



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 6, 2020 – 01:11 PM BST

PDB ID : 2RGU
Title : Crystal structure of complex of human DPP4 and inhibitor
Authors : Nar, H.; Himmelsbach, F.; Eckhardt, M.
Deposited on : 2007-10-05
Resolution : 2.60 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 : 2.13.1
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) : 2.13.1

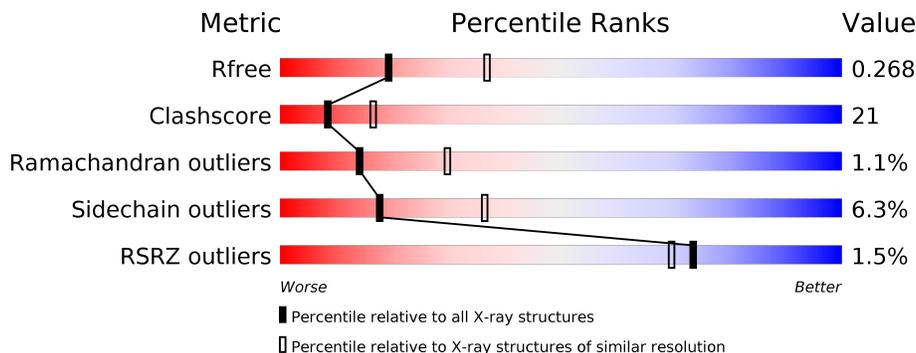
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	734	
1	B	734	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	A	795	X	-	-	-
2	NAG	A	796	X	-	-	-
2	NAG	B	793	X	-	-	-
2	NAG	B	794	X	-	-	-
2	NAG	B	796	X	-	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12323 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.

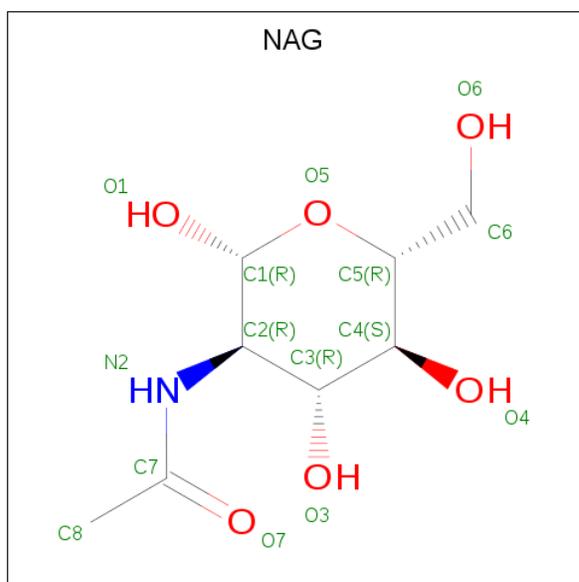
- Molecule 1 is a protein called Dipeptidyl peptidase 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	728	5963	3827	982	1128	26	0	0	0
1	B	728	5963	3827	982	1128	26	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

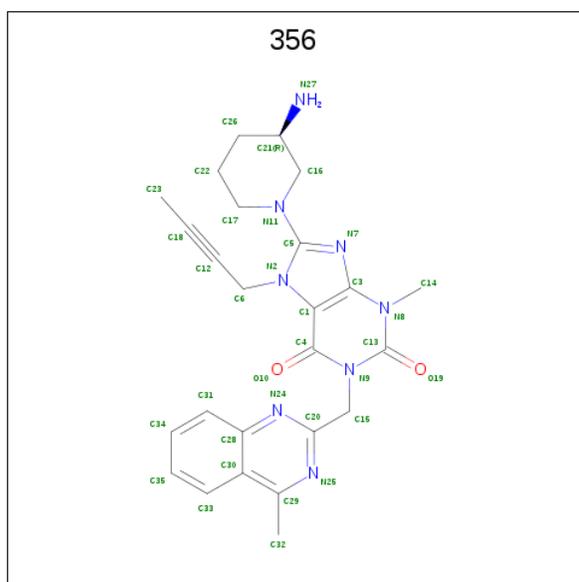
Chain	Residue	Modelled	Actual	Comment	Reference
A	767	HIS	-	expression tag	UNP P27487
A	768	HIS	-	expression tag	UNP P27487
A	769	HIS	-	expression tag	UNP P27487
A	770	HIS	-	expression tag	UNP P27487
A	771	HIS	-	expression tag	UNP P27487
A	772	HIS	-	expression tag	UNP P27487
B	767	HIS	-	expression tag	UNP P27487
B	768	HIS	-	expression tag	UNP P27487
B	769	HIS	-	expression tag	UNP P27487
B	770	HIS	-	expression tag	UNP P27487
B	771	HIS	-	expression tag	UNP P27487
B	772	HIS	-	expression tag	UNP P27487

