



Full wwPDB X-ray Structure Validation Report i

Feb 26, 2014 – 10:56 PM GMT

PDB ID : 2H51
Title : Crystal structure of human caspase-1 (Glu390->Asp and Arg286->Lys) in complex with 3-[2-(2-benzyloxycarbonylamino-3-methyl-butyrylamino)-propionylamino]-4-oxo-pentanoicacid (z-VAD-FMK)
Authors : Scheer, J.M.; Wells, J.A.; Romanowski, M.J.
Deposited on : 2006-05-25
Resolution : 2.10 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

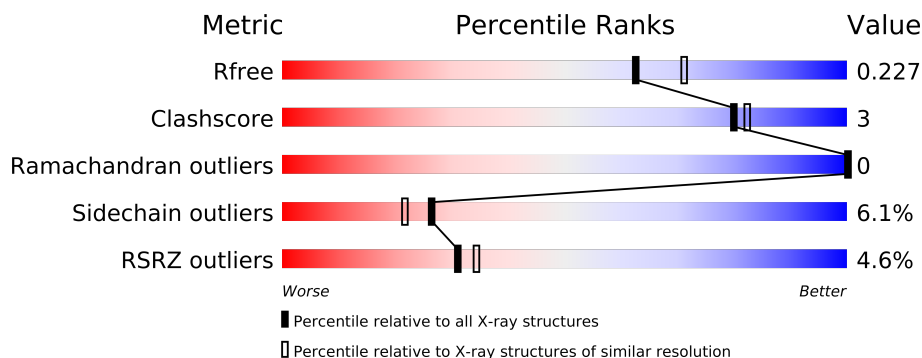
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.10 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}	66092	3012 (2.10-2.10)
Clashscore	79885	3649 (2.10-2.10)
Ramachandran outliers	78287	3610 (2.10-2.10)
Sidechain outliers	78261	3611 (2.10-2.10)
RSRZ outliers	66119	3013 (2.10-2.10)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	178	
2	B	88	
3	C	5	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2283 atoms, of which 0 are hydrogen and 0 are deuterium.

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	167	Total	C	N	O	S	0	4	0
			1314	827	226	250	11			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	286	LYS	ARG	ENGINEERED	UNP P29466

- Molecule 2 is a protein called Caspase-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	87	Total	C	N	O	S	0	4	0
			723	461	125	130	7			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	390	ASP	GLU	ENGINEERED	UNP P29466

- Molecule 3 is a protein called N-[(benzyloxy)carbonyl]-L-valyl-N-[(2S)-1-carboxy-4-fluoro-3-oxobutan-2-yl]-L-alaninamide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	5	Total	C	N	O	0	0	1
			31	21	3	7			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	127	Total	O	0	0
			127	127		

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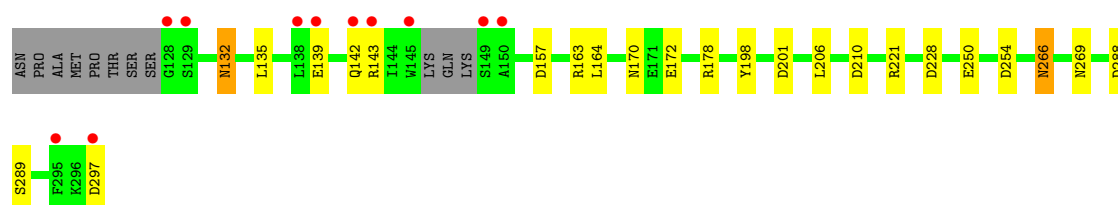
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	87	Total	O	0	0
			87	87		
4	C	1	Total	O	0	0
			1	1		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 2: Caspase-1

Chain B: 



• Molecule 3: N-[(benzyloxy)carbonyl]-L-valyl-N-[(2S)-1-carboxy-4-fluoro-3-oxobutan-2-yl]-L-alaninamide

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	63.16Å 63.16Å 141.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.10 20.00 – 2.10	Depositor EDS
% Data completeness (in resolution range)	93.8 (20.00-2.10) 93.8 (20.00-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.83 (at 2.09Å)	Xtriage
Refinement program	REFMAC 5.1.19	Depositor
R, R_{free}	0.180 , 0.236 0.179 , 0.227	Depositor DCC
R_{free} test set	834 reflections (5.37%)	DCC
Wilson B-factor (Å ²)	19.4	Xtriage
Anisotropy	0.164	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 37.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 16666 reflections (0.006%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2283	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.45% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PHQ, CF0

