



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 08:53 AM UTC

PDB ID : 3EWJ / pdb_00003ewj
Title : Crystal structure of catalytic domain of TACE with carboxylate inhibitor
Authors : Orth, P.
Deposited on : 2008-10-15
Resolution : 1.80 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

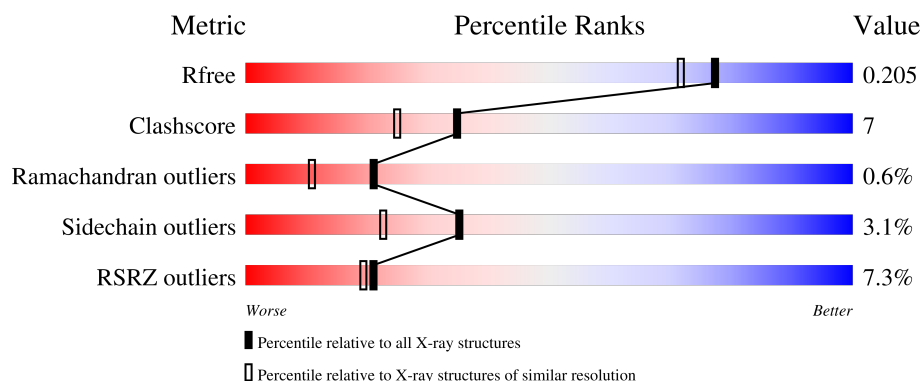
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	271	5% 85% 8% 6%
1	B	271	9% 74% 18% 6%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4497 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 ADAM 17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	254	Total	C	N	O	S	0	1	0
			2002	1262	331	396	13			
1	B	255	Total	C	N	O	S	0	1	0
			1999	1259	334	392	14			

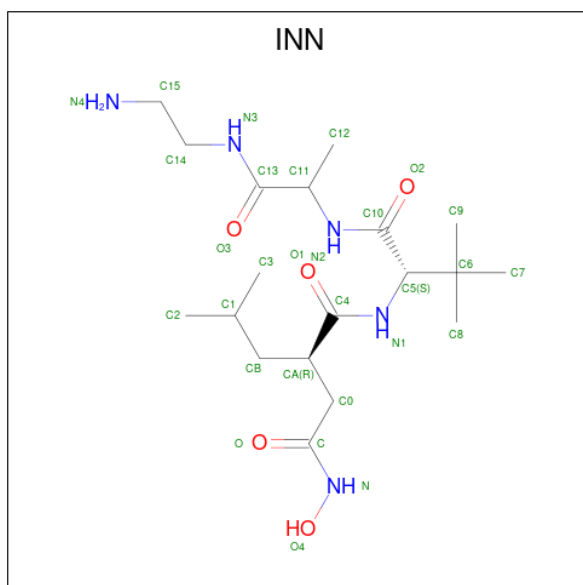
There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	266	ALA	SER	engineered mutation	UNP P78536
A	353	GLY	VAL	engineered mutation	UNP P78536
A	452	GLN	ASN	engineered mutation	UNP P78536
A	478	GLY	-	expression tag	UNP P78536
A	479	SER	-	expression tag	UNP P78536
A	480	HIS	-	expression tag	UNP P78536
A	481	HIS	-	expression tag	UNP P78536
A	482	HIS	-	expression tag	UNP P78536
A	483	HIS	-	expression tag	UNP P78536
A	484	HIS	-	expression tag	UNP P78536
A	485	HIS	-	expression tag	UNP P78536
B	266	ALA	SER	engineered mutation	UNP P78536
B	353	GLY	VAL	engineered mutation	UNP P78536
B	452	GLN	ASN	engineered mutation	UNP P78536
B	478	GLY	-	expression tag	UNP P78536
B	479	SER	-	expression tag	UNP P78536
B	480	HIS	-	expression tag	UNP P78536
B	481	HIS	-	expression tag	UNP P78536
B	482	HIS	-	expression tag	UNP P78536
B	483	HIS	-	expression tag	UNP P78536
B	484	HIS	-	expression tag	UNP P78536
B	485	HIS	-	expression tag	UNP P78536

