



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 04:44 AM UTC

PDB ID : 5AAV / pdb_00005aav
Title : Optimization of a novel binding motif to to (E)-3-(3,5-difluoro-4-((1R,3R)-2-(2-fluoro-2-methylpropyl)-3-methyl-2,3,4,9-tetrahydro-1H-pyrido(3,4-b)indol-1-yl)phenyl)acrylic acid (AZD9496), a potent and orally bioavailable selective estrogen receptor downregulator and antagonist
Authors : Norman, R.A.; Bradbury, R.H.; de Almeida, C.; Andrews, D.M.; Ballard, P.; Buttar, D.; Callis, R.J.; Currie, G.S.; Curwen, J.O.; Davies, C.D.; de Savi, C.; Donald, C.S.; Feron, L.J.L.; Glossop, S.C.; Hayter, B.R.; Karoutchi, G.; Lamont, S.G.; MacFaul, P.; Moss, T.; Pearson, S.E.; Rabow, A.A.; Tonge, M.; Walker, G.E.; Weir, H.M.; Wilson, Z.
Deposited on : 2015-07-29
Resolution : 1.95 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)

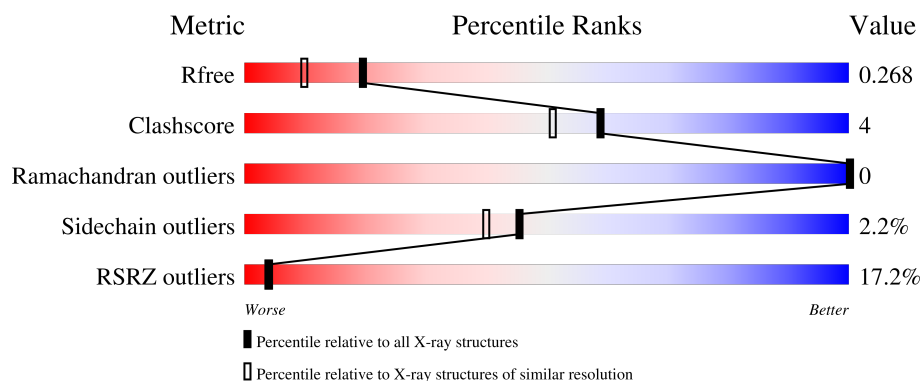
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	252	
2	B	252	

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

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3661 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 ESTROGEN RECEPTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	232	Total	C	N	O	S	0	4	0
			1839	1181	318	323	17			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	303	GLY	-	expression tag	UNP P03372
A	304	SER	-	expression tag	UNP P03372
A	305	HIS	-	expression tag	UNP P03372
A	306	MET	-	expression tag	UNP P03372
A	381	SER	CYS	engineered mutation	UNP P03372
A	417	SER	CYS	engineered mutation	UNP P03372
A	530	SER	CYS	engineered mutation	UNP P03372
A	536	SER	LEU	engineered mutation	UNP P03372

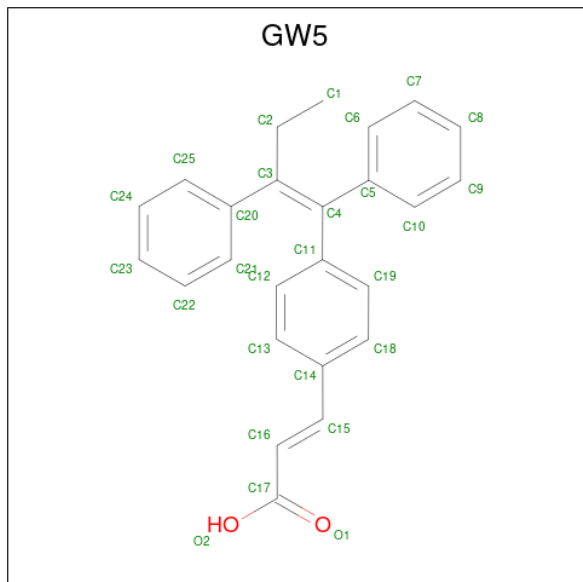
- Molecule 2 is a protein called ESTROGEN RECEPTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	209	Total	C	N	O	S	0	1	0
			1602	1030	276	284	12			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	303	GLY	-	expression tag	UNP P03372
B	304	SER	-	expression tag	UNP P03372
B	305	HIS	-	expression tag	UNP P03372
B	381	SER	CYS	engineered mutation	UNP P03372
B	417	SER	CYS	engineered mutation	UNP P03372
B	530	SER	CYS	engineered mutation	UNP P03372
B	536	SER	LEU	engineered mutation	UNP P03372

