



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:33 PM UTC

PDB ID : 1NW9 / pdb_00001nw9
Title : STRUCTURE OF CASPASE-9 IN AN INHIBITORY COMPLEX WITH XIAP-BIR3
Authors : Shiozaki, E.N.; Chai, J.; Rigotti, D.J.; Riedl, S.J.; Li, P.; Srinivasula, S.M.; Alnemri, E.S.; Fairman, R.; Shi, Y.
Deposited on : 2003-02-05
Resolution : 2.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

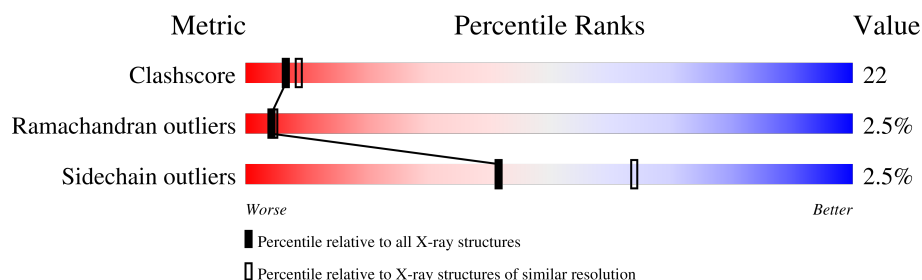
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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))
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	98	
2	B	277	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2590 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 Baculoviral IAP repeat-containing protein 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	91	Total	C	N	O	S	0	0	0
			746	481	127	134	4			

- Molecule 2 is a protein called caspase 9, apoptosis-related cysteine protease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	238	Total	C	N	O	S	9	0	0
			1843	1176	316	336	15			

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

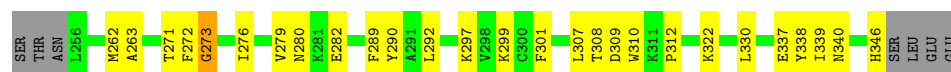
3 Residue-property plots [i](#)

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.

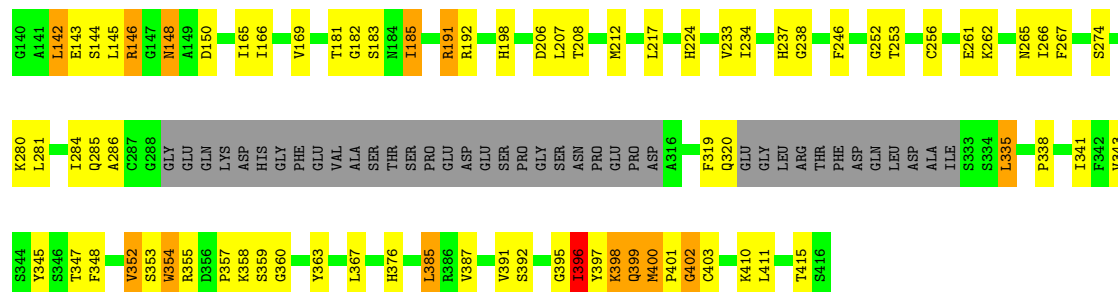
- Molecule 1: Baculoviral IAP repeat-containing protein 4

Chain A: 



- Molecule 2: caspase 9, apoptosis-related cysteine protease

Chain B: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	104.40Å 104.40Å 170.30Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.40	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.230 , 0.235	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2590	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section:
ZN

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	0.36	0/772	0.84	0/1046
2	B	0.42	0/1884	0.97	8/2543 (0.3%)
All	All	0.40	0/2656	0.93	8/3589 (0.2%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	397	TYR	N-CA-C	-7.10	95.67	110.80
2	B	252	GLY	N-CA-C	-7.08	101.70	112.89
2	B	396	ILE	N-CA-C	6.12	122.06	109.34
2	B	237	HIS	N-CA-C	-5.98	102.48	110.55
2	B	385	LEU	N-CA-C	-5.56	105.30	111.36
2	B	208	THR	N-CA-C	-5.39	103.78	110.41
2	B	198	HIS	N-CA-C	5.33	119.09	112.58
2	B	212	MET	N-CA-C	-5.27	105.61	111.36

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	746	0	696	29	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1843	0	1832	84	1
3	A	1	0	0	0	0
All	All	2590	0	2528	110	1

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 22.

