



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:32 AM UTC

PDB ID : 7Y8G / pdb_00007y8g
Title : Estrogen Receptor Alpha Ligand Binding Domain Y537S Mutant in Complex with an Inhibitor 30a and GRIP Peptide
Authors : Min, J.; Hu, H.B.; Yang, Y.; Dong, C.E.; Zhou, H.B.; Chen, C.-C.; Guo, R.-T.
Deposited on : 2022-06-23
Resolution : 2.14 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

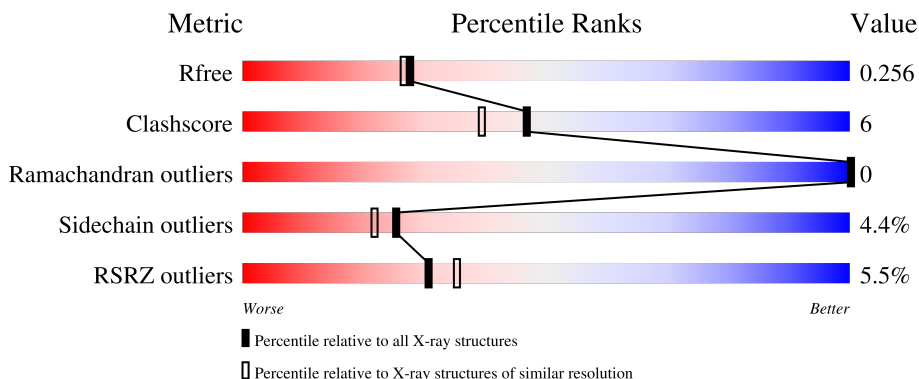
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.14 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	3689 (2.16-2.12)
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)
RSRZ outliers	180081	3691 (2.16-2.12)

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	260	3% 79% 12% 9%
1	B	260	6% 76% 14% 9%
2	C	8	75% 25%
2	D	8	38% 38% 50% 12%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4188 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	237	Total	C	N	O	S	0	2	0
			1893	1209	328	337	19			
1	B	236	Total	C	N	O	S	0	0	0
			1874	1200	319	336	19			

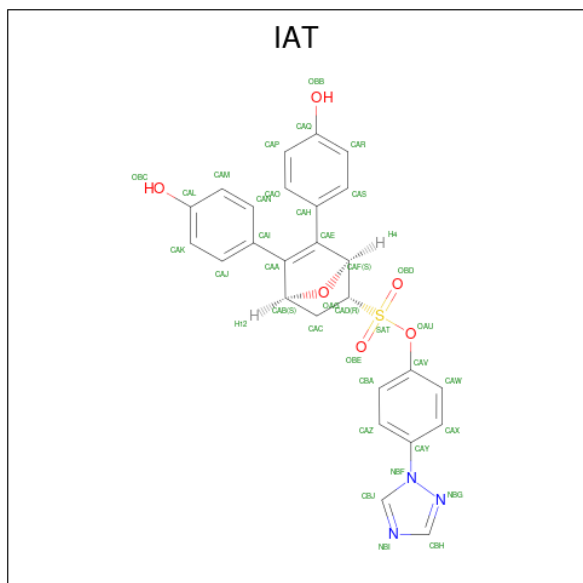
There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	295	ALA	-	linker	UNP P03372
A	296	GLY	-	linker	UNP P03372
A	297	ALA	-	linker	UNP P03372
A	298	GLY	-	linker	UNP P03372
A	299	ALA	-	linker	UNP P03372
A	300	GLY	-	linker	UNP P03372
A	301	ALA	-	linker	UNP P03372
A	302	GLY	-	linker	UNP P03372
A	303	ALA	-	linker	UNP P03372
A	304	GLY	-	linker	UNP P03372
A	537	SER	TYR	engineered mutation	UNP P03372
B	295	ALA	-	linker	UNP P03372
B	296	GLY	-	linker	UNP P03372
B	297	ALA	-	linker	UNP P03372
B	298	GLY	-	linker	UNP P03372
B	299	ALA	-	linker	UNP P03372
B	300	GLY	-	linker	UNP P03372
B	301	ALA	-	linker	UNP P03372
B	302	GLY	-	linker	UNP P03372
B	303	ALA	-	linker	UNP P03372
B	304	GLY	-	linker	UNP P03372
B	537	SER	TYR	engineered mutation	UNP P03372

