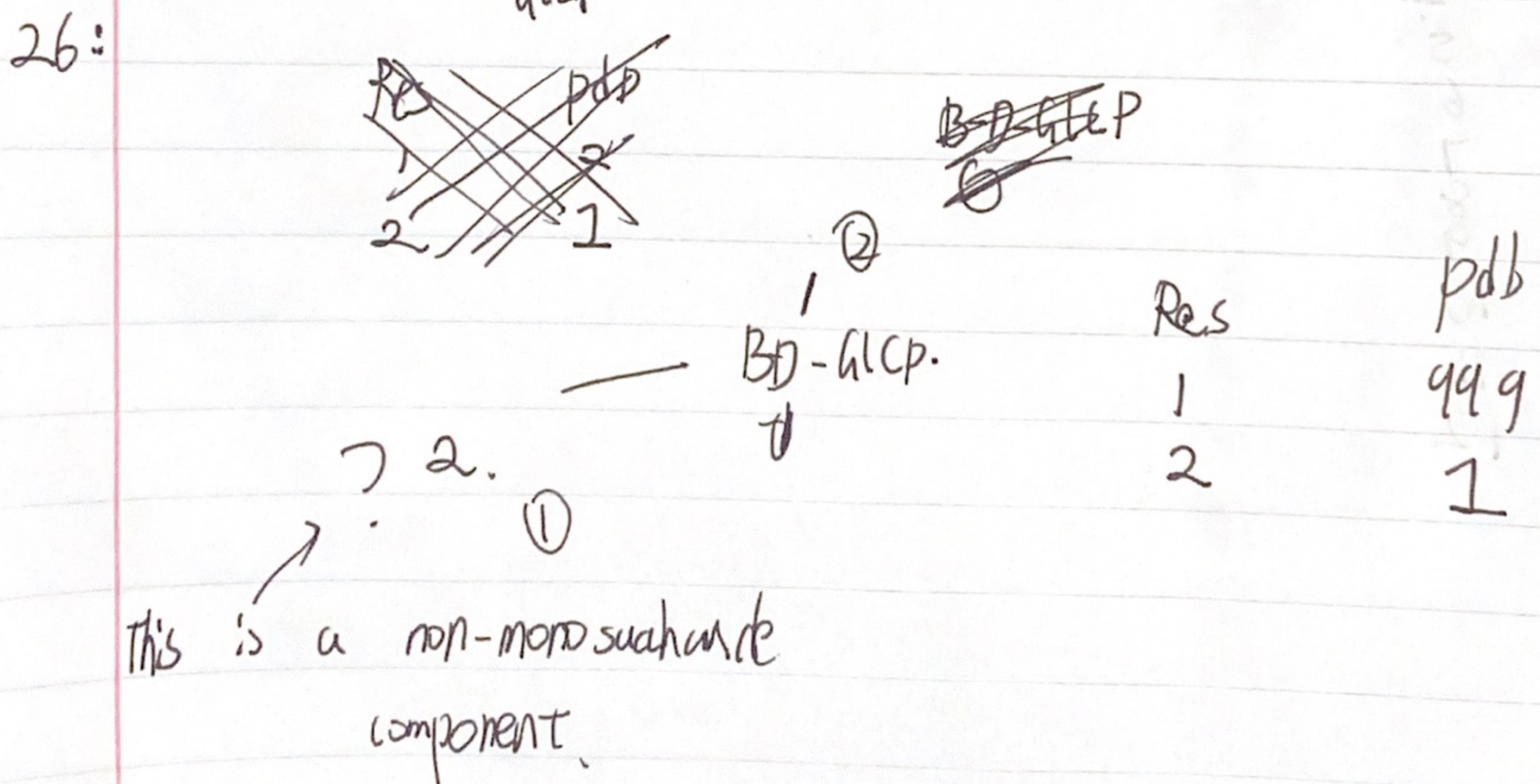
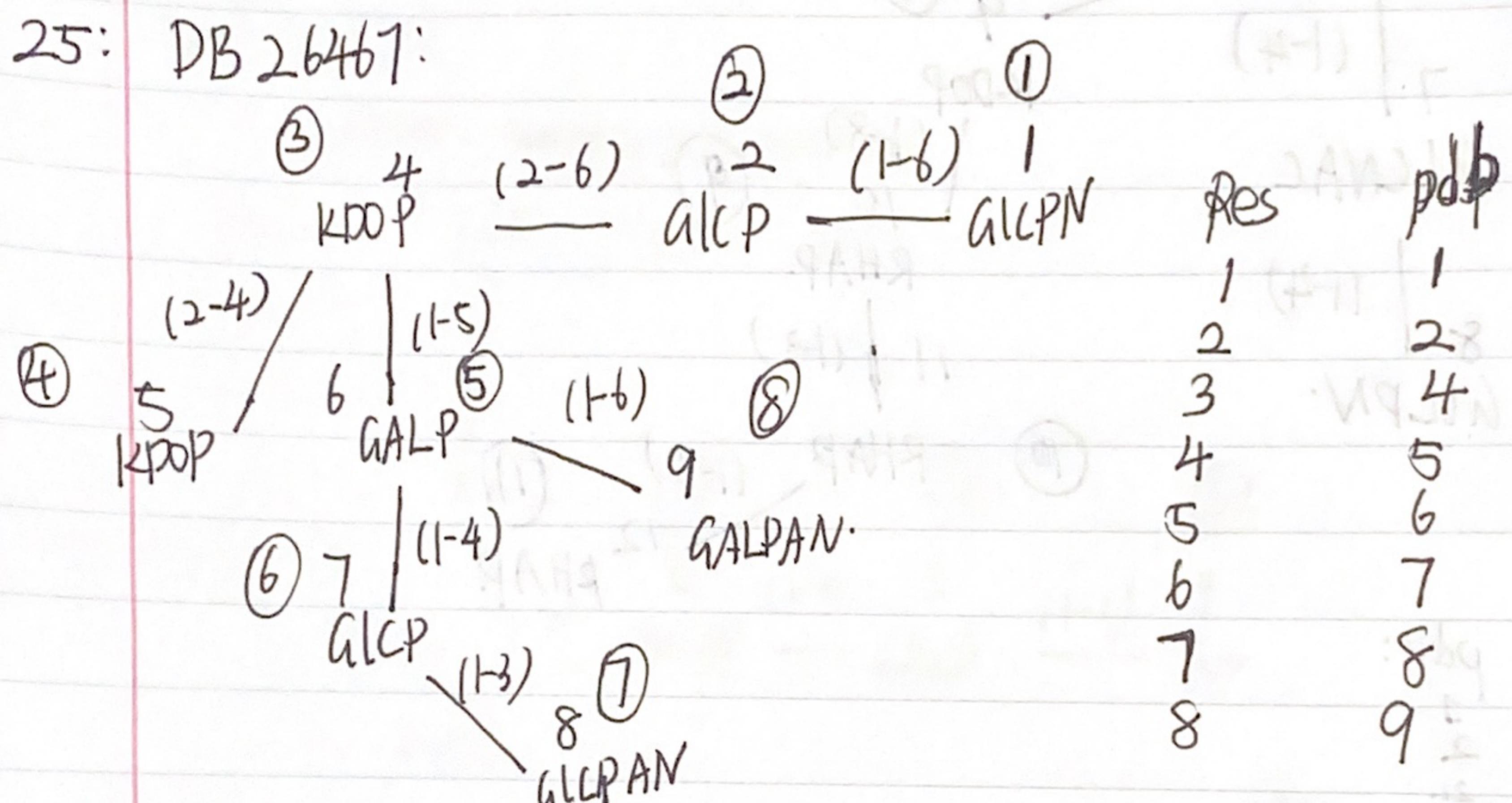
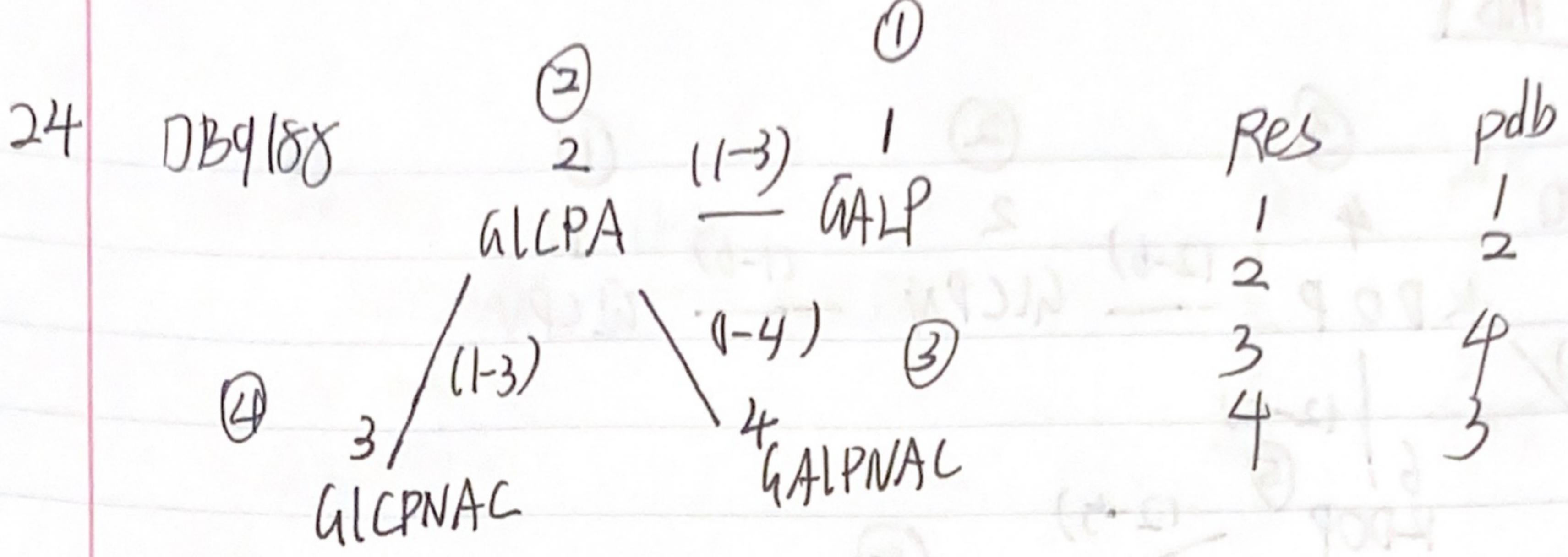
Res	pdB. amy
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8

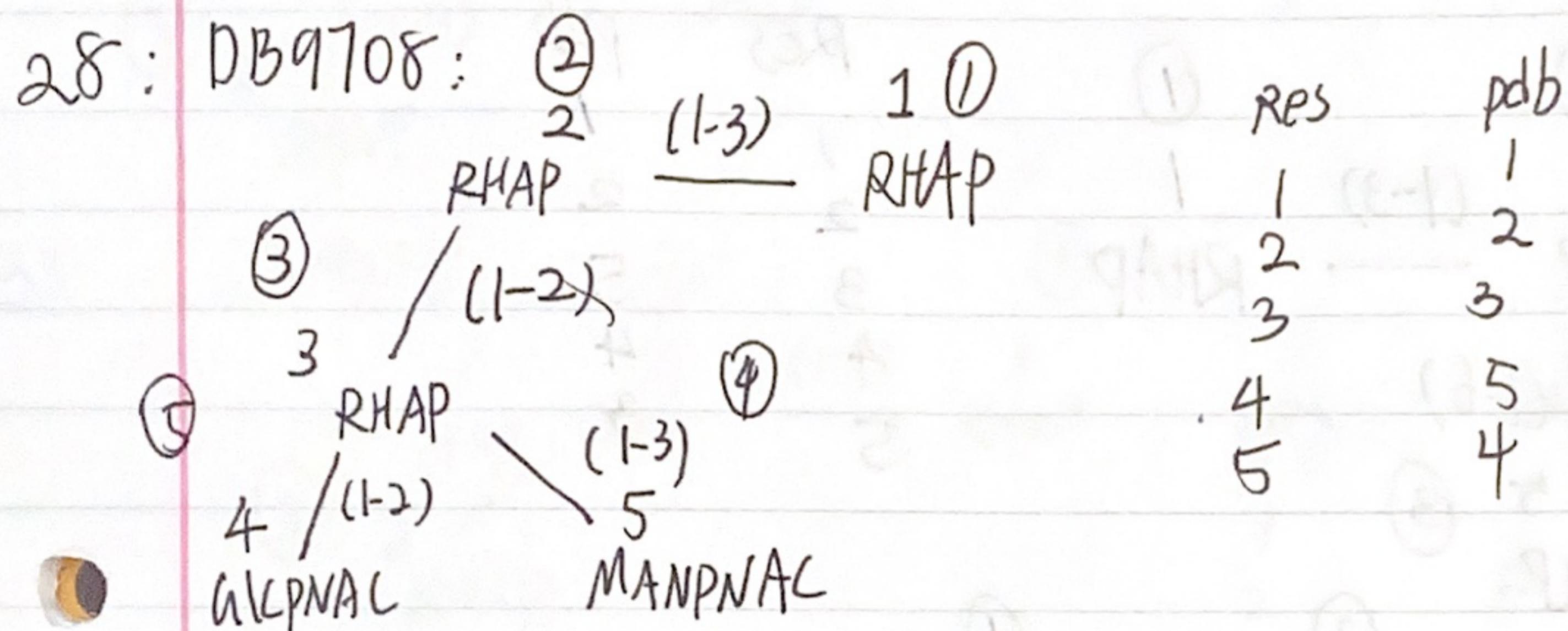
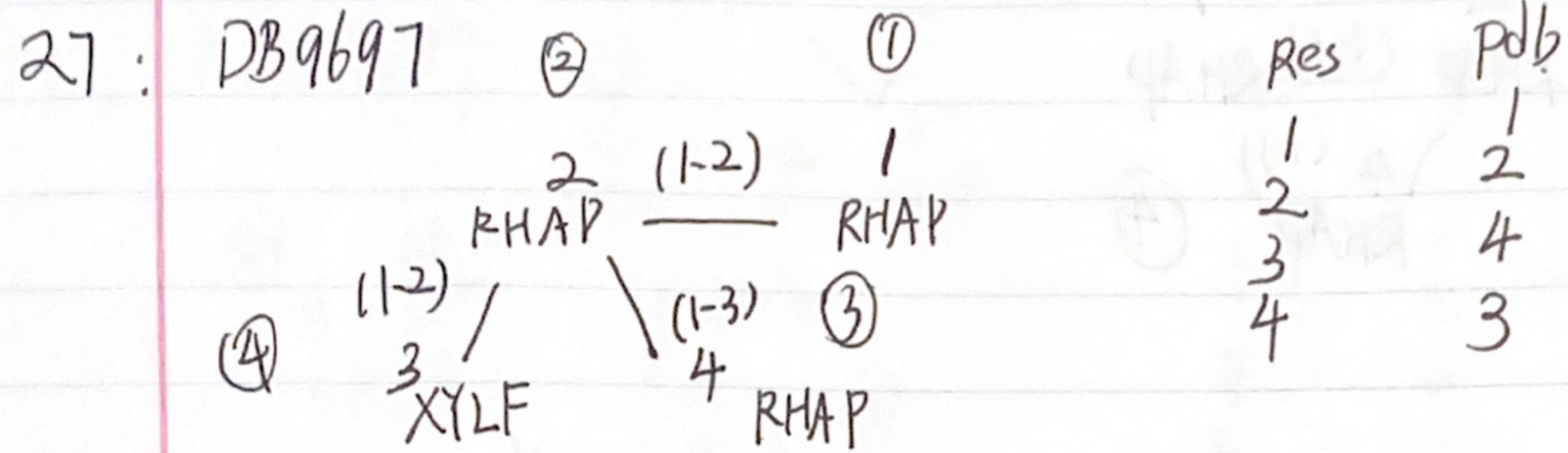
I check this

