



wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 3, 2016 – 07:28 AM EDT

PDB ID : 5DQC
Title : Co-crystal of BACE1 with compound 0211
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Deposited on : 2015-09-14
Resolution : 2.47 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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027790
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) : rb-20027790

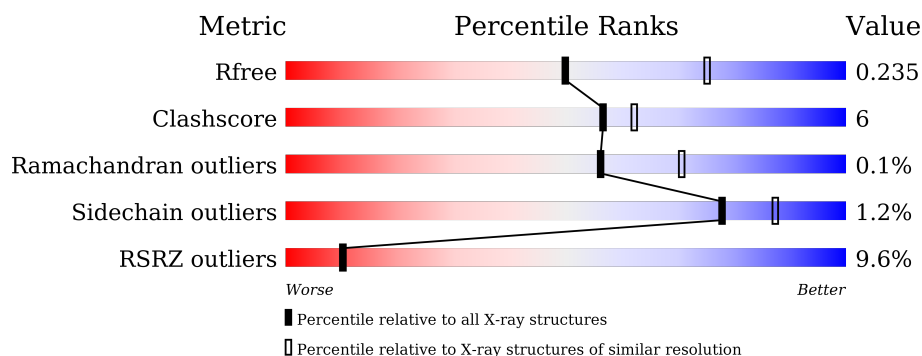
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.47 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	4776 (2.50-2.42)
Clashscore	102246	1030 (2.48-2.44)
Ramachandran outliers	100387	1024 (2.48-2.44)
Sidechain outliers	100360	1024 (2.48-2.44)
RSRZ outliers	91569	4787 (2.50-2.42)

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	390	<div> <div>6%</div> <div> <div></div> <div>83%</div> <div>12%</div> <div>• 5%</div> </div> </div>
1	B	390	<div> <div>14%</div> <div> <div></div> <div>79%</div> <div>14%</div> <div>• 5%</div> </div> </div>
1	C	390	<div> <div>7%</div> <div> <div></div> <div>85%</div> <div>11%</div> <div>•</div> </div> </div>

2 Entry composition [i](#)

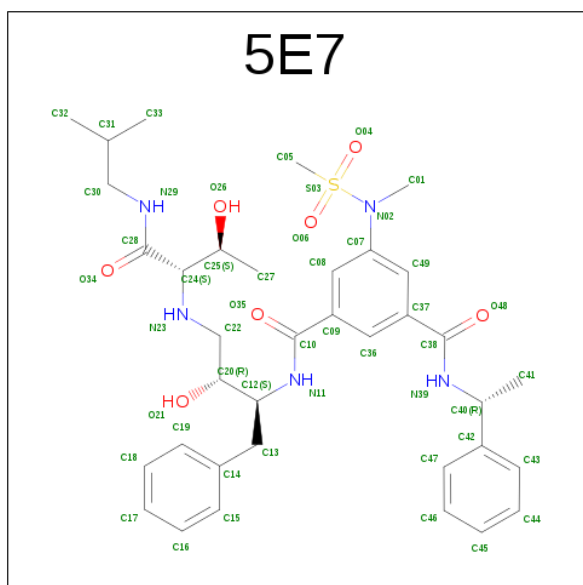
There are 3 unique types of molecules in this entry. The entry contains 9054 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	372	Total	C	N	O	S	2	0	0
			2929	1877	488	550	14			
1	B	369	Total	C	N	O	S	10	0	0
			2910	1868	484	544	14			
1	C	373	Total	C	N	O	S	4	0	0
			2940	1882	489	555	14			

- Molecule 2 is N-[(2S,3R)-3-hydroxy-4-({(2S,3S)-3-hydroxy-1-[(2-methylpropyl)amino]-1-oxobutan-2-yl}amino)-1-phenylbutan-2-yl]-5-[methyl(methylsulfonyl)amino]-N'-[(1R)-1-phenylethyl]benzene-1,3-dicarboxamide (three-letter code: 5E7) (formula: C₃₆H₄₉N₅O₇S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			49	36	5	7	1		
2	B	1	Total	C	N	O	S	0	0
			49	36	5	7	1		

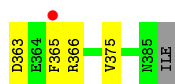
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	S	0	0
			49	36	5	7	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	47	Total	O	0	0
			47	47		
3	B	35	Total	O	0	0
			35	35		
3	C	46	Total	O	0	0
			46	46		



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	81.95Å 103.40Å 100.83Å 90.00° 102.66° 90.00°	Depositor
Resolution (Å)	45.77 – 2.47 45.77 – 2.47	Depositor EDS
% Data completeness (in resolution range)	89.3 (45.77-2.47) 84.3 (45.77-2.47)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 2.45Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.185 , 0.235 0.185 , 0.235	Depositor DCC
R_{free} test set	1894 reflections (3.79%)	DCC
Wilson B-factor (Å ²)	53.9	Xtriage
Anisotropy	0.050	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 51.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9054	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.23% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 5E7

