

Full wwPDB X-ray Structure Validation Report (i)

Sep 13, 2020 - 09:40 PM BST

PDB ID : 5L8A

Title: Targeting the PEX14-PEX5 interaction by small molecules provides novel ther-

apeutic routes to treat trypanosomiases.

Authors: Dawidowski, M.; Emmanouilidis, L.; Sattler, M.; Popowicz, G.M.

Deposited on : 2016-06-07

Resolution : 1.57 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 following versions of software and data (see references (1)) were used in the production of this report:

Mol Probity : 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : FAILED

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

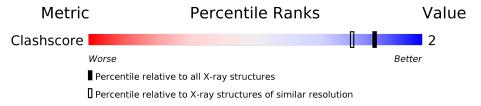
Validation Pipeline (wwPDB-VP) : 2.14.4.dev1

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 1.57 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	Similar resolution
Metric	$(\# ext{Entries})$	$(\# ext{Entries}, ext{resolution range}(ext{Å}))$
Clashscore	141614	5861 (1.60-1.56)

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 <=5%

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain		
1	A	69	90%		10%
1	В	69	87%	•	10%
1	С	69	86%	•	10%
1	D	69	83%	6% •	10%



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 2370 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 Peroxin 14.

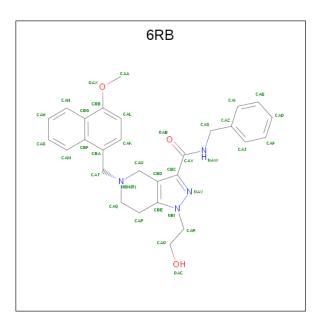
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1 A	۸ 60	Total	С	N	О	S	0	0	0
1	A	62	488	305	88	94	1	U	U	
1	В	62	Total	С	N	О	S	0	0	0
1	Ъ		480	299	90	90	1		U	0
1	С	62	Total	С	N	О	S	0	0	0
1		02	486	303	91	91	1	0	0	U
1	D	62	Total	С	N	О	S	0	0	0
1		02	490	306	89	94	1	U	U	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q8IEW2
A	-1	ALA	_	expression tag	UNP Q8IEW2
A	0	MET	_	expression tag	UNP Q8IEW2
A	1	TRP	_	expression tag	UNP Q8IEW2
В	-2	GLY	_	expression tag	UNP Q8IEW2
В	-1	ALA	_	expression tag	UNP Q8IEW2
В	0	MET	_	expression tag	UNP Q8IEW2
В	1	TRP	_	expression tag	UNP Q8IEW2
С	-2	GLY	_	expression tag	UNP Q8IEW2
С	-1	ALA	_	expression tag	UNP Q8IEW2
С	0	MET	_	expression tag	UNP Q8IEW2
С	1	TRP	_	expression tag	UNP Q8IEW2
D	-2	GLY	_	expression tag	UNP Q8IEW2
D	-1	ALA	-	expression tag	UNP Q8IEW2
D	0	MET	-	expression tag	UNP Q8IEW2
D	1	TRP	-	expression tag	UNP Q8IEW2

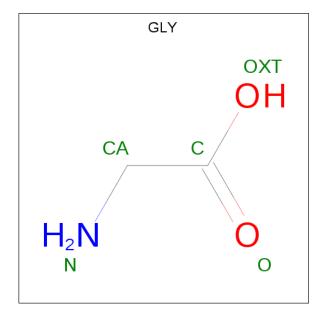
• Molecule 2 is 1-(2-hydroxyethyl)-5-[(4-methoxynaphthalen-1-yl)methyl]- $\{N\}$ -(phenylmethyl)-6,7-dihydro-4 $\{H\}$ -pyrazolo[4,3-c]pyridine-3-carboxamide (three-letter code: 6RB) (formula: $C_{28}H_{30}N_4O_3$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	Λ	1	Total C N O	0	0
2	A	1	35 28 4 3	0	0
2	D	1	Total C N O	0	0
2	Б	1	35 28 4 3	0	
2	С	1	Total C N O	0	0
2		1	35 28 4 3	0	0
2	D	1	Total C N O	0	0
	ש	1	35 28 4 3	0	0

