



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 06:46 PM BST

PDB ID : 6G1W
Title : Crystal structure of Torpedo Californica acetylcholinesterase in complex with 2-{1-[2-(6-Chloro-1,2,3,4-tetrahydroacridin-9-ylamino)ethyl]-1H-1,2,3-triazol-4-yl}-N-[4-(hydroxy)-3-methoxybenzyl]acetamide
Authors : Coquelle, N.; Colletier, J.P.
Deposited on : 2018-03-22
Resolution : 1.90 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

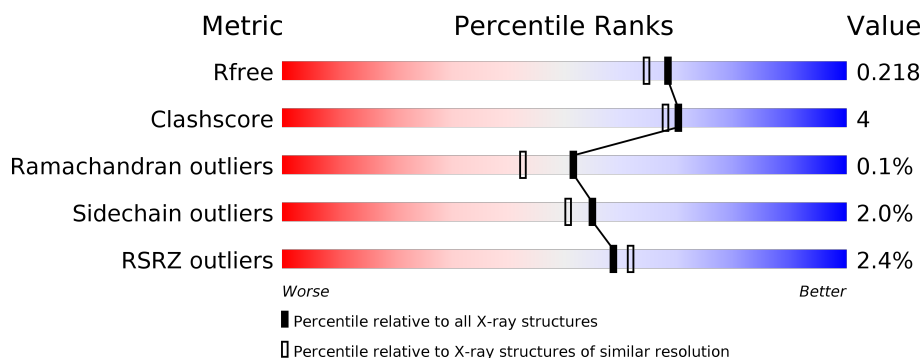
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 on 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	565	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between; align-items: center;"> % <div style="width: 85%; height: 10px; background-color: green;"></div> <div style="width: 8%; height: 10px; background-color: yellow;"></div> <div style="width: 6%; height: 10px; background-color: grey;"></div> </div> <div style="display: flex; justify-content: space-between; align-items: center;"> 85% 8% • 6% </div> </div>
1	B	565	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between; align-items: center;"> 3% <div style="width: 87%; height: 10px; background-color: green;"></div> <div style="width: 6%; height: 10px; background-color: yellow;"></div> <div style="width: 6%; height: 10px; background-color: grey;"></div> </div> <div style="display: flex; justify-content: space-between; align-items: center;"> 87% 6% • 6% </div> </div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 9640 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 Acetylcholinesterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	530	Total	C	N	O	S	0	10	0
			4269	2744	719	782	24			
1	B	532	Total	C	N	O	S	0	11	0
			4295	2758	721	791	25			

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



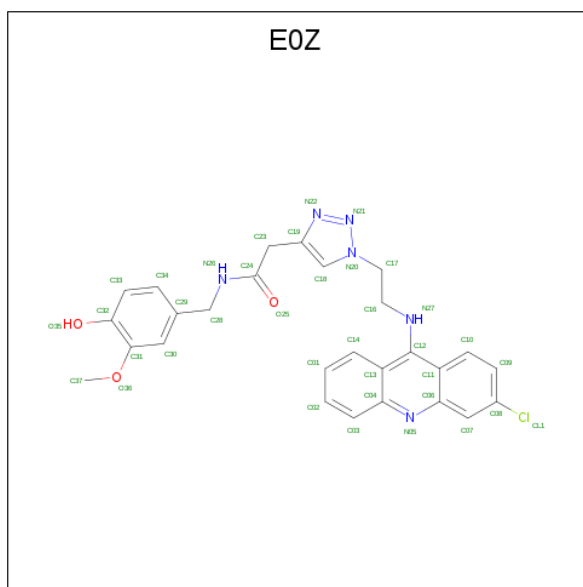
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is 2-[1-[2-[(3-chloranylacridin-9-yl)amino]ethyl]-1,2,3-triazol-4-yl]- {N}-[(3-methoxy-4-oxidanyl-phenyl)methyl]ethanamide (three-letter code: E0Z) (formula: C₂₇H₂₅ClN₆O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	0
			37	27	1	6	3	
3	B	1	Total	C	Cl	N	O	0
			37	27	1	6	3	

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	2	Total	Cl	0
			2	2	
4	A	3	Total	Cl	0
			3	3	

