



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 11:52 pm GMT

PDB ID : 2DYM
Title : The crystal structure of *Saccharomyces cerevisiae* Atg5- Atg16(1-46) complex
Authors : Matsushita, M.; Suzuki, N.N.; Inagaki, F.
Deposited on : 2006-09-15
Resolution : 2.20 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 : trunk28620
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) : recalc28949

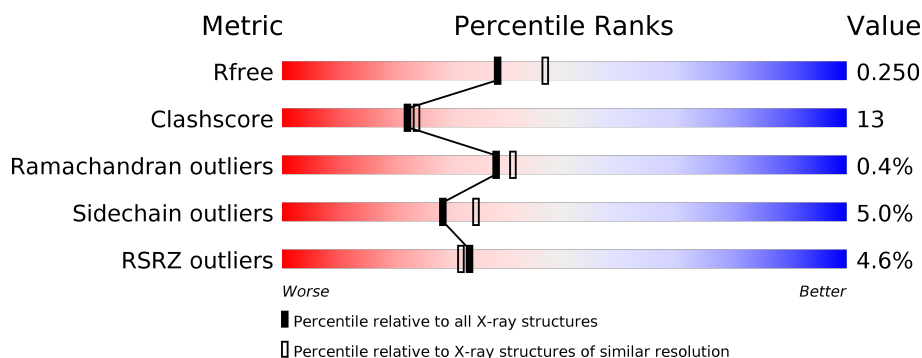
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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.



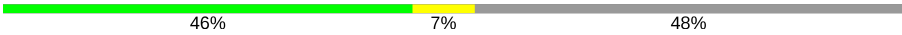

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	4002 (2.20-2.20)
Clashscore	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)
RSRZ outliers	101464	4033 (2.20-2.20)

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	297	<div> <div>2%</div> <div> <div></div> <div>66%</div> <div>17%</div> <div>•</div> <div>14%</div> </div> </div>
1	C	297	<div> <div>5%</div> <div> <div></div> <div>61%</div> <div>21%</div> <div>•</div> <div>15%</div> </div> </div>
1	E	297	<div> <div>4%</div> <div> <div></div> <div>60%</div> <div>21%</div> <div>•</div> <div>17%</div> </div> </div>
1	G	297	<div> <div>6%</div> <div> <div></div> <div>68%</div> <div>18%</div> <div>•</div> <div>12%</div> </div> </div>
2	B	46	<div> <div>2%</div> <div> <div></div> <div>35%</div> <div>15%</div> <div>•</div> <div>48%</div> </div> </div>
2	D	46	<div> <div></div> <div> <div></div> <div>48%</div> <div></div> <div>•</div> <div>48%</div> </div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	F	46	 46% 7% 48%
2	H	46	 48% • 48%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9196 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 Autophagy protein 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	254	Total	C	N	O	S	0	0	0
			2041	1339	339	353	10			
1	C	251	Total	C	N	O	S	0	0	0
			1989	1306	327	345	11			
1	E	247	Total	C	N	O	S	0	0	0
			1970	1298	326	336	10			
1	G	262	Total	C	N	O	S	0	0	0
			2064	1355	339	359	11			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	CLONING ARTIFACT	UNP Q12380
A	-1	ALA	-	CLONING ARTIFACT	UNP Q12380
A	0	HIS	-	CLONING ARTIFACT	UNP Q12380
C	-2	GLY	-	CLONING ARTIFACT	UNP Q12380
C	-1	ALA	-	CLONING ARTIFACT	UNP Q12380
C	0	HIS	-	CLONING ARTIFACT	UNP Q12380
E	-2	GLY	-	CLONING ARTIFACT	UNP Q12380
E	-1	ALA	-	CLONING ARTIFACT	UNP Q12380
E	0	HIS	-	CLONING ARTIFACT	UNP Q12380
G	-2	GLY	-	CLONING ARTIFACT	UNP Q12380
G	-1	ALA	-	CLONING ARTIFACT	UNP Q12380
G	0	HIS	-	CLONING ARTIFACT	UNP Q12380

- Molecule 2 is a protein called Autophagy protein 16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	24	Total	C	N	O	S	0	0	0
			202	124	38	39	1			
2	D	24	Total	C	N	O	S	0	0	0
			203	124	38	40	1			