- Molecule 3 is (2E)-3-{4-[(1E)-1,2-DIPHENYLBUT-1-ENYL]PHENYL}ACRYLIC ACID (CCD ID: GW5) (formula: C₂₅H₂₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			27	25	2		
3	B	1	Total	C	O	0	0
			27	25	2		

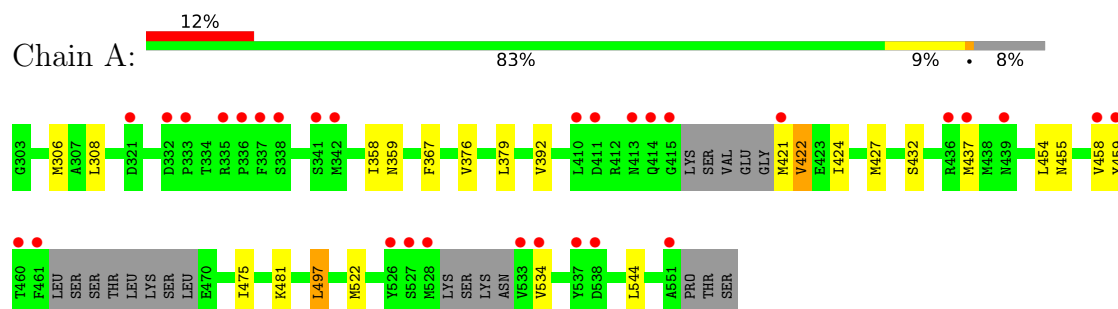
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	103	Total	O	0	0
			103	103		
4	B	63	Total	O	0	0
			63	63		

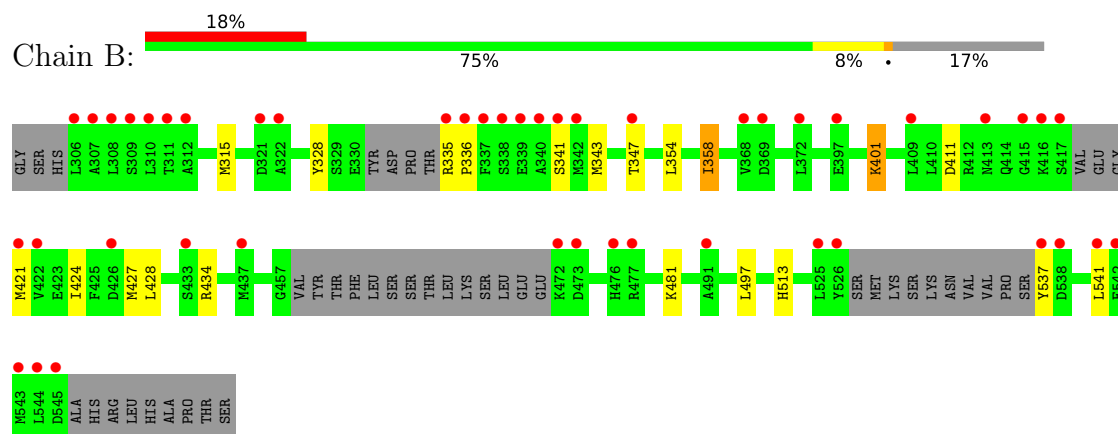
3 Residue-property plots [i](#)

