



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 20, 2020 – 01:04 PM EST

PDB ID : 4TQ0
Title : Crystal structure of human ATG5-ATG16N69
Authors : Kim, J.H.; Hong, S.B.; Song, H.K.
Deposited on : 2014-06-10
Resolution : 2.70 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

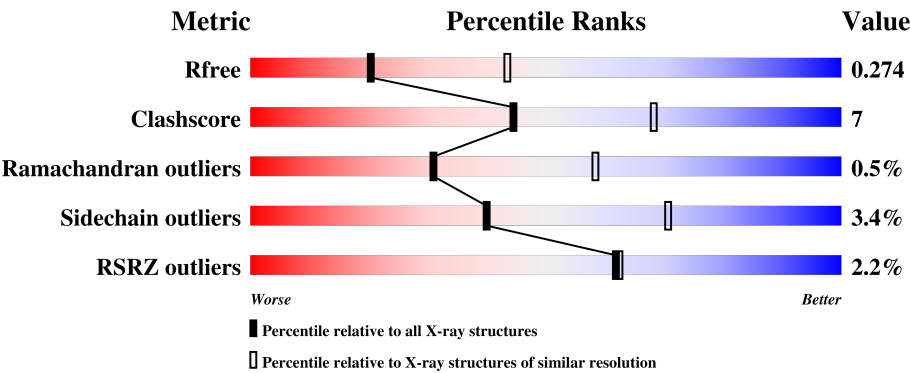
MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.4
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.4

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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.



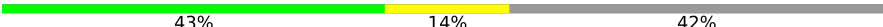
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	111664	2449 (2.70-2.70)
Clashscore	122126	2756 (2.70-2.70)
Ramachandran outliers	120053	2716 (2.70-2.70)
Sidechain outliers	120020	2716 (2.70-2.70)
RSRZ outliers	108989	2376 (2.70-2.70)

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	289	<div><div>%</div><div><div></div><div>71%</div><div>13%</div><div>•</div><div>16%</div></div></div>
1	C	289	<div><div>2%</div><div><div></div><div>67%</div><div>18%</div><div>•</div><div>14%</div></div></div>
1	E	289	<div><div>3%</div><div><div></div><div>67%</div><div>15%</div><div>•</div><div>16%</div></div></div>
2	B	69	<div><div>%</div><div><div></div><div>49%</div><div>7%</div><div>•</div><div>42%</div></div></div>
2	D	69	<div><div></div><div><div></div><div>46%</div><div>7%</div><div></div><div>46%</div></div></div>

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Mol	Chain	Length	Quality of chain
2	F	69	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: a green segment on the left labeled '43%', a yellow segment in the middle labeled '14%', and a grey segment on the right labeled '42%'.

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 7219 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	244	Total	C	N	O	S	0	0	0
			1999	1306	329	353	11			
1	C	248	Total	C	N	O	S	0	0	0
			2033	1327	333	362	11			
1	E	243	Total	C	N	O	S	0	0	0
			1987	1294	330	352	11			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	expression tag	UNP Q9H1Y0
A	-12	GLY	-	expression tag	UNP Q9H1Y0
A	-11	SER	-	expression tag	UNP Q9H1Y0
A	-10	SER	-	expression tag	UNP Q9H1Y0
A	-9	HIS	-	expression tag	UNP Q9H1Y0
A	-8	HIS	-	expression tag	UNP Q9H1Y0
A	-7	HIS	-	expression tag	UNP Q9H1Y0
A	-6	HIS	-	expression tag	UNP Q9H1Y0
A	-5	HIS	-	expression tag	UNP Q9H1Y0
A	-4	HIS	-	expression tag	UNP Q9H1Y0
A	-3	SER	-	expression tag	UNP Q9H1Y0
A	-2	GLN	-	expression tag	UNP Q9H1Y0
A	-1	GLY	-	expression tag	UNP Q9H1Y0
A	0	SER	-	expression tag	UNP Q9H1Y0
C	-13	MET	-	expression tag	UNP Q9H1Y0
C	-12	GLY	-	expression tag	UNP Q9H1Y0
C	-11	SER	-	expression tag	UNP Q9H1Y0
C	-10	SER	-	expression tag	UNP Q9H1Y0
C	-9	HIS	-	expression tag	UNP Q9H1Y0
C	-8	HIS	-	expression tag	UNP Q9H1Y0
C	-7	HIS	-	expression tag	UNP Q9H1Y0
C	-6	HIS	-	expression tag	UNP Q9H1Y0
C	-5	HIS	-	expression tag	UNP Q9H1Y0

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	HIS	-	expression tag	UNP Q9H1Y0
C	-3	SER	-	expression tag	UNP Q9H1Y0
C	-2	GLN	-	expression tag	UNP Q9H1Y0
C	-1	GLY	-	expression tag	UNP Q9H1Y0
C	0	SER	-	expression tag	UNP Q9H1Y0
E	-13	MET	-	expression tag	UNP Q9H1Y0
E	-12	GLY	-	expression tag	UNP Q9H1Y0
E	-11	SER	-	expression tag	UNP Q9H1Y0
E	-10	SER	-	expression tag	UNP Q9H1Y0
E	-9	HIS	-	expression tag	UNP Q9H1Y0
E	-8	HIS	-	expression tag	UNP Q9H1Y0
E	-7	HIS	-	expression tag	UNP Q9H1Y0
E	-6	HIS	-	expression tag	UNP Q9H1Y0
E	-5	HIS	-	expression tag	UNP Q9H1Y0
E	-4	HIS	-	expression tag	UNP Q9H1Y0
E	-3	SER	-	expression tag	UNP Q9H1Y0
E	-2	GLN	-	expression tag	UNP Q9H1Y0
E	-1	GLY	-	expression tag	UNP Q9H1Y0
E	0	SER	-	expression tag	UNP Q9H1Y0

