



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 3, 2023 – 01:24 AM EDT

PDB ID : 1I51
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 : 4.02b-467
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.34

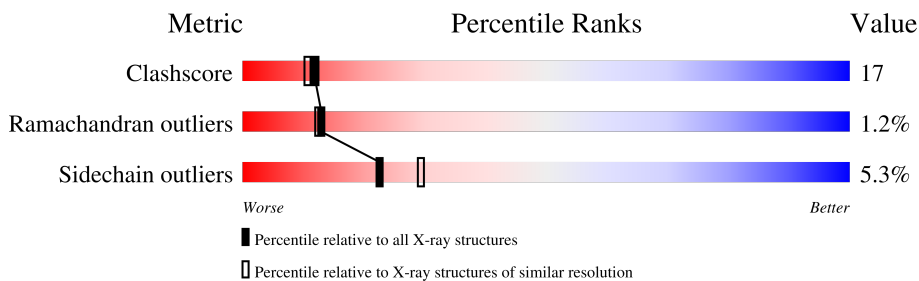
1 Overall quality at a glance

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	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)

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	
1	C	148	
2	B	105	
2	D	105	
3	E	117	
3	F	117	

2 Entry composition [i](#)

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
			Total	C	N	O	S			
1	A	139	1089	686	187	205	11	0	0	0
1	C	139	1089	686	187	205	11	0	0	0

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
			Total	C	N	O	S			
2	B	92	758	487	128	139	4	0	0	0
2	D	92	758	487	128	139	4	0	0	0

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

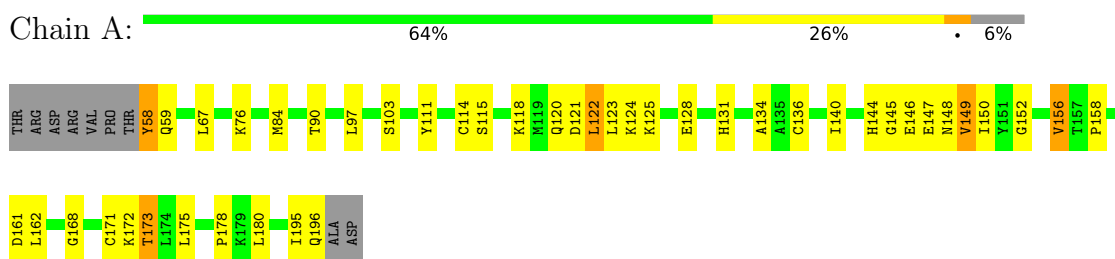
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	E	18	140	86	24	30	0	0	0
3	F	18	140	86	24	30	0	0	0

3 Residue-property plots [i](#)

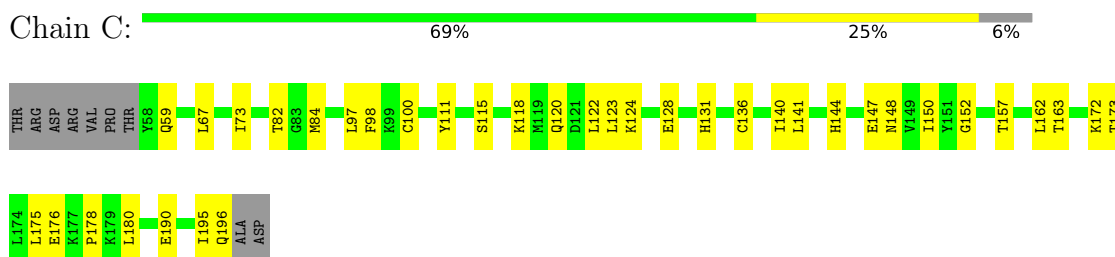
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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.

