



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 16, 2023 – 08:02 AM EDT

PDB ID : 2HWR
Title : Structural basis for the structure-activity relationships of Peroxisome Proliferator-Activated Receptor agonists
Authors : Peng, Y.H.; Lu, I.L.; Mahindroo, N.; Lin, C.H.; Hsieh, H.P.; Wu, S.Y.
Deposited on : 2006-08-01
Resolution : 2.34 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 ⓘ 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 ⓘ](#)) 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 : 2.36
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) : 2.36

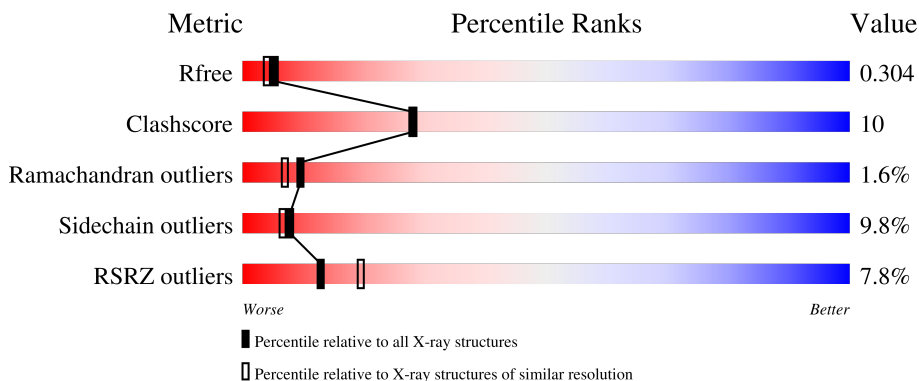
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.34 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	2096 (2.36-2.32)
Clashscore	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (2.36-2.32)
RSRZ outliers	127900	2067 (2.36-2.32)

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 $\leq 5\%$. 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.

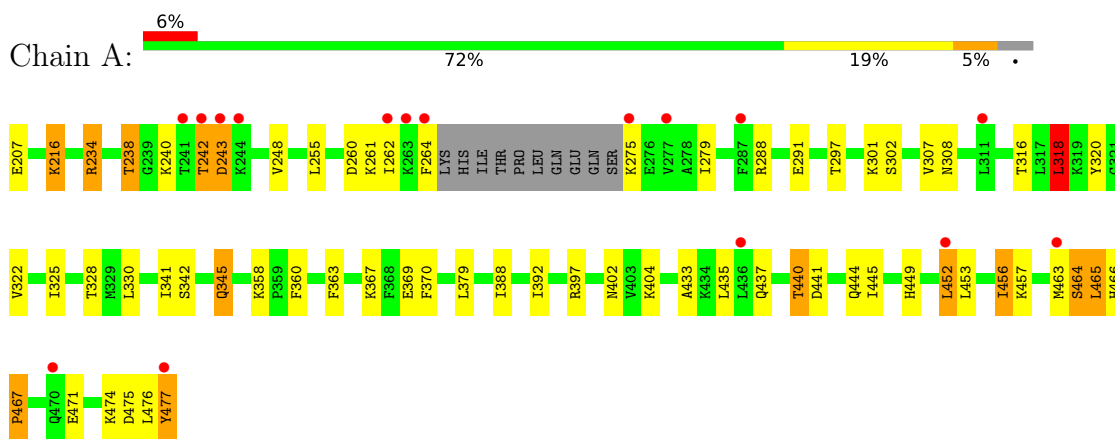
Mol	Chain	Length	Quality of chain
1	A	271	 6% 72% 19% 5%
1	B	271	 9% 68% 22% 7%

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	35	Total 35	O 35	0	0
3	B	42	Total 42	O 42	0	0

