



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:29 PM UTC

PDB ID : 4O8F / pdb_00004o8f
Title : Crystal Structure of the complex between PPARgamma mutant R357A and rosiglitazone
Authors : Pochetti, G.; Montanari, R.; Capelli, D.; Chiaraluce, R.; Consalvi, V.; Lori, C.; Loiodice, F.; Laghezza, A.; Pasquo, A.; Cervoni, L.; Aschi, M.
Deposited on : 2013-12-27
Resolution : 2.60 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

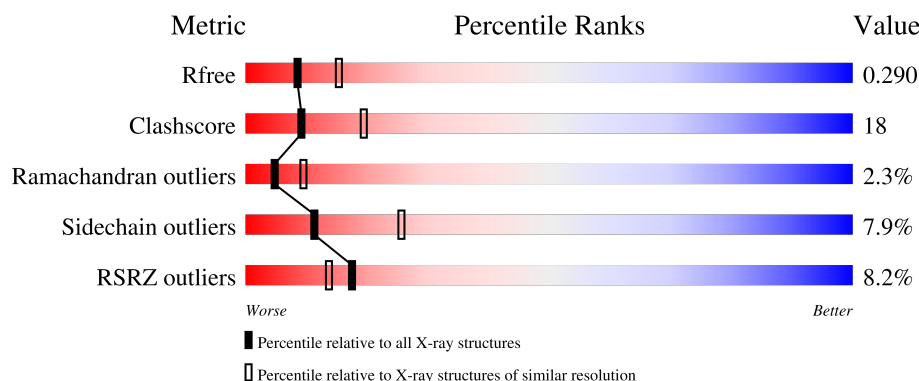
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (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 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	287	
1	B	287	

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	BRL	B	501	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4114 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.

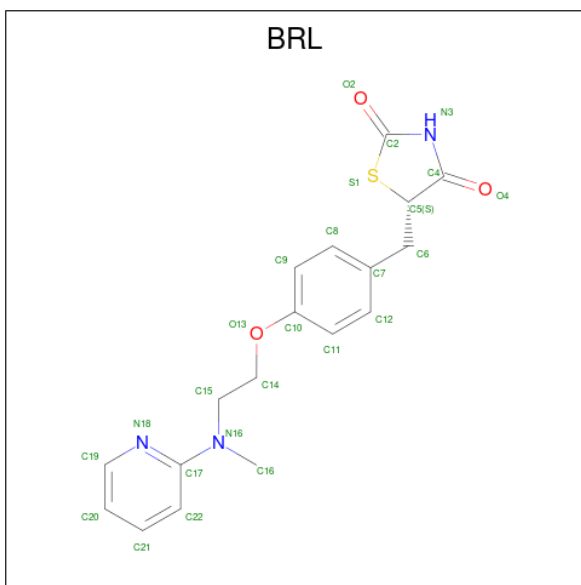
- Molecule 1 is a protein called Peroxisome proliferator-activated receptor gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	252	Total	C	N	O	S	0	0	0
			2013	1304	324	376	9			
1	B	249	Total	C	N	O	S	0	0	0
			1990	1288	321	372	9			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	191	GLY	-	expression tag	UNP P37231
A	192	SER	-	expression tag	UNP P37231
A	193	HIS	-	expression tag	UNP P37231
A	194	MET	-	expression tag	UNP P37231
A	357	ALA	ARG	engineered mutation	UNP P37231
B	191	GLY	-	expression tag	UNP P37231
B	192	SER	-	expression tag	UNP P37231
B	193	HIS	-	expression tag	UNP P37231
B	194	MET	-	expression tag	UNP P37231
B	357	ALA	ARG	engineered mutation	UNP P37231

- Molecule 2 is 2,4-THIAZOLIDINEDIONE, 5-[[4-[2-(METHYL-2-PYRIDINYLAMINO)ETHOXY]PHENYL]METHYL]-(9CL) (CCD ID: BRL) (formula: C₁₈H₁₉N₃O₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			25	18	3	3	1		
2	B	1	Total	C	N	O	S	0	0
			25	18	3	3	1		