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	Total	C	N	O	0	0
			15	8	1	6		
2	A	1	Total	C	N	O	0	0
			15	8	1	6		
2	A	1	Total	C	N	O	0	0
			15	8	1	6		
2	A	1	Total	C	N	O	0	0
			15	8	1	6		
2	B	1	Total	C	N	O	0	0
			15	8	1	6		
2	B	1	Total	C	N	O	0	0
			15	8	1	6		
2	B	1	Total	C	N	O	0	0
			15	8	1	6		

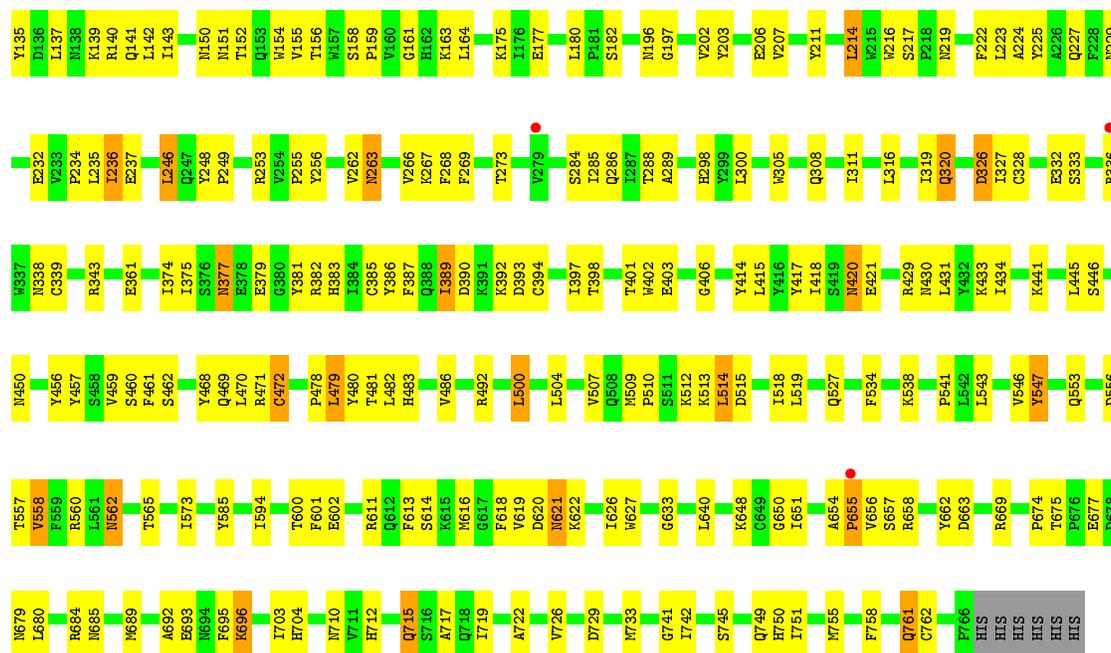
- Molecule 3 is 8-[(3R)-3-Aminopiperidin-1-yl]-7-but-2-yn-1-yl-3-methyl-1-[(4-methylquinazolin-2-yl)methyl]-3,7-dihydro-1H-purine-2,6-dione (three-letter code: 356) (formula: C₂₅H₂₈N₈O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			35	25	8	2		
3	B	1	Total	C	N	O	0	0
			35	25	8	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	96	Total	O	0	0
			96	96		
4	B	111	Total	O	0	0
			111	111		



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.30Å 67.10Å 419.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.60 33.18 – 2.60	Depositor EDS
% Data completeness (in resolution range)	97.5 (40.00-2.60) 97.6 (33.18-2.60)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.58 (at 2.61Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.217 , 0.276 0.212 , 0.268	Depositor DCC
R_{free} test set	2878 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	53.5	Xtrriage
Anisotropy	0.654	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 37.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.034 for k,h,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12323	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.67% 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: 356, NAG

