



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 05:34 PM UTC

PDB ID : 2HWQ / pdb_00002hwq
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 : 1.97 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

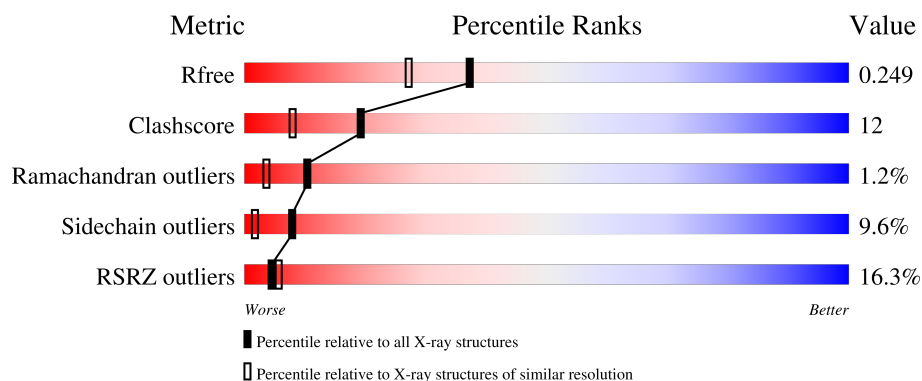
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.97 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}	180053	1506 (1.98-1.98)
Clashscore	190562	1534 (1.98-1.98)
Ramachandran outliers	187476	1518 (1.98-1.98)
Sidechain outliers	187428	1518 (1.98-1.98)
RSRZ outliers	180081	1506 (1.98-1.98)

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	14% 72% 20% • •
1	B	271	17% 71% 18% • 7%

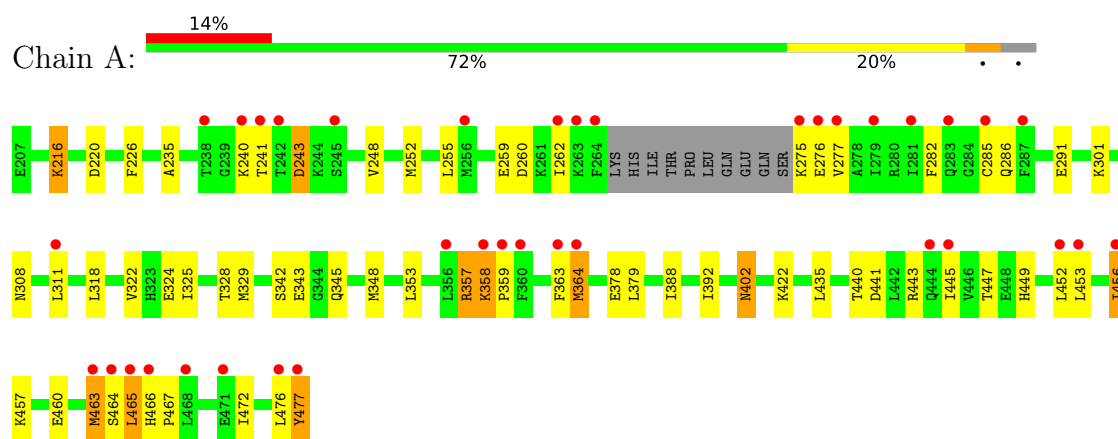
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	113	Total	O	0	0
			113	113		

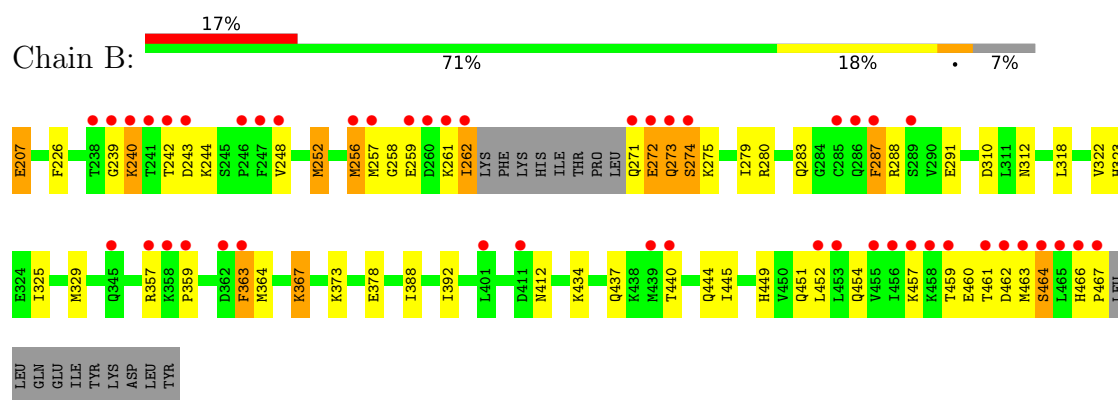
3 Residue-property plots [i](#)