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	0.28	0/3003	0.48	1/4079 (0.0%)
1	B	0.30	1/2984 (0.0%)	0.52	1/4053 (0.0%)
1	C	0.29	0/3014	0.49	0/4093
All	All	0.29	1/9001 (0.0%)	0.50	2/12225 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	270	TRP	CB-CG	5.29	1.59	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	195	ARG	NE-CZ-NH1	-5.08	117.76	120.30
1	B	267	LEU	CA-CB-CG	5.01	126.82	115.30

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	2929	0	2846	30	0
1	B	2910	0	2835	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2940	0	2849	37	0
2	A	49	0	49	0	0
2	B	49	0	49	4	0
2	C	49	0	49	2	0
3	A	47	0	0	2	1
3	B	35	0	0	1	0
3	C	46	0	0	5	1
All	All	9054	0	8677	108	1

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 6.

The worst 5 of 108 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:C:195:ARG:HB3	1:C:197:TRP:HZ3	1.36	0.91
1:B:59:THR:O	1:B:96:ARG:NH2	2.09	0.86
1:A:134:GLU:OE1	3:A:501:HOH:O	1.95	0.83
1:B:122:ALA:O	3:B:501:HOH:O	2.02	0.77
1:C:169:SER:OG	3:C:501:HOH:O	1.96	0.75

All (1) 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)
3:A:525:HOH:O	3:C:544:HOH:O[2_646]	1.90	0.30

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	366/390 (94%)	360 (98%)	6 (2%)	0	100	100
1	B	363/390 (93%)	346 (95%)	16 (4%)	1 (0%)	46	57
1	C	367/390 (94%)	355 (97%)	12 (3%)	0	100	100
All	All	1096/1170 (94%)	1061 (97%)	34 (3%)	1 (0%)	56	71

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	278	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	317/332 (96%)	312 (98%)	5 (2%)	70	83
1	B	316/332 (95%)	310 (98%)	6 (2%)	65	79
1	C	319/332 (96%)	319 (100%)	0	100	100
All	All	952/996 (96%)	941 (99%)	11 (1%)	78	87

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	325	SER
1	B	58	SER
1	B	263	LEU
1	A	197	TRP
1	B	96	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	266	GLN
1	B	266	GLN

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Mol	Chain	Res	Type
1	B	278	ASN
1	B	360	HIS

5.3.3 RNA ⓘ

There are no RNA molecules 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 ⓘ

3 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$
2	5E7	A	401	-	50,51,51	1.21	5 (10%)	64,71,71	1.89	18 (28%)
2	5E7	B	401	-	50,51,51	1.47	6 (12%)	64,71,71	1.98	17 (26%)
2	5E7	C	401	-	50,51,51	1.37	6 (12%)	64,71,71	1.87	18 (28%)

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
2	5E7	A	401	-	-	0/56/56/56	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	5E7	B	401	-	-	0/56/56/56	0/3/3/3
2	5E7	C	401	-	-	0/56/56/56	0/3/3/3

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	5E7	C10-N11	2.25	1.39	1.34
2	C	401	5E7	C10-N11	2.43	1.39	1.34
2	A	401	5E7	C38-N39	2.44	1.39	1.34
2	B	401	5E7	C24-C28	2.55	1.59	1.52
2	A	401	5E7	C20-C12	2.65	1.58	1.54

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	5E7	C49-C37-C36	-3.63	115.27	119.62
2	A	401	5E7	C49-C37-C36	-3.43	115.51	119.62
2	C	401	5E7	C49-C37-C36	-3.43	115.51	119.62
2	C	401	5E7	O04-S03-O06	-3.19	114.28	118.74
2	A	401	5E7	O48-C38-N39	-3.09	116.86	122.45

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
2	B	401	5E7	4	0
2	C	401	5E7	2	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	372/390 (95%)	0.46	24 (6%)	22 24	39, 57, 82, 101	12 (3%)
1	B	369/390 (94%)	0.74	54 (14%)	3 3	38, 62, 100, 115	25 (6%)
1	C	373/390 (95%)	0.49	29 (7%)	16 16	40, 56, 78, 111	15 (4%)
All	All	1114/1170 (95%)	0.56	107 (9%)	10 10	38, 58, 89, 115	52 (4%)

The worst 5 of 107 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	272	ALA	7.1
1	B	386	ILE	5.7
1	B	257	PHE	5.6
1	C	257	PHE	5.4
1	B	273	GLY	5.3

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 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(\AA^2)	Q<0.9
2	5E7	A	401	49/49	0.97	0.21	1.08	40,50,58,66	0
2	5E7	C	401	49/49	0.97	0.21	1.04	36,45,52,54	0
2	5E7	B	401	49/49	0.94	0.22	1.01	46,54,63,66	0

6.5 Other polymers [i](#)

There are no such residues in this entry.