



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 10:59 AM UTC

PDB ID : 2G0G / pdb_00002g0g
Title : Structure-based drug design of a novel family of PPAR partial agonists: virtual screening, x-ray crystallography and in vitro/in vivo biological activities
Authors : Lu, I.L.; Peng, Y.H.; Huang, C.F.; Lin, Y.T.; Hsu, J.T.A.; Wu, S.Y.
Deposited on : 2006-02-13
Resolution : 2.54 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

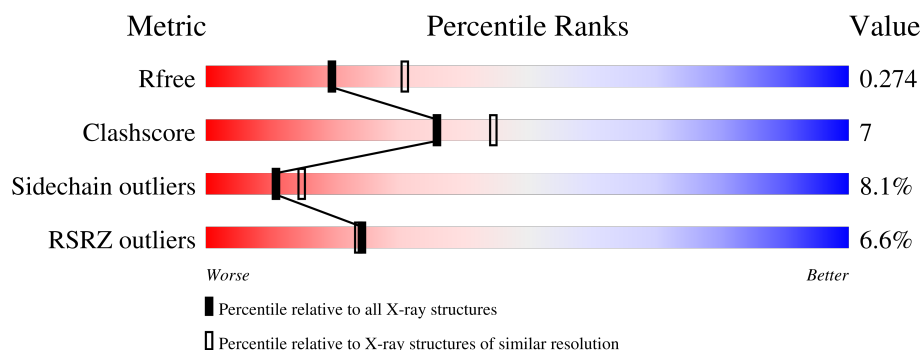
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.54 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	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

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	5% 73% 25% .
1	B	271	8% 79% 18% .

2 Entry composition [i](#)

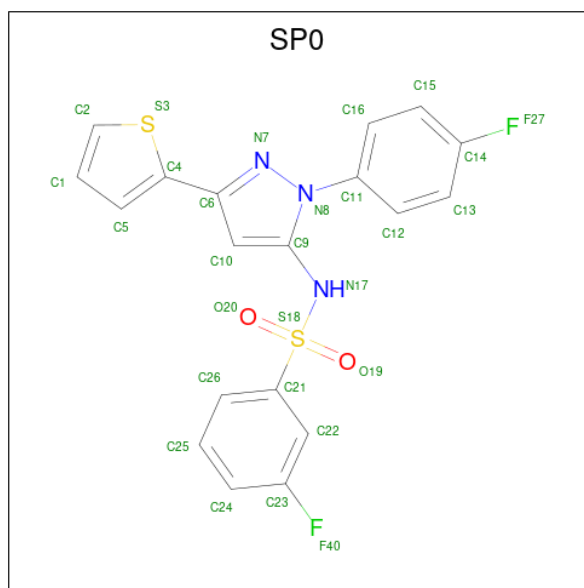
There are 3 unique types of molecules in this entry. The entry contains 4472 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Peroxisome proliferator-activated receptor gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	271	Total	C	N	O	S	0	0	0
			2177	1406	355	406	10			
1	B	271	Total	C	N	O	S	0	0	0
			2177	1406	355	406	10			

- Molecule 2 is 3-FLUORO-N-[1-(4-FLUOROPHENYL)-3-(2-THIENYL)-1H-PYRAZOL-5-YL]BENZENESULFONAMIDE (CCD ID: SP0) (formula: C₁₉H₁₃F₂N₃O₂S₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			28	19	2	3	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	32	Total	O	0	0
			32	32		

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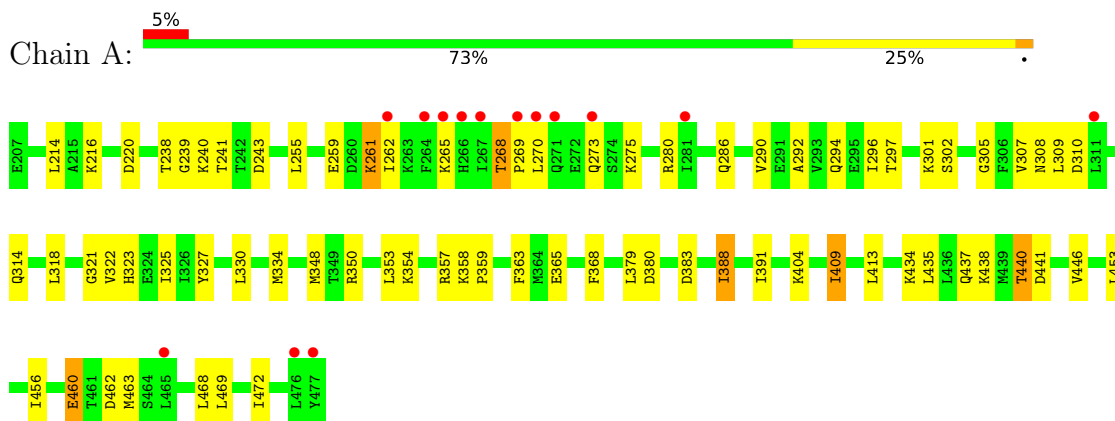
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	58	Total	O	0	0
			58	58		