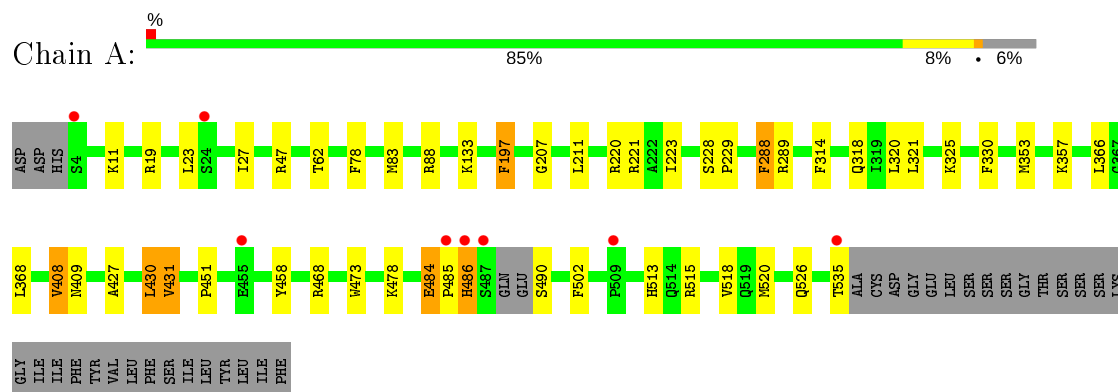
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	447	Total 447	O 447	0	0
5	B	466	Total 466	O 466	0	0

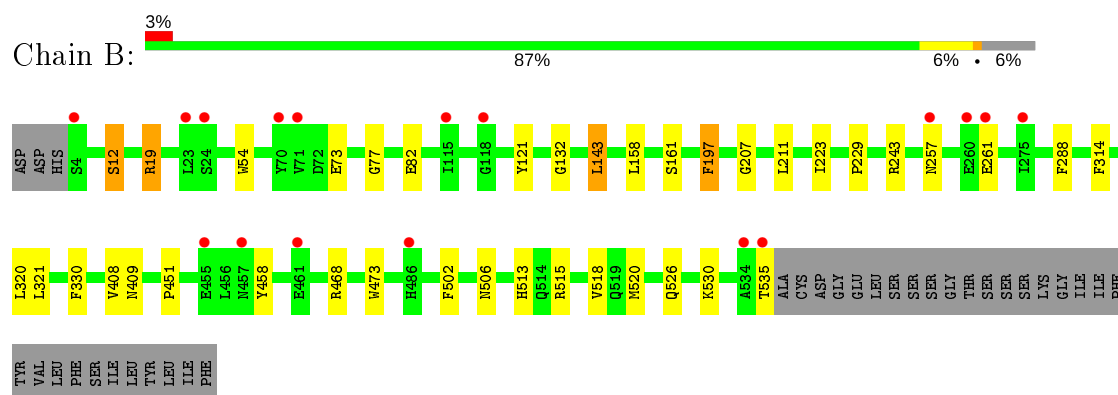
3 Residue-property plots

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: Acetylcholinesterase



• Molecule 1: Acetylcholinesterase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	91.82Å 106.81Å 151.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.70 – 1.90 46.16 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.7 (45.70-1.90) 99.9 (46.16-1.90)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 1.90Å)	Xtriage
Refinement program	PHENIX (1.10.1 _2155: ???)	Depositor
R, R_{free}	0.188 , 0.218 0.188 , 0.218	Depositor DCC
R_{free} test set	5888 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	28.9	Xtriage
Anisotropy	0.823	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 48.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9640	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.03 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.9067e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: E0Z, NAG, CL

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	0.38	0/4420	0.54	0/5998
1	B	0.38	0/4451	0.54	0/6041
All	All	0.38	0/8871	0.54	0/12039

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

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	4269	0	4142	38	0
1	B	4295	0	4157	22	0
2	A	42	0	39	0	0
2	B	42	0	39	0	0
3	A	37	0	0	4	0
3	B	37	0	0	1	0
4	A	3	0	0	0	0
4	B	2	0	0	1	0
5	A	447	0	0	15	0
5	B	466	0	0	7	0
All	All	9640	0	8377	61	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 4.