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	56.02Å 88.67Å 58.02Å 90.00° 90.24° 90.00°	Depositor
Resolution (Å)	30.00 – 1.97 30.00 – 1.97	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-1.97) 99.3 (30.00-1.97)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.90 (at 1.96Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.239 , 0.265 0.227 , 0.249	Depositor DCC
R_{free} test set	1999 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	28.4	Xtriage
Anisotropy	0.091	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 45.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for l,k,-h 0.032 for h,-k,-l 0.019 for l,-k,h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4347	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.38% 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: DRY

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	0.56	1/2131 (0.0%)	0.91	0/2868
1	B	0.52	0/2049	0.92	0/2759
All	All	0.54	1/4180 (0.0%)	0.92	0/5627

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	477	TYR	C-OXT	13.55	1.50	1.23

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	2096	0	2157	53	0
1	B	2017	0	2069	45	0
2	A	39	0	30	9	0
3	A	82	0	0	4	0
3	B	113	0	0	14	0
All	All	4347	0	4256	98	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 12.

All (98) 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:207:GLU:HB3	3:B:196:HOH:O	1.47	1.11
1:B:444:GLN:HB3	3:B:197:HOH:O	1.66	0.95
1:A:353:LEU:HD22	1:A:364:MET:SD	2.08	0.92
1:A:364:MET:SD	2:A:1101:DRY:HAC1	2.18	0.84
1:A:282:PHE:CE1	2:A:1101:DRY:HAJ	2.17	0.80
1:A:364:MET:HA	2:A:1101:DRY:HAA2	1.64	0.80
1:B:378:GLU:HG2	3:B:148:HOH:O	1.86	0.74
1:B:252:MET:HE1	3:B:173:HOH:O	1.88	0.73
1:A:466:HIS:CG	1:A:467:PRO:HD2	2.23	0.73
1:B:275:LYS:HE3	1:B:462:ASP:OD1	1.90	0.72
1:A:276:GLU:OE2	1:A:357:ARG:HD3	1.92	0.69
1:A:216:LYS:O	1:A:216:LYS:HE2	1.94	0.68
1:A:282:PHE:CD1	2:A:1101:DRY:HAJ	2.32	0.64
1:A:443:ARG:O	1:A:447:THR:HG23	1.98	0.63
1:A:325:ILE:HD11	1:A:392:ILE:HG13	1.81	0.63
1:A:364:MET:HB3	2:A:1101:DRY:HAB1	1.84	0.60
1:A:358:LYS:HB3	1:A:359:PRO:HD3	1.84	0.58
1:B:288:ARG:HH11	1:B:291:GLU:HB3	1.68	0.58
1:B:357:ARG:HG2	1:B:359:PRO:HD2	1.86	0.58
1:B:258:GLY:HA2	1:B:261:LYS:HB2	1.84	0.57
1:A:325:ILE:HG12	1:A:388:ILE:HG23	1.86	0.57
1:A:364:MET:CA	2:A:1101:DRY:HAA2	2.34	0.57
1:B:252:MET:O	1:B:256:MET:HG2	2.05	0.56
1:B:207:GLU:HG3	3:B:170:HOH:O	2.05	0.56
1:B:283:GLN:NE2	1:B:462:ASP:OD2	2.38	0.56
1:A:364:MET:HB3	2:A:1101:DRY:CAB	2.36	0.56
1:B:325:ILE:HD11	1:B:392:ILE:HG13	1.87	0.56
1:B:271:GLN:HG3	1:B:272:GLU:N	2.21	0.55
1:A:422:LYS:HG3	3:A:125:HOH:O	2.06	0.54
1:B:226:PHE:CG	1:B:329:MET:HE1	2.43	0.54
1:A:457:LYS:HG3	3:A:172:HOH:O	2.07	0.54
1:B:261:LYS:HG2	3:B:137:HOH:O	2.09	0.53
1:B:310:ASP:OD1	1:B:312:ASN:HB2	2.09	0.53
1:B:412:ASN:HB3	3:B:122:HOH:O	2.09	0.53
1:A:348:MET:SD	1:A:353:LEU:HD21	2.49	0.52
1:B:363:PHE:CE2	1:B:452:LEU:HG	2.44	0.52