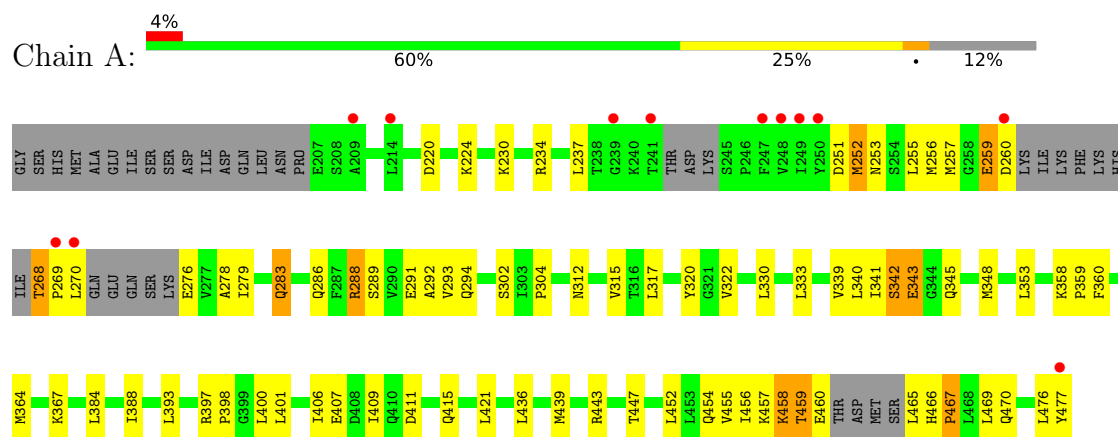
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	38	Total	O	0	0
			38	38		
3	B	23	Total	O	0	0
			23	23		

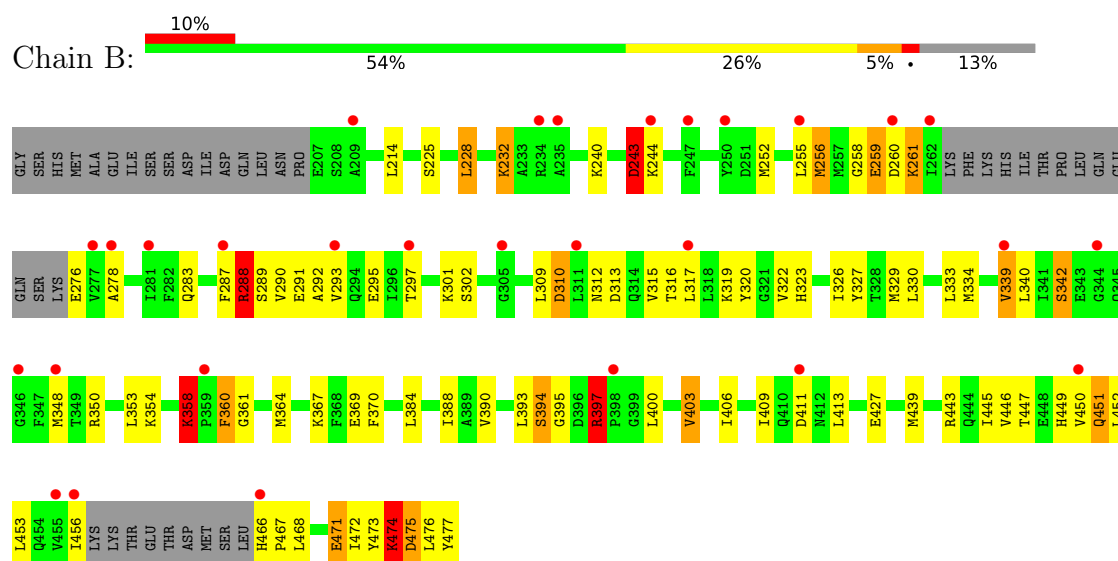
3 Residue-property plots [i](#)

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	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	85.70Å 87.10Å 163.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	61.09 – 2.60 61.09 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.4 (61.09-2.60) 94.6 (61.09-2.60)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.14 (at 2.62Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496, CNS	Depositor
R, R_{free}	0.234 , 0.297 0.239 , 0.290	Depositor DCC
R_{free} test set	1906 reflections (9.90%)	wwPDB-VP
Wilson B-factor (Å ²)	60.6	Xtriage
Anisotropy	0.353	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 61.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.167 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4114	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.42% 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: BRL

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	0.65	0/2045	1.03	7/2754 (0.3%)
1	B	0.67	0/2023	1.08	6/2726 (0.2%)
All	All	0.66	0/4068	1.06	13/5480 (0.2%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	471	GLU	N-CA-C	-8.32	100.87	111.02
1	A	268	THR	CA-C-N	-7.88	112.64	120.21
1	A	268	THR	C-N-CA	-7.88	112.64	120.21
1	A	358	LYS	CA-C-N	-6.67	112.12	119.19
1	A	358	LYS	C-N-CA	-6.67	112.12	119.19
1	B	397	ARG	CA-C-N	6.31	125.73	118.85
1	B	397	ARG	C-N-CA	6.31	125.73	118.85
1	A	251	ASP	CA-C-N	-6.12	112.94	122.37
1	A	251	ASP	C-N-CA	-6.12	112.94	122.37
1	B	288	ARG	N-CA-C	-5.58	105.58	112.90
1	A	458	LYS	N-CA-C	-5.54	101.78	110.36
1	B	451	GLN	N-CA-C	-5.24	105.57	111.28
1	B	358	LYS	CA-CB-CG	5.04	124.18	114.10

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	2013	0	2063	56	0
1	B	1990	0	2038	97	0
2	A	25	0	19	3	0
2	B	25	0	19	9	0
3	A	38	0	0	1	0
3	B	23	0	0	2	0
All	All	4114	0	4139	149	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 18.