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: ESTROGEN RECEPTOR



• Molecule 2: ESTROGEN RECEPTOR



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	105.49Å 51.54Å 83.70Å 90.00° 90.90° 90.00°	Depositor
Resolution (Å)	44.32 – 1.95 44.32 – 1.95	Depositor EDS
% Data completeness (in resolution range)	98.8 (44.32-1.95) 98.8 (44.32-1.95)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.46 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.196 , 0.234 (Not available) , 0.268	Depositor DCC
R_{free} test set	1653 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	25.9	Xtriage
Anisotropy	0.103	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 51.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.021 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3661	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.70% 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: GW5

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	0.70	0/1887	0.95	1/2554 (0.0%)
2	B	0.68	0/1630	0.86	0/2206
All	All	0.69	0/3517	0.91	1/4760 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	422	VAL	N-CA-C	5.34	115.78	110.23

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	1839	0	1852	20	1
2	B	1602	0	1598	16	1
3	A	27	0	21	0	0
3	B	27	0	21	4	0
4	A	103	0	0	0	0
4	B	63	0	0	0	0
All	All	3661	0	3492	31	1

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 4.

All (31) 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:459:TYR:HD2	2:B:513[B]:HIS:CD2	2.08	0.72
1:A:376:VAL:HG22	1:A:544:LEU:HD12	1.75	0.67
1:A:459:TYR:HB2	2:B:513[B]:HIS:HD2	1.61	0.65
1:A:454:LEU:O	1:A:458:VAL:HG13	1.98	0.63
1:A:306:MET:HE2	1:A:306:MET:HA	1.88	0.55
1:A:459:TYR:CD2	2:B:513[B]:HIS:CD2	2.91	0.55
2:B:343:MET:O	2:B:347:THR:HG23	2.07	0.55
2:B:424:ILE:HA	2:B:427:MET:HE3	1.88	0.54
1:A:424:ILE:HG22	1:A:427:MET:HE3	1.92	0.51
1:A:424:ILE:HA	1:A:427:MET:HE3	1.91	0.51
1:A:497:LEU:HD21	2:B:497:LEU:HD22	1.92	0.51
2:B:315:MET:HE3	2:B:481:LYS:HG2	1.93	0.51
2:B:401:LYS:HD3	2:B:411:ASP:HB3	1.93	0.50
1:A:455:ASN:O	1:A:458:VAL:HG22	2.12	0.49
3:B:1546:GW5:H22A	3:B:1546:GW5:C10	2.41	0.49
1:A:459:TYR:OH	2:B:434:ARG:NE	2.46	0.49
2:B:354:LEU:O	2:B:358:ILE:HD12	2.13	0.48
1:A:358:ILE:HG23	1:A:544:LEU:HD23	1.95	0.47
1:A:458:VAL:HG11	1:A:475:ILE:HG21	1.95	0.47
1:A:458:VAL:CG1	1:A:475:ILE:HG21	2.46	0.45
1:A:367:PHE:HZ	1:A:379:LEU:HD23	1.81	0.45
1:A:367:PHE:CZ	1:A:379:LEU:CD2	3.00	0.44
2:B:428:LEU:HD11	3:B:1546:GW5:H11	1.99	0.44
1:A:459:TYR:HB2	2:B:513[B]:HIS:CD2	2.48	0.43
1:A:392:VAL:HG13	1:A:432:SER:HA	1.99	0.42
2:B:335:ARG:CB	2:B:336:PRO:HD3	2.49	0.42
2:B:343:MET:HE1	3:B:1546:GW5:H13	2.00	0.42
2:B:347:THR:HG22	3:B:1546:GW5:H15	2.01	0.42
2:B:537:TYR:O	2:B:541:LEU:HB2	2.20	0.42
1:A:308:LEU:O	1:A:481:LYS:HE2	2.20	0.41
1:A:522:MET:HE1	1:A:534:VAL:HG11	2.02	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:359[A]:ASN:ND2	2:B:328:TYR:OH[3_455]	1.98	0.22

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	228/252 (90%)	226 (99%)	2 (1%)	0	100	100
2	B	200/252 (79%)	196 (98%)	4 (2%)	0	100	100
All	All	428/504 (85%)	422 (99%)	6 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	201/226 (89%)	197 (98%)	4 (2%)	48	43
2	B	169/226 (75%)	165 (98%)	4 (2%)	43	36
All	All	370/452 (82%)	362 (98%)	8 (2%)	45	40

