



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 6BFK
Title : Caspase-3 Mutant- T245A
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Deposited on : 2017-10-26
Resolution : 1.75 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
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
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)	:	2.37.1

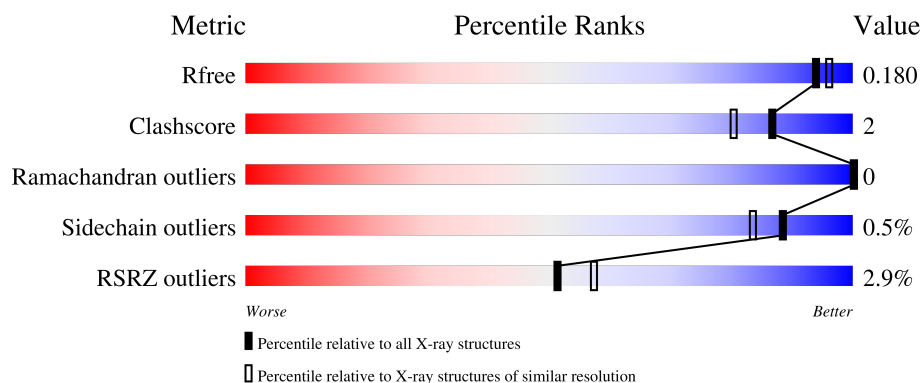
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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	175	<div> <div>3%</div> <div>79%</div> <div>18%</div> </div>
1	B	175	<div> <div>3%</div> <div>78%</div> <div>18%</div> </div>
2	C	103	<div> <div>2%</div> <div>84%</div> <div>7%</div> <div>9%</div> </div>
2	D	103	<div> <div>%</div> <div>86%</div> <div>10%</div> </div>
3	E	6	<div> <div>33%</div> <div>50%</div> <div>17%</div> </div>

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Mol	Chain	Length	Quality of chain
3	F	6	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4530 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-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	143	Total	C	N	O	S	0	7	0
			1168	723	211	223	11			
1	B	143	Total	C	N	O	S	0	7	0
			1174	723	212	228	11			

- Molecule 2 is a protein called Caspase-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	94	Total	C	N	O	S	0	2	0
			793	523	127	137	6			
2	D	93	Total	C	N	O	S	0	1	0
			783	515	126	136	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	245	ALA	THR	engineered mutation	UNP P42574
C	278	HIS	-	expression tag	UNP P42574
D	245	ALA	THR	engineered mutation	UNP P42574
D	278	HIS	-	expression tag	UNP P42574

- Molecule 3 is a protein called AC-ASP-GLU-VAL-ASP-CMK.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	F	6	Total	C	N	O	0	0	1
			36	21	4	11			
3	E	6	Total	C	N	O	0	0	1
			36	21	4	11			

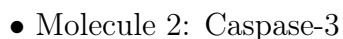
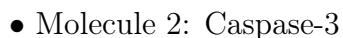
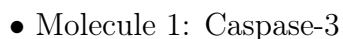
- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

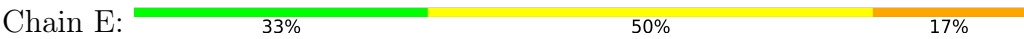
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	2	Total Na 2 2	0	0
4	C	1	Total Na 1 1	0	0
4	B	1	Total Na 1 1	0	0
4	D	1	Total Na 1 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	172	Total O 172 172	0	0
5	C	81	Total O 81 81	0	0
5	B	186	Total O 186 186	0	0
5	D	77	Total O 77 77	0	0
5	F	10	Total O 10 10	0	0
5	E	9	Total O 9 9	0	0

- Molecule 1: Caspase-3





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	128.72Å 69.00Å 85.38Å 90.00° 131.16° 90.00°	Depositor
Resolution (Å)	36.04 – 1.75 36.04 – 1.75	Depositor EDS
% Data completeness (in resolution range)	99.5 (36.04-1.75) 98.4 (36.04-1.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 1.75Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.153 , 0.180 0.153 , 0.180	Depositor DCC
R_{free} test set	2014 reflections (3.58%)	wwPDB-VP
Wilson B-factor (Å ²)	20.8	Xtriage
Anisotropy	0.220	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 36.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.469 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	4530	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.08% 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: ACE, NA, OQE

