



wwPDB X-ray Structure Validation Summary Report ⓘ

May 13, 2020 – 04:54 am BST

PDB ID : 4JYG
Title : Crystal structure of RARbeta LBD in complex with agonist BMS411 [4-{|(5,5-dimethyl-8-phenyl-5,6-dihydronaphthalen-2-yl)carbonyl|amino}benzoic acid]
Authors : Nadendla, E.K.; Teyssier, C.; Germain, P.; Delfosse, V.; Bourguet, W.
Deposited on : 2013-03-29
Resolution : 2.35 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 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 : 2.11
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) : 2.11

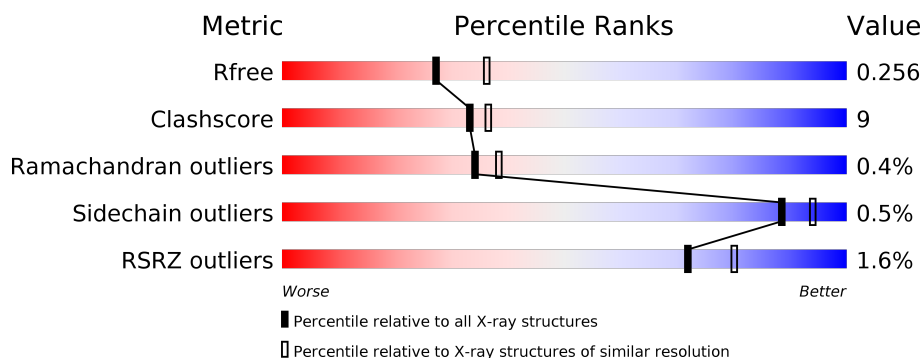
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

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 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	267	
1	B	267	
2	F	13	
2	G	13	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4196 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 Retinoic acid receptor beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	239	Total	C	N	O	S	1	1	0
			1876	1195	312	353	16			
1	B	240	Total	C	N	O	S	0	3	0
			1844	1179	298	350	17			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	148	MET	-	EXPRESSION TAG	UNP P10826
A	149	GLY	-	EXPRESSION TAG	UNP P10826
A	150	SER	-	EXPRESSION TAG	UNP P10826
A	151	SER	-	EXPRESSION TAG	UNP P10826
A	152	HIS	-	EXPRESSION TAG	UNP P10826
A	153	HIS	-	EXPRESSION TAG	UNP P10826
A	154	HIS	-	EXPRESSION TAG	UNP P10826
A	155	HIS	-	EXPRESSION TAG	UNP P10826
A	156	HIS	-	EXPRESSION TAG	UNP P10826
A	157	HIS	-	EXPRESSION TAG	UNP P10826
A	158	SER	-	EXPRESSION TAG	UNP P10826
A	159	SER	-	EXPRESSION TAG	UNP P10826
A	160	GLY	-	EXPRESSION TAG	UNP P10826
A	161	LEU	-	EXPRESSION TAG	UNP P10826
A	162	VAL	-	EXPRESSION TAG	UNP P10826
A	163	PRO	-	EXPRESSION TAG	UNP P10826
A	164	ARG	-	EXPRESSION TAG	UNP P10826
A	165	GLY	-	EXPRESSION TAG	UNP P10826
A	166	SER	-	EXPRESSION TAG	UNP P10826
A	167	HIS	-	EXPRESSION TAG	UNP P10826
A	168	MET	-	EXPRESSION TAG	UNP P10826
A	407	MET	LEU	SEE REMARK 999	UNP P10826
B	148	MET	-	EXPRESSION TAG	UNP P10826
B	149	GLY	-	EXPRESSION TAG	UNP P10826
B	150	SER	-	EXPRESSION TAG	UNP P10826

