



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 04:44 PM UTC

PDB ID : 1I51 / pdb_00001i51
Title : CRYSTAL STRUCTURE OF CASPASE-7 COMPLEXED WITH XIAP
Authors : Chai, J.; Shi, Y.
Deposited on : 2001-02-23
Resolution : 2.45 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

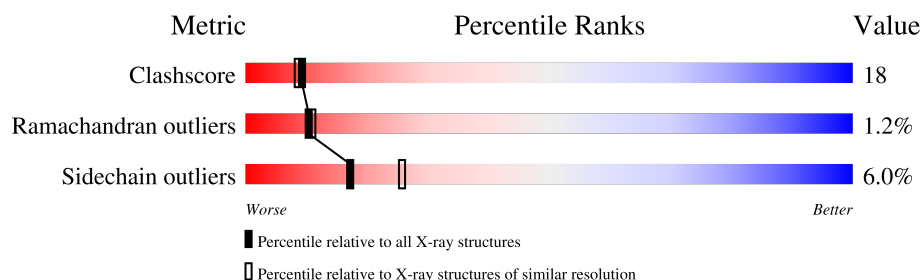
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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))
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	148	62% 28% • • 6%
1	C	148	67% 26% • 6%
2	B	105	63% 22% • 12%
2	D	105	50% 30% 8% 12%
3	E	117	7% 8% • 85%
3	F	117	7% 8% • 85%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3974 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 CASPASE-7 SUBUNIT P20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	139	Total	C	N	O	S	0	0	0
			1089	686	187	205	11			
1	C	139	Total	C	N	O	S	0	0	0
			1089	686	187	205	11			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	169	ALA	ASP	engineered mutation	UNP P55210
C	169	ALA	ASP	engineered mutation	UNP P55210

- Molecule 2 is a protein called CASPASE-7 SUBUNIT P11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	92	Total	C	N	O	S	0	0	0
			758	487	128	139	4			
2	D	92	Total	C	N	O	S	0	0	0
			758	487	128	139	4			

- Molecule 3 is a protein called X-LINKED INHIBITOR OF APOPTOSIS PROTEIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	18	Total	C	N	O	0	0	0
			140	86	24	30			
3	F	18	Total	C	N	O	0	0	0
			140	86	24	30			

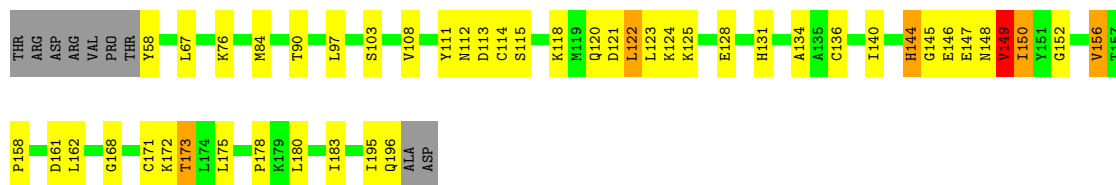
3 Residue-property plots [i](#)

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. 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. 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.

Note EDS was not executed.

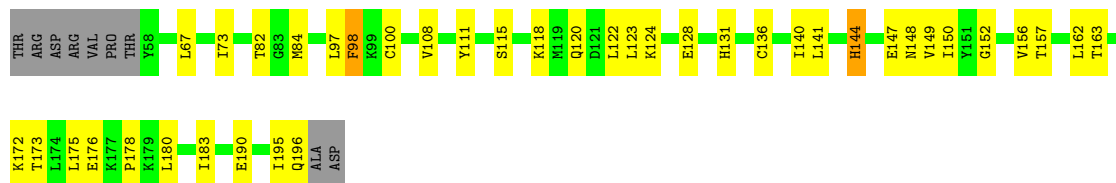
• Molecule 1: CASPASE-7 SUBUNIT P20

Chain A: 



• Molecule 1: CASPASE-7 SUBUNIT P20

Chain C: 



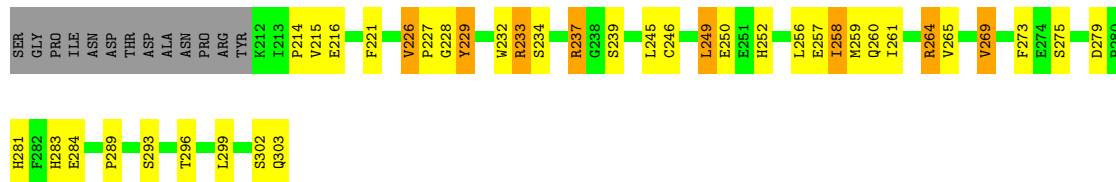
• Molecule 2: CASPASE-7 SUBUNIT P11

Chain B: 



• Molecule 2: CASPASE-7 SUBUNIT P11

Chain D: 



