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FIG. 1

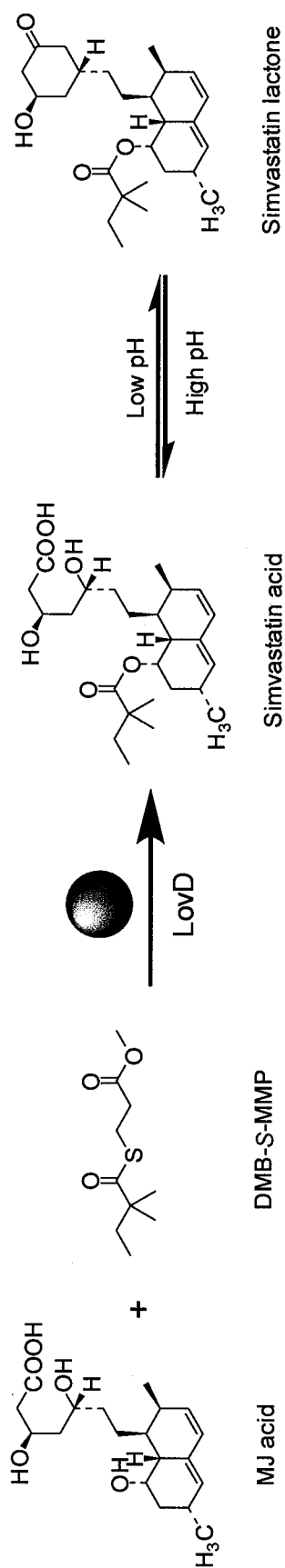


FIG. 2

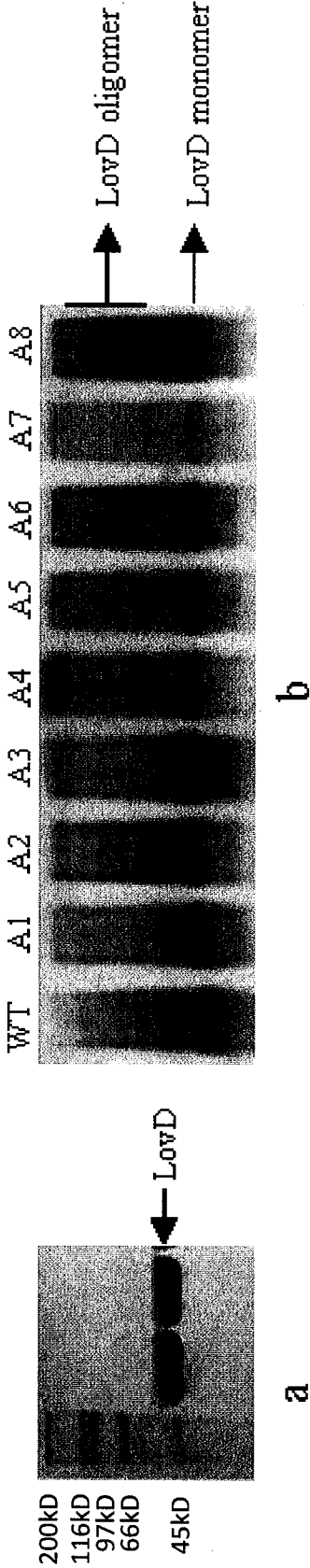


FIG. 3

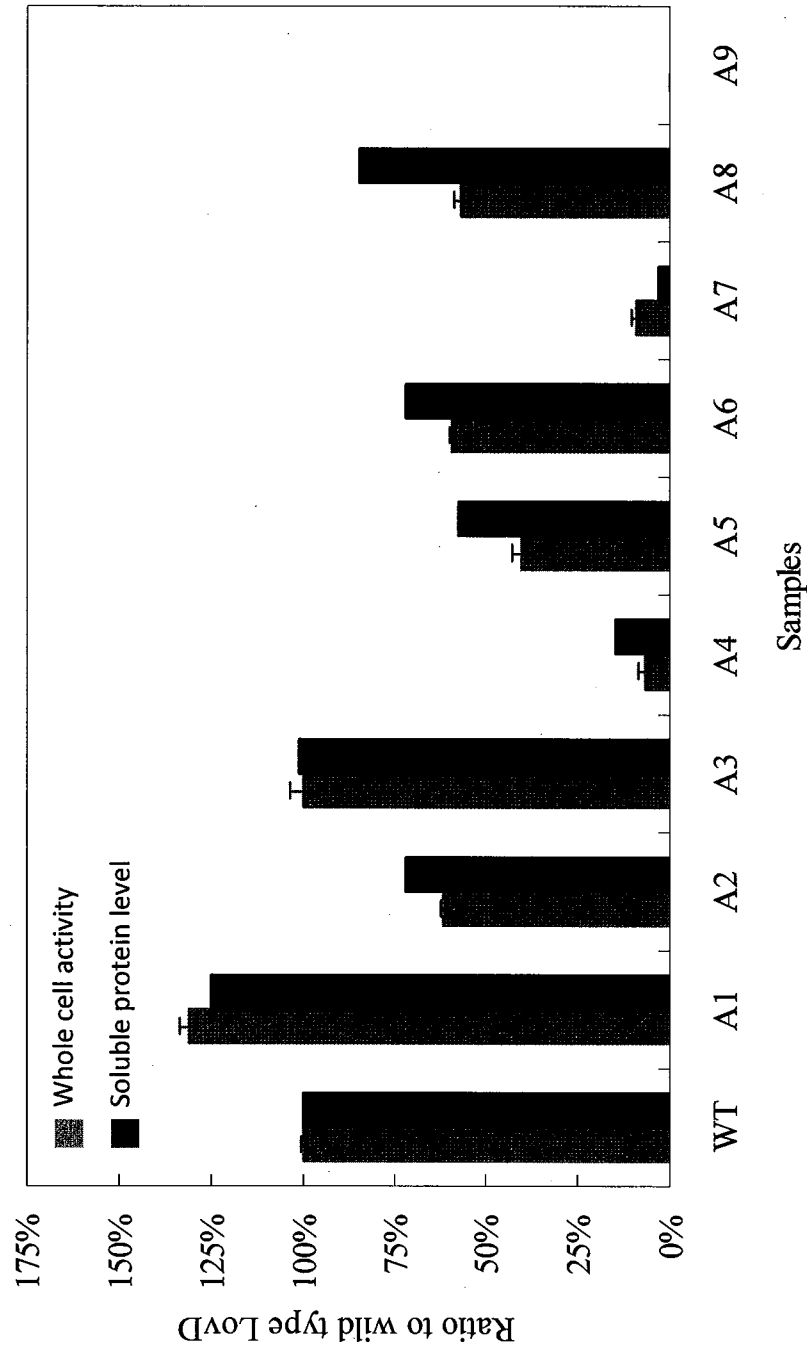


FIG. 4