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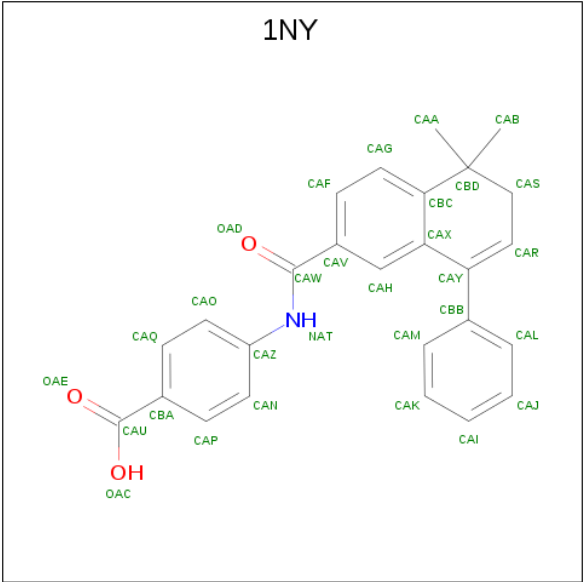
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Chain	Residue	Modelled	Actual	Comment	Reference
B	151	SER	-	EXPRESSION TAG	UNP P10826
B	152	HIS	-	EXPRESSION TAG	UNP P10826
B	153	HIS	-	EXPRESSION TAG	UNP P10826
B	154	HIS	-	EXPRESSION TAG	UNP P10826
B	155	HIS	-	EXPRESSION TAG	UNP P10826
B	156	HIS	-	EXPRESSION TAG	UNP P10826
B	157	HIS	-	EXPRESSION TAG	UNP P10826
B	158	SER	-	EXPRESSION TAG	UNP P10826
B	159	SER	-	EXPRESSION TAG	UNP P10826
B	160	GLY	-	EXPRESSION TAG	UNP P10826
B	161	LEU	-	EXPRESSION TAG	UNP P10826
B	162	VAL	-	EXPRESSION TAG	UNP P10826
B	163	PRO	-	EXPRESSION TAG	UNP P10826
B	164	ARG	-	EXPRESSION TAG	UNP P10826
B	165	GLY	-	EXPRESSION TAG	UNP P10826
B	166	SER	-	EXPRESSION TAG	UNP P10826
B	167	HIS	-	EXPRESSION TAG	UNP P10826
B	168	MET	-	EXPRESSION TAG	UNP P10826
B	407	MET	LEU	SEE REMARK 999	UNP P10826

- Molecule 2 is a protein called Steroid Receptor Coactivator 1.

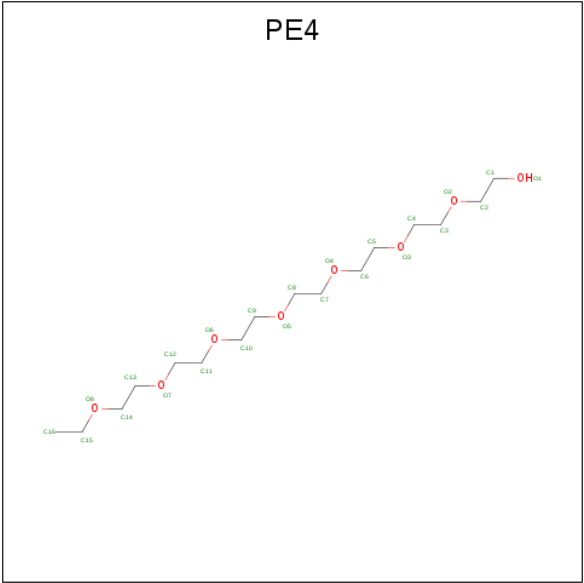
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	F	11	Total	C	N	O	0	0	0
			83	54	18	11			
2	G	11	Total	C	N	O	0	0	0
			95	61	20	14			

- Molecule 3 is 4-{{[(5,5-dimethyl-8-phenyl-5,6-dihydronaphthalen-2-yl)carbonyl]amino}benzoic acid (three-letter code: 1NY) (formula: C₂₆H₂₃NO₃).