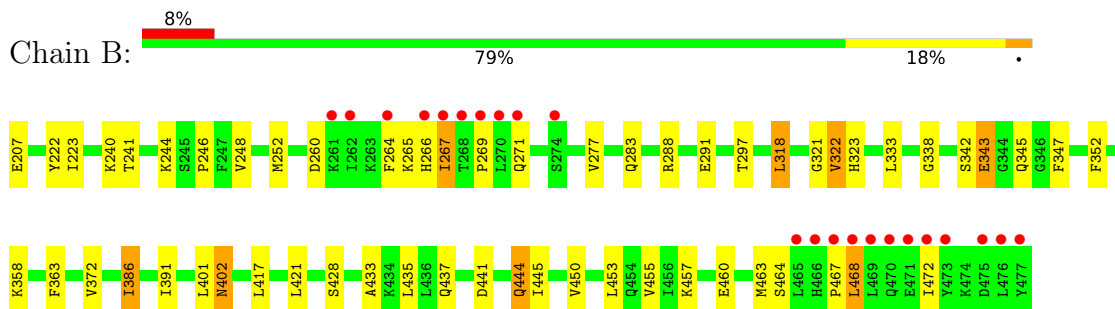
3 Residue-property plots

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	56.42Å 88.81Å 58.26Å 90.00° 89.99° 90.00°	Depositor
Resolution (Å)	20.00 – 2.54 20.00 – 2.54	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.54) 98.9 (20.00-2.54)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.36 (at 2.54Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.216 , 0.264 (Not available) , 0.274	Depositor DCC
R_{free} test set	975 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	44.2	Xtriage
Anisotropy	0.356	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 41.7	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 0.033 for h,-k,-l 0.027 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4472	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.76% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SP0

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	0.46	0/2215	1.29	5/2985 (0.2%)
1	B	0.48	0/2215	1.30	14/2985 (0.5%)
All	All	0.47	0/4430	1.29	19/5970 (0.3%)

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	363	PHE	N-CA-C	7.37	118.96	111.07
1	A	268	THR	CA-C-N	6.91	128.48	119.84
1	A	268	THR	C-N-CA	6.91	128.48	119.84
1	B	391	ILE	N-CA-C	6.85	117.00	110.42
1	B	267	ILE	N-CA-C	6.56	122.99	109.34
1	B	352	PHE	N-CA-C	6.11	117.61	111.07
1	B	322	VAL	N-CA-CB	-6.02	103.83	110.51
1	B	321	GLY	CA-C-N	5.91	128.22	120.60
1	B	321	GLY	C-N-CA	5.91	128.22	120.60
1	A	440	THR	N-CA-C	-5.81	104.38	112.45
1	B	358	LYS	CA-C-N	-5.69	112.72	119.84
1	B	358	LYS	C-N-CA	-5.69	112.72	119.84
1	A	409	ILE	N-CA-C	-5.65	105.22	110.53
1	B	323	HIS	N-CA-C	5.48	117.69	111.11
1	B	428	SER	CB-CA-C	-5.47	102.11	111.41
1	A	391	ILE	N-CA-C	5.38	115.58	110.42
1	B	460	GLU	N-CA-C	5.32	118.33	110.46
1	B	222	TYR	N-CA-C	-5.22	105.59	111.28
1	B	277	VAL	N-CA-C	5.03	115.75	110.62

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	2177	0	2241	42	0
1	B	2177	0	2241	24	0
2	A	28	0	13	1	0
3	A	32	0	0	3	0
3	B	58	0	0	4	0
All	All	4472	0	4495	65	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 7.