• Molecule 3: X-LINKED INHIBITOR OF APOPTOSIS PROTEIN

ALA	GLY	LEU	TYR	THR	ILE	GLY	ASP	GLN	VAL	GLN	CYS	PHE	CYS	CYS	GLY	GLY	LYS	LEU	ASN	TRP	GLU	PRO	CYS	ASP	ARG	ALA	TRP	GLU	HIS	ARG	ASN	ARG	GLY	ASN	CYS	PHE	VAL	LEU	GLY	ASN	LEU	ASN	ILE	ARG	SER	THR	PRO	ALA	SER		
ARG	HIS	PHE	ALA	LEU	ASP	ARG	PRO	SER	GLU	T135	T136	L141	R142	T143	G144	Q145	V146	V147	D148	I149	S150	D151	T152	ILE	TVR	PRO	ARG	ASN	PRO	ALA	MET	TVR	CYS	GLU	ALA	ARG	LEU	LYS	SER	PHE	GLN	ASN	TRP	PRO	TVR	HIS	LEU	THR	PRO	ALA	SER

Chain F: 7% 8% . 85%

GLY	LEU	TYR	TYR	THR	GLY	ILE	GLY	ASP	GLN	VAL	GLN	CYS	PHE	CYS	CYS	GLY	GLY	LEU	LEU	LYS	ASN	TRP	GLU	PRO	CYS	ASP	ARG	ALA	ALA	TRP	SER	GLU	HIS	ARG	HIS	ARG	ARG	GLY	ASN	ASN	LEU	ASN	ASN	ILE	ARG	SER	GLY															
ARG	ASP	HIS	PHE	ALA	LEU	ASP	ARG	PRO	SER	GLY	T135	T136	A137	D138		R142	T143	G144	Q145		I149	S150	D151	T152	ILE	TYR	PRO	ARG	ASN	PRO	ALA	ALA	MET	TYR	CYS	GLY	GLU	GLU	ALA	ARG	LEU	LYS	SER	PHE	GLN	ASN	TRP	PRO	ASN	ASN	TYR	ASP	HIS	THR	PRO	ARG	GLU	LEU	ALA	ALA	SER	ALA

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	89.60Å 89.60Å 185.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.45	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.45)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.233 , 0.272	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3974	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

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	0.41	0/1106	0.95	5/1482 (0.3%)
1	C	0.47	0/1106	0.98	4/1482 (0.3%)
2	B	0.46	0/780	0.97	4/1054 (0.4%)
2	D	0.46	0/780	1.04	4/1054 (0.4%)
3	E	0.40	0/141	0.76	0/192
3	F	0.46	0/141	0.69	0/192
All	All	0.45	0/4054	0.97	17/5456 (0.3%)

There are no bond length outliers.

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	152	GLY	N-CA-C	-8.78	98.71	112.58
1	A	152	GLY	N-CA-C	-8.67	99.41	112.41
1	A	144	HIS	N-CA-C	-6.85	101.30	110.55
2	D	232	TRP	N-CA-C	6.71	119.96	110.50
1	C	108	VAL	N-CA-C	6.68	117.71	108.89

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	1089	0	1080	38	0
1	C	1089	0	1080	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	758	0	731	19	0
2	D	758	0	731	41	0
3	E	140	0	133	8	0
3	F	140	0	133	12	0
All	All	3974	0	3888	142	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 18.

The worst 5 of 142 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:115:SER:H	1:C:118:LYS:HD2	1.29	0.94
2:B:259:MET:HE2	2:D:259:MET:HE2	1.47	0.92
1:C:111:TYR:CE2	1:C:122:LEU:HD11	2.05	0.91
2:D:258:ILE:CD1	2:D:299:LEU:HB3	2.03	0.88
1:C:131:HIS:H	1:C:173:THR:HG21	1.39	0.87

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	137/148 (93%)	126 (92%)	10 (7%)	1 (1%)	18	24
1	C	137/148 (93%)	130 (95%)	6 (4%)	1 (1%)	18	24
2	B	90/105 (86%)	88 (98%)	2 (2%)	0	100	100
2	D	90/105 (86%)	87 (97%)	3 (3%)	0	100	100
3	E	16/117 (14%)	14 (88%)	0	2 (12%)	0	0
3	F	16/117 (14%)	14 (88%)	0	2 (12%)	0	0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	486/740 (66%)	459 (94%)	21 (4%)	6 (1%)	10 11

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	E	151	ASP
3	F	151	ASP
3	E	150	SER
1	A	171	CYS
1	C	82	THR

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	118/126 (94%)	109 (92%)	9 (8%)	12 15
1	C	118/126 (94%)	113 (96%)	5 (4%)	26 39
2	B	84/95 (88%)	80 (95%)	4 (5%)	23 34
2	D	84/95 (88%)	76 (90%)	8 (10%)	8 8
3	E	16/102 (16%)	16 (100%)	0	100 100
3	F	16/102 (16%)	16 (100%)	0	100 100
All	All	436/646 (68%)	410 (94%)	26 (6%)	17 26

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

Mol	Chain	Res	Type
1	C	98	PHE
1	C	180	LEU
2	D	264	ARG
1	C	156	VAL
2	D	226	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	303	GLN
3	F	145	GLN
3	F	136	HIS
1	C	88	ASN
2	D	281	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 [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.