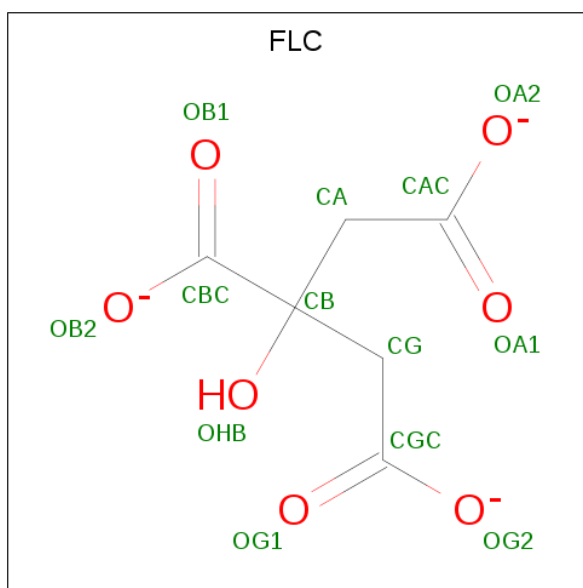
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			30	26	1	3		
3	B	1	Total	C	N	O	0	0
			30	26	1	3		

- Molecule 4 is 2-{2-[2-(2-{2-[2-(2-ETHOXY-ETHOXY)-ETHOXY]-ETHOXY}-ETHOXY)-ETHOXY]-ETHOXY}-ETHANOL (three-letter code: PE4) (formula: C₁₆H₃₄O₈).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			24	16	8		

- Molecule 5 is CITRATE ANION (three-letter code: FLC) (formula: $C_6H_5O_7$).

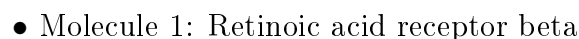


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	G	1	Total	C	O	0	0
			13	6	7		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	136	Total	O	0	0
			136	136		
6	B	54	Total	O	0	0
			54	54		
6	F	3	Total	O	0	0
			3	3		
6	G	8	Total	O	0	0
			8	8		

- Molecule 1: Retinoic acid receptor beta



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.24Å 84.83Å 108.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.50 – 2.35 48.01 – 2.35	Depositor EDS
% Data completeness (in resolution range)	97.1 (39.50-2.35) 97.1 (48.01-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.75 (at 2.34Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.199 , 0.257 0.196 , 0.256	Depositor DCC
R_{free} test set	1120 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	33.6	Xtriage
Anisotropy	0.747	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.2	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	4196	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.88% 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: PE4, FLC, 1NY

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	0.23	0/1910	0.40	0/2585
1	B	0.22	0/1884	0.40	0/2558
2	F	0.19	0/84	0.36	0/113
2	G	0.22	0/96	0.41	0/127
All	All	0.22	0/3974	0.40	0/5383

There are no bond length outliers.

There are no bond angle outliers.

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	1876	0	1908	33	0
1	B	1844	0	1838	31	0
2	F	83	0	78	2	0
2	G	95	0	99	3	0
3	A	30	0	22	1	0
3	B	30	0	22	1	0
4	B	24	0	34	5	0
5	G	13	0	5	3	0
6	A	136	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	54	0	0	4	0
6	F	3	0	0	0	0
6	G	8	0	0	0	0
All	All	4196	0	4006	69	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 9.

The worst 5 of 69 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)
4:B:501:PE4:H21	6:B:648:HOH:O	1.82	0.79
1:A:378:ARG:HG3	1:B:375:THR:HG23	1.69	0.73
1:B:301:LEU:HD11	1:B:380:ILE:HG12	1.74	0.68
1:A:238:ARG:HD2	6:A:613:HOH:O	1.96	0.65
1:A:180:LEU:HD12	1:A:240:PRO:HG2	1.79	0.65

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	238/267 (89%)	234 (98%)	4 (2%)	0	100	100
1	B	241/267 (90%)	228 (95%)	11 (5%)	2 (1%)	19	20
2	F	9/13 (69%)	9 (100%)	0	0	100	100
2	G	9/13 (69%)	9 (100%)	0	0	100	100
All	All	497/560 (89%)	480 (97%)	15 (3%)	2 (0%)	34	38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	361	PRO
1	B	364	PRO