 \bullet Molecule 3 is GLYCINE (three-letter code: GLY) (formula: $\mathrm{C_2H_5NO_2}).$



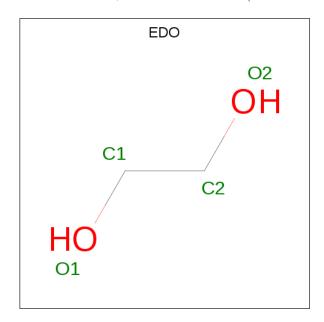


Mol	Chain	Residues	${f Atoms}$				ZeroOcc	AltConf
3	Α	1	Total	С	N	О	0	0
	11	1	5	2	1	2		

• Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	С	1	Total Na 1 1	0	0

 \bullet Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $\mathrm{C_2H_6O_2}).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	D	1	Total C O 4 2 2	0	0

• Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	
6	Α	84	Total O	0	\cap	
	11	04	84 84		O	
6	В	63	Total O	0	0	
0	0 D	0.5	63 - 63	0		
6	С	68	Total O	0	0	
0	C	00	68 68	0	U	
6	D	61	Total O	0	0	
0	ש	01	61 61	U	U	



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. 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. 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.

Note EDS failed to run properly.

• Molecule 1: Peroxin 14





4 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants	36.10Å 36.28Å 55.31Å	Depositor
a, b, c, α , β , γ	94.12° 105.87° 100.54°	Depositor
Resolution (Å)	27.79 - 1.57	Depositor
% Data completeness	92.5 (27.79-1.57)	Depositor
(in resolution range)	, , , , , , , , , , , , , , , , , , , ,	
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.84 (at 1.57Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.191 , 0.252	Depositor
Wilson B-factor (A^2)	15.3	Xtriage
Anisotropy	0.069	Xtriage
L-test for twinning ²	$ < L >=0.47, < L^2>=0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2370	wwPDB-VP
Average B, all atoms (\mathring{A}^2)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 10.81% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: 6RB, EDO, NA

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		
IVIOI	Chain	RMSZ	# Z >5	RMSZ	# Z > 5	
1	A	0.85	0/493	0.79	0/658	
1	В	0.74	0/485	0.76	0/648	
1	С	0.83	0/491	0.77	0/655	
1	D	0.84	0/495	0.95	$5/660 \ (0.8\%)$	
All	All	0.81	0/1964	0.82	$5/2621 \ (0.2\%)$	

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
1	D	23	VAL	CB-CA-C	6.95	124.60	111.40
1	D	25	ARG	NE-CZ-NH1	6.16	123.38	120.30
1	D	23	VAL	CA-CB-CG1	5.79	119.59	110.90
1	D	25	ARG	NE-CZ-NH2	-5.47	117.57	120.30
1	D	22	ARG	NE-CZ-NH1	5.36	122.98	120.30

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	488	0	504	0	0
1	В	480	0	493	1	1

Continued on next page...



Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	С	486	0	504	5	0
1	D	490	0	511	2	1
2	A	35	0	0	0	0
2	В	35	0	0	1	0
2	С	35	0	0	0	0
2	D	35	0	0	0	0
3	A	5	0	2	0	0
4	С	1	0	0	0	0
5	D	4	0	6	0	0
6	A	84	0	0	0	0
6	В	63	0	0	1	0
6	С	68	0	0	5	1
6	D	61	0	0	2	1
All	All	2370	0	2020	9	2

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 2.

All (9) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{array}{ll} ext{Interatomic} \ ext{distance} \ (ext{\AA}) \end{array}$	Clash overlap (Å)
1:D:60:GLU:HG3	6:D:234:HOH:O	1.75	0.87
1:C:63:ARG:NH1	6:C:202:HOH:O	2.31	0.64
1:B:36:LYS:HE2	6:B:248:HOH:O	2.09	0.52
1:C:5:SER:CB	6:C:249:HOH:O	2.58	0.51
1:D:13:ASN:ND2	6:D:204:HOH:O	2.47	0.48
1:C:5:SER:HA	6:C:249:HOH:O	2.13	0.48
1:C:24:ARG:HD2	6:C:256:HOH:O	2.19	0.42
1:C:63:ARG:CZ	6:C:202:HOH:O	2.67	0.41
2:B:101:6RB:OAB	2:B:101:6RB:CAU	2.67	0.40