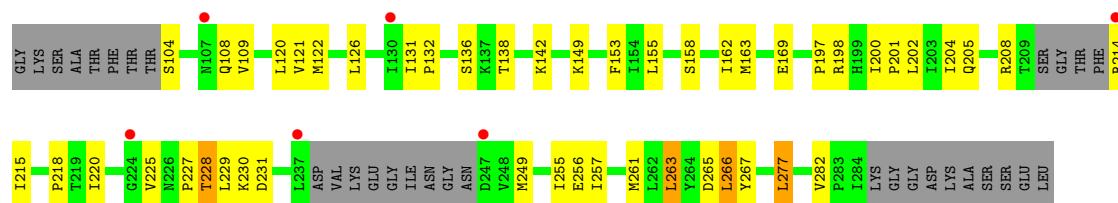
Continued on next page...

Continued from previous page...

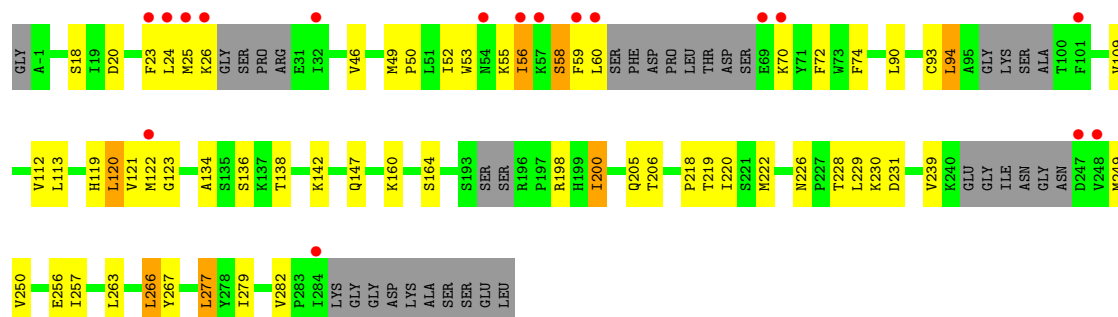
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	24	Total	C	N	O	S	0	0	0
			203	124	38	40	1			
2	H	24	Total	C	N	O	S	0	0	0
			203	124	38	40	1			

- Molecule 3 is water.

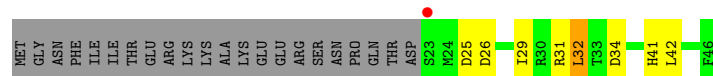
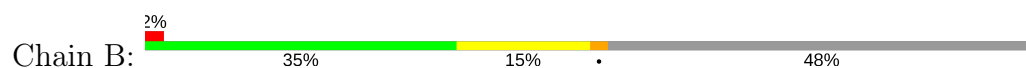
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	76	Total	O	0	0
			76	76		
3	B	8	Total	O	0	0
			8	8		
3	C	61	Total	O	0	0
			61	61		
3	D	12	Total	O	0	0
			12	12		
3	E	73	Total	O	0	0
			73	73		
3	F	15	Total	O	0	0
			15	15		
3	G	65	Total	O	0	0
			65	65		
3	H	11	Total	O	0	0
			11	11		



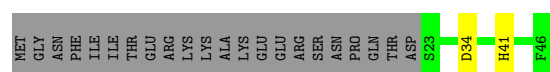
• Molecule 1: Autophagy protein 5



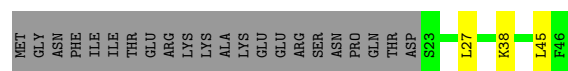
• Molecule 2: Autophagy protein 16



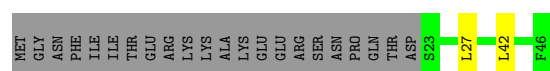
• Molecule 2: Autophagy protein 16



• Molecule 2: Autophagy protein 16



• Molecule 2: Autophagy protein 16



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	66.35Å 104.42Å 112.15Å 90.00° 92.11° 90.00°	Depositor
Resolution (Å)	49.38 – 2.20 49.38 – 2.10	Depositor EDS
% Data completeness (in resolution range)	96.5 (49.38-2.20) 94.9 (49.38-2.10)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.83 (at 2.10Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.219 , 0.250 0.219 , 0.250	Depositor DCC
R_{free} test set	7451 reflections (9.95%)	DCC
Wilson B-factor (Å ²)	35.3	Xtriage
Anisotropy	0.415	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 58.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.025 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9196	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 28.66 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.7741e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [i](#)