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	207/238 (87%)	207 (100%)	0	100	100
1	B	199/238 (84%)	198 (100%)	1 (0%)	88	94
2	F	7/12 (58%)	7 (100%)	0	100	100
2	G	10/12 (83%)	9 (90%)	1 (10%)	7	6
All	All	423/500 (85%)	421 (100%)	2 (0%)	88	94

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	245	LEU
2	G	639	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	291	HIS
2	F	634	HIS
1	B	291	HIS
1	A	274	GLN
1	A	404	GLN

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 ⓘ

4 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	$\# Z > 2$
5	FLC	G	701	-	3,12,12	1.04	0	3,17,17	1.70	1 (33%)
4	PE4	B	501	-	23,23,23	0.58	0	22,22,22	0.48	0
3	1NY	B	502	-	31,33,33	2.90	10 (32%)	42,48,48	1.63	5 (11%)
3	1NY	A	501	-	31,33,33	2.72	10 (32%)	42,48,48	1.94	11 (26%)

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
5	FLC	G	701	-	-	1/6/16/16	-
4	PE4	B	501	-	-	10/21/21/21	-
3	1NY	B	502	-	-	0/12/32/32	0/4/4/4
3	1NY	A	501	-	-	0/12/32/32	0/4/4/4

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	502	1NY	CAR-CAY	10.34	1.42	1.34
3	A	501	1NY	CAR-CAY	9.39	1.41	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	1NY	CBB-CAY	-5.92	1.40	1.49
3	B	502	1NY	CBA-CAU	-5.89	1.41	1.47
3	B	502	1NY	CBD-CBC	5.47	1.61	1.53

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	502	1NY	CAS-CAR-CAY	-6.22	109.94	122.93
3	A	501	1NY	CBB-CAY-CAR	-5.93	112.82	120.58
3	A	501	1NY	CAS-CAR-CAY	-5.01	112.45	122.93
3	B	502	1NY	CBB-CAY-CAR	-4.57	114.59	120.58
3	B	502	1NY	CAB-CBD-CBC	3.98	116.95	110.10

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	501	PE4	C6-C5-O3-C4
4	B	501	PE4	C12-C11-O6-C10
5	G	701	FLC	OHB-CB-CG-CGC
4	B	501	PE4	C16-C15-O8-C14
4	B	501	PE4	C7-C8-O5-C9

