wwPDB X-ray Structure Validation Summary Report (i)

Aug 30, 2023 – 10:04 AM EDT

PDB ID	:	3N4L
Title	:	BACE-1 in complex with ELN380842
Authors	:	Yao, N.H.
Deposited on	:	2010-05-21
Resolution	:	2.70 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 (i) 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 (i)) were used in the production of this report:

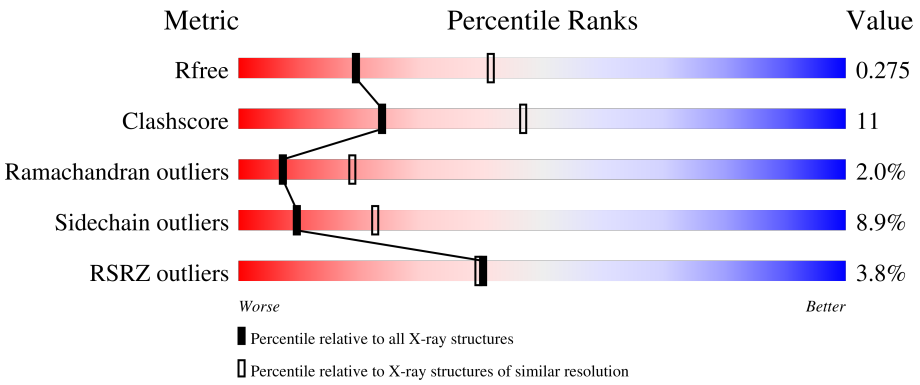
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 <=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	406	3%, 72%, 20%, • 8%
1	B	406	3%, 65%, 23%, • 8%
1	C	406	4%, 60%, 28%, • 8%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 8982 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
			Total	C	N	O	S			
1	A	375	2953	1892	490	557	14	0	0	0
1	B	375	2942	1887	490	551	14	0	0	0
1	C	375	2947	1887	490	556	14	0	0	0

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P56817
A	399	ARG	-	expression tag	UNP P56817
A	400	SER	-	expression tag	UNP P56817
A	401	HIS	-	expression tag	UNP P56817
A	402	HIS	-	expression tag	UNP P56817
A	403	HIS	-	expression tag	UNP P56817
A	404	HIS	-	expression tag	UNP P56817
A	405	HIS	-	expression tag	UNP P56817
A	406	HIS	-	expression tag	UNP P56817
B	1	MET	-	initiating methionine	UNP P56817
B	399	ARG	-	expression tag	UNP P56817
B	400	SER	-	expression tag	UNP P56817
B	401	HIS	-	expression tag	UNP P56817
B	402	HIS	-	expression tag	UNP P56817
B	403	HIS	-	expression tag	UNP P56817
B	404	HIS	-	expression tag	UNP P56817
B	405	HIS	-	expression tag	UNP P56817
B	406	HIS	-	expression tag	UNP P56817
C	1	MET	-	initiating methionine	UNP P56817
C	399	ARG	-	expression tag	UNP P56817
C	400	SER	-	expression tag	UNP P56817
C	401	HIS	-	expression tag	UNP P56817
C	402	HIS	-	expression tag	UNP P56817

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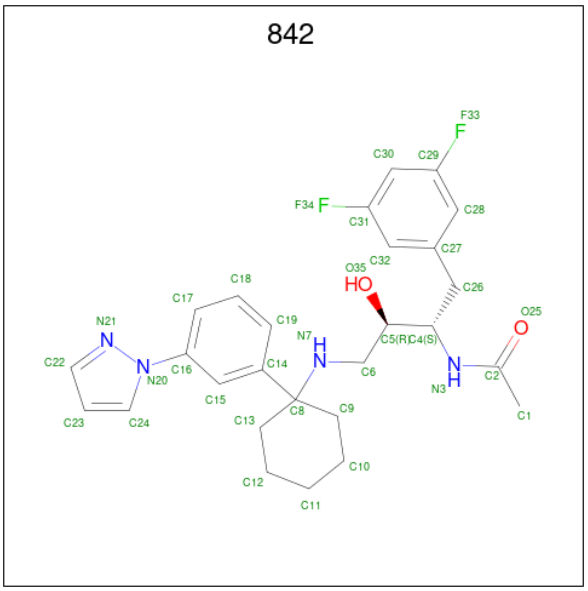
Chain	Residue	Modelled	Actual	Comment	Reference
C	403	HIS	-	expression tag	UNP P56817
C	404	HIS	-	expression tag	UNP P56817
C	405	HIS	-	expression tag	UNP P56817
C	406	HIS	-	expression tag	UNP P56817

