



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:04 AM UTC

PDB ID : 2B1Z / pdb_00002b1z
Title : Human estrogen receptor alpha ligand-binding domain in complex with 17methyl-17alpha-dihydroequilenin and a glucocorticoid interacting protein 1 NR box II peptide
Authors : Rajan, S.S.; Hsieh, R.W.; Sharma, S.K.; Greene, G.L.
Deposited on : 2005-09-16
Resolution : 1.78 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

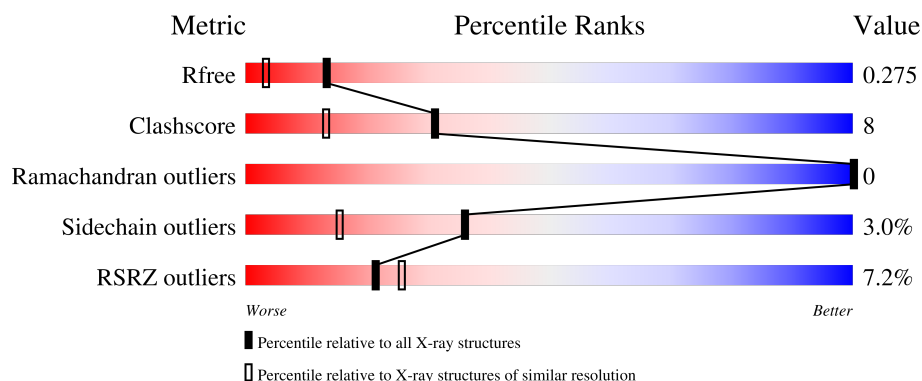
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.78 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	1365 (1.78-1.78)
Clashscore	190562	1395 (1.78-1.78)
Ramachandran outliers	187476	1382 (1.78-1.78)
Sidechain outliers	187428	1382 (1.78-1.78)
RSRZ outliers	180081	1365 (1.78-1.78)

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	257	5% 77% 13% 9%
1	B	257	9% 75% 16% 7%
2	C	13	54% 8% 38%
2	D	13	54% 8% 8% 31%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4127 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	235	Total	C	N	O	S	0	4	0
			1905	1217	326	338	24			
1	B	238	Total	C	N	O	S	0	2	0
			1919	1228	325	342	24			

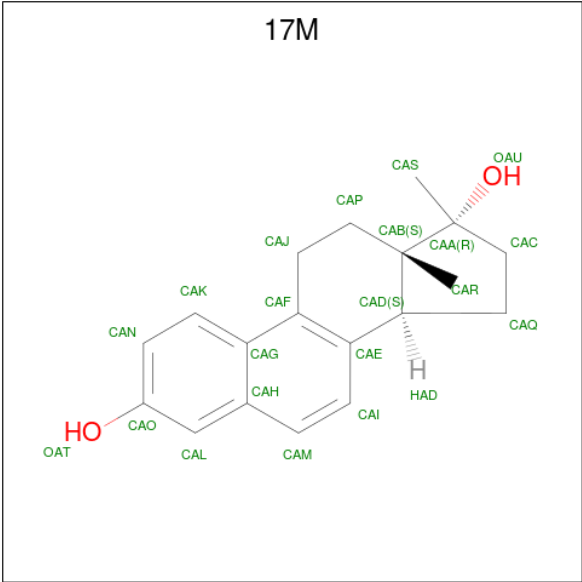
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	381	CME	CYS	modified residue	UNP P03372
A	417	CME	CYS	modified residue	UNP P03372
A	530	CME	CYS	modified residue	UNP P03372
A	537	SER	TYR	engineered mutation	UNP P03372
B	381	CME	CYS	modified residue	UNP P03372
B	417	CME	CYS	modified residue	UNP P03372
B	530	CME	CYS	modified residue	UNP P03372
B	537	SER	TYR	engineered mutation	UNP P03372