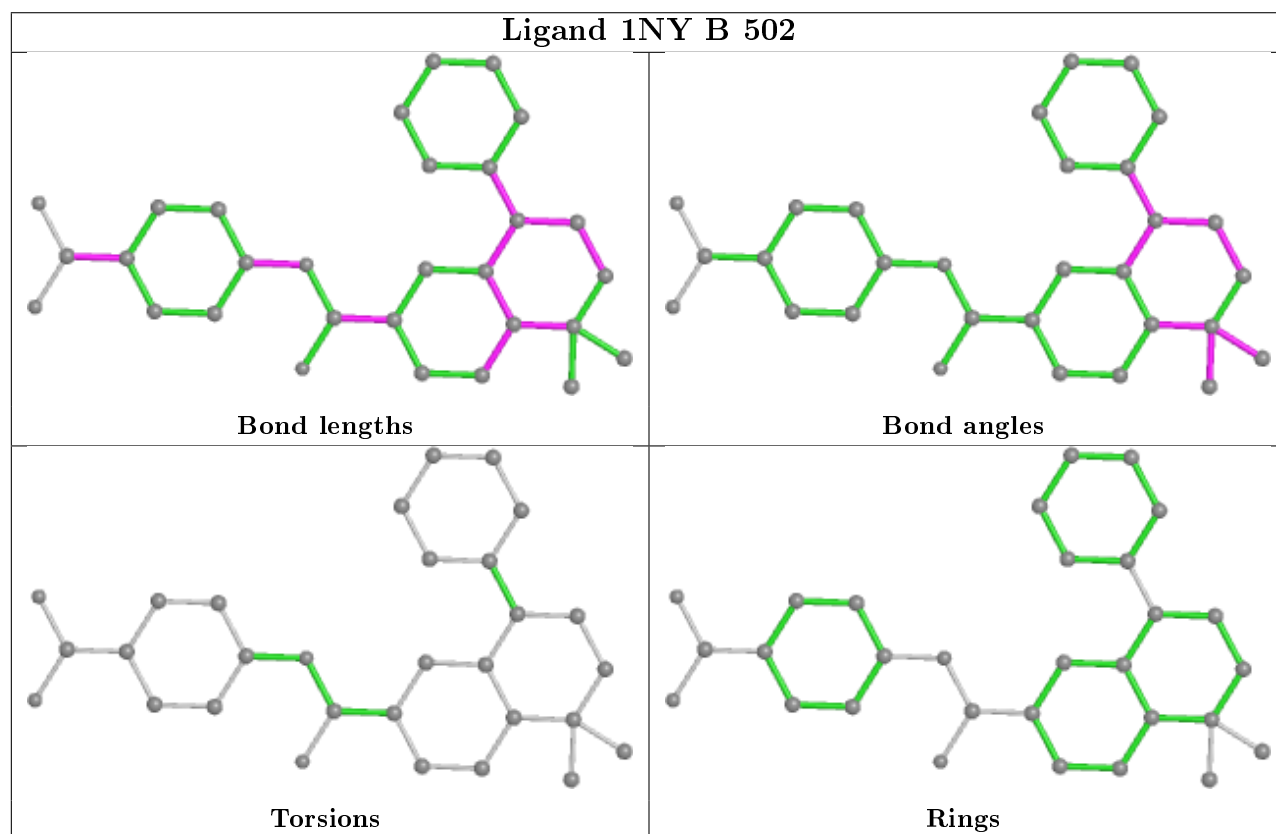
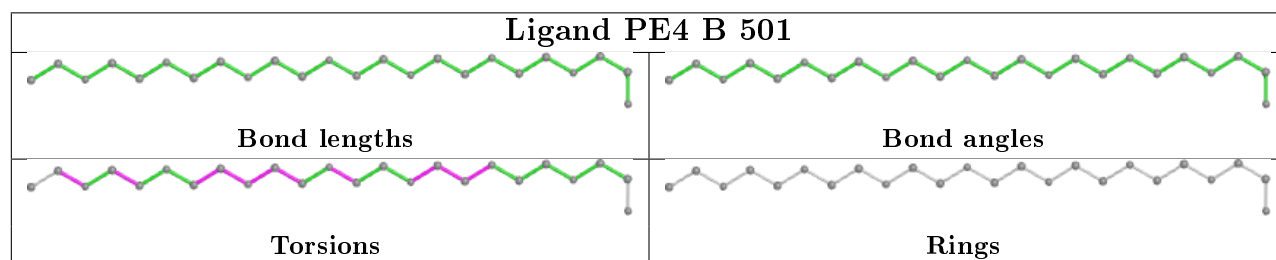
There are no ring outliers.