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

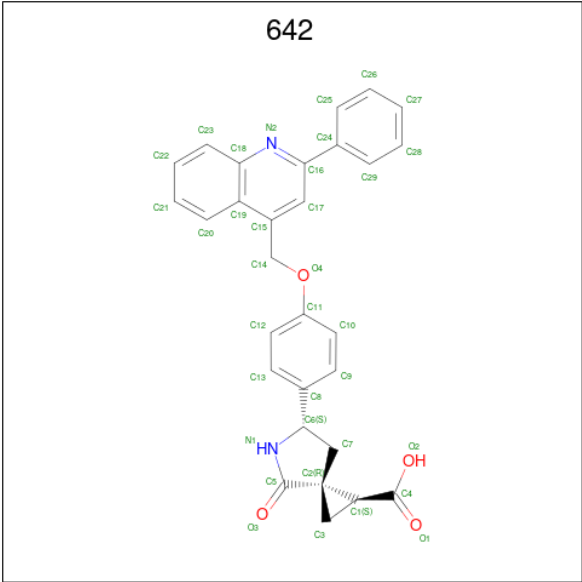
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

- Molecule 3 is N-{(2R)-2-[2-(hydroxyamino)-2-oxoethyl]-4-methylpentanoyl}-3-methyl-L-valyl-N-(2-aminoethyl)-L-alaninamide (CCD ID: INN) (formula: C₁₉H₃₇N₅O₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			29	19	5	5		

- Molecule 4 is (1S,3R,6S)-4-oxo-6-{4-[(2-phenylquinolin-4-yl)methoxy]phenyl}-5-azaspiro[2.4]heptane-1-carboxylic acid (CCD ID: 642) (formula: C₂₉H₂₄N₂O₄).

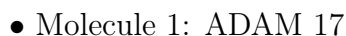


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			35	29	2	4		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	193	Total	O	0	0
			193	193		
5	B	237	Total	O	0	0
			237	237		

- Molecule 1: ADAM 17



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.40Å 76.18Å 103.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.86 – 1.80 36.86 – 1.81	Depositor EDS
% Data completeness (in resolution range)	80.9 (36.86-1.80) 97.4 (36.86-1.81)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.13 (at 1.81Å)	Xtriage
Refinement program	BUSTER-TNT 2.1.1	Depositor
R, R_{free}	0.181 , 0.210 0.180 , 0.205	Depositor DCC
R_{free} test set	987 reflections (1.91%)	wwPDB-VP
Wilson B-factor (Å ²)	19.4	Xtriage
Anisotropy	0.155	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.016 for k,h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4497	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.65% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 642, ZN, INN

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	0.57	1/2050 (0.0%)	0.87	4/2767 (0.1%)
1	B	0.52	0/2050	0.88	6/2768 (0.2%)
All	All	0.55	1/4100 (0.0%)	0.87	10/5535 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	435	MET	SD-CE	5.43	1.93	1.79

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	313	ASP	N-CA-C	-6.30	99.74	109.76
1	A	313	ASP	N-CA-C	-6.29	100.53	109.96
1	A	345	MET	N-CA-C	5.99	119.91	112.24
1	B	414	GLU	N-CA-C	-5.63	101.84	109.95
1	B	434	VAL	N-CA-C	5.47	117.89	111.05
1	B	237	ARG	N-CA-C	5.37	116.94	111.14
1	B	280	GLU	N-CA-C	-5.35	106.43	113.12
1	B	314	VAL	N-CA-C	5.29	116.64	110.62
1	A	239	MET	N-CA-C	-5.24	106.95	113.55
1	A	326	ALA	N-CA-C	5.14	117.28	111.11

