



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 16, 2021 – 08:08 PM EDT

PDB ID : 1SC1  
Title : Crystal structure of an active-site ligand-free form of the human caspase-1 C285A mutant  
Authors : Romanowski, M.J.; Scheer, J.M.; O'Brien, T.; McDowell, R.S.  
Deposited on : 2004-02-11  
Resolution : 2.60 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

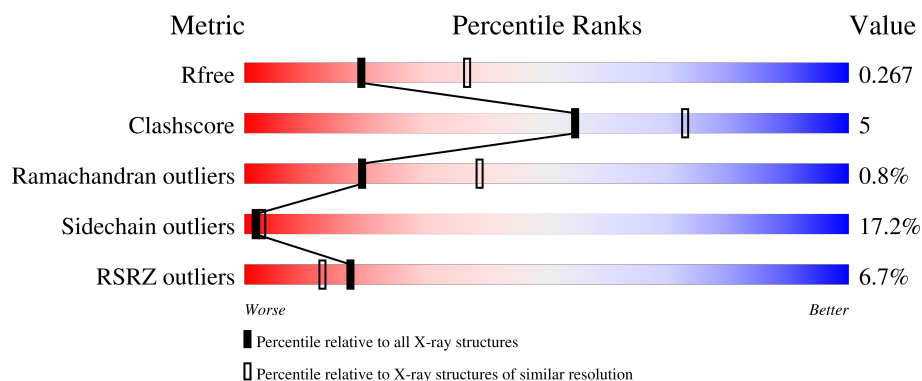
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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))
$R_{free}$	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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  $\geq 3$ , 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	178	 7% 69% 23% 6%
2	B	88	 5% 68% 28% 6%

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2091 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 Interleukin-1 beta convertase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	167	Total	C	N	O	S	0	0	0
			1312	824	229	249	10			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	285	ALA	CYS	engineered mutation	UNP P29466

- Molecule 2 is a protein called Interleukin-1 beta convertase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	88	Total	C	N	O	S	0	0	0
			718	457	126	128	7			

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Cl	0	0
			1	1		

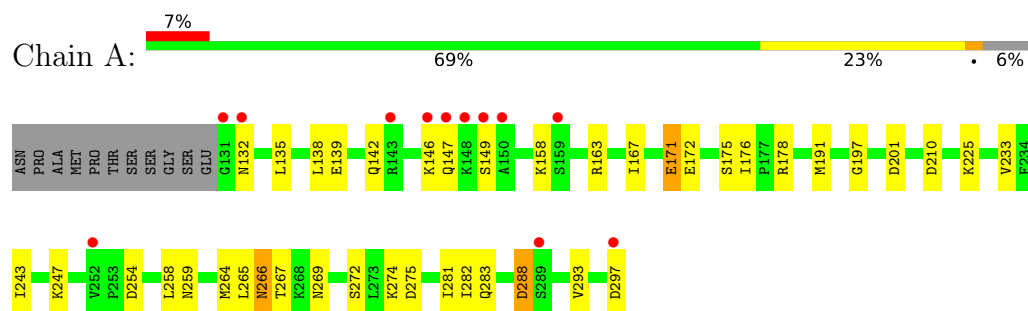
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	36	Total	O	0	0
			36	36		
4	B	24	Total	O	0	0
			24	24		

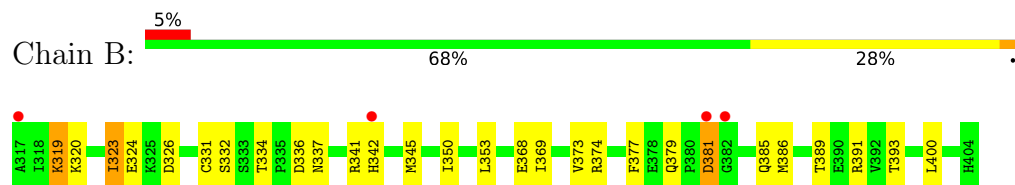
### 3 Residue-property plots [i](#)

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: Interleukin-1 beta convertase



- Molecule 2: Interleukin-1 beta convertase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	71.78Å 71.78Å 118.45Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.60 19.77 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.6 (20.00-2.60) 99.6 (19.77-2.60)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.02 (at 2.59Å)	Xtriage
Refinement program	REFMAC 5.1.19	Depositor
R, $R_{free}$	0.231 , 0.273 0.228 , 0.267	Depositor DCC
$R_{free}$ test set	537 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	49.5	Xtriage
Anisotropy	0.589	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 46.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	0.000 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	2091	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.71% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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](#)

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

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	0.35	0/1334	0.72	5/1796 (0.3%)
2	B	0.40	0/738	0.69	3/995 (0.3%)
All	All	0.37	0/2072	0.71	8/2791 (0.3%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	297	ASP	CB-CG-OD2	7.14	124.72	118.30
1	A	201	ASP	CB-CG-OD2	6.62	124.26	118.30
1	A	254	ASP	CB-CG-OD2	5.96	123.67	118.30
2	B	326	ASP	CB-CG-OD2	5.89	123.60	118.30
1	A	288	ASP	CB-CG-OD2	5.63	123.37	118.30
1	A	210	ASP	CB-CG-OD2	5.39	123.15	118.30
2	B	336	ASP	CB-CG-OD2	5.27	123.05	118.30
2	B	381	ASP	CB-CG-OD2	5.07	122.87	118.30

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	1312	0	1331	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	718	0	693	10	0
3	B	1	0	0	0	0
4	A	36	0	0	3	0
4	B	24	0	0	0	0
All	All	2091	0	2024	21	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 5.