[23]



Res:	pdp:
1	1
2	2
3	4
4	5
5	6
6	7
7	8
8	9
9	10
10	11
11	12

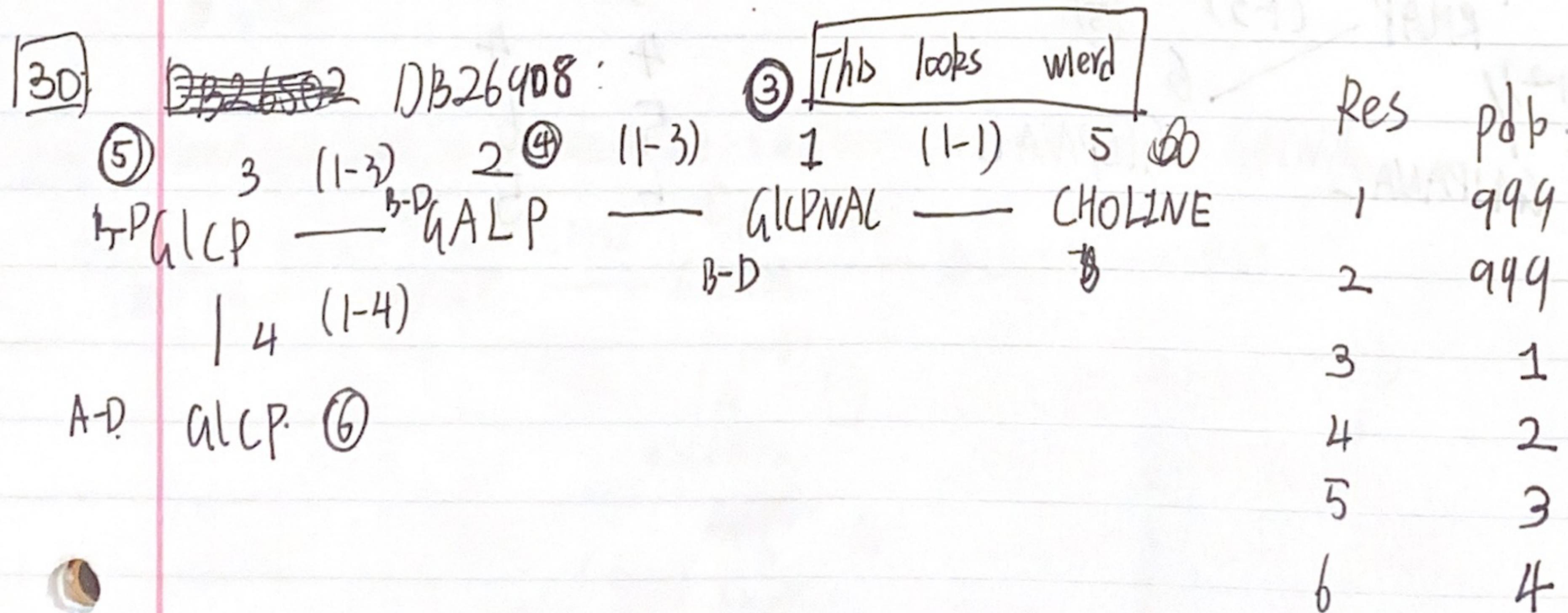


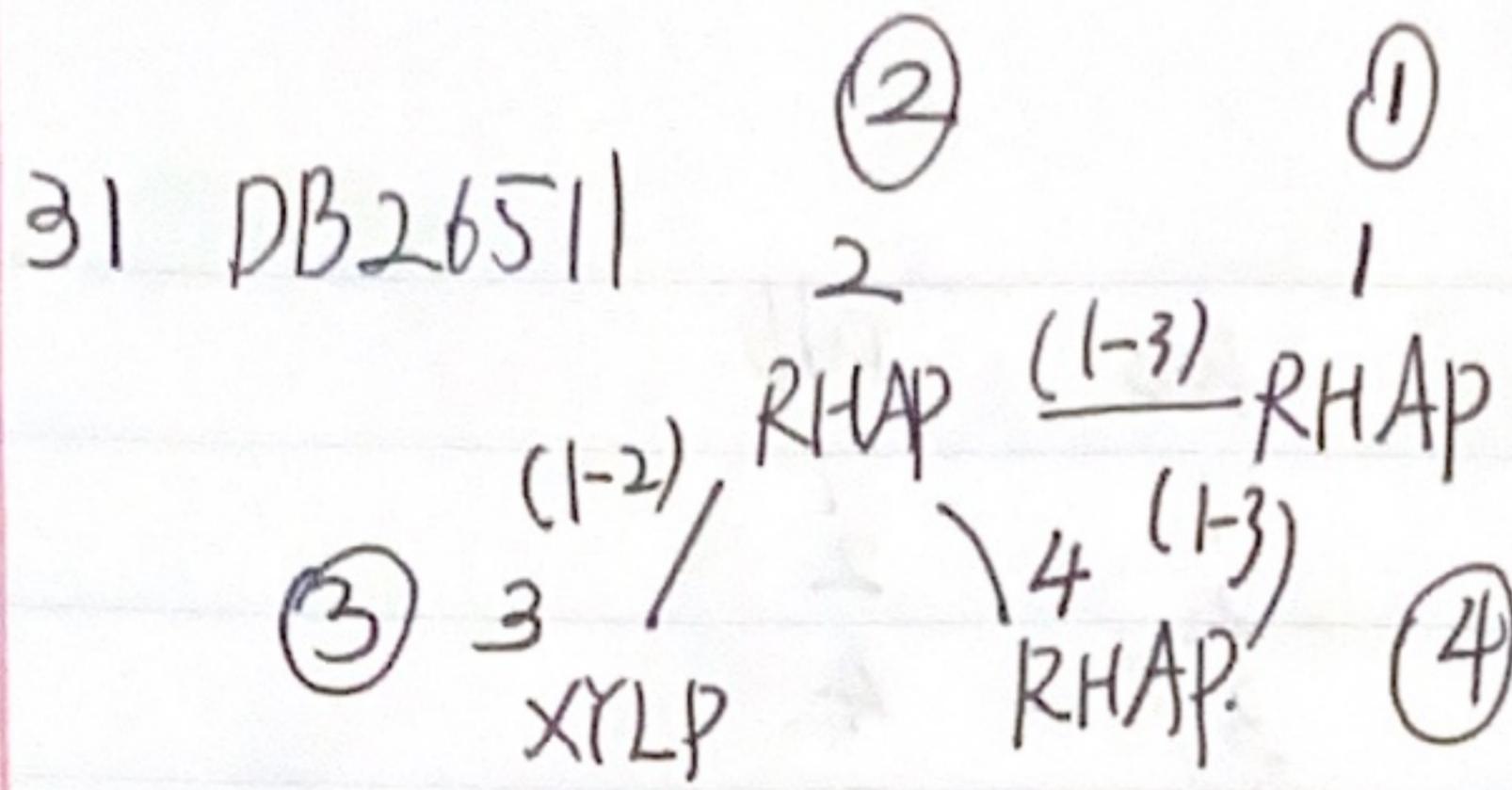


29: DB26502

1-1, ... 9-9.

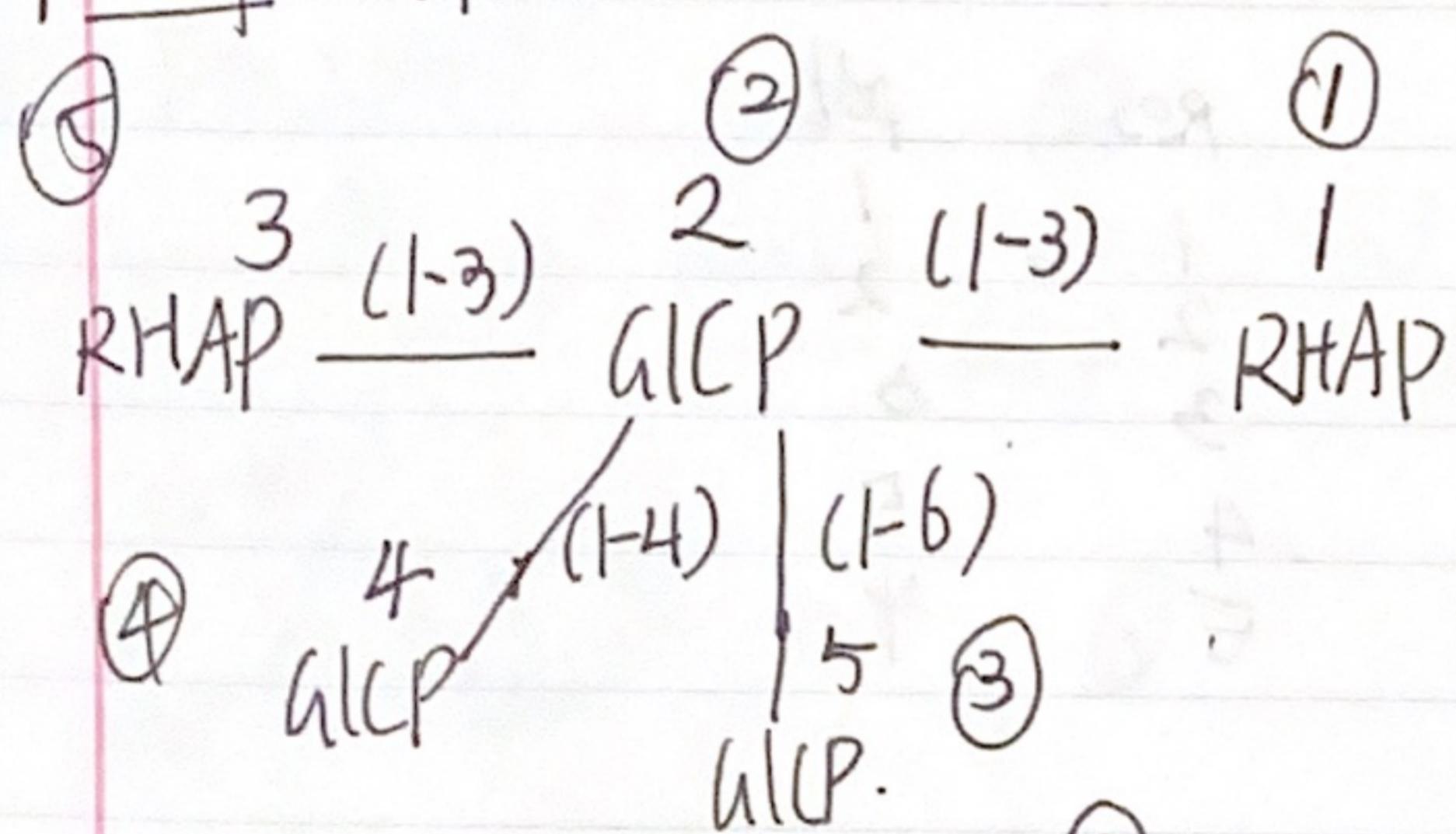
Included in nonlinear-progress-record.txt.