All (149) 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:319:LYS:HE2	1:B:320:TYR:HE1	1.18	1.08
1:A:401:LEU:HD22	1:B:232:LYS:HD3	1.45	0.97
1:B:289:SER:HB2	2:B:501:BRL:H8	1.45	0.96
1:B:319:LYS:HE2	1:B:320:TYR:CE1	2.04	0.90
1:B:319:LYS:HG2	1:B:320:TYR:HD1	1.37	0.89
1:A:293:VAL:HG22	1:A:322:VAL:HG21	1.61	0.83
1:B:358:LYS:HG2	1:B:360:PHE:H	1.45	0.82
1:A:288:ARG:HA	1:A:291:GLU:HG2	1.62	0.80
1:B:394:SER:OG	1:B:395:GLY:N	2.14	0.79
1:B:471:GLU:O	1:B:474:LYS:HD3	1.86	0.75
1:A:401:LEU:HD22	1:B:232:LYS:CD	2.19	0.73
1:B:258:GLY:O	1:B:261:LYS:N	2.23	0.70
1:B:474:LYS:O	1:B:476:LEU:N	2.24	0.70
1:B:453:LEU:HD11	2:B:501:BRL:O2	1.93	0.69
1:A:465:LEU:O	1:A:470:GLN:NE2	2.26	0.68
1:A:289:SER:OG	2:A:501:BRL:H5	1.94	0.67
1:B:323:HIS:HE1	1:B:473:TYR:OH	1.77	0.67
1:B:339:VAL:HG11	2:B:501:BRL:H162	1.75	0.67
1:A:447:THR:HG22	1:A:477:TYR:CE1	2.30	0.67
1:B:312:ASN:HA	1:B:315:VAL:HG22	1.75	0.66
1:A:458:LYS:O	1:A:460:GLU:N	2.27	0.66
1:B:364:MET:HE2	2:B:501:BRL:H163	1.78	0.66
1:A:443:ARG:O	1:A:447:THR:HG23	1.97	0.65
1:B:319:LYS:HG2	1:B:320:TYR:CD1	2.27	0.64
1:A:447:THR:HG22	1:A:477:TYR:HE1	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:466:HIS:CG	1:A:467:PRO:HD2	2.35	0.62
1:B:258:GLY:O	1:B:259:GLU:C	2.42	0.62
1:A:317:LEU:HD11	1:A:406:ILE:HD12	1.79	0.62
1:B:288:ARG:O	1:B:292:ALA:N	2.31	0.61
1:B:390:VAL:HG12	1:B:439:MET:HE1	1.83	0.60
1:B:339:VAL:CG1	2:B:501:BRL:H162	2.31	0.60
1:B:397:ARG:HB2	1:B:400:LEU:HG	1.84	0.59
1:B:323:HIS:O	1:B:326:ILE:HG13	2.02	0.59
1:B:353:LEU:HD13	1:B:364:MET:HG3	1.85	0.59
1:B:367:LYS:N	1:B:367:LYS:HD3	2.18	0.58
1:B:214:LEU:HD21	1:B:413:LEU:HD23	1.85	0.58
1:B:319:LYS:HG3	1:B:474:LYS:HZ3	1.68	0.58
1:A:367:LYS:H	1:A:367:LYS:HD2	1.67	0.57
1:A:253:ASN:O	1:A:257:MET:HG3	2.05	0.57
1:B:354:LYS:HA	1:B:361:GLY:O	2.05	0.57
1:B:310:ASP:OD1	1:B:313:ASP:N	2.27	0.56
1:A:384:LEU:O	1:A:388:ILE:HG12	2.05	0.56
1:A:342:SER:O	1:A:345:GLN:HG3	2.06	0.56
1:B:319:LYS:HD2	1:B:474:LYS:HE2	1.88	0.56
1:B:310:ASP:OD1	1:B:312:ASN:N	2.38	0.56
1:B:393:LEU:HD22	1:B:409:ILE:HB	1.87	0.56
1:B:472:ILE:HA	1:B:474:LYS:NZ	2.22	0.55
1:A:397:ARG:HB2	1:A:400:LEU:HG	1.86	0.55
1:A:401:LEU:HD13	1:B:232:LYS:HE3	1.89	0.55
1:A:467:PRO:O	1:A:470:GLN:OE1	2.25	0.55
1:B:258:GLY:O	1:B:260:ASP:N	2.40	0.54