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	2002	0	1895	14	0
1	B	1999	0	1889	44	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	29	0	36	3	0
4	B	35	0	22	2	0
5	A	193	0	0	2	0
5	B	237	0	0	9	0
All	All	4497	0	3842	59	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (59) 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:304:TYR:HE1	1:B:316:MET:HE1	1.36	0.88
1:B:304:TYR:CE1	1:B:316:MET:HE1	2.14	0.82
1:B:443:ASP:HA	5:B:619:HOH:O	1.82	0.79
1:B:446:ASN:HA	1:B:449[B]:MET:HE3	1.67	0.77
1:B:221:MET:CG	1:B:472:GLU:HG2	2.16	0.76
1:B:221:MET:HG2	1:B:472:GLU:HG2	1.74	0.69
1:B:449[A]:MET:HE1	5:B:111:HOH:O	1.97	0.64
1:B:222:LYS:HE2	1:B:470:PHE:O	1.96	0.64
1:A:439:ALA:O	3:A:4:INN:H11	1.99	0.63
1:B:350:LEU:HD13	5:B:583:HOH:O	2.02	0.60
1:B:221:MET:HG3	1:B:472:GLU:HG2	1.83	0.59
1:B:273:LYS:HB3	1:B:273:LYS:NZ	2.18	0.59
1:B:289:GLN:HG2	1:B:297:HIS:CG	2.40	0.57
1:B:375:LYS:HD3	5:B:562:HOH:O	2.06	0.56
1:B:273:LYS:HB3	1:B:273:LYS:HZ2	1.72	0.55
1:B:446:ASN:HA	1:B:449[B]:MET:CE	2.37	0.54
1:A:390:TYR:OH	3:A:4:INN:H151	2.09	0.53
1:B:378:ILE:C	1:B:378:ILE:HD12	2.34	0.53
1:B:283:ARG:NH2	1:B:328:GLU:OE2	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:323:PHE:CE1	1:B:376:LYS:HE2	2.44	0.52
1:A:218:PRO:N	5:A:524:HOH:O	2.43	0.52
1:A:344[A]:ASP:OD2	1:A:345:MET:HG3	2.10	0.51
1:B:261:ILE:HD13	5:B:143:HOH:O	2.11	0.50
1:B:264:ASN:ND2	5:B:523:HOH:O	2.43	0.50
1:A:302:LYS:HE3	1:A:307:GLU:HB2	1.93	0.50
1:A:440:VAL:O	1:A:441:SER:HB2	2.11	0.49
1:B:221:MET:HG2	1:B:221:MET:O	2.10	0.49
1:B:248:THR:OG1	1:B:284:ILE:HD11	2.12	0.49
1:A:350:LEU:HD13	5:A:74:HOH:O	2.12	0.48
1:B:448:LYS:HE3	5:B:504:HOH:O	2.13	0.48
4:B:1:642:H7	4:B:1:642:O1	2.14	0.47
1:B:304:TYR:CG	1:B:305:PRO:HA	2.49	0.47
1:B:347:THR:HG23	4:B:1:642:O3	2.15	0.47
1:B:221:MET:HE3	1:B:472:GLU:HG3	1.97	0.47
1:A:254:LEU:C	1:A:254:LEU:HD23	2.40	0.46
1:B:448:LYS:NZ	5:B:603:HOH:O	2.47	0.46
1:B:359:ASN:HA	5:B:97:HOH:O	2.15	0.45
1:A:439:ALA:O	1:A:440:VAL:HG23	2.17	0.45
1:B:273:LYS:NZ	1:B:273:LYS:CB	2.80	0.45
1:B:327:GLU:H	1:B:327:GLU:CD	2.24	0.45
1:B:221:MET:HE3	1:B:472:GLU:CG	2.47	0.45
1:A:223:ASN:C	1:A:223:ASN:HD22	2.25	0.44
1:B:292:LYS:N	1:B:295:GLU:OE2	2.32	0.44
1:B:316:MET:HE2	1:B:316:MET:HB3	1.84	0.44
1:B:221:MET:HG3	1:B:472:GLU:OE1	2.18	0.44
1:B:279:ILE:HG21	1:B:282:ILE:HG13	2.00	0.44
1:A:424:ALA:N	1:A:425:PRO:HD3	2.32	0.43
1:B:330:SER:HB3	1:B:379:TYR:CE1	2.53	0.43
1:B:357:ARG:O	1:B:360:SER:HB2	2.19	0.43
1:B:292:LYS:HB3	1:B:293:PRO:CD	2.50	0.42
1:A:439:ALA:HB2	3:A:4:INN:H21	2.02	0.42
1:B:292:LYS:HB3	1:B:293:PRO:HD2	2.02	0.41
1:B:248:THR:O	1:B:252:ILE:HG13	2.20	0.41
1:B:283:ARG:NE	1:B:328:GLU:OE2	2.53	0.41
1:A:323:PHE:CD1	1:A:376:LYS:HE2	2.57	0.40
1:A:315:LYS:O	1:A:319:GLU:HG3	2.21	0.40
1:B:254:LEU:HD23	1:B:254:LEU:C	2.45	0.40
1:B:266:ALA:HB2	1:B:273:LYS:NZ	2.36	0.40
1:B:263:ARG:NE	1:B:276:GLY:HA3	2.36	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	251/271 (93%)	246 (98%)	3 (1%)	2 (1%)	16	6
1	B	254/271 (94%)	250 (98%)	3 (1%)	1 (0%)	30	19
All	All	505/542 (93%)	496 (98%)	6 (1%)	3 (1%)	21	11

