



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 10:22 PM GMT

PDB ID : 1T9D  
Title : Crystal Structure Of Yeast Acetohydroxyacid Synthase In Complex With A Sulfonyleurea Herbicide, Metsulfuron methyl  
Authors : McCourt, J.A.; Pang, S.S.; Guddat, L.W.; Duggleby, R.G.  
Deposited on : 2004-05-16  
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

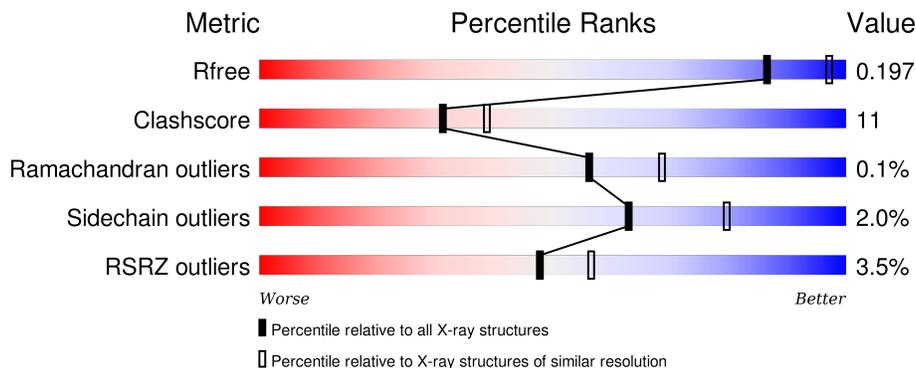
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	677	 74% 13% • 12%
1	B	677	 67% 18% 14%
1	C	677	 11% 63% 20% • 15%
1	D	677	 74% 14% • 12%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	1MM	C	2695	-	X	-	-
7	PYD	A	703	-	X	-	X
7	PYD	B	1703	-	X	-	X
7	PYD	C	2703	-	X	-	X
7	PYD	D	3703	-	X	-	X

## 2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 20377 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Acetolactate synthase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	596	4548	2879	783	865	21	0	6	0
1	B	582	4392	2788	758	827	19	0	3	0
1	C	575	4323	2742	746	816	19	0	2	0
1	D	596	4528	2867	781	860	20	0	5	0

There are 188 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	11	MET	-	CLONING ARTIFACT	UNP P07342
A	12	HIS	-	CLONING ARTIFACT	UNP P07342
A	13	HIS	-	CLONING ARTIFACT	UNP P07342
A	14	HIS	-	CLONING ARTIFACT	UNP P07342
A	15	HIS	-	CLONING ARTIFACT	UNP P07342
A	16	HIS	-	CLONING ARTIFACT	UNP P07342
A	17	HIS	-	CLONING ARTIFACT	UNP P07342
A	18	SER	-	CLONING ARTIFACT	UNP P07342
A	19	SER	-	CLONING ARTIFACT	UNP P07342
A	20	GLY	-	CLONING ARTIFACT	UNP P07342
A	21	LEU	-	CLONING ARTIFACT	UNP P07342
A	22	VAL	-	CLONING ARTIFACT	UNP P07342
A	23	PRO	-	CLONING ARTIFACT	UNP P07342
A	24	ARG	-	CLONING ARTIFACT	UNP P07342
A	25	GLY	-	CLONING ARTIFACT	UNP P07342
A	26	SER	-	CLONING ARTIFACT	UNP P07342
A	27	GLY	-	CLONING ARTIFACT	UNP P07342
A	28	MET	-	CLONING ARTIFACT	UNP P07342
A	29	LYS	-	CLONING ARTIFACT	UNP P07342
A	30	GLU	-	CLONING ARTIFACT	UNP P07342
A	31	THR	-	CLONING ARTIFACT	UNP P07342