- Molecule 2 is a protein called Nuclear receptor coactivator 2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	8	Total	C	N	O	0	0	0
			71	47	15	9			
2	D	9	Total	C	N	O	0	0	0
			79	51	16	12			

- Molecule 3 is 17-METHYL-17-ALPHA-DIHYDROEQUILENIN (CCD ID: 17M) (formula: $C_{19}H_{22}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			21	19	2		
3	B	1	Total	C	O	0	0
			21	19	2		

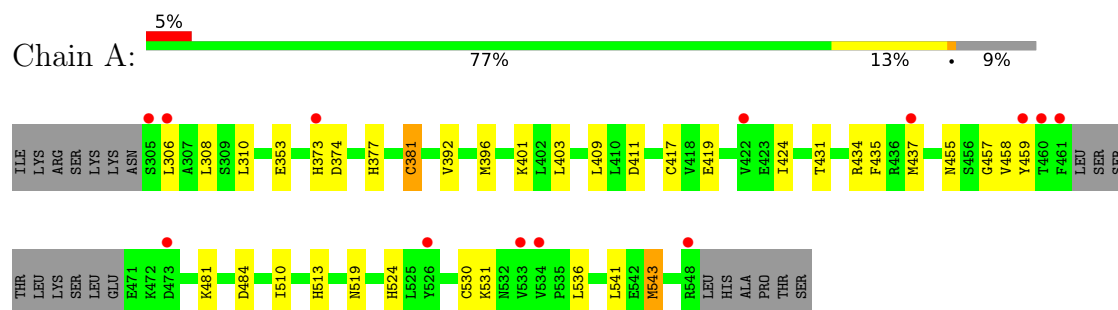
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	53	Total	O	0	1
			54	54		
4	B	56	Total	O	0	0
			56	56		
4	D	1	Total	O	0	0
			1	1		

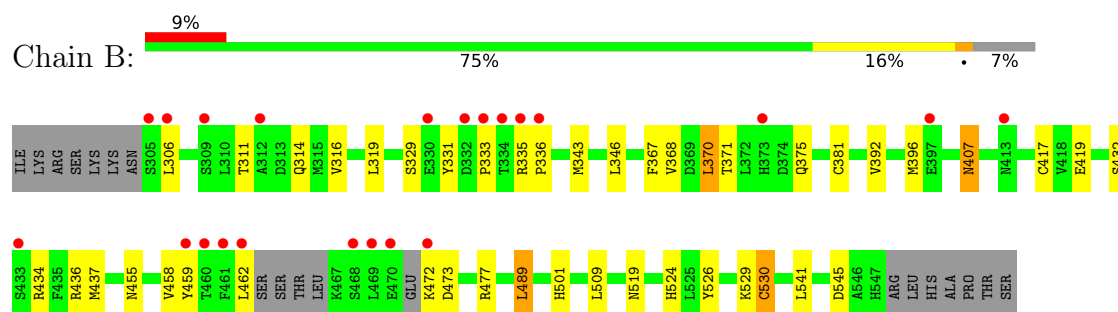
3 Residue-property plots

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: Nuclear receptor coactivator 2



• Molecule 2: Nuclear receptor coactivator 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	55.92Å 83.80Å 58.52Å 90.00° 108.94° 90.00°	Depositor
Resolution (Å)	20.00 – 1.78 20.00 – 1.78	Depositor EDS
% Data completeness (in resolution range)	98.6 (20.00-1.78) 98.5 (20.00-1.78)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.45 (at 1.78Å)	Xtriage
Refinement program	REFMAC 5.2.0005, XTALVIEW	Depositor
R, R_{free}	0.204 , 0.238 (Not available) , 0.275	Depositor DCC
R_{free} test set	2441 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	25.5	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 47.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.021 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4127	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 5.65% 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: CME, 17M

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	0.37	0/1911	0.66	0/2577
1	B	0.41	0/1919	0.68	0/2586
2	C	0.34	0/71	0.66	0/93
2	D	0.35	0/79	0.63	0/104
All	All	0.39	0/3980	0.67	0/5360

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1905	0	1947	32	0
1	B	1919	0	1972	40	0
2	C	71	0	84	1	0
2	D	79	0	88	2	0
3	A	21	0	21	4	0
3	B	21	0	21	4	0
4	A	54	0	0	0	0
4	B	56	0	0	2	0
4	D	1	0	0	0	0
All	All	4127	0	4133	67	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 8.

