



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 07:33 AM UTC

PDB ID : 7CFC / pdb_00007cfc
Title : Drosophila melanogaster Krimper eTud1-Ago3 complex
Authors : Hu, H.; Li, S.
Deposited on : 2020-06-25
Resolution : 2.40 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
Xtrriage (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

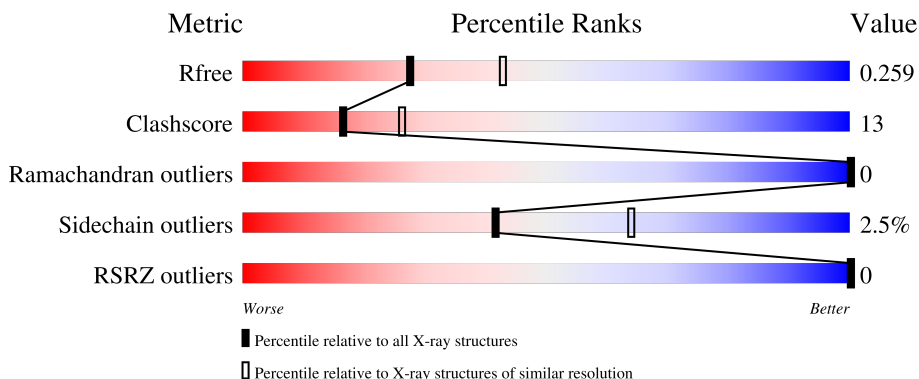
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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.



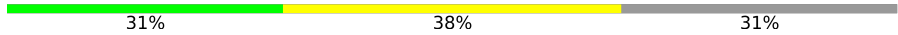

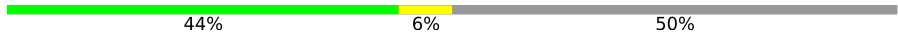
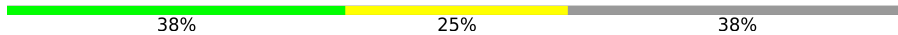
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	242	
1	B	242	
1	C	242	
1	D	242	
1	E	242	

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Mol	Chain	Length	Quality of chain
2	F	16	
2	G	16	
2	H	16	
2	I	16	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 7515 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 FI20010p1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	178	1407	888	241	272	6	0	0	0
1	B	178	1407	888	241	272	6	0	0	0
1	C	179	1415	894	242	273	6	0	0	0
1	D	179	1415	894	242	273	6	0	0	0
1	E	161	1258	795	212	245	6	0	0	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	271	SER	-	expression tag	UNP A1ZAC4
B	271	SER	-	expression tag	UNP A1ZAC4
C	271	SER	-	expression tag	UNP A1ZAC4
D	271	SER	-	expression tag	UNP A1ZAC4
E	271	SER	-	expression tag	UNP A1ZAC4

- Molecule 2 is a protein called Protein argonaute-3.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	F	11	90	55	21	14	0	0	0
2	G	11	90	55	21	14	0	0	0
2	H	8	66	41	14	11	0	0	0
2	I	10	79	49	17	13	0	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	63	Total O 63 63	0	0
3	B	73	Total O 73 73	0	0
3	C	52	Total O 52 52	0	0
3	D	36	Total O 36 36	0	0
3	E	54	Total O 54 54	0	0
3	F	1	Total O 1 1	0	0
3	H	9	Total O 9 9	0	0

4 Data and refinement statistics i

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	88.46Å 88.46Å 181.70Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.51 – 2.40 47.51 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.2 (47.51-2.40) 99.2 (47.51-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.41 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.234 , 0.259 0.236 , 0.259	Depositor DCC
R_{free} test set	3078 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	47.2	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 29.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.022 for -h,-k,l 0.480 for h,-h-k,-l 0.022 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7515	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.17% 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	0.13	0/1433	0.33	0/1949
1	B	0.15	0/1433	0.35	0/1949
1	C	0.12	0/1441	0.35	0/1960
1	D	0.41	1/1441 (0.1%)	0.46	0/1960
1	E	0.52	0/1281	0.90	5/1744 (0.3%)
2	F	0.12	0/89	0.38	0/116
2	G	0.30	0/89	0.51	0/116
2	H	0.12	0/65	0.34	0/86
2	I	0.18	0/78	0.63	0/102
All	All	0.30	1/7350 (0.0%)	0.51	5/9982 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	463	PRO	C-O	-6.78	1.15	1.23