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	0.39	0/6135	0.65	0/8344
1	B	0.41	0/6135	0.67	1/8344 (0.0%)
All	All	0.40	0/12270	0.66	1/16688 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	60	LEU	CA-CB-CG	5.47	127.89	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	5963	0	5685	269	0
1	B	5963	0	5685	231	0
2	A	60	0	60	21	0
2	B	60	0	60	14	0
3	A	35	0	28	0	0
3	B	35	0	28	1	0
4	A	96	0	0	28	0
4	B	111	0	0	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	12323	0	11546	492	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 21.

The worst 5 of 492 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:85:ASN:ND2	2:B:794:NAG:H1	1.30	1.42
1:B:85:ASN:HD21	2:B:794:NAG:C1	1.43	1.31
1:A:229:ASN:HD21	2:A:796:NAG:C1	1.72	1.01
1:B:403:GLU:H	1:B:420:ASN:HD21	1.09	0.98
1:A:85:ASN:ND2	2:A:794:NAG:H1	1.79	0.96

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	726/734 (99%)	657 (90%)	59 (8%)	10 (1%)	11	22
1	B	726/734 (99%)	662 (91%)	58 (8%)	6 (1%)	19	39
All	All	1452/1468 (99%)	1319 (91%)	117 (8%)	16 (1%)	14	30

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	320	GLN
1	B	140	ARG
1	B	333	SER
1	B	393	ASP

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Mol	Chain	Res	Type
1	A	111	GLY

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	653/659 (99%)	611 (94%)	42 (6%)	17	35
1	B	653/659 (99%)	613 (94%)	40 (6%)	18	38
All	All	1306/1318 (99%)	1224 (94%)	82 (6%)	18	36

5 of 82 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	710	ASN
1	B	51	ASN
1	B	655	PRO
1	A	715	GLN
1	A	736	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	679	ASN
1	A	750	HIS
1	B	685	ASN
1	A	710	ASN
1	A	731	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](#)

10 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	356	B	902	-	32,39,39	1.91	10 (31%)	35,57,57	2.85	10 (28%)
3	356	A	901	-	32,39,39	1.72	10 (31%)	35,57,57	2.74	10 (28%)
2	NAG	A	796	-	15,15,15	0.44	0	21,21,21	0.72	1 (4%)
2	NAG	B	794	-	15,15,15	0.36	0	21,21,21	0.66	0
2	NAG	B	793	-	15,15,15	0.49	0	21,21,21	0.63	0
2	NAG	A	793	-	15,15,15	0.30	0	21,21,21	0.64	0
2	NAG	B	797	-	15,15,15	0.48	0	21,21,21	0.71	0
2	NAG	B	796	-	15,15,15	0.34	0	21,21,21	0.91	1 (4%)
2	NAG	A	794	-	15,15,15	0.46	0	21,21,21	0.84	1 (4%)
2	NAG	A	795	-	15,15,15	0.43	0	21,21,21	0.56	0

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	356	B	902	-	-	1/6/22/22	0/5/5/5
3	356	A	901	-	-	2/6/22/22	0/5/5/5
2	NAG	A	796	-	1/1/6/7	2/6/26/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	794	-	1/1/6/7	2/6/26/26	0/1/1/1
2	NAG	B	793	-	1/1/6/7	4/6/26/26	0/1/1/1
2	NAG	A	793	-	-	2/6/26/26	0/1/1/1
2	NAG	B	797	-	-	2/6/26/26	0/1/1/1
2	NAG	B	796	-	1/1/6/7	2/6/26/26	0/1/1/1
2	NAG	A	794	-	-	2/6/26/26	0/1/1/1
2	NAG	A	795	-	1/1/6/7	2/6/26/26	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	902	356	C3-N7	-4.85	1.28	1.33
3	B	902	356	C5-N7	-3.63	1.28	1.35
3	A	901	356	C3-N7	-3.58	1.30	1.33
3	B	902	356	C30-C28	3.28	1.47	1.42
3	B	902	356	C6-N2	3.10	1.53	1.48