All (67) 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:524:HIS:HD2	3:B:202:17M:HAS1	1.03	1.12
1:A:524:HIS:HD2	3:A:201:17M:HAS1	1.21	1.06
1:B:524:HIS:CD2	3:B:202:17M:HAS1	1.96	1.00
1:A:524:HIS:CD2	3:A:201:17M:HAS1	2.04	0.93
1:A:519:ASN:HD22	1:B:519:ASN:HD22	0.94	0.90
1:A:519:ASN:ND2	1:B:519:ASN:HD22	1.72	0.85
1:B:329:SER:H	1:B:407:ASN:HD21	1.20	0.84
1:A:519:ASN:HD22	1:B:519:ASN:ND2	1.74	0.83
1:A:458:VAL:HG13	1:A:459:TYR:CD1	2.22	0.74
1:B:335:ARG:HG2	1:B:336:PRO:HD2	1.75	0.69
1:B:407:ASN:HD22	1:B:407:ASN:H	1.44	0.66
1:B:396:MET:O	1:B:436:ARG:HD3	2.03	0.59
1:A:403:LEU:HD13	1:A:409:LEU:HD13	1.85	0.58
1:B:331:TYR:CE2	1:B:333:PRO:HA	2.38	0.58
1:B:331:TYR:CZ	1:B:333:PRO:HA	2.38	0.57
1:A:484:ASP:OD1	1:B:501:HIS:HE1	1.88	0.57
1:A:513[A]:HIS:CE1	1:B:459:TYR:CD2	2.94	0.56
1:A:381[B]:CME:HZ2	1:A:381[B]:CME:HA	1.87	0.56
1:B:501:HIS:HD2	4:B:54:HOH:O	1.88	0.56
1:A:419:GLU:O	1:A:524:HIS:HE1	1.89	0.55
1:B:311:THR:H	1:B:314:GLN:HE21	1.53	0.55
1:A:524:HIS:HD2	3:A:201:17M:CAS	2.08	0.54
1:B:335:ARG:HG2	1:B:336:PRO:CD	2.38	0.53
1:B:434:ARG:CD	1:B:437:MET:HE3	2.38	0.53
1:B:311:THR:H	1:B:314:GLN:NE2	2.05	0.53
1:B:392:VAL:HG13	1:B:432:SER:HA	1.91	0.53
1:B:434:ARG:HD3	1:B:437:MET:HE3	1.91	0.51
1:A:392:VAL:HG11	1:A:431:THR:HG22	1.92	0.51
1:B:346:LEU:HB3	3:B:202:17M:HAJ1	1.91	0.51
1:B:392:VAL:HG13	1:B:432:SER:CA	2.40	0.51
1:B:419:GLU:O	1:B:524:HIS:HE1	1.95	0.50
2:D:689:ILE:HG22	2:D:693:LEU:HD22	1.93	0.50
1:A:434:ARG:NE	1:B:459:TYR:OH	2.44	0.50
1:B:455:ASN:O	1:B:458:VAL:HG12	2.12	0.49
1:B:316:VAL:HG21	1:B:489:LEU:HD11	1.94	0.49
1:A:455:ASN:O	1:A:458:VAL:HG12	2.13	0.49
1:A:308:LEU:HA	1:A:481:LYS:HD2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:308:LEU:HA	1:A:481:LYS:CD	2.43	0.48
1:A:403:LEU:CD1	1:A:409:LEU:HD13	2.43	0.48
1:B:473:ASP:O	1:B:477:ARG:HG3	2.14	0.48
1:A:434:ARG:HA	1:A:437:MET:HE3	1.96	0.47
1:A:435:PHE:HE1	1:A:510:ILE:HG21	1.80	0.47
1:A:458:VAL:HG13	1:A:459:TYR:HD1	1.78	0.47
2:D:689:ILE:HG22	2:D:693:LEU:CD2	2.44	0.46
1:A:353:GLU:OE1	3:A:201:17M:OAT	2.33	0.45
1:A:536:LEU:N	1:A:536:LEU:HD12	2.32	0.45
1:B:371:THR:O	1:B:375:GLN:HG3	2.17	0.45
1:B:529:LYS:HG3	1:B:530:CME:N	2.31	0.45
1:A:396:MET:HE2	1:A:396:MET:HB3	1.73	0.44
1:B:434:ARG:HA	1:B:437:MET:HG2	1.99	0.44
1:B:541:LEU:O	1:B:545:ASP:HB2	2.18	0.44
1:B:526:TYR:OH	1:B:530:CME:HZ2	2.17	0.44
1:A:543:MET:HE1	2:C:690:LEU:HD22	1.99	0.44
1:B:407:ASN:HD22	1:B:407:ASN:N	2.09	0.43
1:A:373[A]:HIS:HD2	1:A:374:ASP:OD1	2.02	0.43
1:A:458:VAL:HG13	1:A:459:TYR:CE1	2.54	0.43
1:A:377:HIS:HE1	1:A:457:GLY:O	2.02	0.42
1:B:367:PHE:O	1:B:370:LEU:HB2	2.20	0.42
1:A:513[A]:HIS:CG	1:B:459:TYR:HD2	2.38	0.42
1:B:368:VAL:HG22	4:B:66:HOH:O	2.19	0.41
1:A:536:LEU:HB2	1:A:541:LEU:HD13	2.03	0.41
1:B:434:ARG:HD2	1:B:437:MET:HE3	2.03	0.41
1:B:343:MET:HE1	3:B:202:17M:HAS3	2.03	0.41
1:B:509:LEU:HD23	1:B:509:LEU:HA	1.90	0.41
1:A:401:LYS:NZ	1:A:411:ASP:OD1	2.46	0.41
1:B:329:SER:N	1:B:407:ASN:HD21	2.02	0.40