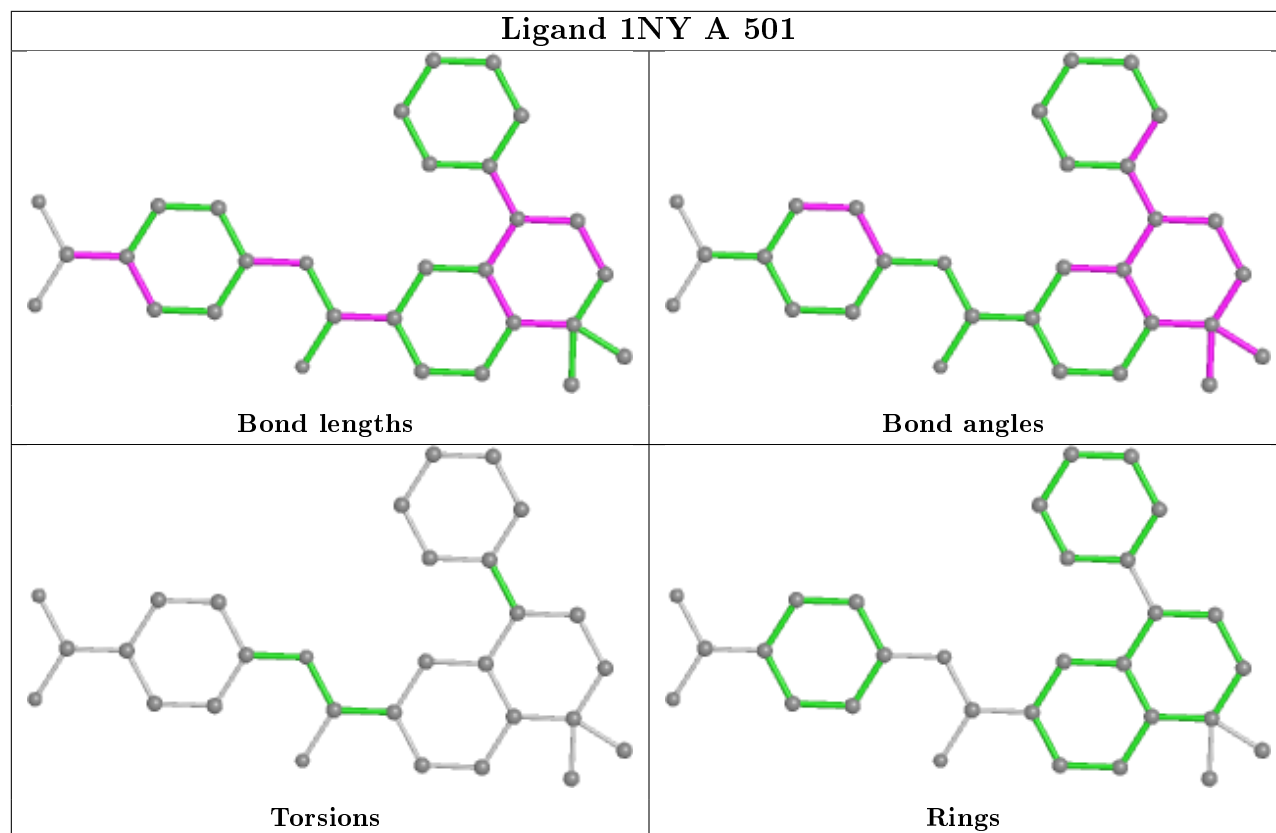
4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	G	701	FLC	3	0
4	B	501	PE4	5	0
3	B	502	1NY	1	0
3	A	501	1NY	1	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 than 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.





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	239/267 (89%)	-0.28	0 100 100	25, 33, 50, 64	2 (0%)
1	B	240/267 (89%)	-0.01	8 (3%) 46 59	31, 43, 62, 92	1 (0%)
2	F	11/13 (84%)	-0.08	0 100 100	44, 50, 60, 60	0
2	G	11/13 (84%)	-0.24	0 100 100	30, 35, 48, 48	0
All	All	501/560 (89%)	-0.15	8 (1%) 72 80	25, 38, 56, 92	3 (0%)

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	362	SER	6.1
1	B	361	PRO	5.5
1	B	360	ARG	4.1
1	B	169	GLU	3.4
1	B	171	TYR	3.2

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](#)

