

**Available structures of Complex II superfamily members:**

enzyme	species	ID code	date	ligands				ProCheck		EDS RSR <sup>3</sup>	
				dicarb	Q-site	Resoln	R <sub>cryst</sub>	R <sub>free</sub>	%MFR <sup>1</sup>		
QFR	<i>E.coli</i>	1KF6	19-NOV-01	OAA? <sup>4</sup>	HQNO	2.70	0.231	0.280	84.8	+0.03	ND <sup>5</sup>
		1KFY	24-NOV-01	OAA? <sup>4</sup>	DNP-19	3.60	0.264	0.301	84.5	+0.05	ND
		1L0V	13-FEB-02	OAA? <sup>4</sup>	MQ,MQ	3.30	0.245	0.290	77.3	-0.08	ND
		2B76	03-OCT-05	citrate	MQ	3.30	0.248	0.284	73.8	-0.35	0.219
	<i>W.succ</i>	1QLA	24-AUG-99			2.20	0.212	0.224	89.0	+0.30	ND
		1QLB	24-AUG-99	fumar.		2.33	0.213	0.223	88.1	+0.19	ND
		1E7P	01-SEP-00	malon.		3.10	0.283	0.291	74.5	-0.18	ND
		2BS2	09-MAY-05	fumar.		1.78	0.229	0.237	90.0	+0.24	0.127
		2BS3	09-MAY-05	citrate		2.19	0.183	0.198	90.0	+0.24	0.148
		2BS4	11-MAY-05	citrate	me <sub>2</sub> NQ	2.76	0.200	0.216	87.6	+0.15	0.162
SQR	<i>E.coli</i>	1NEK	11-DEC-02	OAA	UQ2	2.60	0.247	0.289	85.9	+0.07	ND
		1NEN	11-DEC-02	OAA	DNP-17	2.90	0.271	0.296	85.1	+0.05	ND
		2ACZ	19-JUL-05	OAA	AA5 <sup>6</sup>	3.10	0.264	0.308	79.7	-0.05	0.235
	<i>Sus</i>	1ZOY	15-MAY-05		UQ	2.40	0.213	0.259	84.4	+0.09	0.188
		1ZP0	16-MAY-05	3NP	TTFA	3.50	0.268	0.293	84.4	+0.12	0.235
	<i>Gallus</i>	1YQ3	01-FEB-05	OAA	UQ?	2.20	0.175	0.223	88.6	+0.06	0.133
		1YQ4	01-FEB-05	3NP	UQ?	2.33	0.202	0.252	87.5	+0.11	0.137
		2FBW	10-DEC-05	OAA	carboxn	2.10	0.187	0.227	89.8	+0.21	0.111
		2H88	06-JUN-06	OAA	??	1.74	0.178	0.206	90.7	+0.18	0.104
		2H89	06-JUN-06	malon	??	2.40	0.226	0.279	85.6	+0.12	0.150

<sup>1</sup> %MFR - percent of residues in most favorable region of Ramachandran

<sup>2</sup> G - overall Procheck G-score on dihedral angles. Higher is better. (G-score on bond angles and lengths is less relevant as it depends mainly on geometric restraints during refinement).

<sup>3</sup> RSR- Real-space R factor- Measure of disagreement between the model and the density. Lower is better.

<sup>4</sup>The authors later speculated that what was modeled as OAA in the *E. coli* QFR structures was actually citrate from the mother liquor.

<sup>5</sup>ND- No data was deposited with these structures so the RSR cannot be calculated.

<sup>6</sup> AA5- Atpenin A5