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	230/257 (90%)	227 (99%)	3 (1%)	0	100	100
1	B	230/257 (90%)	228 (99%)	2 (1%)	0	100	100
2	C	6/13 (46%)	6 (100%)	0	0	100	100
2	D	7/13 (54%)	7 (100%)	0	0	100	100
All	All	473/540 (88%)	468 (99%)	5 (1%)	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	210/229 (92%)	205 (98%)	5 (2%)	43	24
1	B	212/229 (93%)	205 (97%)	7 (3%)	33	13
2	C	8/13 (62%)	8 (100%)	0	100	100
2	D	9/13 (69%)	8 (89%)	1 (11%)	6	0
All	All	439/484 (91%)	426 (97%)	13 (3%)	36	15

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	306	LEU
1	A	310	LEU
1	A	424	ILE
1	A	531	LYS
1	A	543	MET
1	B	306	LEU
1	B	319	LEU
1	B	370	LEU
1	B	407	ASN
1	B	462	LEU
1	B	472	LYS
1	B	489	LEU
2	D	693	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	359	ASN
1	A	377	HIS
1	A	439	ASN
1	A	488	HIS
1	A	498	GLN
1	A	524	HIS
1	B	314	GLN
1	B	356	HIS
1	B	407	ASN
1	B	413	ASN
1	B	455	ASN
1	B	474	HIS
1	B	501	HIS
1	B	516	HIS
1	B	519	ASN
1	B	524	HIS
2	D	691	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