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A	32	ALA	-	CLONING ARTIFACT	UNP P07342
A	33	ALA	-	CLONING ARTIFACT	UNP P07342
A	34	ALA	-	CLONING ARTIFACT	UNP P07342
A	35	LYS	-	CLONING ARTIFACT	UNP P07342
A	36	PHE	-	CLONING ARTIFACT	UNP P07342
A	37	GLU	-	CLONING ARTIFACT	UNP P07342
A	38	ARG	-	CLONING ARTIFACT	UNP P07342
A	39	GLN	-	CLONING ARTIFACT	UNP P07342
A	40	HIS	-	CLONING ARTIFACT	UNP P07342
A	41	MET	-	CLONING ARTIFACT	UNP P07342
A	42	ASP	-	CLONING ARTIFACT	UNP P07342
A	43	SER	-	CLONING ARTIFACT	UNP P07342
A	44	PRO	-	CLONING ARTIFACT	UNP P07342
A	45	ASP	-	CLONING ARTIFACT	UNP P07342
A	46	LEU	-	CLONING ARTIFACT	UNP P07342
A	47	GLY	-	CLONING ARTIFACT	UNP P07342
A	48	THR	-	CLONING ARTIFACT	UNP P07342
A	49	ASP	-	CLONING ARTIFACT	UNP P07342
A	50	ASP	-	CLONING ARTIFACT	UNP P07342
A	51	ASP	-	CLONING ARTIFACT	UNP P07342
A	52	ASP	-	CLONING ARTIFACT	UNP P07342
A	53	LYS	-	CLONING ARTIFACT	UNP P07342
A	54	ALA	-	CLONING ARTIFACT	UNP P07342
A	55	MET	-	CLONING ARTIFACT	UNP P07342
A	56	GLY	-	CLONING ARTIFACT	UNP P07342
A	57	SER	-	CLONING ARTIFACT	UNP P07342
B	11	MET	-	CLONING ARTIFACT	UNP P07342
B	12	HIS	-	CLONING ARTIFACT	UNP P07342
B	13	HIS	-	CLONING ARTIFACT	UNP P07342
B	14	HIS	-	CLONING ARTIFACT	UNP P07342
B	15	HIS	-	CLONING ARTIFACT	UNP P07342
B	16	HIS	-	CLONING ARTIFACT	UNP P07342
B	17	HIS	-	CLONING ARTIFACT	UNP P07342
B	18	SER	-	CLONING ARTIFACT	UNP P07342
B	19	SER	-	CLONING ARTIFACT	UNP P07342
B	20	GLY	-	CLONING ARTIFACT	UNP P07342
B	21	LEU	-	CLONING ARTIFACT	UNP P07342
B	22	VAL	-	CLONING ARTIFACT	UNP P07342
B	23	PRO	-	CLONING ARTIFACT	UNP P07342
B	24	ARG	-	CLONING ARTIFACT	UNP P07342
B	25	GLY	-	CLONING ARTIFACT	UNP P07342
B	26	SER	-	CLONING ARTIFACT	UNP P07342

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
B	27	GLY	-	CLONING ARTIFACT	UNP P07342
B	28	MET	-	CLONING ARTIFACT	UNP P07342
B	29	LYS	-	CLONING ARTIFACT	UNP P07342
B	30	GLU	-	CLONING ARTIFACT	UNP P07342
B	31	THR	-	CLONING ARTIFACT	UNP P07342
B	32	ALA	-	CLONING ARTIFACT	UNP P07342
B	33	ALA	-	CLONING ARTIFACT	UNP P07342
B	34	ALA	-	CLONING ARTIFACT	UNP P07342
B	35	LYS	-	CLONING ARTIFACT	UNP P07342
B	36	PHE	-	CLONING ARTIFACT	UNP P07342
B	37	GLU	-	CLONING ARTIFACT	UNP P07342
B	38	ARG	-	CLONING ARTIFACT	UNP P07342
B	39	GLN	-	CLONING ARTIFACT	UNP P07342
B	40	HIS	-	CLONING ARTIFACT	UNP P07342
B	41	MET	-	CLONING ARTIFACT	UNP P07342
B	42	ASP	-	CLONING ARTIFACT	UNP P07342
B	43	SER	-	CLONING ARTIFACT	UNP P07342
B	44	PRO	-	CLONING ARTIFACT	UNP P07342
B	45	ASP	-	CLONING ARTIFACT	UNP P07342
B	46	LEU	-	CLONING ARTIFACT	UNP P07342
B	47	GLY	-	CLONING ARTIFACT	UNP P07342
B	48	THR	-	CLONING ARTIFACT	UNP P07342
B	49	ASP	-	CLONING ARTIFACT	UNP P07342
B	50	ASP	-	CLONING ARTIFACT	UNP P07342
B	51	ASP	-	CLONING ARTIFACT	UNP P07342
B	52	ASP	-	CLONING ARTIFACT	UNP P07342
B	53	LYS	-	CLONING ARTIFACT	UNP P07342
B	54	ALA	-	CLONING ARTIFACT	UNP P07342
B	55	MET	-	CLONING ARTIFACT	UNP P07342
B	56	GLY	-	CLONING ARTIFACT	UNP P07342
B	57	SER	-	CLONING ARTIFACT	UNP P07342
C	11	MET	-	CLONING ARTIFACT	UNP P07342
C	12	HIS	-	CLONING ARTIFACT	UNP P07342
C	13	HIS	-	CLONING ARTIFACT	UNP P07342
C	14	HIS	-	CLONING ARTIFACT	UNP P07342
C	15	HIS	-	CLONING ARTIFACT	UNP P07342
C	16	HIS	-	CLONING ARTIFACT	UNP P07342
C	17	HIS	-	CLONING ARTIFACT	UNP P07342
C	18	SER	-	CLONING ARTIFACT	UNP P07342
C	19	SER	-	CLONING ARTIFACT	UNP P07342
C	20	GLY	-	CLONING ARTIFACT	UNP P07342
C	21	LEU	-	CLONING ARTIFACT	UNP P07342