5.1 Standard geometry [i](#)

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	0.37	0/2095	0.62	0/2850
1	C	0.34	0/2041	0.60	0/2777
1	E	0.36	0/2022	0.61	0/2751
1	G	0.34	0/2118	0.60	0/2888
2	B	0.39	0/203	0.53	0/271
2	D	0.34	0/204	0.46	0/272
2	F	0.35	0/204	0.48	0/272
2	H	0.35	0/204	0.47	0/272
All	All	0.35	0/9091	0.60	0/12353

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	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	48	TYR	Sidechain

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	2041	0	2013	47	0
1	C	1989	0	1948	65	0
1	E	1970	0	1956	54	0
1	G	2064	0	2005	62	0
2	B	202	0	196	4	0
2	D	203	0	199	3	0
2	F	203	0	199	3	0
2	H	203	0	199	3	0
3	A	76	0	0	3	0
3	B	8	0	0	0	0
3	C	61	0	0	0	0
3	D	12	0	0	0	0
3	E	73	0	0	0	0
3	F	15	0	0	0	0
3	G	65	0	0	0	0
3	H	11	0	0	0	0
All	All	9196	0	8715	232	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 13.

The worst 5 of 232 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:C:228:THR:HG22	1:C:231:ASP:H	1.40	0.87
1:G:49:MET:HA	1:G:49:MET:HE2	1.58	0.86
1:E:205:GLN:HG2	1:E:215:ILE:HG12	1.57	0.85
1:E:228:THR:HG22	1:E:231:ASP:H	1.44	0.80
1:C:266:LEU:HD13	1:C:277:LEU:HD11	1.63	0.80

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	242/297 (82%)	235 (97%)	7 (3%)	0	100	100
1	C	239/297 (80%)	229 (96%)	8 (3%)	2 (1%)	22	21
1	E	235/297 (79%)	226 (96%)	8 (3%)	1 (0%)	38	41
1	G	250/297 (84%)	243 (97%)	6 (2%)	1 (0%)	38	41
2	B	22/46 (48%)	22 (100%)	0	0	100	100
2	D	22/46 (48%)	22 (100%)	0	0	100	100
2	F	22/46 (48%)	22 (100%)	0	0	100	100
2	H	22/46 (48%)	22 (100%)	0	0	100	100
All	All	1054/1372 (77%)	1021 (97%)	29 (3%)	4 (0%)	38	41

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	26	LYS
1	E	54	ASN
1	G	56	ILE
1	C	27	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	A	223/271 (82%)	210 (94%)	13 (6%)	23	27
1	C	214/271 (79%)	204 (95%)	10 (5%)	30	37
1	E	214/271 (79%)	201 (94%)	13 (6%)	22	25
1	G	221/271 (82%)	212 (96%)	9 (4%)	35	44
2	B	22/43 (51%)	19 (86%)	3 (14%)	4	3
2	D	23/43 (54%)	23 (100%)	0	100	100
2	F	23/43 (54%)	23 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	H	23/43 (54%)	23 (100%)	0	100	100
All	All	963/1256 (77%)	915 (95%)	48 (5%)	28	34

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	228	THR
1	E	6	GLN
1	G	226	ASN
1	C	263	LEU
1	C	266	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	217	GLN
1	E	10	ASN
1	G	205	GLN
2	D	41	HIS
1	E	47	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	254/297 (85%)	0.08	6 (2%) 59 57	23, 41, 67, 86	0
1	C	251/297 (84%)	0.26	15 (5%) 23 22	26, 47, 74, 89	0
1	E	247/297 (83%)	0.10	12 (4%) 30 29	24, 42, 70, 83	0
1	G	262/297 (88%)	0.22	17 (6%) 20 18	24, 44, 75, 92	0
2	B	24/46 (52%)	-0.24	1 (4%) 37 35	24, 37, 52, 59	0
2	D	24/46 (52%)	-0.13	0 100 100	26, 38, 52, 55	0
2	F	24/46 (52%)	-0.32	0 100 100	25, 36, 45, 53	0
2	H	24/46 (52%)	-0.16	0 100 100	29, 39, 58, 69	0
All	All	1110/1372 (80%)	0.13	51 (4%) 33 32	23, 42, 71, 92	0

The worst 5 of 51 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	25	MET	5.7
1	G	23	PHE	5.4
1	C	284	ILE	5.3
1	G	69	GLU	5.3
1	C	213	PHE	5.1

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

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.