8 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	CME	B	381[A]	-	8,9,10	0.86	0	6,9,11	2.98	3 (50%)
1	CME	A	381[B]	-	8,9,10	0.81	0	6,9,11	2.64	2 (33%)
1	CME	B	530	1	8,9,10	0.85	0	6,9,11	2.62	3 (50%)
1	CME	B	417	1	8,9,10	0.88	0	6,9,11	3.22	2 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	CME	A	417	1	8,9,10	0.88	0	6,9,11	3.14	2 (33%)
1	CME	A	530	1	8,9,10	0.79	0	6,9,11	3.24	2 (33%)
1	CME	A	381[A]	-	8,9,10	0.84	0	6,9,11	3.37	2 (33%)
1	CME	B	381[B]	-	8,9,10	0.81	0	6,9,11	2.86	2 (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
1	CME	B	381[A]	-	-	1/5/8/10	-
1	CME	A	381[B]	-	-	2/5/8/10	-
1	CME	B	530	1	-	1/5/8/10	-
1	CME	B	417	1	-	3/5/8/10	-
1	CME	A	417	1	-	1/5/8/10	-
1	CME	A	530	1	-	3/5/8/10	-
1	CME	A	381[A]	-	-	1/5/8/10	-
1	CME	B	381[B]	-	-	2/5/8/10	-

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	381[A]	CME	CB-SG-SD	6.18	119.84	103.86
1	A	530	CME	CB-SG-SD	6.10	119.64	103.86
1	A	417	CME	CB-SG-SD	5.76	118.76	103.86
1	B	417	CME	CB-SG-SD	5.68	118.56	103.86
1	A	381[A]	CME	CE-SD-SG	5.15	126.07	103.46
1	B	417	CME	CE-SD-SG	5.06	125.69	103.46
1	B	381[A]	CME	CB-SG-SD	4.97	116.72	103.86
1	B	381[B]	CME	CE-SD-SG	4.89	124.93	103.46
1	A	530	CME	CE-SD-SG	4.86	124.82	103.46
1	B	381[A]	CME	CE-SD-SG	4.78	124.44	103.46
1	A	381[B]	CME	CE-SD-SG	4.56	123.50	103.46
1	B	381[B]	CME	CB-SG-SD	4.54	115.62	103.86
1	A	417	CME	CE-SD-SG	4.50	123.20	103.46
1	B	530	CME	CE-SD-SG	4.27	122.21	103.46
1	A	381[B]	CME	CB-SG-SD	4.26	114.88	103.86
1	B	530	CME	CB-SG-SD	4.16	114.61	103.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	530	CME	CA-CB-SG	-2.09	105.88	114.45
1	B	381[A]	CME	CA-CB-SG	-2.05	106.05	114.45

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	381[B]	CME	SD-CE-CZ-OH
1	A	417	CME	SD-CE-CZ-OH
1	A	530	CME	CA-CB-SG-SD
1	B	381[A]	CME	SD-CE-CZ-OH
1	B	381[B]	CME	SD-CE-CZ-OH
1	B	417	CME	CE-SD-SG-CB
1	B	417	CME	CZ-CE-SD-SG
1	B	530	CME	SD-CE-CZ-OH
1	A	381[A]	CME	CE-SD-SG-CB
1	A	381[B]	CME	CE-SD-SG-CB
1	B	381[B]	CME	CE-SD-SG-CB
1	A	530	CME	CE-SD-SG-CB
1	A	530	CME	SD-CE-CZ-OH
1	B	417	CME	SD-CE-CZ-OH

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	381[B]	CME	1	0
1	B	530	CME	2	0

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	17M	A	201	-	24,24,24	1.59	1 (4%)	36,39,39	1.73	6 (16%)
3	17M	B	202	-	24,24,24	1.61	1 (4%)	36,39,39	1.72	7 (19%)

