



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:40 PM UTC

PDB ID : 6TI2 / pdb_00006ti2
Title : Structure of the Ustilago maydis chorismate mutase 1 in complex with KWL1-b from Zea mays
Authors : Altegoer, F.; Bange, G.
Deposited on : 2019-11-21
Resolution : 2.75 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

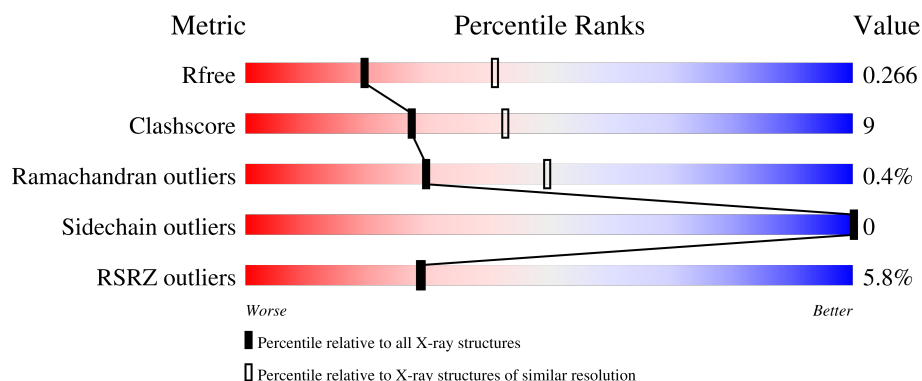
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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}	180053	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	B	278	4% 72% 22% 6%
1	C	278	4% 76% 17% 6%
2	A	199	8% 62% 20% 18%
2	E	199	6% 68% 13% 18%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6613 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 Chromosome 16, whole genome shotgun sequence.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	262	Total	C	N	O	S	0	0	0
			2059	1298	365	393	3			
1	C	262	Total	C	N	O	S	0	0	0
			2059	1298	365	393	3			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	21	MET	-	initiating methionine	UNP A0A0D1DWQ2
B	291	LEU	-	expression tag	UNP A0A0D1DWQ2
B	292	GLU	-	expression tag	UNP A0A0D1DWQ2
B	293	HIS	-	expression tag	UNP A0A0D1DWQ2
B	294	HIS	-	expression tag	UNP A0A0D1DWQ2
B	295	HIS	-	expression tag	UNP A0A0D1DWQ2
B	296	HIS	-	expression tag	UNP A0A0D1DWQ2
B	297	HIS	-	expression tag	UNP A0A0D1DWQ2
B	298	HIS	-	expression tag	UNP A0A0D1DWQ2
C	21	MET	-	initiating methionine	UNP A0A0D1DWQ2
C	291	LEU	-	expression tag	UNP A0A0D1DWQ2
C	292	GLU	-	expression tag	UNP A0A0D1DWQ2
C	293	HIS	-	expression tag	UNP A0A0D1DWQ2
C	294	HIS	-	expression tag	UNP A0A0D1DWQ2
C	295	HIS	-	expression tag	UNP A0A0D1DWQ2
C	296	HIS	-	expression tag	UNP A0A0D1DWQ2
C	297	HIS	-	expression tag	UNP A0A0D1DWQ2
C	298	HIS	-	expression tag	UNP A0A0D1DWQ2

- Molecule 2 is a protein called Ripening-related protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	163	Total	C	N	O	S	0	0	0
			1238	749	224	252	13			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	163	Total	C	N	O	S	0	0	0
			1238	749	224	252	13			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	199	HIS	-	expression tag	UNP K7U7F7
E	200	HIS	-	expression tag	UNP K7U7F7
E	201	HIS	-	expression tag	UNP K7U7F7
E	202	HIS	-	expression tag	UNP K7U7F7
E	203	HIS	-	expression tag	UNP K7U7F7
E	204	HIS	-	expression tag	UNP K7U7F7
A	199	HIS	-	expression tag	UNP K7U7F7
A	200	HIS	-	expression tag	UNP K7U7F7
A	201	HIS	-	expression tag	UNP K7U7F7
A	202	HIS	-	expression tag	UNP K7U7F7
A	203	HIS	-	expression tag	UNP K7U7F7
A	204	HIS	-	expression tag	UNP K7U7F7

