



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 07:54 AM GMT

PDB ID : 3CKP  
Title : Crystal structure of BACE-1 in complex with inhibitor  
Authors : Min, K.  
Deposited on : 2008-03-16  
Resolution : 2.30 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](mailto: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.

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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  
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

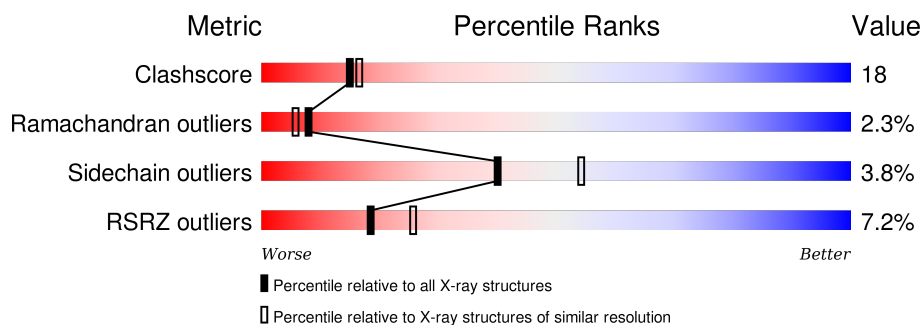
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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  $\geq 3$ , 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	412	<div> <div>4%</div> <div>63% 28% 8%</div> </div>
1	B	412	<div> <div>7%</div> <div>62% 27% 9%</div> </div>
1	C	412	<div> <div>8%</div> <div>47% 40% 8%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9210 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 Beta-secretase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	379	Total	C	N	O	S	0	0	0
			2974	1904	496	560	14			
1	B	376	Total	C	N	O	S	0	0	0
			2956	1894	492	556	14			
1	C	377	Total	C	N	O	S	0	0	0
			2967	1900	494	559	14			

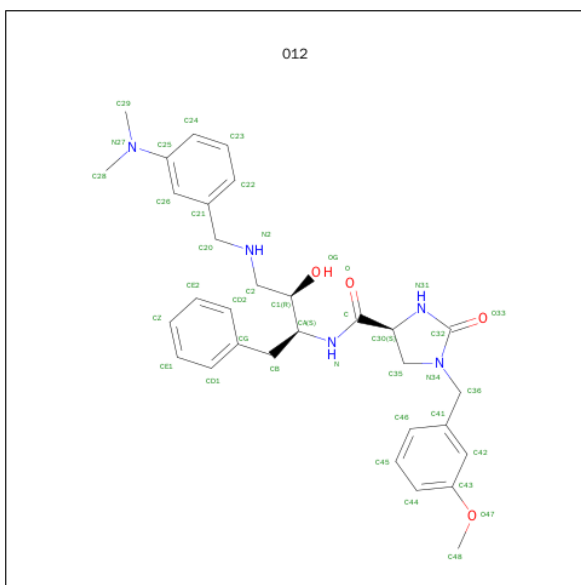
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	LYS	ARG	ENGINEERED	UNP P56817
A	-5	LYS	ARG	ENGINEERED	UNP P56817
B	-6	LYS	ARG	ENGINEERED	UNP P56817
B	-5	LYS	ARG	ENGINEERED	UNP P56817
C	-6	LYS	ARG	ENGINEERED	UNP P56817
C	-5	LYS	ARG	ENGINEERED	UNP P56817

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Cl	0	0
			2	2		
2	A	5	Total	Cl	0	0
			5	5		
2	C	2	Total	Cl	0	0
			2	2		

- Molecule 3 is (4S)-N-[(1S,2R)-1-BENZYL-3-{[3-(DIMETHYLAMINO)BENZYL]AMINO}-2-HYDROXYPROPYL]-1-(3-METHOXYBENZYL)-2-OXOIMIDAZOLIDINE-4-CARBOX AMIDE (three-letter code: 012) (formula: C<sub>31</sub>H<sub>39</sub>N<sub>5</sub>O<sub>4</sub>).