- Molecule 2 is N-[(1S,2R)-1-(3,5-difluorobenzyl)-2-hydroxy-3-({1-[3-(1H-pyrazol-1-yl)phenyl]cyclohexyl}amino)propyl]acetamide (three-letter code: 842) (formula: $C_{27}H_{32}F_2N_4O_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	F	N	O		
2	A	1	35	27	2	4	2	0	0
2	B	1	35	27	2	4	2	0	0
2	C	1	35	27	2	4	2	0	0

- Molecule 3 is water.

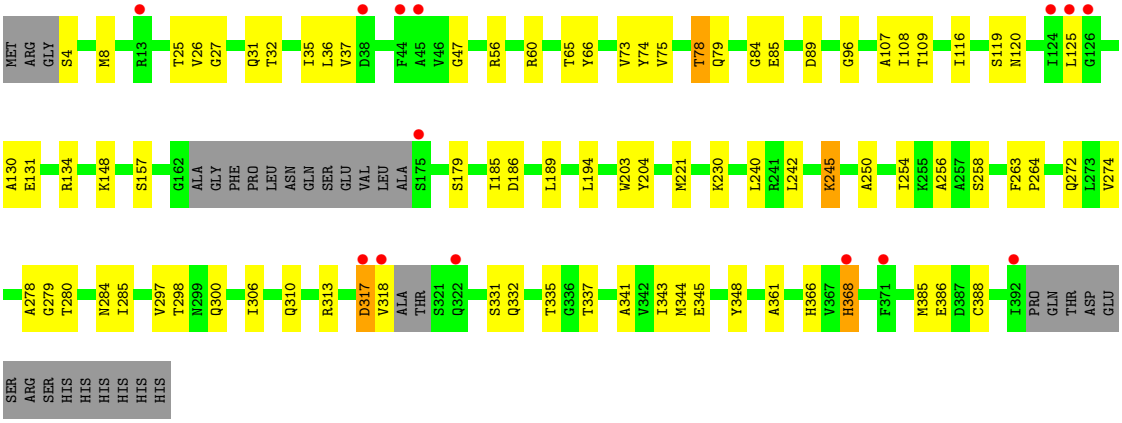
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	12	12	12	0	0
3	B	14	14	14	0	0
3	C	9	9	9	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