All (21) 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:A:283:GLN:HG3	4:A:40:HOH:O	1.95	0.67
1:A:266:ASN:HD22	1:A:266:ASN:C	1.98	0.67
2:B:374:ARG:NH2	2:B:389:THR:OG1	2.32	0.61
1:A:266:ASN:ND2	1:A:269:ASN:H	2.02	0.56
1:A:266:ASN:HB2	2:B:323:ILE:O	2.05	0.56
2:B:369:ILE:O	2:B:373:VAL:HG23	2.07	0.54
2:B:374:ARG:HG2	2:B:386:MET:SD	2.49	0.53
1:A:266:ASN:OD1	2:B:323:ILE:HD12	2.08	0.52
1:A:171:GLU:HG2	4:A:57:HOH:O	2.11	0.51
2:B:319:LYS:HE2	2:B:320:LYS:H	1.76	0.51
1:A:266:ASN:HD21	1:A:269:ASN:H	1.58	0.50
1:A:267:THR:HG23	1:A:274:LYS:HB2	1.93	0.50
2:B:323:ILE:HG13	2:B:324:GLU:N	2.27	0.50
1:A:258:LEU:HD22	1:A:282:ILE:HD13	1.93	0.49
1:A:163:ARG:HB2	1:A:197:GLY:O	2.13	0.48
1:A:281:ILE:HD13	2:B:353:LEU:HD21	1.96	0.47
2:B:332:SER:HB2	2:B:385:GLN:OE1	2.16	0.46
4:A:59:HOH:O	2:B:350:ILE:HD11	2.15	0.45
1:A:167:ILE:HG12	1:A:233:VAL:HB	2.01	0.43
1:A:236:SER:HB3	1:A:243:ILE:HG23	2.02	0.42
1:A:274:LYS:O	1:A:275:ASP:HB2	2.20	0.41

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	165/178 (93%)	154 (93%)	10 (6%)	1 (1%)	25	47
2	B	86/88 (98%)	81 (94%)	4 (5%)	1 (1%)	13	27
All	All	251/266 (94%)	235 (94%)	14 (6%)	2 (1%)	19	39

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	149	SER
2	B	381	ASP

### 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	148/157 (94%)	123 (83%)	25 (17%)	2	3
2	B	79/79 (100%)	65 (82%)	14 (18%)	2	3
All	All	227/236 (96%)	188 (83%)	39 (17%)	2	3

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	132	ASN
1	A	135	LEU
1	A	138	LEU
1	A	139	GLU

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Mol	Chain	Res	Type
1	A	142	GLN
1	A	146	LYS
1	A	147	GLN
1	A	158	LYS
1	A	171	GLU
1	A	172	GLU
1	A	175	SER
1	A	176	ILE
1	A	178	ARG
1	A	191	MET
1	A	225	LYS
1	A	235	MET
1	A	241	GLU
1	A	247	LYS
1	A	259	ASN
1	A	264	MET
1	A	265	LEU
1	A	266	ASN
1	A	272	SER
1	A	288	ASP
1	A	293	VAL
2	B	319	LYS
2	B	323	ILE
2	B	331	CYS
2	B	334	THR
2	B	337	ASN
2	B	341	ARG
2	B	342	HIS
2	B	345	MET
2	B	368	GLU
2	B	377	PHE
2	B	379	GLN
2	B	391	ARG
2	B	393	THR
2	B	400	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	170	ASN
1	A	263	ASN
1	A	266	ASN

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Mol	Chain	Res	Type
1	A	269	ASN
2	B	356	HIS
2	B	358	GLN
2	B	404	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 monosaccharides 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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	167/178 (93%)	0.09	13 (7%) 13 9	24, 49, 91, 105	0
2	B	88/88 (100%)	-0.02	4 (4%) 33 26	23, 44, 83, 88	0
All	All	255/266 (95%)	0.05	17 (6%) 17 13	23, 47, 87, 105	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	131	GLY	6.3
1	A	150	ALA	4.4
1	A	148	LYS	4.0
2	B	381	ASP	4.0
1	A	289	SER	3.9
1	A	149	SER	3.7
2	B	342	HIS	3.4
1	A	252	VAL	3.1
1	A	147	GLN	2.9
2	B	382	GLY	2.7
1	A	146	LYS	2.7
2	B	317	ALA	2.5
1	A	143	ARG	2.5
1	A	241	GLU	2.5
1	A	159	SER	2.3
1	A	297	ASP	2.2
1	A	132	ASN	2.1

### 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 monosaccharides 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, 95<sup>th</sup> 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
3	CL	B	1	1/1	0.94	0.10	33,33,33,33	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.