



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 25, 2026 – 03:16 PM EDT

PDB ID : 4P1W / pdb_00004p1w
Title : Crystal structure of Atg13(17BR)-Atg17-Atg29-Atg31 complex
Authors : Fujioka, Y.; Noda, N.N.
Deposited on : 2014-02-27
Resolution : 3.20 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

<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

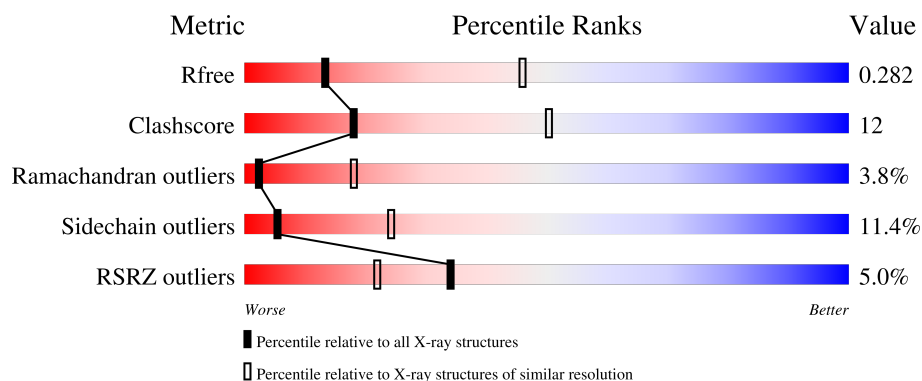
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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 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	A	74	5% 80% 15% . .
1	D	74	11% 78% 9% . 11%
2	B	151	3% 61% 21% 7% . 11%
2	E	151	6% 56% 22% 5% . 17%
3	C	413	3% 66% 26% . .

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Mol	Chain	Length	Quality of chain
3	F	413	5% 70% 20% • 6%
4	G	13	38% 8% 54%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8904 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 Atg29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	72	Total	C	N	O	S	0	0	0
			448	285	79	83	1			
1	D	66	Total	C	N	O	S	0	0	0
			400	250	71	78	1			

- Molecule 2 is a protein called Atg31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	135	Total	C	N	O	S	0	0	0
			1009	642	167	198	2			
2	E	126	Total	C	N	O	S	0	0	0
			948	603	159	184	2			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	146	HIS	-	expression tag	UNP C5DEB9
B	147	HIS	-	expression tag	UNP C5DEB9
B	148	HIS	-	expression tag	UNP C5DEB9
B	149	HIS	-	expression tag	UNP C5DEB9
B	150	HIS	-	expression tag	UNP C5DEB9
B	151	HIS	-	expression tag	UNP C5DEB9
E	146	HIS	-	expression tag	UNP C5DEB9
E	147	HIS	-	expression tag	UNP C5DEB9
E	148	HIS	-	expression tag	UNP C5DEB9
E	149	HIS	-	expression tag	UNP C5DEB9
E	150	HIS	-	expression tag	UNP C5DEB9
E	151	HIS	-	expression tag	UNP C5DEB9

- Molecule 3 is a protein called Atg17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	399	Total	C	N	O	S	0	0	0
			3073	1927	527	607	12			
3	F	389	Total	C	N	O	S	0	0	0
			2980	1865	515	589	11			

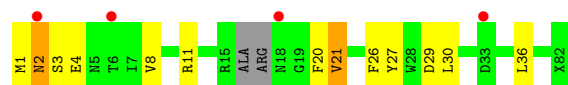
- Molecule 4 is a protein called Atg13 17BR.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	G	6	Total	C	N	O	0	0	0
			46	29	9	8			

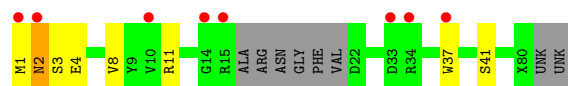
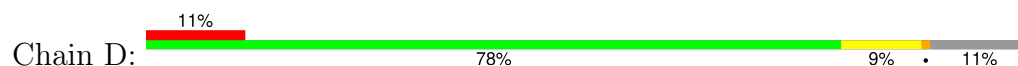
3 Residue-property plots [i](#)

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.

