



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 3E4C / pdb_00003e4c
Title : Procaspase-1 zymogen domain crystal structure
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Deposited on : 2008-08-11
Resolution : 2.05 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)	:	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

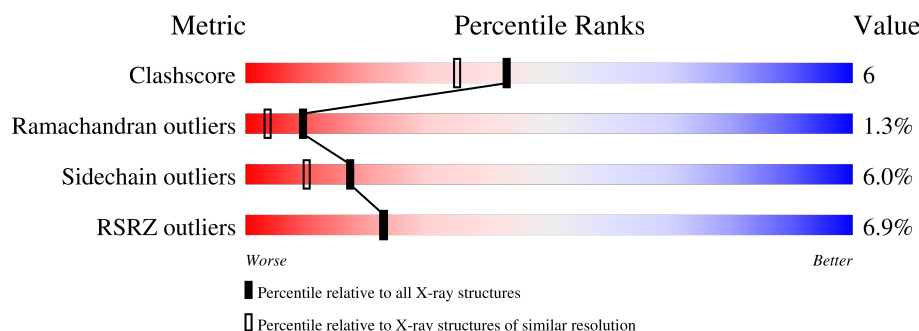
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)
RSRZ outliers	180081	2260 (2.04-2.04)

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	302	5% 76% 12% • 10%
1	B	302	8% 74% 13% • 11%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4423 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-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	271	Total	C	N	O	S	0	12	0
			2149	1351	371	410	17			
1	B	269	Total	C	N	O	S	0	12	0
			2137	1345	369	406	17			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	103	GLN	-	expression tag	UNP P29466
A	285	ALA	CYS	engineered mutation	UNP P29466
B	103	GLN	-	expression tag	UNP P29466
B	285	ALA	CYS	engineered mutation	UNP P29466

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mg	0	0
			1	1		

- Molecule 3 is water.

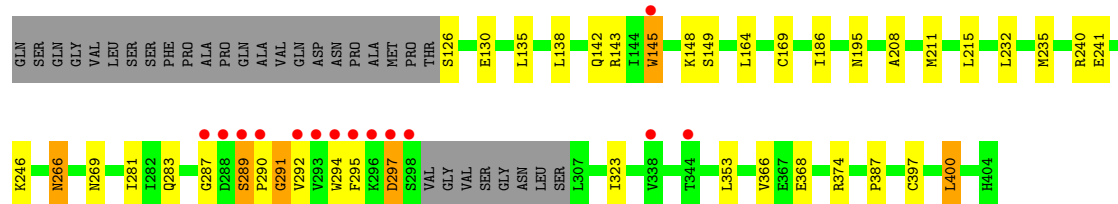
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	69	Total	O	0	0
			69	69		
3	B	67	Total	O	0	0
			67	67		

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.

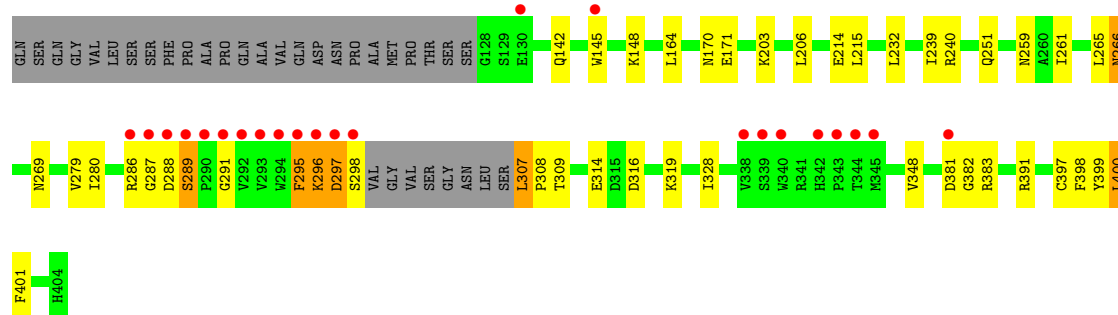
• Molecule 1: Caspase-1

Chain A: 



• Molecule 1: Caspase-1

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	56.10Å 58.00Å 60.12Å 105.95° 119.60° 92.77°	Depositor
Resolution (Å)	20.00 – 2.05 20.00 – 2.05	Depositor EDS
% Data completeness (in resolution range)	96.6 (20.00-2.05) 96.5 (20.00-2.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.78 (at 2.06Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.200 , 0.263 0.212 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	35.6	Xtriage
Anisotropy	0.133	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 62.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4423	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.58% 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