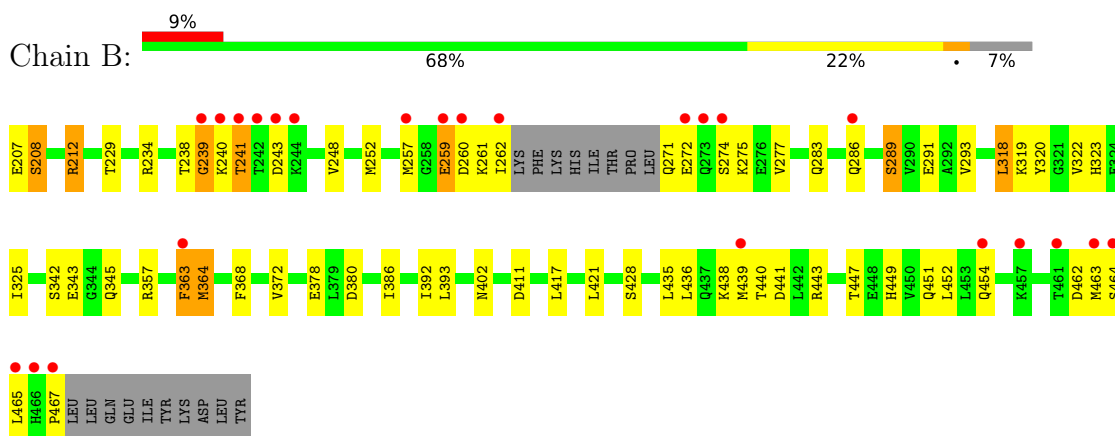
3 Residue-property plots [i](#)

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: Peroxisome proliferator-activated receptor gamma



- Molecule 1: Peroxisome proliferator-activated receptor gamma



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	56.76Å 89.78Å 58.77Å 90.00° 90.32° 90.00°	Depositor
Resolution (Å)	30.00 – 2.34 29.39 – 2.33	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-2.34) 98.4 (29.39-2.33)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.21 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.233 , 0.316 0.231 , 0.304	Depositor DCC
R_{free} test set	1274 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	34.6	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 42.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.004 for l,k,-h 0.029 for h,-k,-l 0.019 for l,-k,h	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4231	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.21% 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: DRD

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	0.95	1/2131 (0.0%)	0.87	3/2868 (0.1%)
1	B	1.01	0/2049	0.96	4/2759 (0.1%)
All	All	0.98	1/4180 (0.0%)	0.91	7/5627 (0.1%)

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	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	369	GLU	CG-CD	5.09	1.59	1.51

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	318	LEU	CB-CG-CD2	-6.41	100.11	111.00
1	B	212	ARG	NE-CZ-NH2	-6.29	117.15	120.30
1	B	318	LEU	CA-CB-CG	5.85	128.75	115.30
1	B	380	ASP	CB-CG-OD1	5.17	122.95	118.30
1	B	212	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	A	397	ARG	NE-CZ-NH2	-5.07	117.77	120.30
1	A	476	LEU	CA-CB-CG	5.04	126.90	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	357	ARG	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	2096	0	2157	46	0
1	B	2017	0	2069	35	0
2	A	41	0	34	8	0
3	A	35	0	0	5	0
3	B	42	0	0	6	0
All	All	4231	0	4260	83	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 10.