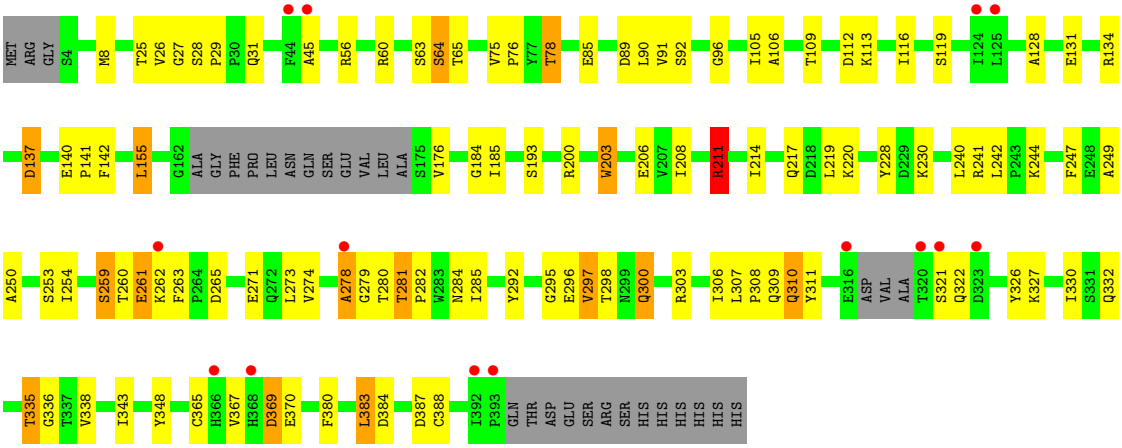
• Molecule 1: Beta-secretase 1

Chain A: 3% 72% 20% • 8%



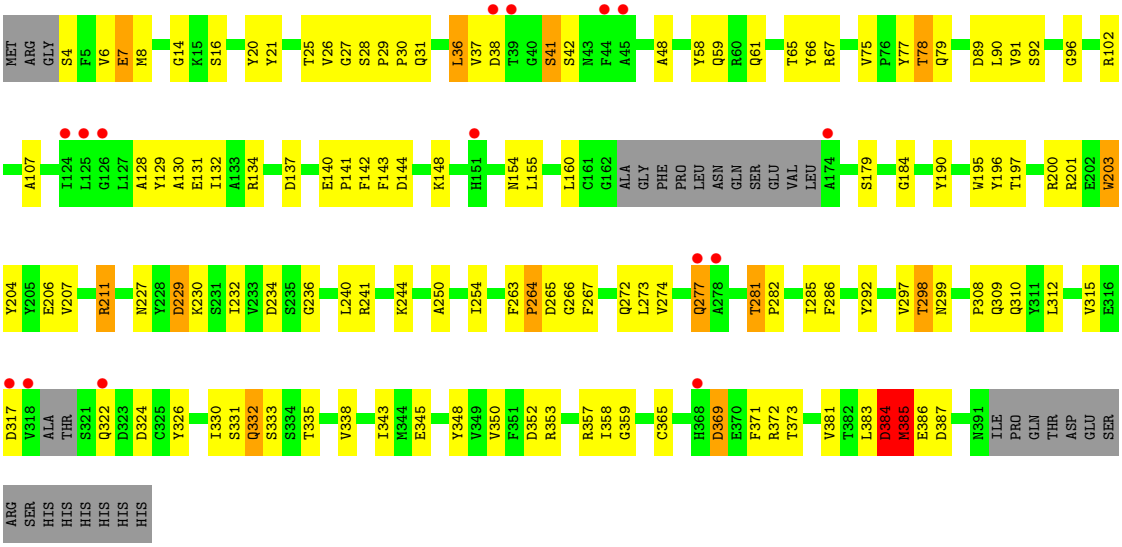
• Molecule 1: Beta-secretase 1

Chain B: 3% 65% 23% • 8%



• Molecule 1: Beta-secretase 1

Chain C: 4% 60% 28% • 8%


MET ARG GLY S4 F5 V6 E7 M8 G14 K15 S16 Y20 Y21 T25 V26 G27 S28 P29 P30 Q31 L36 V37 D38 T39 G40 S41 S42 N43 F44 A45 A48 Y58 Q59 R60 Q61 T65 Y66 R67 V75 P76 Y77 T78 Q79 D89 L90 V91 S92 G96 R102
A107 I124 L125 G126 L127 A128 Y129 A130 E131 I132 A133 R134 D137 E140 P141 F142 F143 D144 K148 H151 N154 L155 L160 C161 G162 ALA GLY PHE PRO LEU ASN GLN SER GLU VAL LEU A174 S179 G184 Y190 W195 Y196 T197 R200 R201 E202 W203
Y204 Y205 E206 V207 R211 N227 Y228 D229 K230 S231 I232 V233 D234 S235 G236 L240 R241 K244 A250 I254 F263 P264 D265 G266 F267 Q272 L273 V274 Q277 A278 T281 P282 I285 F286 Y292 V297 T298 N299 P308 Q309 Q310 Y311 L312 V315 E316
D317 V318 ALA THR S321 Q322 D323 D324 G325 Y326 I330 S331 Q332 S333 S334 T335 V338 I343 M344 E345 Y348 V349 V350 F351 D352 R353 R357 I358 G359 G365 H368 D369 E370 F371 R372 T373 V381 T382 L383 D384 M385 E386 D387 N391 ILE PRO GLN THR ASP GLU SER
ARG SER HIS HIS HIS HIS HIS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	83.05Å 105.58Å 101.58Å 90.00° 104.63° 90.00°	Depositor
Resolution (Å)	28.00 – 2.70 28.24 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.7 (28.00-2.70) 98.8 (28.24-2.70)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.57 (at 2.72Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.223 , 0.283 0.216 , 0.275	Depositor DCC
R_{free} test set	2329 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	74.1	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 35.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	8982	wwPDB-VP
Average B, all atoms (Å^2)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.68% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: 842