5.1 Standard geometry

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

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	0/2193	0.86	2/2957 (0.1%)
1	B	0.77	1/2181 (0.0%)	0.95	2/2941 (0.1%)
All	All	0.74	1/4374 (0.0%)	0.91	4/5898 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	280	ILE	CA-CB	-5.24	1.47	1.54

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	289[B]	SER	CA-C-N	5.90	125.57	119.56
1	B	289[B]	SER	C-N-CA	5.90	125.57	119.56
1	A	289[A]	SER	CA-C-N	5.70	126.96	119.84
1	A	289[A]	SER	C-N-CA	5.70	126.96	119.84

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2149	0	2116	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2137	0	2103	35	0
2	B	1	0	0	0	0
3	A	69	0	0	1	0
3	B	67	0	0	2	0
All	All	4423	0	4219	53	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 6.

All (53) 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:B:148:LYS:NZ	1:B:397:CYS:SG	2.26	1.08
1:A:148:LYS:NZ	1:A:397:CYS:SG	2.27	1.07
1:B:142:GLN:HG3	3:B:405:HOH:O	1.72	0.88
1:B:259:ASN:HD22	1:B:391:ARG:HH22	1.20	0.87
1:A:290[A]:PRO:O	1:A:291[A]:GLY:O	1.92	0.85
1:B:266:ASN:C	1:B:266:ASN:HD22	1.86	0.83
1:A:266:ASN:HD22	1:A:266:ASN:C	1.93	0.76
1:B:295[B]:PHE:O	1:B:296[B]:LYS:CB	2.37	0.72
1:B:297[B]:ASP:O	1:B:298[B]:SER:HB3	1.89	0.72
1:B:297[B]:ASP:O	1:B:298[B]:SER:CB	2.39	0.71
1:B:287[B]:GLY:O	1:B:289[B]:SER:N	2.26	0.69
1:B:295[B]:PHE:O	1:B:296[B]:LYS:HB2	1.93	0.68
1:A:266:ASN:ND2	1:A:269:ASN:H	1.93	0.66
1:B:295[B]:PHE:O	1:B:296[B]:LYS:HG2	1.98	0.64
1:B:142:GLN:HE21	1:B:142:GLN:HA	1.63	0.64
1:A:208:ALA:HA	1:A:211:MET:HE3	1.79	0.63
1:B:295[B]:PHE:O	1:B:296[B]:LYS:CG	2.48	0.62
1:B:251:GLN:OE1	1:B:251:GLN:N	2.34	0.61
1:A:266:ASN:HD21	1:A:269:ASN:H	1.51	0.58
1:B:266:ASN:C	1:B:266:ASN:ND2	2.56	0.57
1:B:297[B]:ASP:N	1:B:297[B]:ASP:OD1	2.36	0.57
1:A:145:TRP:O	1:A:149:SER:HB3	2.07	0.54
1:B:286:ARG:HG2	1:B:291[B]:GLY:HA2	1.89	0.54
1:A:374:ARG:HD3	1:A:387:PRO:O	2.09	0.52
1:B:328:ILE:HG23	1:B:328:ILE:O	2.09	0.51
1:B:287[B]:GLY:C	1:B:289[B]:SER:N	2.69	0.51
1:B:142:GLN:HA	1:B:142:GLN:NE2	2.27	0.50
1:A:169:CYS:HB2	1:A:235:MET:HE3	1.94	0.49
1:A:368:GLU:OE1	1:B:148:LYS:NZ	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:142:GLN:CG	3:B:405:HOH:O	2.43	0.49
1:A:289[A]:SER:HB2	1:A:290[A]:PRO:HD2	1.93	0.49
1:A:366:VAL:HG12	1:A:400:LEU:CD2	2.44	0.48
1:A:126:SER:N	3:A:434:HOH:O	2.47	0.48
1:B:266:ASN:ND2	1:B:269:ASN:H	2.11	0.47
1:B:399:TYR:HB2	1:B:401:PHE:CE2	2.48	0.47
1:B:279:VAL:CG2	1:B:398:PHE:HE2	2.28	0.46
1:B:314:GLU:O	1:B:319:LYS:HE3	2.16	0.46
1:B:295[B]:PHE:C	1:B:296[B]:LYS:HG2	2.42	0.45
1:B:148:LYS:CE	1:B:397:CYS:SG	3.04	0.45
1:B:170:ASN:ND2	1:B:206:LEU:H	2.16	0.44
1:B:381:ASP:O	1:B:382:GLY:C	2.60	0.43
1:B:307:LEU:N	1:B:308:PRO:CD	2.82	0.43
1:A:169:CYS:HB3	1:A:186:ILE:HD11	2.01	0.42
1:B:203:LYS:HB3	1:B:206:LEU:HD11	2.00	0.42
1:A:130:GLU:O	1:A:195:ASN:HB3	2.19	0.42
1:A:240:ARG:HB3	1:A:241:GLU:OE1	2.19	0.42
1:A:266:ASN:HB2	1:A:323:ILE:O	2.20	0.42
1:A:148:LYS:CE	1:A:397:CYS:SG	3.08	0.41
1:B:328:ILE:O	1:B:328:ILE:CG2	2.67	0.41
1:B:239:ILE:O	1:B:240:ARG:C	2.64	0.41
1:B:261:ILE:O	1:B:265:LEU:HD23	2.21	0.41
1:A:281:ILE:HD13	1:A:353:LEU:HD21	2.03	0.41
1:B:400:LEU:O	1:B:401:PHE:C	2.64	0.40