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	421	MET
1	A	422	VAL
1	A	437	MET

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Mol	Chain	Res	Type
1	A	497	LEU
2	B	341	SER
2	B	358	ILE
2	B	401	LYS
2	B	421	MET

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	439	ASN
1	A	474	HIS
1	A	488	HIS
1	A	513	HIS
1	A	519	ASN
2	B	519	ASN
2	B	524	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
3	GW5	A	1552	-	29,29,29	1.46	5 (17%)	38,38,38	1.17	3 (7%)
3	GW5	B	1546	-	29,29,29	1.33	3 (10%)	38,38,38	1.53	7 (18%)

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
3	GW5	A	1552	-	-	2/23/23/23	0/3/3/3
3	GW5	B	1546	-	-	1/23/23/23	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1546	GW5	O1-C17	4.71	1.34	1.23
3	A	1552	GW5	O1-C17	4.30	1.33	1.23
3	A	1552	GW5	O2-C17	-2.97	1.22	1.30
3	B	1546	GW5	O2-C17	-2.61	1.23	1.30
3	A	1552	GW5	C12-C11	2.51	1.43	1.39
3	A	1552	GW5	C21-C20	2.34	1.43	1.39
3	A	1552	GW5	C25-C20	2.18	1.42	1.39
3	B	1546	GW5	C4-C3	2.18	1.39	1.35

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1546	GW5	C12-C11-C4	-3.54	114.80	120.91
3	B	1546	GW5	C2-C3-C4	-2.98	120.49	123.46
3	B	1546	GW5	C18-C19-C11	-2.58	118.04	120.80
3	B	1546	GW5	C7-C6-C5	-2.36	118.05	120.36
3	B	1546	GW5	C25-C20-C3	-2.30	118.03	121.00
3	B	1546	GW5	C12-C11-C19	2.27	121.45	118.57
3	A	1552	GW5	C25-C20-C3	-2.18	118.20	121.00
3	A	1552	GW5	O2-C17-C16	2.13	124.00	116.16
3	B	1546	GW5	C2-C3-C20	2.08	117.47	114.48
3	A	1552	GW5	C13-C14-C18	2.04	120.69	117.65

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1552	GW5	C13-C14-C15-C16
3	B	1546	GW5	C1-C2-C3-C20
3	A	1552	GW5	C18-C14-C15-C16

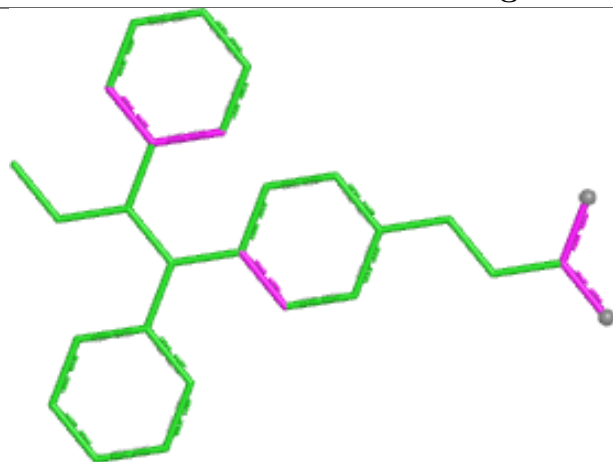
There are no ring outliers.

1 monomer is involved in 4 short contacts:

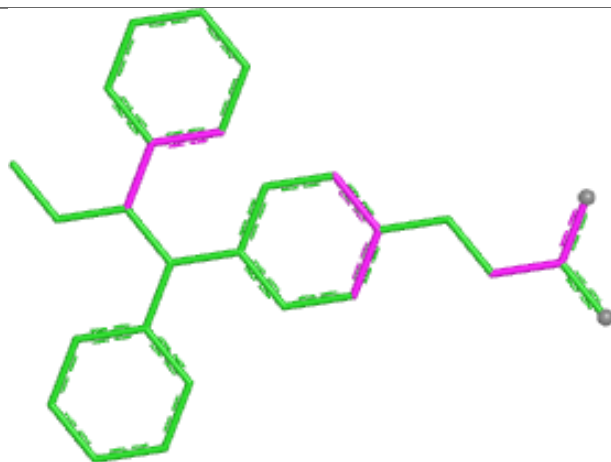
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1546	GW5	4	0

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.