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	902	356	C21-C16-N11	-7.38	100.35	109.64
3	A	901	356	C20-N24-C28	7.24	121.45	116.54
3	B	902	356	C20-N24-C28	6.46	120.92	116.54
3	B	902	356	C20-N25-C29	5.97	122.47	117.26
3	A	901	356	C21-C16-N11	-5.70	102.46	109.64

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	796	NAG	C1
2	B	794	NAG	C1
2	B	793	NAG	C1
2	B	796	NAG	C1
2	A	795	NAG	C1

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	902	356	N9-C15-C20-N25
3	A	901	356	C18-C12-C6-N2

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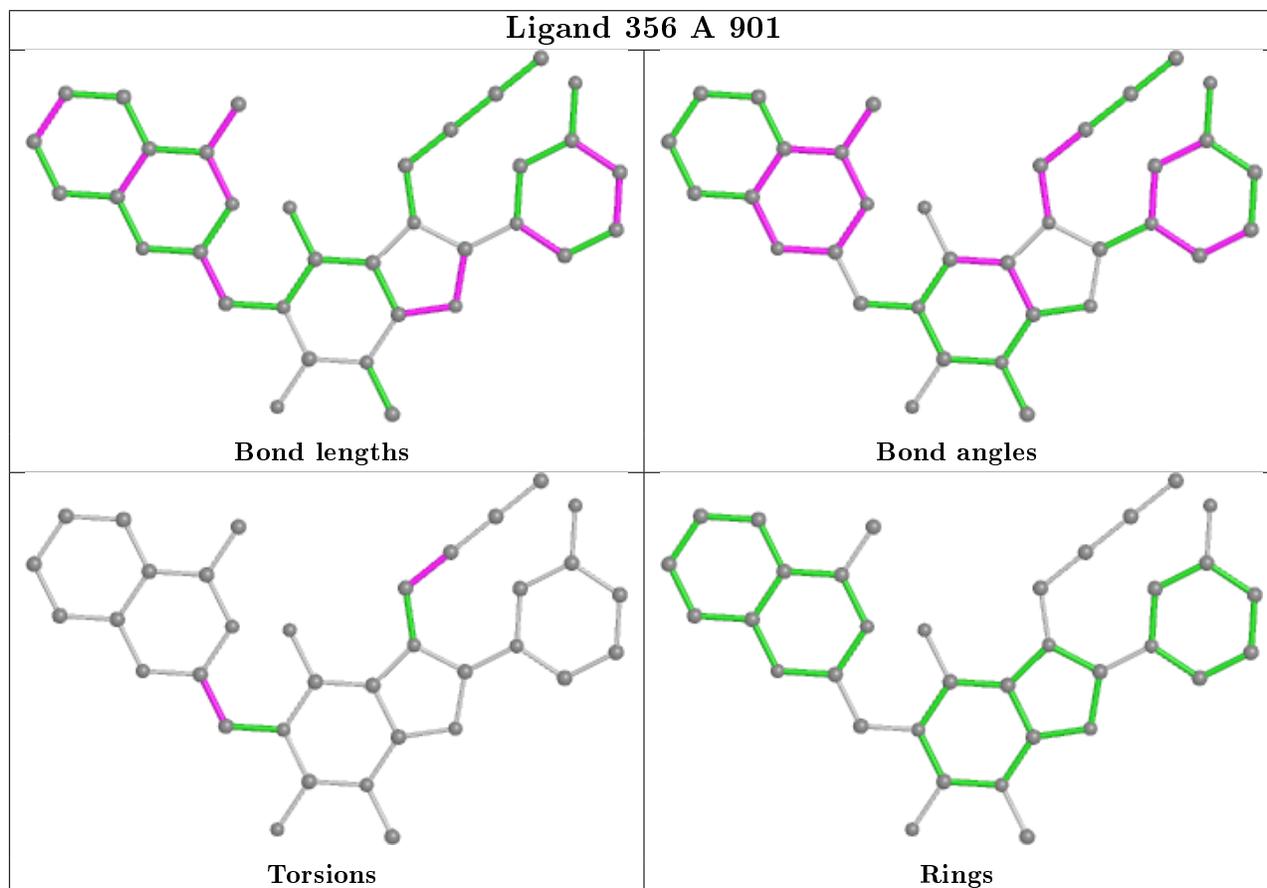
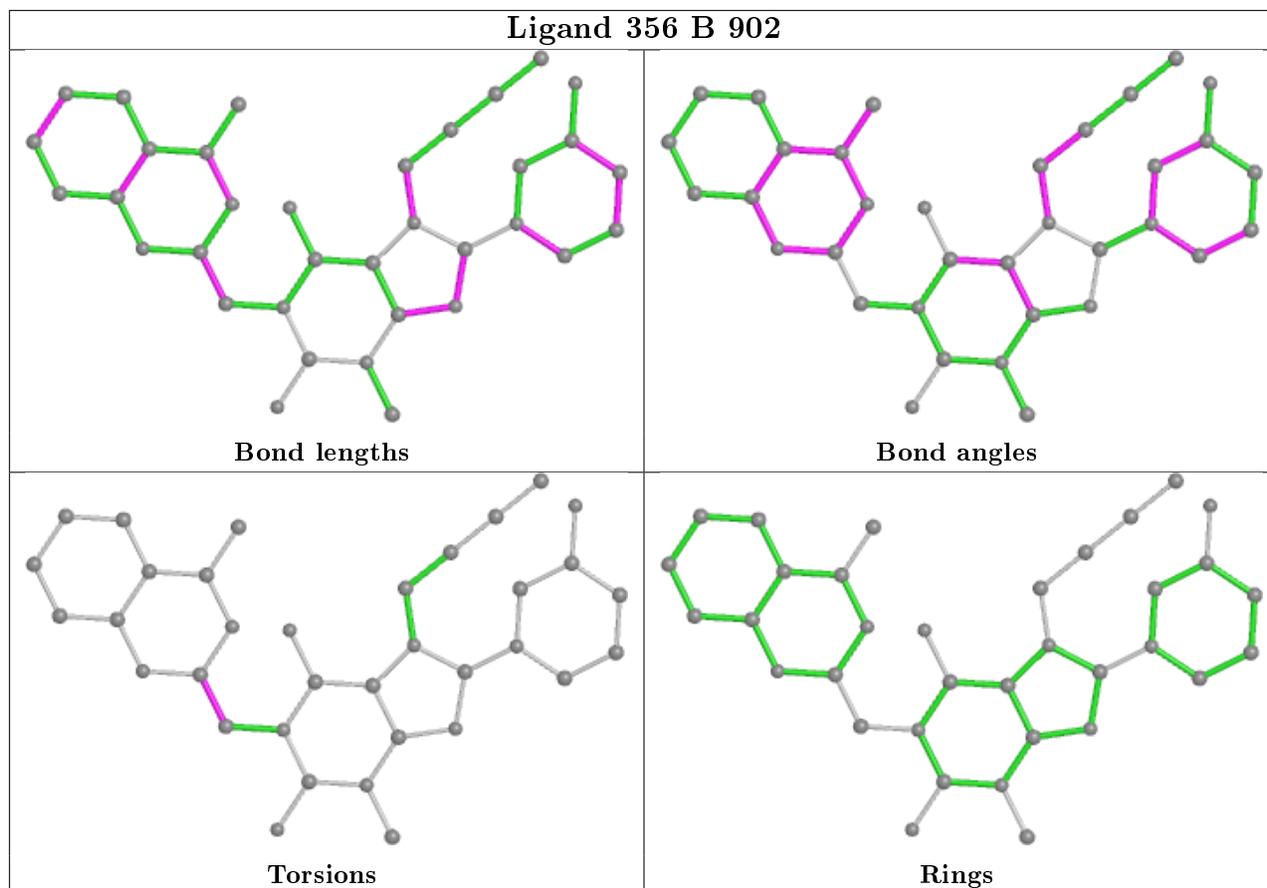
Mol	Chain	Res	Type	Atoms
2	A	793	NAG	C4-C5-C6-O6
2	A	793	NAG	O5-C5-C6-O6
2	B	793	NAG	C4-C5-C6-O6

There are no ring outliers.