- Molecule 2 is a protein called Grip peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	8	Total 67	C 44	N 14	O 9	0	0	0
2	D	8	Total 67	C 44	N 14	O 9	0	0	0

- Molecule 3 is [4-(1,2,4-triazol-1-yl)phenyl] (1 {S},2 {R},4 {S})-5,6-bis(4-hydroxyphenyl)-7-oxabicyclo[2.2.1]hept-5-ene-2-sulfonate (CCD ID: IAT) (formula: C₂₆H₂₁N₃O₆S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 36	C 26	N 3	O 6	S 1	0	0
3	B	1	Total 36	C 26	N 3	O 6	S 1	0	0

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			7	4	3		
4	B	1	Total	C	O	0	0
			7	4	3		

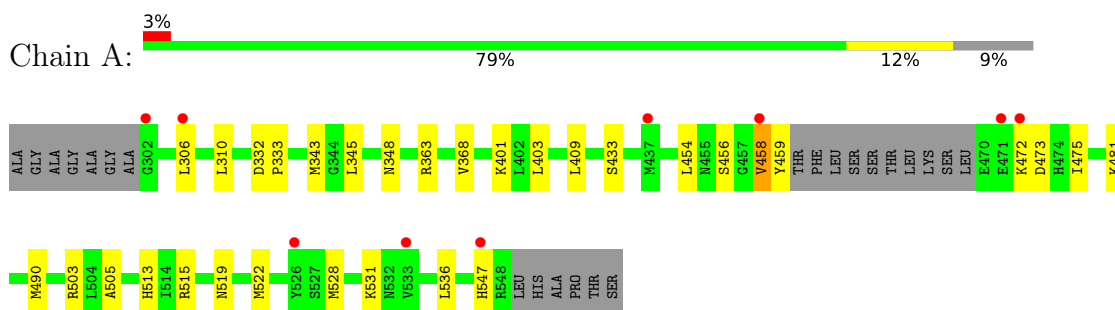
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	113	Total	O	0	0
			113	113		
5	C	4	Total	O	0	0
			4	4		
5	B	82	Total	O	0	0
			82	82		
5	D	2	Total	O	0	0
			2	2		

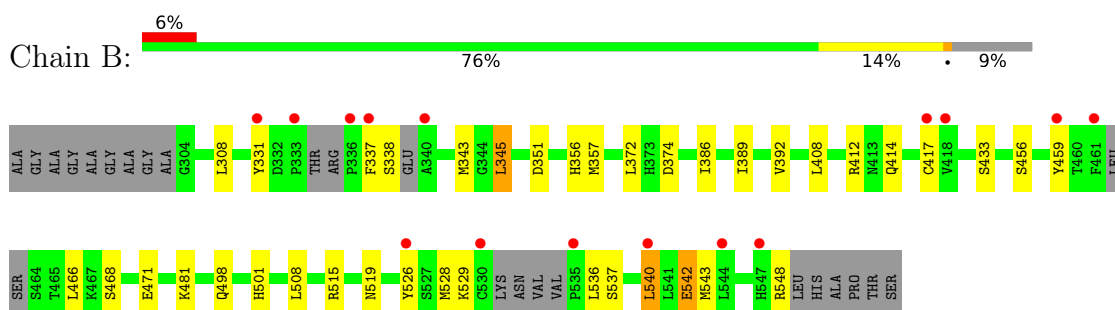
3 Residue-property plots

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.