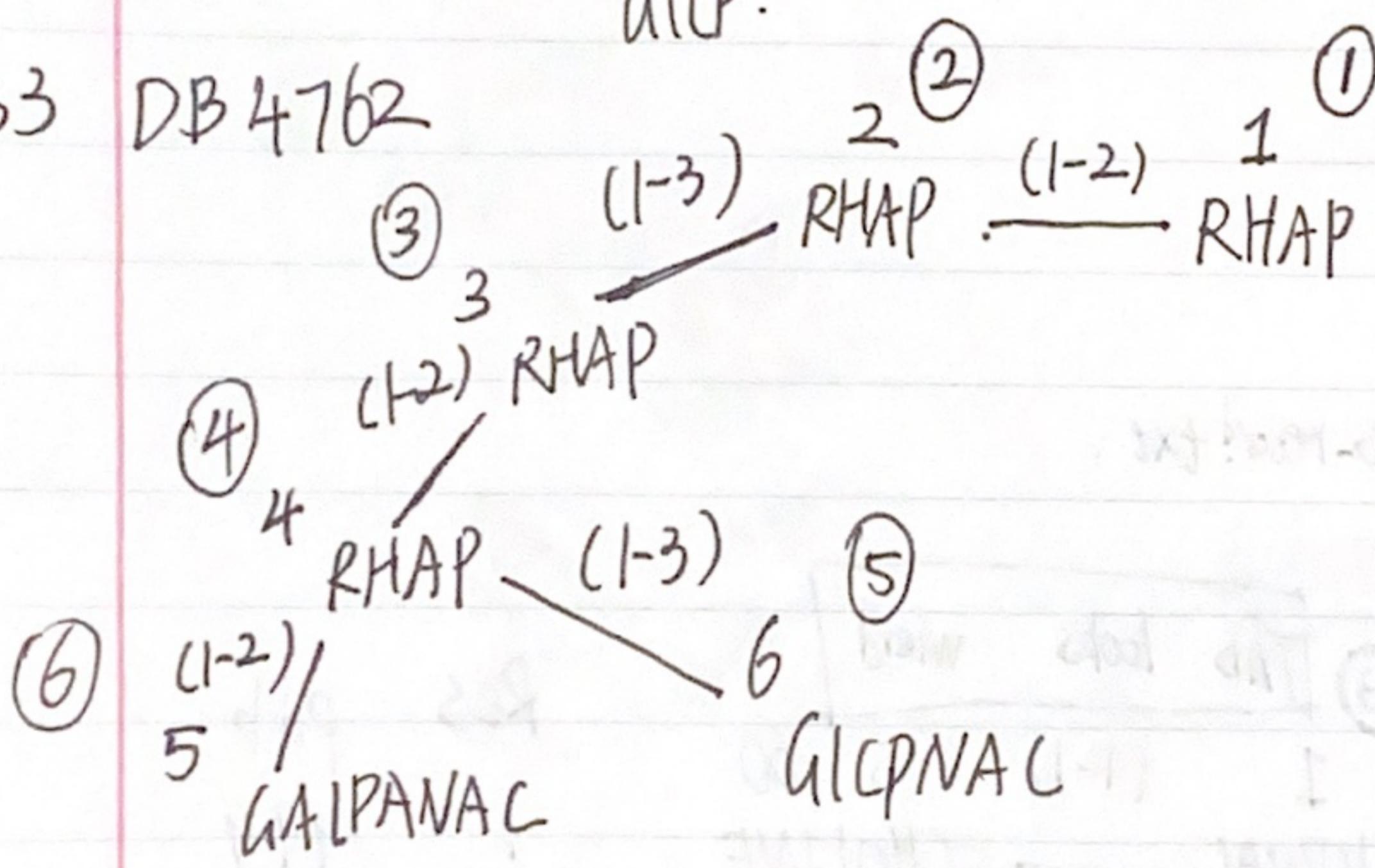
✓

32 DB9917



Res	pdb
1	1
2	2
3	5
4	4
5	3

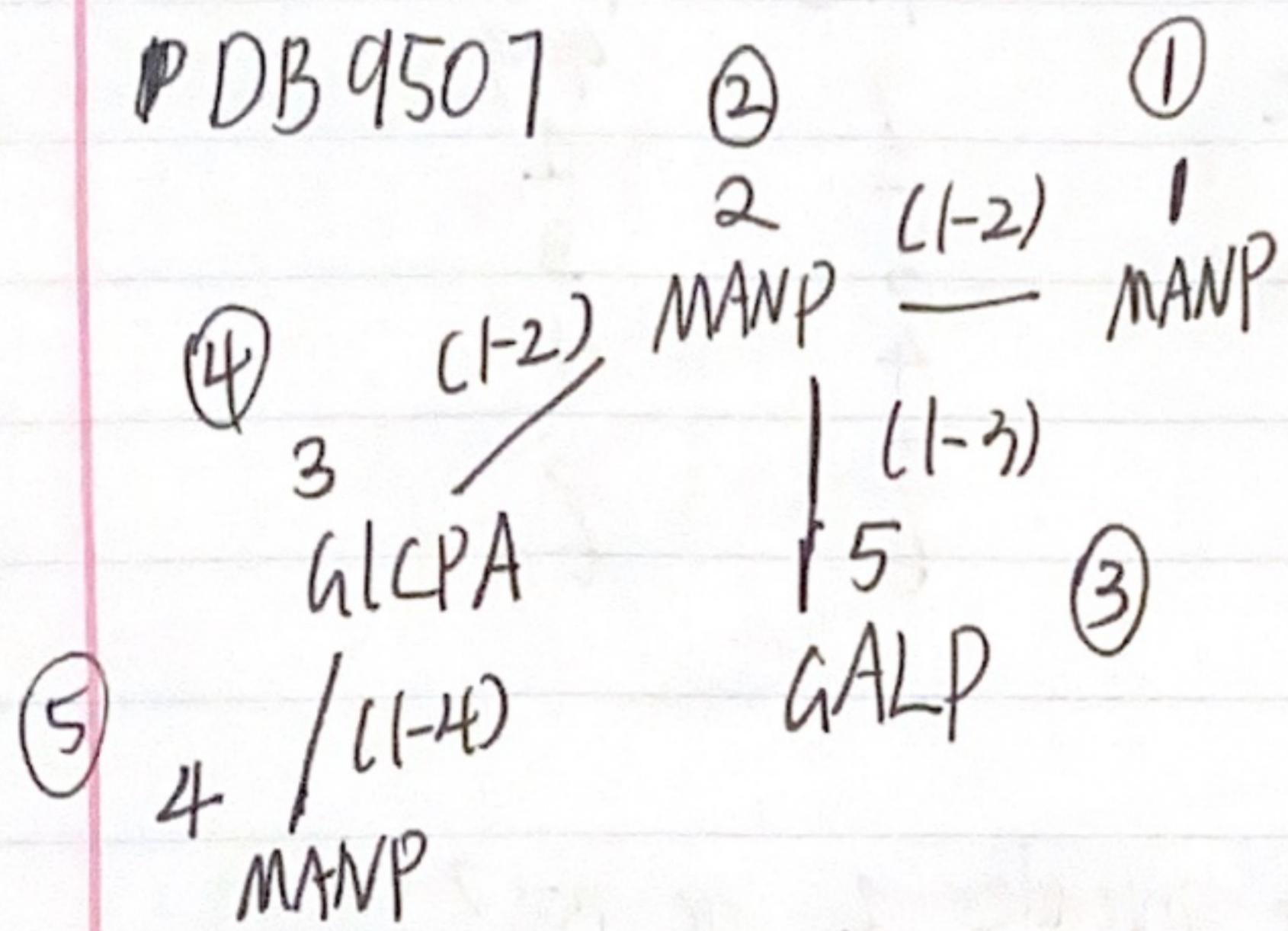
33 DB4762



Res	pdb
1	1
2	2
3	3
4	4
5	6
6	5

34

PDB 9507

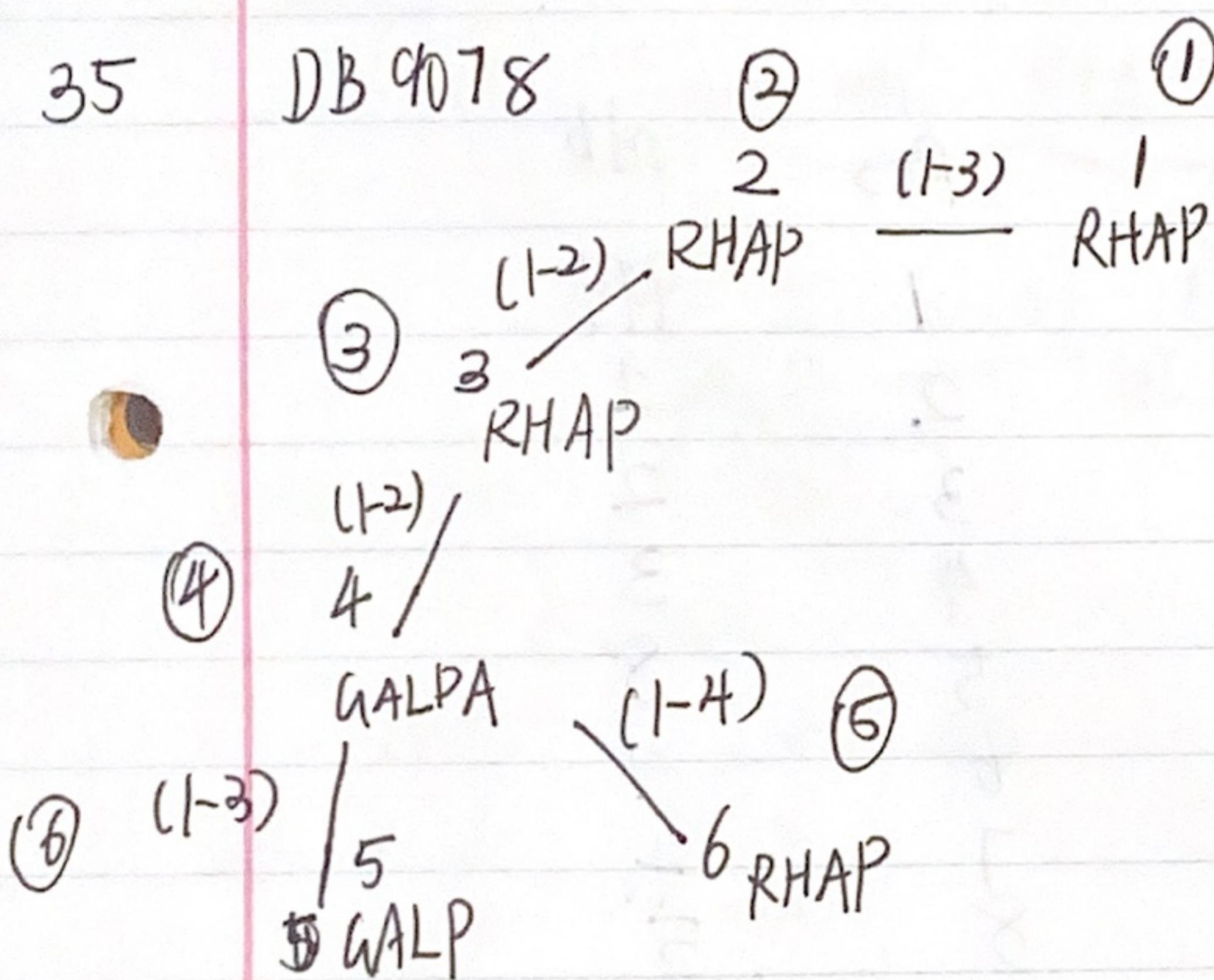


Res      pdb

1	1
2	2
3	5
4	3
5	4

35

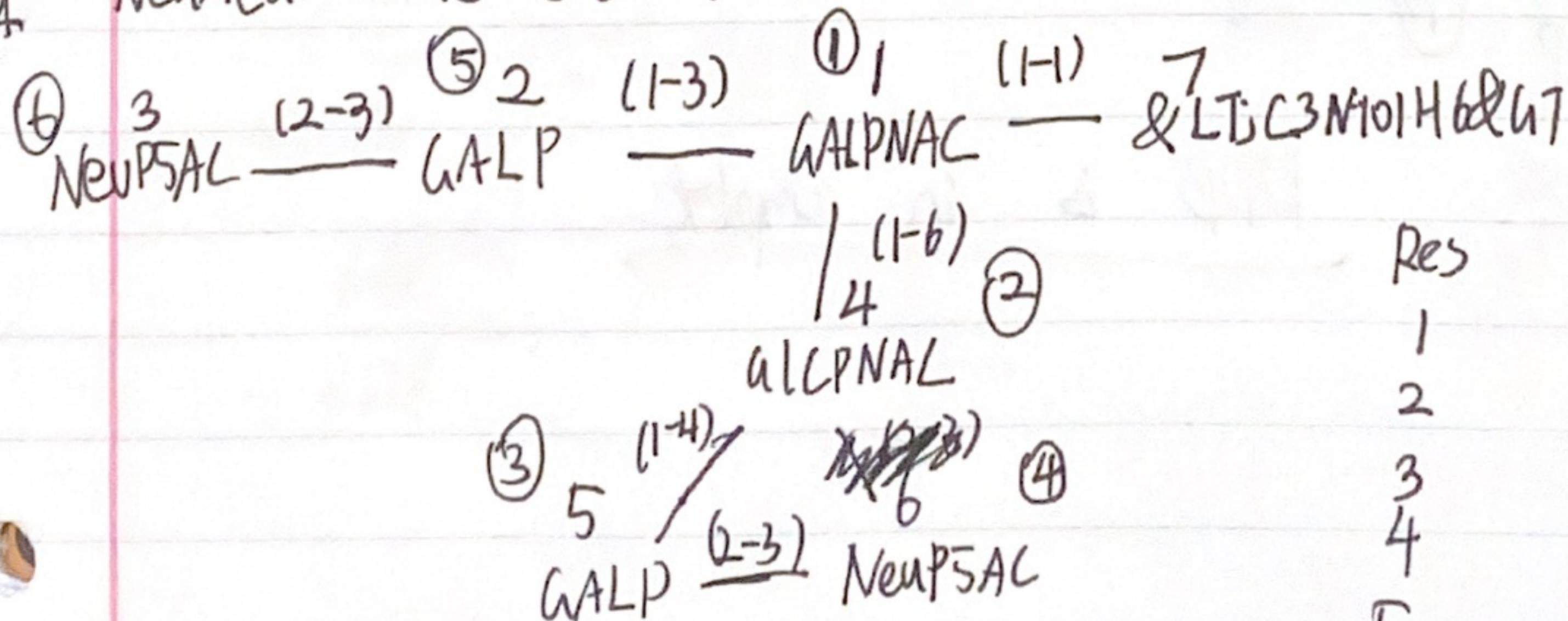
DB 9078



Res      pdb

1	1
2	2
3	3
4	4
5	6
6	5

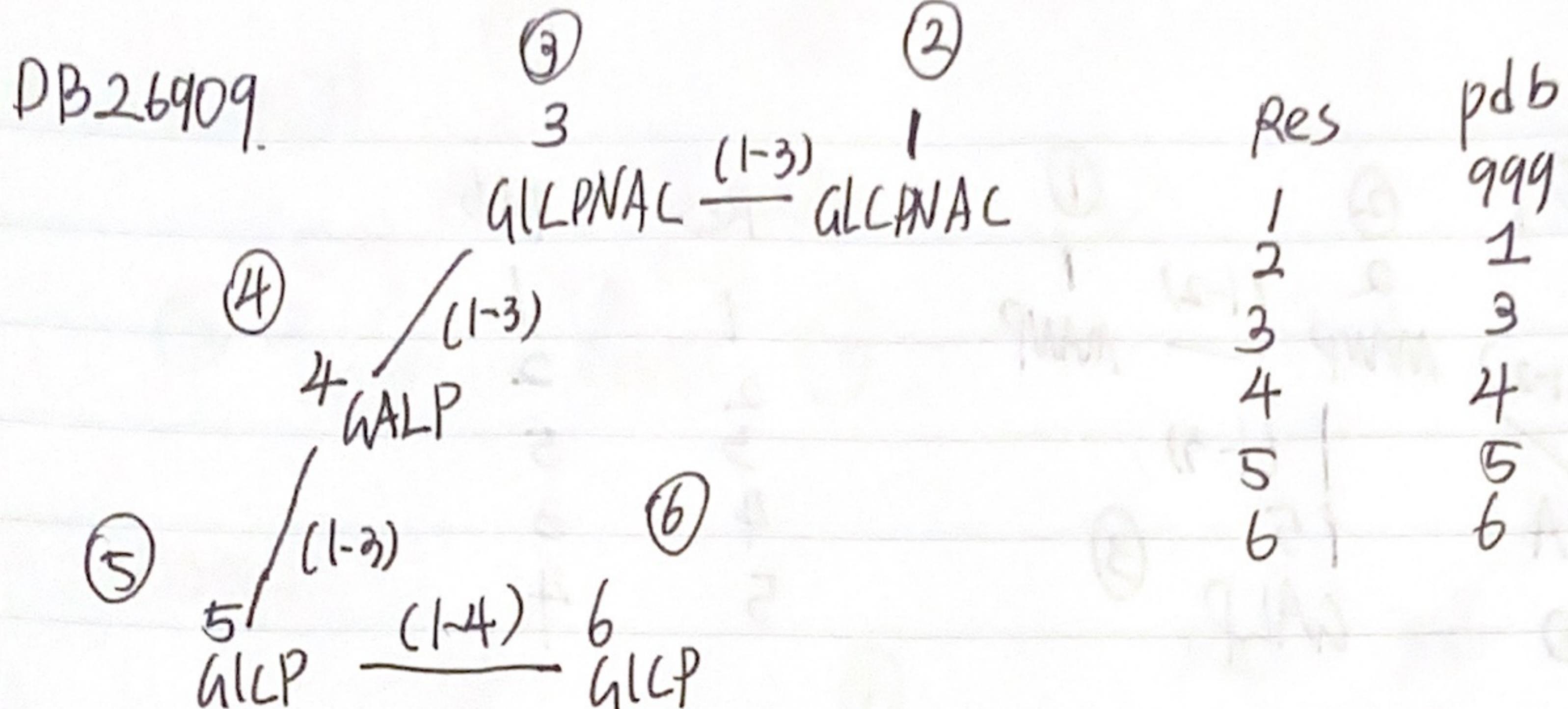
36 NeuAc<sub>2</sub>-3Gal<sub>b</sub>1-3( NeuAc<sub>2</sub>-3Gal<sub>b</sub>1-4 GlcNAc b1-6) GalNAc.