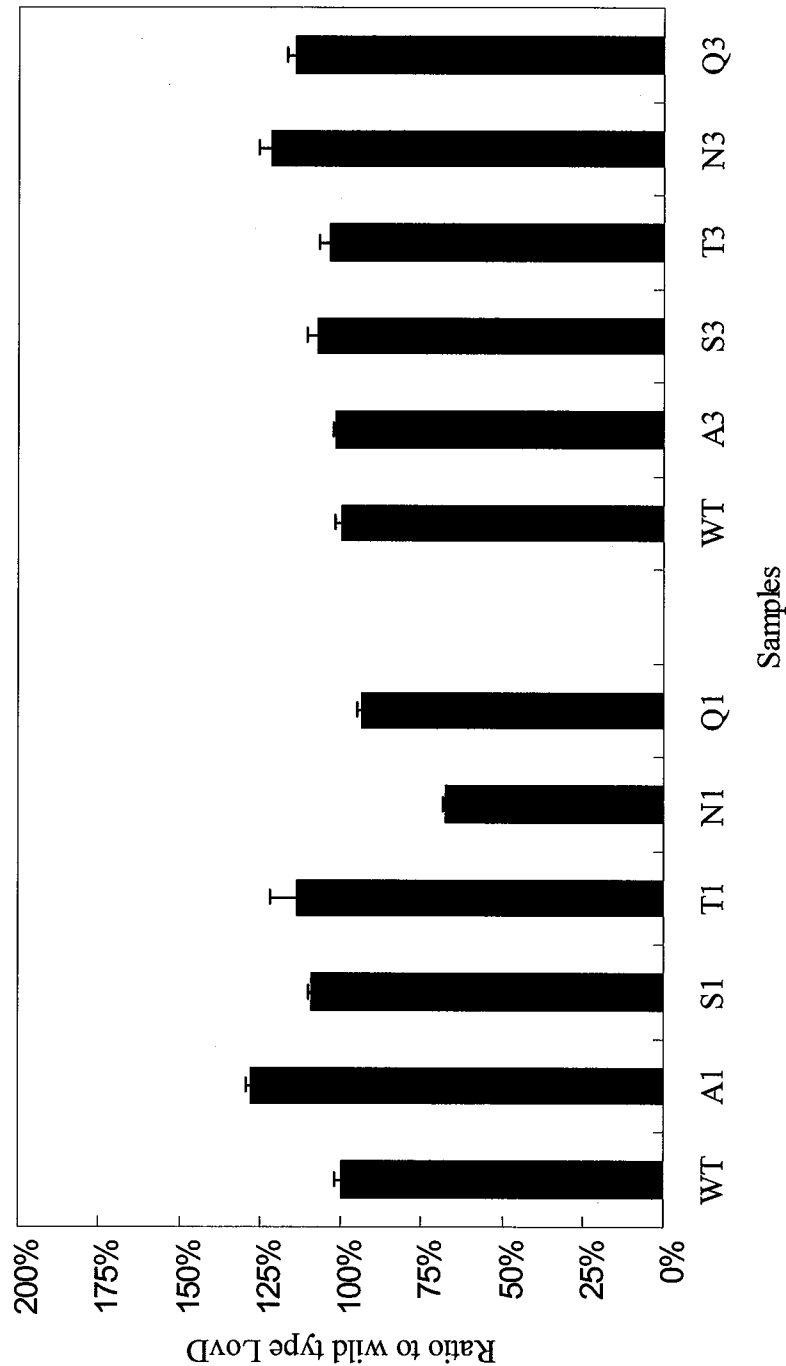


FIG. 5

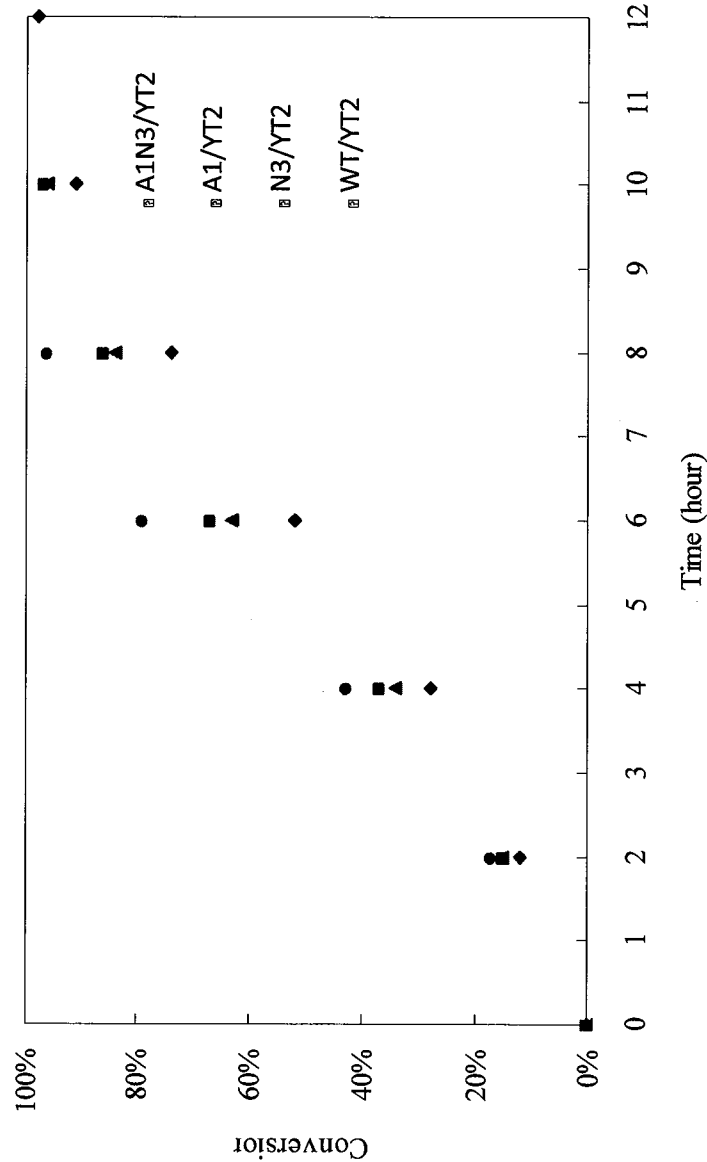


FIG. 6

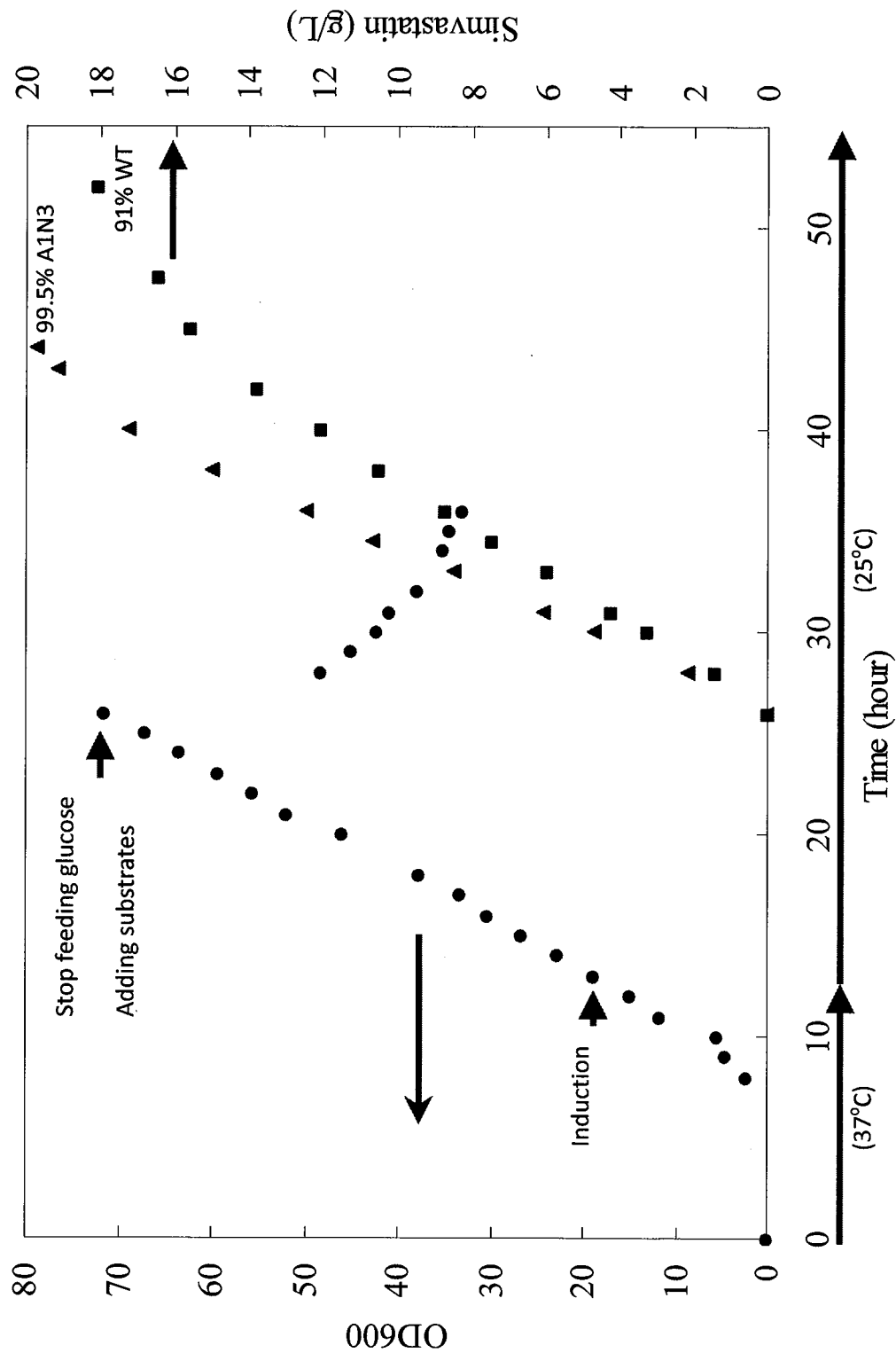
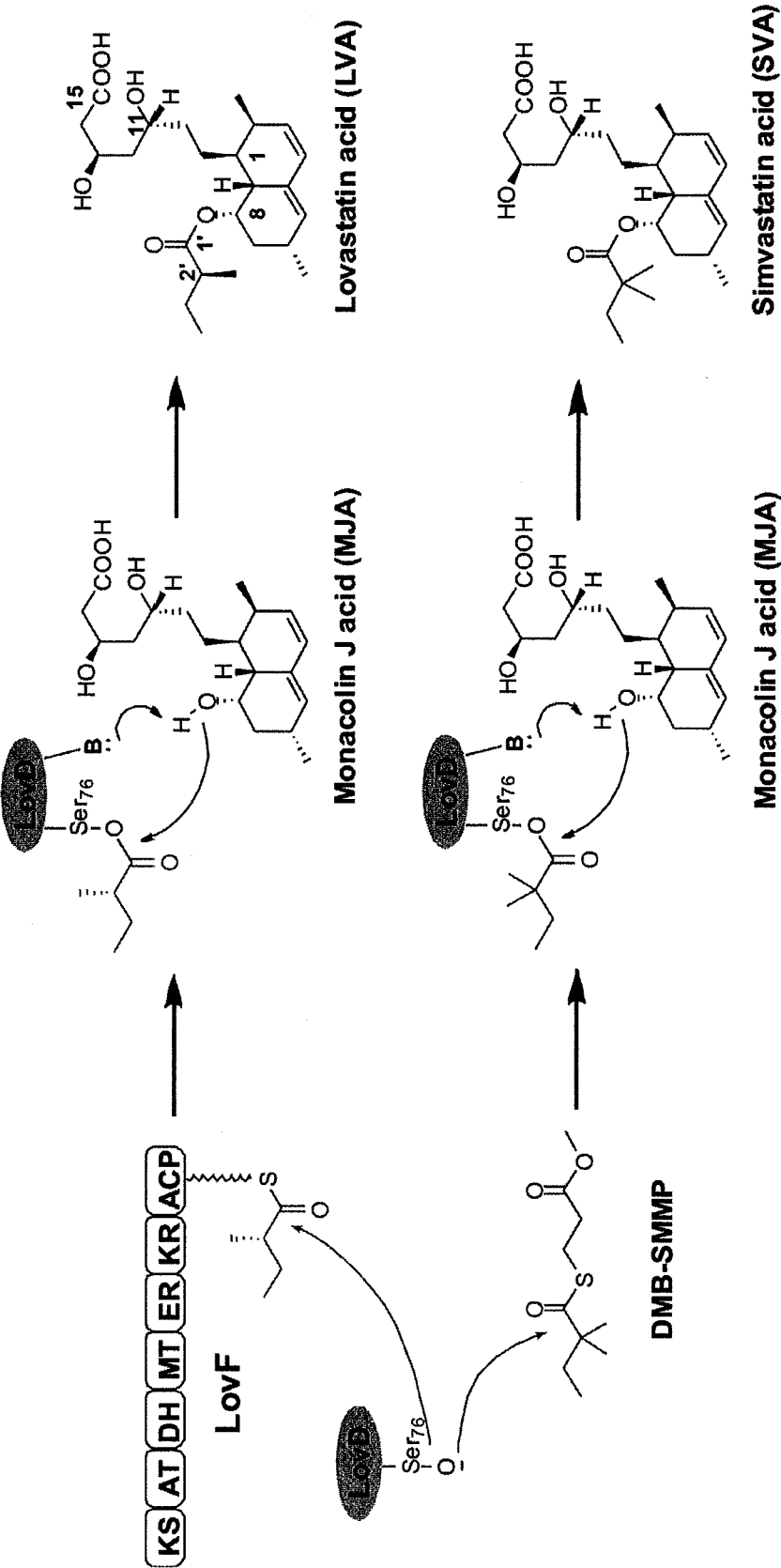
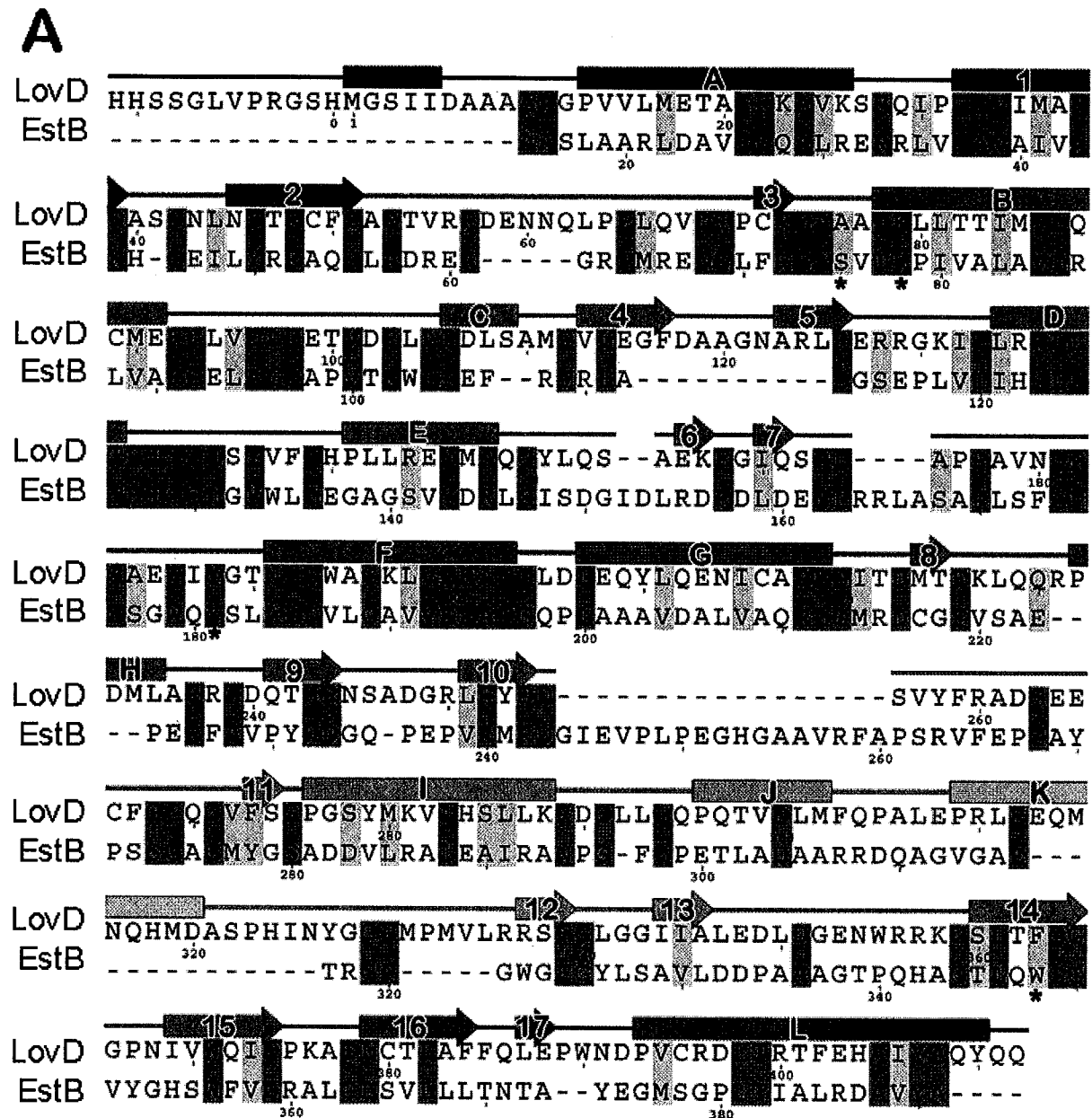