- Molecule 2 is a protein called Autophagy-related protein 16-1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	40	Total	C	N	O	0	0	0
			354	221	73	60			
2	D	37	Total	C	N	O	0	0	0
			326	205	66	55			
2	F	40	Total	C	N	O	0	0	0
			358	224	74	60			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	43	Total	O	0	0
			43	43		
3	B	4	Total	O	0	0
			4	4		
3	C	54	Total	O	0	0
			54	54		
3	D	6	Total	O	0	0
			6	6		
3	E	49	Total	O	0	0
			49	49		

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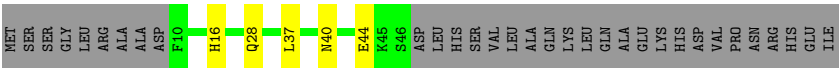
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	F	6	Total	O	0	0
			6	6		



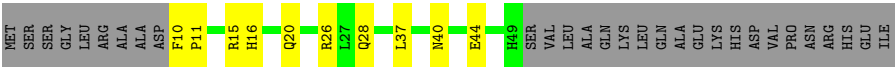
● Molecule 2: Autophagy-related protein 16-1



● Molecule 2: Autophagy-related protein 16-1



● Molecule 2: Autophagy-related protein 16-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	93.09Å 93.09Å 245.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.09 – 2.70 37.09 – 2.70	Depositor EDS
% Data completeness (in resolution range)	92.3 (37.09-2.70) 92.3 (37.09-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.17 (at 2.68Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.203 , 0.274 0.203 , 0.274	Depositor DCC
R_{free} test set	1830 reflections (6.46%)	wwPDB-VP
Wilson B-factor (Å ²)	27.0	Xtriage
Anisotropy	0.066	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 37.3	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	0.90	EDS
Total number of atoms	7219	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.16% 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	A	0.54	0/2060	0.66	1/2800 (0.0%)
1	C	0.53	0/2094	0.66	1/2845 (0.0%)
1	E	0.47	0/2047	0.67	0/2782
2	B	0.56	0/360	0.62	0/481
2	D	0.54	0/331	0.74	0/441
2	F	0.52	0/364	0.70	0/485
All	All	0.52	0/7256	0.67	2/9834 (0.0%)

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.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	121	ILE	CG1-CB-CG2	-6.63	96.81	111.40
1	A	188	ARG	NE-CZ-NH2	-5.24	117.68	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	57	GLN	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	1999	0	1918	24	0
1	C	2033	0	1970	35	0
1	E	1987	0	1916	35	0
2	B	354	0	353	5	0
2	D	326	0	331	3	0
2	F	358	0	364	8	0
3	A	43	0	0	2	0
3	B	4	0	0	1	0
3	C	54	0	0	1	0
3	D	6	0	0	0	0
3	E	49	0	0	5	0
3	F	6	0	0	2	0
All	All	7219	0	6852	98	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 7.

The worst 5 of 98 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:F:10:PHE:O	2:F:15:ARG:NH1	2.14	0.80
1:A:176:PRO:HG2	1:A:179:GLU:HG3	1.69	0.75
2:F:28:GLN:NE2	3:F:104:HOH:O	2.13	0.73
1:E:199:ILE:HD11	1:E:222:VAL:HG12	1.71	0.71
1:C:41:ARG:NH2	1:C:88:ASP:OD1	2.24	0.70

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	A	234/289 (81%)	228 (97%)	6 (3%)	0	100	100
1	C	240/289 (83%)	236 (98%)	4 (2%)	0	100	100
1	E	235/289 (81%)	227 (97%)	4 (2%)	4 (2%)	10	25
2	B	38/69 (55%)	37 (97%)	1 (3%)	0	100	100
2	D	35/69 (51%)	35 (100%)	0	0	100	100
2	F	38/69 (55%)	37 (97%)	1 (3%)	0	100	100
All	All	820/1074 (76%)	800 (98%)	16 (2%)	4 (0%)	31	58

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	58	LYS
1	E	117	SER
1	E	208	ALA
1	E	273	PRO

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	214/266 (80%)	208 (97%)	6 (3%)	47	77
1	C	220/266 (83%)	211 (96%)	9 (4%)	33	63
1	E	213/266 (80%)	206 (97%)	7 (3%)	41	71
2	B	37/63 (59%)	35 (95%)	2 (5%)	24	51
2	D	34/63 (54%)	33 (97%)	1 (3%)	45	75
2	F	38/63 (60%)	37 (97%)	1 (3%)	49	79
All	All	756/987 (77%)	730 (97%)	26 (3%)	40	71

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	116	PRO
1	C	196	ARG
1	E	209	ASP
1	C	118	LYS
1	C	173	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	57	GLN
2	F	28	GLN
1	C	191	GLN
1	A	158	GLN
1	E	191	GLN

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	244/289 (84%)	-0.47	3 (1%) 79 80	9, 21, 53, 74	0
1	C	248/289 (85%)	-0.36	5 (2%) 65 66	10, 24, 53, 72	0
1	E	243/289 (84%)	-0.05	10 (4%) 37 35	15, 31, 70, 103	0
2	B	40/69 (57%)	-0.28	1 (2%) 57 58	18, 29, 58, 71	0
2	D	37/69 (53%)	-0.42	0 100 100	15, 29, 48, 51	0
2	F	40/69 (57%)	-0.45	0 100 100	14, 26, 52, 64	0
All	All	852/1074 (79%)	-0.31	19 (2%) 62 62	9, 26, 60, 103	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	177	ALA	6.0
1	E	195	GLU	5.5
1	E	138	LYS	4.7
1	C	208	ALA	4.1
1	E	194	THR	3.9

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.