All (2) 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	$egin{array}{l} ext{Interatomic} \ ext{distance } (ext{Å}) \end{array}$	$egin{array}{c} ext{Clash} \ ext{overlap } (ext{Å}) \end{array}$
6:C:266:HOH:O	6:D:261:HOH:O[1_656]	2.06	0.14
1:B:66:SER:OXT	1:D:25:ARG:NH2[1_656]	2.18	0.02



5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains (i)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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)

Of 7 ligands modelled in this entry, 1 is monoatomic - leaving 6 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	Tuno	Chain	Res	Link	В	ond leng	gths	В	ond ang	gles
MIGI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
2	6RB	С	101	_	38,39,39	2.31	11 (28%)	44,54,54	3.64	16 (36%)
2	6RB	D	101	-	38,39,39	1.87	10 (26%)	44,54,54	4.64	15 (34%)
2	6RB	A	101	-	38,39,39	2.39	9 (23%)	44,54,54	2.11	16 (36%)
3	GLY	A	102	-	1,4,4	0.25	0	0,4,4	0.00	-
5	EDO	D	102	-	3,3,3	0.35	0	2,2,2	0.35	0
2	6RB	В	101	_	38,39,39	2.18	11 (28%)	44,54,54	4.21	19 (43%)



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	6RB	С	101	-	-	4/14/27/27	0/5/5/5
2	6RB	D	101	-	-	4/14/27/27	0/5/5/5
2	6RB	A	101	_	-	1/14/27/27	0/5/5/5
3	GLY	A	102	_	-	0/0/2/2	-
5	EDO	D	102	_	-	0/1/1/1	-
2	6RB	В	101	-	-	3/14/27/27	0/5/5/5

All (41) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(A)
2	A	101	6RB	CBC-CAY	-9.00	1.37	1.50
2	С	101	6RB	CBC-CAY	-7.55	1.39	1.50
2	В	101	6RB	CBC-CAY	-7.10	1.39	1.50
2	D	101	6RB	CBC-CAY	-5.70	1.42	1.50
2	A	101	6RB	CAU-CBD	-5.44	1.40	1.51
2	A	101	6RB	CAP-CBE	-4.81	1.38	1.50
2	A	101	6RB	CAT-NBH	4.74	1.56	1.47
2	С	101	6RB	CAR-NBI	4.42	1.54	1.47
2	D	101	6RB	CAU-CBD	-4.28	1.42	1.51
2	С	101	6RB	CAT-NBH	4.22	1.55	1.47
2	В	101	6RB	CAQ-CAP	4.07	1.59	1.51
2	В	101	6RB	CAS-CAZ	-4.02	1.42	1.51
2	В	101	6RB	CAU-CBD	-3.86	1.43	1.51
2	С	101	6RB	CAS-CAZ	-3.77	1.43	1.51
2	С	101	6RB	CAP-CBE	-3.75	1.41	1.50
2	В	101	6RB	CAR-NBI	3.67	1.53	1.47
2	С	101	6RB	CAS-NAW	-3.63	1.39	1.46
2	С	101	6RB	CAU-CBD	-3.63	1.44	1.51
2	В	101	6RB	CAT-NBH	3.62	1.54	1.47
2	A	101	6RB	CAQ-CAP	3.52	1.58	1.51
2	D	101	6RB	CAP-CBE	-3.45	1.42	1.50
2	С	101	6RB	CAQ-CAP	3.18	1.58	1.51
2	В	101	6RB	CAS-NAW	-2.96	1.40	1.46
2	D	101	6RB	CAS-NAW	-2.95	1.40	1.46
2	В	101	6RB	CAP-CBE	-2.90	1.43	1.50
2	D	101	6RB	CAH-CAN	2.85	1.43	1.36
2	С	101	6RB	CBE-CBD	-2.82	1.34	1.38
2	A	101	6RB	CAG-CAM	2.81	1.43	1.36

 $Continued\ on\ next\ page...$



Continued from previous page...