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
C	22	VAL	-	CLONING ARTIFACT	UNP P07342
C	23	PRO	-	CLONING ARTIFACT	UNP P07342
C	24	ARG	-	CLONING ARTIFACT	UNP P07342
C	25	GLY	-	CLONING ARTIFACT	UNP P07342
C	26	SER	-	CLONING ARTIFACT	UNP P07342
C	27	GLY	-	CLONING ARTIFACT	UNP P07342
C	28	MET	-	CLONING ARTIFACT	UNP P07342
C	29	LYS	-	CLONING ARTIFACT	UNP P07342
C	30	GLU	-	CLONING ARTIFACT	UNP P07342
C	31	THR	-	CLONING ARTIFACT	UNP P07342
C	32	ALA	-	CLONING ARTIFACT	UNP P07342
C	33	ALA	-	CLONING ARTIFACT	UNP P07342
C	34	ALA	-	CLONING ARTIFACT	UNP P07342
C	35	LYS	-	CLONING ARTIFACT	UNP P07342
C	36	PHE	-	CLONING ARTIFACT	UNP P07342
C	37	GLU	-	CLONING ARTIFACT	UNP P07342
C	38	ARG	-	CLONING ARTIFACT	UNP P07342
C	39	GLN	-	CLONING ARTIFACT	UNP P07342
C	40	HIS	-	CLONING ARTIFACT	UNP P07342
C	41	MET	-	CLONING ARTIFACT	UNP P07342
C	42	ASP	-	CLONING ARTIFACT	UNP P07342
C	43	SER	-	CLONING ARTIFACT	UNP P07342
C	44	PRO	-	CLONING ARTIFACT	UNP P07342
C	45	ASP	-	CLONING ARTIFACT	UNP P07342
C	46	LEU	-	CLONING ARTIFACT	UNP P07342
C	47	GLY	-	CLONING ARTIFACT	UNP P07342
C	48	THR	-	CLONING ARTIFACT	UNP P07342
C	49	ASP	-	CLONING ARTIFACT	UNP P07342
C	50	ASP	-	CLONING ARTIFACT	UNP P07342
C	51	ASP	-	CLONING ARTIFACT	UNP P07342
C	52	ASP	-	CLONING ARTIFACT	UNP P07342
C	53	LYS	-	CLONING ARTIFACT	UNP P07342
C	54	ALA	-	CLONING ARTIFACT	UNP P07342
C	55	MET	-	CLONING ARTIFACT	UNP P07342
C	56	GLY	-	CLONING ARTIFACT	UNP P07342
C	57	SER	-	CLONING ARTIFACT	UNP P07342
D	11	MET	-	CLONING ARTIFACT	UNP P07342
D	12	HIS	-	CLONING ARTIFACT	UNP P07342
D	13	HIS	-	CLONING ARTIFACT	UNP P07342
D	14	HIS	-	CLONING ARTIFACT	UNP P07342
D	15	HIS	-	CLONING ARTIFACT	UNP P07342
D	16	HIS	-	CLONING ARTIFACT	UNP P07342

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
D	17	HIS	-	CLONING ARTIFACT	UNP P07342
D	18	SER	-	CLONING ARTIFACT	UNP P07342
D	19	SER	-	CLONING ARTIFACT	UNP P07342
D	20	GLY	-	CLONING ARTIFACT	UNP P07342
D	21	LEU	-	CLONING ARTIFACT	UNP P07342
D	22	VAL	-	CLONING ARTIFACT	UNP P07342
D	23	PRO	-	CLONING ARTIFACT	UNP P07342
D	24	ARG	-	CLONING ARTIFACT	UNP P07342
D	25	GLY	-	CLONING ARTIFACT	UNP P07342
D	26	SER	-	CLONING ARTIFACT	UNP P07342
D	27	GLY	-	CLONING ARTIFACT	UNP P07342
D	28	MET	-	CLONING ARTIFACT	UNP P07342
D	29	LYS	-	CLONING ARTIFACT	UNP P07342
D	30	GLU	-	CLONING ARTIFACT	UNP P07342
D	31	THR	-	CLONING ARTIFACT	UNP P07342
D	32	ALA	-	CLONING ARTIFACT	UNP P07342
D	33	ALA	-	CLONING ARTIFACT	UNP P07342
D	34	ALA	-	CLONING ARTIFACT	UNP P07342
D	35	LYS	-	CLONING ARTIFACT	UNP P07342
D	36	PHE	-	CLONING ARTIFACT	UNP P07342
D	37	GLU	-	CLONING ARTIFACT	UNP P07342
D	38	ARG	-	CLONING ARTIFACT	UNP P07342
D	39	GLN	-	CLONING ARTIFACT	UNP P07342
D	40	HIS	-	CLONING ARTIFACT	UNP P07342
D	41	MET	-	CLONING ARTIFACT	UNP P07342
D	42	ASP	-	CLONING ARTIFACT	UNP P07342
D	43	SER	-	CLONING ARTIFACT	UNP P07342
D	44	PRO	-	CLONING ARTIFACT	UNP P07342
D	45	ASP	-	CLONING ARTIFACT	UNP P07342
D	46	LEU	-	CLONING ARTIFACT	UNP P07342
D	47	GLY	-	CLONING ARTIFACT	UNP P07342
D	48	THR	-	CLONING ARTIFACT	UNP P07342
D	49	ASP	-	CLONING ARTIFACT	UNP P07342
D	50	ASP	-	CLONING ARTIFACT	UNP P07342
D	51	ASP	-	CLONING ARTIFACT	UNP P07342
D	52	ASP	-	CLONING ARTIFACT	UNP P07342
D	53	LYS	-	CLONING ARTIFACT	UNP P07342
D	54	ALA	-	CLONING ARTIFACT	UNP P07342
D	55	MET	-	CLONING ARTIFACT	UNP P07342
D	56	GLY	-	CLONING ARTIFACT	UNP P07342
D	57	SER	-	CLONING ARTIFACT	UNP P07342