All (65) 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:A:354:LYS:HE2	1:A:365:GLU:HG2	1.57	0.86
1:A:325:ILE:HD12	1:A:388:ILE:HG13	1.61	0.82
1:A:327:TYR:HE2	1:A:446:VAL:HG22	1.54	0.72
1:B:421:LEU:HD11	1:B:435:LEU:HD23	1.75	0.69
1:A:292:ALA:O	1:A:296:ILE:HG12	1.93	0.69
1:B:401:LEU:C	1:B:402:ASN:HD22	2.02	0.67
1:B:240:LYS:HG3	1:B:241:THR:HG22	1.78	0.65
1:A:296:ILE:HD12	1:A:325:ILE:HG21	1.82	0.62
1:A:350:ARG:HG3	1:A:368:PHE:CD2	2.34	0.62
1:A:379:LEU:HD11	1:A:435:LEU:HD13	1.82	0.61
1:A:434:LYS:HA	1:A:437:GLN:HE21	1.68	0.59
1:B:288:ARG:HH11	1:B:291:GLU:HB3	1.70	0.57
1:B:402:ASN:HD22	1:B:402:ASN:N	2.02	0.57
1:B:444:GLN:HB3	3:B:72:HOH:O	2.03	0.57
1:B:433:ALA:O	1:B:437:GLN:HG3	2.06	0.55
1:A:214:LEU:HD21	1:A:413:LEU:HD23	1.89	0.54
1:A:261:LYS:HA	1:A:261:LYS:HE3	1.90	0.53
1:B:402:ASN:N	1:B:402:ASN:ND2	2.54	0.53
1:A:297:THR:HG23	1:A:318:LEU:HD21	1.92	0.52
1:A:309:LEU:O	1:A:310:ASP:C	2.53	0.52
1:B:441:ASP:O	1:B:445:ILE:HD12	2.09	0.52
1:A:290:VAL:HG13	1:A:468:LEU:HD23	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:265:LYS:HG3	1:B:266:HIS:H	1.76	0.51
1:A:327:TYR:CE2	1:A:446:VAL:HG22	2.42	0.51
1:A:348:MET:SD	1:A:353:LEU:HD21	2.51	0.49
1:A:321:GLY:O	1:A:325:ILE:HG12	2.12	0.49
1:B:297:THR:HG23	1:B:318:LEU:HD21	1.95	0.49
1:A:239:GLY:C	1:A:241:THR:H	2.20	0.49
1:A:307:VAL:HG22	3:A:86:HOH:O	2.13	0.48
1:A:296:ILE:HD12	1:A:325:ILE:CG2	2.42	0.48
1:A:330:LEU:O	1:A:334:MET:HG3	2.13	0.48
1:B:386:ILE:HB	1:B:417:LEU:HD13	1.96	0.48
1:B:271:GLN:HG2	1:B:283:GLN:HE21	1.79	0.47
1:A:323:HIS:HE1	1:A:472:ILE:HG22	1.79	0.46
2:A:101:SP0:C16	2:A:101:SP0:H17	2.29	0.46
1:B:269:PRO:HA	3:B:88:HOH:O	2.16	0.46
1:B:372:VAL:HG12	3:B:28:HOH:O	2.15	0.46
1:A:301:LYS:CD	1:B:468:LEU:HB2	2.46	0.46
1:A:456:ILE:O	1:A:460:GLU:HB2	2.16	0.45
1:A:325:ILE:HG23	1:A:388:ILE:HG13	1.98	0.45
1:A:357:ARG:HG2	1:A:359:PRO:HD2	1.97	0.45
1:A:310:ASP:O	1:A:314:GLN:HG3	2.16	0.45
1:A:259:GLU:C	1:A:261:LYS:H	2.23	0.45
1:A:438:LYS:HE2	3:A:64:HOH:O	2.17	0.45
1:A:259:GLU:O	1:A:262:ILE:HG13	2.18	0.44
1:B:463:MET:O	1:B:464:SER:HB2	2.18	0.44
1:B:338:GLY:HA3	1:B:347:PHE:CZ	2.53	0.43
1:B:271:GLN:HG2	1:B:283:GLN:NE2	2.33	0.43
1:A:325:ILE:HG23	1:A:388:ILE:CG1	2.49	0.43
1:A:290:VAL:O	1:A:294:GLN:HG3	2.19	0.42
1:B:244:LYS:HG2	3:B:90:HOH:O	2.18	0.42
1:A:305:GLY:HA2	1:A:308:ASN:HD22	1.85	0.42
1:B:260:ASP:C	1:B:264:PHE:HB2	2.44	0.42
1:A:404:LYS:NZ	3:A:50:HOH:O	2.52	0.42
1:A:301:LYS:NZ	1:B:467:PRO:HD2	2.36	0.41
1:A:268:THR:HA	1:A:269:PRO:HD3	1.97	0.41
1:A:273:GLN:HA	1:A:280:ARG:CD	2.50	0.41
1:A:290:VAL:HG22	1:A:469:LEU:HG	2.02	0.41
1:A:330:LEU:HG	1:A:334:MET:HE3	2.02	0.41
1:A:380:ASP:OD1	1:A:383:ASP:N	2.48	0.40
1:A:380:ASP:OD1	1:A:380:ASP:C	2.64	0.40
1:B:342:SER:O	1:B:343:GLU:C	2.62	0.40
1:A:358:LYS:HB3	1:A:359:PRO:HD3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:THR:CG2	1:A:240:LYS:HG3	2.52	0.40
1:B:246:PRO:HA	1:B:345:GLN:O	2.21	0.40