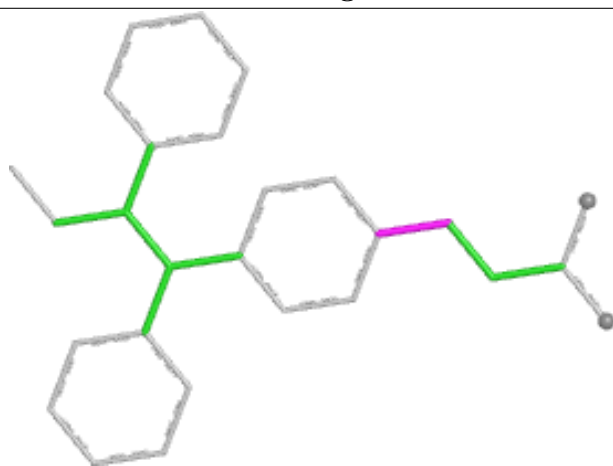
Ligand GW5 A 1552



Bond lengths



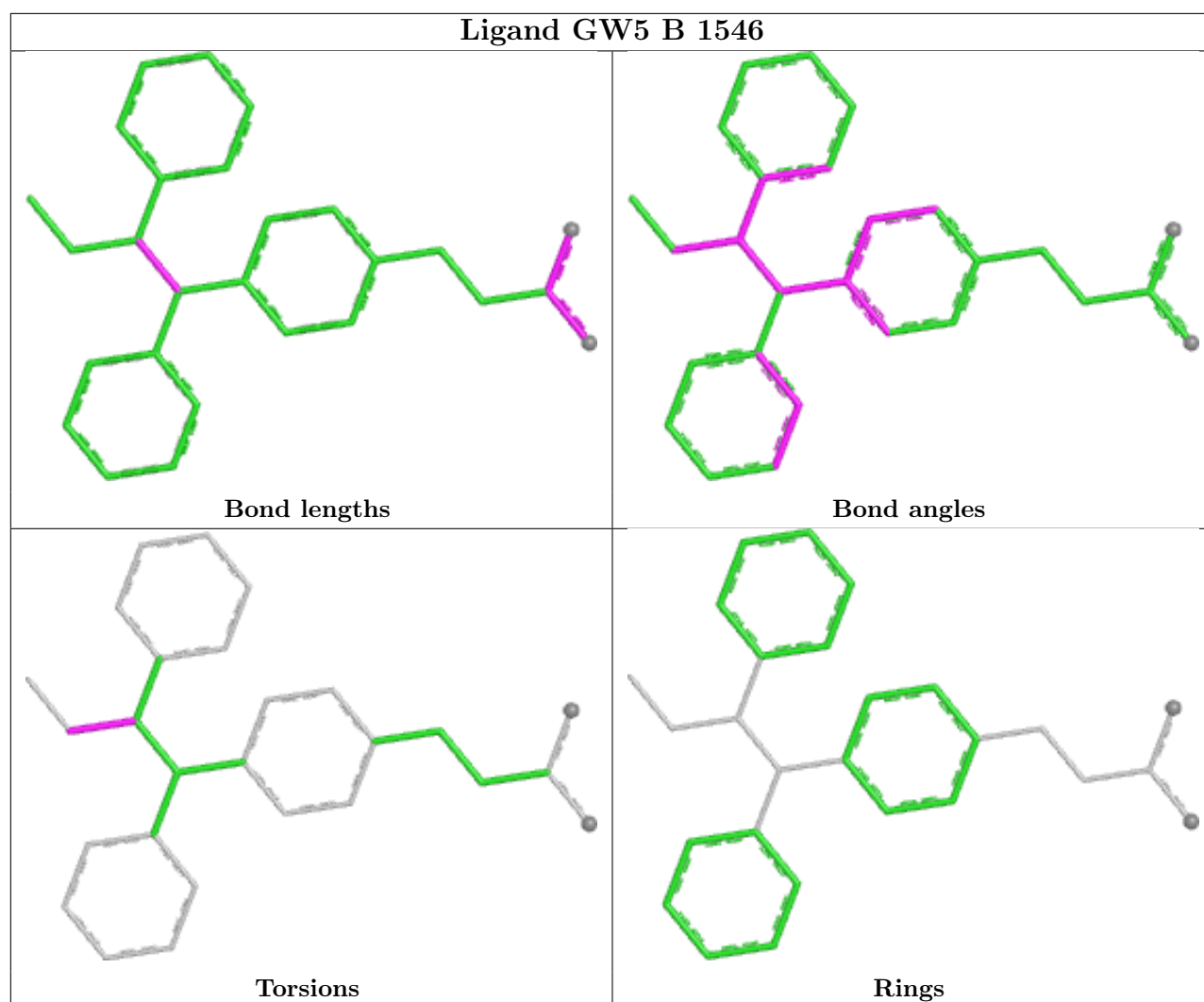
Bond angles



Torsions



Rings



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	232/252 (92%)	0.78	30 (12%) 7 9	11, 26, 48, 62	4 (1%)
2	B	209/252 (82%)	1.11	46 (22%) 2 2	10, 26, 58, 70	1 (0%)
All	All	441/504 (87%)	0.94	76 (17%) 4 4	10, 26, 51, 70	5 (1%)

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	461	PHE	7.2
2	B	338	SER	6.1
2	B	306	LEU	5.5
2	B	537	TYR	5.2
2	B	526	TYR	5.2
1	A	459	TYR	4.7
2	B	321	ASP	4.6
2	B	339	GLU	4.5
2	B	422	VAL	4.3
1	A	413	ASN	4.3
1	A	533	VAL	4.2
2	B	413	ASN	4.1
1	A	337	PHE	4.0
1	A	526	TYR	3.9
2	B	342	MET	3.6
2	B	341	SER	3.5
2	B	337	PHE	3.4
2	B	340	ALA	3.4
2	B	307	ALA	3.2
1	A	321	ASP	3.2
2	B	417	SER	3.2
1	A	528	MET	3.0
2	B	421	MET	3.0
2	B	472	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	537	TYR	2.9
2	B	525	LEU	2.9