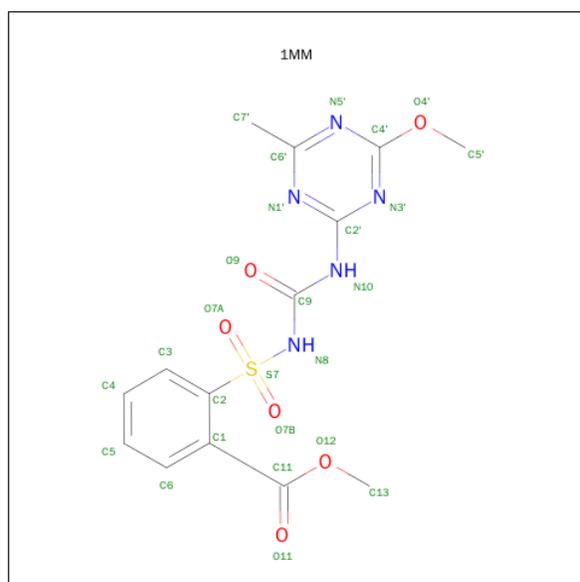
- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total K 1 1	0	0
2	A	1	Total K 1 1	0	0
2	D	1	Total K 1 1	0	0
2	C	1	Total K 1 1	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Mg 1 1	0	0
3	A	1	Total Mg 1 1	0	0
3	D	1	Total Mg 1 1	0	0
3	C	1	Total Mg 1 1	0	0

- Molecule 4 is METHYL 2-[(4-METHOXY-6-METHYL-1,3,5-TRIAZIN-2-YL)AMINO]CARBONYL]AMINO)SULFONYL]BENZOATE (three-letter code: 1MM) (formula: C<sub>14</sub>H<sub>15</sub>N<sub>5</sub>O<sub>6</sub>S).



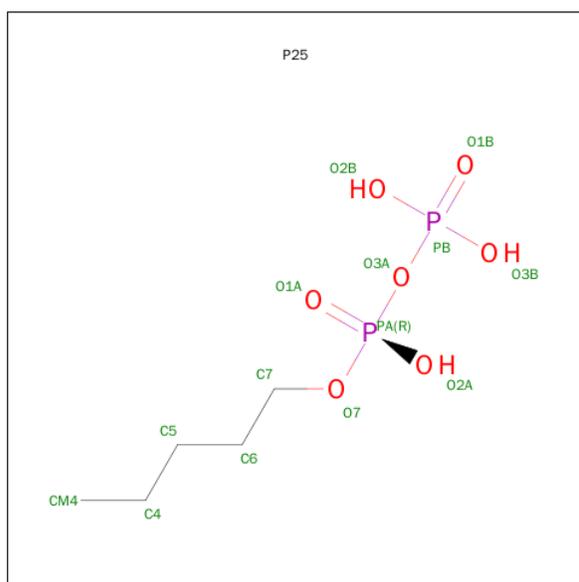
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			26	14	5	6	1		

*Continued on next page...*

Continued from previous page...