1:B:262:ILE:HG22	3:B:137:HOH:O	2.10	0.52
1:B:288:ARG:NH1	1:B:291:GLU:HB3	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:325:ILE:HD11	1:B:392:ILE:CG1	2.41	0.51
1:A:308:ASN:ND2	1:B:291:GLU:OE2	2.40	0.51
1:A:456:ILE:CG2	1:A:463:MET:HE3	2.40	0.51
1:A:255:LEU:HD21	1:A:277:VAL:HG13	1.93	0.51
1:B:259:GLU:OE1	1:B:280:ARG:NH2	2.34	0.50
1:B:259:GLU:CD	1:B:280:ARG:HH22	2.19	0.50
1:A:363:PHE:CD1	1:A:452:LEU:HD23	2.48	0.49
1:B:226:PHE:CD1	1:B:329:MET:HE1	2.47	0.48
1:A:357:ARG:NH2	1:A:460:GLU:OE1	2.47	0.48
1:B:367:LYS:HD2	1:B:367:LYS:N	2.27	0.48
1:A:363:PHE:CE1	1:A:452:LEU:HB3	2.49	0.47
1:B:412:ASN:CB	3:B:122:HOH:O	2.62	0.47
1:A:449:HIS:HE1	2:A:1101:DRY:CAL	2.28	0.47
1:B:467:PRO:HG3	3:B:131:HOH:O	2.13	0.47
1:A:466:HIS:CE1	1:A:467:PRO:HG2	2.50	0.46
1:A:243:ASP:OD1	1:A:243:ASP:N	2.49	0.46
1:B:364:MET:O	1:B:367:LYS:HB2	2.15	0.46
1:A:226:PHE:CG	1:A:329:MET:HE1	2.50	0.46
1:B:467:PRO:HB3	3:B:131:HOH:O	2.15	0.46
1:A:282:PHE:O	1:A:285:CYS:HB2	2.15	0.46
1:A:325:ILE:HG12	1:A:388:ILE:HD12	1.98	0.45
1:A:325:ILE:HD11	1:A:392:ILE:CG1	2.46	0.45
1:B:279:ILE:HD13	1:B:462:ASP:CB	2.46	0.45
1:B:287:PHE:HB3	3:B:138:HOH:O	2.15	0.45
1:A:342:SER:O	1:A:345:GLN:HG2	2.17	0.45
1:B:273:GLN:O	1:B:274:SER:HB3	2.17	0.45
1:A:465:LEU:HD13	1:A:465:LEU:N	2.32	0.44
1:B:325:ILE:HG12	1:B:388:ILE:HG23	1.99	0.44
1:A:226:PHE:CD1	1:A:329:MET:HE1	2.52	0.44
1:A:456:ILE:HG22	1:A:463:MET:HE3	1.99	0.44
1:A:472:ILE:O	1:A:476:LEU:HD13	2.17	0.44
1:B:434:LYS:HA	1:B:437:GLN:HE21	1.82	0.44
1:A:286:GLN:NE2	1:A:465:LEU:HD12	2.32	0.44
1:B:363:PHE:HE1	1:B:449:HIS:CE1	2.35	0.44
1:B:258:GLY:HA2	1:B:261:LYS:CB	2.48	0.44
1:B:467:PRO:N	3:B:118:HOH:O	2.50	0.44
2:A:1101:DRY:HAN	2:A:1101:DRY:HAB2	1.92	0.43
1:A:357:ARG:O	1:A:359:PRO:HD2	2.18	0.43
1:A:463:MET:HE2	1:A:463:MET:HB2	1.89	0.43
1:A:452:LEU:HD12	1:A:452:LEU:HA	1.86	0.43
1:A:311:LEU:HD12	1:A:311:LEU:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:328:THR:HG21	1:A:388:ILE:HD11	2.00	0.42
1:B:257:MET:HE3	1:B:257:MET:HB3	1.70	0.42
1:B:463:MET:O	1:B:464:SER:CB	2.67	0.42
1:A:363:PHE:CZ	1:A:452:LEU:HB3	2.54	0.42
1:A:255:LEU:HD21	1:A:277:VAL:CG1	2.49	0.42
1:B:240:LYS:HE3	1:B:240:LYS:HB2	1.75	0.42
1:A:353:LEU:HD22	1:A:364:MET:CE	2.49	0.42
1:A:402:ASN:ND2	3:A:168:HOH:O	2.52	0.41
1:B:243:ASP:OD1	1:B:244:LYS:HG2	2.20	0.41
1:A:358:LYS:HB3	1:A:359:PRO:CD	2.48	0.41
1:B:459:THR:O	1:B:460:GLU:HG2	2.20	0.41
1:A:262:ILE:HG12	3:A:177:HOH:O	2.19	0.41
1:B:363:PHE:HE1	1:B:449:HIS:ND1	2.18	0.41
1:A:441:ASP:O	1:A:445:ILE:HG12	2.21	0.41
1:A:259:GLU:O	1:A:262:ILE:HG13	2.20	0.41
1:A:379:LEU:HD11	1:A:435:LEU:HD13	2.02	0.41
1:A:235:ALA:HB1	1:A:240:LYS:HD3	2.04	0.40
1:B:445:ILE:HD13	3:B:182:HOH:O	2.21	0.40
1:A:324:GLU:OE2	1:A:443:ARG:HD3	2.21	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%)	248 (96%)	7 (3%)	2 (1%)	16	7
1	B	249/271 (92%)	236 (95%)	9 (4%)	4 (2%)	7	2
All	All	506/542 (93%)	484 (96%)	16 (3%)	6 (1%)	10	3