All (83) 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)
2:A:101:DRD:HAK2	2:A:101:DRD:HAP	1.49	0.94
1:B:364:MET:HE3	3:B:6:HOH:O	1.74	0.88
1:B:271:GLN:HG3	1:B:272:GLU:H	1.40	0.84
1:B:378:GLU:HG2	3:B:57:HOH:O	1.79	0.82
1:A:463:MET:HG3	1:A:464:SER:H	1.46	0.80
1:B:342:SER:O	1:B:345:GLN:HG3	1.81	0.80
1:A:477:TYR:O	1:A:477:TYR:HD1	1.67	0.78
1:B:271:GLN:HG3	1:B:272:GLU:N	1.99	0.78
1:A:275:LYS:HG2	1:A:279:ILE:HG21	1.68	0.76
1:B:283:GLN:NE2	1:B:462:ASP:OD2	2.20	0.75
1:A:463:MET:HG3	1:A:464:SER:N	2.03	0.72
1:A:216:LYS:O	1:A:216:LYS:HE2	1.93	0.69
2:A:101:DRD:HAP	2:A:101:DRD:CAK	2.21	0.69
1:A:449:HIS:HA	1:A:452:LEU:HD22	1.74	0.69
1:A:477:TYR:O	1:A:477:TYR:CD1	2.45	0.69
1:A:260:ASP:C	1:A:262:ILE:H	1.97	0.68
1:A:325:ILE:HD11	1:A:392:ILE:HG13	1.77	0.67
1:A:234:ARG:O	1:A:238:THR:HB	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:471:GLU:HG2	3:A:70:HOH:O	1.95	0.66
1:B:443:ARG:O	1:B:447:THR:HG23	1.96	0.65
1:A:474:LYS:HE2	1:A:475:ASP:OD2	1.96	0.64
1:B:325:ILE:HD11	1:B:392:ILE:HG13	1.83	0.60
1:A:370:PHE:HB2	1:A:445:ILE:HD11	1.84	0.60
1:A:238:THR:CG2	1:A:240:LYS:HG3	2.33	0.59
1:A:308:ASN:ND2	1:B:291:GLU:HG2	2.17	0.59
1:A:345:GLN:HE21	1:A:345:GLN:HA	1.68	0.57
1:B:229:THR:HA	3:B:71:HOH:O	2.04	0.57
1:A:457:LYS:HG2	1:A:463:MET:SD	2.45	0.56
1:A:379:LEU:HD11	1:A:435:LEU:HD13	1.87	0.56
1:A:444:GLN:CB	3:A:72:HOH:O	2.53	0.56
1:B:436:LEU:O	1:B:439:MET:HB2	2.04	0.56
1:A:260:ASP:C	1:A:262:ILE:N	2.59	0.56
1:A:297:THR:OG1	1:A:318:LEU:HD21	2.06	0.56
1:A:275:LYS:HG2	1:A:279:ILE:CG2	2.34	0.56
1:A:444:GLN:HB3	3:A:72:HOH:O	2.06	0.55
1:A:325:ILE:HG23	1:A:388:ILE:HD12	1.90	0.54
1:B:451:GLN:HA	1:B:454:GLN:HG2	1.89	0.54
1:A:449:HIS:O	1:A:452:LEU:HB2	2.08	0.53
1:A:330:LEU:HD21	2:A:101:DRD:HAB2	1.91	0.53
1:B:392:ILE:HG22	1:B:393:LEU:HD22	1.92	0.52
1:A:367:LYS:HG2	2:A:101:DRD:HAA2	1.92	0.52
1:B:252:MET:SD	1:B:277:VAL:HG11	2.49	0.52
1:B:208:SER:O	1:B:212:ARG:HG2	2.10	0.51
1:B:289:SER:O	1:B:293:VAL:HG23	2.10	0.51
1:A:363:PHE:CZ	1:A:452:LEU:HB3	2.45	0.51
1:A:440:THR:O	1:A:444:GLN:HG3	2.11	0.50
1:B:319:LYS:HE3	1:B:320:TYR:CE1	2.47	0.50
1:B:275:LYS:HE3	1:B:462:ASP:CG	2.32	0.49
1:B:364:MET:CE	3:B:6:HOH:O	2.44	0.49
2:A:101:DRD:CAK	2:A:101:DRD:CAP	2.90	0.48
1:B:257:MET:O	1:B:261:LYS:HB2	2.13	0.47
1:A:433:ALA:O	1:A:437:GLN:HG3	2.15	0.47
1:A:328:THR:HG21	1:A:388:ILE:HD11	1.97	0.46
1:B:463:MET:SD	1:B:465:LEU:HD13	2.56	0.46
1:B:363:PHE:HE1	1:B:449:HIS:CE1	2.34	0.46
1:A:242:THR:HG23	1:A:242:THR:O	2.14	0.45
1:A:238:THR:HG22	1:A:240:LYS:HG3	1.97	0.45
1:A:341:ILE:HD12	2:A:101:DRD:HAV	1.97	0.45
1:B:259:GLU:OE2	1:B:259:GLU:HA	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:402:ASN:HB3	3:A:16:HOH:O	2.15	0.45
1:B:238:THR:HB	1:B:239:GLY:H	1.50	0.44
1:B:363:PHE:CE1	1:B:449:HIS:CE1	3.05	0.44
1:A:288:ARG:HG3	2:A:101:DRD:HBN3	1.99	0.43
1:B:212:ARG:HA	1:B:212:ARG:HD2	1.84	0.43
1:B:438:LYS:HA	1:B:438:LYS:HD2	1.59	0.43
1:B:368:PHE:O	1:B:372:VAL:HG23	2.18	0.43
1:A:307:VAL:HG22	3:A:25:HOH:O	2.18	0.42
1:A:238:THR:HG22	1:A:240:LYS:H	1.84	0.42
1:B:286:GLN:OE1	1:B:465:LEU:HG	2.20	0.42
1:B:241:THR:O	1:B:243:ASP:OD1	2.37	0.42
1:A:288:ARG:NH1	1:A:291:GLU:OE1	2.53	0.41
1:A:477:TYR:CD1	1:A:477:TYR:C	2.93	0.41
1:B:386:ILE:HB	1:B:417:LEU:HD13	2.03	0.41
1:A:437:GLN:O	1:A:440:THR:HG23	2.20	0.41
2:A:101:DRD:HAK2	2:A:101:DRD:CAP	2.35	0.41
1:B:467:PRO:HA	3:B:36:HOH:O	2.20	0.41
1:A:316:THR:O	1:A:320:TYR:HD1	2.03	0.41
1:A:466:HIS:HA	1:A:467:PRO:HD2	1.78	0.41
1:A:325:ILE:HG12	1:A:388:ILE:HG23	2.03	0.40
1:A:360:PHE:CE1	1:A:456:ILE:HD11	2.55	0.40
1:B:421:LEU:HD11	1:B:435:LEU:HD23	2.04	0.40
1:B:447:THR:HG23	3:B:46:HOH:O	2.21	0.40
1:A:301:LYS:HZ2	1:B:467:PRO:N	2.19	0.40