FIG. 7



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FIG. 8A



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FIG. 8D

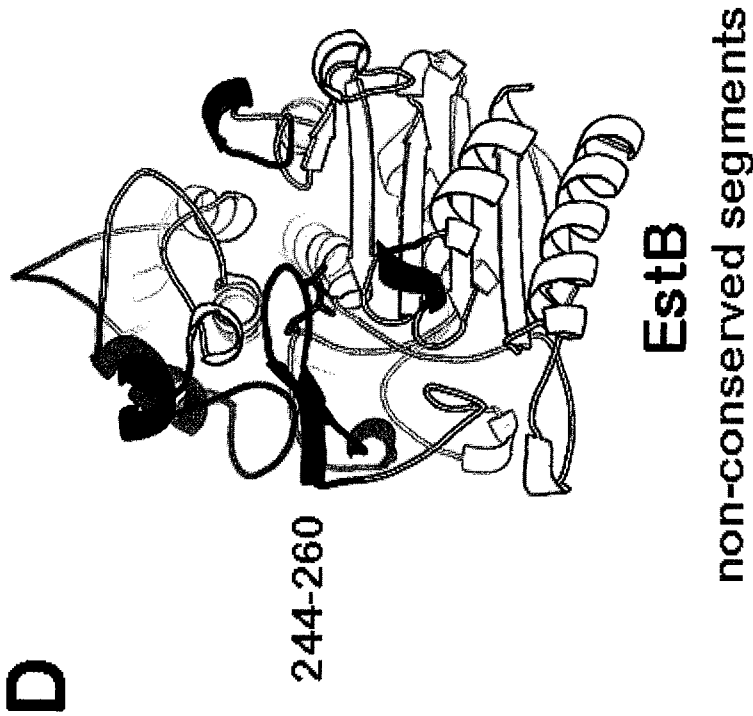
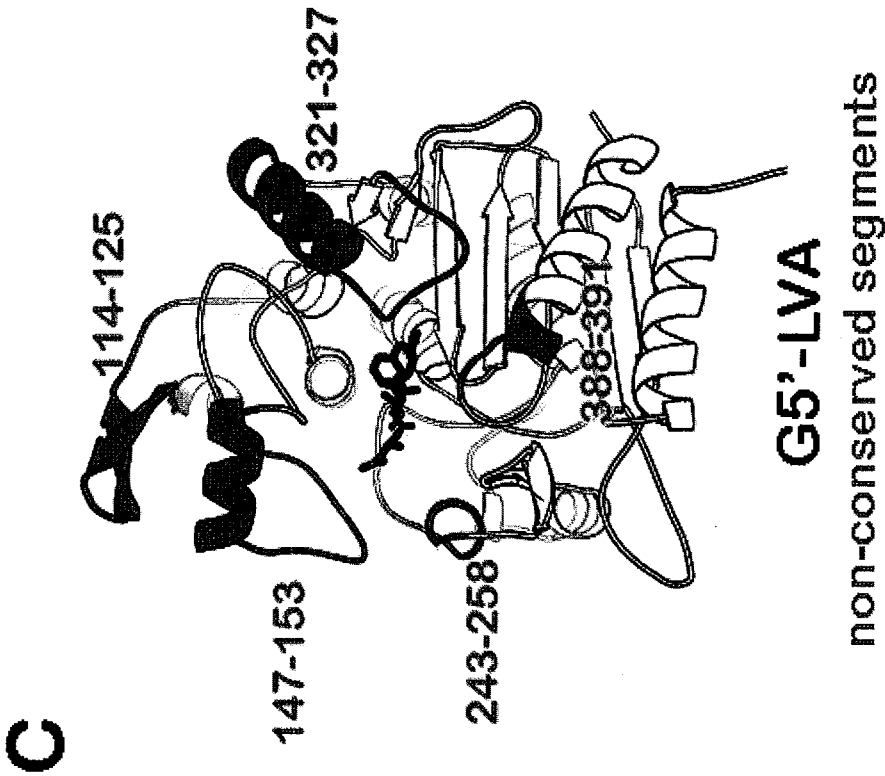


FIG. 8C



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FIG. 8E



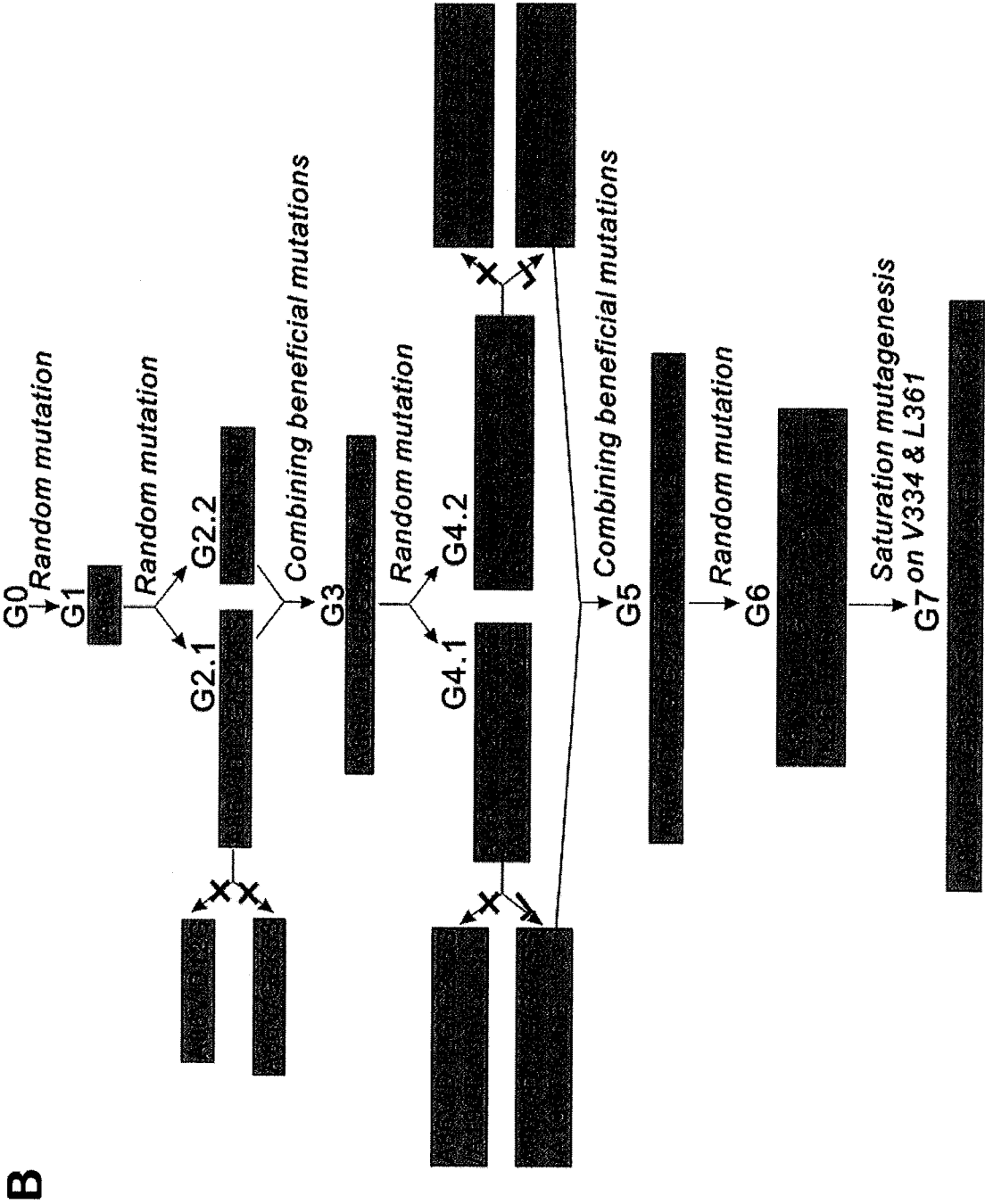
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FIG. 9A