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	358	LYS
1	A	464	SER
1	B	274	SER
1	B	464	SER
1	B	242	THR
1	B	239	GLY

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	234/244 (96%)	211 (90%)	23 (10%)	7	1
1	B	226/244 (93%)	205 (91%)	21 (9%)	8	2
All	All	460/488 (94%)	416 (90%)	44 (10%)	8	2

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	216	LYS
1	A	220	ASP
1	A	241	THR
1	A	243	ASP
1	A	248	VAL
1	A	252	MET
1	A	260	ASP
1	A	275	LYS
1	A	291	GLU
1	A	301	LYS
1	A	318	LEU
1	A	322	VAL
1	A	343	GLU
1	A	357	ARG
1	A	364	MET
1	A	378	GLU
1	A	402	ASN
1	A	440	THR

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Mol	Chain	Res	Type
1	A	453	LEU
1	A	456	ILE
1	A	463	MET
1	A	465	LEU
1	A	477	TYR
1	B	207	GLU
1	B	240	LYS
1	B	248	VAL
1	B	252	MET
1	B	256	MET
1	B	262	ILE
1	B	272	GLU
1	B	273	GLN
1	B	287	PHE
1	B	318	LEU
1	B	322	VAL
1	B	323	HIS
1	B	363	PHE
1	B	367	LYS
1	B	373	LYS
1	B	440	THR
1	B	451	GLN
1	B	454	GLN
1	B	457	LYS
1	B	461	THR
1	B	466	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	283	GLN
1	A	294	GLN
1	A	402	ASN
1	A	449	HIS
1	A	451	GLN
1	B	273	GLN
1	B	402	ASN
1	B	437	GLN
1	B	454	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	DRY	A	1101	-	43,43,43	1.34	4 (9%)	59,59,59	1.10	3 (5%)

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	DRY	A	1101	-	-	9/23/23/23	0/5/5/5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	DRY	CAH-NAM	-3.43	1.33	1.39
2	A	1101	DRY	CAG-CAF	-3.39	1.34	1.43
2	A	1101	DRY	CAV-CAU	3.18	1.54	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	DRY	CAT-CAU	2.66	1.53	1.49

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	DRY	CBJ-OB1-CAI	-3.71	110.99	117.63
2	A	1101	DRY	CAZ-CAY-CBD	-2.51	118.77	122.57
2	A	1101	DRY	CAV-CAU-CAT	2.12	124.18	120.18

There are no chirality outliers.

