



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 26, 2026 – 12:35 PM EDT

PDB ID : 5OAJ / pdb_00005oaj
Title : Crystal structure of mutant AChBP in complex with tropisetron (T53F, Q74R, Y110A, I135S, G162E)
Authors : Dawson, A.; Hunter, W.N.; de Souza, J.O.; Trumper, P.
Deposited on : 2017-06-22
Resolution : 2.47 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

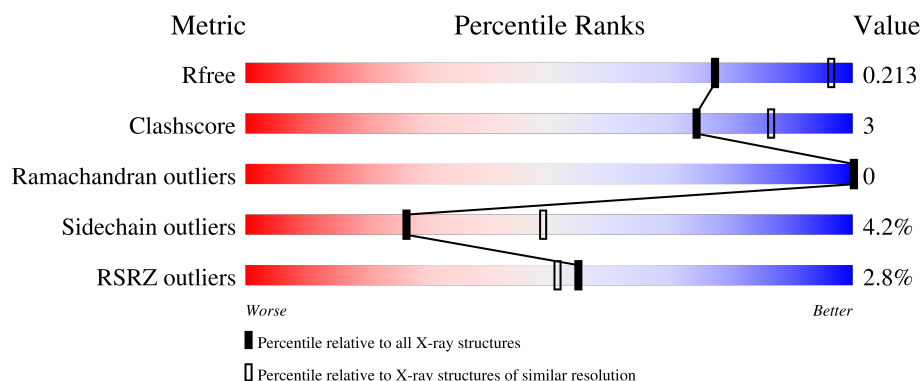
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.47 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	7589 (2.50-2.46)
Clashscore	190562	8295 (2.50-2.46)
Ramachandran outliers	187476	8164 (2.50-2.46)
Sidechain outliers	187428	8166 (2.50-2.46)
RSRZ outliers	180081	7593 (2.50-2.46)

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	249	 2% 76% 6% 17%
1	B	249	 5% 81% 6% 11%
1	C	249	 2% 79% 1% 18%
1	D	249	 0% 77% 5% 17%
1	E	249	 0% 74% 8% 17%

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Mol	Chain	Length	Quality of chain
1	F	249	
1	G	249	
1	H	249	
1	I	249	
1	J	249	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	E	603	-	-	X	-
4	FLC	G	601	-	X	-	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 17553 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 Soluble acetylcholine receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	206	Total	C	N	O	S	0	0	0
			1649	1042	272	326	9			
1	B	221	Total	C	N	O	S	0	0	0
			1781	1127	296	349	9			
1	C	205	Total	C	N	O	S	0	0	0
			1638	1036	268	325	9			
1	D	206	Total	C	N	O	S	0	0	0
			1649	1042	272	326	9			
1	E	206	Total	C	N	O	S	0	1	0
			1654	1045	273	327	9			
1	F	206	Total	C	N	O	S	0	0	0
			1649	1042	272	326	9			
1	G	205	Total	C	N	O	S	0	6	0
			1679	1060	274	334	11			
1	H	206	Total	C	N	O	S	0	0	0
			1649	1042	272	326	9			
1	I	206	Total	C	N	O	S	0	0	0
			1649	1042	272	326	9			
1	J	213	Total	C	N	O	S	0	0	0
			1710	1082	280	339	9			