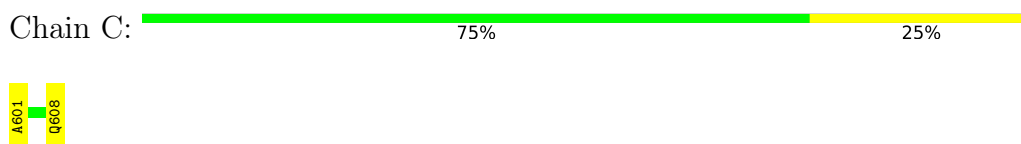
- Molecule 1: Estrogen receptor



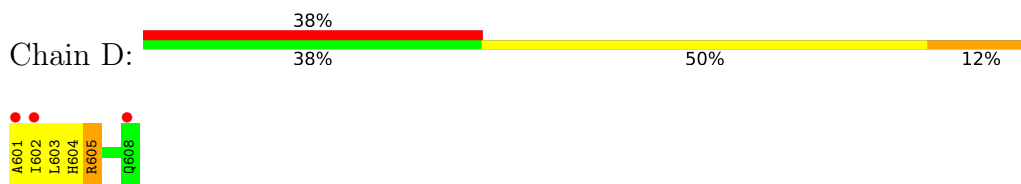
- Molecule 1: Estrogen receptor



- Molecule 2: Grip peptide



- Molecule 2: Grip peptide



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	52.63Å 101.86Å 195.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.32 – 2.14 35.32 – 2.14	Depositor EDS
% Data completeness (in resolution range)	99.3 (35.32-2.14) 99.3 (35.32-2.14)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.64 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.185 , 0.248 0.195 , 0.256	Depositor DCC
R_{free} test set	1418 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	31.6	Xtriage
Anisotropy	0.621	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 38.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4188	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.52% 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: PEG, IAT

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	1.01	0/1935	1.40	1/2613 (0.0%)
1	B	1.04	0/1906	1.42	0/2567
2	C	0.95	0/67	1.37	1/89 (1.1%)
2	D	1.02	0/67	1.58	0/89
All	All	1.03	0/3975	1.41	2/5358 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	608	GLN	CA-C-O	-5.84	110.86	120.80
1	A	332	ASP	CB-CA-C	5.45	117.20	109.08

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	1893	0	1937	20	0
1	B	1874	0	1919	28	0
2	C	67	0	76	1	0
2	D	67	0	76	7	0
3	A	36	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	36	0	0	0	0
4	A	7	0	10	0	0
4	B	7	0	10	0	0
5	A	113	0	0	4	0
5	B	82	0	0	2	0
5	C	4	0	0	1	0
5	D	2	0	0	1	0
All	All	4188	0	4028	46	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 6.

All (46) 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:519:ASN:HD22	1:B:519:ASN:ND2	1.65	0.93
1:A:519:ASN:ND2	1:B:519:ASN:HD22	1.66	0.91
1:A:519:ASN:HD22	1:B:519:ASN:HD22	0.83	0.77
1:A:456:SER:HA	1:A:515:ARG:NH2	2.09	0.67
1:A:528:MET:CE	1:A:536:LEU:HD21	2.25	0.66
1:A:528:MET:HE3	1:A:536:LEU:HD21	1.78	0.65
1:B:543:MET:HE1	2:D:603:LEU:HD22	1.80	0.64
1:A:348:ASN:ND2	5:A:701:HOH:O	2.24	0.61
1:B:356:HIS:HD2	5:B:709:HOH:O	1.83	0.61
1:B:526:TYR:O	1:B:529:LYS:HG2	2.02	0.59
1:B:337:PHE:CE2	1:B:417:CYS:SG	2.97	0.57
2:D:604:HIS:HE1	5:D:701:HOH:O	1.87	0.57
1:A:459:TYR:C	5:A:760:HOH:O	2.49	0.55
1:B:528:MET:CE	1:B:536:LEU:HD21	2.37	0.54
1:B:543:MET:HE1	2:D:603:LEU:HD13	1.87	0.54
1:B:351:ASP:OD1	1:B:540:LEU:HD23	2.09	0.52
1:B:528:MET:HE3	1:B:536:LEU:HD21	1.90	0.52
1:B:343:MET:HE2	1:B:528:MET:SD	2.50	0.51
1:B:357:MET:HE2	1:B:386:ILE:HG22	1.93	0.51
1:B:374:ASP:OD2	1:B:471:GLU:OE1	2.29	0.51
1:A:513[B]:HIS:CG	1:B:459:TYR:HD2	2.30	0.50
1:A:481:LYS:NZ	5:A:706:HOH:O	2.43	0.50
1:A:363:ARG:NH1	5:A:707:HOH:O	2.45	0.48
1:B:356:HIS:CD2	5:B:709:HOH:O	2.64	0.48
1:A:343:MET:HE2	1:A:528:MET:SD	2.53	0.48
1:B:456:SER:HA	1:B:515:ARG:NH2	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:308:LEU:O	1:B:481:LYS:HE2	2.14	0.48
1:B:389:ILE:HA	1:B:392:VAL:HG22	1.98	0.46
1:A:403:LEU:HD13	1:A:409:LEU:HD13	1.97	0.46
1:A:310:LEU:O	1:A:481:LYS:HE2	2.15	0.46
1:A:454:LEU:O	1:A:458:VAL:HG23	2.16	0.46
2:C:601:ALA:HA	5:C:703:HOH:O	2.15	0.46
1:B:542:GLU:OE2	2:D:602:ILE:N	2.32	0.45
1:B:351:ASP:OD2	1:B:537:SER:OG	2.29	0.45
1:B:543:MET:CE	2:D:603:LEU:HD22	2.46	0.45
1:B:337:PHE:O	1:B:337:PHE:CD2	2.70	0.45
1:B:331:TYR:CD1	1:B:345:LEU:HD22	2.52	0.44
1:A:505:ALA:HA	1:B:508:LEU:CD1	2.47	0.44
2:D:601:ALA:O	2:D:605:ARG:HG3	2.17	0.43
1:A:490:MET:HE2	1:A:503:ARG:HG2	2.00	0.43
1:A:522:MET:HE3	1:A:547:HIS:CE1	2.52	0.43
1:B:345:LEU:HD12	1:B:408:LEU:CD2	2.49	0.43
1:B:372:LEU:HD23	2:D:604:HIS:NE2	2.34	0.43
1:A:458:VAL:CG2	1:A:475:ILE:HG21	2.49	0.42
1:B:498:GLN:HA	1:B:501:HIS:CE1	2.55	0.42
1:A:333:PRO:HB3	1:A:345:LEU:HD11	2.02	0.41