Res      pdb

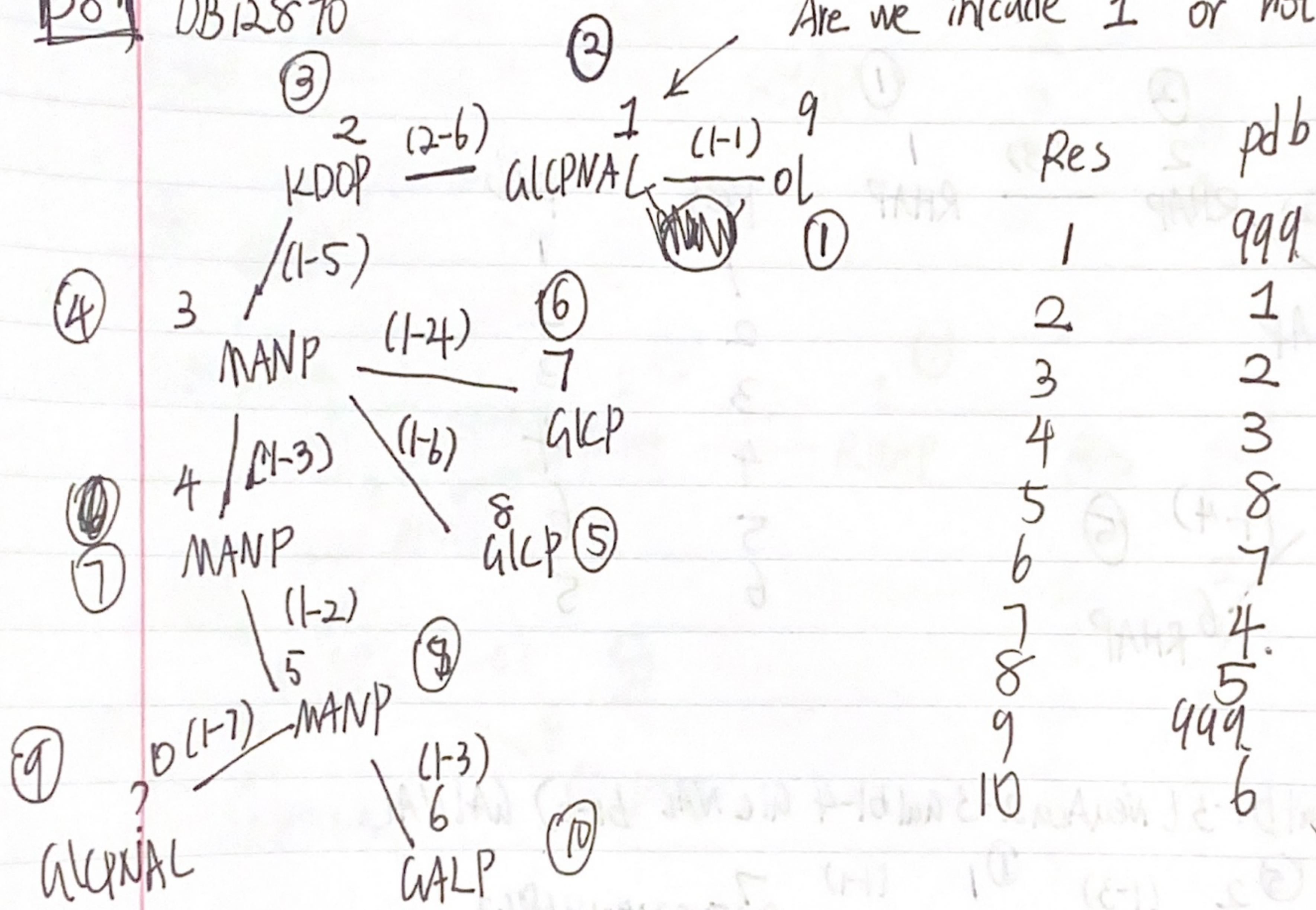
1	1
2	4
3	5
4	6
5	2
6	3

37



38

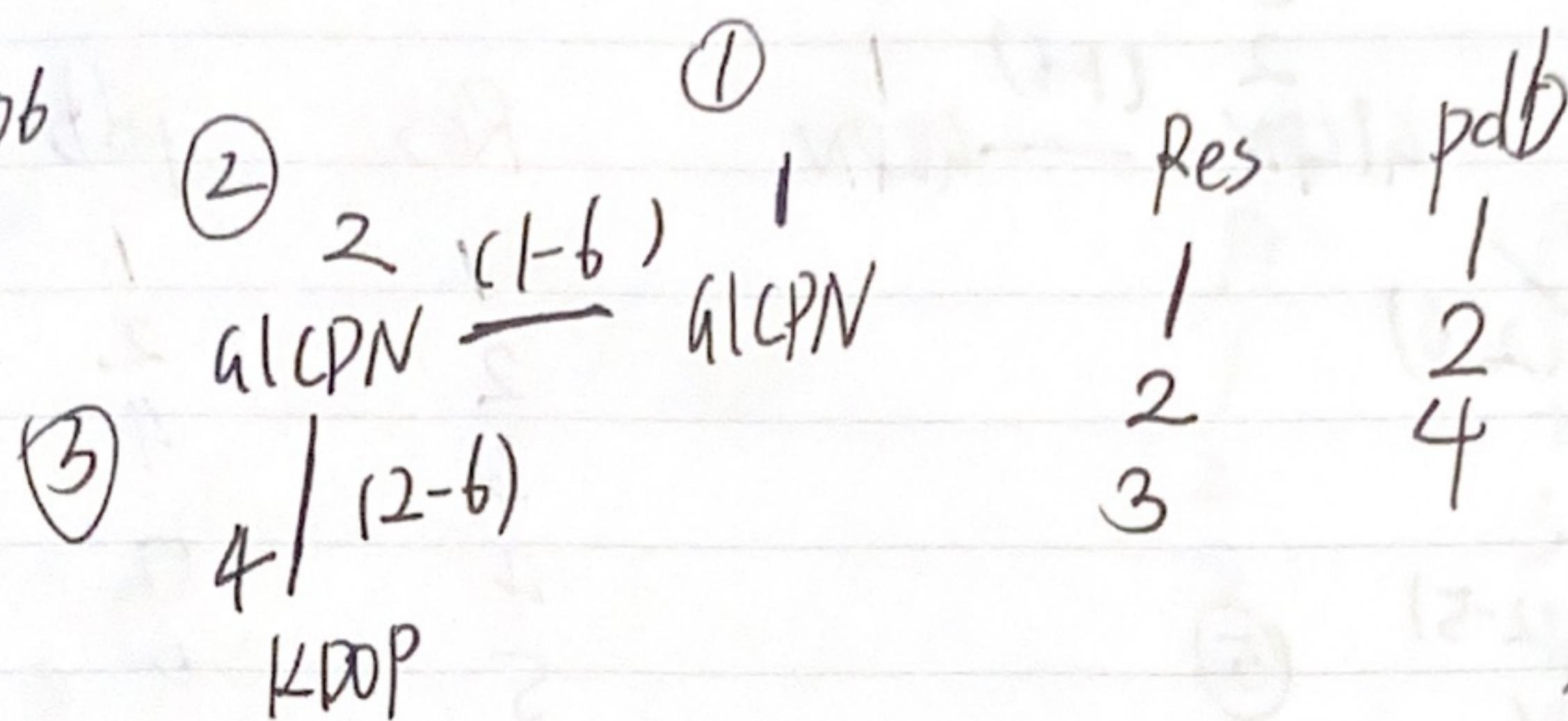
DB12870



PDB is in complete

39

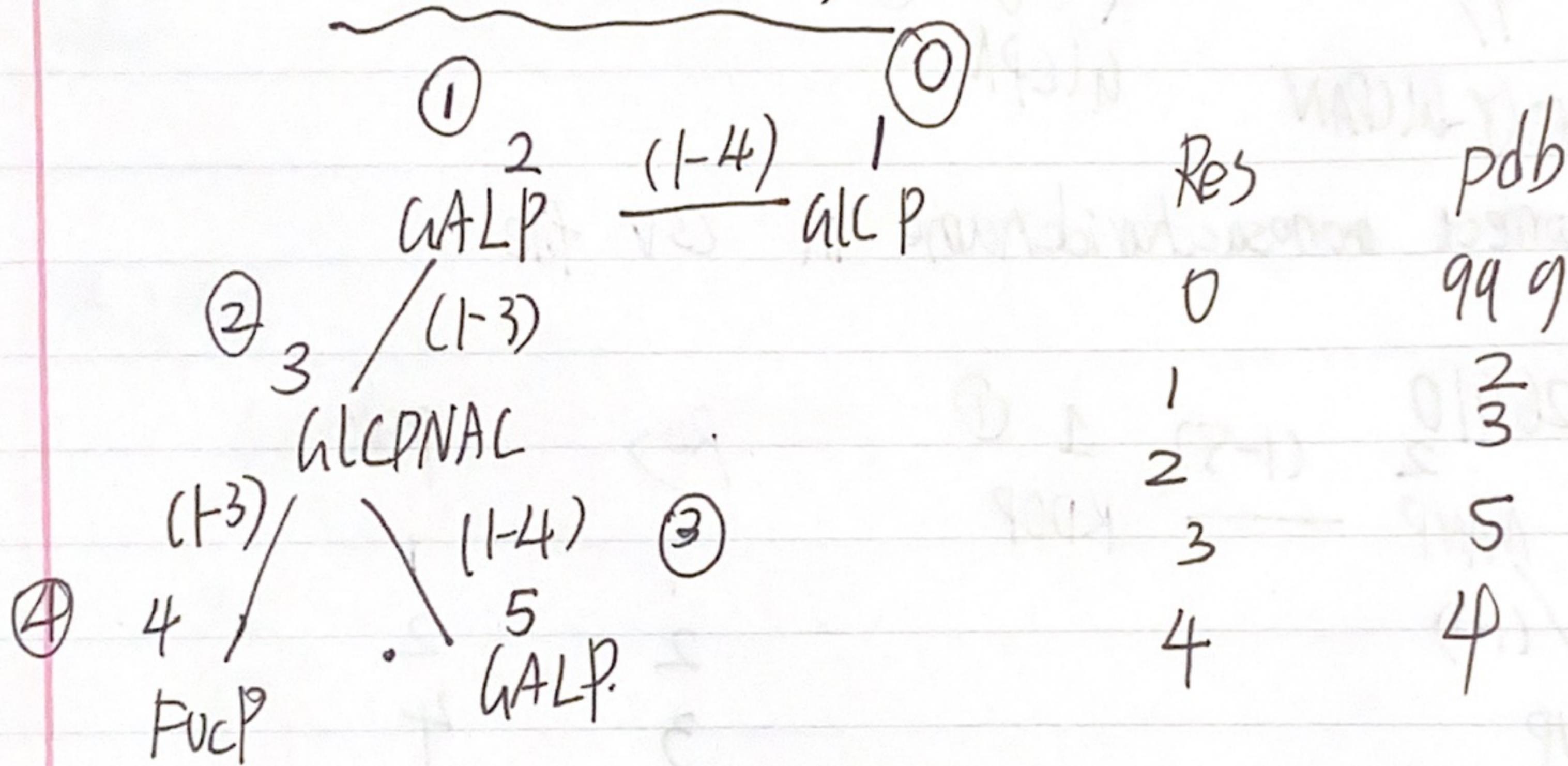
DB22506



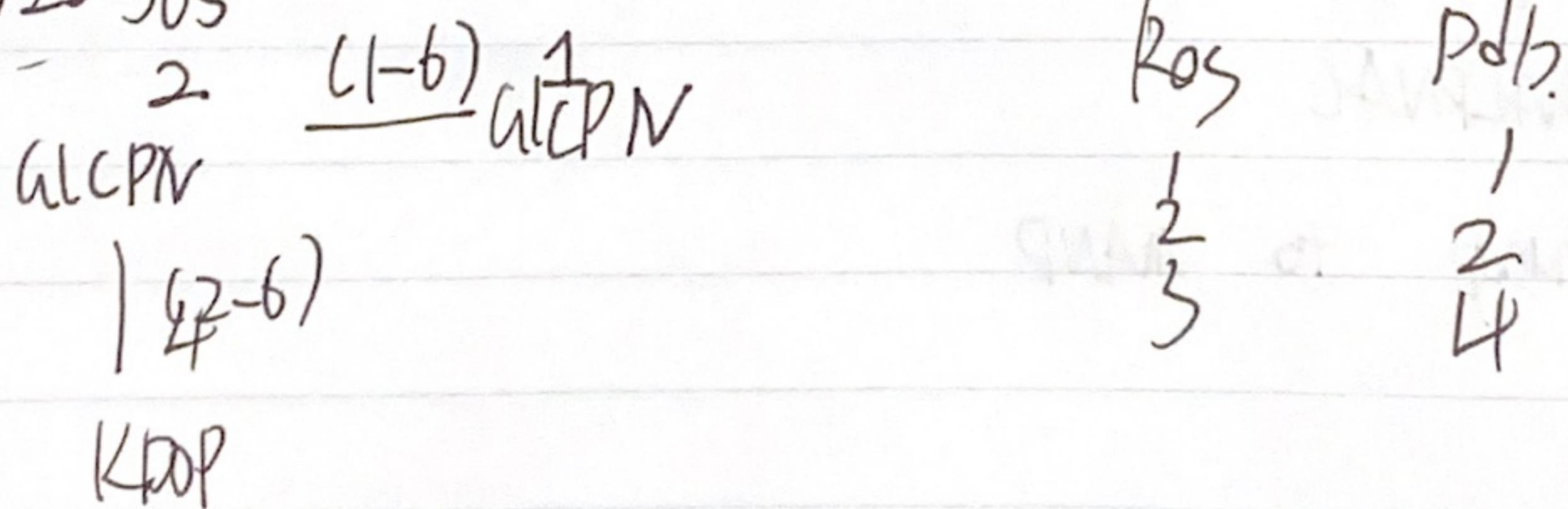
40

LFucpa 1-3 [Dgalpb 1-4] DhcpNAcb 1-3 Dhgalbb 1-4 Dhlc.

$\uparrow$  starts with HIA HIB. which to use?