A

FIG. 9B



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FIG. 10

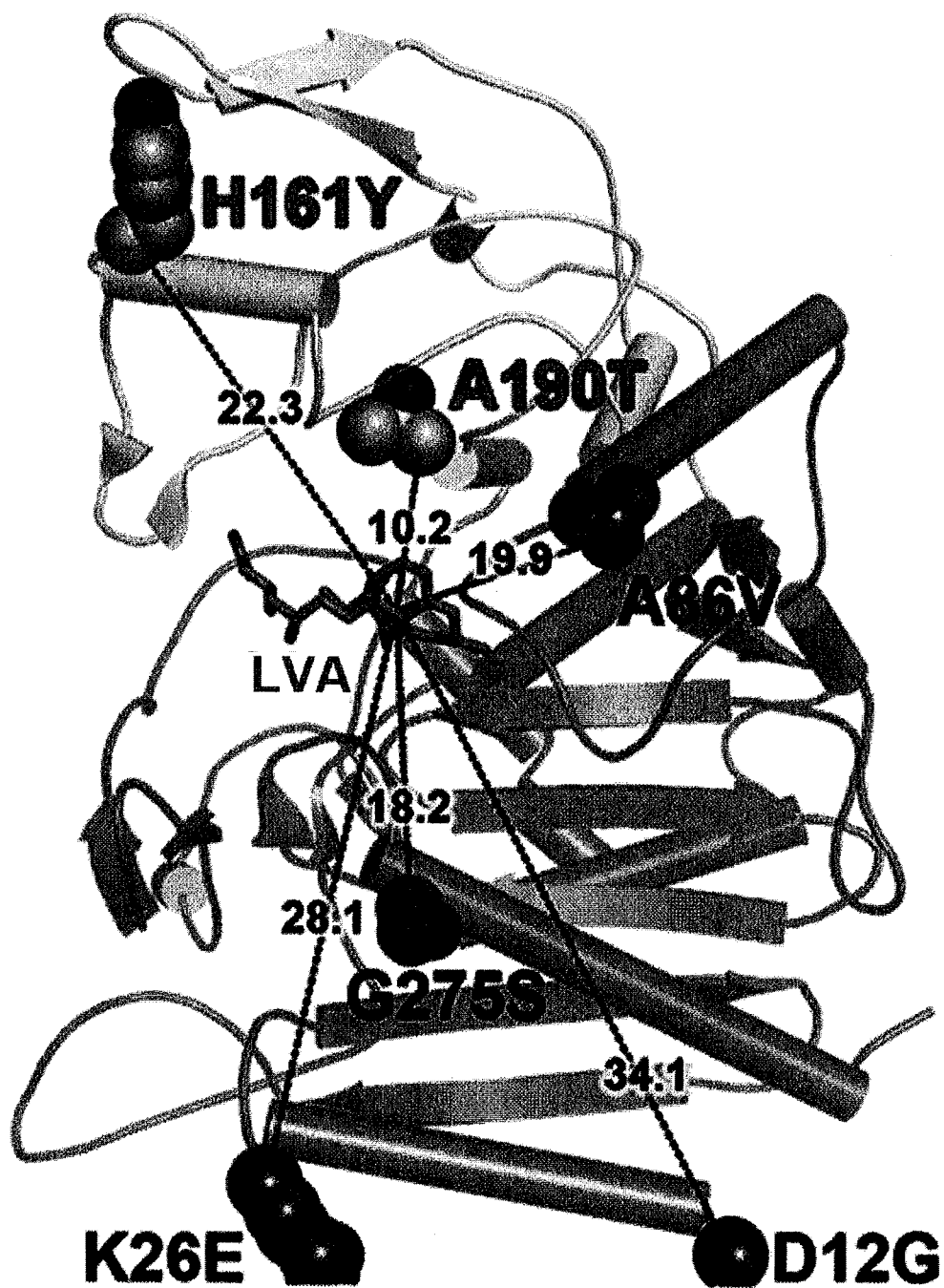


FIG. 11

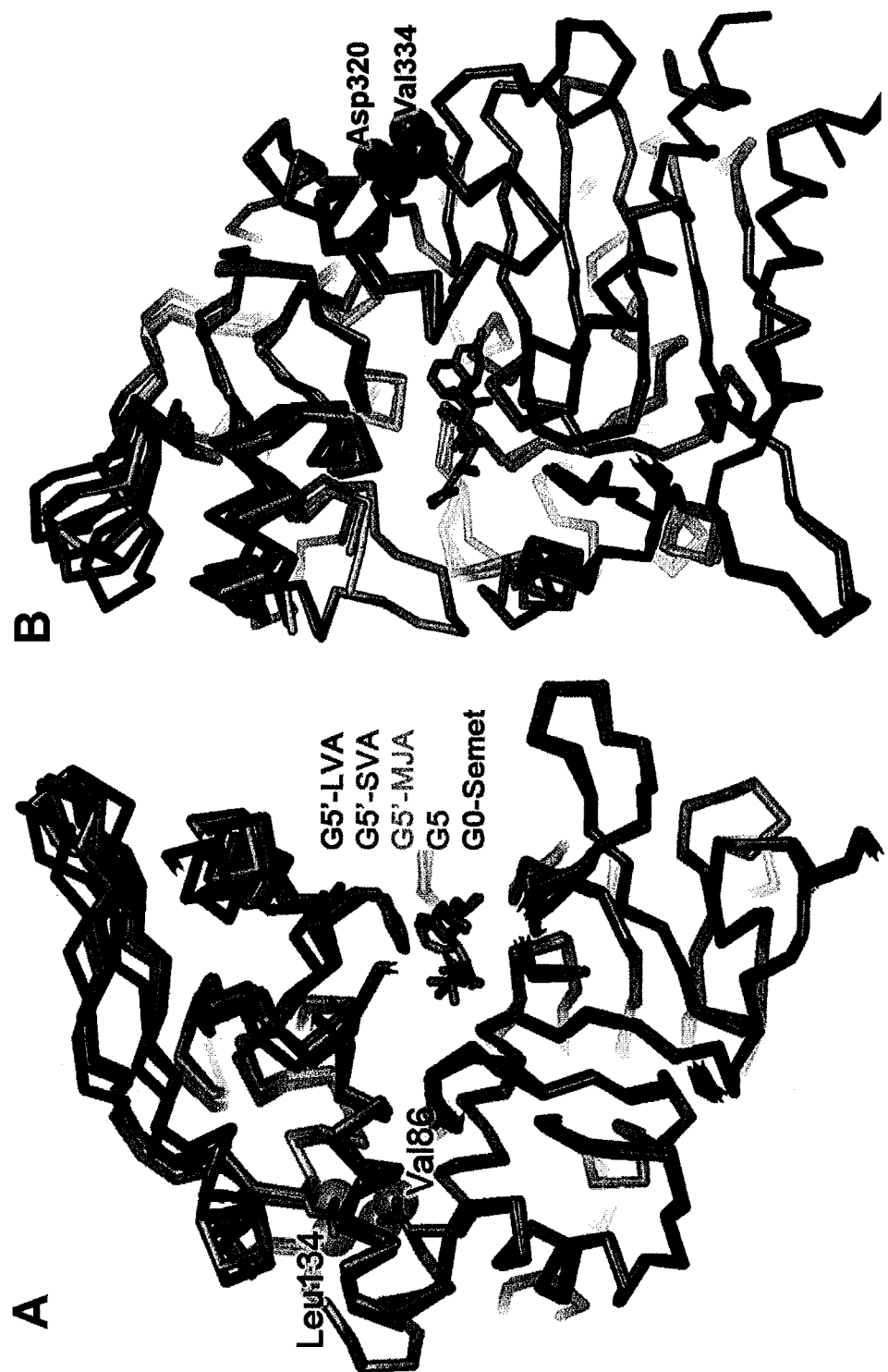


FIG. 12

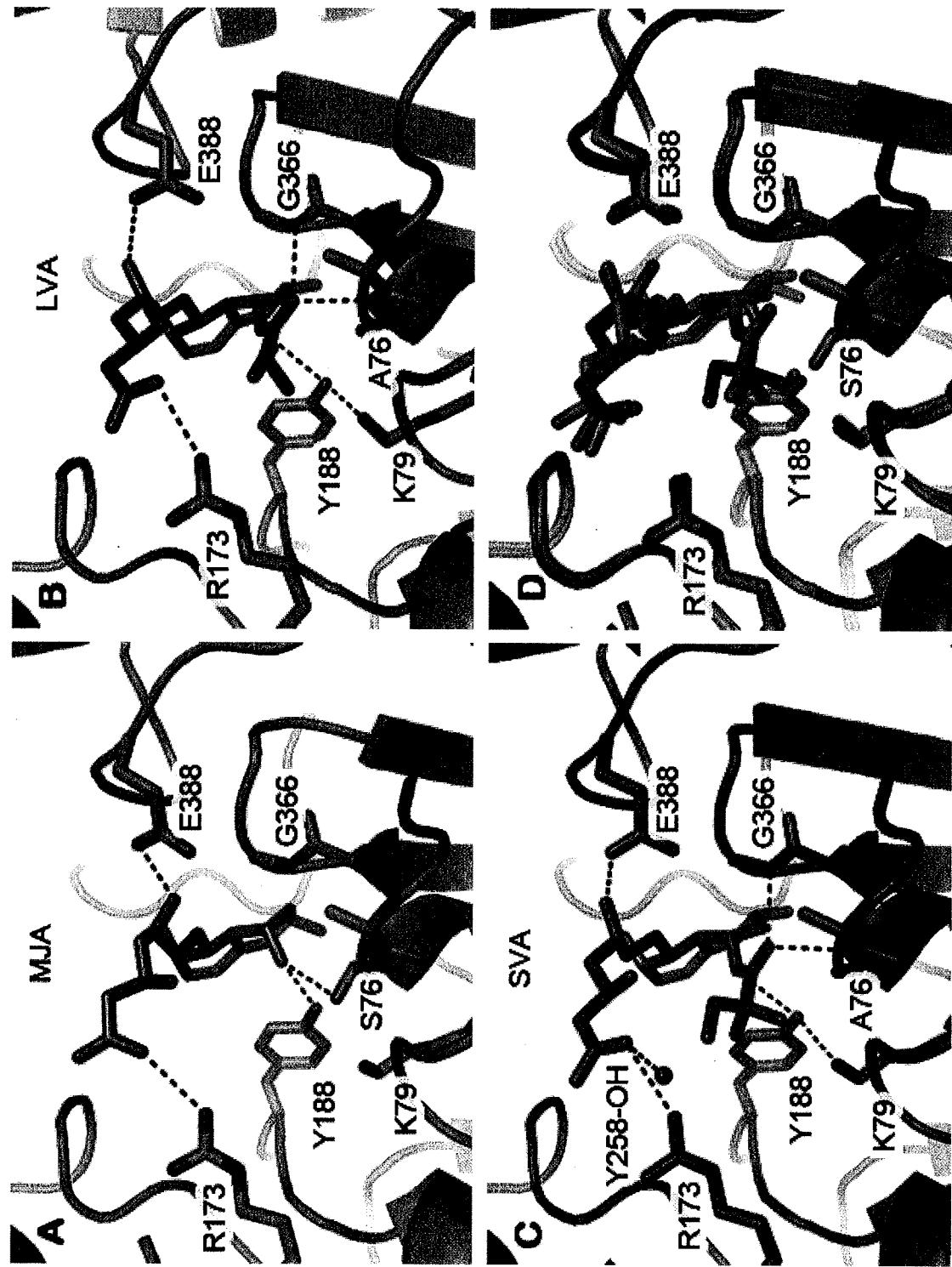


FIG. 13

FIG. 13: . Amino acid substitutions and characterization of LovD variants

Mutations	Whole cell Activity*	k_{cat} (min ⁻¹)	K_M of MJA (mM) †	K_M of DMB-SMMP (mM ⁻¹) ‡	Soluble protein (mg/L) §	T_m (°C) ¶
G0	1	0.66±0.03	0.77±0.17	0.67±0.12	138±11	39.5±0.4
G1 A86V	1.2	0.79±0.03	0.74±0.16	0.66±0.19	140±5.4	41±0.7
G2.1 A86V D12G G275S	1.9	1.14±0.03	0.91±0.17	0.62±0.10	184±8.7	40.5±0.4
G2.2 A86V A190T	1.8	1.20±0.09	0.74±0.21	0.69±0.17	168±17	41±0.4
G3 A86V D12G A190T G275S	3.6	1.86±0.09	0.77±0.11	0.70±0.19	205±23	41±0.4
G4.1 A86V D12G A190T G275S	4.8	2.13±0.03	0.70±0.24	0.66±0.16	183±18	43.5±0.7
A10V K26E						
G4.2 A86V D12G A190T G275S	5.2	2.16±0.12	0.80±0.24	0.64±0.16	221±9.3	42.5±1.9
H161Y K227R						
G5 A86V D12G A190T G275S	6.4	2.61±0.03	0.74±0.03	0.69±0.14	206±5.7	46.5±0.4
K26E H161Y						
G6 A86V D12G A190T G275S	9.3	3.30±0.06	0.70±0.07	0.63±0.15	212±3.9	47±0.1
K26E H161Y V334D L361M						
G7 A86V D12G A190T G275S	11.2	4.80±0.06	0.70±0.04	0.69±0.17	214±6.3	48.5±0.7
K26E H161Y V334F						