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	257/271 (95%)	239 (93%)	12 (5%)	6 (2%)	6 3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	249/271 (92%)	237 (95%)	10 (4%)	2 (1%)	19	20
All	All	506/542 (93%)	476 (94%)	22 (4%)	8 (2%)	9	7

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	358	LYS
1	A	464	SER
1	B	274	SER
1	A	243	ASP
1	A	261	LYS
1	A	465	LEU
1	B	239	GLY
1	A	467	PRO

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	234/244 (96%)	212 (91%)	22 (9%)	8	7
1	B	226/244 (93%)	203 (90%)	23 (10%)	7	6
All	All	460/488 (94%)	415 (90%)	45 (10%)	8	6

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	207	GLU
1	A	216	LYS
1	A	234	ARG
1	A	238	THR
1	A	242	THR
1	A	243	ASP
1	A	248	VAL
1	A	255	LEU

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Mol	Chain	Res	Type
1	A	264	PHE
1	A	302	SER
1	A	318	LEU
1	A	322	VAL
1	A	342	SER
1	A	345	GLN
1	A	404	LYS
1	A	440	THR
1	A	441	ASP
1	A	452	LEU
1	A	453	LEU
1	A	456	ILE
1	A	465	LEU
1	A	477	TYR
1	B	207	GLU
1	B	208	SER
1	B	234	ARG
1	B	240	LYS
1	B	241	THR
1	B	248	VAL
1	B	259	GLU
1	B	260	ASP
1	B	262	ILE
1	B	289	SER
1	B	318	LEU
1	B	322	VAL
1	B	323	HIS
1	B	343	GLU
1	B	363	PHE
1	B	364	MET
1	B	402	ASN
1	B	411	ASP
1	B	428	SER
1	B	440	THR
1	B	441	ASP
1	B	452	LEU
1	B	464	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	294	GLN

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Mol	Chain	Res	Type
1	A	345	GLN
1	B	253	ASN
1	B	271	GLN
1	B	273	GLN
1	B	402	ASN
1	B	437	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](#)

1 ligand is 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	DRD	A	101	-	43,45,45	1.65	8 (18%)	59,64,64	1.27	5 (8%)

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	DRD	A	101	-	-	12/29/29/29	0/5/5/5

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	101	DRD	CAG-CAH	4.98	1.58	1.53
2	A	101	DRD	CAO-NAT	-4.93	1.33	1.39
2	A	101	DRD	CBA-CBB	3.46	1.55	1.49
2	A	101	DRD	CBC-CBB	3.31	1.55	1.49
2	A	101	DRD	CAE-CBK	2.30	1.42	1.38
2	A	101	DRD	CAU-NAT	-2.28	1.35	1.38
2	A	101	DRD	OAF-CAG	2.26	1.49	1.45
2	A	101	DRD	CBL-CBK	2.14	1.56	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	101	DRD	CAG-OAF-CAS	3.40	129.13	121.87
2	A	101	DRD	OAF-CAS-CAN	3.39	118.25	114.16
2	A	101	DRD	OAD-CAE-CBJ	-2.66	118.21	123.97
2	A	101	DRD	OAD-CAE-CBK	2.58	120.95	117.00
2	A	101	DRD	OAF-CAG-CAH	-2.34	106.80	109.99

There are no chirality outliers.