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(\mathbf{\mathring{A}})$	Ideal(Å)
2	В	101	6RB	CAH-CAN	2.75	1.43	1.36
2	A	101	6RB	CAT-CBA	-2.69	1.45	1.52
2	D	101	6RB	CAT-NBH	2.53	1.52	1.47
2	D	101	6RB	CAT-CBA	-2.47	1.45	1.52
2	A	101	6RB	CAS-CAZ	-2.45	1.46	1.51
2	D	101	6RB	CAS-CAZ	-2.36	1.46	1.51
2	D	101	6RB	CBE-CBD	-2.35	1.35	1.38
2	В	101	6RB	CAG-CAM	2.31	1.42	1.36
2	В	101	6RB	CBE-CBD	-2.28	1.35	1.38
2	D	101	6RB	CBC-CBD	-2.12	1.37	1.41
2	A	101	6RB	CBC-CBD	-2.07	1.37	1.41
2	С	101	6RB	CAK-CAL	2.03	1.42	1.38
2	С	101	6RB	CAF-CAJ	2.03	1.43	1.38

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}({}^o)$	$Ideal(^{o})$
2	D	101	6RB	CBC-CAY-NAW	21.78	136.90	115.67
2	В	101	6RB	CBC-CAY-NAW	18.71	133.91	115.67
2	С	101	6RB	CBC-CAY-NAW	15.68	130.96	115.67
2	D	101	6RB	CAR-NBI-CBE	-11.47	113.89	128.48
2	D	101	6RB	OAB-CAY-NAW	-9.57	103.54	122.61
2	В	101	6RB	OAB-CAY-NAW	-8.36	105.96	122.61
2	D	101	6RB	CAS-NAW-CAY	8.30	141.44	121.81
2	С	101	6RB	CAR-NBI-CBE	-7.89	118.44	128.48
2	С	101	6RB	OAB-CAY-NAW	-6.96	108.75	122.61
2	С	101	6RB	CBD-CAU-NBH	6.60	120.53	111.56
2	В	101	6RB	CAG-CAH-CAN	-6.40	111.47	120.44
2	D	101	6RB	CAA-OAX-CBB	6.28	126.53	117.75
2	С	101	6RB	CAS-NAW-CAY	6.17	136.40	121.81
2	В	101	6RB	CBD-CAU-NBH	5.95	119.65	111.56
2	В	101	6RB	CAS-NAW-CAY	5.92	135.83	121.81
2	D	101	6RB	CAY-CBC-NAV	5.88	135.32	120.57
2	В	101	6RB	CAY-CBC-NAV	5.29	133.84	120.57
2	В	101	6RB	CAH-CAN-CBG	5.22	128.13	120.89
2	С	101	6RB	CAZ-CAS-NAW	-4.99	102.35	113.05
2	В	101	6RB	CAZ-CAS-NAW	-4.96	102.41	113.05
2	A	101	6RB	CAA-OAX-CBB	4.83	124.50	117.75
2	В	101	6RB	OAX-CBB-CBG	4.71	119.06	114.46
2	A	101	6RB	CBE-NBI-NAV	-4.18	107.29	112.10
2	В	101	6RB	CAL-CAK-CBA	4.00	126.89	119.70
2	В	101	6RB	CAR-NBI-CBE	-3.92	123.49	128.48

Continued on next page...



Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\mathbf{Ideal}(^o)$
2	Α	101	6RB	OAX-CBB-CBG	3.84	118.22	114.46
2	A	101	6RB	CBD-CAU-NBH	3.84	116.78	111.56
2	С	101	6RB	CAL-CAK-CBA	3.76	126.45	119.70
2	D	101	6RB	CAP-CAQ-NBH	-3.72	107.03	111.07
2	A	101	6RB	CAT-NBH-CAU	3.57	117.97	111.62
2	D	101	6RB	CAT-CBA-CBF	3.52	126.08	119.93
2	В	101	6RB	CBE-NBI-NAV	-3.50	108.08	112.10
2	В	101	6RB	CAM-CBF-CBG	-3.49	114.11	118.45
2	В	101	6RB	CAK-CBA-CBF	-3.46	114.16	119.08
2	С	101	6RB	CAT-CBA-CBF	3.44	125.94	119.93
2	С	101	6RB	CAY-CBC-NAV	3.42	129.15	120.57
2	Α	101	6RB	CAT-NBH-CAQ	3.41	118.66	111.06
2	В	101	6RB	CAL-CBB-CBG	-3.38	115.22	121.15
2	A	101	6RB	CAT-CBA-CBF	3.37	125.81	119.93
2	A	101	6RB	CBD-CBE-NBI	3.32	109.44	106.79
2	В	101	6RB	CAT-NBH-CAU	3.31	117.50	111.62
2	С	101	6RB	OAX-CBB-CBG	3.26	117.64	114.46
2	С	101	6RB	CBE-NBI-NAV	-3.21	108.41	112.10
2	В	101	6RB	CBB-CBG-CBF	3.11	123.30	118.49
2	D	101	6RB	CBE-NBI-NAV	-3.08	108.57	112.10
2	A	101	6RB	CAL-CAK-CBA	2.98	125.06	119.70
2	A	101	6RB	CAR-NBI-CBE	2.94	132.22	128.48
2	С	101	6RB	CBB-CBG-CBF	2.91	123.00	118.49
2	D	101	6RB	CBD-CAU-NBH	2.90	115.50	111.56
2	A	101	6RB	CAQ-CAP-CBE	-2.85	108.10	113.16
2	A	101	6RB	CAU-NBH-CAQ	-2.65	106.53	109.91
2	D	101	6RB	CAL-CAK-CBA	2.55	124.29	119.70
2	D	101	6RB	CAU-NBH-CAQ	2.49	113.10	109.91
2	D	101	6RB	CAZ-CAS-NAW	-2.48	107.73	113.05
2	С	101	6RB	CAT-NBH-CAU	2.48	116.03	111.62
2	В	101	6RB	CAH-CAG-CAM	2.47	123.90	120.44
2	D	101	6RB	OAC-CAO-CAR	-2.44	101.52	110.82
2	A	101	6RB	CAG-CAH-CAN	-2.42	117.05	120.44
2	С	101	6RB	CBA-CAT-NBH	2.38	117.54	114.14
2	D	101	6RB	OAX-CBB-CBG	2.25	116.65	114.46
2	A	101	6RB	CAK-CBA-CBF	-2.23	115.90	119.08
2	A	101	6RB	CBB-CBG-CBF	2.16	121.83	118.49
2	В	101	6RB	CBD-CBE-NBI	2.11	108.47	106.79
2	С	101	6RB	CAP-CAQ-NBH	2.05	113.30	111.07
2	С	101	6RB	CAQ-CAP-CBE	2.03	116.77	113.16
2	A	101	6RB	CAP-CAQ-NBH	2.00	113.25	111.07

There are no chirality outliers.



All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	101	6RB	CAO-CAR-NBI-CBE
2	D	101	6RB	CAO-CAR-NBI-NAV
2	D	101	6RB	CBC-CAY-NAW-CAS
2	В	101	6RB	OAC-CAO-CAR-NBI
2	В	101	6RB	CBC-CAY-NAW-CAS
2	С	101	6RB	CBC-CAY-NAW-CAS
2	D	101	6RB	OAB-CAY-NAW-CAS
2	С	101	6RB	OAB-CAY-NAW-CAS
2	В	101	6RB	OAB-CAY-NAW-CAS
2	С	101	6RB	CAO-CAR-NBI-CBE
2	С	101	6RB	CAO-CAR-NBI-NAV
2	A	101	6RB	CBA-CAT-NBH-CAQ

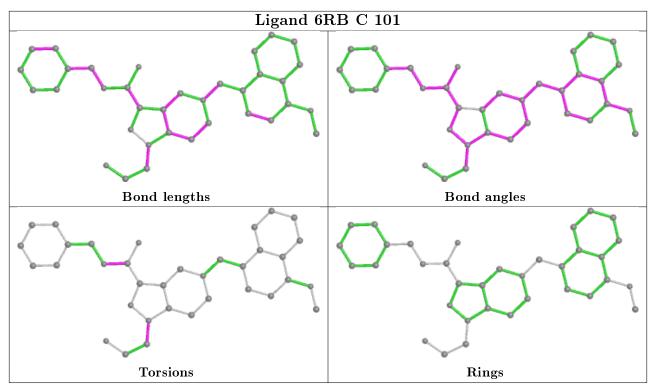
There are no ring outliers.