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	419	ILE	N-CA-C	-6.03	107.62	113.53
1	E	456	ASN	CA-C-N	5.66	130.39	122.36
1	E	456	ASN	C-N-CA	5.66	130.39	122.36
1	E	416	PRO	N-CA-C	5.56	121.43	113.47
1	E	457	SER	N-CA-C	5.51	119.00	111.39

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	1407	0	1390	18	0
1	B	1407	0	1390	8	0
1	C	1415	0	1401	17	0
1	D	1415	0	1401	32	0
1	E	1258	0	1233	100	0
2	F	90	0	103	9	0
2	G	90	0	103	5	0
2	H	66	0	74	1	0
2	I	79	0	90	10	0
3	A	63	0	0	1	0
3	B	73	0	0	0	0
3	C	52	0	0	2	0
3	D	36	0	0	7	0
3	E	54	0	0	1	0
3	F	1	0	0	0	0
3	H	9	0	0	0	0
All	All	7515	0	7185	186	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 186 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:E:357:GLN:OE1	1:E:414:LYS:HD2	1.44	1.18
1:E:321:THR:CG2	1:E:448:LYS:HG2	1.80	1.11
1:E:309:LYS:HE2	1:E:457:SER:HB2	1.19	1.08
2:F:10:ILE:HG22	2:F:14:LYS:CE	1.87	1.05
2:F:10:ILE:CG2	2:F:14:LYS:HE3	1.86	1.05

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	176/242 (73%)	172 (98%)	4 (2%)	0	100	100
1	B	176/242 (73%)	173 (98%)	3 (2%)	0	100	100
1	C	177/242 (73%)	174 (98%)	3 (2%)	0	100	100
1	D	177/242 (73%)	176 (99%)	1 (1%)	0	100	100
1	E	157/242 (65%)	151 (96%)	6 (4%)	0	100	100
2	F	9/16 (56%)	9 (100%)	0	0	100	100
2	G	9/16 (56%)	9 (100%)	0	0	100	100
2	H	6/16 (38%)	6 (100%)	0	0	100	100
2	I	8/16 (50%)	8 (100%)	0	0	100	100
All	All	895/1274 (70%)	878 (98%)	17 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	157/215 (73%)	157 (100%)	0	100	100
1	B	157/215 (73%)	157 (100%)	0	100	100
1	C	158/215 (74%)	158 (100%)	0	100	100
1	D	158/215 (74%)	155 (98%)	3 (2%)	50	71
1	E	140/215 (65%)	124 (89%)	16 (11%)	5	8
2	F	9/13 (69%)	9 (100%)	0	100	100
2	G	9/13 (69%)	8 (89%)	1 (11%)	6	9
2	H	7/13 (54%)	7 (100%)	0	100	100
2	I	8/13 (62%)	8 (100%)	0	100	100
All	All	803/1127 (71%)	783 (98%)	20 (2%)	42	64

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	420	LYS
1	E	457	SER
2	G	4	ARG
1	E	458	THR
1	E	309	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	306	GLN
1	D	317	ASN
1	E	444	ASN
1	D	438	ASN
1	D	452	HIS

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

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	178/242 (73%)	-1.50	0 100 100	32, 46, 63, 67	0
1	B	178/242 (73%)	-1.49	0 100 100	33, 46, 61, 82	0
1	C	179/242 (73%)	-1.39	0 100 100	35, 50, 69, 77	0
1	D	179/242 (73%)	-1.39	0 100 100	34, 49, 67, 73	0
1	E	161/242 (66%)	-1.08	0 100 100	62, 85, 99, 111	0
2	F	11/16 (68%)	-1.16	0 100 100	58, 67, 78, 87	0
2	G	11/16 (68%)	-1.23	0 100 100	60, 65, 85, 88	0
2	H	8/16 (50%)	-1.26	0 100 100	54, 58, 67, 68	0
2	I	10/16 (62%)	-1.22	0 100 100	55, 65, 71, 77	0
All	All	915/1274 (71%)	-1.37	0 100 100	32, 51, 89, 111	0

There are no RSRZ outliers to report.

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.