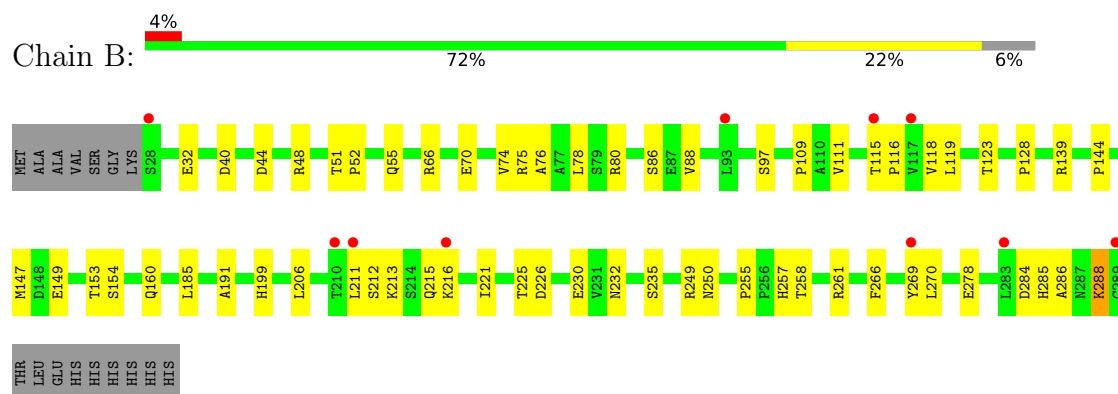
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	3	Total	O	0	0
			3	3		
3	C	7	Total	O	0	0
			7	7		
3	E	7	Total	O	0	0
			7	7		
3	A	2	Total	O	0	0
			2	2		

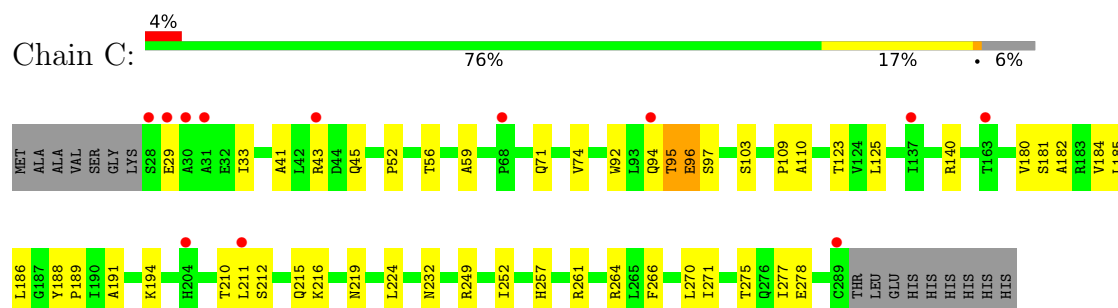
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

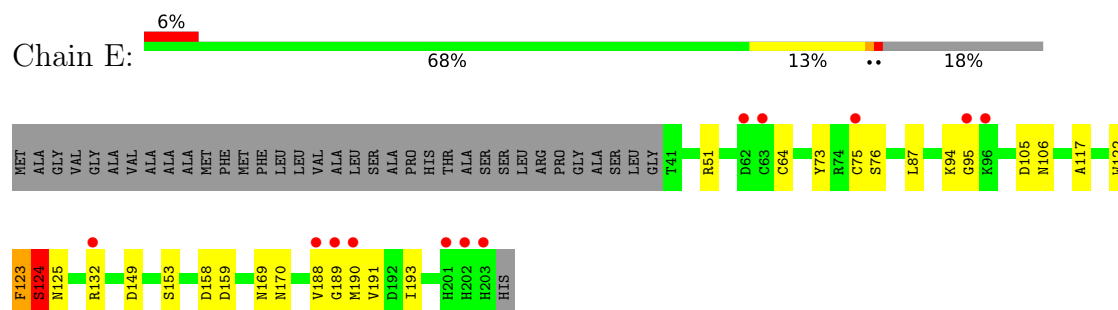
- Molecule 1: Chromosome 16, whole genome shotgun sequence