All (12) torsion outliers are listed below:

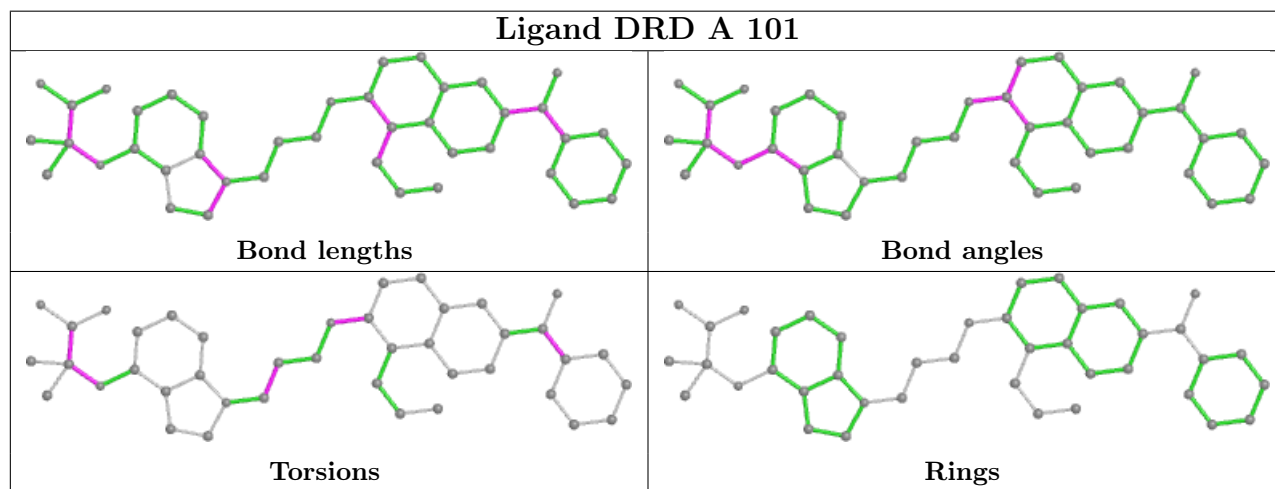
Mol	Chain	Res	Type	Atoms
2	A	101	DRD	NAT-CAA-CAB-CAC
2	A	101	DRD	CAH-CAG-OAF-CAS
2	A	101	DRD	OAF-CAG-CAH-OAJ
2	A	101	DRD	CAV-CBA-CBB-OBO
2	A	101	DRD	CAZ-CBA-CBB-OBO
2	A	101	DRD	CAZ-CBA-CBB-CBC
2	A	101	DRD	CAV-CBA-CBB-CBC
2	A	101	DRD	CAL-CAG-OAF-CAS
2	A	101	DRD	CBJ-CAE-OAD-CAC
2	A	101	DRD	CBK-CAE-OAD-CAC
2	A	101	DRD	CAK-CAG-OAF-CAS
2	A	101	DRD	CAK-CAG-CAH-OAJ

There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	101	DRD	8	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

6.1 Protein, DNA and RNA chains

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	261/271 (96%)	0.29	16 (6%) 21 30	19, 35, 66, 96	0
1	B	253/271 (93%)	0.39	24 (9%) 8 13	15, 31, 83, 119	0
All	All	514/542 (94%)	0.34	40 (7%) 13 19	15, 33, 75, 119	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	465	LEU	11.3
1	A	264	PHE	8.7
1	B	241	THR	7.6
1	B	467	PRO	7.2
1	B	272	GLU	6.5
1	B	464	SER	6.2
1	B	273	GLN	6.0
1	B	274	SER	5.8
1	B	242	THR	5.7
1	B	243	ASP	5.6
1	A	477	TYR	5.3
1	A	262	ILE	5.0
1	B	240	LYS	4.5
1	B	466	HIS	4.4
1	A	242	THR	4.4
1	B	454	GLN	4.1
1	B	260	ASP	4.0
1	B	461	THR	3.9
1	B	463	MET	3.8
1	B	244	LYS	3.7
1	A	287	PHE	3.6
1	B	363	PHE	3.6
1	A	275	LYS	3.2
1	B	439	MET	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	239	GLY	2.9
1	A	241	THR	2.8
1	B	259	GLU	2.8
1	B	262	ILE	2.8
1	B	257	MET	2.6
1	A	463	MET	2.6
1	A	243	ASP	2.6
1	B	457	LYS	2.3
1	A	263	LYS	2.3
1	A	436	LEU	2.2
1	A	452	LEU	2.2
1	A	470	GLN	2.2
1	A	244	LYS	2.2
1	A	277	VAL	2.1
1	B	286	GLN	2.1
1	A	311	LEU	2.1