2	B	310	LEU	2.9
1	A	458	VAL	2.9
1	A	411	ASP	2.8
2	B	473	ASP	2.8
2	B	544	LEU	2.8
2	B	336	PRO	2.7
1	A	534	VAL	2.7
2	B	542	GLU	2.7
2	B	415	GLY	2.7
1	A	414	GLN	2.7
1	A	527	SER	2.7
2	B	397	GLU	2.7
1	A	538	ASP	2.7
2	B	416	LYS	2.6
2	B	433	SER	2.6
1	A	332	ASP	2.6
1	A	415	GLY	2.6
2	B	541	LEU	2.6
1	A	460	THR	2.5
2	B	543	MET	2.5
2	B	335	ARG	2.5
1	A	437	MET	2.5
1	A	551	ALA	2.4
2	B	309	SER	2.4
1	A	436	ARG	2.3
2	B	369	ASP	2.3
2	B	372	LEU	2.3
2	B	409	LEU	2.3
2	B	322	ALA	2.3
1	A	336	PRO	2.3
2	B	437	MET	2.3
2	B	308	LEU	2.3
2	B	311	THR	2.3
1	A	338	SER	2.3
2	B	347	THR	2.3
2	B	538	ASP	2.2
2	B	545	ASP	2.2
1	A	410	LEU	2.2
2	B	426	ASP	2.2
1	A	342	MET	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	312	ALA	2.1
1	A	335	ARG	2.1
2	B	476	HIS	2.1
2	B	491	ALA	2.1
1	A	439	ASN	2.1
2	B	477	ARG	2.1
1	A	333	PRO	2.0
2	B	368	VAL	2.0
1	A	341	SER	2.0
1	A	421	MET	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](#)