All (61) 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:520[B]:MET:SD	5:B:951:HOH:O	2.16	1.01
1:A:520[B]:MET:SD	5:A:750:HOH:O	2.21	0.97
1:A:520[A]:MET:SD	5:A:1057:HOH:O	2.43	0.75
1:B:526:GLN:NE2	5:B:701:HOH:O	2.15	0.75
4:B:605:CL:CL	5:B:1045:HOH:O	2.43	0.73
1:A:353:MET:SD	5:A:1146:HOH:O	2.49	0.70
1:A:47:ARG:NH1	5:A:708:HOH:O	2.25	0.69
1:B:243:ARG:NH2	5:B:705:HOH:O	2.29	0.65
1:A:490:SER:N	5:A:713:HOH:O	2.30	0.65
1:A:485:PRO:O	5:A:701:HOH:O	2.14	0.64
1:A:11:LYS:NZ	5:A:712:HOH:O	2.29	0.64
1:A:427:ALA:HB3	1:A:430:LEU:HD22	1.79	0.63
1:A:78:PHE:CZ	1:A:431:VAL:HG13	2.36	0.60
3:A:604:E0Z:O35	5:A:702:HOH:O	2.16	0.58
1:A:211:LEU:HD23	1:A:314:PHE:HB3	1.86	0.57
1:A:220:ARG:HG3	1:A:221:ARG:HG3	1.86	0.56
1:B:211:LEU:HD23	1:B:314:PHE:HB3	1.88	0.54
1:A:409:ASN:HB3	5:A:1066:HOH:O	2.08	0.54
1:A:451:PRO:HA	1:A:458:TYR:CD1	2.44	0.53
1:B:409:ASN:HB3	5:B:1078:HOH:O	2.10	0.52
1:A:62:THR:HG23	1:A:88[B]:ARG:NH2	2.25	0.51
1:A:478:LYS:NZ	5:A:717:HOH:O	2.38	0.51
1:A:221:ARG:HD3	1:A:318:GLN:OE1	2.11	0.51
1:B:121:TYR:OH	3:B:604:E0Z:C18	2.60	0.50
1:A:468:ARG:NH1	5:A:703:HOH:O	2.16	0.49
1:B:321:LEU:HD11	1:B:408:VAL:HG23	1.94	0.49
1:A:325:LYS:HE2	5:A:960:HOH:O	2.13	0.49
1:A:357:LYS:HD3	1:A:368:LEU:HD11	1.95	0.49
1:B:132:GLY:HA3	1:B:143:LEU:HD22	1.95	0.48
1:B:77:GLY:N	1:B:82:GLU:OE2	2.35	0.48
1:B:451:PRO:HA	1:B:458:TYR:CD1	2.48	0.48
1:B:257:ASN:HB2	1:B:261:GLU:OE1	2.14	0.48
1:A:207:GLY:HA3	1:A:229:PRO:HD3	1.96	0.47
1:A:535:THR:O	5:A:704:HOH:O	2.20	0.47
1:A:502:PHE:CZ	1:A:513:HIS:HB2	2.50	0.46
1:B:197:PHE:HB3	1:B:223:ILE:HB	1.96	0.46
1:A:19[B]:ARG:HD3	5:A:858:HOH:O	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:502:PHE:CZ	1:B:513:HIS:HB2	2.52	0.45
1:A:223:ILE:HA	1:A:320:LEU:O	2.16	0.45
1:A:23:LEU:O	5:A:705:HOH:O	2.21	0.45
1:A:484:GLU:O	1:A:486:HIS:N	2.46	0.44
1:A:288:PHE:H	3:A:604:E0Z:C28	2.31	0.44
1:A:366:LEU:HD13	1:B:530:LYS:HG2	2.00	0.44
1:B:197:PHE:CB	1:B:223:ILE:HB	2.48	0.43
1:A:515:ARG:HB3	1:A:518:VAL:HB	2.00	0.43
1:A:289:ARG:HB2	3:A:604:E0Z:C37	2.48	0.43
1:B:158:LEU:O	1:B:161[A]:SER:OG	2.26	0.43
1:B:223:ILE:HA	1:B:320:LEU:O	2.19	0.43
1:B:207:GLY:HA3	1:B:229:PRO:HD3	2.01	0.43
1:B:515:ARG:HB3	1:B:518:VAL:HB	2.01	0.43
1:A:330:PHE:HZ	3:A:604:E0Z:C18	2.31	0.42
1:A:228:SER:HB2	1:A:229:PRO:HD2	2.02	0.42
1:B:12:SER:HB2	1:B:54:TRP:CZ3	2.54	0.42
1:B:19:ARG:HD3	5:B:742:HOH:O	2.20	0.41
1:A:83:MET:HE2	1:A:83:MET:HB2	1.94	0.41
1:A:321:LEU:HD21	1:A:408:VAL:HG23	2.02	0.41
1:A:485:PRO:O	1:A:486:HIS:HB2	2.21	0.41
1:B:506:ASN:HB2	5:B:764:HOH:O	2.21	0.41
1:A:27:ILE:HD11	1:A:133:LYS:HB2	2.02	0.41
1:A:197:PHE:CB	1:A:223:ILE:HB	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	536/565 (95%)	514 (96%)	21 (4%)	1 (0%)	47	38
1	B	541/565 (96%)	521 (96%)	20 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1077/1130 (95%)	1035 (96%)	41 (4%)	1 (0%)	51 43