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	0.79	0/3027	0.82	1/4112 (0.0%)
1	B	0.80	1/3017 (0.0%)	0.82	1/4100 (0.0%)
1	C	0.79	0/3021	0.85	2/4105 (0.0%)
All	All	0.79	1/9065 (0.0%)	0.83	4/12317 (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	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	388	CYS	CB-SG	-5.36	1.73	1.81

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	385	MET	N-CA-C	-5.97	94.88	111.00
1	B	211	ARG	NE-CZ-NH1	5.15	122.88	120.30
1	A	344	MET	CG-SD-CE	5.12	108.39	100.20
1	C	90	LEU	CA-CB-CG	5.08	126.97	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	384	ASP	Peptide
1	C	385	MET	Peptide

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	2953	0	2862	48	0
1	B	2942	0	2850	67	0
1	C	2947	0	2849	85	0
2	A	35	0	32	3	0
2	B	35	0	32	3	0
2	C	35	0	32	3	0
3	A	12	0	0	0	0
3	B	14	0	0	0	0
3	C	9	0	0	0	0
All	All	8982	0	8657	197	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 11.

The worst 5 of 197 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:297:VAL:O	1:C:298:THR:HG22	1.39	1.18
1:B:211:ARG:HH11	1:B:211:ARG:HB2	1.22	1.03
1:A:317:ASP:HA	1:A:318:VAL:HB	1.50	0.93
1:B:296:GLU:H	1:B:300:GLN:HE21	1.12	0.93
1:C:384:ASP:C	1:C:386:GLU:H	1.69	0.93

There are no symmetry-related clashes.

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	369/406 (91%)	346 (94%)	19 (5%)	4 (1%)	14	34
1	B	369/406 (91%)	323 (88%)	35 (10%)	11 (3%)	4	10
1	C	369/406 (91%)	322 (87%)	40 (11%)	7 (2%)	8	20
All	All	1107/1218 (91%)	991 (90%)	94 (8%)	22 (2%)	7	19

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	370	GLU
1	A	278	ALA
1	A	279	GLY
1	B	64	SER
1	B	128	ALA

5.3.2 Protein sidechains (i)

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	321/348 (92%)	301 (94%)	20 (6%)	18	40
1	B	318/348 (91%)	284 (89%)	34 (11%)	6	15
1	C	319/348 (92%)	288 (90%)	31 (10%)	8	19
All	All	958/1044 (92%)	873 (91%)	85 (9%)	9	22

5 of 85 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	36	LEU
1	C	267	PHE
1	C	78	THR
1	C	179	SER
1	C	281	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	310	GLN
1	C	299	ASN
1	B	284	ASN
1	C	272	GLN
1	B	217	GLN

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)

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	842	C	407	-	33,38,38	0.89	2 (6%)	41,53,53	1.94	12 (29%)
2	842	A	407	-	33,38,38	0.98	1 (3%)	41,53,53	1.53	6 (14%)
2	842	B	407	-	33,38,38	0.88	1 (3%)	41,53,53	1.74	6 (14%)

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	842	C	407	-	-	3/24/38/38	0/4/4/4
2	842	A	407	-	-	2/24/38/38	0/4/4/4
2	842	B	407	-	-	8/24/38/38	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	407	842	C32-C31	2.30	1.41	1.37
2	A	407	842	F34-C31	-2.22	1.31	1.36
2	C	407	842	C28-C29	2.12	1.41	1.37
2	B	407	842	C28-C29	2.08	1.41	1.37

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	407	842	C23-C24-N20	-4.76	103.95	106.78
2	B	407	842	C23-C24-N20	-4.74	103.97	106.78
2	C	407	842	C27-C28-C29	4.73	123.11	118.81
2	B	407	842	C4-N3-C2	4.20	128.89	122.90
2	C	407	842	C18-C17-C16	3.94	123.48	121.25

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	407	842	O35-C5-C6-N7
2	B	407	842	C1-C2-N3-C4
2	B	407	842	C26-C4-C5-O35
2	B	407	842	O25-C2-N3-C4
2	B	407	842	C5-C6-N7-C8