All (110) 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:B:396:ILE:HD12	2:B:399:GLN:HB2	1.35	1.03
2:B:347:THR:OG1	2:B:398:LYS:HD3	1.66	0.95
1:A:279:VAL:HG21	1:A:310:TRP:HB3	1.47	0.93
2:B:400:MET:C	2:B:402:GLY:H	1.79	0.89
1:A:340:ASN:OD1	2:B:402:GLY:HA2	1.74	0.88
1:A:262:MET:HE1	1:A:271:THR:HG21	1.55	0.88
2:B:142:LEU:HD23	2:B:142:LEU:H	1.40	0.87
2:B:191:ARG:HH11	2:B:191:ARG:HB3	1.41	0.85
2:B:396:ILE:HD12	2:B:399:GLN:CB	2.08	0.83
2:B:392:SER:HA	2:B:396:ILE:HG13	1.61	0.82
2:B:392:SER:HA	2:B:396:ILE:CG1	2.14	0.78
2:B:352:VAL:HG22	2:B:359:SER:HB2	1.65	0.78
2:B:400:MET:C	2:B:402:GLY:N	2.37	0.76
1:A:279:VAL:HG21	1:A:310:TRP:CB	2.16	0.75
2:B:191:ARG:HH12	2:B:192:ARG:HG3	1.54	0.71
1:A:262:MET:HE1	1:A:271:THR:CG2	2.22	0.70
2:B:347:THR:H	2:B:398:LYS:NZ	1.89	0.70
1:A:297:LYS:HG2	1:A:308:THR:OG1	1.93	0.69
2:B:166:ILE:HD12	2:B:207:LEU:HD12	1.74	0.68
2:B:391:VAL:O	2:B:396:ILE:HD11	1.95	0.67
2:B:347:THR:H	2:B:398:LYS:HZ3	1.44	0.66
2:B:181:THR:HG21	2:B:358:LYS:HG2	1.77	0.66
1:A:262:MET:HE3	1:A:290:TYR:CG	2.31	0.65
2:B:391:VAL:C	2:B:396:ILE:HD11	2.22	0.65
2:B:262:LYS:O	2:B:266:ILE:HG12	1.97	0.65
2:B:281:LEU:HD11	2:B:411:LEU:HD21	1.80	0.64
1:A:308:THR:HG22	1:A:309:ASP:N	2.13	0.64
1:A:308:THR:HG22	1:A:309:ASP:H	1.63	0.63
2:B:234:ILE:HB	2:B:284:ILE:HD12	1.81	0.62
1:A:322:LYS:HG3	1:A:346:HIS:HE1	1.63	0.62
2:B:191:ARG:HH12	2:B:192:ARG:CG	2.14	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:396:ILE:HG23	2:B:399:GLN:HB2	1.83	0.60
2:B:398:LYS:HE3	2:B:400:MET:H	1.67	0.60
1:A:330:LEU:HD21	1:A:339:ILE:HD12	1.84	0.59
2:B:400:MET:O	2:B:402:GLY:N	2.34	0.59
2:B:401:PRO:O	2:B:402:GLY:C	2.46	0.59
2:B:145:LEU:HD21	2:B:410:LYS:HD2	1.85	0.58
2:B:191:ARG:HH11	2:B:191:ARG:CB	2.14	0.58
2:B:319:PHE:O	2:B:320:GLN:HB3	2.04	0.58
1:A:330:LEU:HG	1:A:339:ILE:HD11	1.87	0.57
2:B:398:LYS:C	2:B:400:MET:N	2.61	0.57
2:B:181:THR:CG2	2:B:358:LYS:HG2	2.36	0.55
2:B:238:GLY:HA3	2:B:286:ALA:HB1	1.88	0.55
2:B:398:LYS:O	2:B:399:GLN:C	2.49	0.55
2:B:142:LEU:HG	2:B:143:GLU:OE2	2.06	0.55
2:B:398:LYS:O	2:B:400:MET:N	2.40	0.55
1:A:322:LYS:HG3	1:A:346:HIS:CE1	2.41	0.55
2:B:347:THR:HG1	2:B:398:LYS:HD3	1.72	0.54
2:B:391:VAL:HG12	2:B:396:ILE:HD11	1.90	0.53
2:B:387:VAL:O	2:B:391:VAL:HG23	2.08	0.53
1:A:292:LEU:HD11	1:A:299:LYS:HG3	1.90	0.52
1:A:337:GLU:H	1:A:337:GLU:CD	2.17	0.52
2:B:355:ARG:O	2:B:357:PRO:HD3	2.08	0.52
1:A:272:PHE:O	1:A:273:GLY:C	2.53	0.52
2:B:343:VAL:O	2:B:403:CYS:HA	2.09	0.52
2:B:400:MET:N	2:B:401:PRO:HD3	2.25	0.51
1:A:276:ILE:C	1:A:276:ILE:HD12	2.35	0.51
2:B:391:VAL:HG12	2:B:396:ILE:CD1	2.41	0.51
2:B:399:GLN:C	2:B:401:PRO:CD	2.84	0.51
2:B:169:VAL:HG22	2:B:183:SER:HB3	1.92	0.50
2:B:395:GLY:O	2:B:396:ILE:HB	2.12	0.50
1:A:279:VAL:CG2	1:A:310:TRP:HB3	2.32	0.50
2:B:191:ARG:NH1	2:B:192:ARG:N	2.60	0.50
2:B:280:LYS:HB2	2:B:341:ILE:HD13	1.94	0.50
2:B:352:VAL:HG13	2:B:360:GLY:O	2.11	0.50
2:B:182:GLY:O	2:B:185:ILE:HG13	2.11	0.50
2:B:348:PHE:N	2:B:398:LYS:HE2	2.28	0.49