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	486	HIS

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	469/494 (95%)	461 (98%)	8 (2%)	60 57
1	B	473/494 (96%)	463 (98%)	10 (2%)	53 48
All	All	942/988 (95%)	924 (98%)	18 (2%)	55 53

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	197	PHE
1	A	288	PHE
1	A	408	VAL
1	A	430	LEU
1	A	431	VAL
1	A	473	TRP
1	A	484	GLU
1	A	526	GLN
1	B	12	SER
1	B	19	ARG
1	B	73	GLU
1	B	143	LEU
1	B	197	PHE
1	B	288	PHE
1	B	330	PHE
1	B	468	ARG
1	B	473	TRP

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Mol	Chain	Res	Type
1	B	535	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 5 are monoatomic - leaving 8 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	$\# Z > 2$
2	NAG	B	601	1	14,14,15	0.35	0	17,19,21	0.44	0
3	E0Z	A	604	-	41,41,41	1.91	8 (19%)	51,57,57	2.27	13 (25%)
3	E0Z	B	604	-	41,41,41	1.90	9 (21%)	51,57,57	2.11	14 (27%)
2	NAG	A	601	1	14,14,15	0.87	1 (7%)	17,19,21	0.83	1 (5%)
2	NAG	B	602	1	14,14,15	0.32	0	17,19,21	0.37	0
2	NAG	A	603	1	14,14,15	0.48	0	17,19,21	0.54	0
2	NAG	B	603	1	14,14,15	0.52	0	17,19,21	0.53	0
2	NAG	A	602	1	14,14,15	0.69	1 (7%)	17,19,21	0.40	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	601	1	-	2/6/23/26	0/1/1/1
3	E0Z	A	604	-	-	8/15/17/17	0/5/5/5
3	E0Z	B	604	-	-	7/15/17/17	0/5/5/5
2	NAG	A	601	1	-	4/6/23/26	0/1/1/1
2	NAG	B	602	1	-	0/6/23/26	0/1/1/1
2	NAG	A	603	1	-	0/6/23/26	0/1/1/1
2	NAG	B	603	1	-	0/6/23/26	0/1/1/1
2	NAG	A	602	1	-	0/6/23/26	0/1/1/1

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	604	E0Z	C24-N26	5.82	1.46	1.33
3	B	604	E0Z	C24-N26	5.71	1.46	1.33
3	A	604	E0Z	C18-C19	5.33	1.44	1.36
3	B	604	E0Z	C18-C19	5.31	1.44	1.36
3	B	604	E0Z	C12-N27	3.77	1.46	1.35
3	A	604	E0Z	C12-N27	3.58	1.46	1.35
3	A	604	E0Z	C11-C06	-3.30	1.37	1.42
3	A	604	E0Z	C23-C19	3.17	1.54	1.51
2	A	601	NAG	O5-C1	3.07	1.48	1.43
3	B	604	E0Z	C23-C19	3.03	1.54	1.51
3	B	604	E0Z	C11-C06	-2.88	1.37	1.42
3	B	604	E0Z	C13-C04	-2.56	1.38	1.42
3	A	604	E0Z	C13-C04	-2.56	1.38	1.42
3	B	604	E0Z	O36-C31	2.45	1.41	1.37
3	A	604	E0Z	O35-C32	2.35	1.41	1.36
3	B	604	E0Z	O35-C32	2.30	1.41	1.36
2	A	602	NAG	O5-C1	-2.18	1.40	1.43
3	A	604	E0Z	C18-N20	-2.05	1.33	1.35
3	B	604	E0Z	O25-C24	-2.01	1.19	1.23