There are 200 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	53	PHE	THR	engineered mutation	UNP Q8WSF8
A	60	VAL	ALA	conflict	UNP Q8WSF8
A	74	ARG	GLN	engineered mutation	UNP Q8WSF8
A	110	ALA	TYR	engineered mutation	UNP Q8WSF8
A	135	SER	ILE	engineered mutation	UNP Q8WSF8
A	155	VAL	ALA	conflict	UNP Q8WSF8
A	162	GLU	GLY	engineered mutation	UNP Q8WSF8
A	237	GLU	-	expression tag	UNP Q8WSF8
A	238	ASN	-	expression tag	UNP Q8WSF8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	239	LEU	-	expression tag	UNP Q8WSF8
A	240	TYR	-	expression tag	UNP Q8WSF8
A	241	PHE	-	expression tag	UNP Q8WSF8
A	242	GLN	-	expression tag	UNP Q8WSF8
A	243	GLY	-	expression tag	UNP Q8WSF8
A	244	HIS	-	expression tag	UNP Q8WSF8
A	245	HIS	-	expression tag	UNP Q8WSF8
A	246	HIS	-	expression tag	UNP Q8WSF8
A	247	HIS	-	expression tag	UNP Q8WSF8
A	248	HIS	-	expression tag	UNP Q8WSF8
A	249	HIS	-	expression tag	UNP Q8WSF8
B	53	PHE	THR	engineered mutation	UNP Q8WSF8
B	60	VAL	ALA	conflict	UNP Q8WSF8
B	74	ARG	GLN	engineered mutation	UNP Q8WSF8
B	110	ALA	TYR	engineered mutation	UNP Q8WSF8
B	135	SER	ILE	engineered mutation	UNP Q8WSF8
B	155	VAL	ALA	conflict	UNP Q8WSF8
B	162	GLU	GLY	engineered mutation	UNP Q8WSF8
B	237	GLU	-	expression tag	UNP Q8WSF8
B	238	ASN	-	expression tag	UNP Q8WSF8
B	239	LEU	-	expression tag	UNP Q8WSF8
B	240	TYR	-	expression tag	UNP Q8WSF8
B	241	PHE	-	expression tag	UNP Q8WSF8
B	242	GLN	-	expression tag	UNP Q8WSF8
B	245	GLY	-	expression tag	UNP Q8WSF8
B	246	HIS	-	expression tag	UNP Q8WSF8
B	247	HIS	-	expression tag	UNP Q8WSF8
B	248	HIS	-	expression tag	UNP Q8WSF8
B	249	HIS	-	expression tag	UNP Q8WSF8
B	250	HIS	-	expression tag	UNP Q8WSF8
B	251	HIS	-	expression tag	UNP Q8WSF8
C	53	PHE	THR	engineered mutation	UNP Q8WSF8
C	60	VAL	ALA	conflict	UNP Q8WSF8
C	74	ARG	GLN	engineered mutation	UNP Q8WSF8
C	110	ALA	TYR	engineered mutation	UNP Q8WSF8
C	135	SER	ILE	engineered mutation	UNP Q8WSF8
C	155	VAL	ALA	conflict	UNP Q8WSF8
C	162	GLU	GLY	engineered mutation	UNP Q8WSF8
C	237	GLU	-	expression tag	UNP Q8WSF8
C	238	ASN	-	expression tag	UNP Q8WSF8
C	239	LEU	-	expression tag	UNP Q8WSF8
C	240	TYR	-	expression tag	UNP Q8WSF8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	241	PHE	-	expression tag	UNP Q8WSF8
C	242	GLN	-	expression tag	UNP Q8WSF8
C	243	GLY	-	expression tag	UNP Q8WSF8
C	244	HIS	-	expression tag	UNP Q8WSF8
C	245	HIS	-	expression tag	UNP Q8WSF8
C	246	HIS	-	expression tag	UNP Q8WSF8
C	247	HIS	-	expression tag	UNP Q8WSF8
C	248	HIS	-	expression tag	UNP Q8WSF8
C	249	HIS	-	expression tag	UNP Q8WSF8
D	53	PHE	THR	engineered mutation	UNP Q8WSF8
D	60	VAL	ALA	conflict	UNP Q8WSF8
D	74	ARG	GLN	engineered mutation	UNP Q8WSF8
D	110	ALA	TYR	engineered mutation	UNP Q8WSF8
D	135	SER	ILE	engineered mutation	UNP Q8WSF8
D	155	VAL	ALA	conflict	UNP Q8WSF8
D	162	GLU	GLY	engineered mutation	UNP Q8WSF8
D	237	GLU	-	expression tag	UNP Q8WSF8
D	238	ASN	-	expression tag	UNP Q8WSF8
D	239	LEU	-	expression tag	UNP Q8WSF8
D	240	TYR	-	expression tag	UNP Q8WSF8
D	241	PHE	-	expression tag	UNP Q8WSF8
D	242	GLN	-	expression tag	UNP Q8WSF8
D	243	GLY	-	expression tag	UNP Q8WSF8
D	244	HIS	-	expression tag	UNP Q8WSF8
D	245	HIS	-	expression tag	UNP Q8WSF8
D	246	HIS	-	expression tag	UNP Q8WSF8
D	247	HIS	-	expression tag	UNP Q8WSF8
D	248	HIS	-	expression tag	UNP Q8WSF8
D	249	HIS	-	expression tag	UNP Q8WSF8
E	53	PHE	THR	engineered mutation	UNP Q8WSF8
E	60	VAL	ALA	conflict	UNP Q8WSF8
E	74	ARG	GLN	engineered mutation	UNP Q8WSF8
E	110	ALA	TYR	engineered mutation	UNP Q8WSF8
E	135	SER	ILE	engineered mutation	UNP Q8WSF8
E	155	VAL	ALA	conflict	UNP Q8WSF8
E	162	GLU	GLY	engineered mutation	UNP Q8WSF8
E	237	GLU	-	expression tag	UNP Q8WSF8
E	238	ASN	-	expression tag	UNP Q8WSF8
E	239	LEU	-	expression tag	UNP Q8WSF8
E	240	TYR	-	expression tag	UNP Q8WSF8
E	241	PHE	-	expression tag	UNP Q8WSF8
E	242	GLN	-	expression tag	UNP Q8WSF8