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	267/302 (88%)	246 (92%)	17 (6%)	4 (2%)	8 2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	265/302 (88%)	249 (94%)	13 (5%)	3 (1%)	11	5
All	All	532/604 (88%)	495 (93%)	30 (6%)	7 (1%)	9	3

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	291[A]	GLY
1	A	297[A]	ASP
1	A	287[A]	GLY
1	B	288[B]	ASP
1	B	296[B]	LYS
1	A	294[A]	TRP
1	B	295[B]	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	242/267 (91%)	227 (94%)	15 (6%)	16	9
1	B	240/267 (90%)	226 (94%)	14 (6%)	18	11
All	All	482/534 (90%)	453 (94%)	29 (6%)	17	10

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	135	LEU
1	A	138	LEU
1	A	142	GLN
1	A	143	ARG
1	A	145	TRP
1	A	164	LEU
1	A	215	LEU
1	A	232	LEU
1	A	246	LYS

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Mol	Chain	Res	Type
1	A	266	ASN
1	A	283	GLN
1	A	292[A]	VAL
1	A	295[A]	PHE
1	A	297[A]	ASP
1	A	400	LEU
1	B	145	TRP
1	B	164	LEU
1	B	171	GLU
1	B	214	GLU
1	B	215	LEU
1	B	232	LEU
1	B	266	ASN
1	B	297[B]	ASP
1	B	307	LEU
1	B	309	THR
1	B	316	ASP
1	B	348	VAL
1	B	383	ARG
1	B	400	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	170	ASN
1	A	195	ASN
1	A	263	ASN
1	A	266	ASN
1	A	358	GLN
1	A	385	GLN
1	B	142	GLN
1	B	147	GLN
1	B	170	ASN
1	B	194	GLN
1	B	259	ASN
1	B	263	ASN
1	B	266	ASN
1	B	269	ASN
1	B	283	GLN

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](#)

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 [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

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	271/302 (89%)	0.07	14 (5%)	33 33	22, 35, 58, 74	12 (4%)
1	B	269/302 (89%)	0.18	23 (8%)	16 16	8, 34, 68, 123	12 (4%)
All	All	540/604 (89%)	0.13	37 (6%)	23 23	8, 35, 61, 123	24 (4%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	287[B]	GLY	6.1
1	A	290[A]	PRO	5.9
1	A	287[A]	GLY	5.5
1	A	296[A]	LYS	5.2
1	B	293[B]	VAL	5.1
1	A	292[A]	VAL	4.7
1	A	294[A]	TRP	4.7
1	A	344	THR	4.6
1	B	289[B]	SER	4.3
1	B	292[B]	VAL	4.2
1	A	289[A]	SER	4.0
1	B	290[B]	PRO	3.9
1	B	343	PRO	3.7
1	B	338	VAL	3.7
1	A	298[A]	SER	3.4
1	B	340	TRP	3.1
1	B	294[B]	TRP	3.0
1	B	130	GLU	3.0
1	B	295[B]	PHE	3.0
1	A	295[A]	PHE	2.9
1	B	298[B]	SER	2.9
1	B	296[B]	LYS	2.8
1	A	297[A]	ASP	2.7
1	B	381	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	286	ARG	2.6
1	B	342	HIS	2.6
1	B	145	TRP	2.6
1	B	297[B]	ASP	2.5
1	A	338	VAL	2.4
1	B	288[B]	ASP	2.4
1	B	339	SER	2.4
1	A	288[A]	ASP	2.3
1	A	293[A]	VAL	2.2
1	A	145	TRP	2.2
1	B	345	MET	2.2
1	B	344	THR	2.1
1	B	291[B]	GLY	2.0

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MG	B	1	1/1	0.99	0.03	34,34,34,34	0

6.5 Other polymers [i](#)

There are no such residues in this entry.