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	235/260 (90%)	232 (99%)	3 (1%)	0	100	100
1	B	226/260 (87%)	220 (97%)	6 (3%)	0	100	100
2	C	6/8 (75%)	6 (100%)	0	0	100	100
2	D	6/8 (75%)	6 (100%)	0	0	100	100
All	All	473/536 (88%)	464 (98%)	9 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	212/225 (94%)	204 (96%)	8 (4%)	29	28
1	B	211/225 (94%)	201 (95%)	10 (5%)	23	19
2	C	7/7 (100%)	7 (100%)	0	100	100
2	D	7/7 (100%)	6 (86%)	1 (14%)	3	1
All	All	437/464 (94%)	418 (96%)	19 (4%)	25	23

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	306	LEU
1	A	368	VAL
1	A	401	LYS
1	A	433	SER
1	A	458	VAL
1	A	472	LYS
1	A	473	ASP
1	A	531	LYS
1	B	338	SER
1	B	345	LEU
1	B	412	ARG
1	B	414	GLN
1	B	433	SER
1	B	466	LEU
1	B	468	SER
1	B	540	LEU
1	B	542	GLU
1	B	548	ARG
2	D	605	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	356	HIS
1	B	413	ASN
1	B	476	HIS
1	B	519	ASN

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 ⓘ

4 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	$\# Z > 2$
4	PEG	A	602	-	6,6,6	0.21	0	5,5,5	0.43	0
4	PEG	B	602	-	6,6,6	0.16	0	5,5,5	0.15	0
3	IAT	B	601	-	40,41,41	3.29	11 (27%)	53,61,61	1.80	14 (26%)
3	IAT	A	601	-	40,41,41	3.19	12 (30%)	53,61,61	2.56	18 (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
4	PEG	A	602	-	-	2/4/4/4	-
4	PEG	B	602	-	-	3/4/4/4	-
3	IAT	B	601	-	-	3/21/47/47	0/7/6/6
3	IAT	A	601	-	-	2/21/47/47	0/7/6/6