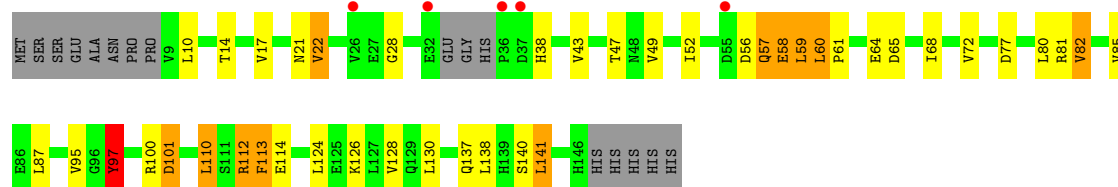
• Molecule 1: Atg29



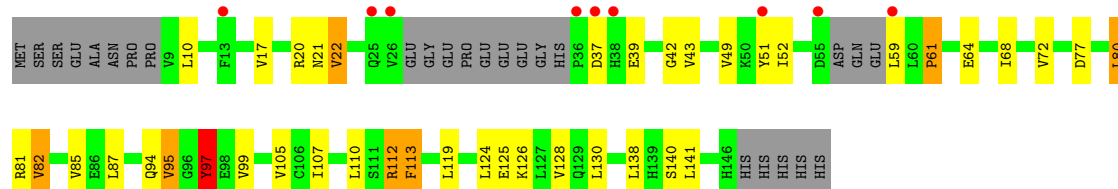
• Molecule 1: Atg29



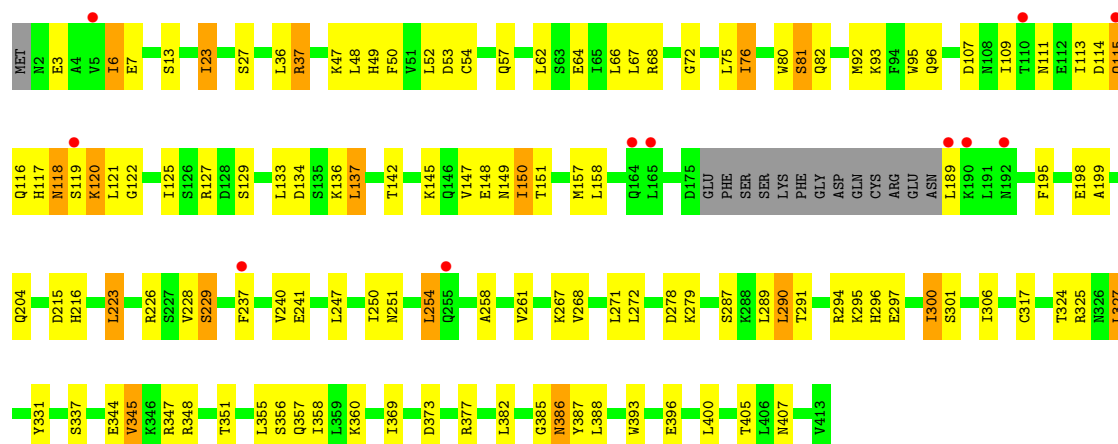
• Molecule 2: Atg31



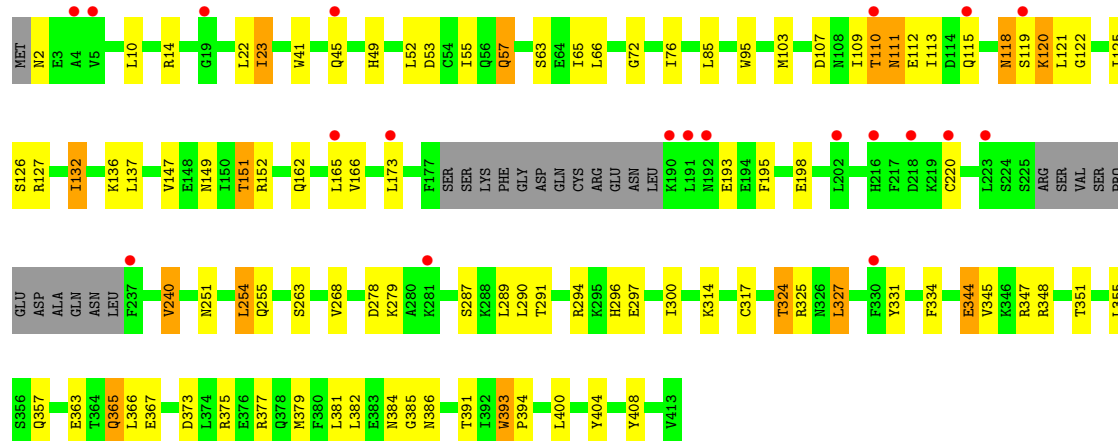
• Molecule 2: Atg31



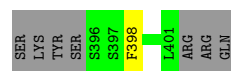
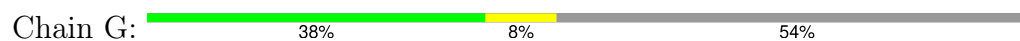
• Molecule 3: Atg17