There are no symmetry-related clashes.

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](#)

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	244/244 (100%)	224 (92%)	20 (8%)	10	14
1	B	225/244 (92%)	207 (92%)	18 (8%)	11	15
All	All	469/488 (96%)	431 (92%)	38 (8%)	11	15

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	216	LYS
1	A	220	ASP
1	A	243	ASP
1	A	255	LEU
1	A	261	LYS
1	A	265	LYS
1	A	270	LEU
1	A	275	LYS
1	A	286	GLN
1	A	302	SER
1	A	322	VAL

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Mol	Chain	Res	Type
1	A	363	PHE
1	A	388	ILE
1	A	409	ILE
1	A	440	THR
1	A	441	ASP
1	A	453	LEU
1	A	460	GLU
1	A	462	ASP
1	A	463	MET
1	B	207	GLU
1	B	223	ILE
1	B	248	VAL
1	B	252	MET
1	B	267	ILE
1	B	318	LEU
1	B	322	VAL
1	B	333	LEU
1	B	343	GLU
1	B	386	ILE
1	B	402	ASN
1	B	444	GLN
1	B	450	VAL
1	B	453	LEU
1	B	455	VAL
1	B	457	LYS
1	B	468	LEU
1	B	472	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	271	GLN
1	A	283	GLN
1	A	294	GLN
1	A	308	ASN
1	A	437	GLN
1	A	451	GLN
1	B	271	GLN
1	B	273	GLN
1	B	283	GLN
1	B	402	ASN
1	B	444	GLN

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Mol	Chain	Res	Type
1	B	454	GLN
1	B	470	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	SP0	A	101	-	31,31,31	2.71	9 (29%)	44,45,45	2.46	18 (40%)

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	SP0	A	101	-	-	1/18/19/19	0/4/4/4

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	101	SP0	N8-N7	-7.15	1.23	1.39
2	A	101	SP0	O19-S18	6.33	1.50	1.43
2	A	101	SP0	O20-S18	6.25	1.50	1.43
2	A	101	SP0	C11-N8	-4.96	1.34	1.43
2	A	101	SP0	C6-C4	-4.60	1.39	1.45
2	A	101	SP0	C10-C6	-3.27	1.33	1.41
2	A	101	SP0	C9-N8	-3.24	1.33	1.36
2	A	101	SP0	C10-C9	-2.93	1.33	1.37
2	A	101	SP0	C9-N17	-2.70	1.33	1.40

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	101	SP0	C6-N7-N8	7.58	110.26	103.99
2	A	101	SP0	C4-C6-N7	4.94	126.02	120.55
2	A	101	SP0	O20-S18-O19	-4.56	113.98	119.52
2	A	101	SP0	C11-N8-N7	4.46	125.13	118.67
2	A	101	SP0	C9-N8-N7	-4.10	108.26	111.82
2	A	101	SP0	C10-C6-N7	-3.89	107.59	111.73
2	A	101	SP0	C10-C9-N17	-3.87	126.29	132.49
2	A	101	SP0	C11-N8-C9	-3.40	126.45	129.78
2	A	101	SP0	C1-C2-S3	-3.18	105.26	113.02
2	A	101	SP0	C10-C9-N8	2.75	108.84	107.01
2	A	101	SP0	C5-C4-S3	-2.74	104.84	111.23
2	A	101	SP0	F40-C23-C24	2.55	122.63	118.55
2	A	101	SP0	C21-S18-N17	2.45	109.96	106.06
2	A	101	SP0	O19-S18-N17	2.17	112.99	106.77
2	A	101	SP0	C24-C23-C22	-2.15	120.39	123.23
2	A	101	SP0	C2-S3-C4	2.10	96.10	92.33
2	A	101	SP0	C22-C21-S18	-2.06	116.95	119.06
2	A	101	SP0	C6-C4-S3	2.06	123.76	120.97