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	601	IAT	CAF-CAE	-9.97	1.39	1.50
3	A	601	IAT	CAD-SAT	9.05	1.98	1.79
3	B	601	IAT	CAH-CAE	-7.99	1.33	1.48
3	B	601	IAT	OBD-SAT	7.03	1.54	1.43
3	B	601	IAT	CAI-CAA	-6.99	1.35	1.48
3	A	601	IAT	CAH-CAE	-6.90	1.35	1.48
3	A	601	IAT	OBD-SAT	6.90	1.54	1.43
3	A	601	IAT	CAI-CAA	-6.81	1.35	1.48
3	A	601	IAT	CAF-CAE	-6.74	1.43	1.50
3	B	601	IAT	CAB-CAA	-6.56	1.43	1.52
3	A	601	IAT	CAB-CAA	-5.97	1.43	1.52
3	A	601	IAT	OBE-SAT	5.65	1.52	1.43
3	B	601	IAT	OBE-SAT	5.44	1.52	1.43
3	B	601	IAT	CAD-SAT	5.41	1.90	1.79
3	B	601	IAT	OAU-SAT	-4.41	1.53	1.60
3	A	601	IAT	CAY-NBF	-3.94	1.35	1.43
3	A	601	IAT	OAU-SAT	-3.75	1.54	1.60
3	A	601	IAT	CAC-CAD	3.54	1.58	1.54
3	B	601	IAT	CAY-NBF	-3.54	1.36	1.43
3	A	601	IAT	OAU-CAV	-2.88	1.38	1.42
3	B	601	IAT	OAU-CAV	-2.85	1.38	1.42
3	B	601	IAT	CAC-CAB	-2.70	1.47	1.53
3	A	601	IAT	CAX-CAW	2.01	1.42	1.38

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	IAT	OBE-SAT-CAD	-8.27	98.28	109.22
3	A	601	IAT	OAU-CAV-CAW	6.38	131.20	118.70
3	A	601	IAT	CAX-CAY-NBF	5.59	126.42	119.58
3	A	601	IAT	OBD-SAT-CAD	5.12	115.99	109.22
3	B	601	IAT	CAB-CAC-CAD	-4.74	96.42	100.61
3	A	601	IAT	CAY-NBF-NBG	4.67	129.06	121.08
3	B	601	IAT	OBE-SAT-CAD	-4.53	103.22	109.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	IAT	CAV-OAU-SAT	4.51	130.42	119.78
3	A	601	IAT	OAU-CAV-CBA	-4.45	109.98	118.70
3	B	601	IAT	OAU-CAV-CAW	4.27	127.06	118.70
3	A	601	IAT	OAG-CAB-CAC	-3.64	97.62	104.73
3	B	601	IAT	CBH-NBG-NBF	3.32	109.44	102.32
3	A	601	IAT	OAG-CAB-CAA	3.31	106.60	101.99
3	A	601	IAT	CAZ-CAY-NBF	-3.24	115.62	119.58
3	B	601	IAT	CBJ-NBF-NBG	-3.08	105.71	109.26
3	B	601	IAT	NBG-CBH-NBI	-2.66	107.30	114.90
3	A	601	IAT	CAD-CAF-CAE	2.56	112.63	105.52
3	B	601	IAT	OAG-CAB-CAA	2.45	105.40	101.99
3	A	601	IAT	CAI-CAA-CAB	2.44	125.64	121.26
3	B	601	IAT	CAN-CAI-CAA	2.38	123.99	120.91
3	A	601	IAT	CBH-NBG-NBF	2.38	107.42	102.32
3	B	601	IAT	CAJ-CAI-CAA	-2.33	117.88	120.91
3	B	601	IAT	OAU-SAT-OBE	2.27	113.74	106.81
3	A	601	IAT	CAZ-CBA-CAV	2.26	122.32	119.73
3	A	601	IAT	CAS-CAH-CAE	-2.25	117.99	120.91
3	A	601	IAT	CAM-CAN-CAI	2.23	123.18	120.80
3	B	601	IAT	CAY-NBF-NBG	2.22	124.88	121.08
3	B	601	IAT	OAU-SAT-OB	2.21	113.55	106.81
3	B	601	IAT	CBJ-NBI-CBH	2.17	108.72	102.85
3	B	601	IAT	OB	2.14	112.05	109.22
3	A	601	IAT	NBG-CBH-NBI	-2.13	108.82	114.90
3	A	601	IAT	CAY-NBF-CBJ	-2.12	123.54	129.17

There are no chirality outliers.