1:B:319:LYS:HG3	1:B:474:LYS:NZ	2.21	0.54
1:B:290:VAL:HG21	1:B:466:HIS:CE1	2.42	0.54
1:A:312:ASN:HA	1:B:243:ASP:OD2	2.08	0.54
1:B:384:LEU:O	1:B:388:ILE:HG12	2.08	0.53
1:B:252:MET:O	1:B:255:LEU:HB3	2.09	0.53
1:B:319:LYS:HE3	1:B:474:LYS:HZ3	1.74	0.53
1:B:450:VAL:HG23	1:B:453:LEU:HB2	1.90	0.52
1:B:288:ARG:HA	1:B:291:GLU:HB3	1.91	0.52
1:A:252:MET:HB2	1:A:255:LEU:HB3	1.92	0.51
1:A:353:LEU:HD13	1:A:364:MET:HG3	1.92	0.51
1:B:466:HIS:CD2	1:B:467:PRO:HD2	2.45	0.51
1:B:225:SER:OG	1:B:295:GLU:O	2.29	0.51
1:A:276:GLU:OE1	1:A:278:ALA:N	2.29	0.51
1:B:228:LEU:HG	1:B:333:LEU:HD21	1.93	0.51
1:B:358:LYS:HD3	1:B:360:PHE:CD2	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:350:ARG:O	1:B:354:LYS:HG3	2.11	0.50
1:B:358:LYS:HD3	1:B:360:PHE:CG	2.46	0.50
1:A:291:GLU:HG3	1:A:292:ALA:N	2.27	0.50
1:B:348:MET:HE2	2:B:501:BRL:H161	1.94	0.50
1:B:474:LYS:O	1:B:475:ASP:C	2.54	0.50
1:B:452:LEU:O	1:B:452:LEU:HG	2.11	0.50
1:B:348:MET:HE3	1:B:353:LEU:HD21	1.93	0.49
1:B:312:ASN:O	1:B:316:THR:N	2.39	0.49
1:B:317:LEU:HD23	1:B:397:ARG:HG2	1.92	0.49
1:B:289:SER:O	1:B:293:VAL:HG23	2.12	0.49
1:A:289:SER:OG	2:A:501:BRL:C5	2.59	0.48
1:B:427:GLU:N	1:B:427:GLU:OE1	2.46	0.48
1:B:353:LEU:HD23	1:B:353:LEU:HA	1.74	0.48
1:A:283:GLN:HA	1:A:286:GLN:HB2	1.95	0.48
1:B:232:LYS:HZ3	1:B:232:LYS:HB3	1.79	0.48
1:A:237:LEU:HD21	1:A:340:LEU:HG	1.96	0.47
1:B:287:PHE:HA	1:B:290:VAL:HG12	1.97	0.47
1:A:259:GLU:OE1	1:A:268:THR:HG21	2.15	0.47
1:A:454:GLN:OE1	1:A:457:LYS:HE3	2.14	0.47
1:A:436:LEU:O	1:A:439:MET:HB2	2.14	0.47
1:A:393:LEU:HD22	1:A:409:ILE:HB	1.95	0.47
1:A:330:LEU:HD21	1:A:364:MET:HE1	1.97	0.47
1:A:401:LEU:CD2	1:B:232:LYS:HD3	2.32	0.47
1:B:370:PHE:HB2	1:B:445:ILE:HD11	1.96	0.47
1:A:333:LEU:HB3	1:A:340:LEU:HB2	1.96	0.46
1:A:411:ASP:O	1:A:415:GLN:HG3	2.16	0.46
1:B:443:ARG:NH2	1:B:477:TYR:OH	2.48	0.46
1:A:455:VAL:O	1:A:459:THR:HB	2.15	0.46
1:B:333:LEU:HB3	1:B:340:LEU:HB2	1.96	0.46
1:B:323:HIS:HE1	1:B:473:TYR:CZ	2.35	0.45
1:B:358:LYS:HG2	1:B:360:PHE:N	2.24	0.45
1:A:302:SER:O	1:A:304:PRO:HD3	2.16	0.45
1:A:268:THR:N	1:A:269:PRO:HD3	2.31	0.45
1:A:359:PRO:HG2	1:A:360:PHE:CE1	2.52	0.45
1:A:421:LEU:HD23	1:A:421:LEU:HA	1.78	0.45
1:B:290:VAL:HG21	1:B:466:HIS:ND1	2.31	0.45