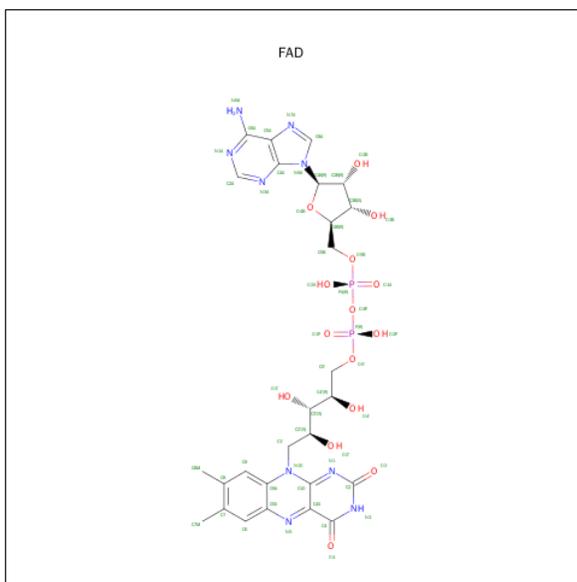
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	S	0	0
			26	14	5	6	1		
4	C	1	Total	C	N	O	S	0	0
			26	14	5	6	1		
4	C	1	Total	C	N	O	S	0	0
			26	14	5	6	1		

- Molecule 5 is PENTYL TRIHYDROGEN DIPHOSPHATE (three-letter code: P25) (formula:  $C_5H_{14}O_7P_2$ ).



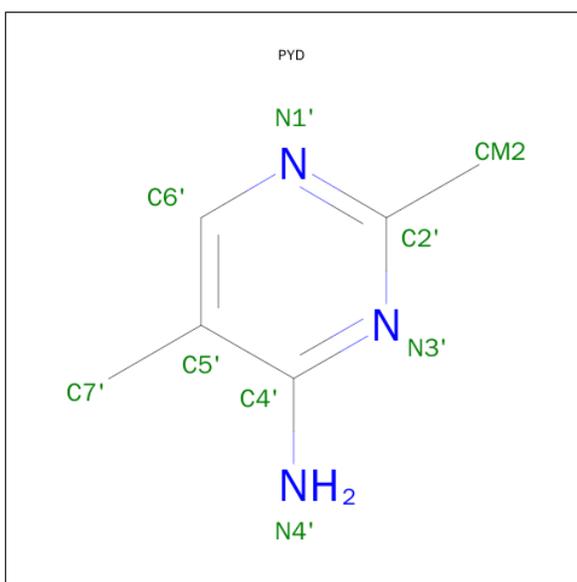
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	O	P	0	0
			14	5	7	2		
5	A	1	Total	C	O	P	0	0
			14	5	7	2		

- Molecule 6 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



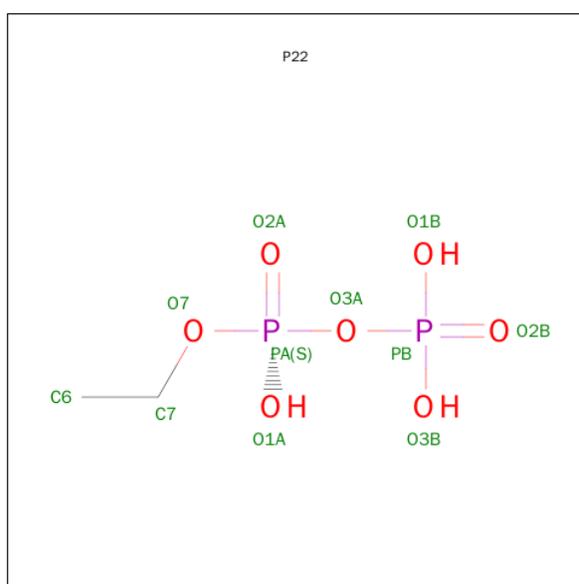
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
6	A	1	Total 53	C 27	N 9	O 15	P 2	0	0
6	B	1	Total 53	C 27	N 9	O 15	P 2	0	0
6	C	1	Total 53	C 27	N 9	O 15	P 2	0	0
6	D	1	Total 53	C 27	N 9	O 15	P 2	0	0

- Molecule 7 is 2,5-DIMETHYL-PYRIMIDIN-4-YLAMINE (three-letter code: PYD) (formula:  $C_6H_9N_3$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C N 9 6 3	0	0
7	B	1	Total C N 9 6 3	0	0
7	C	1	Total C N 9 6 3	0	0
7	D	1	Total C N 9 6 3	0	0

- Molecule 8 is ETHYL DIHYDROGEN DIPHOSPHATE (three-letter code: P22) (formula:  $C_2H_8O_7P_2$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	D	1	Total C O P 11 2 7 2	0	0
8	C	1	Total C O P 11 2 7 2	0	0

- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	671	Total O 671 671	1	0
9	B	468	Total O 468 468	0	0
9	C	400	Total O 400 400	0	0