There are no chirality outliers.

All (1) torsion outliers are listed below:

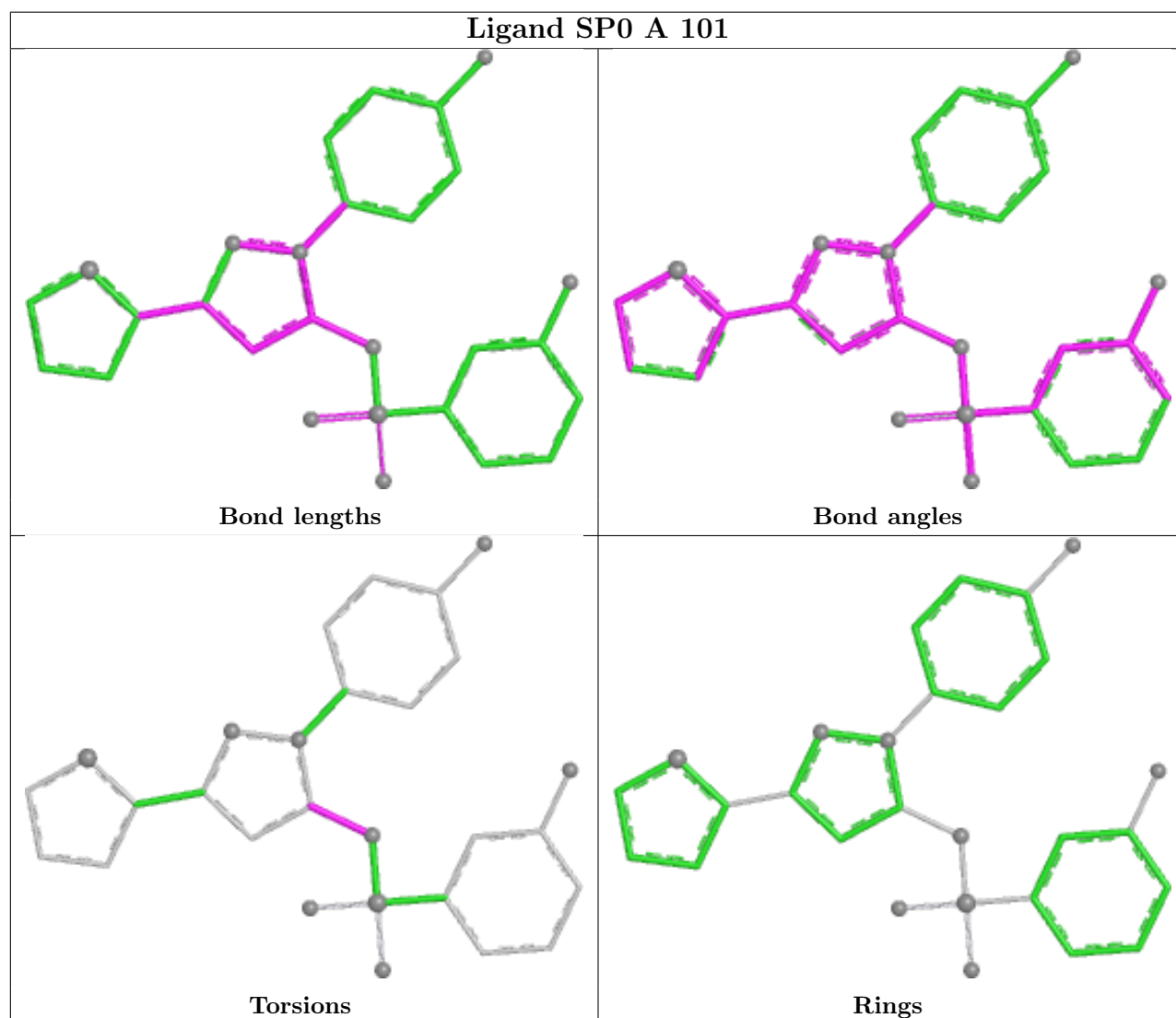
Mol	Chain	Res	Type	Atoms
2	A	101	SP0	N8-C9-N17-S18

