



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 26, 2017 – 08:47 AM EDT

PDB ID : 5Y7O
Title : Crystal structure of folding sensor region of UGGT from *Thermomyces dubon-
tii*
Authors : Satoh, T.; Song, C.; Zhu, T.; Toshimori, T.; Murata, K.; Hayashi, Y.;
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Deposited on : unknown
Resolution : 3.10 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

<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
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	rb-20030345

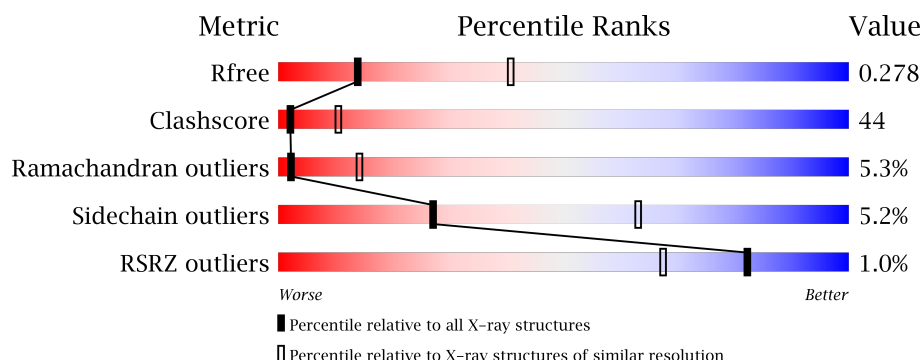
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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}	100719	1001 (3.12-3.08)
Clashscore	112137	1099 (3.12-3.08)
Ramachandran outliers	110173	1057 (3.12-3.08)
Sidechain outliers	110143	1057 (3.12-3.08)
RSRZ outliers	101464	1006 (3.12-3.08)

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 ≥ 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	1130	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -5px; left: 0; width: 100%; height: 1px; background-color: red;"></div> <div style="position: absolute; bottom: 0; left: 0; width: 100%; height: 10px;"> <div style="width: 29%; background-color: green;"></div> <div style="width: 15%; background-color: yellow;"></div> <div style="width: 5%; background-color: orange;"></div> <div style="width: 5%; background-color: red;"></div> <div style="width: 44%; background-color: grey;"></div> </div> </div> <div>29% 44% 6% • 19%</div> </div>
1	B	1130	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -5px; left: 0; width: 100%; height: 1px; background-color: red;"></div> <div style="position: absolute; bottom: 0; left: 0; width: 100%; height: 10px;"> <div style="width: 29%; background-color: green;"></div> <div style="width: 16%; background-color: yellow;"></div> <div style="width: 5%; background-color: orange;"></div> <div style="width: 5%; background-color: red;"></div> <div style="width: 45%; background-color: grey;"></div> </div> </div> <div>29% 45% 6% • 19%</div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 14318 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.

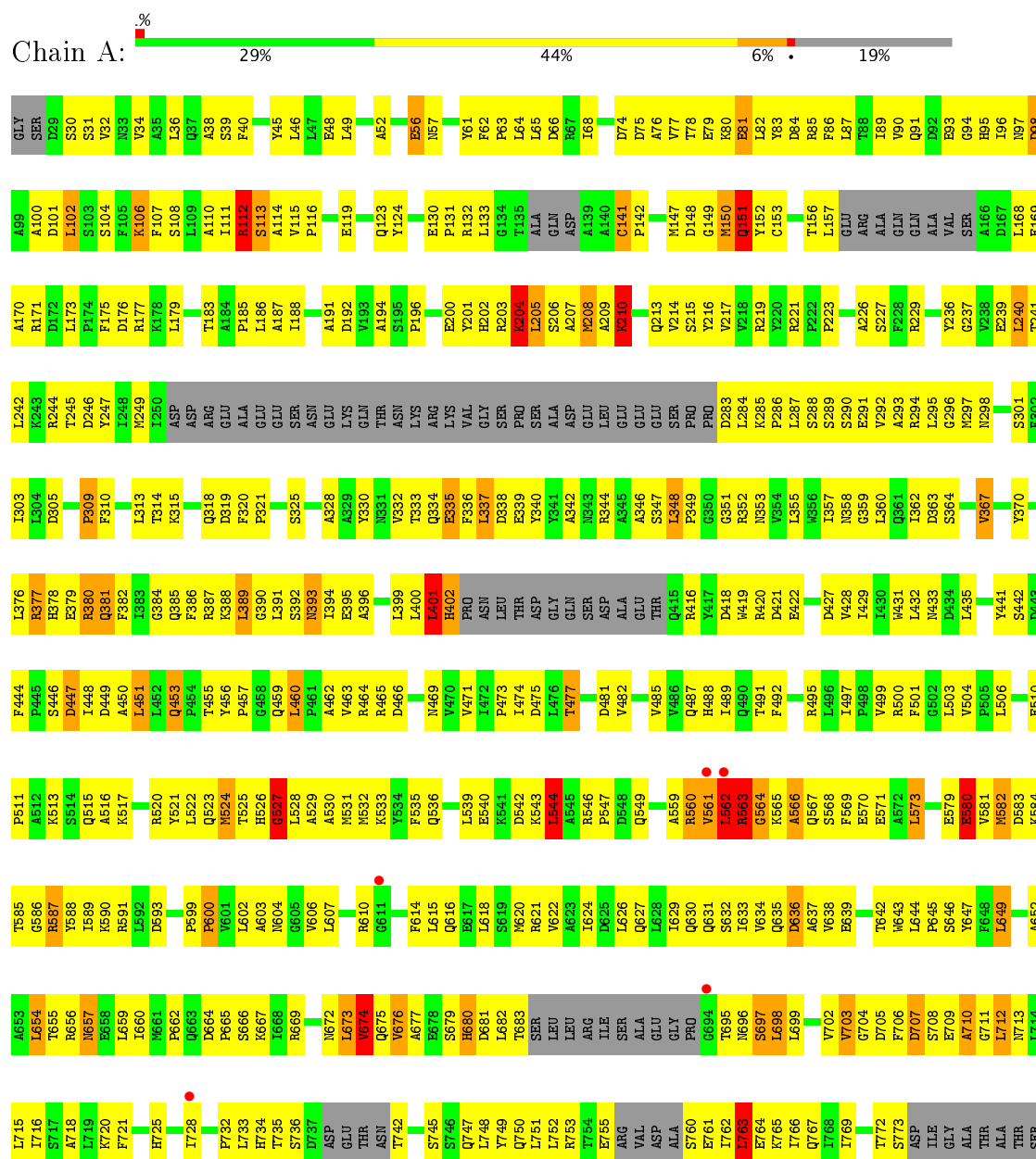
- Molecule 1 is a protein called UGGT.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	913	Total	C	N	O	S	Se	0	0	0
			7159	4556	1224	1362	2	15			
1	B	913	Total	C	N	O	S	Se	0	0	0
			7159	4556	1224	1362	2	15			