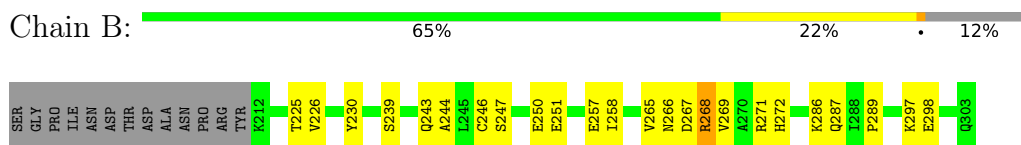
- Molecule 1: CASPASE-7 SUBUNIT P20



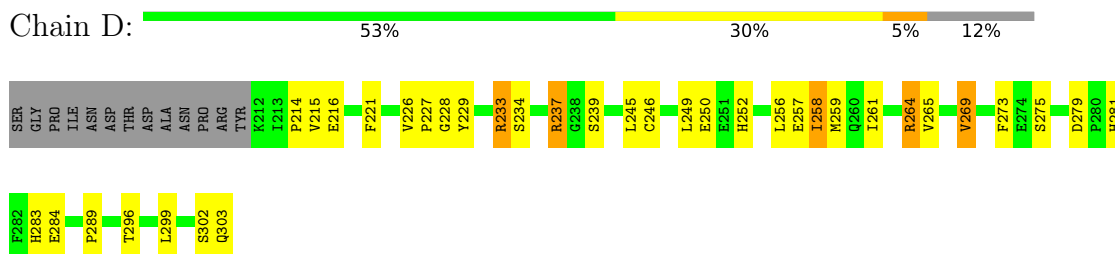
- Molecule 1: CASPASE-7 SUBUNIT P20



- Molecule 2: CASPASE-7 SUBUNIT P11



- Molecule 2: CASPASE-7 SUBUNIT P11



- Molecule 3: X-LINKED INHIBITOR OF APOPTOSIS PROTEIN

Chain E:  7% 8% . 85%

ARG	ASP	GLY	HIS	PHE	TYR	ALA	THR	LEU	GLY	ASP	ARG	PRO	SER	GLN	VAL	T1135	H1136	L1141	R1142	T1143	G1144	Q1145	V1146	D1148	I1149	S1150	D1151	T1152	ILE	TYR	PRO	ARG	ALA	ASN	TRP	PRO	ALA	GLY	HIS	MET	TYR	ARG	CYS	GLU	GLY	ALA	ARG	ASN	LEU	CYS	LEU	LYS	SER	PHE	VAL	GLN	ASN	TRP	ARG	ASN	PRO	ASP	TYR	ALA	HIS	LEU	THR	PRO	ARG	GLU	LEU	ALA	SER
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ALA	GLY	LEU	TYR	PHE	TYR	THR	LEU	GLY	ASP	ILE	GLY	ASP	SER	GLN	VAL	GLN	CYS	PHE	CYS	CYS	GLY	GLY	GLY	LYS	LEU	LYS	ASN	TRP	GLU	PRO	CYS	ASP	PRO	ARG	ALA	ASN	TRP	SER	TRP	SER	GLU	HIS	ARG	ARG	HIS	GLY	HIS	PHE	PRO	ALA	ASN	ARG	LEU	CYS	PHE	SER	PHE	VAL	VAL	LEU	GLY	TRP	ARG	ASN	ASN	PRO	ASP	TYR	ASN	ILE	ALA	HIS	ARG	LEU	THR	PRO	PRO	ARG	GLU	LEU	ALA	SER
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• Molecule 3: X-LINKED INHIBITOR OF APOPTOSIS PROTEIN

Chain F:  7% 8% . 85%

ARG	ASP	GLY	HIS	PHE	TYR	ALA	THR	LEU	GLY	ASP	ARG	PRO	SER	GLN	VAL	T1135	H1136	A1137	D1138	R1142	T1143	G1144	Q1145	I1149	S1150	D1151	T1152	ILE	TYR	PRO	ARG	ALA	ASN	TRP	PRO	ALA	GLY	HIS	MET	TYR	ARG	CYS	GLU	GLY	ALA	ARG	ASN	LEU	CYS	PHE	SER	PHE	VAL	LEU	GLN	ASN	TRP	ARG	ASN	ASN	PRO	ASP	TYR	ASN	ILE	ALA	HIS	ARG	LEU	THR	PRO	PRO	ARG	GLU	LEU	ALA	SER	ALA
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GLY	LEU	TYR	TYR	THR	GLY	ILE	GLY	ASP	GLN	VAL	GLN	CYS	PHE	CYS	CYS	GLY	GLY	LYS	LEU	LYS	ASN	TRP	GLU	PRO	CYS	ASP	ARG	PRO	ALA	ALA	TRP	SER	GLU	HIS	HIS	ARG	TYR	ARG	ARG	HIS	PHE	PRO	ASN	ASN	LEU	PHE	PHE	VAL	LEU	GLY	ARG	ASN	ASN	LEU	ASN	ASN	ILE	ILE	ARG	SER	GLU
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4 Data and refinement statistics

Xtrriage (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.	Xtrriage
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	0.38	0/1106	0.65	1/1482 (0.1%)
1	C	0.40	0/1106	0.64	1/1482 (0.1%)
2	B	0.41	0/780	0.63	0/1054
2	D	0.42	0/780	0.68	0/1054
3	E	0.38	0/141	0.53	0/192
3	F	0.35	0/141	0.51	0/192
All	All	0.40	0/4054	0.64	2/5456 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	152	GLY	N-CA-C	-5.76	98.71	113.10
1	A	152	GLY	N-CA-C	-5.48	99.41	113.10

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	35	0
1	C	1089	0	1080	37	0
2	B	758	0	731	19	0
2	D	758	0	731	40	0
3	E	140	0	133	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	140	0	133	12	0
All	All	3974	0	3888	135	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 17.

The worst 5 of 135 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
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
2:D:233:ARG:HA	2:D:239:SER:HA	1.55	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%)	22	25
1	C	137/148 (93%)	130 (95%)	6 (4%)	1 (1%)	22	25
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
All	All	486/740 (66%)	459 (94%)	21 (4%)	6 (1%)	13	12

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 [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	118/126 (94%)	109 (92%)	9 (8%)	13	15
1	C	118/126 (94%)	114 (97%)	4 (3%)	37	48
2	B	84/95 (88%)	80 (95%)	4 (5%)	25	33
2	D	84/95 (88%)	78 (93%)	6 (7%)	14	17
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%)	413 (95%)	23 (5%)	22	29

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	67	LEU
2	D	233	ARG
1	C	180	LEU
2	D	234	SER
1	A	156	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	136	HIS
3	E	145	GLN
1	C	120	GLN
2	D	303	GLN

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Mol	Chain	Res	Type
1	C	112	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 monosaccharides 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.