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	0.34	0/1354	0.68	6/1825 (0.3%)
2	B	0.41	0/765	0.72	4/1031 (0.4%)
3	C	2.36	1/19 (5.3%)	1.24	0/25
All	All	0.43	1/2138 (0.0%)	0.70	10/2881 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	4	ASP	C-O	10.17	1.42	1.23

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	365	ASP	CB-CG-OD2	6.18	123.86	118.30
1	A	201	ASP	CB-CG-OD2	5.92	123.63	118.30
1	A	254	ASP	CB-CG-OD2	5.91	123.61	118.30
1	A	157	ASP	CB-CG-OD2	5.66	123.39	118.30
1	A	228	ASP	CB-CG-OD2	5.65	123.38	118.30
2	B	390[A]	ASP	CB-CG-OD2	5.46	123.21	118.30
2	B	390[B]	ASP	CB-CG-OD2	5.46	123.21	118.30
1	A	288	ASP	CB-CG-OD2	5.11	122.90	118.30
1	A	297	ASP	CB-CG-OD2	5.09	122.88	118.30
2	B	326	ASP	CB-CG-OD2	5.03	122.83	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1314	0	1322	10	0
2	B	723	0	691	6	0
3	C	31	0	24	0	0
4	A	127	0	0	1	0
4	B	87	0	0	1	0
4	C	1	0	0	0	0
All	All	2283	0	2037	14	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 3.

All (14) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:390[A]:ASP:OD2	4:B:491:HOH:O	1.98	0.81
1:A:266:ASN:HD22	1:A:266:ASN:C	1.91	0.74
1:A:170:ASN:HD21	1:A:206:LEU:H	1.43	0.65
1:A:170:ASN:ND2	1:A:206:LEU:H	1.97	0.63
1:A:266:ASN:ND2	1:A:269:ASN:H	2.02	0.56
1:A:132:ASN:HB3	4:A:561:HOH:O	2.08	0.54
1:A:266:ASN:ND2	1:A:266:ASN:C	2.63	0.52
2:B:357:MET:CE	2:B:369:ILE:HD13	2.44	0.47
1:A:163:ARG:HB3	1:A:198:TYR:CD2	2.51	0.45
2:B:357:MET:HA	2:B:357:MET:HE2	2.00	0.44
2:B:341:ARG:HA	2:B:347:SER:HA	2.00	0.43
1:A:289:SER:HB3	2:B:337:ASN:HD22	1.83	0.43
1:A:266:ASN:HB2	2:B:323:ILE:O	2.19	0.42
1:A:206:LEU:HB3	1:A:210:ASP:HB2	2.00	0.42

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	167/178 (94%)	164 (98%)	3 (2%)	0	100	100
2	B	88/88 (100%)	87 (99%)	1 (1%)	0	100	100
3	C	1/5 (20%)	1 (100%)	0	0	100	100
All	All	256/271 (94%)	252 (98%)	4 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	151/158 (96%)	140 (93%)	11 (7%)	20	15
2	B	83/79 (105%)	80 (96%)	3 (4%)	47	46
3	C	2/2 (100%)	2 (100%)	0	100	100
All	All	236/239 (99%)	222 (94%)	14 (6%)	26	23

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	132	ASN
1	A	135	LEU
1	A	139	GLU
1	A	142	GLN
1	A	143	ARG
1	A	164	LEU
1	A	172	GLU
1	A	178	ARG

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Mol	Chain	Res	Type
1	A	221	ARG
1	A	250	GLU
1	A	266	ASN
2	B	319	LYS
2	B	359	GLU
2	B	378	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	132	ASN
1	A	170	ASN
1	A	266	ASN
1	A	269	ASN
2	B	337	ASN
2	B	358	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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 ⓘ

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	167/178 (93%)	0.04	11 (6%) 18 20	5, 12, 38, 70	0
2	B	87/88 (98%)	-0.33	1 (1%) 77 81	6, 10, 19, 27	0
3	C	5/5 (100%)	-0.35	0 100 100	15, 16, 20, 22	0
All	All	259/271 (95%)	-0.09	12 (4%) 31 34	5, 11, 30, 70	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	297	ASP	8.0
1	A	149	SER	5.1
1	A	150	ALA	4.5
1	A	145	TRP	3.8
1	A	142	GLN	3.6
1	A	129	SER	3.6
1	A	128	GLY	3.5
1	A	143	ARG	3.4
1	A	138	LEU	3.1
1	A	139	GLU	2.8
1	A	295	PHE	2.4
2	B	381	ASP	2.1

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.