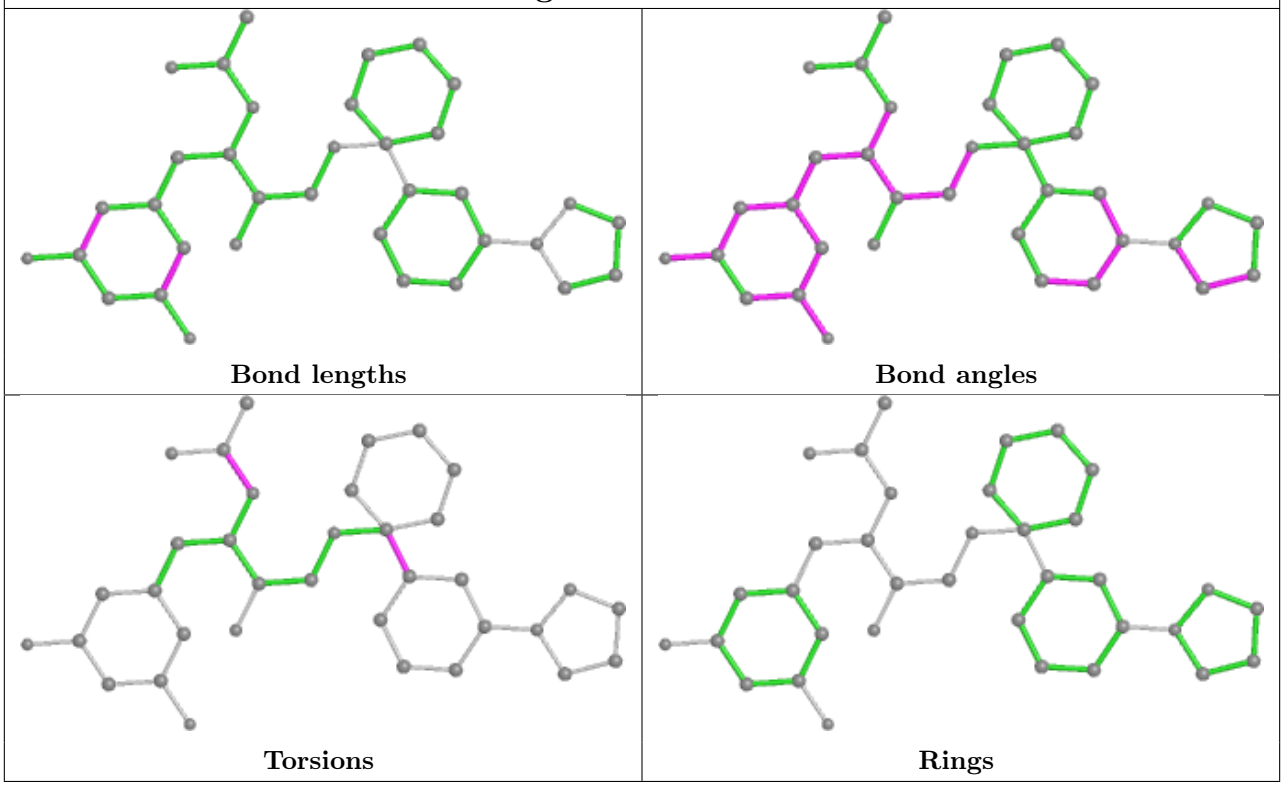
There are no ring outliers.

3 monomers are involved in 9 short contacts:

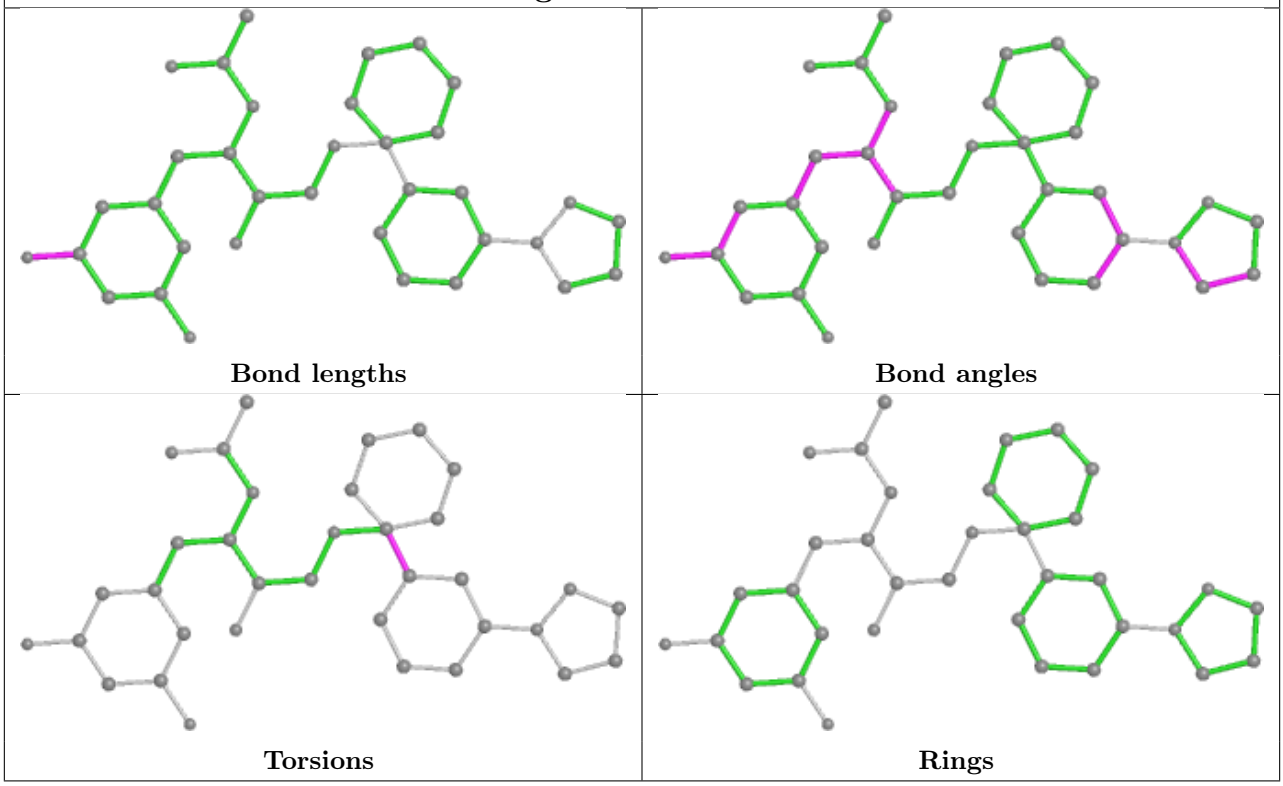
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	407	842	3	0
2	A	407	842	3	0
2	B	407	842	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