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	17M	A	201	-	-	-	0/4/4/4
3	17M	B	202	-	-	-	0/4/4/4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	202	17M	CAB-CAD	-5.56	1.51	1.58
3	A	201	17M	CAB-CAD	-5.45	1.51	1.58

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	201	17M	CAA-CAB-CAD	-5.92	97.21	103.61
3	B	202	17M	CAA-CAB-CAD	-5.19	98.00	103.61
3	B	202	17M	CAP-CAB-CAA	-4.04	114.25	117.38
3	A	201	17M	CAP-CAB-CAA	-3.86	114.39	117.38
3	A	201	17M	CAR-CAB-CAD	-3.79	111.83	115.94
3	B	202	17M	CAR-CAB-CAD	-3.47	112.18	115.94
3	B	202	17M	CAS-CAA-CAB	-3.45	110.70	114.09
3	A	201	17M	CAR-CAB-CAA	3.18	111.41	108.61
3	B	202	17M	CAC-CAQ-CAD	-3.06	99.68	103.17
3	B	202	17M	CAR-CAB-CAA	2.65	110.94	108.61
3	A	201	17M	CAK-CAG-CAF	-2.50	118.78	122.57
3	A	201	17M	CAC-CAQ-CAD	-2.44	100.39	103.17
3	B	202	17M	CAR-CAB-CAP	2.09	112.55	109.69

There are no chirality outliers.

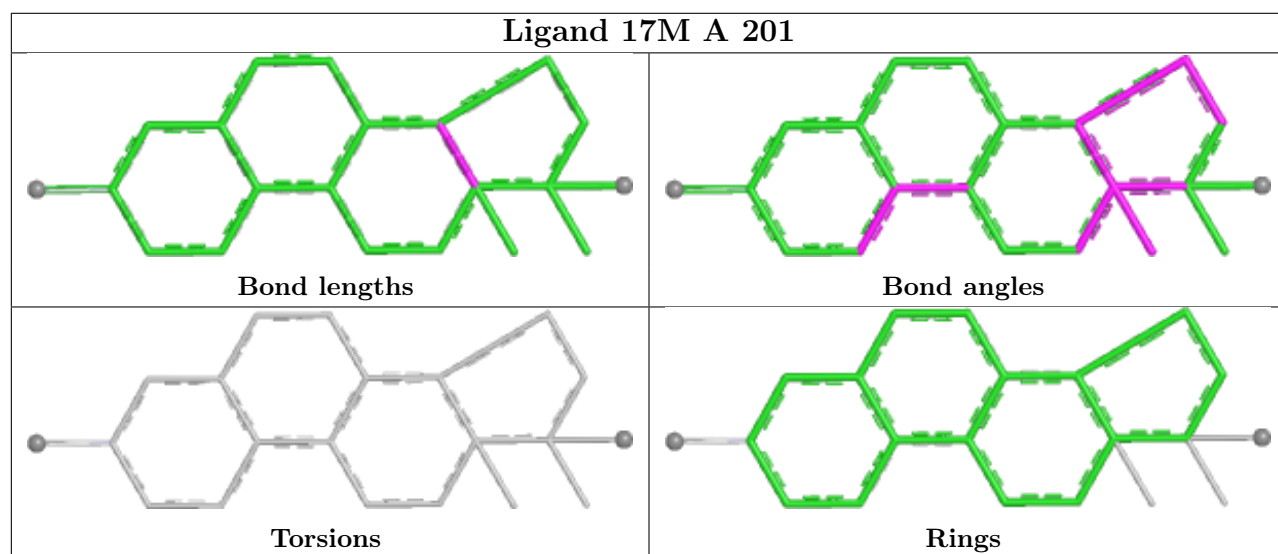
There are no torsion outliers.