All (9) torsion outliers are listed below:

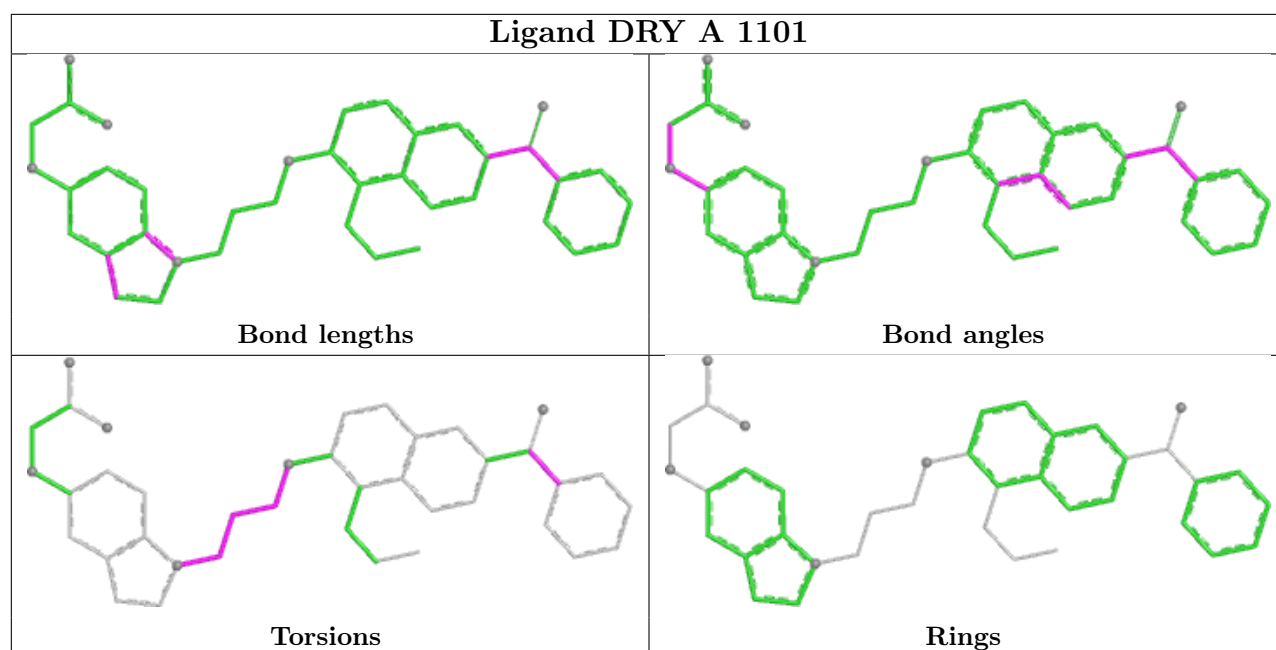
Mol	Chain	Res	Type	Atoms
2	A	1101	DRY	NAM-CAA-CAB-CAC
2	A	1101	DRY	CAA-CAB-CAC-OAD
2	A	1101	DRY	CAO-CAT-CAU-OBH
2	A	1101	DRY	CAS-CAT-CAU-OBH
2	A	1101	DRY	CAO-CAT-CAU-CAV
2	A	1101	DRY	CAS-CAT-CAU-CAV
2	A	1101	DRY	CAB-CAA-NAM-CAH
2	A	1101	DRY	CAB-CAA-NAM-CAN
2	A	1101	DRY	CAB-CAC-OAD-CAE

There are no ring outliers.

1 monomer is involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1101	DRY	9	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%)	0.78	37 (14%) 6 8	15, 30, 63, 89	0
1	B	253/271 (93%)	0.88	47 (18%) 3 4	14, 27, 75, 92	0
All	All	514/542 (94%)	0.83	84 (16%) 4 6	14, 29, 70, 92	0

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	363	PHE	9.2
1	B	465	LEU	8.6
1	B	467	PRO	8.6
1	B	262	ILE	8.2
1	A	264	PHE	7.1
1	B	241	THR	6.0
1	A	262	ILE	6.0
1	B	466	HIS	5.6
1	B	242	THR	5.1
1	B	461	THR	5.1
1	A	359	PRO	5.0
1	B	274	SER	4.7
1	A	452	LEU	4.6
1	B	259	GLU	4.5
1	B	239	GLY	4.5
1	B	462	ASP	4.4
1	B	463	MET	4.2
1	B	273	GLN	4.2
1	B	260	ASP	4.0
1	A	477	TYR	4.0
1	A	263	LYS	4.0
1	B	464	SER	4.0
1	A	358	LYS	3.9
1	A	364	MET	3.8