FIG. 14

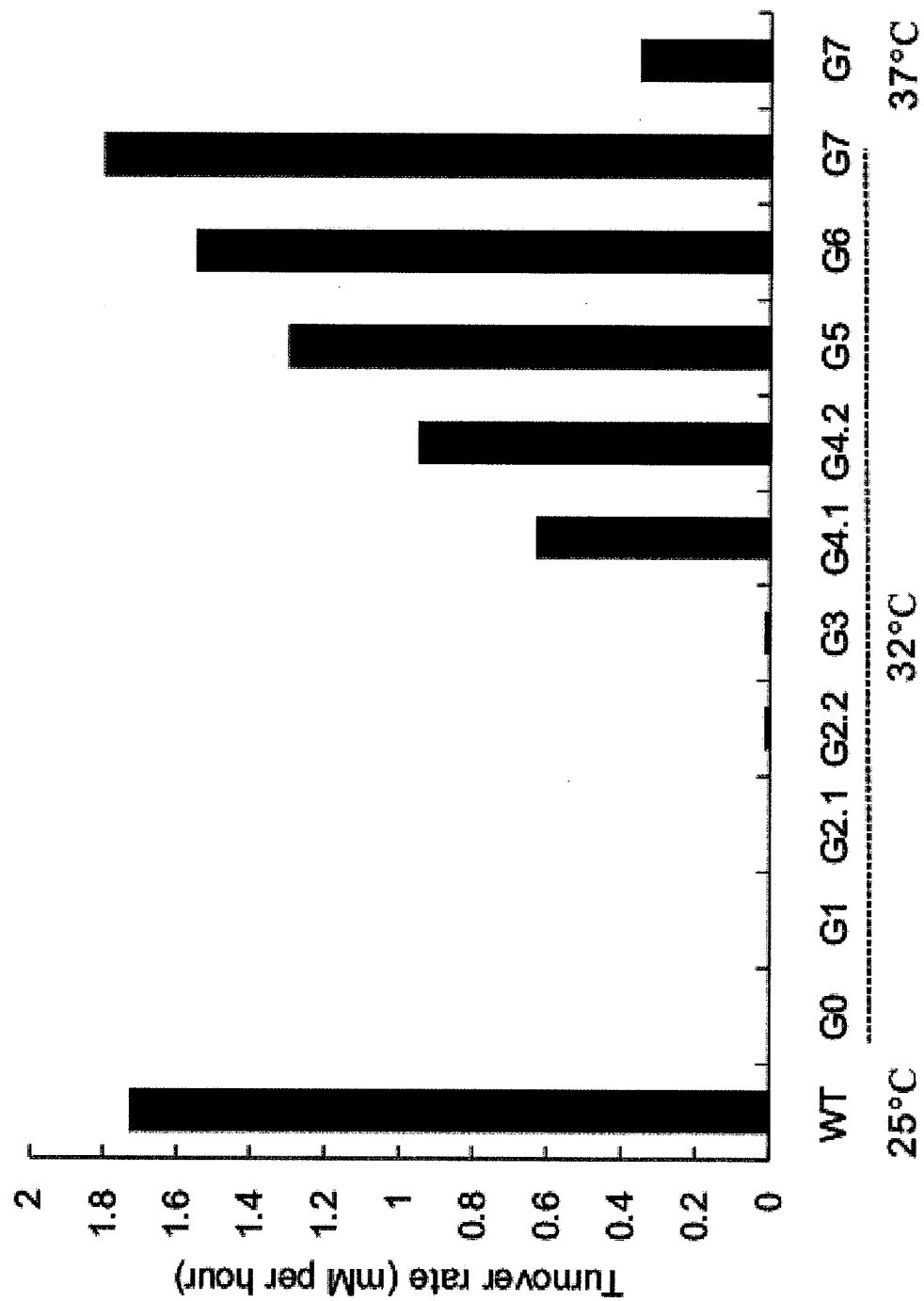
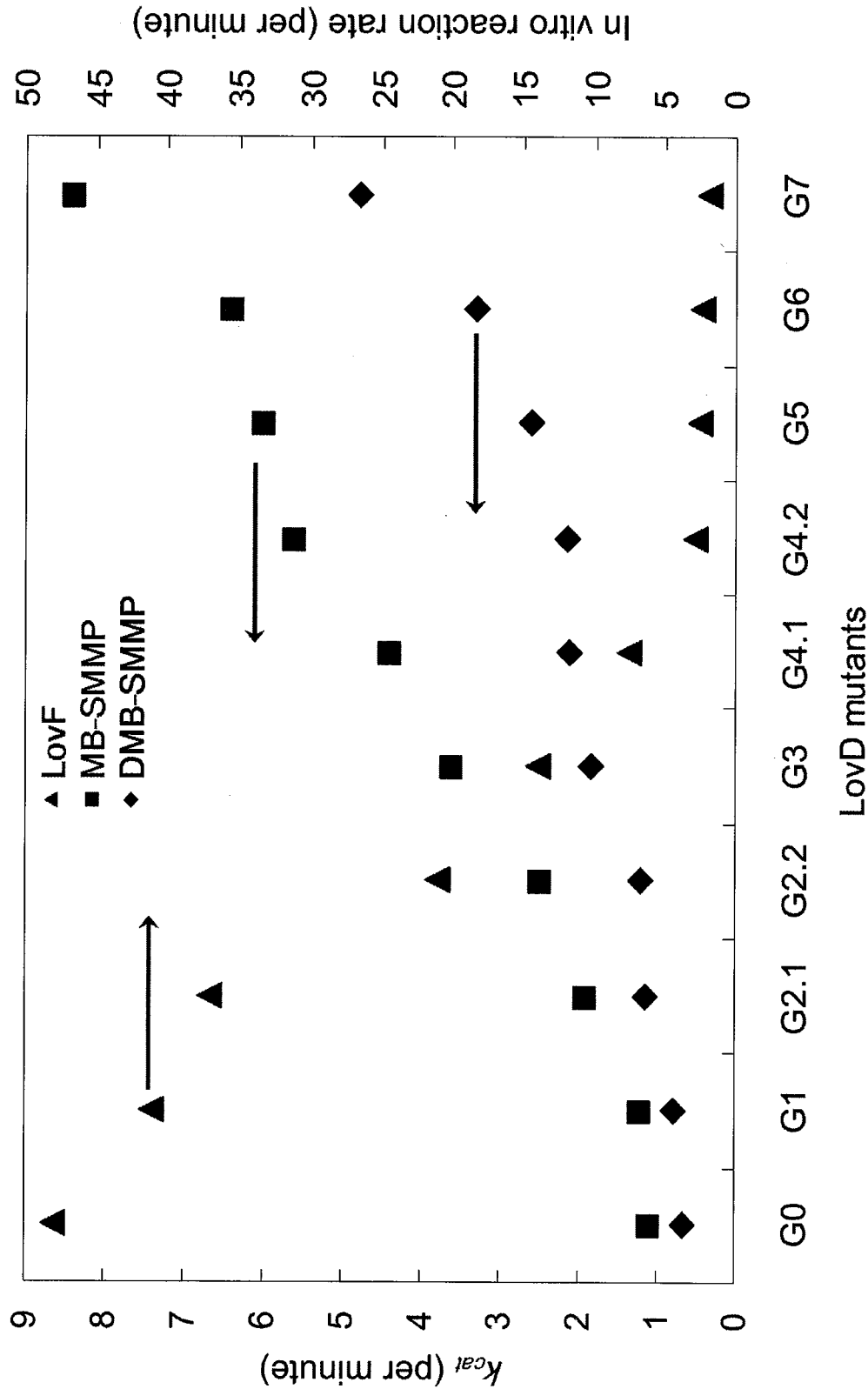
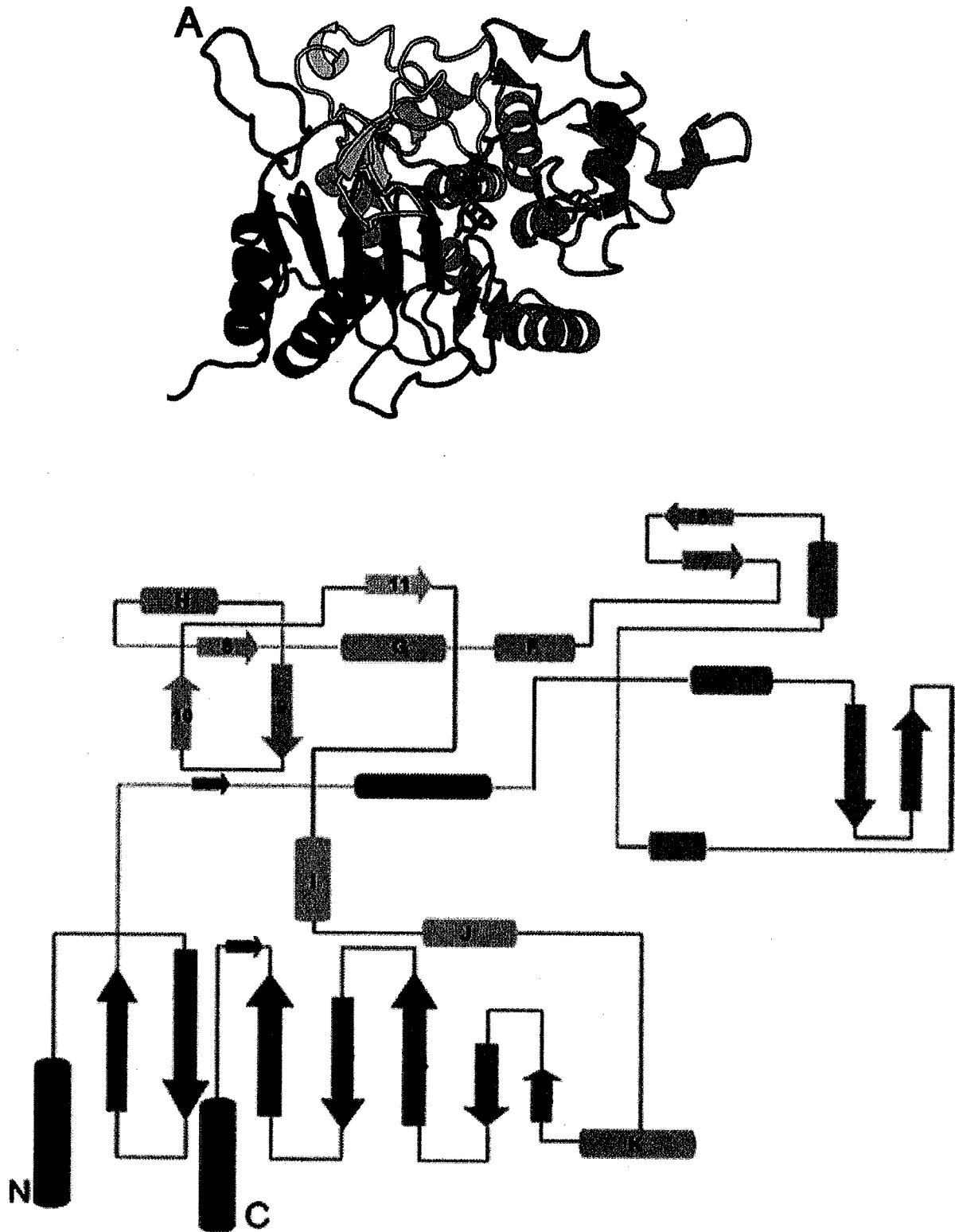