1:A:341:ILE:HD13	1:A:348:MET:HE3	1.99	0.45
1:B:403:VAL:O	1:B:406:ILE:HG12	2.16	0.45
1:B:443:ARG:O	1:B:446:VAL:HG22	2.16	0.45
1:B:468:LEU:O	1:B:472:ILE:HG13	2.17	0.45
1:A:288:ARG:O	1:A:291:GLU:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:322:VAL:O	1:B:326:ILE:HG23	2.17	0.44
1:B:283:GLN:HB3	1:B:287:PHE:CZ	2.53	0.44
1:B:310:ASP:CG	1:B:313:ASP:H	2.19	0.44
1:B:475:ASP:N	1:B:475:ASP:OD1	2.50	0.44
1:B:450:VAL:HA	1:B:453:LEU:HG	1.99	0.44
1:A:348:MET:HE3	1:A:348:MET:HB2	1.82	0.43
1:A:289:SER:O	1:A:293:VAL:HG23	2.18	0.43
1:B:334:MET:HG2	1:B:339:VAL:HB	2.00	0.43
1:A:230:LYS:O	1:A:234:ARG:HG2	2.18	0.43
1:A:252:MET:HA	1:A:255:LEU:H	1.84	0.43
1:A:452:LEU:HD12	1:A:452:LEU:HA	1.86	0.43
1:B:302:SER:HA	3:B:618:HOH:O	2.19	0.43
1:B:397:ARG:HB2	1:B:400:LEU:CG	2.46	0.43
1:B:278:ALA:HB1	1:B:360:PHE:CD2	2.54	0.43
1:B:276:GLU:HG3	1:B:278:ALA:H	1.84	0.42
1:A:320:TYR:CZ	1:A:476:LEU:HD12	2.54	0.42
1:A:397:ARG:HA	1:A:398:PRO:HD3	1.83	0.42
1:B:256:MET:C	1:B:258:GLY:N	2.72	0.42
1:B:330:LEU:HD21	2:B:501:BRL:H141	2.01	0.42
1:A:466:HIS:O	1:A:467:PRO:C	2.63	0.42
1:B:472:ILE:C	1:B:474:LYS:HZ2	2.28	0.42
1:B:252:MET:O	1:B:256:MET:HE2	2.20	0.41
1:B:243:ASP:OD1	1:B:243:ASP:N	2.53	0.41
1:B:330:LEU:HD12	1:B:330:LEU:HA	1.79	0.41
1:A:359:PRO:HG2	1:A:360:PHE:CD1	2.54	0.41
1:B:258:GLY:C	1:B:260:ASP:N	2.78	0.41
1:B:329:MET:HE2	1:B:329:MET:HB3	1.96	0.41
1:A:260:ASP:OD2	3:A:616:HOH:O	2.21	0.41
1:B:319:LYS:CD	1:B:474:LYS:HE2	2.50	0.41
1:B:348:MET:HE1	2:B:501:BRL:H22	2.03	0.41
1:B:327:TYR:CE2	1:B:446:VAL:HG12	2.56	0.41
1:B:449:HIS:NE2	2:B:501:BRL:C2	2.83	0.41
1:A:288:ARG:CA	1:A:291:GLU:HG2	2.41	0.41
1:A:469:LEU:HD23	1:A:469:LEU:HA	1.88	0.41
1:B:394:SER:HB3	1:B:397:ARG:NE	2.36	0.41
1:A:220:ASP:O	1:A:224:LYS:HG3	2.21	0.41
1:B:288:ARG:NH1	3:B:619:HOH:O	2.50	0.41
1:B:293:VAL:HG22	1:B:322:VAL:HG21	2.03	0.41
1:B:283:GLN:HB3	1:B:287:PHE:CE2	2.56	0.40
1:A:291:GLU:O	1:A:294:GLN:HG2	2.21	0.40
2:A:501:BRL:H22	2:A:501:BRL:H161	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:309:LEU:HD22	1:B:406:ILE:HG22	2.03	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	242/287 (84%)	221 (91%)	18 (7%)	3 (1%)	10	23
1	B	243/287 (85%)	215 (88%)	20 (8%)	8 (3%)	3	5
All	All	485/574 (84%)	436 (90%)	38 (8%)	11 (2%)	5	9