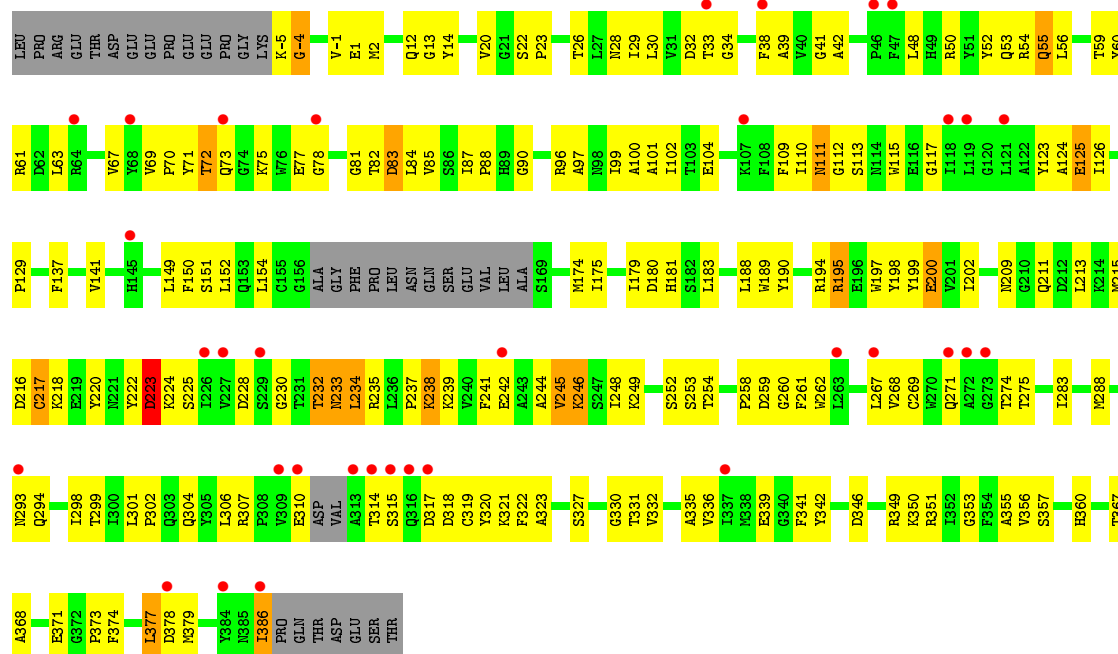
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 40	C 31	N 5	O 4	0	0
3	B	1	Total 40	C 31	N 5	O 4	0	0
3	C	1	Total 40	C 31	N 5	O 4	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	81	Total O 81 81	0	0
4	B	64	Total O 64 64	0	0
4	C	39	Total O 39 39	0	0



• Molecule 1: Beta-secretase 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	224.06 Å   105.65 Å   63.70 Å 90.00°   101.47°   90.00°	Depositor
Resolution (Å)	19.97 – 2.30 29.98 – 2.30	Depositor EDS
% Data completeness (in resolution range)	87.3 (19.97-2.30) 87.2 (29.98-2.30)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.06 (at 2.29 Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.245   ,   0.304 0.258   ,   (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	31.3	Xtriage
Anisotropy	0.689	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 41.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 61353 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	9210	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.04% 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, 0.375 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: 012, 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	0.46	0/3048	0.72	2/4138 (0.0%)
1	B	0.43	0/3031	0.71	1/4119 (0.0%)
1	C	0.43	0/3041	0.70	2/4129 (0.0%)
All	All	0.44	0/9120	0.71	5/12386 (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
1	C	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	223	ASP	N-CA-C	-6.58	93.24	111.00
1	B	198	TYR	N-CA-C	-5.77	95.43	111.00
1	C	198	TYR	N-CA-C	-5.65	95.74	111.00
1	A	198	TYR	N-CA-C	-5.64	95.78	111.00
1	A	342	TYR	N-CA-C	-5.42	96.36	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	52	TYR	Sidechain



## 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	2974	0	2889	85	0
1	B	2956	0	2865	99	0
1	C	2967	0	2886	134	0
2	A	5	0	0	1	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
3	A	40	0	39	5	0
3	B	40	0	39	1	0
3	C	40	0	39	6	0
4	A	81	0	0	3	0
4	B	64	0	0	2	0
4	C	39	0	0	2	0
All	All	9210	0	8757	313	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 18.