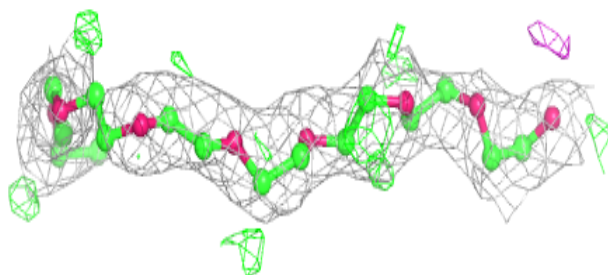
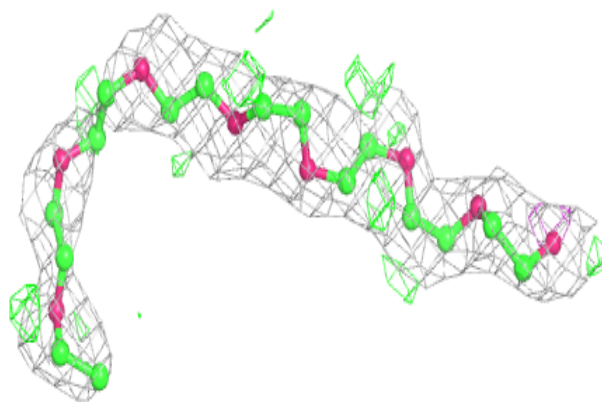
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	PE4	B	501	24/24	0.81	0.17	47,55,72,77	0
5	FLC	G	701	13/13	0.86	0.14	34,42,45,45	0
3	1NY	B	502	30/30	0.95	0.12	31,33,36,37	0
3	1NY	A	501	30/30	0.97	0.12	19,24,30,32	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.

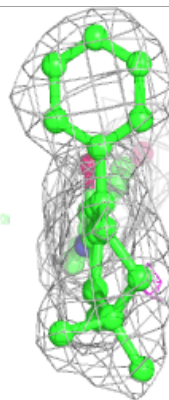
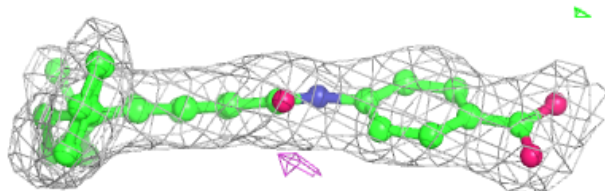
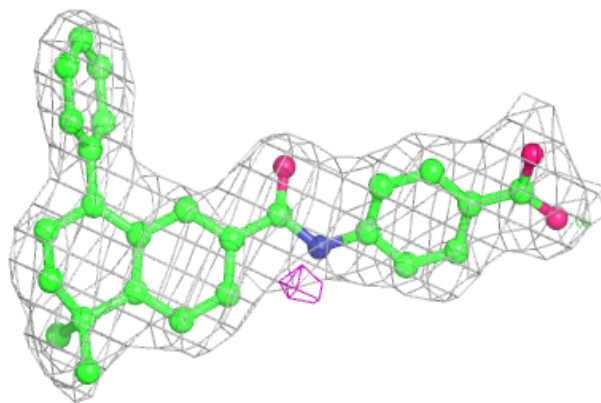
Electron density around PE4 B 501:

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

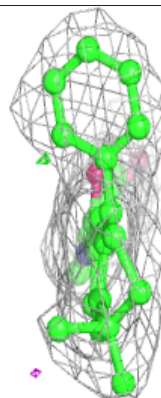
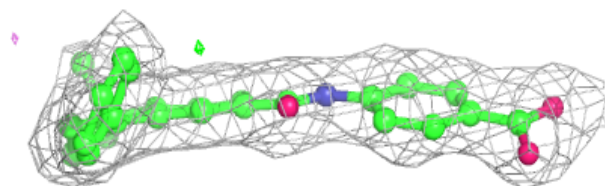
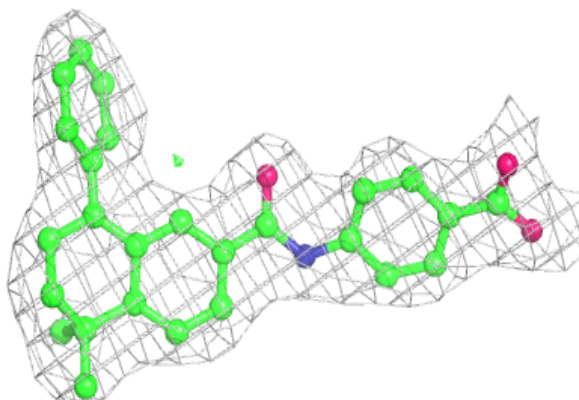


Electron density around 1NY B 502:

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

**Electron density around 1NY A 501:**

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



6.5 Other polymers ⓘ

There are no such residues in this entry.