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	441	SER
1	A	365	CYS
1	B	365	CYS

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	213/231 (92%)	210 (99%)	3 (1%)	59	52
1	B	211/231 (91%)	201 (95%)	10 (5%)	23	11
All	All	424/462 (92%)	411 (97%)	13 (3%)	35	23

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

Mol	Chain	Res	Type
1	A	223	ASN
1	A	280	GLU
1	A	428	ASP

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Mol	Chain	Res	Type
1	B	221	MET
1	B	222	LYS
1	B	273	LYS
1	B	280	GLU
1	B	281	GLN
1	B	283	ARG
1	B	325	ILE
1	B	344	ASP
1	B	373	VAL
1	B	429	GLN

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

Mol	Chain	Res	Type
1	A	223	ASN
1	A	281	GLN
1	A	377	ASN
1	A	456	GLN
1	A	467	GLN
1	B	264	ASN
1	B	269	ASN
1	B	281	GLN
1	B	320	GLN
1	B	359	ASN
1	B	429	GLN
1	B	444	HIS
1	B	452	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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	642	B	1	2	39,40,40	1.53	7 (17%)	49,59,59	1.84	8 (16%)
3	INN	A	4	2	28,28,28	1.11	3 (10%)	35,38,38	2.05	9 (25%)

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	642	B	1	2	-	0/17/40/40	0/6/6/6
3	INN	A	4	2	-	6/40/40/40	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1	642	O1-C4	4.86	1.36	1.22
4	B	1	642	C17-C16	3.13	1.44	1.39
4	B	1	642	C18-N2	-2.68	1.33	1.37
4	B	1	642	C10-C11	2.63	1.43	1.38
4	B	1	642	C16-N2	2.58	1.36	1.33
3	A	4	INN	C0-CA	2.44	1.58	1.53
3	A	4	INN	CB-CA	2.40	1.59	1.53
4	B	1	642	C13-C8	2.25	1.42	1.39
4	B	1	642	C22-C23	2.06	1.41	1.36
3	A	4	INN	C10-N2	2.06	1.38	1.34

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1	642	O2-C4-C1	6.18	127.98	113.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	4	INN	O4-N-C	-5.93	111.03	119.79
4	B	1	642	C8-C6-N1	-5.85	106.11	112.81
3	A	4	INN	C6-C5-N1	-4.58	104.78	111.94
3	A	4	INN	C10-C5-N1	3.84	118.36	109.47
4	B	1	642	O1-C4-C1	-3.83	112.40	123.02
3	A	4	INN	C13-C11-N2	-3.81	102.16	111.59
3	A	4	INN	C0-CA-C4	-3.54	104.68	109.71
4	B	1	642	C15-C19-C18	3.17	120.56	117.76
3	A	4	INN	CA-C0-C	-3.14	106.17	112.33
3	A	4	INN	O1-C4-CA	-2.99	117.58	122.19
4	B	1	642	C17-C16-C24	-2.97	117.79	121.82
3	A	4	INN	C12-C11-N2	2.77	115.47	110.38
4	B	1	642	C3-C1-C4	2.65	123.55	119.11
4	B	1	642	C22-C23-C18	2.35	123.30	120.09
4	B	1	642	O3-C5-C2	-2.23	123.40	125.21
3	A	4	INN	C11-N2-C10	2.01	125.55	121.32