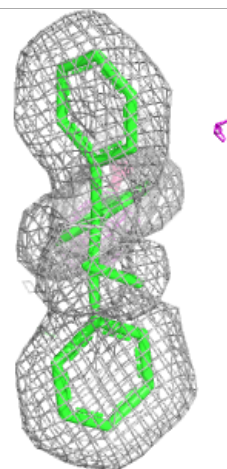
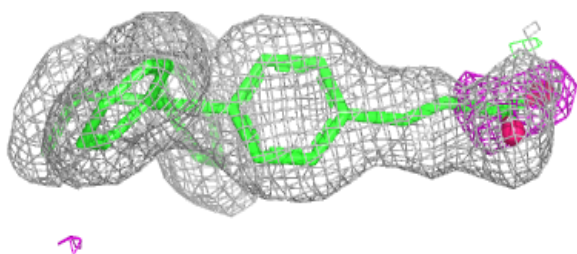
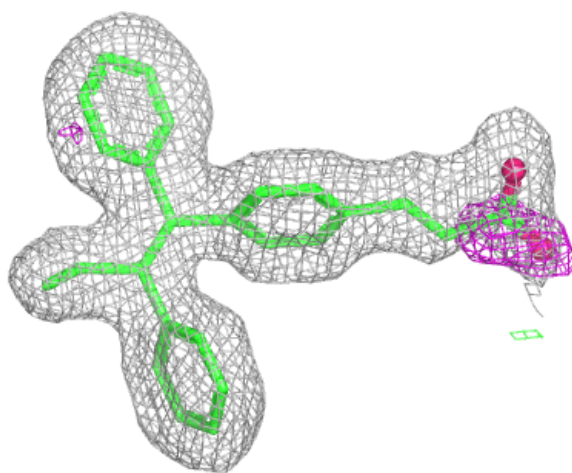
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GW5	A	1552	27/27	0.91	0.07	16,17,26,28	0
3	GW5	B	1546	27/27	0.91	0.08	21,21,33,34	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.

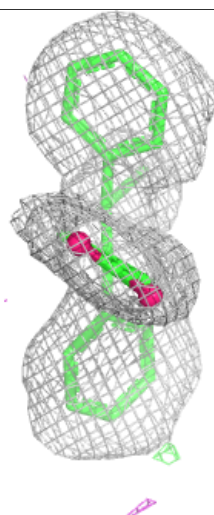
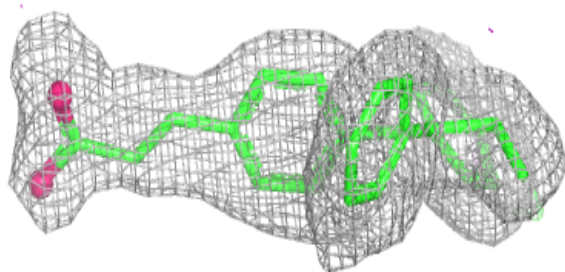
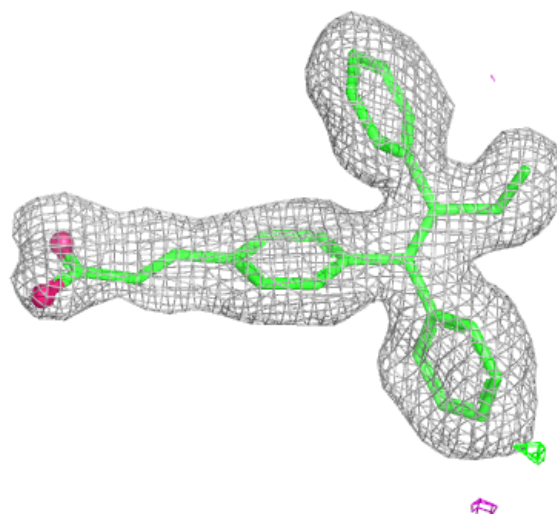
Electron density around GW5 A 1552:

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



Electron density around GW5 B 1546:

$2mF_o-DF_c$ (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.