• Molecule 3: Atg17



• Molecule 4: Atg13 17BR



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	148.35Å 63.99Å 184.60Å 90.00° 109.25° 90.00°	Depositor
Resolution (Å)	44.26 – 3.20 44.26 – 3.20	Depositor EDS
% Data completeness (in resolution range)	89.7 (44.26-3.20) 89.7 (44.26-3.20)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.09 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.257 , 0.293 0.248 , 0.282	Depositor DCC
R_{free} test set	5548 reflections (10.17%)	wwPDB-VP
Wilson B-factor (Å ²)	78.5	Xtriage
Anisotropy	0.406	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 84.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8904	wwPDB-VP
Average B, all atoms (Å ²)	117.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.85% 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 [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	0.71	0/300	0.85	0/410
1	D	0.67	0/261	0.83	0/358
2	B	0.76	0/1026	0.99	1/1400 (0.1%)
2	E	0.65	0/963	0.91	2/1314 (0.2%)
3	C	0.74	0/3115	0.97	5/4224 (0.1%)
3	F	0.62	0/3018	0.93	2/4092 (0.0%)
4	G	0.59	0/46	0.53	0/59
All	All	0.69	0/8729	0.94	10/11857 (0.1%)

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	F	393	TRP	CA-C-N	6.85	128.40	119.84
3	F	393	TRP	C-N-CA	6.85	128.40	119.84
3	C	115	GLN	N-CA-C	6.77	125.22	110.80
2	E	68	ILE	N-CA-C	6.52	117.14	110.82
3	C	114	ASP	CA-C-N	5.89	132.79	121.54

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	448	0	271	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	400	0	210	7	0
2	B	1009	0	925	36	0
2	E	948	0	874	35	0
3	C	3073	0	2869	91	0
3	F	2980	0	2754	64	0
4	G	46	0	45	2	0
All	All	8904	0	7948	206	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 12.

The worst 5 of 206 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)
3:C:111:ASN:HA	3:C:120:LYS:HA	1.40	1.03
3:C:109:ILE:HG21	3:C:121:LEU:HD13	1.48	0.93
3:F:111:ASN:HA	3:F:120:LYS:HA	1.48	0.92
1:D:8:VAL:HG12	2:E:72:VAL:HB	1.65	0.77
3:C:96:GLN:HE21	3:C:133:LEU:HB2	1.50	0.77

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	37/74 (50%)	32 (86%)	2 (5%)	3 (8%)	1	4
1	D	33/74 (45%)	29 (88%)	2 (6%)	2 (6%)	1	9
2	B	131/151 (87%)	108 (82%)	13 (10%)	10 (8%)	1	5
2	E	120/151 (80%)	98 (82%)	12 (10%)	10 (8%)	0	4
3	C	395/413 (96%)	352 (89%)	35 (9%)	8 (2%)	6	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	F	383/413 (93%)	352 (92%)	22 (6%)	9 (2%)	5	29
4	G	4/13 (31%)	2 (50%)	2 (50%)	0	100	100
All	All	1103/1289 (86%)	973 (88%)	88 (8%)	42 (4%)	2	18

5 of 42 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	SER
1	A	21	VAL
2	B	57	GLN
2	B	64	GLU
2	B	113	PHE

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	23/39 (59%)	22 (96%)	1 (4%)	26	59
1	D	17/39 (44%)	17 (100%)	0	100	100
2	B	103/140 (74%)	89 (86%)	14 (14%)	3	18
2	E	98/140 (70%)	90 (92%)	8 (8%)	10	39
3	C	316/383 (82%)	277 (88%)	39 (12%)	4	22
3	F	300/383 (78%)	264 (88%)	36 (12%)	5	23
4	G	5/12 (42%)	5 (100%)	0	100	100
All	All	862/1136 (76%)	764 (89%)	98 (11%)	5	24

5 of 98 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	80	LEU
3	F	118	ASN
2	E	97	TYR
3	F	22	LEU

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Mol	Chain	Res	Type
3	F	151	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	56	GLN
3	F	357	GLN
3	F	74	ASN
3	F	251	ASN
3	C	138	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	D	1

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Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	43:LEU	C	52:UNK	N	12.71
1	A	43:LEU	C	52:UNK	N	11.09

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	41/74 (55%)	0.60	4 (9%) 13 9	102, 122, 150, 152	0
1	D	37/74 (50%)	0.89	8 (21%) 2 2	118, 137, 150, 152	0
2	B	135/151 (89%)	0.28	5 (3%) 45 28	69, 104, 169, 183	0
2	E	126/151 (83%)	0.36	9 (7%) 22 14	79, 124, 165, 185	0
3	C	399/413 (96%)	-0.03	11 (2%) 55 35	61, 100, 165, 195	0
3	F	389/413 (94%)	0.22	20 (5%) 33 21	80, 118, 181, 240	0
4	G	6/13 (46%)	0.33	0 100 100	116, 137, 147, 156	0
All	All	1133/1289 (87%)	0.19	57 (5%) 34 22	61, 113, 174, 240	0

The worst 5 of 57 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	37	ASP	5.7
3	C	119	SER	5.6
2	B	36	PRO	5.6
3	F	190	LYS	5.1
3	F	165	LEU	5.0

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.