*Continued on next page...*

*Continued from previous page...*

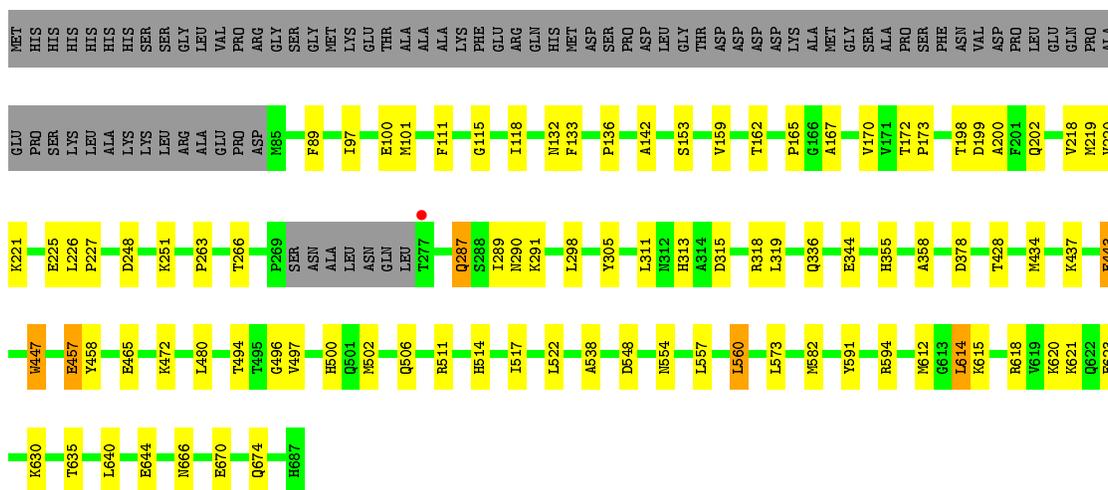
<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
9	D	637	Total 637	O 637	0	0

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

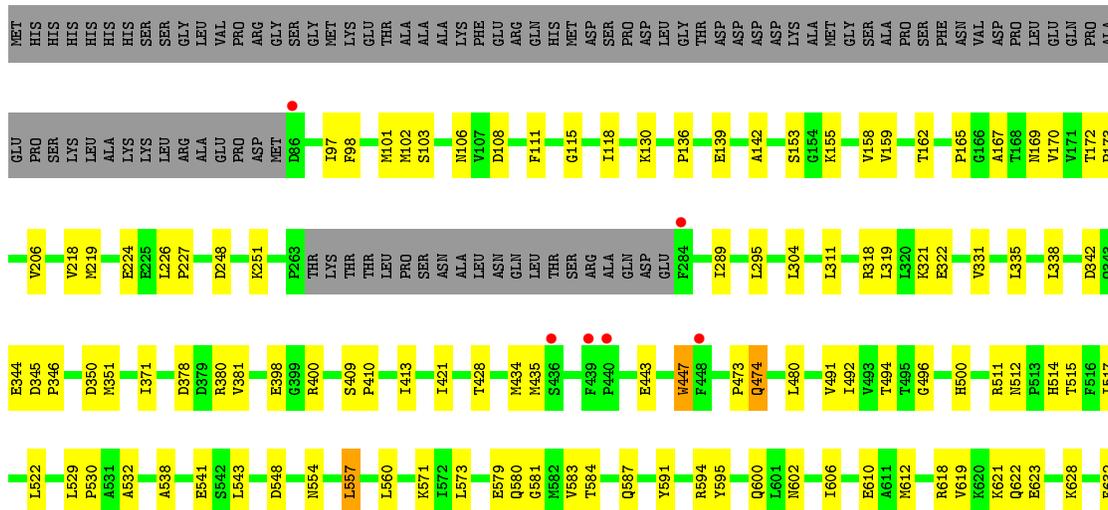
- Molecule 1: Acetolactate synthase, mitochondrial

Chain A: 



- Molecule 1: Acetolactate synthase, mitochondrial

Chain B: 





## 4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	218.35Å 218.35Å 361.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.30 94.27 – 2.30	Depositor EDS
% Data completeness (in resolution range)	80.1 (50.00-2.30) 79.9 (94.27-2.30)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.73 (at 2.29Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.164 , 0.195 0.167 , 0.197	Depositor DCC
$R_{free}$ test set	15236 reflections (9.95%)	DCC
Wilson B-factor (Å <sup>2</sup> )	28.5	Xtrriage
Anisotropy	0.342	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 62.6	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Outliers	0 of 160659 reflections	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	20377	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.63% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, K, P25, 1MM, P22, PYD, FAD

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.32	0/4666	0.59	0/6332
1	B	0.29	0/4497	0.55	0/6111
1	C	0.27	0/4423	0.53	0/6014
1	D	0.31	0/4642	0.58	0/6301
All	All	0.30	0/18228	0.56	0/24758

