



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 09:59 PM GMT

PDB ID : 1RHQ
Title : CRYSTAL STRUCTURE OF THE COMPLEX OF CASPASE-3 WITH A BROMOMETHOXYPHENYL INHIBITOR
Authors : Becker, J.W.; Rotonda, J.; Soisson, S.M.
Deposited on : 2003-11-14
Resolution : 3.00 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

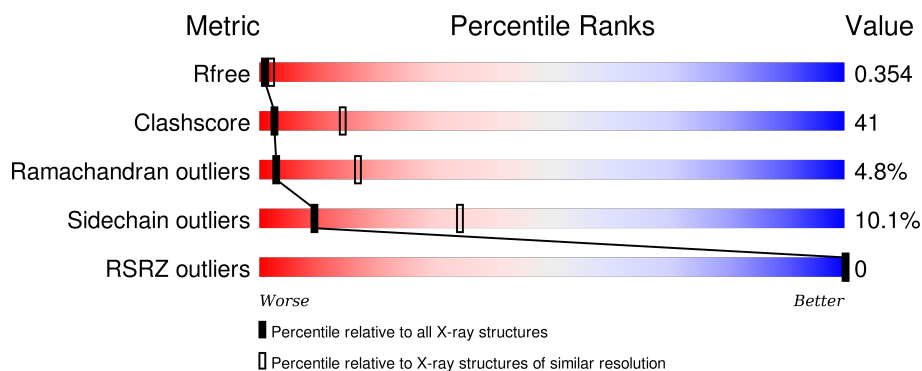
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	91344	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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. 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	147	
1	D	147	
2	B	102	
2	E	102	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3812 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	140	Total	C	N	O	S	0	0	0
			1113	688	201	215	9			
1	D	140	Total	C	N	O	S	0	0	0
			1113	688	201	215	9			

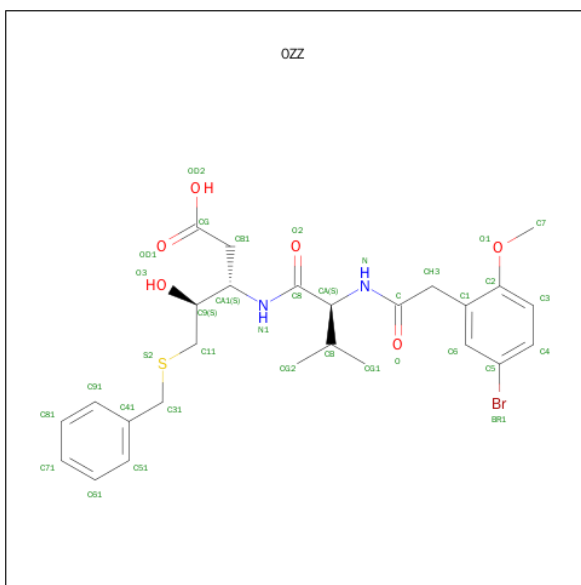
- Molecule 2 is a protein called Caspase-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	91	Total	C	N	O	S	0	0	0
			757	499	119	134	5			
2	E	91	Total	C	N	O	S	0	0	0
			757	499	119	134	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	324	GLU	ASP	ISOFORM BETA	UNP P42574
E	324	GLU	ASP	ISOFORM BETA	UNP P42574

- Molecule 3 is 5-S-BENZYL-3-({N-[(5-BROMO-2-METHOXYPHENYL)ACETYL]-L-VALYL}AMINO)-2,3-DIDEOXY-5-THIO-D-ERYTHRO-PENTONIC ACID (three-letter code: 0ZZ) (formula: C₂₆H₃₃BrN₂O₆S).

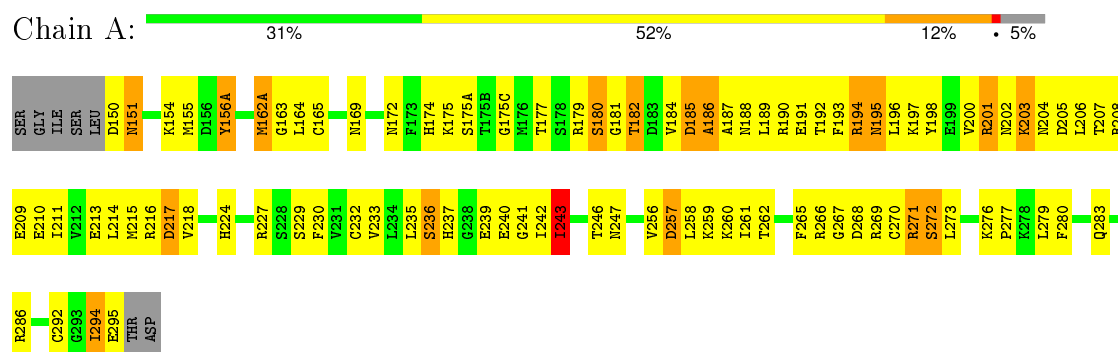


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total 36	Br 1	C 26	N 2	O 6	S 1	0	0
3	D	1	Total 36	Br 1	C 26	N 2	O 6	S 1	0	0