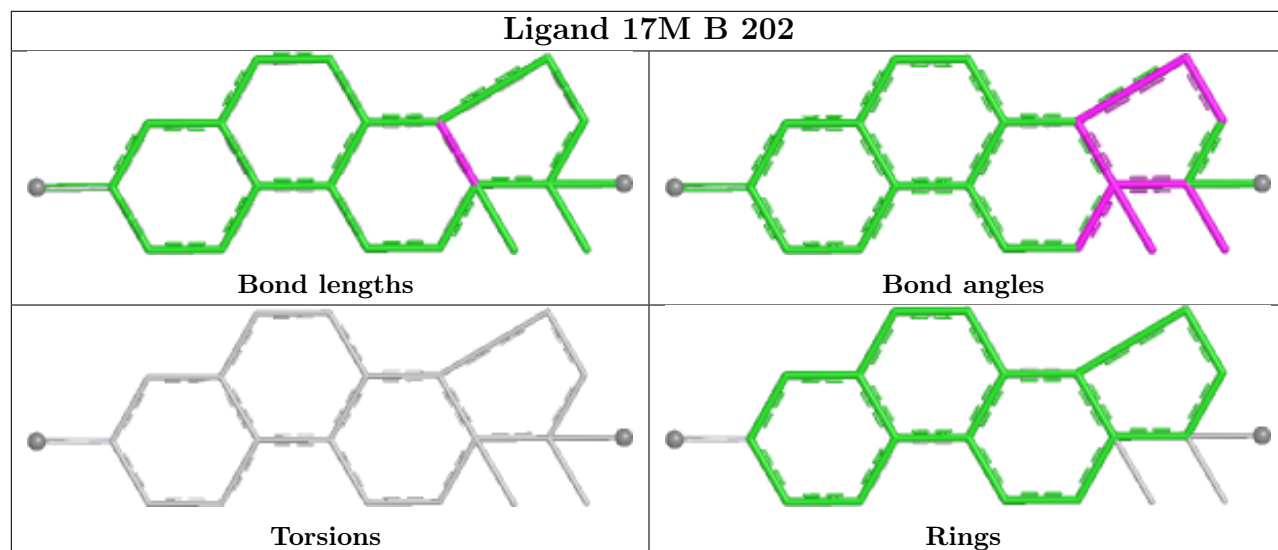
There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	201	17M	4	0
3	B	202	17M	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.





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	232/257 (90%)	0.42	13 (5%) 30 36	14, 26, 41, 60	2 (0%)
1	B	235/257 (91%)	0.71	22 (9%) 14 16	14, 26, 46, 60	1 (0%)
2	C	8/13 (61%)	0.61	0 100 100	26, 29, 34, 37	0
2	D	9/13 (69%)	1.13	0 100 100	23, 28, 36, 41	0
All	All	484/540 (89%)	0.57	35 (7%) 21 26	14, 26, 45, 60	3 (0%)

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	334	THR	7.8
1	B	333	PRO	5.7
1	B	459	TYR	5.7
1	B	462	LEU	4.7
1	A	306	LEU	4.3
1	B	461	PHE	4.2
1	A	534	VAL	3.9
1	B	305	SER	3.7
1	B	306	LEU	3.5
1	B	460	THR	3.4
1	A	459	TYR	3.4
1	A	373[A]	HIS	3.4
1	A	461	PHE	3.3
1	A	533	VAL	3.0
1	A	437	MET	2.9
1	B	336	PRO	2.8
1	B	413	ASN	2.8
1	B	332	ASP	2.7
1	B	433	SER	2.7
1	B	469	LEU	2.7
1	B	470	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	373	HIS	2.6
1	B	309	SER	2.6
1	B	468	SER	2.6
1	B	397	GLU	2.6
1	B	312	ALA	2.5
1	A	526	TYR	2.4
1	B	330	GLU	2.4
1	A	422	VAL	2.2
1	A	548	ARG	2.2
1	A	473	ASP	2.2
1	B	335	ARG	2.2
1	A	460	THR	2.1
1	B	472	LYS	2.1
1	A	305	SER	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	CME	A	530	10/11	0.78	0.18	36,38,56,56	0
1	CME	B	417	10/11	0.79	0.14	28,32,53,53	0
1	CME	B	530	10/11	0.91	0.12	22,26,51,53	0
1	CME	A	381[A]	10/11	0.92	0.12	22,24,36,41	6
1	CME	A	381[B]	10/11	0.92	0.12	22,24,37,39	6
1	CME	A	417	10/11	0.92	0.10	29,33,54,56	0
1	CME	B	381[A]	10/11	0.96	0.08	22,24,39,39	6
1	CME	B	381[B]	10/11	0.96	0.08	22,24,37,40	6