FIG. 15



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FIG. 16A



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FIG. 16B

B

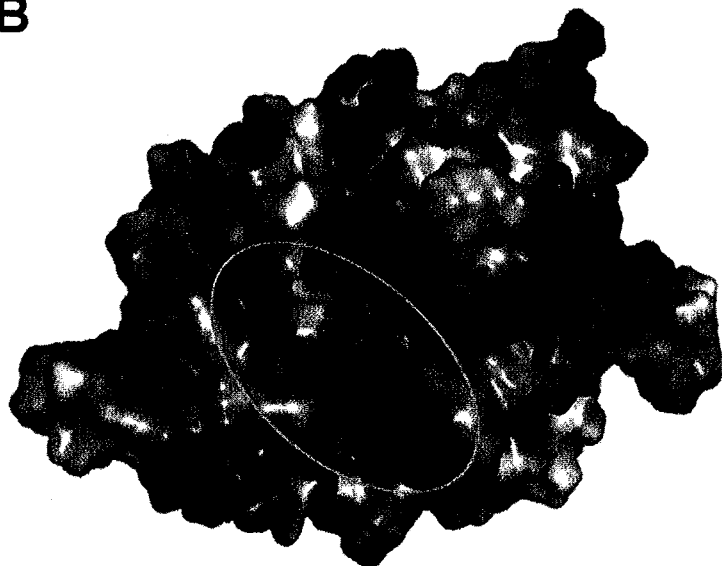


FIG. 16C

C

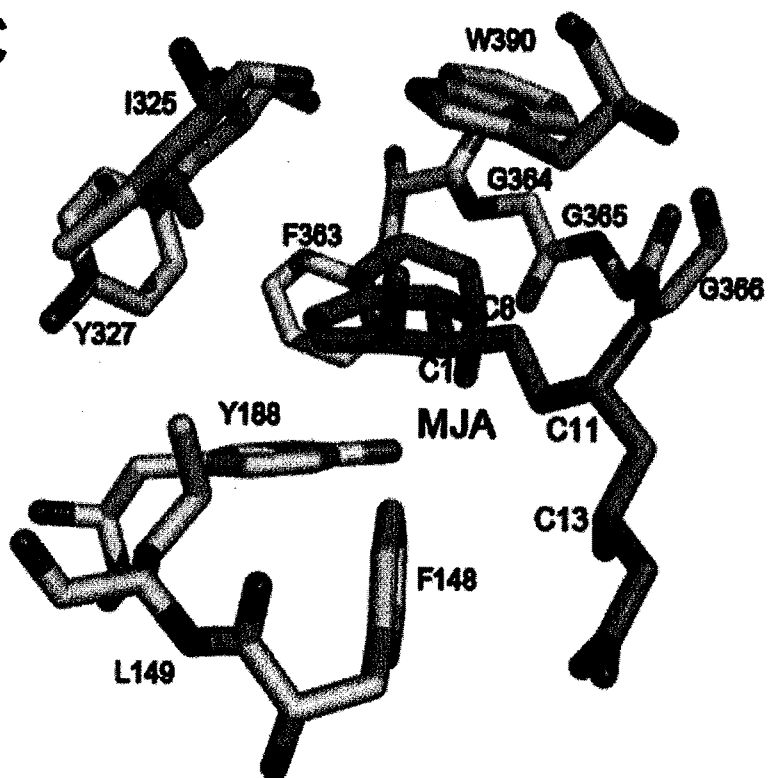


FIG. 17

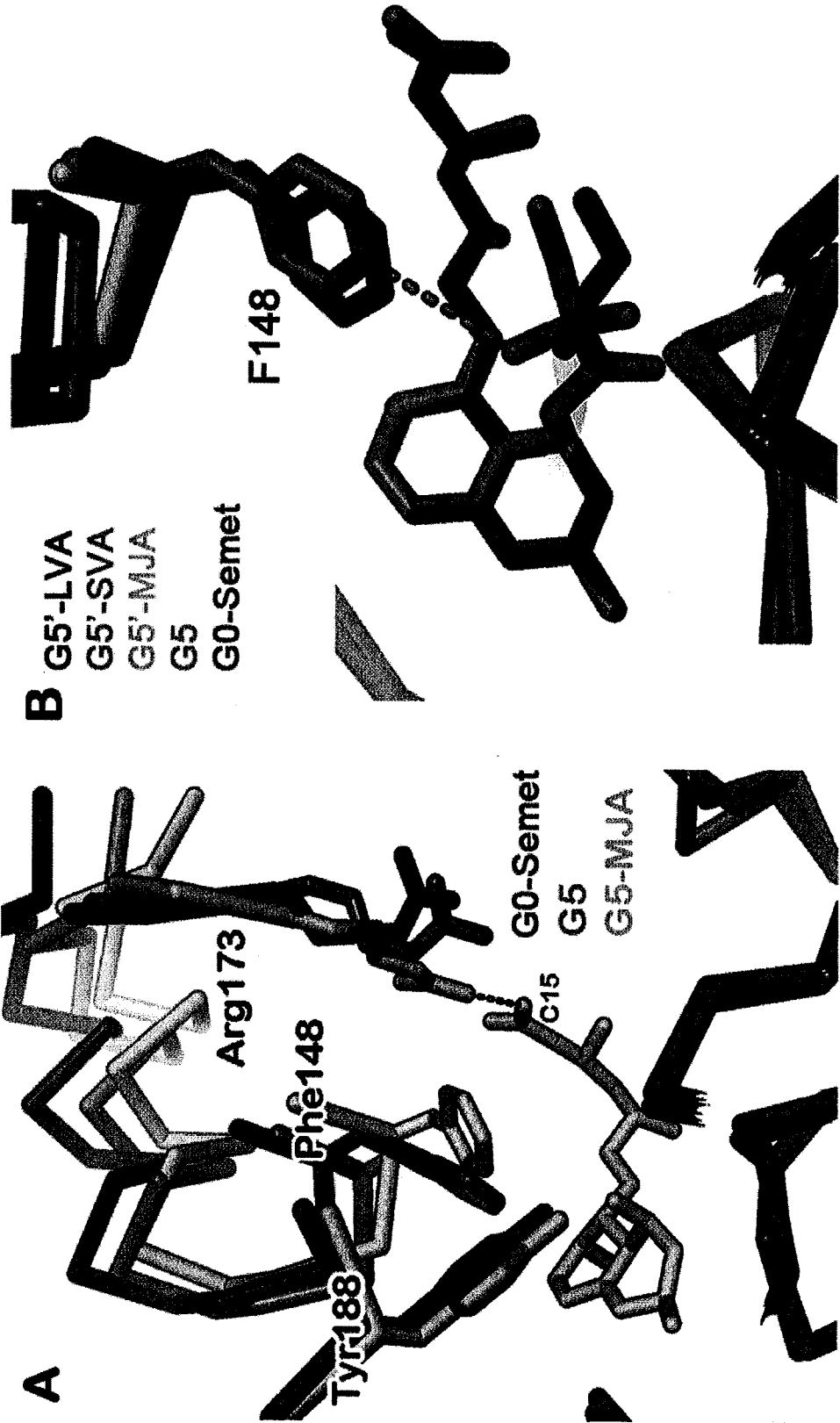


FIG. 18A

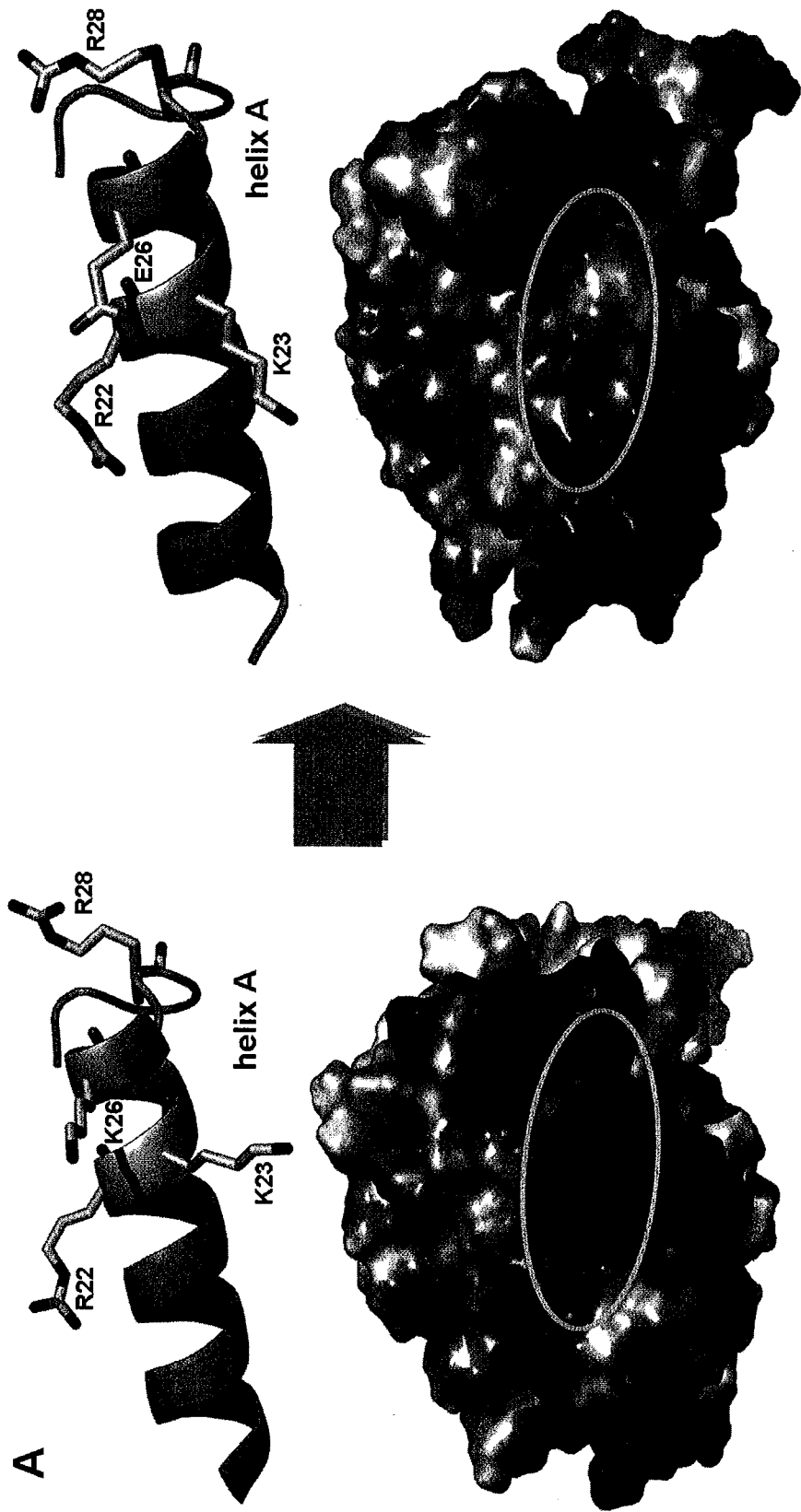


FIG. 18B

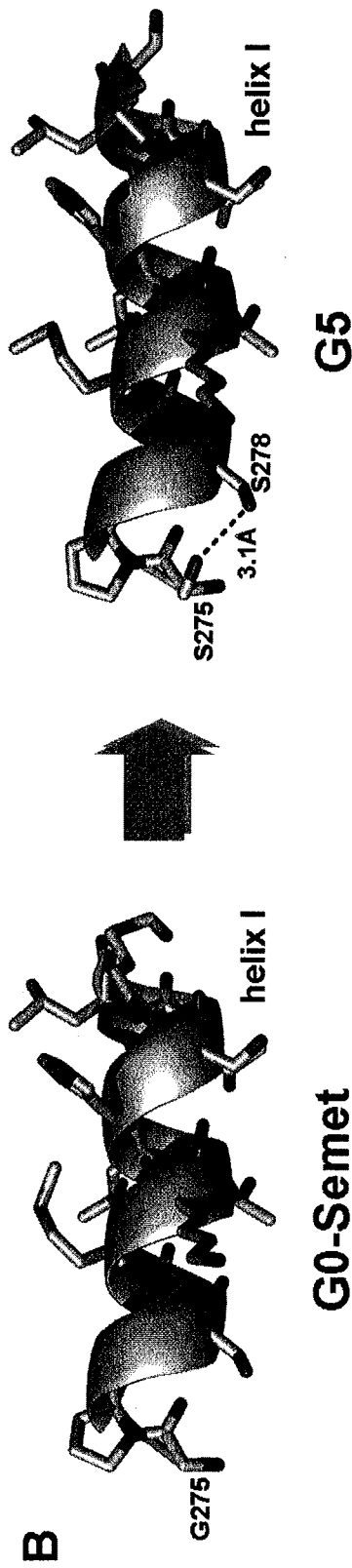


FIG. 19B

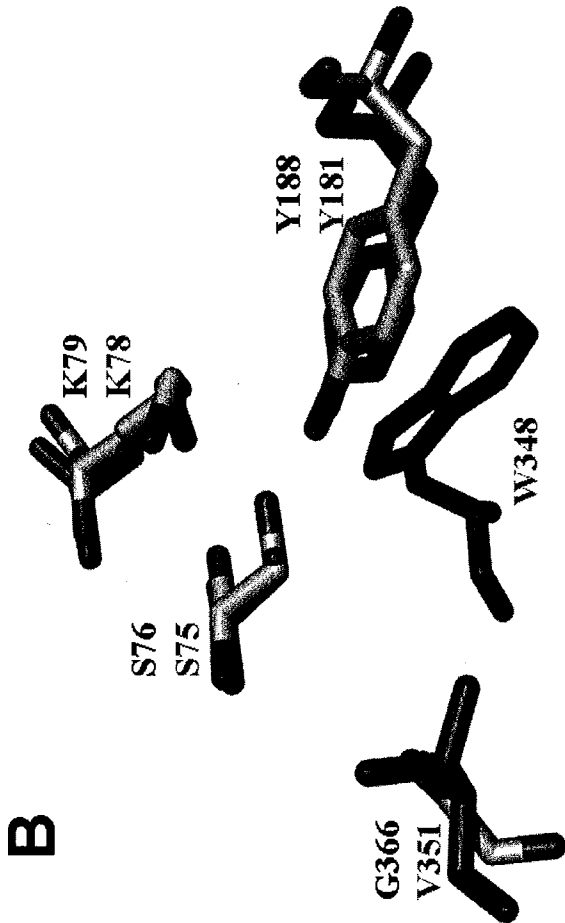


FIG. 19A

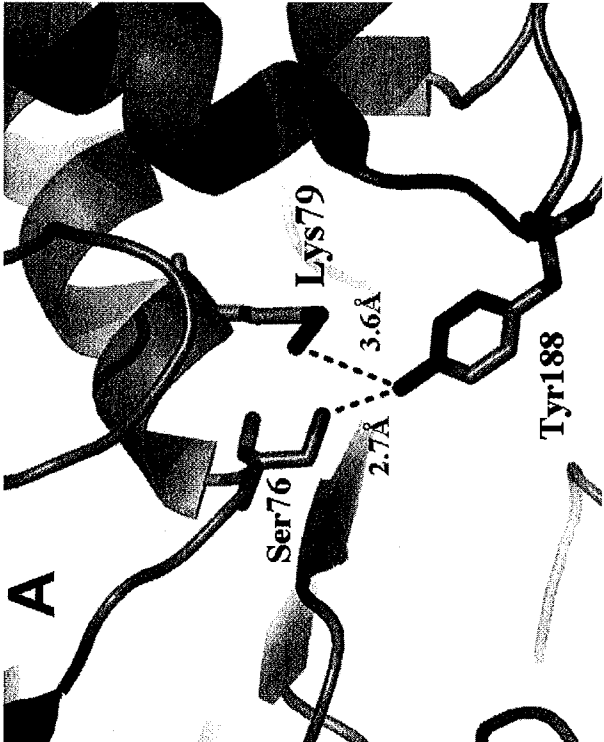


FIG. 19C

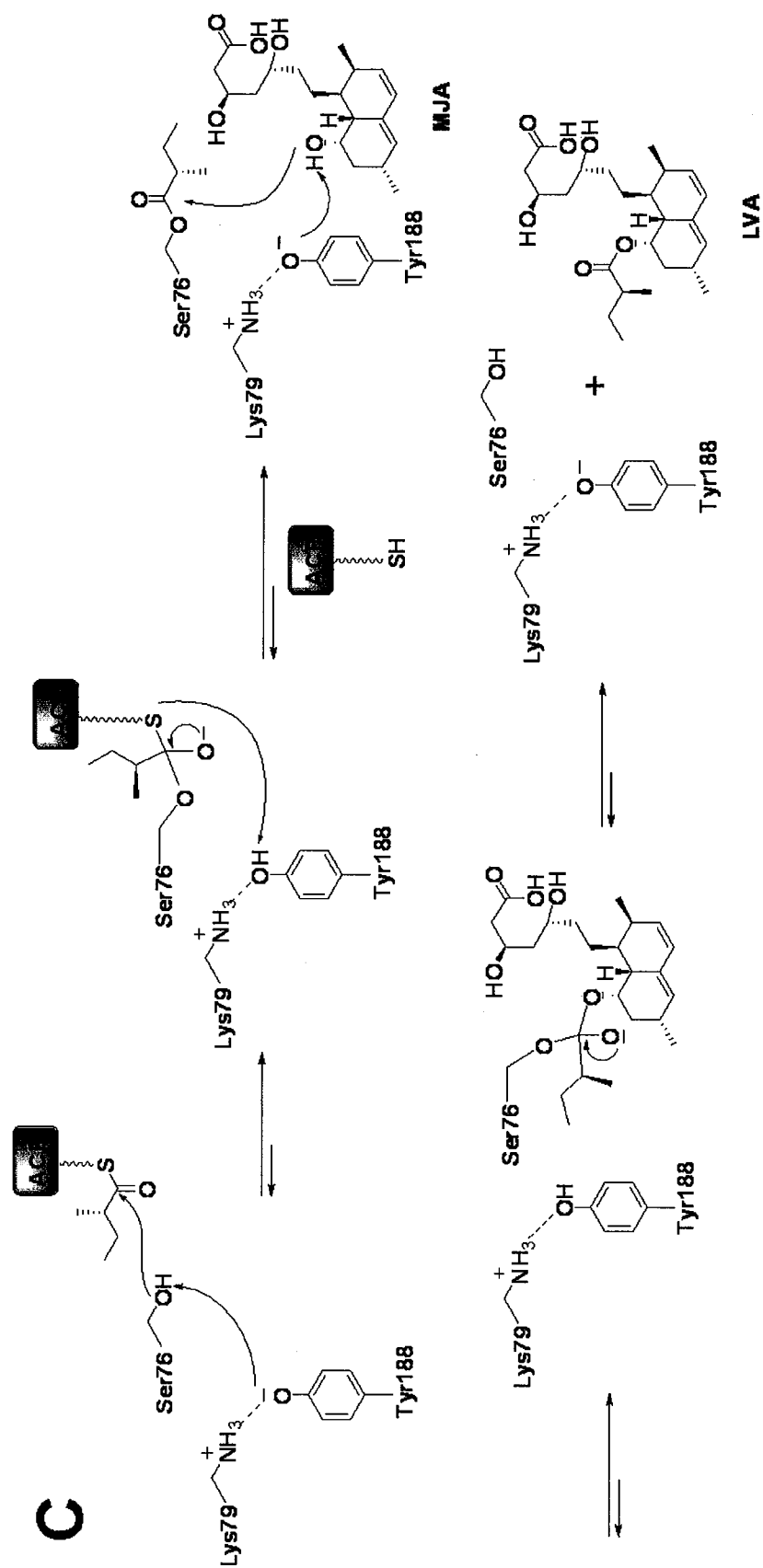


FIG. 20: Statistics of X-ray data collection and atomic refinement (numbers in parentheses refer to the outer shell of data).

Protein	G0	SeMet G0	G5	G5	G5'	G5'	G5'	G5'
Ligand	none	none	none	MJA	MJA	SVA	SVA	LVA
Data collection								
Space group	P1	C2	P2 ₁ 2 ₁ 2 ₁	P2 ₁ 2 ₁ 2 ₁	P2 ₁ 2 ₁ 2 ₁	P2 ₁ 2 ₁ 2 ₁	P2 ₁ 2 ₁ 2 ₁	P2 ₁ 2 ₁ 2 ₁
Cell dimensions								
<i>a</i> , <i>b</i> , <i>c</i> (Å)	56.7, 79.7, 104.1	209.5, 85.2, 104.0	58.2, 75.0, 131.6	58.5, 75.2, 133.5	58.0, 75.2, 132.7	58.5, 75.1, 131.8	59.0, 75.2, 131.7	