9 monomers are involved in 36 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	902	356	1	0
2	A	796	NAG	6	0
2	B	794	NAG	6	0
2	B	793	NAG	2	0
2	A	793	NAG	3	0
2	B	797	NAG	1	0
2	B	796	NAG	5	0
2	A	794	NAG	6	0
2	A	795	NAG	6	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

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, 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	728/734 (99%)	-0.10	16 (2%) 62 56	36, 55, 82, 98	0
1	B	728/734 (99%)	-0.23	6 (0%) 86 84	34, 48, 72, 86	0
All	All	1456/1468 (99%)	-0.17	22 (1%) 73 70	34, 51, 77, 98	0

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	39	SER	5.0
1	B	279	VAL	3.5
1	A	279	VAL	3.2
1	B	97	GLU	3.1
1	A	97	GLU	3.0

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](#)

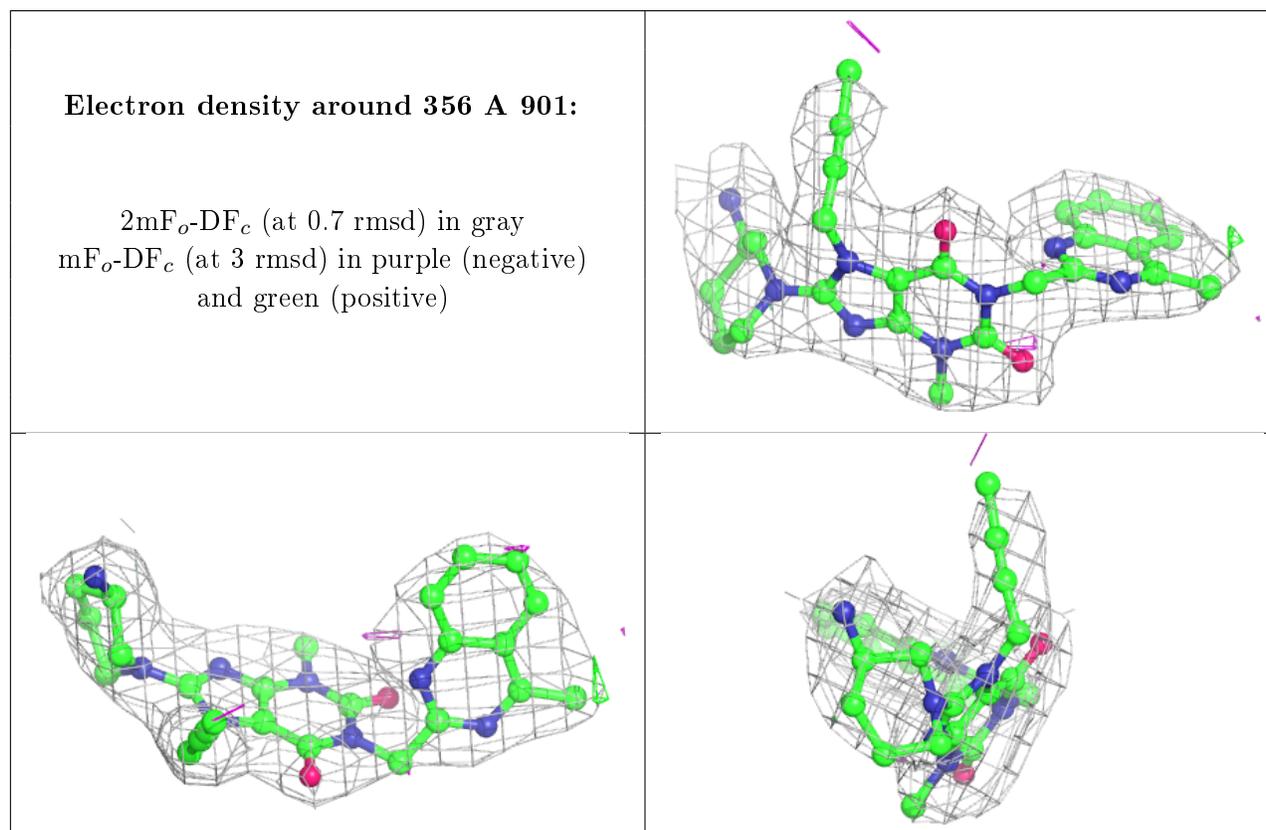
There are no monosaccharides in this entry.