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Chain	Residue	Modelled	Actual	Comment	Reference
E	243	GLY	-	expression tag	UNP Q8WSF8
E	244	HIS	-	expression tag	UNP Q8WSF8
E	245	HIS	-	expression tag	UNP Q8WSF8
E	246	HIS	-	expression tag	UNP Q8WSF8
E	247	HIS	-	expression tag	UNP Q8WSF8
E	248	HIS	-	expression tag	UNP Q8WSF8
E	249	HIS	-	expression tag	UNP Q8WSF8
F	53	PHE	THR	engineered mutation	UNP Q8WSF8
F	60	VAL	ALA	conflict	UNP Q8WSF8
F	74	ARG	GLN	engineered mutation	UNP Q8WSF8
F	110	ALA	TYR	engineered mutation	UNP Q8WSF8
F	135	SER	ILE	engineered mutation	UNP Q8WSF8
F	155	VAL	ALA	conflict	UNP Q8WSF8
F	162	GLU	GLY	engineered mutation	UNP Q8WSF8
F	237	GLU	-	expression tag	UNP Q8WSF8
F	238	ASN	-	expression tag	UNP Q8WSF8
F	239	LEU	-	expression tag	UNP Q8WSF8
F	240	TYR	-	expression tag	UNP Q8WSF8
F	241	PHE	-	expression tag	UNP Q8WSF8
F	242	GLN	-	expression tag	UNP Q8WSF8
F	243	GLY	-	expression tag	UNP Q8WSF8
F	244	HIS	-	expression tag	UNP Q8WSF8
F	245	HIS	-	expression tag	UNP Q8WSF8
F	246	HIS	-	expression tag	UNP Q8WSF8
F	247	HIS	-	expression tag	UNP Q8WSF8
F	248	HIS	-	expression tag	UNP Q8WSF8
F	249	HIS	-	expression tag	UNP Q8WSF8
G	53	PHE	THR	engineered mutation	UNP Q8WSF8
G	60	VAL	ALA	conflict	UNP Q8WSF8
G	74	ARG	GLN	engineered mutation	UNP Q8WSF8
G	110	ALA	TYR	engineered mutation	UNP Q8WSF8
G	135	SER	ILE	engineered mutation	UNP Q8WSF8
G	155	VAL	ALA	conflict	UNP Q8WSF8
G	162	GLU	GLY	engineered mutation	UNP Q8WSF8
G	237	GLU	-	expression tag	UNP Q8WSF8
G	238	ASN	-	expression tag	UNP Q8WSF8
G	239	LEU	-	expression tag	UNP Q8WSF8
G	240	TYR	-	expression tag	UNP Q8WSF8
G	241	PHE	-	expression tag	UNP Q8WSF8
G	242	GLN	-	expression tag	UNP Q8WSF8
G	243	GLY	-	expression tag	UNP Q8WSF8
G	244	HIS	-	expression tag	UNP Q8WSF8