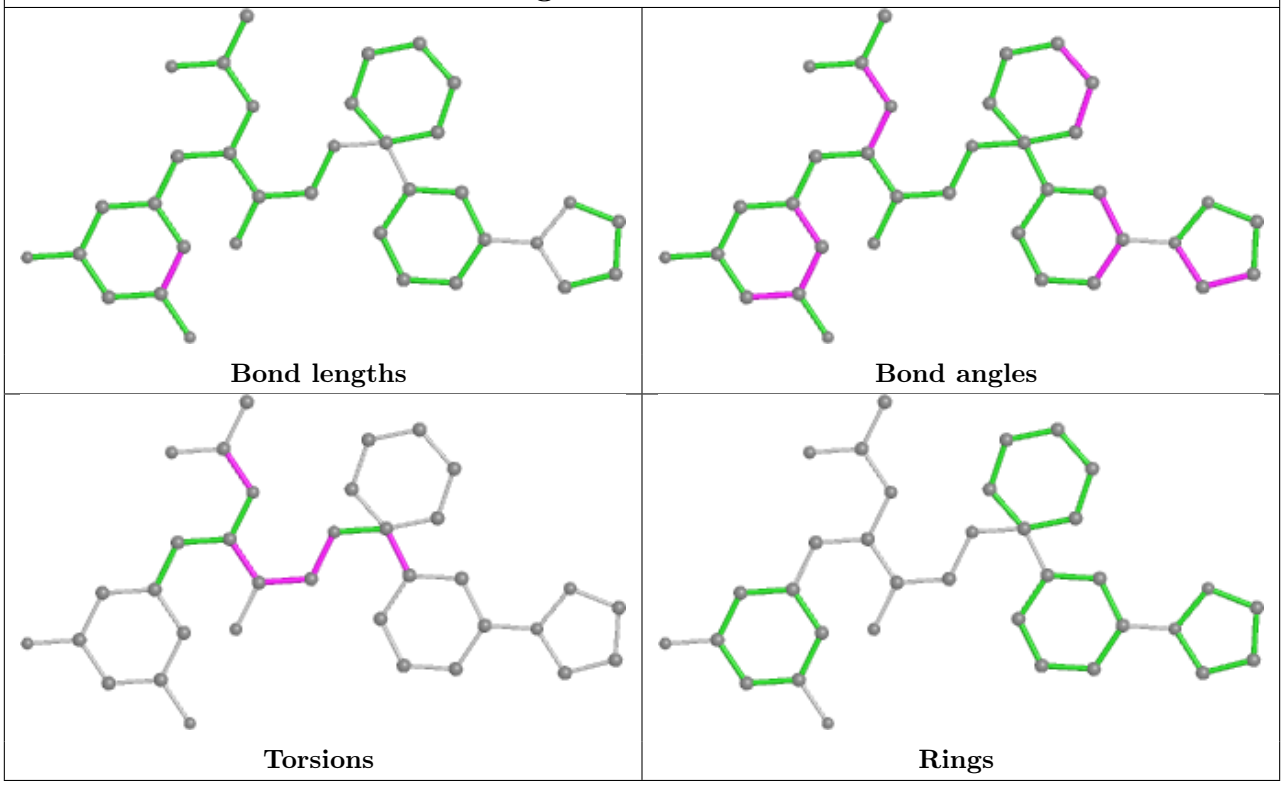
Ligand 842 C 407



Ligand 842 A 407



Ligand 842 B 407



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	375/406 (92%)	0.01	14 (3%)	41	41	43, 66, 99, 111	0
1	B	375/406 (92%)	-0.00	14 (3%)	41	41	44, 67, 99, 114	0
1	C	375/406 (92%)	-0.04	15 (4%)	38	37	45, 66, 99, 112	0
All	All	1125/1218 (92%)	-0.01	43 (3%)	40	39	43, 66, 99, 114	0

The worst 5 of 43 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	393	PRO	5.7
1	C	318	VAL	5.5
1	A	175	SER	4.2
1	A	392	ILE	4.1
1	A	125	LEU	4.1

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 (i)

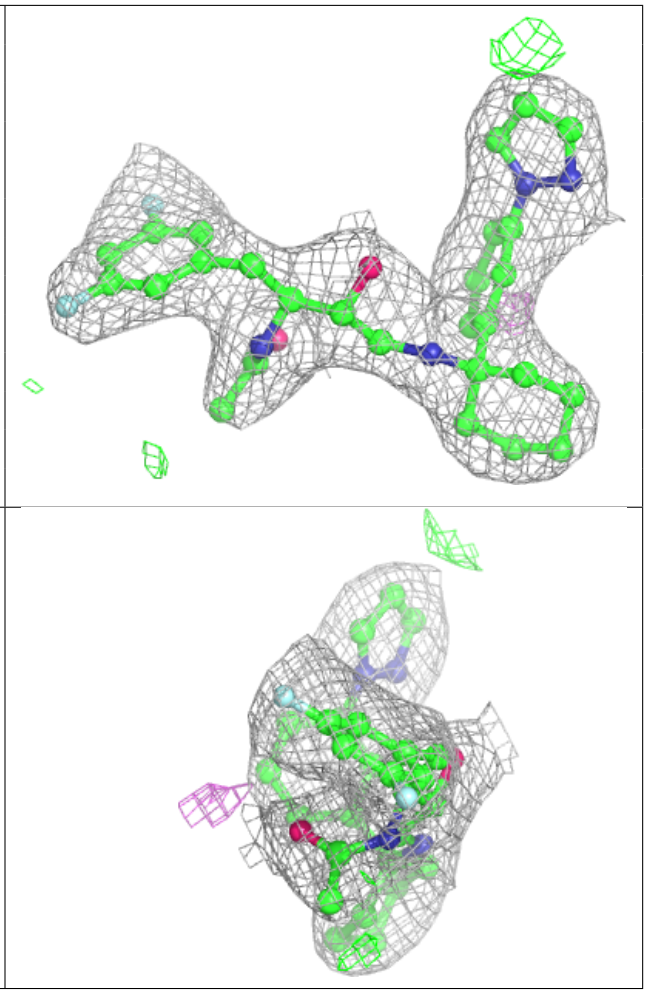
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	842	A	407	35/35	0.94	0.15	44,50,61,63	0
2	842	B	407	35/35	0.96	0.14	44,50,63,65	0
2	842	C	407	35/35	0.96	0.14	44,49,63,66	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