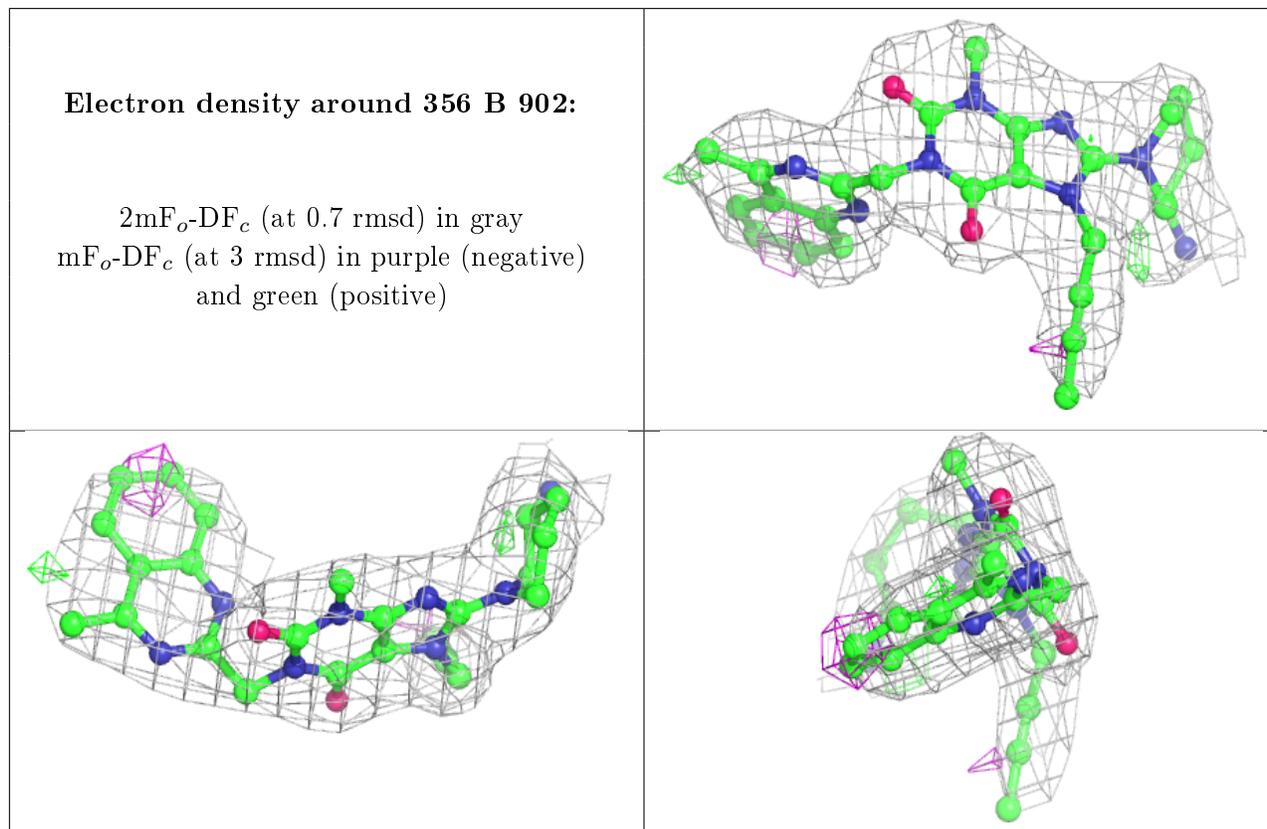
6.4 Ligands [i](#)

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(\AA^2)	Q<0.9
2	NAG	B	793	15/15	0.81	0.22	98,99,100,100	0
2	NAG	A	795	15/15	0.82	0.32	99,99,100,100	0
2	NAG	A	796	15/15	0.86	0.19	79,80,81,82	0
2	NAG	B	797	15/15	0.88	0.14	92,93,93,93	0
2	NAG	B	796	15/15	0.91	0.17	65,65,66,67	0
2	NAG	A	793	15/15	0.92	0.17	95,96,96,97	0
2	NAG	A	794	15/15	0.93	0.18	68,68,69,69	0
3	356	A	901	35/35	0.93	0.20	40,42,45,46	0
3	356	B	902	35/35	0.94	0.23	34,36,45,48	0
2	NAG	B	794	15/15	0.94	0.16	50,52,54,57	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.