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	4	INN	N3-C14-C15-N4
3	A	4	INN	N2-C11-C13-N3
3	A	4	INN	N2-C11-C13-O3
3	A	4	INN	N-C-C0-CA
3	A	4	INN	C13-C11-N2-C10
3	A	4	INN	C12-C11-C13-N3

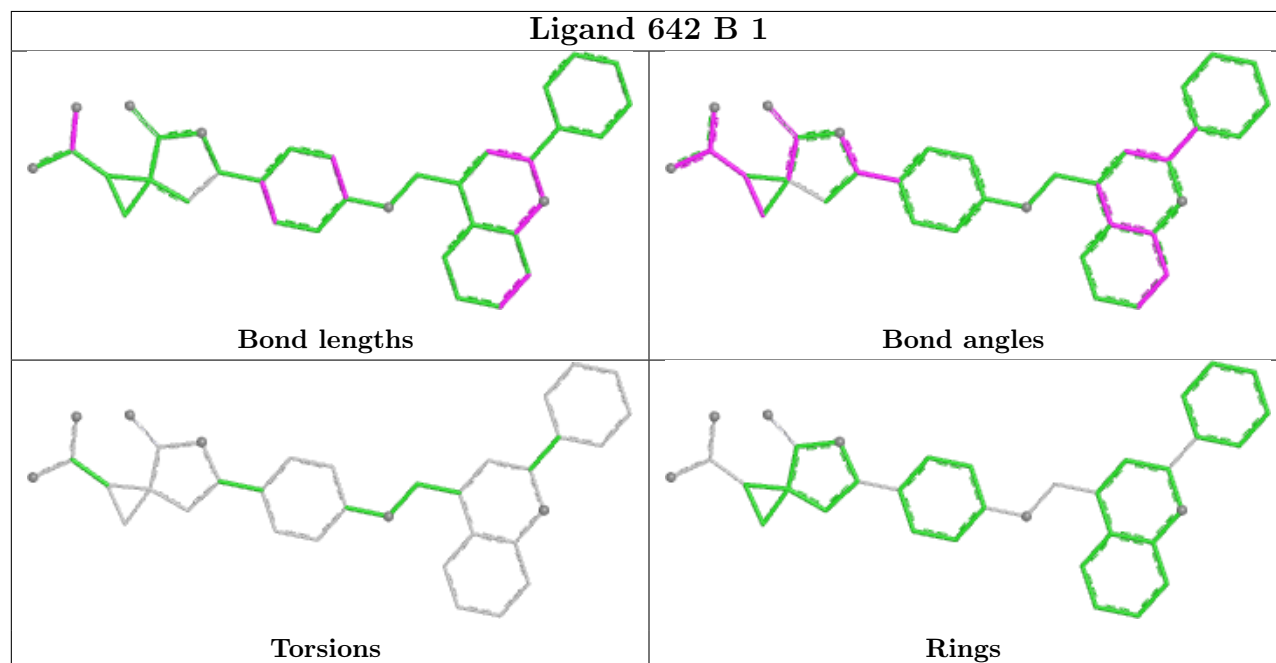
There are no ring outliers.