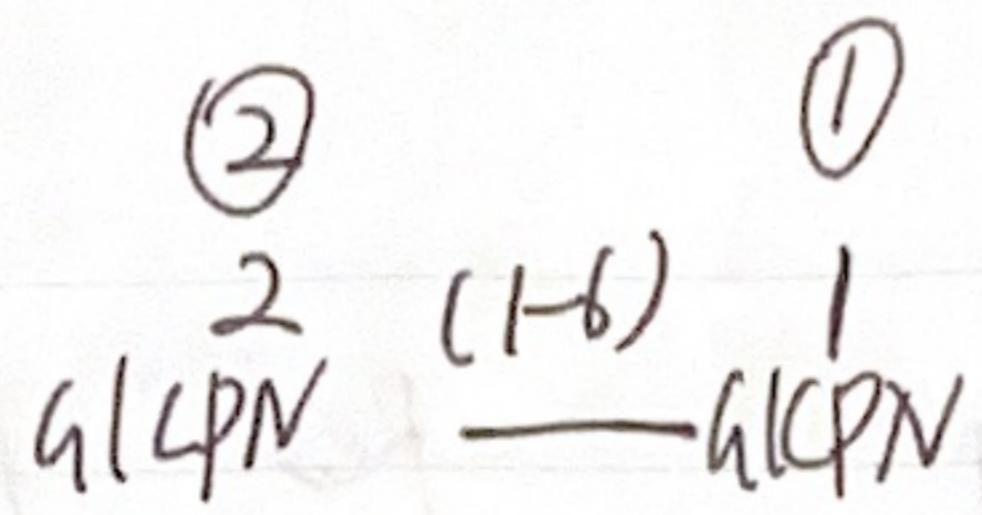


41

PB22505  $\leftarrow$  this is exactly same as 22506

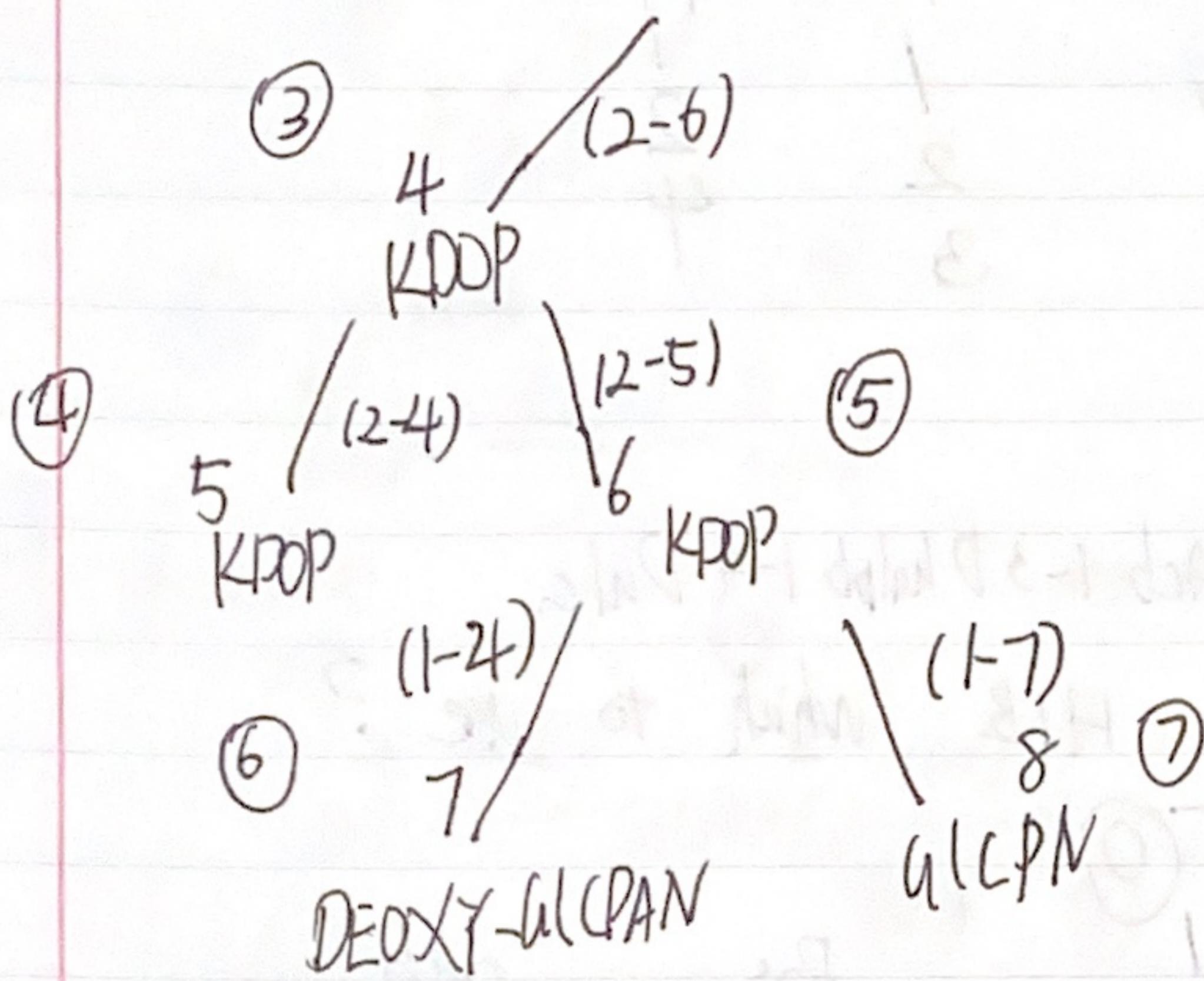
42

DB26879



Res              pdb

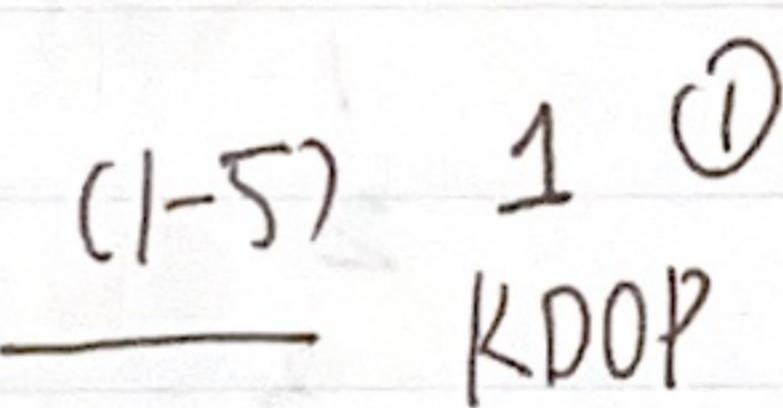
1	1
2	2
3	4
4	5
5	6
6	7
7	8



Needs correct monosaccharide name in CSV file

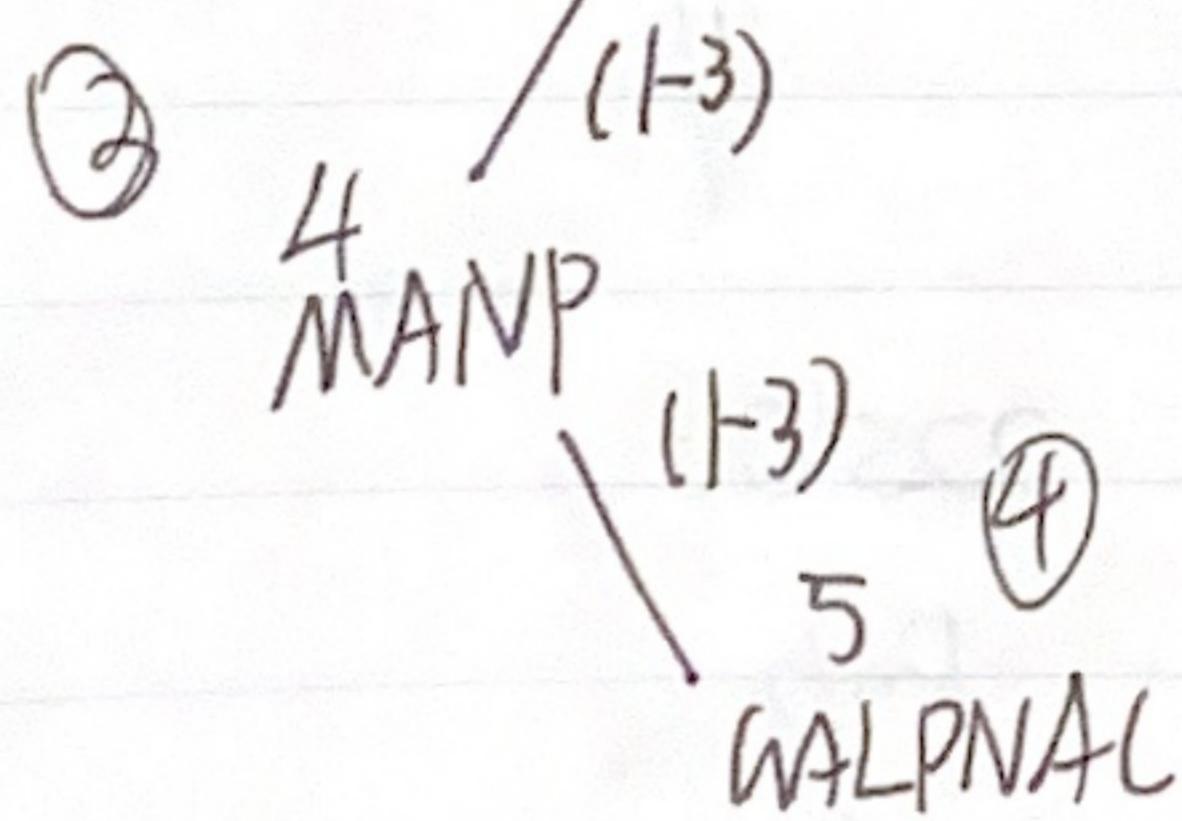
43

DB26910



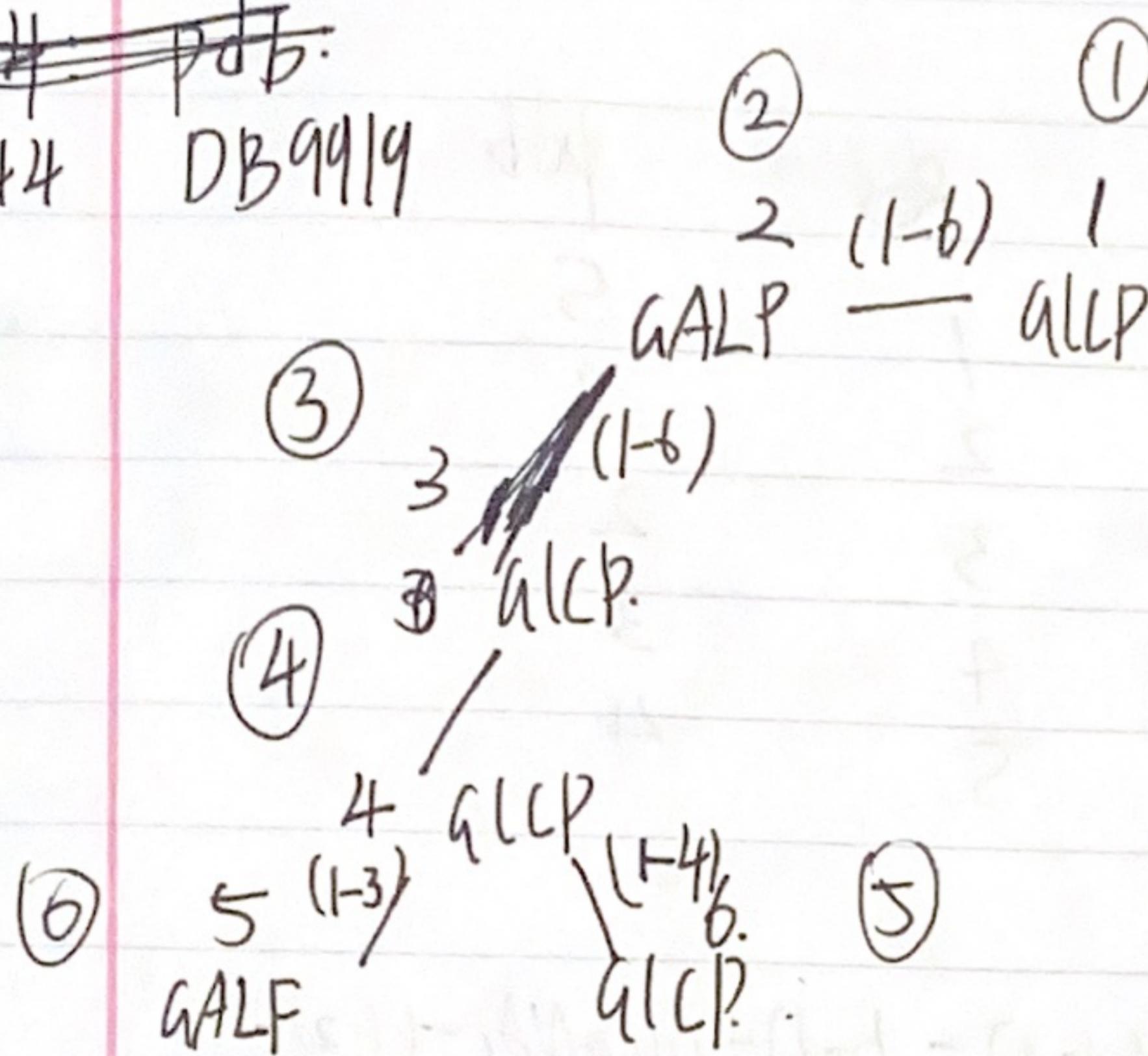