□□□ (°)	94.1, 91.6, 106.8	90.0, 117.5, 90.0	90.0, 90.0, 90.0	90.0, 90.0, 90.0	90.0, 90.0, 90.0	90.0, 90.0, 90.0	90.0, 90.0, 90.0	
protomers/asymmetr ic unit	4	4	1	1	1	1	1	1
Resolution (Å)	100.00-3.40 (3.66-3.40)	80.00-2.50 (2.59-2.50)	90.00-2.00 (2.07-2.00)	60.00-2.00 (2.07-2.00)	60.00-2.05 (2.12-2.05)	60.00-2.00 (2.07-2.00)	60.00-2.00 (2.07-2.00)	27/28 60.00-2.00 (2.07-2.00)
<i>R</i> _{merge} (%)	20.8 (43.4)	11.8 (45.3)	4.9 (37.8)	15.6 (39.6)	6.8 (40.2)	6.9 (31.4)	11.8 (39.6)	
<i>I</i> / □□	5.1 (2.9)	10.2 (1.7)	47.2 (6.5)	13.0 (4.8)	38.3 (6.6)	19.5 (3.9)	13.33 (4.64)	
Completeness (%)	99.3 (98.9)	89.9 (46.7)	99.9 (100.0)	99.8 (100.0)	99.9 (99.8)	97.7 (99.6)	98.5 (99.5)	
Redundancy	3.7 (3.7)	5.3 (3.0)	11.6 (11.7)	6.2 (6.4)	15.4 (12.9)	4.9 (4.9)	6.4 (6.5)	
wavelength (Å)	0.9793	0.9793	0.9794	0.9794	0.9792 &1.5418	0.9717	0.9795	
Refinement								
Resolution (Å)	103.7-3.4 (3.5-3.4)	65.9-2.50 (2.56-2.50)	65.80-2.00 (2.05-2.00)	46.18-2.00 (2.05-2.00)	49.86-2.05 (2.10-2.05)	49.51-2.00 (2.05-2.00)	46.42-2.00 (2.06-2.00)	
No. reflections	22457 (1669)	47728 (1657)	37539 (2837)	38325 (2910)	35223 (2686)	36938 (2714)	37005 (2671)	