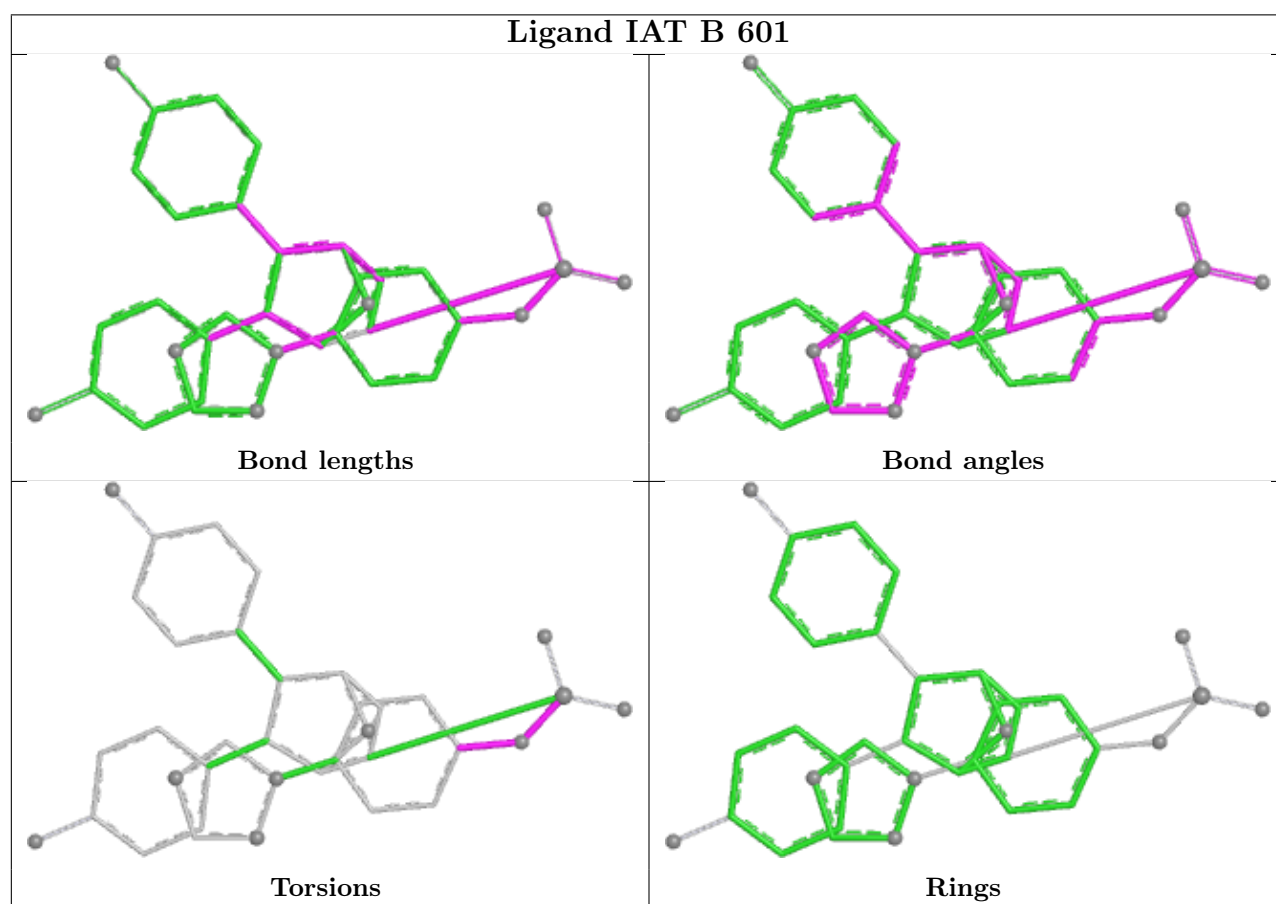
All (10) torsion outliers are listed below:

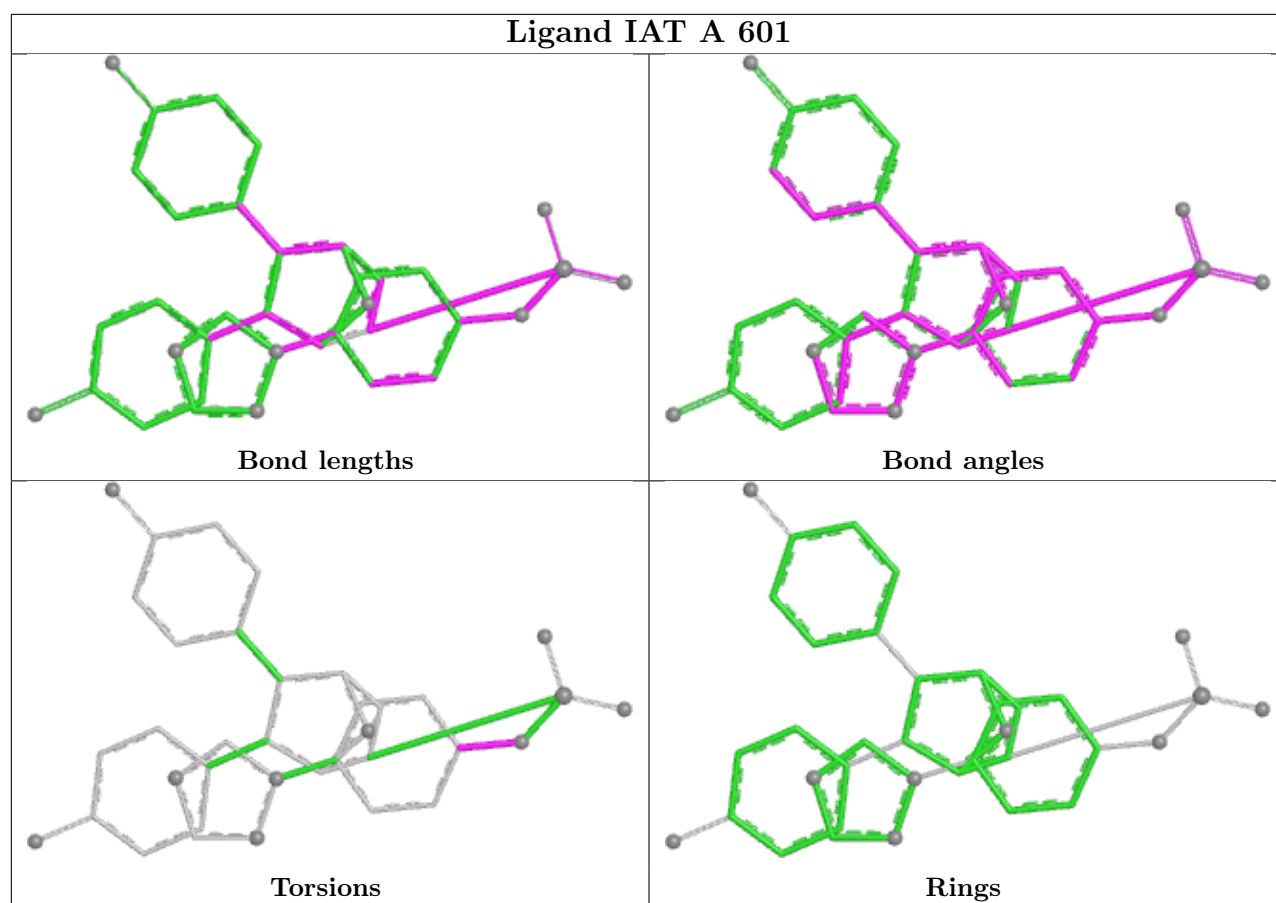
Mol	Chain	Res	Type	Atoms
3	B	601	IAT	CAW-CAV-OAU-SAT
3	B	601	IAT	CBA-CAV-OAU-SAT
4	A	602	PEG	C4-C3-O2-C2
3	A	601	IAT	CAW-CAV-OAU-SAT
3	A	601	IAT	CBA-CAV-OAU-SAT
4	B	602	PEG	O2-C3-C4-O4
4	A	602	PEG	O1-C1-C2-O2
4	B	602	PEG	O1-C1-C2-O2
3	B	601	IAT	CAV-OAU-SAT-OBE
4	B	602	PEG	C4-C3-O2-C2

There are no ring outliers.

No monomer is involved in short contacts.