Res              pdb

1	1
2	2
3	4
4	5



HEPP change to MANP

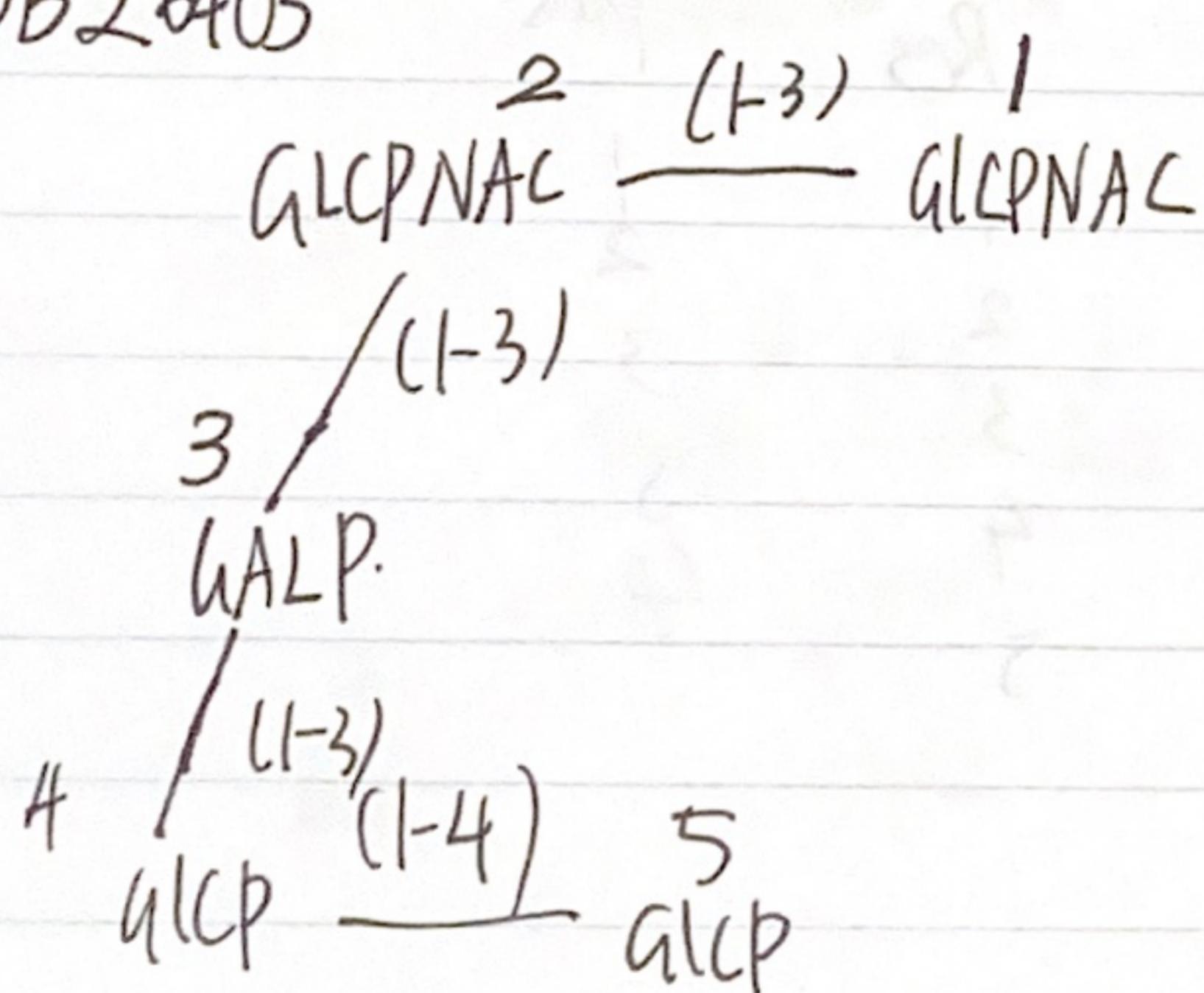
~~44~~ pdB.  
DB9919



Res pdB  
1 1  
2 2  
3 3  
4 4  
5 6  
6 5

45

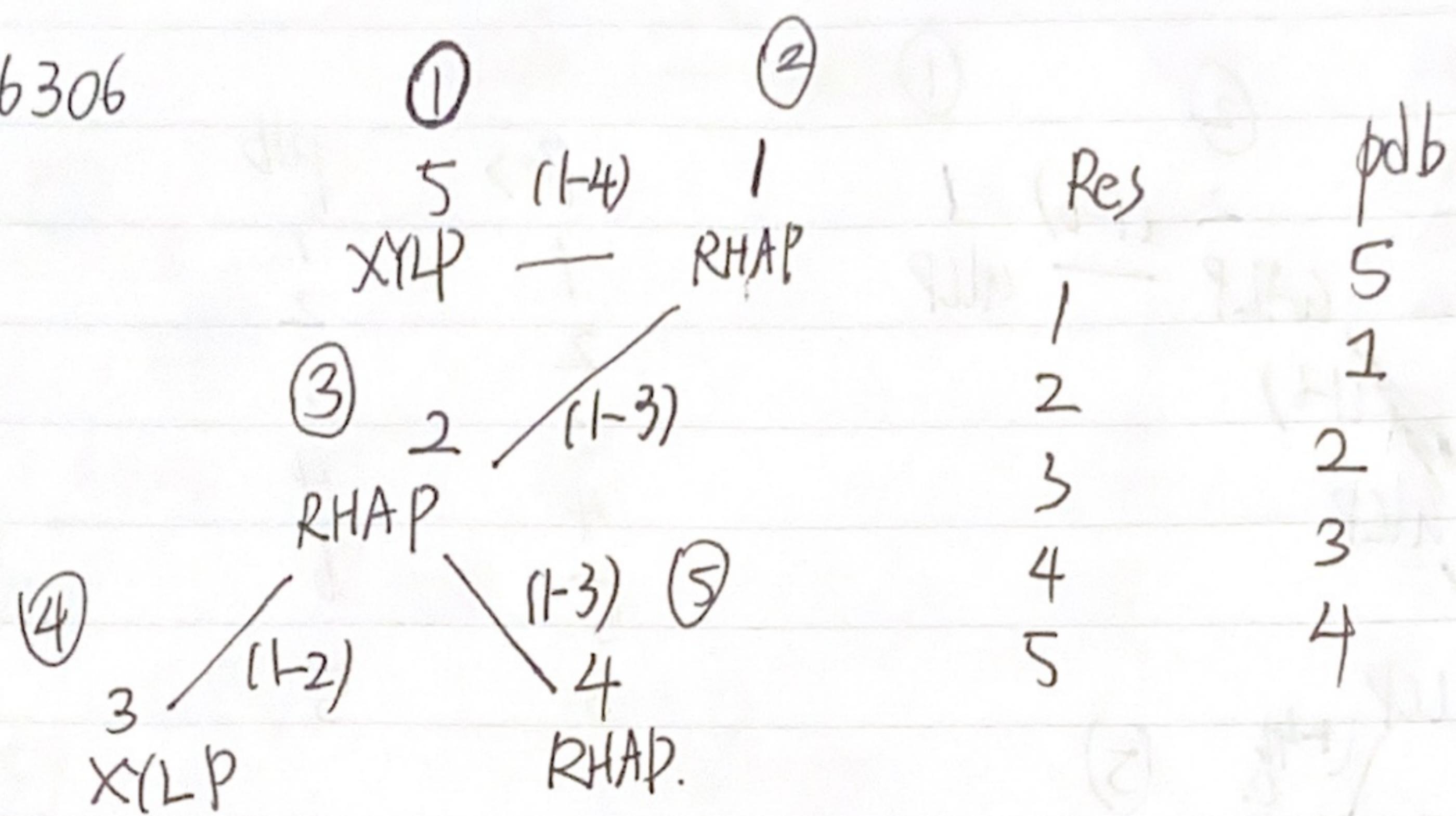
DB26403





46

DB26306



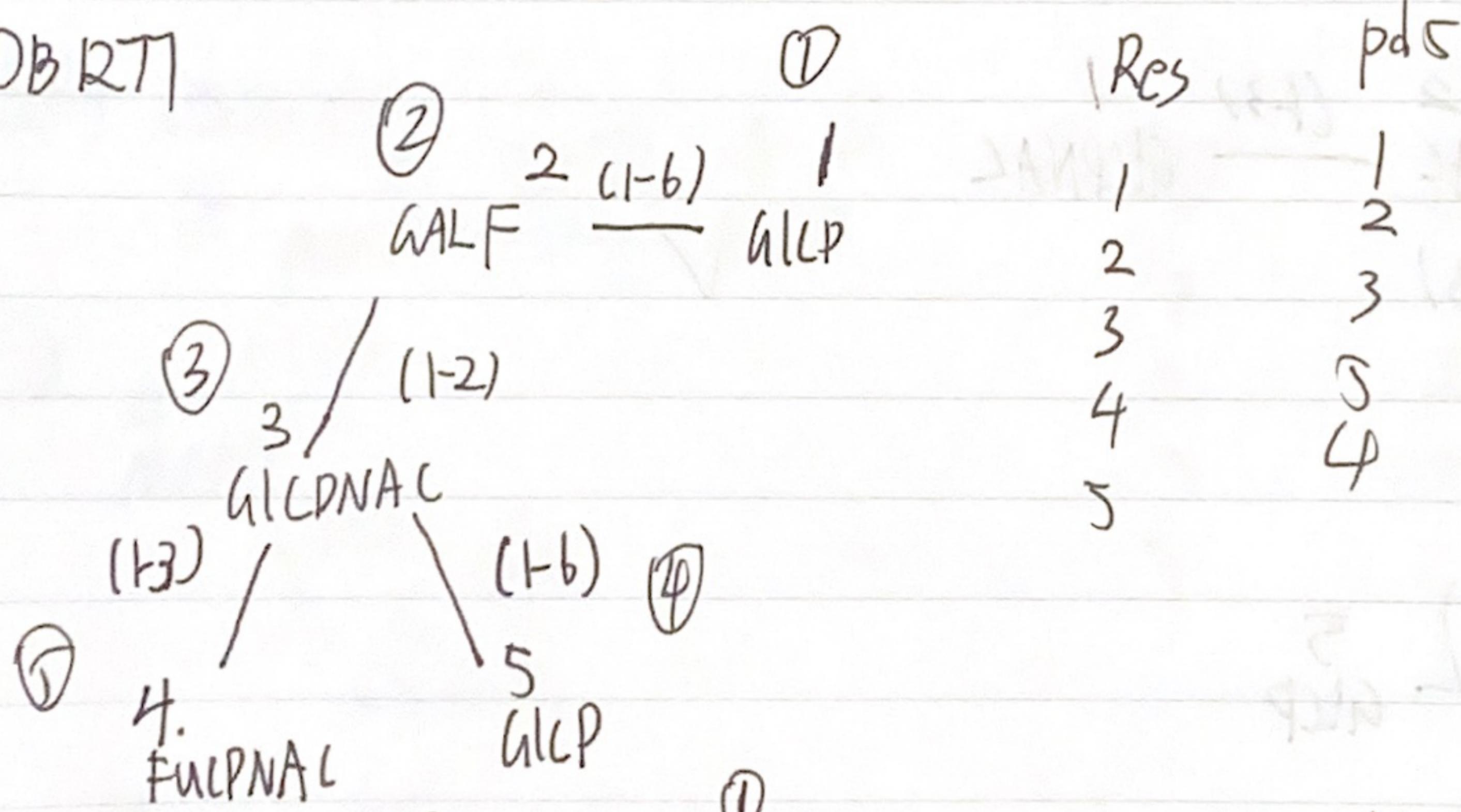
47

Repeat-4)-a-D-Manp-(1-4)-a-D-GalpA-(1-3)-b-D-GlcNAc-(1-2)-  
a-D-Galp-(1-3)-a-L-Rhap2NAc-(1-8)