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4548	0	4521	77	0
1	B	4392	0	4352	106	0
1	C	4323	0	4263	135	0
1	D	4528	0	4494	83	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	26	0	15	2	0
4	B	26	0	15	5	0
4	C	52	0	30	4	0
5	A	14	0	11	2	0
5	B	14	0	11	1	0
6	A	53	0	31	1	0
6	B	53	0	31	1	0
6	C	53	0	31	1	0
6	D	53	0	31	1	0
7	A	9	0	9	0	0
7	B	9	0	9	0	0
7	C	9	0	9	0	0
7	D	9	0	9	0	0
8	C	11	0	5	0	0
8	D	11	0	5	1	0
9	A	671	0	0	9	0
9	B	468	0	0	12	0
9	C	400	0	0	18	0
9	D	637	0	0	12	0
All	All	20377	0	17882	389	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 389 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:594[A]:ARG:HG3	1:D:594[A]:ARG:HH11	1.16	1.04
1:C:114:PRO:HG2	1:D:580:GLN:HE22	1.25	1.00
1:A:313:HIS:HD2	1:A:315:ASP:H	1.19	0.91
1:C:619:VAL:HG22	1:C:628:LYS:HG3	1.54	0.89
1:B:580:GLN:HG3	5:B:698:P25:H72	1.54	0.87

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	598/677 (88%)	587 (98%)	11 (2%)	0	100	100
1	B	581/677 (86%)	568 (98%)	12 (2%)	1 (0%)	52	64
1	C	573/677 (85%)	551 (96%)	21 (4%)	1 (0%)	52	64
1	D	597/677 (88%)	586 (98%)	11 (2%)	0	100	100
All	All	2349/2708 (87%)	2292 (98%)	55 (2%)	2 (0%)	56	68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	350	ASP
1	C	350	ASP

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	488/556 (88%)	477 (98%)	11 (2%)	58	75
1	B	464/556 (84%)	457 (98%)	7 (2%)	72	85
1	C	453/556 (82%)	442 (98%)	11 (2%)	57	74
1	D	483/556 (87%)	471 (98%)	12 (2%)	55	73
All	All	1888/2224 (85%)	1847 (98%)	41 (2%)	63	77

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	295	LEU
1	C	447	TRP
1	D	594[A]	ARG
1	C	347	LYS
1	C	400	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	132	ASN
1	C	474	GLN
1	D	450	GLN
1	C	312	ASN
1	C	500	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 8 are monoatomic - leaving 16 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	P25	A	1698	3	11,13,13	1.91	4 (36%)	16,18,18	3.02	6 (37%)
4	1MM	A	695	-	27,27,27	4.08	19 (70%)	37,38,38	4.34	16 (43%)
6	FAD	A	701	-	48,58,58	2.59	20 (41%)	54,89,89	2.28	11 (20%)
7	PYD	A	703	-	9,9,9	7.66	6 (66%)	11,12,12	3.73	5 (45%)
4	1MM	B	1695	-	27,27,27	4.32	18 (66%)	37,38,38	4.40	16 (43%)
6	FAD	B	1701	-	48,58,58	2.80	21 (43%)	54,89,89	2.29	10 (18%)
7	PYD	B	1703	-	9,9,9	7.68	5 (55%)	11,12,12	3.77	5 (45%)
5	P25	B	698	3	11,13,13	1.88	4 (36%)	16,18,18	2.98	6 (37%)
4	1MM	C	2695	-	27,27,27	4.15	19 (70%)	37,38,38	4.33	18 (48%)
6	FAD	C	2701	-	48,58,58	2.85	21 (43%)	54,89,89	2.30	9 (16%)
7	PYD	C	2703	-	9,9,9	7.88	6 (66%)	11,12,12	3.70	5 (45%)
4	1MM	C	3695	-	27,27,27	4.29	19 (70%)	37,38,38	4.42	16 (43%)
8	P22	C	3702	3	8,10,10	1.94	2 (25%)	12,15,15	1.20	1 (8%)
8	P22	D	2702	3	8,10,10	2.00	4 (50%)	12,15,15	1.10	0
6	FAD	D	3701	-	48,58,58	2.65	21 (43%)	54,89,89	2.28	10 (18%)
7	PYD	D	3703	-	9,9,9	7.74	6 (66%)	11,12,12	3.56	6 (54%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	P25	A	1698	3	-	0/13/13/13	0/0/0/0
4	1MM	A	695	-	-	0/23/23/23	0/2/2/2
6	FAD	A	701	-	-	0/30/50/50	0/6/6/6
7	PYD	A	703	-	-	0/0/0/0	0/1/1/1
4	1MM	B	1695	-	-	0/23/23/23	0/2/2/2
6	FAD	B	1701	-	-	0/30/50/50	0/6/6/6
7	PYD	B	1703	-	-	0/0/0/0	0/1/1/1
5	P25	B	698	3	-	0/13/13/13	0/0/0/0
4	1MM	C	2695	-	-	0/23/23/23	0/2/2/2
6	FAD	C	2701	-	-	0/30/50/50	0/6/6/6
7	PYD	C	2703	-	-	0/0/0/0	0/1/1/1
4	1MM	C	3695	-	-	0/23/23/23	0/2/2/2
8	P22	C	3702	3	-	0/10/10/10	0/0/0/0
8	P22	D	2702	3	-	0/10/10/10	0/0/0/0
6	FAD	D	3701	-	-	0/30/50/50	0/6/6/6
7	PYD	D	3703	-	-	0/0/0/0	0/1/1/1