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	604	E0Z	C37-O36-C31	-7.98	105.48	117.53
3	B	604	E0Z	C23-C24-N26	5.80	124.02	116.19
3	A	604	E0Z	O36-C31-C32	5.09	121.95	114.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	604	E0Z	C16-C17-N20	-4.84	103.05	110.90
3	A	604	E0Z	O36-C31-C30	-4.73	115.98	124.12
3	B	604	E0Z	O36-C31-C32	4.73	121.42	114.57
3	B	604	E0Z	C28-N26-C24	-4.45	115.41	122.34
3	A	604	E0Z	C17-N20-C18	-4.25	119.83	129.82
3	B	604	E0Z	C18-C19-N22	-3.90	105.54	111.34
3	B	604	E0Z	C13-C04-N05	-3.90	119.70	123.35
3	A	604	E0Z	N22-N21-N20	3.85	110.22	107.31
3	B	604	E0Z	C06-N05-C04	3.77	123.18	117.86
3	B	604	E0Z	C11-C06-N05	-3.73	119.86	123.35
3	A	604	E0Z	C06-N05-C04	3.68	123.05	117.86
3	A	604	E0Z	C11-C06-N05	-3.61	119.97	123.35
3	B	604	E0Z	C16-C17-N20	-3.57	105.10	110.90
3	A	604	E0Z	C13-C04-N05	-3.41	120.16	123.35
3	B	604	E0Z	N22-N21-N20	3.21	109.73	107.31
3	B	604	E0Z	O25-C24-N26	-3.17	117.03	123.01
3	A	604	E0Z	C16-N27-C12	-3.14	118.59	129.84
3	B	604	E0Z	C37-O36-C31	-3.02	112.97	117.53
3	B	604	E0Z	O36-C31-C30	-2.89	119.14	124.12
3	A	604	E0Z	C18-C19-N22	-2.77	107.23	111.34
2	A	601	NAG	C1-O5-C5	2.49	115.56	112.19
3	A	604	E0Z	C10-C11-C06	2.49	121.11	118.33
3	A	604	E0Z	C10-C11-C12	-2.40	119.23	123.40
3	B	604	E0Z	C17-N20-C18	-2.03	125.03	129.82
3	B	604	E0Z	C14-C13-C12	-2.03	119.88	123.40

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	604	E0Z	N27-C16-C17-N20
3	A	604	E0Z	C16-C17-N20-C18
3	A	604	E0Z	C16-C17-N20-N21
3	B	604	E0Z	N27-C16-C17-N20
3	B	604	E0Z	C16-C17-N20-C18
3	B	604	E0Z	C16-C17-N20-N21
2	A	601	NAG	O5-C5-C6-O6
3	A	604	E0Z	C32-C31-O36-C37
2	A	601	NAG	C4-C5-C6-O6
2	B	601	NAG	C8-C7-N2-C2
2	B	601	NAG	O7-C7-N2-C2
2	A	601	NAG	C8-C7-N2-C2