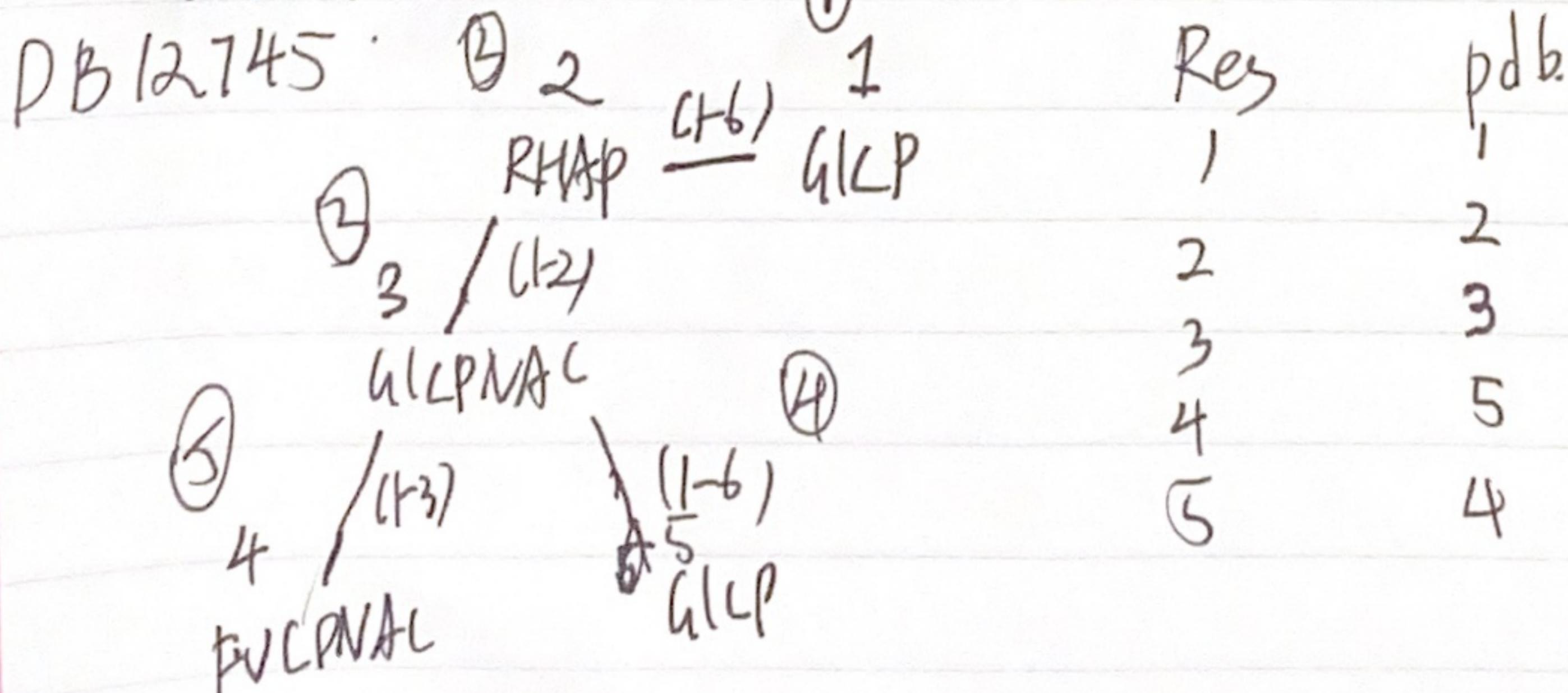
✓

48

DB RTI



49



50

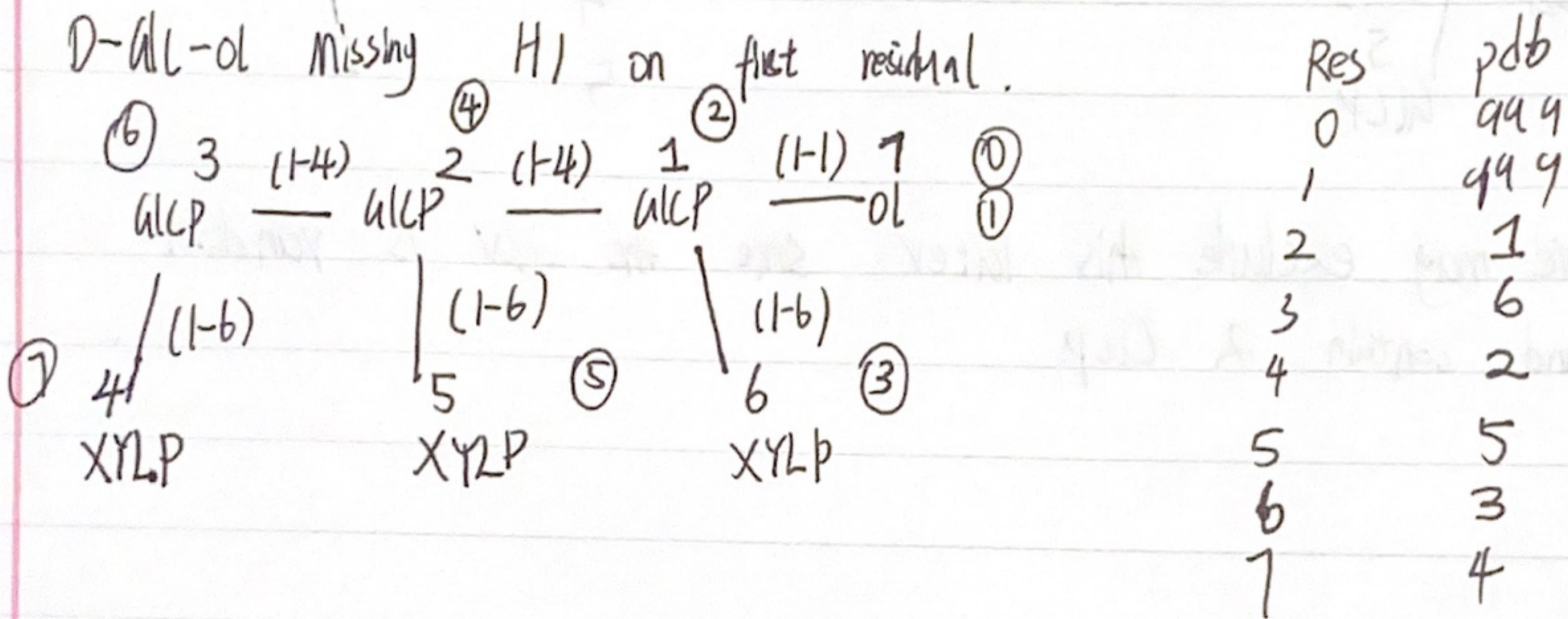
DB26810

Rare α-L-6-deoxy-Talp.



[51]

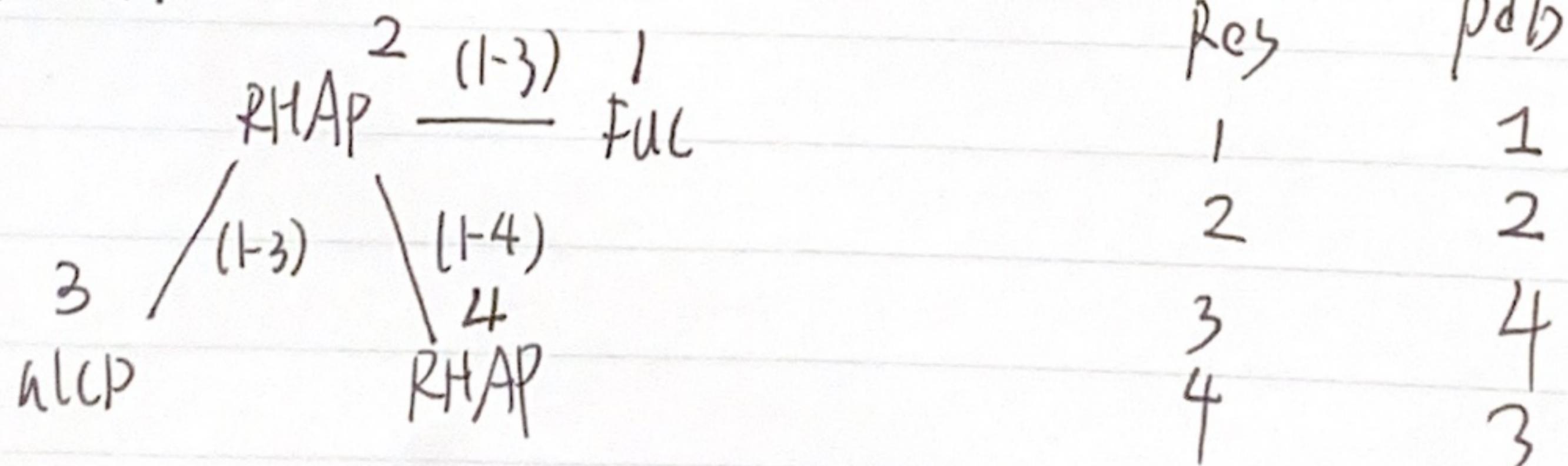
DB 3758

D-Gal-Ol missing H<sub>1</sub> on first residual.