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](#)

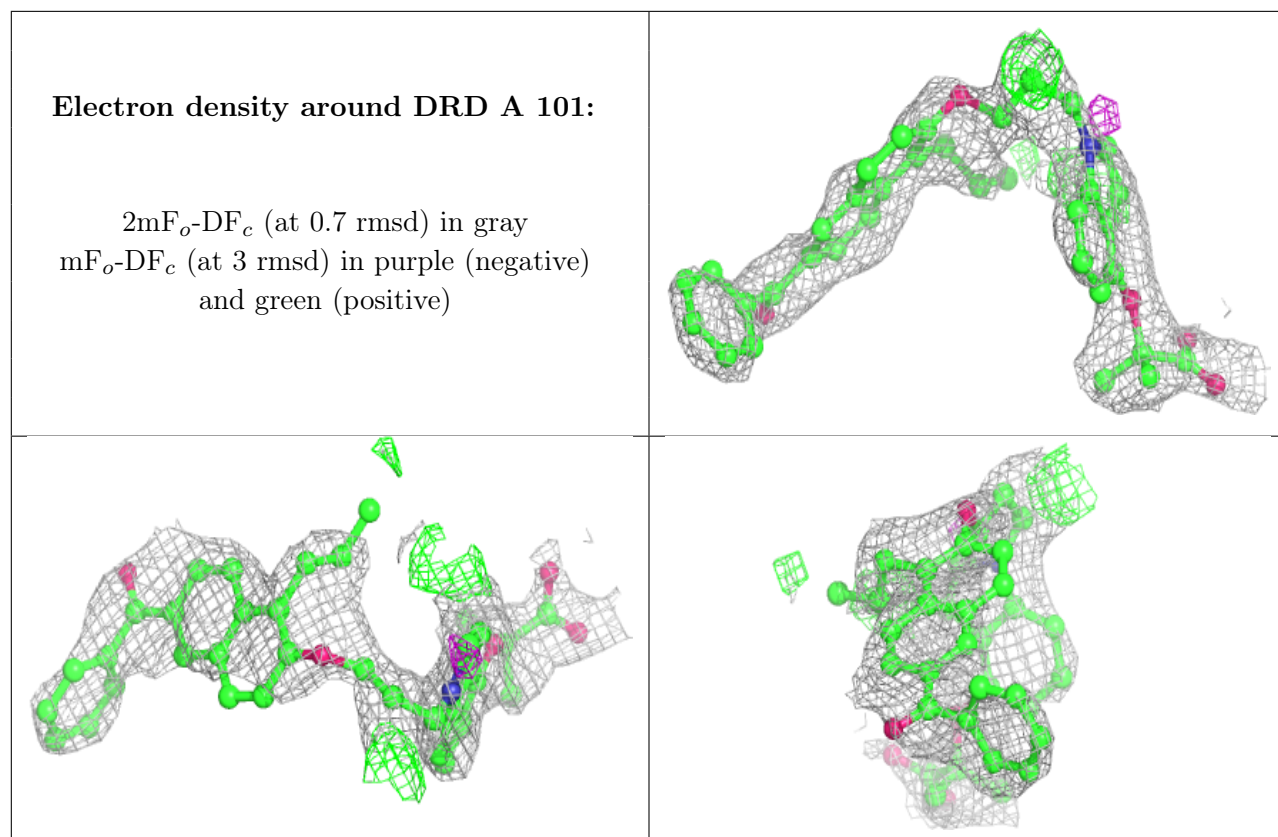
There are no monosaccharides in this entry.

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	DRD	A	101	41/41	0.71	0.26	60,75,76,77	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.