<i>R</i> _{work} / <i>R</i> _{free} (%)	23.1/27.5 (31.9/35.5)	24.8/29.0 (35.6/40.5)	17.9/20.6 (20.4/24.4)	17.9/21.3 (21.5/26.1)	17.7/20.9 (19.8/23.7)	17.6/20.9 (23.1/25.1)	16.2/18.9 (18.3/21.8)	
No. atoms								

Protein	12328	12547	3289	3332	3355	3351	3343
Ligand/ion 1	0	65 (sulfate)	13 (PEG)	48 (MJA)	24 (MJA)	31(SVA)	30
Ligand/ion 2	0	0	6 (glycerol)	12 (formate)	8 (dithiothreitol)	0	0
Water	0	21	151	275	157	179	230
<i>B</i> -factors (Å ²)							
Protein	6.3	51.7	34.4	27.6	35.4	32.2	31.4
Ligand/ion 1	n/a	68.0 (SO ₄)	58.6 (PEG)	58.8 (MJA)	46.5 (MJA)	45.5 (SVA)	38.3 (LVA)
Ligand/ion 1	n/a	n/a	58.2 (glycerol)	38.6 (formate)	74.2 (dithiothreitol)	n/a	n/a
Water	n/a	39.4	36.9	32.8	37.6	36.1	37.2
R.M.S. deviations							
Bond lengths (Å)	0.011	0.006	0.009	0.009	0.008	0.008	0.008
Bond angles (°)	1.3	0.995	1.199	1.230	1.202	1.193	1.193
Ramachandran Plot (%)							
most favored	88.0	90.0	91.2	89.4	89.7	90.3	90.6
additionally allowed	11.4	9.7	8.5	10.3	10.0	9.4	9.1
generously allowed	0.6	0.3	0.3	0.3	0.3	0.3	0.3
disallowed	0.0	0.0	0.0	0.0	0.0	0.0	0.0
PDB ID code	3HL9	3HLB	3HLC	3HLD	3HLE	3HLF	3HLG

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FIG. 20 (Continued)