- Molecule 1: Chromosome 16, whole genome shotgun sequence

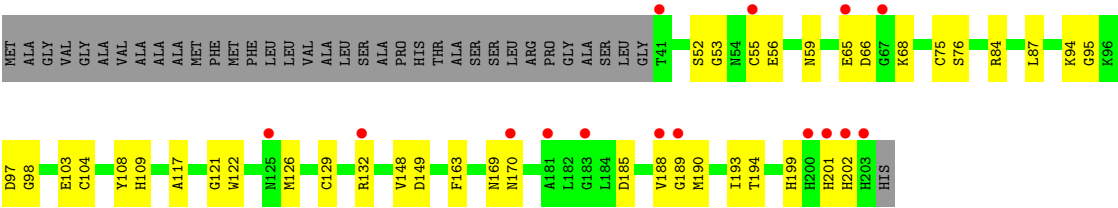


- Molecule 2: Ripening-related protein 3



- Molecule 2: Ripening-related protein 3





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	57.74Å 124.58Å 98.21Å 90.00° 96.22° 90.00°	Depositor
Resolution (Å)	47.99 – 2.75 47.99 – 2.75	Depositor EDS
% Data completeness (in resolution range)	98.4 (47.99-2.75) 93.4 (47.99-2.75)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.70 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.224 , 0.263 0.228 , 0.266	Depositor DCC
R_{free} test set	1768 reflections (4.18%)	wwPDB-VP
Wilson B-factor (Å ²)	66.4	Xtriage
Anisotropy	0.240	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 36.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6613	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.22% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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	B	0.25	1/2098 (0.0%)	0.50	2/2856 (0.1%)
1	C	0.22	0/2098	0.56	4/2856 (0.1%)
2	A	0.31	0/1269	0.67	2/1724 (0.1%)
2	E	0.42	2/1269 (0.2%)	0.66	1/1724 (0.1%)
All	All	0.29	3/6734 (0.0%)	0.58	9/9160 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1
2	E	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	132	ARG	CD-NE	5.97	1.54	1.46
1	B	288	LYS	CB-CG	5.45	1.68	1.52
2	E	132	ARG	CG-CD	-5.03	1.37	1.52

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	288	LYS	CA-CB-CG	8.04	130.17	114.10
1	B	288	LYS	CB-CG-CD	7.87	129.40	111.30
1	C	96	GLU	CA-CB-CG	-7.32	99.47	114.10
2	A	132	ARG	NE-CZ-NH1	-7.28	114.22	121.50
2	E	124	SER	N-CA-CB	-6.49	99.53	110.49

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	94	GLN	Peptide
2	E	123	PHE	Peptide

5.2 Too-close contacts

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	B	2059	0	2079	39	0
1	C	2059	0	2079	37	0
2	A	1238	0	1112	32	0
2	E	1238	0	1112	18	0
3	A	2	0	0	0	0
3	B	3	0	0	0	0
3	C	7	0	0	1	0
3	E	7	0	0	0	0
All	All	6613	0	6382	118	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 9.

The worst 5 of 118 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)
2:A:185:ASP:O	2:A:188:VAL:HG12	1.54	1.05
1:B:249:ARG:NH2	1:C:232:ASN:OD1	2.06	0.87
1:C:96:GLU:O	1:C:96:GLU:HG3	1.75	0.85
1:B:66:ARG:NH1	1:B:160:GLN:OE1	2.13	0.82
1:B:119:LEU:HD12	1:B:123:THR:HG21	1.63	0.81

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	B	260/278 (94%)	250 (96%)	10 (4%)	0	100	100
1	C	260/278 (94%)	250 (96%)	10 (4%)	0	100	100
2	A	161/199 (81%)	149 (92%)	11 (7%)	1 (1%)	21	38
2	E	161/199 (81%)	148 (92%)	11 (7%)	2 (1%)	10	20
All	All	842/954 (88%)	797 (95%)	42 (5%)	3 (0%)	30	50

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	124	SER
2	A	189	GLY
2	E	189	GLY

5.3.2 Protein sidechains

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	B	231/244 (95%)	231 (100%)	0	100	100
1	C	231/244 (95%)	231 (100%)	0	100	100
2	A	137/160 (86%)	137 (100%)	0	100	100
2	E	137/160 (86%)	137 (100%)	0	100	100
All	All	736/808 (91%)	736 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	201	HIS
2	A	59	ASN
1	C	208	ASN
1	C	229	GLN
2	E	170	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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, 95th 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 ²)	Q<0.9
1	B	262/278 (94%)	0.48	10 (3%) 44 41	46, 75, 104, 114	0
1	C	262/278 (94%)	0.46	12 (4%) 37 36	48, 72, 105, 113	0
2	A	163/199 (81%)	0.69	15 (9%) 14 14	47, 67, 104, 119	0
2	E	163/199 (81%)	0.59	12 (7%) 20 20	46, 66, 95, 116	0
All	All	850/954 (89%)	0.54	49 (5%) 29 29	46, 71, 104, 119	0

The worst 5 of 49 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	188	VAL	7.8
2	E	189	GLY	6.3
2	A	189	GLY	5.9
2	A	203	HIS	5.4
2	A	132	ARG	5.2

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.