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	310	ASP
1	B	475	ASP
1	B	358	LYS
1	A	467	PRO
1	B	394	SER
1	A	342	SER
1	A	343	GLU
1	B	474	LYS
1	B	243	ASP
1	B	259	GLU
1	B	342	SER

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	224/257 (87%)	211 (94%)	13 (6%)	18	39
1	B	221/257 (86%)	199 (90%)	22 (10%)	7	16
All	All	445/514 (87%)	410 (92%)	35 (8%)	11	26

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	252	MET
1	A	256	MET
1	A	259	GLU
1	A	270	LEU
1	A	279	ILE
1	A	283	GLN
1	A	288	ARG
1	A	315	VAL
1	A	339	VAL
1	A	343	GLU
1	A	407	GLU
1	A	456	ILE
1	A	459	THR
1	B	228	LEU
1	B	232	LYS
1	B	240	LYS
1	B	243	ASP
1	B	244	LYS
1	B	256	MET
1	B	261	LYS
1	B	288	ARG
1	B	297	THR
1	B	301	LYS
1	B	339	VAL
1	B	342	SER
1	B	358	LYS
1	B	360	PHE
1	B	369	GLU
1	B	397	ARG
1	B	403	VAL
1	B	411	ASP
1	B	447	THR
1	B	451	GLN

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Mol	Chain	Res	Type
1	B	456	ILE
1	B	474	LYS

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	312	ASN
1	A	430	GLN
1	B	314	GLN
1	B	323	HIS
1	B	430	GLN
1	B	451	GLN
1	B	466	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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
2	BRL	B	501	-	27,27,27	1.57	4 (14%)	36,36,36	3.23	14 (38%)
2	BRL	A	501	-	27,27,27	1.81	6 (22%)	36,36,36	3.33	12 (33%)

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	BRL	B	501	-	-	1/14/26/26	0/3/3/3
2	BRL	A	501	-	-	1/14/26/26	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	BRL	C2-S1	5.09	1.80	1.76
2	A	501	BRL	C4-N3	-3.92	1.32	1.37
2	B	501	BRL	C4-N3	-3.77	1.32	1.37
2	A	501	BRL	C11-C10	3.53	1.45	1.38
2	B	501	BRL	C11-C10	2.96	1.44	1.38
2	B	501	BRL	C2-S1	2.94	1.78	1.76
2	B	501	BRL	C17-N16	2.22	1.42	1.37
2	A	501	BRL	C12-C11	2.18	1.42	1.38
2	A	501	BRL	C17-N16	2.11	1.42	1.37
2	A	501	BRL	C2-N3	-2.08	1.34	1.36

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	BRL	S1-C2-N3	-9.60	103.69	110.44
2	B	501	BRL	S1-C2-N3	-9.21	103.97	110.44
2	A	501	BRL	C4-C5-S1	-8.19	99.08	105.93
2	B	501	BRL	C5-S1-C2	8.17	97.92	92.77
2	B	501	BRL	C4-C5-S1	-8.09	99.17	105.93
2	A	501	BRL	C4-N3-C2	7.94	123.49	118.20
2	A	501	BRL	C5-S1-C2	7.59	97.55	92.77
2	B	501	BRL	C4-N3-C2	7.46	123.18	118.20
2	A	501	BRL	C5-C4-N3	4.95	116.18	111.99
2	A	501	BRL	O2-C2-S1	4.91	129.05	124.61
2	B	501	BRL	C5-C4-N3	4.46	115.77	111.99
2	B	501	BRL	C19-N18-C17	4.28	123.03	116.81
2	A	501	BRL	C19-N18-C17	4.12	122.79	116.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	BRL	O2-C2-S1	3.87	128.11	124.61
2	A	501	BRL	O4-C4-N3	-2.65	121.80	124.93
2	A	501	BRL	C14-C15-N16	-2.47	107.60	112.44
2	B	501	BRL	O4-C4-N3	-2.45	122.04	124.93
2	A	501	BRL	C7-C6-C5	-2.39	109.92	113.35
2	B	501	BRL	C22-C17-N18	-2.21	119.10	123.46
2	B	501	BRL	C14-O13-C10	-2.14	112.36	117.93
2	B	501	BRL	O2-C2-N3	2.12	127.92	125.76
2	A	501	BRL	C22-C17-N18	-2.11	119.30	123.46
2	A	501	BRL	C14-O13-C10	-2.10	112.47	117.93
2	B	501	BRL	C14-C15-N16	-2.08	108.37	112.44
2	B	501	BRL	N18-C17-N16	2.03	119.82	116.62
2	B	501	BRL	C6-C5-S1	-2.02	110.35	113.32

There are no chirality outliers.