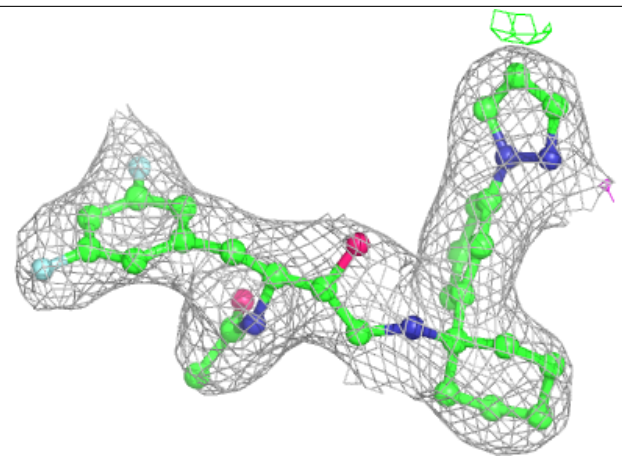
Electron density around 842 A 407:

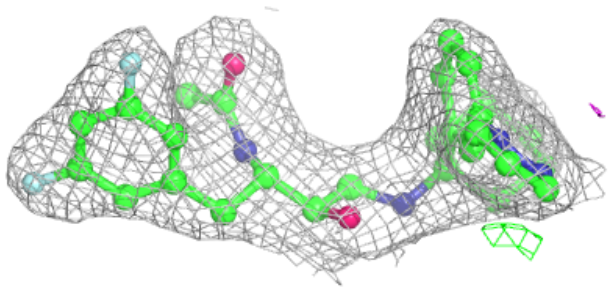
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

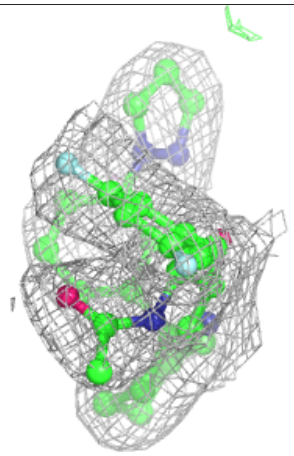


Electron density around 842 B 407:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

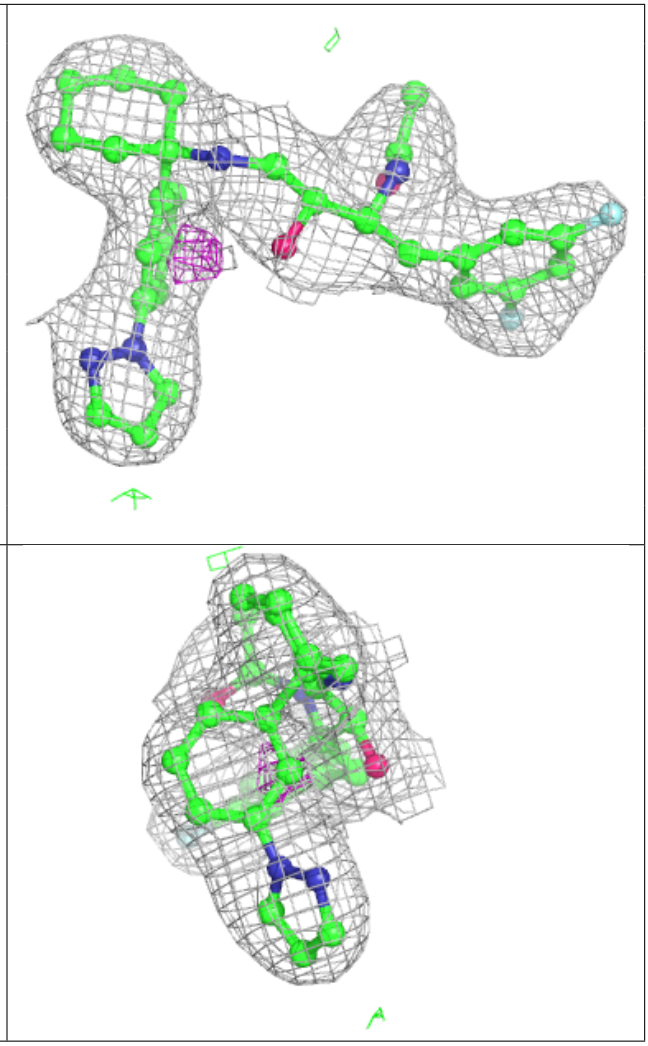






Electron density around 842 C 407:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.