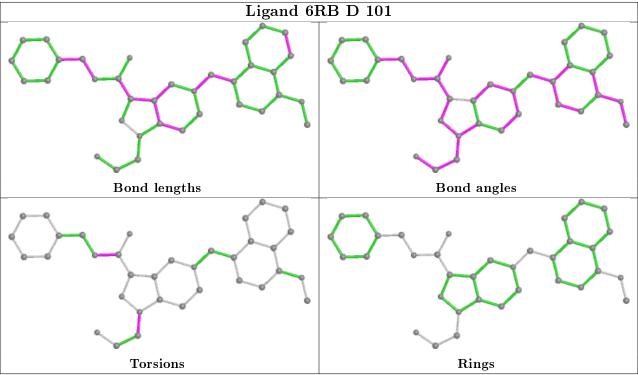
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	101	6RB	1	0

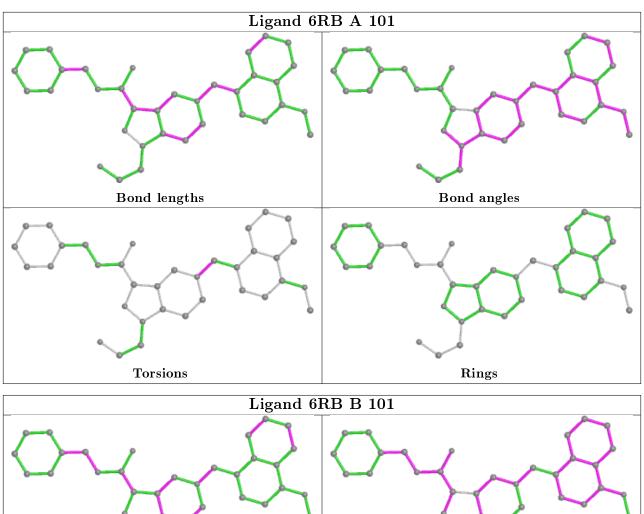
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.

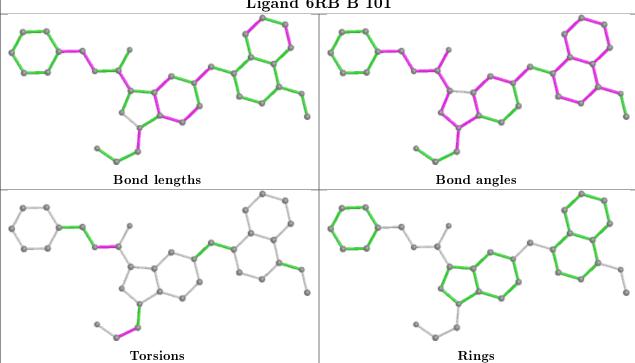












5.7 Other polymers (i)

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)

EDS failed to run properly - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates (i)

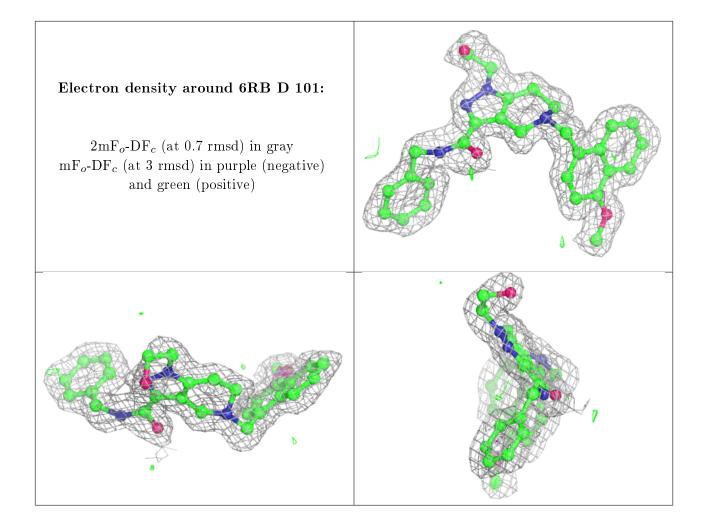
EDS failed to run properly - this section is therefore empty.