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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: UGGT





Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 1 2	Depositor
Cell constants a, b, c, α , β , γ	195.09Å 195.09Å 142.26Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.97 – 3.10 19.97 – 3.10	Depositor EDS
% Data completeness (in resolution range)	98.0 (19.97-3.10) 98.0 (19.97-3.10)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 3.09Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.232 , 0.278 0.232 , 0.278	Depositor DCC
R_{free} test set	2730 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	110.4	Xtriage
Anisotropy	0.256	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 108.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.55$, $\langle L^2 \rangle = 0.40$	Xtriage
Estimated twinning fraction	0.478 for -h,-k,l	Xtriage
Reported twinning fraction	0.500 for -h,-k,l	Depositor
Outliers	0 of 54601 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14318	wwPDB-VP
Average B, all atoms (Å ²)	123.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.67% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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	A	0.66	3/7286 (0.0%)	1.09	30/9871 (0.3%)
1	B	0.62	3/7286 (0.0%)	1.02	29/9871 (0.3%)
All	All	0.64	6/14572 (0.0%)	1.05	59/19742 (0.3%)

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	A	0	14
1	B	0	9
All	All	0	23

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	211	GLU	CB-CG	-8.01	1.36	1.52
1	B	209	ALA	CA-CB	-7.33	1.37	1.52
1	A	895	TRP	CB-CG	-7.16	1.37	1.50
1	B	211	GLU	CG-CD	-6.12	1.42	1.51
1	A	563	ARG	CG-CD	-5.51	1.38	1.51

The worst 5 of 59 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	401	LEU	CB-CG-CD2	-18.33	79.83	111.00
1	A	763	LEU	CB-CG-CD1	-13.06	88.80	111.00
1	A	205	LEU	CA-CB-CG	-8.87	94.90	115.30
1	A	573	LEU	CB-CG-CD2	-8.71	96.20	111.00
1	A	564	GLY	N-CA-C	8.65	134.73	113.10

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	150	MSE	Peptide
1	A	151	GLN	Peptide
1	A	204	LYS	Peptide
1	A	391	LEU	Peptide
1	A	456	TYR	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	A	7159	0	7156	685	0
1	B	7159	0	7156	576	1
All	All	14318	0	14312	1254	1

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 44.

The worst 5 of 1254 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:A:703:VAL:HG22	1:A:804:ARG:HH11	1.15	1.10
1:A:380:ARG:HH11	1:A:912:ILE:HD12	1.02	1.07
1:B:210:LYS:HB2	1:B:211:GLU:HG2	1.11	1.06
1:A:433:ASN:HD22	1:A:500:ARG:HA	1.21	1.04
1:B:420:ARG:HE	1:B:649:LEU:HD21	1.22	1.00

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:456:TYR:OH	1:B:456:TYR:OH[5_554]	2.09	0.11

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	893/1130 (79%)	685 (77%)	155 (17%)	53 (6%)	2	12
1	B	893/1130 (79%)	696 (78%)	155 (17%)	42 (5%)	3	17
All	All	1786/2260 (79%)	1381 (77%)	310 (17%)	95 (5%)	2	14

5 of 95 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	56	GLU
1	A	61	TYR
1	A	148	ASP
1	A	348	LEU
1	A	524	MSE

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	782/948 (82%)	737 (94%)	45 (6%)	23	59
1	B	782/948 (82%)	746 (95%)	36 (5%)	31	68
All	All	1564/1896 (82%)	1483 (95%)	81 (5%)	27	63

5 of 81 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	821	THR

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Mol	Chain	Res	Type
1	B	89	ILE
1	B	846	MSE
1	A	837	LYS
1	A	924	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	675	GLN
1	A	853	HIS
1	B	488	HIS
1	A	549	GLN
1	B	469	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 carbohydrates 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	A	898/1130 (79%)	-0.34	9 (1%) 82 67	70, 117, 187, 345	0
1	B	898/1130 (79%)	-0.34	9 (1%) 82 67	76, 115, 181, 279	0
All	All	1796/2260 (79%)	-0.34	18 (1%) 82 67	70, 116, 185, 345	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	819	THR	6.7
1	B	820	SER	5.6
1	B	94	GLY	5.1
1	A	728	ILE	4.5
1	A	1039	LEU	4.3

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.