2:B:400:MET:N	2:B:401:PRO:CD	2.76	0.48
2:B:396:ILE:HD12	2:B:399:GLN:CG	2.43	0.48
2:B:142:LEU:H	2:B:142:LEU:CD2	2.19	0.48
2:B:285:GLN:NE2	2:B:363:TYR:CD2	2.82	0.47
1:A:289:PHE:CE1	1:A:307:LEU:HD23	2.50	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:330:LEU:HG	1:A:339:ILE:CD1	2.45	0.47
2:B:352:VAL:HG22	2:B:359:SER:CB	2.39	0.47
2:B:246:PHE:CE1	2:B:338:PRO:HG2	2.50	0.47
1:A:262:MET:HE3	1:A:290:TYR:CB	2.45	0.46
2:B:396:ILE:HG23	2:B:399:GLN:CB	2.45	0.46
2:B:354:TRP:CE2	2:B:355:ARG:HG3	2.50	0.46
2:B:206:ASP:HA	2:B:253:THR:HG21	1.98	0.46
1:A:308:THR:HG1	2:B:319:PHE:HD2	1.62	0.45
2:B:185:ILE:HD11	2:B:360:GLY:HA3	1.97	0.45
2:B:144:SER:O	2:B:148:ASN:HB2	2.16	0.45
2:B:261:GLU:HG3	2:B:265:ASN:ND2	2.32	0.44
1:A:280:ASN:OD1	1:A:282:GLU:HB2	2.17	0.44
2:B:352:VAL:CG2	2:B:359:SER:HB2	2.42	0.44
2:B:367:LEU:HD23	2:B:367:LEU:C	2.43	0.44
2:B:142:LEU:O	2:B:146:ARG:HG3	2.18	0.44
2:B:376:HIS:HA	2:B:415:THR:HG21	2.00	0.44
2:B:398:LYS:HZ1	2:B:400:MET:C	2.26	0.44
2:B:217:LEU:HD23	2:B:266:ILE:HG23	1.99	0.44
1:A:262:MET:CE	1:A:271:THR:HG21	2.36	0.44
2:B:398:LYS:CE	2:B:400:MET:H	2.30	0.44
2:B:165:ILE:HG12	2:B:233:VAL:HB	2.01	0.43
1:A:338:TYR:HD2	1:A:339:ILE:HD13	1.84	0.43
2:B:395:GLY:O	2:B:396:ILE:CB	2.66	0.43
2:B:148:ASN:OD1	2:B:150:ASP:HB2	2.20	0.42
2:B:345:TYR:O	2:B:401:PRO:HA	2.20	0.42
2:B:385:LEU:O	2:B:385:LEU:HD23	2.20	0.42
2:B:399:GLN:C	2:B:401:PRO:HD3	2.45	0.42
1:A:262:MET:HE3	1:A:290:TYR:HB2	2.01	0.42
2:B:345:TYR:O	2:B:400:MET:O	2.38	0.42
2:B:267:PHE:CD2	2:B:267:PHE:N	2.88	0.41
2:B:398:LYS:NZ	2:B:400:MET:HB3	2.35	0.41
1:A:263:ALA:HA	1:A:301:PHE:CD1	2.55	0.41
2:B:335:LEU:HD23	2:B:335:LEU:N	2.35	0.41
1:A:308:THR:CG2	1:A:309:ASP:N	2.81	0.41
2:B:319:PHE:O	2:B:320:GLN:CB	2.69	0.41
1:A:340:ASN:CG	2:B:402:GLY:HA2	2.43	0.41
2:B:224:HIS:N	2:B:274:SER:OG	2.50	0.40
2:B:352:VAL:CG2	2:B:353:SER:N	2.84	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:256:CYS:SG	2:B:256:CYS:SG[8_556]	1.97	0.23

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	89/98 (91%)	84 (94%)	3 (3%)	2 (2%)	5	6
2	B	232/277 (84%)	213 (92%)	13 (6%)	6 (3%)	4	4
All	All	321/375 (86%)	297 (92%)	16 (5%)	8 (2%)	4	5

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	402	GLY
1	A	273	GLY
2	B	396	ILE
2	B	399	GLN
1	A	312	PRO
2	B	148	ASN
2	B	354	TRP
2	B	400	MET

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	76/83 (92%)	76 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	B	205/238 (86%)	198 (97%)	7 (3%)	32 54
All	All	281/321 (88%)	274 (98%)	7 (2%)	42 64

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	142	LEU
2	B	146	ARG
2	B	185	ILE
2	B	191	ARG
2	B	335	LEU
2	B	352	VAL
2	B	398	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	319	GLN
1	A	346	HIS
2	B	167	ASN
2	B	245	GLN
2	B	285	GLN
2	B	373	GLN
2	B	376	HIS
2	B	399	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

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

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.