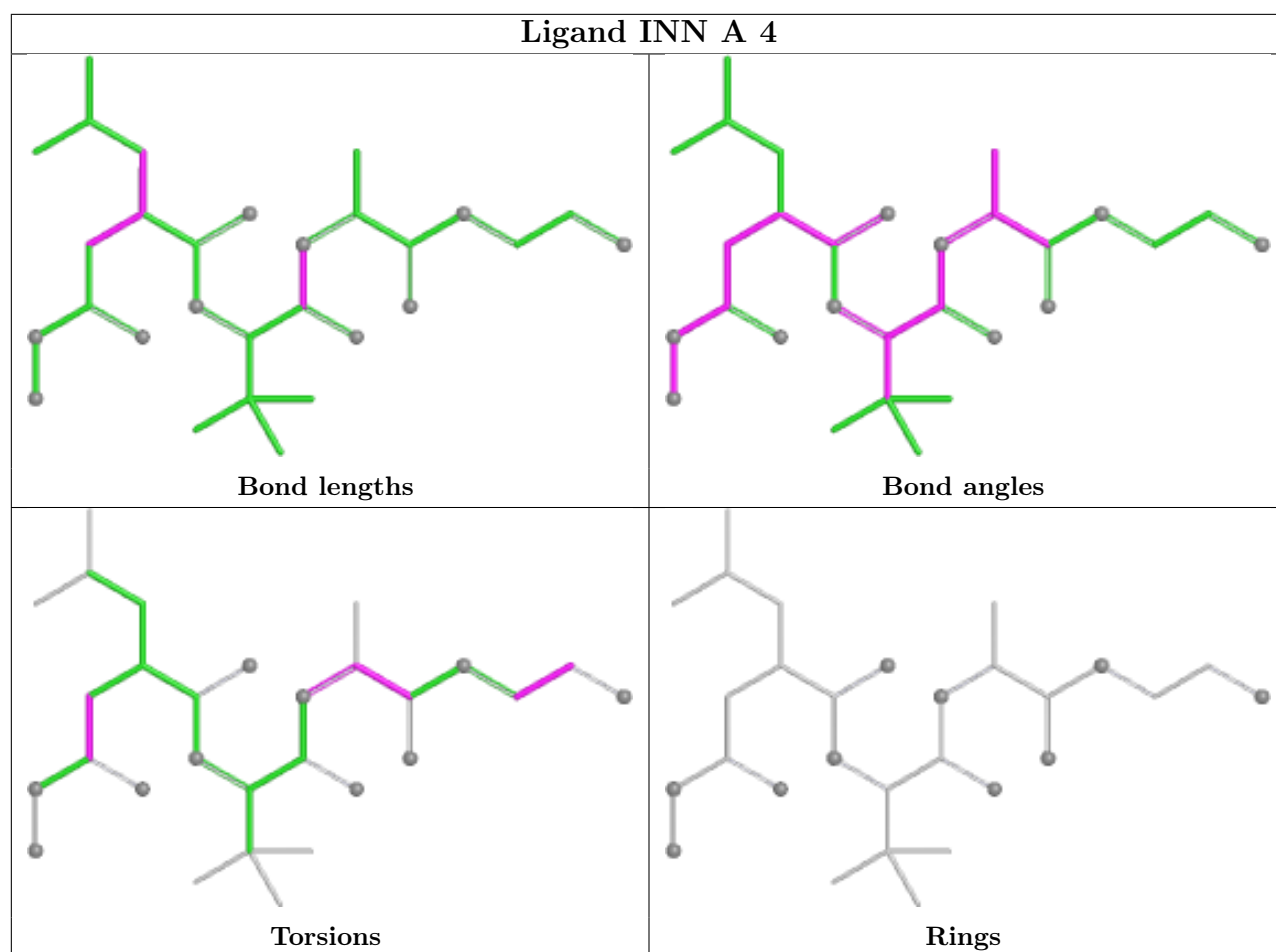
2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1	642	2	0
3	A	4	INN	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 [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	254/271 (93%)	-0.11	13 (5%) 33 32	10, 19, 44, 68	2 (0%)
1	B	255/271 (94%)	0.31	24 (9%) 14 12	12, 25, 47, 75	1 (0%)
All	All	509/542 (93%)	0.10	37 (7%) 21 19	10, 22, 47, 75	3 (0%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	440	VAL	8.0
1	A	475	ASN	7.0
1	B	474	SER	5.0
1	B	356	PRO	4.7
1	A	356	PRO	4.7
1	B	441	SER	4.4
1	B	358	ALA	4.3
1	B	360	SER	4.0
1	A	218	PRO	4.0
1	A	355	SER	4.0
1	B	221	MET	3.9
1	A	439	ALA	3.9
1	B	442	GLY	3.8
1	B	355	SER	3.8
1	A	445	GLU	3.7
1	A	361	HIS	3.6
1	B	440	VAL	3.2
1	B	220	PRO	3.1
1	B	448	LYS	3.0
1	A	442	GLY	2.9
1	A	441	SER	2.8
1	B	293	PRO	2.8
1	B	271	GLY	2.8
1	B	359	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	373	VAL	2.7
1	B	369	TYR	2.5
1	B	292	LYS	2.5
1	B	439	ALA	2.5
1	B	291	VAL	2.5
1	B	464	SER	2.4
1	A	429	GLN	2.3
1	A	221	MET	2.3
1	B	357	ARG	2.1
1	B	361	HIS	2.1
1	B	270	ALA	2.1
1	A	293	PRO	2.0
1	B	272	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](#)