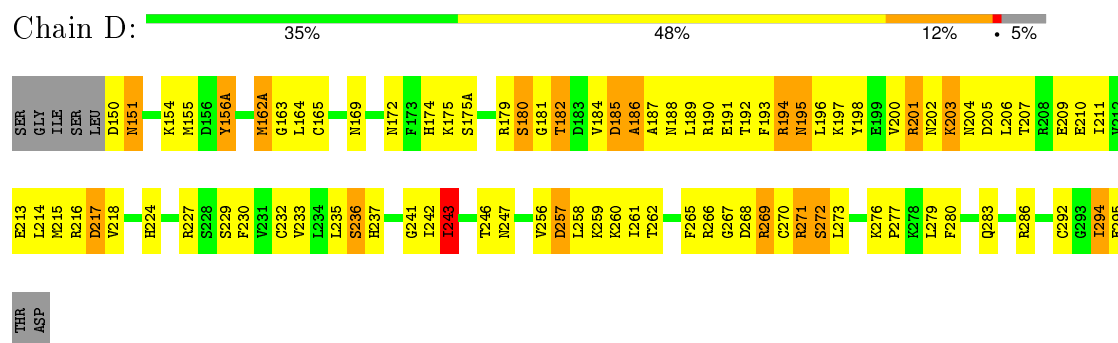
3 Residue-property plots

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.

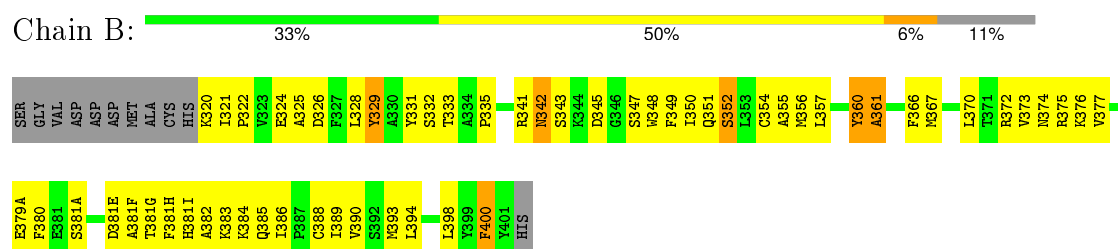
• Molecule 1: Caspase-3



• Molecule 1: Caspase-3



• Molecule 2: Caspase-3



• Molecule 2: Caspase-3



E379A	SER
F380	GLY
E381	VAL
S381A	ASP
D381E	ASP
A381F	MET
F381G	ALA
F381H	CYS
H381I	HIS
A382	K320
K383	L321
K384	P322
Q385	G323
I386	E324
F387	A325
C388	D326
I389	F327
V390	L328
S392	G329
M393	A330
L394	V331
L398	S332
F399	T333
F400	A334
Y401	P335
HIS	R341
	N342
	S343
	K344
	D345
	G346
	S347
	K348
	F349
	L350
	Q351
	S352
	L353
	C354
	A355
	K356
	L357
	V360
	A361
	F366
	K367
	L370
	T371
	K372
	V373
	K374
	K375
	K376
	V377

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	110.30Å 96.90Å 70.90Å 90.00° 128.06° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00 20.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	84.4 (20.00-3.00) 77.3 (20.00-3.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.12 (at 2.98Å)	Xtriage
Refinement program	CNX 2002	Depositor
R, R_{free}	0.273 , 0.354 0.270 , 0.354	Depositor DCC
R_{free} test set	1178 reflections (13.17%)	DCC
Wilson B-factor (Å ²)	21.2	Xtriage
Anisotropy	0.419	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.19 , -26.6	EDS
Estimated twinning fraction	0.268 for -h-2*k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Outliers	0 of 11439 reflections	Xtriage
F_o, F_c correlation	0.78	EDS
Total number of atoms	3812	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.76% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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:
0ZZ

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	0.44	0/1128	0.77	0/1510
1	D	0.45	0/1128	0.77	0/1510
2	B	0.49	0/780	0.75	1/1053 (0.1%)
2	E	0.49	0/780	0.75	1/1053 (0.1%)
All	All	0.47	0/3816	0.76	2/5126 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	360	TYR	N-CA-C	5.16	124.94	111.00
2	B	360	TYR	N-CA-C	5.15	124.91	111.00

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	1113	0	1106	111	4
1	D	1113	0	1106	111	3
2	B	757	0	740	59	0
2	E	757	0	740	61	3
3	A	36	0	31	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	36	0	31	3	0
All	All	3812	0	3754	313	7

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 41.