6.4 Ligands (i)

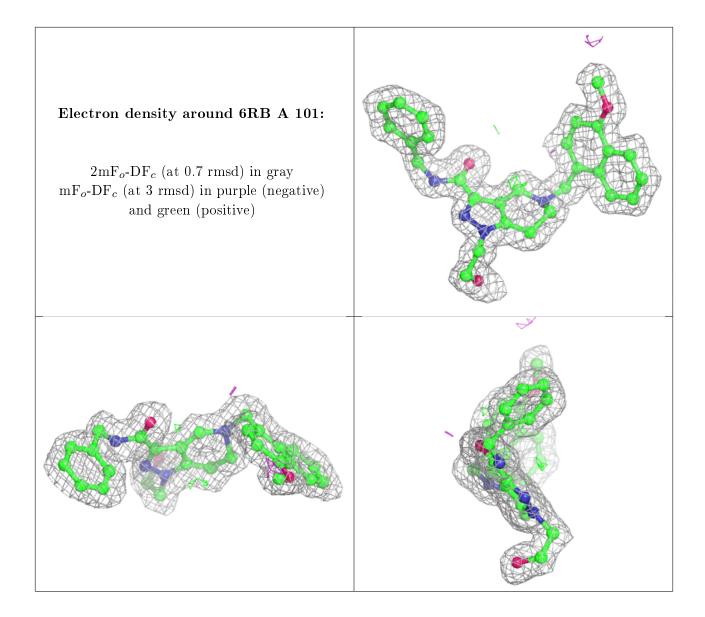
EDS failed to run properly - this section is therefore empty.

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.

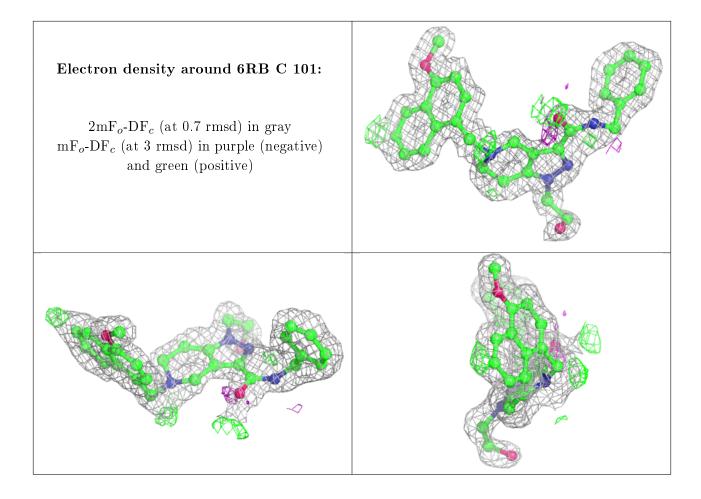




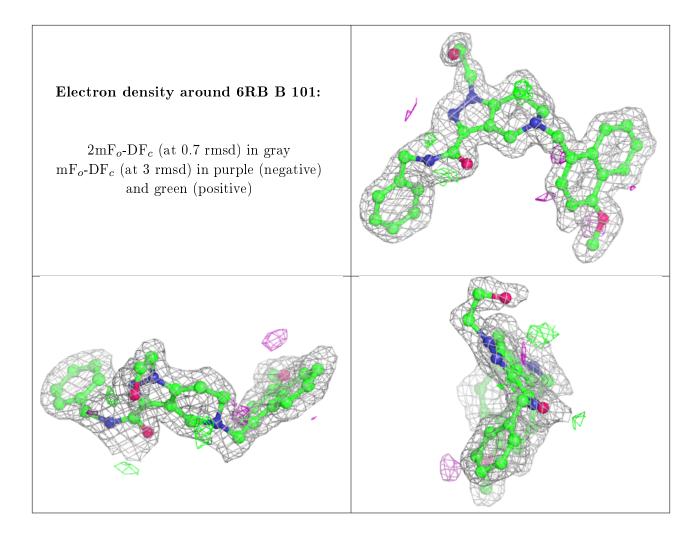












6.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.