The worst 5 of 195 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1695	1MM	C2'-N10	-6.23	1.32	1.39
4	A	695	1MM	C2'-N10	-6.07	1.32	1.39
4	C	2695	1MM	C2'-N10	-5.96	1.32	1.39
4	C	3695	1MM	C2'-N10	-5.46	1.32	1.39
4	A	695	1MM	C9-N10	-3.82	1.30	1.37

The worst 5 of 140 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	2695	1MM	C3-C2-S7	-11.67	103.17	117.39
4	B	1695	1MM	C3-C2-S7	-11.41	103.49	117.39
4	A	695	1MM	C3-C2-S7	-11.38	103.53	117.39
4	C	3695	1MM	C3-C2-S7	-11.28	103.65	117.39
7	B	1703	PYD	C5'-C6'-N1'	-6.97	119.02	125.23

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

11 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1698	P25	2	0
4	A	695	1MM	2	0
6	A	701	FAD	1	0
4	B	1695	1MM	5	0
6	B	1701	FAD	1	0
5	B	698	P25	1	0
4	C	2695	1MM	2	0
6	C	2701	FAD	1	0
4	C	3695	1MM	2	0
8	D	2702	P22	1	0
6	D	3701	FAD	1	0

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q < 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å <sup>2</sup> )	Q < 0.9
1	A	596/677 (88%)	-0.20	1 (0%) 95 97	15, 25, 41, 76	0
1	B	582/677 (85%)	-0.09	6 (1%) 84 88	19, 38, 62, 84	0
1	C	575/677 (84%)	0.54	75 (13%) 5 7	23, 49, 99, 114	0
1	D	596/677 (88%)	-0.25	1 (0%) 95 97	18, 28, 43, 74	1 (0%)
All	All	2349/2708 (86%)	-0.00	83 (3%) 48 56	15, 32, 77, 114	1 (0%)

The worst 5 of 83 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	438	ILE	7.1
1	C	264	THR	5.7
1	C	445	SER	5.4
1	C	263	PRO	5.4
1	C	432	GLY	5.1

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
7	PYD	B	1703	9/9	0.90	0.26	11.63	35,37,38,38	0
7	PYD	C	2703	9/9	0.84	0.28	8.78	39,40,42,44	0
7	PYD	D	3703	9/9	0.81	0.25	7.37	43,46,49,51	0
7	PYD	A	703	9/9	0.90	0.22	6.68	33,37,39,39	0
4	1MM	A	695	26/26	0.98	0.14	1.75	21,25,30,30	0
5	P25	A	1698	14/14	0.98	0.14	1.26	18,22,33,36	0
4	1MM	C	3695	26/26	0.97	0.17	1.25	48,51,53,56	0
4	1MM	C	2695	26/26	0.98	0.12	0.88	27,30,31,34	0
6	FAD	A	701	53/53	0.99	0.15	0.82	13,18,23,24	0
5	P25	B	698	14/14	0.97	0.13	0.53	25,29,42,44	0
2	K	A	1696	1/1	1.00	0.12	0.40	24,24,24,24	0
6	FAD	D	3701	53/53	0.99	0.13	0.24	17,21,24,25	0
2	K	D	2696	1/1	0.99	0.12	0.21	26,26,26,26	0
4	1MM	B	1695	26/26	0.98	0.12	0.07	30,35,38,39	0
8	P22	D	2702	11/11	0.99	0.12	-0.00	21,24,27,30	0
6	FAD	B	1701	53/53	0.98	0.12	-0.17	30,33,36,37	0
8	P22	C	3702	11/11	0.98	0.12	-0.27	38,40,44,45	0
6	FAD	C	2701	53/53	0.97	0.14	-0.44	48,51,55,57	0
3	MG	C	3699	1/1	0.96	0.08	-1.53	36,36,36,36	0
3	MG	D	2699	1/1	0.97	0.07	-1.94	24,24,24,24	0
3	MG	A	1699	1/1	0.99	0.08	-1.98	19,19,19,19	0
2	K	C	3696	1/1	0.97	0.06	-2.59	61,61,61,61	0
2	K	B	696	1/1	0.99	0.06	-3.11	45,45,45,45	0
3	MG	B	699	1/1	0.99	0.04	-3.27	25,25,25,25	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.