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	101	SP0	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

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	271/271 (100%)	0.09	14 (5%)	33 32	27, 48, 107, 138	0
1	B	271/271 (100%)	0.11	22 (8%)	18 17	22, 40, 132, 158	0
All	All	542/542 (100%)	0.10	36 (6%)	24 24	22, 44, 123, 158	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	268	THR	8.0
1	B	476	LEU	6.6
1	B	477	TYR	6.2
1	B	467	PRO	5.1
1	A	477	TYR	4.9
1	B	465	LEU	4.8
1	B	468	LEU	4.5
1	B	472	ILE	3.9
1	A	264	PHE	3.7
1	B	270	LEU	3.3
1	B	262	ILE	3.1
1	A	262	ILE	3.0
1	B	475	ASP	3.0
1	B	471	GLU	2.9
1	B	470	GLN	2.9
1	B	469	LEU	2.9
1	A	266	HIS	2.8
1	A	267	ILE	2.7
1	B	269	PRO	2.6
1	B	264	PHE	2.6
1	B	473	TYR	2.6
1	B	267	ILE	2.5
1	A	273	GLN	2.5
1	B	271	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	466	HIS	2.4
1	A	271	GLN	2.4
1	A	465	LEU	2.3
1	A	269	PRO	2.3
1	B	266	HIS	2.3
1	B	261	LYS	2.3
1	A	270	LEU	2.3
1	A	265	LYS	2.2
1	B	274	SER	2.2
1	A	311	LEU	2.1
1	A	281	ILE	2.1
1	A	476	LEU	2.0

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

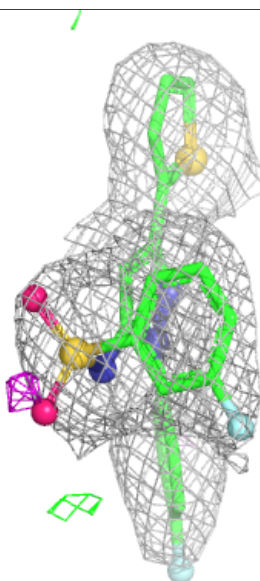
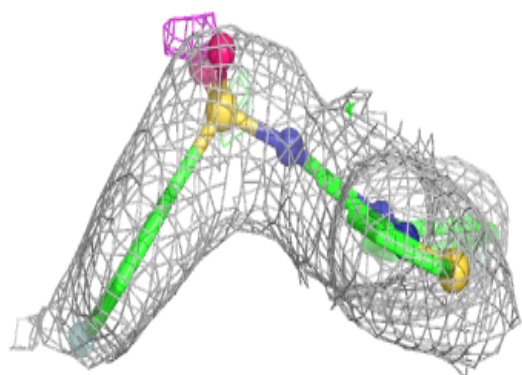
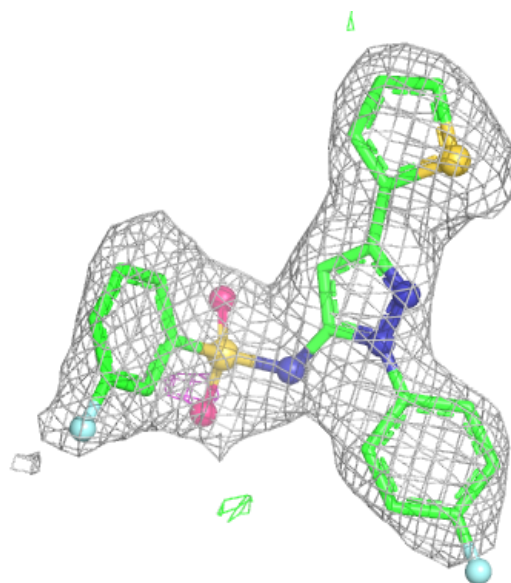
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	SP0	A	101	28/28	0.86	0.11	78,82,85,89	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 SP0 A 101:

$2mF_o-DF_c$ (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.