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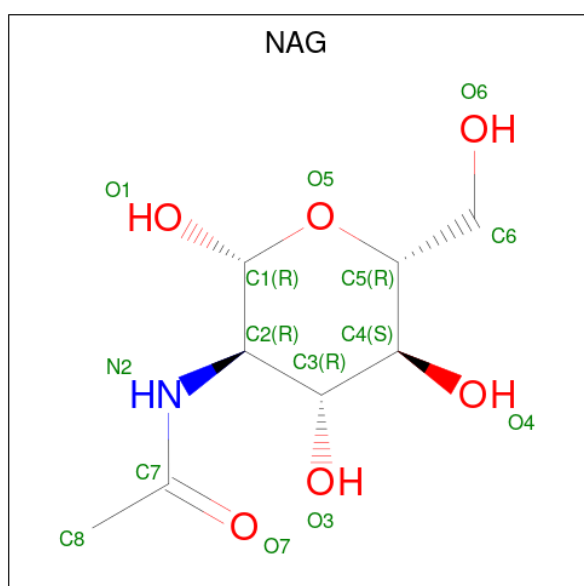
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G	245	HIS	-	expression tag	UNP Q8WSF8
G	246	HIS	-	expression tag	UNP Q8WSF8
G	247	HIS	-	expression tag	UNP Q8WSF8
G	248	HIS	-	expression tag	UNP Q8WSF8
G	249	HIS	-	expression tag	UNP Q8WSF8
H	53	PHE	THR	engineered mutation	UNP Q8WSF8
H	60	VAL	ALA	conflict	UNP Q8WSF8
H	74	ARG	GLN	engineered mutation	UNP Q8WSF8
H	110	ALA	TYR	engineered mutation	UNP Q8WSF8
H	135	SER	ILE	engineered mutation	UNP Q8WSF8
H	155	VAL	ALA	conflict	UNP Q8WSF8
H	162	GLU	GLY	engineered mutation	UNP Q8WSF8
H	237	GLU	-	expression tag	UNP Q8WSF8
H	238	ASN	-	expression tag	UNP Q8WSF8
H	239	LEU	-	expression tag	UNP Q8WSF8
H	240	TYR	-	expression tag	UNP Q8WSF8
H	241	PHE	-	expression tag	UNP Q8WSF8
H	242	GLN	-	expression tag	UNP Q8WSF8
H	243	GLY	-	expression tag	UNP Q8WSF8
H	244	HIS	-	expression tag	UNP Q8WSF8
H	245	HIS	-	expression tag	UNP Q8WSF8
H	246	HIS	-	expression tag	UNP Q8WSF8
H	247	HIS	-	expression tag	UNP Q8WSF8
H	248	HIS	-	expression tag	UNP Q8WSF8
H	249	HIS	-	expression tag	UNP Q8WSF8
I	53	PHE	THR	engineered mutation	UNP Q8WSF8
I	60	VAL	ALA	conflict	UNP Q8WSF8
I	74	ARG	GLN	engineered mutation	UNP Q8WSF8
I	110	ALA	TYR	engineered mutation	UNP Q8WSF8
I	135	SER	ILE	engineered mutation	UNP Q8WSF8
I	155	VAL	ALA	conflict	UNP Q8WSF8
I	162	GLU	GLY	engineered mutation	UNP Q8WSF8
I	237	GLU	-	expression tag	UNP Q8WSF8
I	238	ASN	-	expression tag	UNP Q8WSF8
I	239	LEU	-	expression tag	UNP Q8WSF8
I	240	TYR	-	expression tag	UNP Q8WSF8
I	241	PHE	-	expression tag	UNP Q8WSF8
I	242	GLN	-	expression tag	UNP Q8WSF8
I	243	GLY	-	expression tag	UNP Q8WSF8
I	244	HIS	-	expression tag	UNP Q8WSF8
I	245	HIS	-	expression tag	UNP Q8WSF8
I	246	HIS	-	expression tag	UNP Q8WSF8

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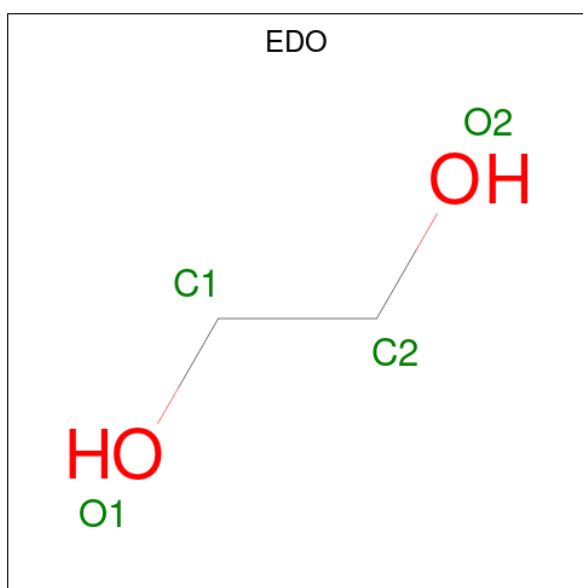
Chain	Residue	Modelled	Actual	Comment	Reference
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I	248	HIS	-	expression tag	UNP Q8WSF8
I	249	HIS	-	expression tag	UNP Q8WSF8
J	53	PHE	THR	engineered mutation	UNP Q8WSF8
J	60	VAL	ALA	conflict	UNP Q8WSF8
J	74	ARG	GLN	engineered mutation	UNP Q8WSF8
J	110	ALA	TYR	engineered mutation	UNP Q8WSF8
J	135	SER	ILE	engineered mutation	UNP Q8WSF8
J	155	VAL	ALA	conflict	UNP Q8WSF8
J	162	GLU	GLY	engineered mutation	UNP Q8WSF8
J	237	GLU	-	expression tag	UNP Q8WSF8
J	238	ASN	-	expression tag	UNP Q8WSF8
J	239	LEU	-	expression tag	UNP Q8WSF8
J	240	TYR	-	expression tag	UNP Q8WSF8
J	241	PHE	-	expression tag	UNP Q8WSF8
J	242	GLN	-	expression tag	UNP Q8WSF8
J	243	GLY	-	expression tag	UNP Q8WSF8
J	244	HIS	-	expression tag	UNP Q8WSF8
J	245	HIS	-	expression tag	UNP Q8WSF8
J	246	HIS	-	expression tag	UNP Q8WSF8
J	247	HIS	-	expression tag	UNP Q8WSF8
J	248	HIS	-	expression tag	UNP Q8WSF8
J	249	HIS	-	expression tag	UNP Q8WSF8