The worst 5 of 313 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:243:ILE:HG23	1:A:256:VAL:HG13	1.41	1.00
1:D:243:ILE:HG23	1:D:256:VAL:HG13	1.41	0.98
1:A:294:ILE:HG13	1:A:295:GLU:H	1.37	0.90
1:D:294:ILE:HG13	1:D:295:GLU:H	1.37	0.88
1:A:279:LEU:HD22	2:B:328:LEU:HD23	1.55	0.88

The worst 5 of 7 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)
1:A:239:GLU:OE2	1:A:239:GLU:OE2[2_758]	0.72	1.48
1:D:174:HIS:NE2	2:E:381(E):ASP:OD1[2_758]	1.49	0.71
1:A:175(C):GLY:O	1:A:175(C):GLY:O[2_758]	1.54	0.66
1:A:175(C):GLY:CA	1:A:177:THR:CG2[2_758]	1.83	0.37
1:A:239:GLU:CD	1:A:239:GLU:OE2[2_758]	1.92	0.28

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	138/147 (94%)	104 (75%)	26 (19%)	8 (6%)	2	12
1	D	138/147 (94%)	104 (75%)	26 (19%)	8 (6%)	2	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	89/102 (87%)	71 (80%)	15 (17%)	3 (3%)	5	25
2	E	89/102 (87%)	71 (80%)	15 (17%)	3 (3%)	5	25
All	All	454/498 (91%)	350 (77%)	82 (18%)	22 (5%)	3	17

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	185	ASP
1	A	267	GLY
1	D	185	ASP
1	D	267	GLY
1	A	186	ALA

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	126/132 (96%)	110 (87%)	16 (13%)	5	23
1	D	126/132 (96%)	110 (87%)	16 (13%)	5	23
2	B	81/90 (90%)	76 (94%)	5 (6%)	23	60
2	E	81/90 (90%)	76 (94%)	5 (6%)	23	60
All	All	414/444 (93%)	372 (90%)	42 (10%)	9	34

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	352	SER
1	D	156(A)	TYR
2	E	342	ASN
2	B	379(A)	GLU
1	D	150	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	359	GLN
1	D	195	ASN
1	D	263	ASN
2	B	342	ASN
1	D	204	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	0ZZ	A	551	1	33,37,37	1.14	2 (6%)	43,49,49	1.15	4 (9%)
3	0ZZ	D	551	1	33,37,37	1.14	2 (6%)	43,49,49	1.16	4 (9%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	0ZZ	A	551	1	-	0/34/36/36	0/2/2/2
3	0ZZ	D	551	1	-	0/34/36/36	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	551	0ZZ	C31-S2	-2.58	1.77	1.82
3	D	551	0ZZ	C31-S2	-2.55	1.77	1.82
3	D	551	0ZZ	O1-C2	4.83	1.44	1.37
3	A	551	0ZZ	O1-C2	4.85	1.44	1.37

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	551	0ZZ	O1-C2-C3	-2.71	119.80	124.35
3	D	551	0ZZ	O1-C2-C3	-2.71	119.80	124.35
3	A	551	0ZZ	C4-C5-C6	-2.07	118.30	121.44
3	D	551	0ZZ	C4-C5-C6	-2.07	118.30	121.44
3	D	551	0ZZ	C7-O1-C2	2.60	121.49	117.54

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	551	0ZZ	3	0
3	D	551	0ZZ	3	0

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, 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	140/147 (95%)	-0.56	0 100 100	7, 13, 39, 46	0
1	D	140/147 (95%)	-0.62	0 100 100	7, 13, 39, 46	0
2	B	91/102 (89%)	-0.66	0 100 100	7, 9, 35, 42	0
2	E	91/102 (89%)	-0.63	0 100 100	7, 9, 35, 42	0
All	All	462/498 (92%)	-0.61	0 100 100	7, 12, 37, 46	0

There are no RSRZ outliers to report.

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	0ZZ	D	551	36/36	0.94	0.16	0.28	7,15,24,24	0
3	0ZZ	A	551	36/36	0.94	0.16	-0.43	7,15,24,24	0

6.5 Other polymers

There are no such residues in this entry.