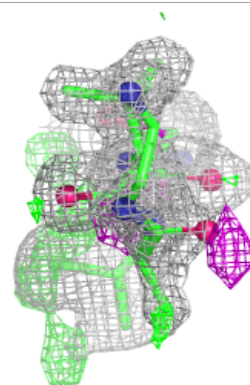
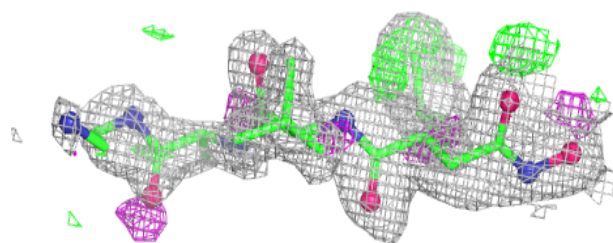
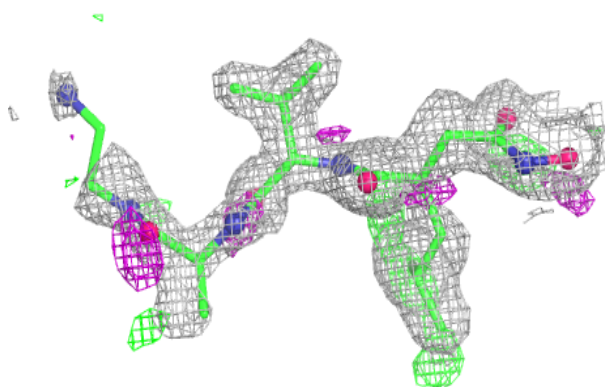
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	INN	A	4	29/29	0.84	0.16	21,33,53,54	0
4	642	B	1	35/35	0.89	0.11	20,29,31,33	0
2	ZN	A	1	1/1	0.99	0.03	21,21,21,21	0
2	ZN	B	2	1/1	1.00	0.01	16,16,16,16	0

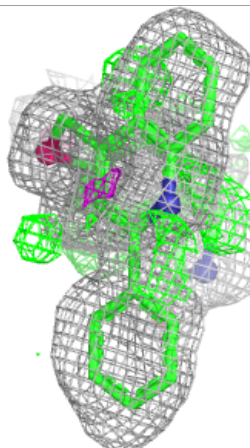
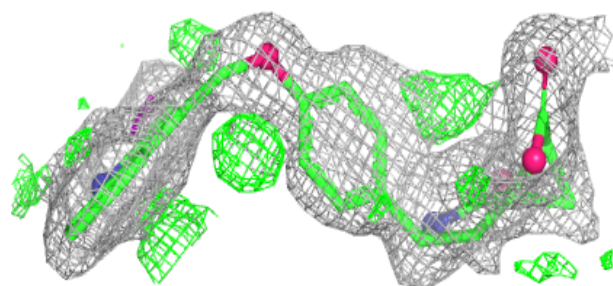
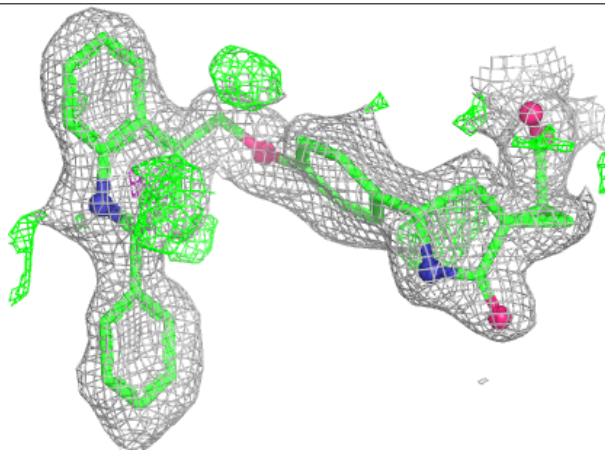
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around INN A 4:

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

**Electron density around 642 B 1:**

$2mF_o-DF_c$ (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.