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,

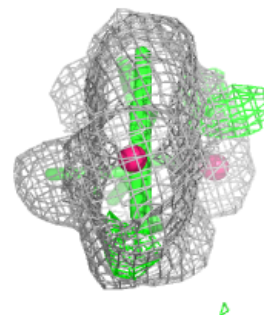
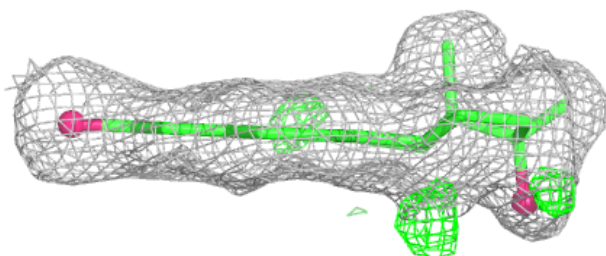
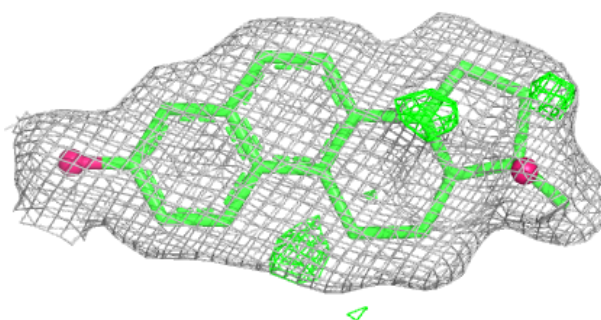
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	17M	A	201	21/21	0.93	0.08	20,23,32,42	0
3	17M	B	202	21/21	0.93	0.07	15,20,24,31	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.

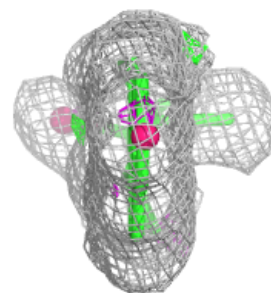
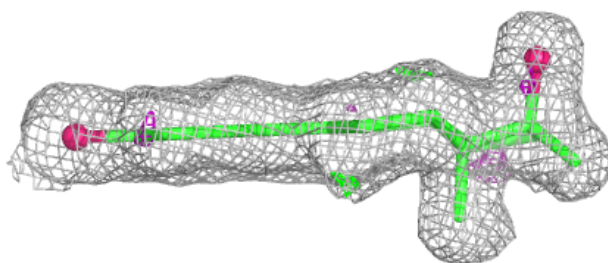
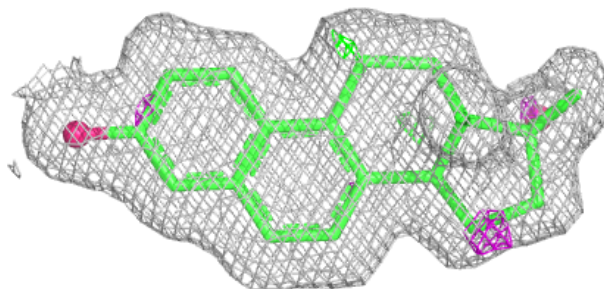
Electron density around 17M A 201:

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 17M B 202:

$2mF_o - DF_c$ (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.