Assigned by connections in .csv

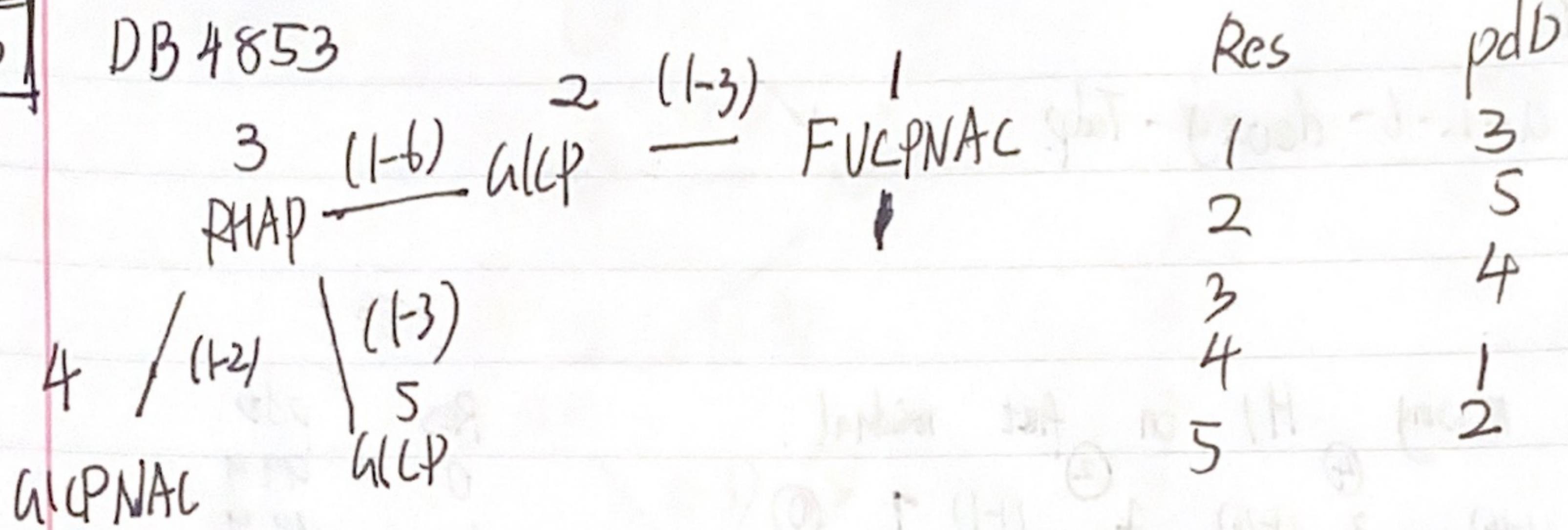
52

DB 4711



53

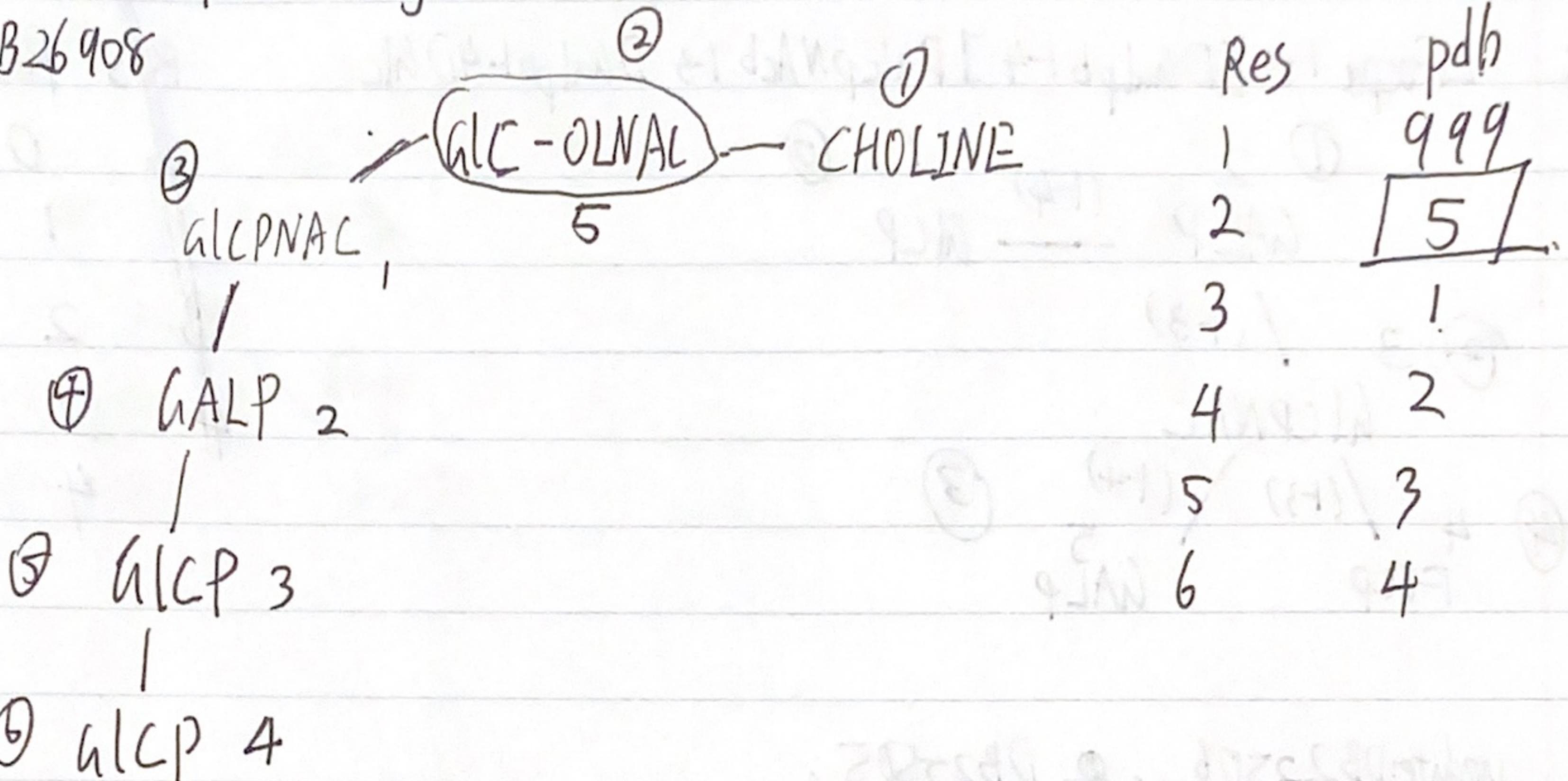
DB 4853



? We may exclude this later. since the .csv is random  
and contain 2 Clp.

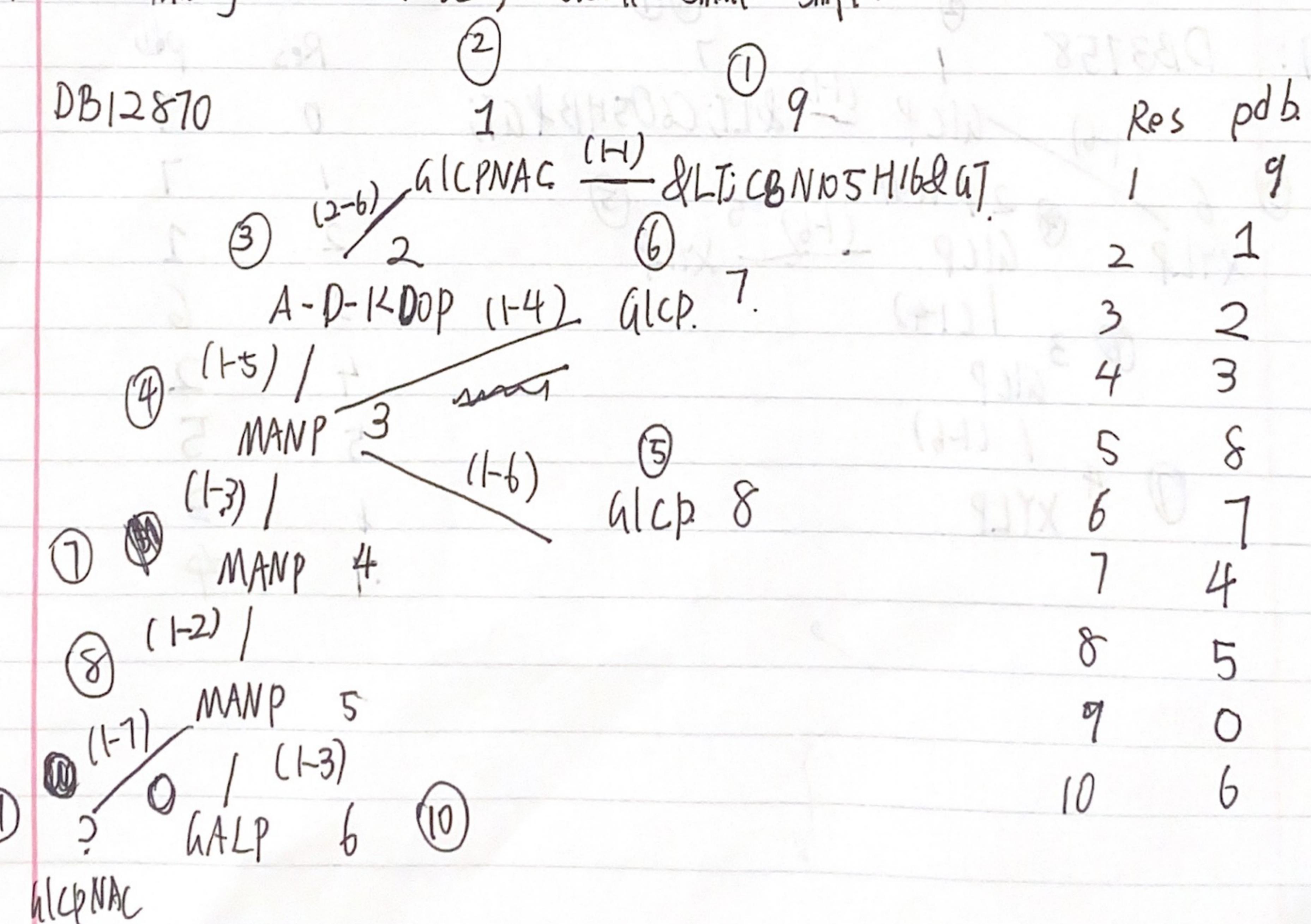
Revised from Ryan's email:

30 : DB26908



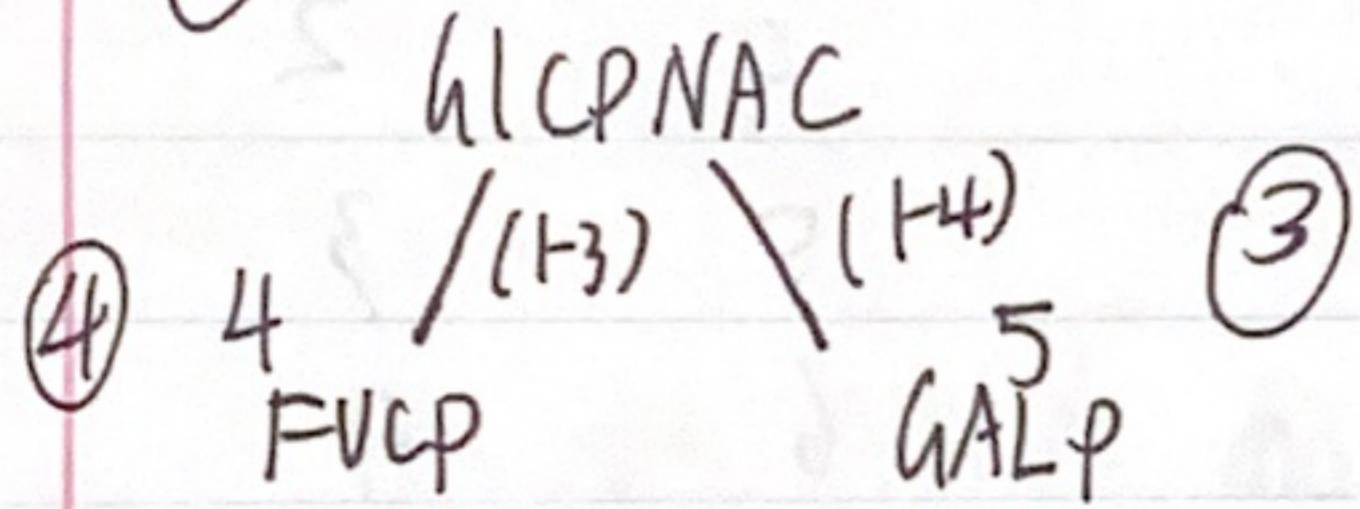
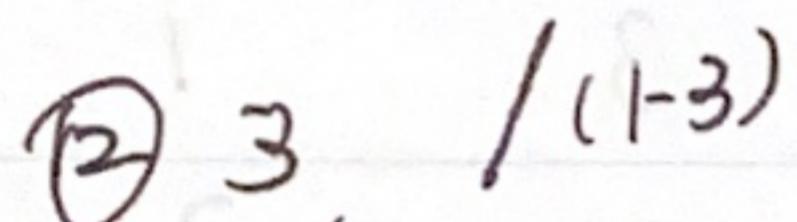
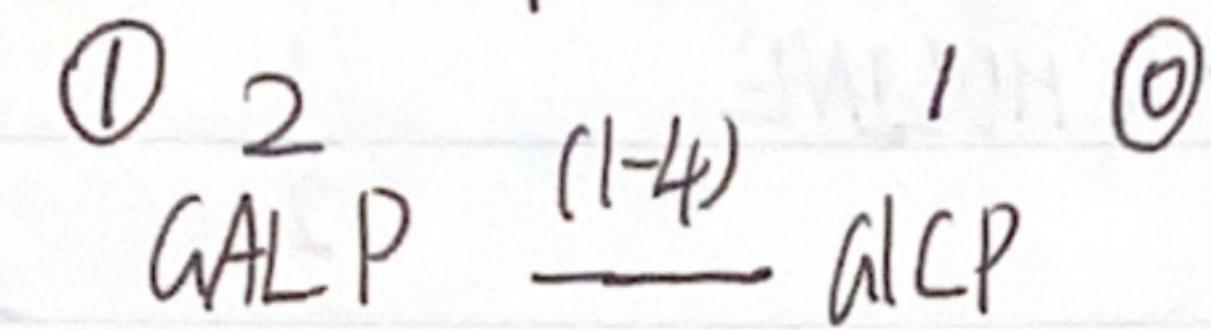
For 5: Missing monosaccharide, overall small shift.

38 : DB12870



40: LFucpa 1-3 [DGalp b1-4] DGalpNAcb 1-3 DGalp b1-4 DGalp

	Res	Res	pdb
①	0	1	
②	1	2	
③	2	3	
④	3	5	
⑤	4	4	

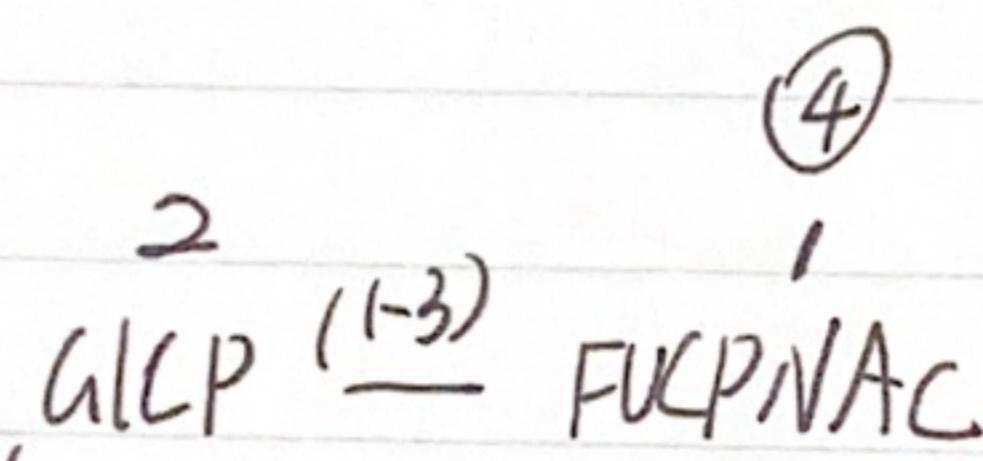


\* update: DB22506, DB22505.

	Res	pdb
51: DB3758	0	7
② 1      7	1	7
③ 6      ④ 2 / (1-4)      ⑤ 5	2	1
XYLp      GlCP      XYLp	3	6
⑥ 3        (1-4)	4	2
GlcP	5	5
⑦ 4        (1-6)	6	3
XYLp	7	4

53:

DB 4853



(1) 3 / (H) ~~N~~

Res  
1

pdB  
3

2 ~~5~~

3 4

4 1

5 2.

RHAP

(2) 4 / (H<sub>2</sub>)  
GICPNAC

$\xrightarrow{(1-3)}$

GICP