All (2) torsion outliers are listed below:

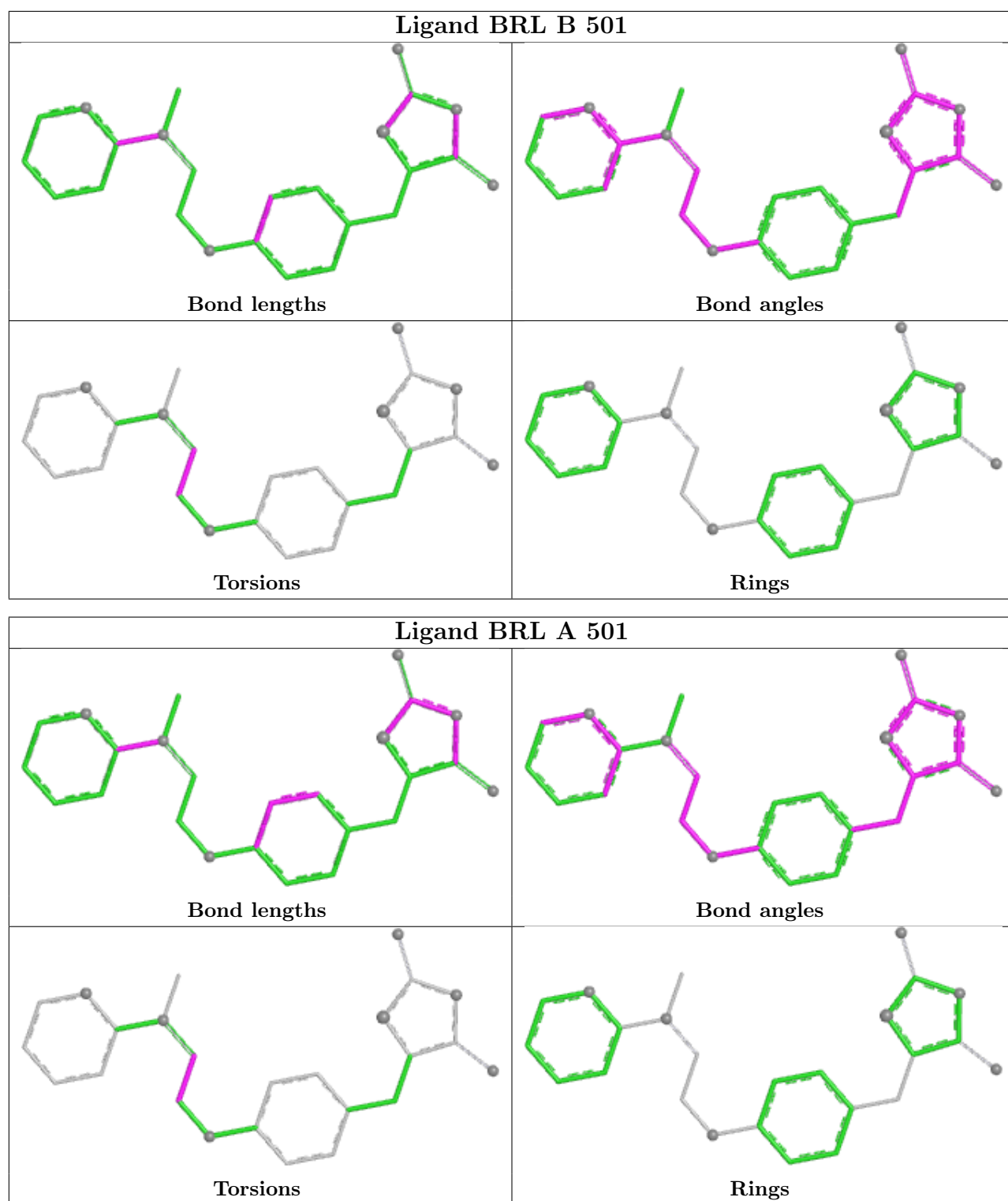
Mol	Chain	Res	Type	Atoms
2	B	501	BRL	O13-C14-C15-N16
2	A	501	BRL	O13-C14-C15-N16

There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	BRL	9	0
2	A	501	BRL	3	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

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	252/287 (87%)	0.34	12 (4%) 35 30	42, 69, 111, 163	0
1	B	249/287 (86%)	0.91	29 (11%) 9 7	45, 85, 125, 147	0
All	All	501/574 (87%)	0.62	41 (8%) 17 14	42, 76, 123, 163	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	297	THR	5.7
1	A	270	LEU	4.5
1	B	456	ILE	4.0
1	B	262	ILE	3.8
1	B	234	ARG	3.7
1	B	293	VAL	3.4
1	A	269	PRO	3.3
1	B	346	GLY	3.2
1	A	249	ILE	2.9
1	B	260	ASP	2.8
1	B	244	LYS	2.7
1	B	209	ALA	2.7
1	A	477	TYR	2.6
1	B	311	LEU	2.6
1	B	466	HIS	2.6
1	B	398	PRO	2.5
1	A	239	GLY	2.5
1	A	248	VAL	2.5
1	A	247	PHE	2.5
1	A	241	THR	2.5
1	A	260	ASP	2.5
1	A	209	ALA	2.4
1	B	277	VAL	2.4
1	B	450	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	250	TYR	2.3
1	B	255	LEU	2.3
1	B	359	PRO	2.3
1	B	344	GLY	2.3
1	B	247	PHE	2.3
1	B	411	ASP	2.3
1	B	250	TYR	2.2
1	A	214	LEU	2.2
1	B	455	VAL	2.2
1	B	235	ALA	2.2
1	B	287	PHE	2.2
1	B	305	GLY	2.2
1	B	278	ALA	2.1
1	B	348	MET	2.1
1	B	281	ILE	2.0
1	B	317	LEU	2.0
1	B	339	VAL	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