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	237/260 (91%)	0.06	9 (3%) 44 49	14, 36, 71, 94	2 (0%)
1	B	236/260 (90%)	0.28	15 (6%) 25 29	24, 40, 94, 114	0
2	C	8/8 (100%)	-0.01	0 100 100	32, 39, 40, 47	0
2	D	8/8 (100%)	1.68	3 (37%) 1 1	63, 77, 92, 98	0
All	All	489/536 (91%)	0.19	27 (5%) 30 35	14, 39, 85, 114	2 (0%)

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	547	HIS	3.8
1	B	535	PRO	3.8
1	B	526	TYR	3.8
1	A	526	TYR	3.5
2	D	601	ALA	3.2
1	B	459	TYR	3.1
1	B	547	HIS	2.9
2	D	602	ILE	2.9
1	A	302	GLY	2.9
1	B	340	ALA	2.9
1	A	458	VAL	2.8
1	B	418	VAL	2.7
1	B	333	PRO	2.6
1	B	544	LEU	2.4
1	A	471	GLU	2.3
1	A	533	VAL	2.3
1	A	437	MET	2.3
1	B	530	CYS	2.2
1	A	472	LYS	2.2
1	B	331	TYR	2.2
1	B	337	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	336	PRO	2.1
1	A	306	LEU	2.1
1	B	417	CYS	2.1
1	B	540	LEU	2.1
2	D	608	GLN	2.1
1	B	461	PHE	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](#)

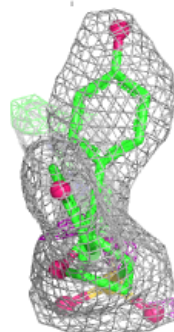
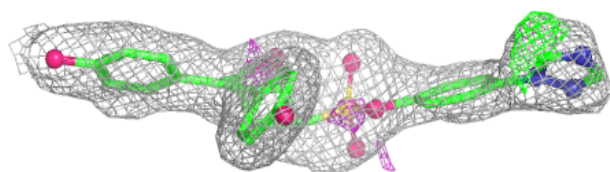
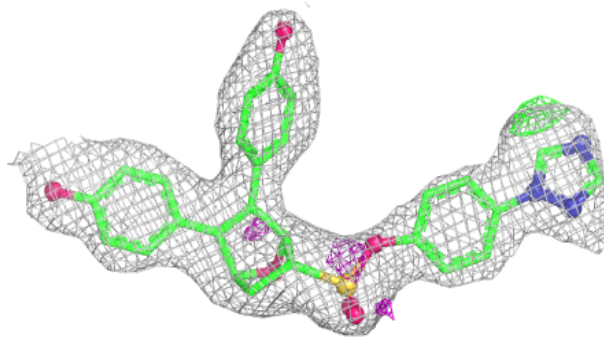
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	IAT	A	601	36/36	0.88	0.12	37,52,88,90	0
4	PEG	A	602	7/7	0.91	0.11	55,58,61,61	0
4	PEG	B	602	7/7	0.91	0.11	58,61,67,71	0
3	IAT	B	601	36/36	0.93	0.10	38,50,107,109	0

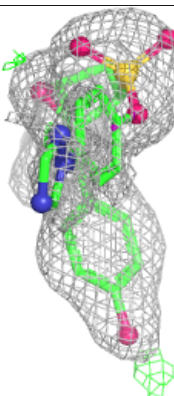
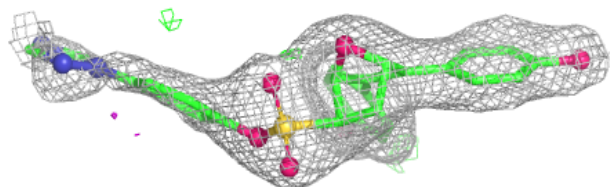
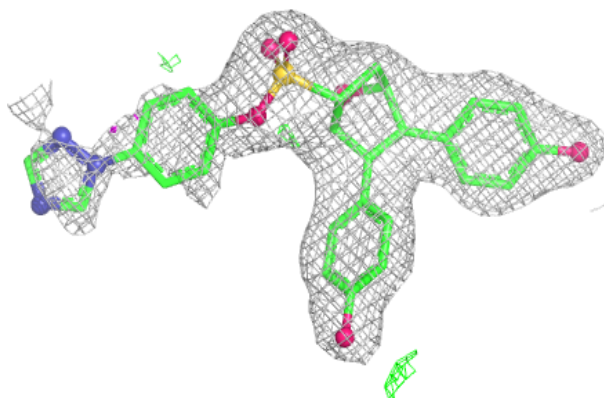
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around IAT A 601:

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

**Electron density around IAT B 601:**

$2mF_o-DF_c$ (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.