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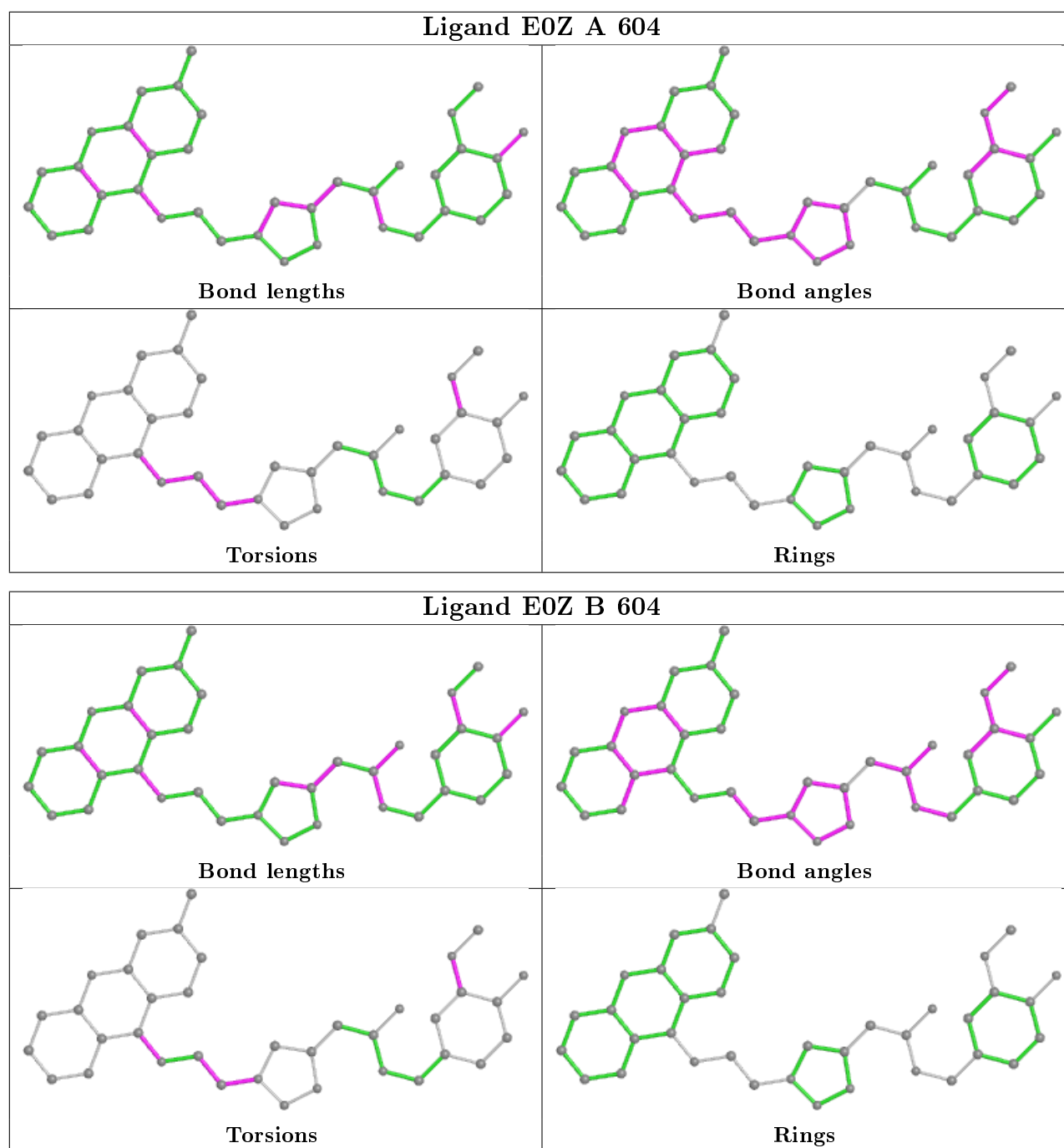
Mol	Chain	Res	Type	Atoms
2	A	601	NAG	O7-C7-N2-C2
3	A	604	E0Z	C30-C31-O36-C37
3	B	604	E0Z	C32-C31-O36-C37
3	A	604	E0Z	C13-C12-N27-C16
3	A	604	E0Z	C11-C12-N27-C16
3	A	604	E0Z	C17-C16-N27-C12
3	B	604	E0Z	C30-C31-O36-C37
3	B	604	E0Z	C13-C12-N27-C16
3	B	604	E0Z	C11-C12-N27-C16

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	604	E0Z	4	0
3	B	604	E0Z	1	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	530/565 (93%)	0.03	8 (1%) 73 76	23, 33, 49, 78	2 (0%)
1	B	532/565 (94%)	0.15	17 (3%) 47 50	23, 33, 50, 79	0
All	All	1062/1130 (93%)	0.09	25 (2%) 59 62	23, 33, 50, 79	2 (0%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	535	THR	6.0
1	A	4	SER	4.1
1	B	23	LEU	3.5
1	A	485	PRO	3.4
1	B	534	ALA	3.3
1	B	257	ASN	3.2
1	B	24	SER	3.2
1	B	486	HIS	3.0
1	B	261	GLU	2.9
1	A	509	PRO	2.9
1	B	260	GLU	2.9
1	B	4	SER	2.8
1	B	71	VAL	2.8
1	B	275	ILE	2.5
1	A	486	HIS	2.5
1	A	535	THR	2.5
1	B	115	ILE	2.4
1	A	455	GLU	2.4
1	B	457	ASN	2.3
1	A	24	SER	2.3
1	B	70	TYR	2.2
1	B	461	GLU	2.2
1	A	487	SER	2.1
1	B	118	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	455	GLU	2.1

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 monosaccharides in this entry.