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Mol	Chain	Res	Type	RSRZ
1	B	458	LYS	3.8
1	A	245	SER	3.7
1	B	455	VAL	3.7
1	B	358	LYS	3.7
1	A	238	THR	3.7
1	A	279	ILE	3.6
1	A	311	LEU	3.4
1	A	363	PHE	3.3
1	A	277	VAL	3.3
1	A	465	LEU	3.3
1	A	242	THR	3.2
1	B	362	ASP	3.2
1	B	456	ILE	3.2
1	A	356	LEU	3.2
1	B	271	GLN	3.2
1	B	440	THR	3.0
1	B	240	LYS	3.0
1	B	457	LYS	2.9
1	B	286	GLN	2.9
1	B	287	PHE	2.9
1	A	468	LEU	2.8
1	B	459	THR	2.8
1	B	238	THR	2.8
1	B	243	ASP	2.8
1	B	452	LEU	2.8
1	A	464	SER	2.7
1	B	247	PHE	2.7
1	A	241	THR	2.7
1	A	275	LYS	2.6
1	B	261	LYS	2.6
1	B	248	VAL	2.6
1	A	476	LEU	2.6
1	B	272	GLU	2.6
1	A	285	CYS	2.5
1	B	357	ARG	2.5
1	B	401	LEU	2.5
1	B	246	PRO	2.4
1	B	453	LEU	2.4
1	A	276	GLU	2.3
1	A	456	ILE	2.3
1	A	444	GLN	2.3
1	A	287	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	256	MET	2.3
1	B	289	SER	2.3
1	A	463	MET	2.3
1	B	439	MET	2.2
1	A	283	GLN	2.2
1	A	445	ILE	2.2
1	B	359	PRO	2.2
1	A	240	LYS	2.2
1	A	471	GLU	2.1
1	B	411	ASP	2.1
1	A	281	ILE	2.1
1	A	256	MET	2.1
1	A	453	LEU	2.1
1	A	360	PHE	2.1
1	B	257	MET	2.1
1	A	466	HIS	2.1
1	B	345	GLN	2.1
1	B	285	CYS	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

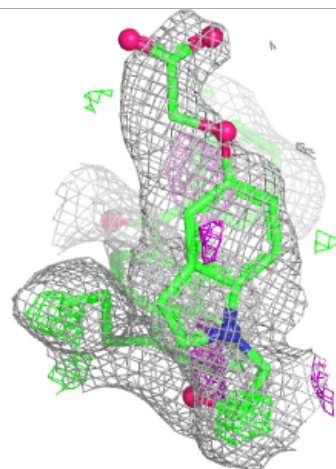
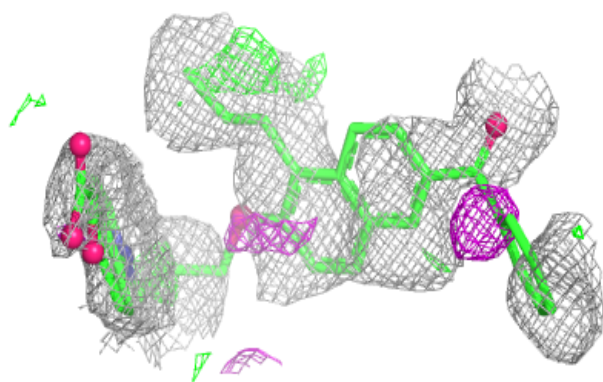
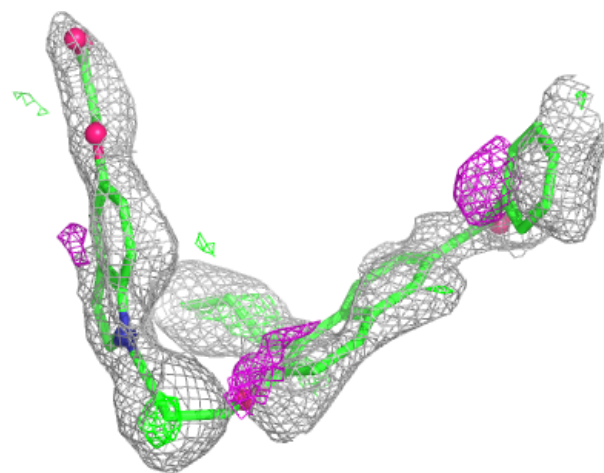
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	DRY	A	1101	39/39	0.49	0.23	65,76,79,80	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 DRY A 1101:

$2mF_o-DF_c$ (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.