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	0/1192	0.53	0/1594
1	B	0.40	0/1192	0.53	0/1595
2	C	0.41	0/821	0.55	0/1109
2	D	0.43	0/808	0.55	0/1090
3	E	2.06	1/32 (3.1%)	1.96	1/43 (2.3%)
3	F	1.84	0/32	1.79	1/43 (2.3%)
All	All	0.47	1/4077 (0.0%)	0.58	2/5474 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	E	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	3	GLU	CD-OE1	-5.55	1.19	1.25

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	1	ACE	O-C-N	8.25	135.90	122.70
3	E	4	VAL	O-C-N	-7.17	111.23	122.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	E	4	VAL	Mainchain

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	1168	0	1165	4	0
1	B	1174	0	1157	6	0
2	C	793	0	773	6	0
2	D	783	0	760	3	0
3	E	36	0	26	3	0
3	F	36	0	26	2	0
4	A	2	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	172	0	0	0	0
5	B	186	0	0	2	0
5	C	81	0	0	1	0
5	D	77	0	0	0	0
5	E	9	0	0	0	0
5	F	10	0	0	0	0
All	All	4530	0	3907	17	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 2.

The worst 5 of 17 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:163:CYS:SG	3:E:5:ASP:O	1.98	1.20
1:A:163:CYS:SG	3:F:6:0QE:C1	2.58	0.91
1:A:163:CYS:SG	3:F:5:ASP:C	2.50	0.90
1:B:163:CYS:SG	3:E:5:ASP:C	2.60	0.80
1:B:80:ASN:OD1	5:B:401:HOH:O	2.10	0.69

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	148/175 (85%)	147 (99%)	1 (1%)	0	100	100
1	B	148/175 (85%)	146 (99%)	2 (1%)	0	100	100
2	C	94/103 (91%)	93 (99%)	1 (1%)	0	100	100
2	D	92/103 (89%)	91 (99%)	1 (1%)	0	100	100
3	E	3/6 (50%)	3 (100%)	0	0	100	100
3	F	3/6 (50%)	3 (100%)	0	0	100	100
All	All	488/568 (86%)	483 (99%)	5 (1%)	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	132/159 (83%)	132 (100%)	0	100	100
1	B	133/159 (84%)	131 (98%)	2 (2%)	65	49
2	C	84/90 (93%)	84 (100%)	0	100	100
2	D	83/90 (92%)	81 (98%)	2 (2%)	49	26
3	E	4/4 (100%)	4 (100%)	0	100	100
3	F	4/4 (100%)	4 (100%)	0	100	100
All	All	440/506 (87%)	436 (99%)	4 (1%)	88	67

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	127[A]	ILE
1	B	127[B]	ILE
2	D	268[A]	MET
2	D	268[B]	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	80	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](#)

Of 5 ligands modelled in this entry, 5 are 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 ⓘ

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, 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	143/175 (81%)	-0.45	6 (4%) 36 42	16, 21, 35, 49	1 (0%)
1	B	143/175 (81%)	-0.37	5 (3%) 44 50	16, 21, 38, 52	1 (0%)
2	C	94/103 (91%)	-0.45	2 (2%) 63 71	15, 19, 36, 72	0
2	D	93/103 (90%)	-0.48	1 (1%) 80 86	15, 19, 34, 72	0
3	E	4/6 (66%)	-0.43	0 100 100	16, 20, 22, 26	0
3	F	4/6 (66%)	-0.28	0 100 100	16, 20, 22, 26	0
All	All	481/568 (84%)	-0.43	14 (2%) 51 57	15, 20, 38, 72	2 (0%)

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	170	CYS	6.2
2	D	278	HIS	6.0
1	A	170	CYS	5.0
1	B	33	LEU	4.7
1	B	171	GLY	3.3

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

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(Å ²)	Q<0.9
4	NA	B	301	1/1	0.98	0.04	23,23,23,23	0
4	NA	A	202	1/1	0.99	0.05	25,25,25,25	0
4	NA	C	301	1/1	0.99	0.04	25,25,25,25	0
4	NA	A	201	1/1	0.99	0.03	22,22,22,22	0
4	NA	D	301	1/1	0.99	0.04	25,25,25,25	0

6.5 Other polymers

There are no such residues in this entry.