6.4 Ligands [i](#)

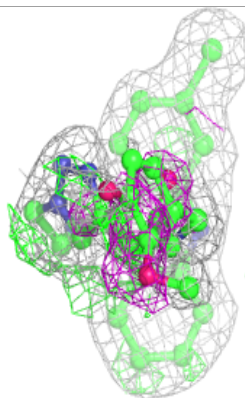
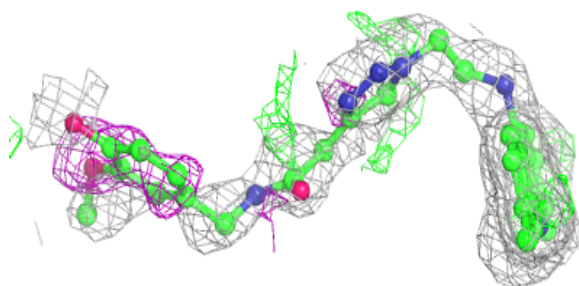
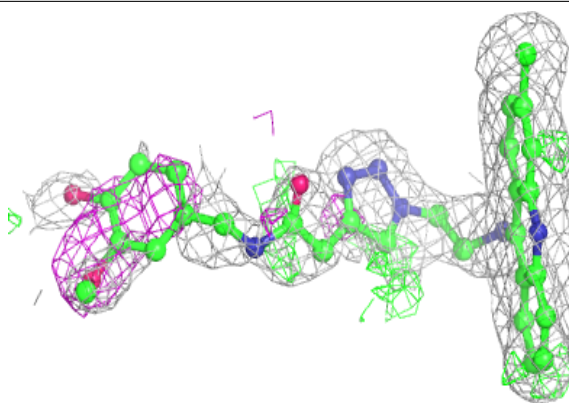
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAG	A	603	14/15	0.69	0.31	63,69,72,76	14
2	NAG	B	603	14/15	0.72	0.35	66,74,79,82	0
2	NAG	B	601	14/15	0.81	0.27	45,55,64,65	0
3	E0Z	A	604	37/37	0.82	0.27	20,34,52,55	37
4	CL	B	606	1/1	0.84	0.10	69,69,69,69	0
2	NAG	A	601	14/15	0.85	0.30	51,62,69,73	0
4	CL	A	605	1/1	0.86	0.11	70,70,70,70	0
4	CL	A	606	1/1	0.88	0.12	55,55,55,55	0
3	E0Z	B	604	37/37	0.89	0.24	23,40,60,62	37
2	NAG	A	602	14/15	0.90	0.10	39,46,56,67	0
2	NAG	B	602	14/15	0.91	0.13	36,42,51,53	0
4	CL	B	605	1/1	0.94	0.06	53,53,53,53	0
4	CL	A	607	1/1	0.94	0.08	66,66,66,66	0

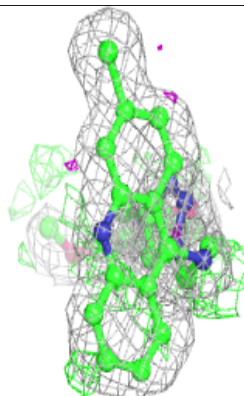
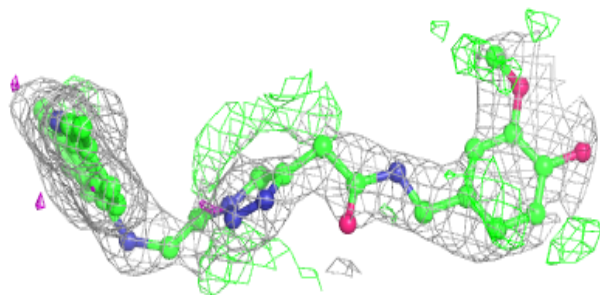
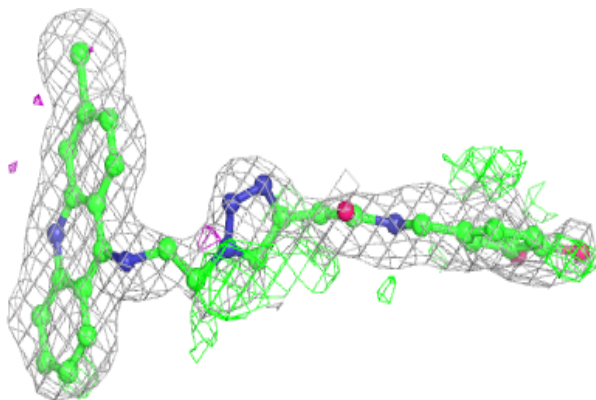
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around E0Z A 604:

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

**Electron density around E0Z B 604:**

$2mF_o-DF_c$ (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.