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:B:53:GLN:HB3	1:B:55:GLN:HE22	1.27	0.96
1:C:55:GLN:HE21	1:C:55:GLN:H	1.11	0.95
1:B:234:LEU:HB2	1:B:336:VAL:HG21	1.47	0.94
1:C:55:GLN:HG2	1:C:56:LEU:HD12	1.53	0.91
1:A:4:ASP:H	1:A:173:SER:HB3	1.39	0.88

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	373/412 (90%)	341 (91%)	27 (7%)	5 (1%)	15	15
1	B	372/412 (90%)	329 (88%)	35 (9%)	8 (2%)	8	6
1	C	371/412 (90%)	324 (87%)	34 (9%)	13 (4%)	4	2
All	All	1116/1236 (90%)	994 (89%)	96 (9%)	26 (2%)	8	6

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	223	ASP
1	B	223	ASP
1	C	125	GLU
1	C	223	ASP
1	C	233	ASN

### 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	321/353 (91%)	309 (96%)	12 (4%)	41	55
1	B	319/353 (90%)	310 (97%)	9 (3%)	51	68
1	C	322/353 (91%)	306 (95%)	16 (5%)	30	41
All	All	962/1059 (91%)	925 (96%)	37 (4%)	40	54

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	197	TRP
1	B	386	ILE
1	C	377	LEU
1	B	234	LEU
1	B	257	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	304	GLN
1	B	316	GLN
1	C	211	GLN
1	B	92	ASN
1	B	111	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](#)

Of 12 ligands modelled in this entry, 9 are monoatomic - leaving 3 for Mogul analysis.

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	012	A	501	-	42,43,43	1.42	4 (9%)	52,58,58	2.05	7 (13%)
3	012	B	502	-	42,43,43	1.41	3 (7%)	52,58,58	2.17	6 (11%)
3	012	C	503	-	42,43,43	1.52	7 (16%)	52,58,58	2.06	6 (11%)

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	012	A	501	-	-	0/32/44/44	0/4/4/4
3	012	B	502	-	-	0/32/44/44	0/4/4/4
3	012	C	503	-	-	0/32/44/44	0/4/4/4

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	503	012	CD1-CG	2.01	1.43	1.38
3	C	503	012	C42-C41	2.04	1.42	1.39
3	C	503	012	C44-C43	2.05	1.42	1.38
3	C	503	012	C24-C25	2.07	1.43	1.39
3	A	501	012	C44-C43	2.13	1.42	1.38

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	502	012	C35-N34-C32	-11.31	98.98	111.67
3	C	503	012	C35-N34-C32	-10.03	100.41	111.67
3	A	501	012	C35-N34-C32	-9.89	100.56	111.67
3	A	501	012	O33-C32-N31	-3.44	119.94	126.77
3	C	503	012	O33-C32-N31	-3.40	120.03	126.77

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	012	5	0
3	B	502	012	1	0
3	C	503	012	6	0

## 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 [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	379/412 (91%)	0.28	18 (4%) 35 44	18, 35, 61, 91	0
1	B	376/412 (91%)	0.51	29 (7%) 16 23	22, 40, 68, 89	0
1	C	377/412 (91%)	0.66	34 (9%) 12 17	25, 50, 74, 105	0
All	All	1132/1236 (91%)	0.48	81 (7%) 18 26	18, 41, 69, 105	0

The worst 5 of 81 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	311	ASP	5.8
1	B	312	VAL	5.3
1	B	145	HIS	4.3
1	A	168	ALA	4.3
1	B	113	SER	4.2

### 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, 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	CL	A	605	1/1	0.98	0.21	1.15	32,32,32,32	0
3	012	B	502	40/40	0.91	0.19	0.27	36,43,50,50	0
2	CL	A	603	1/1	0.99	0.16	0.26	21,21,21,21	0
3	012	A	501	40/40	0.93	0.15	0.06	30,37,45,45	0
3	012	C	503	40/40	0.91	0.19	-0.04	40,45,58,58	0
2	CL	B	602	1/1	0.97	0.18	-0.79	23,23,23,23	0
2	CL	A	607	1/1	0.98	0.09	-2.00	34,34,34,34	0
2	CL	C	609	1/1	0.96	0.06	-3.08	43,43,43,43	0
2	CL	A	608	1/1	0.96	0.08	-3.16	39,39,39,39	0
2	CL	A	601	1/1	0.98	0.27	-	12,12,12,12	0
2	CL	B	606	1/1	0.98	0.08	-	36,36,36,36	0
2	CL	C	604	1/1	0.98	0.18	-	32,32,32,32	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.