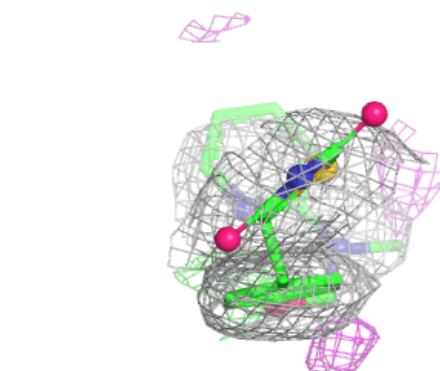
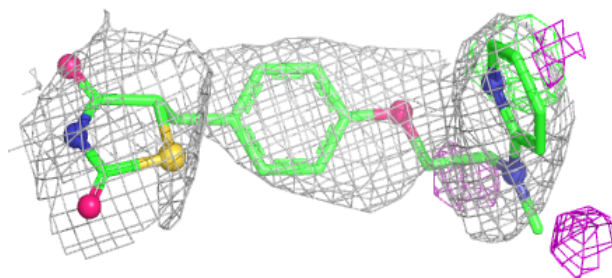
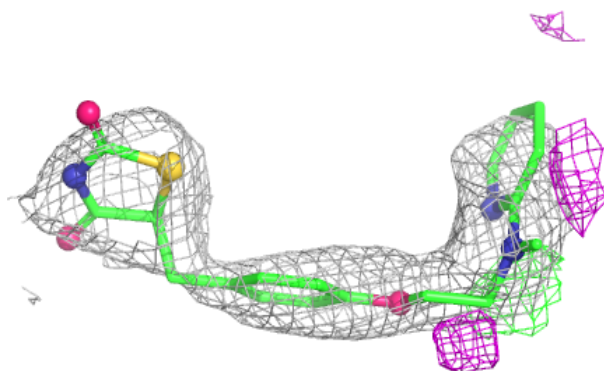
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	BRL	B	501	25/25	0.80	0.18	80,94,113,117	0
2	BRL	A	501	25/25	0.88	0.15	61,73,77,91	0

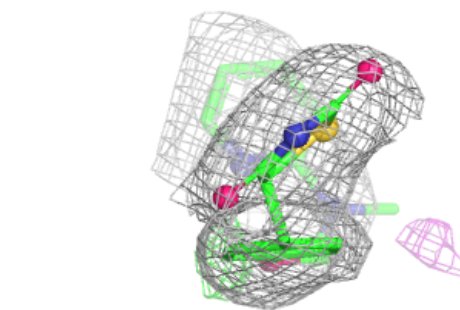
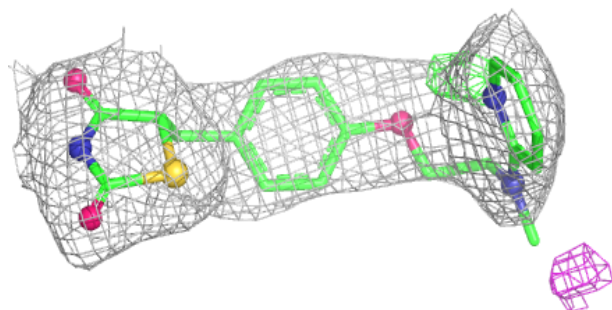
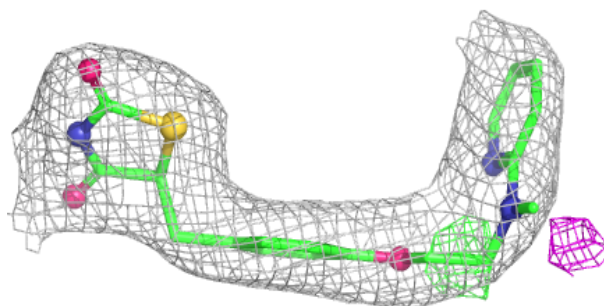
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around BRL B 501:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around BRL A 501:**

$2mF_o-DF_c$ (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.