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: 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	E	1	Total	C	N	O	0	0
			14	8	1	5		
2	H	1	Total	C	N	O	0	0
			14	8	1	5		
2	I	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		

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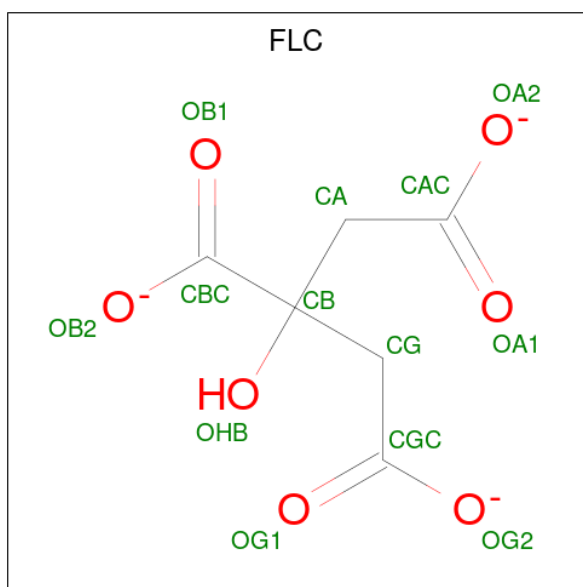
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	F	1	Total 4	C 2	O 2	0	0
3	F	1	Total 4	C 2	O 2	0	0
3	F	1	Total 4	C 2	O 2	0	0
3	F	1	Total 4	C 2	O 2	0	0
3	F	1	Total 4	C 2	O 2	0	0
3	G	1	Total 4	C 2	O 2	0	0
3	G	1	Total 4	C 2	O 2	0	0
3	G	1	Total 4	C 2	O 2	0	0
3	G	1	Total 4	C 2	O 2	0	0

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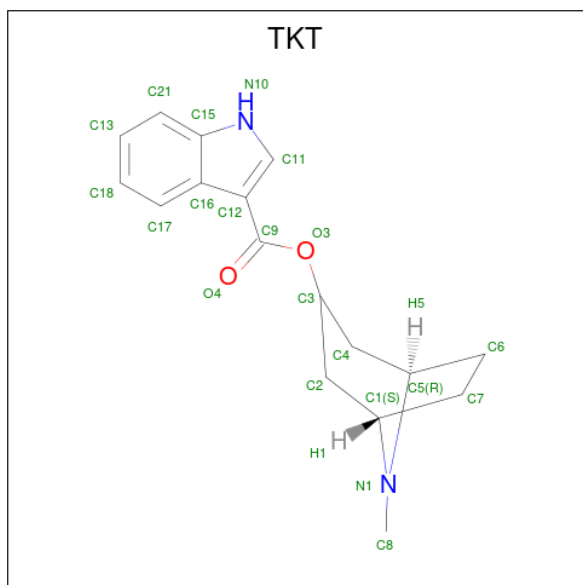
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	H	1	Total 4	C 2	O 2	0	0
3	H	1	Total 4	C 2	O 2	0	0
3	H	1	Total 4	C 2	O 2	0	0
3	H	1	Total 4	C 2	O 2	0	0
3	I	1	Total 4	C 2	O 2	0	0
3	I	1	Total 4	C 2	O 2	0	0
3	I	1	Total 4	C 2	O 2	0	0
3	I	1	Total 4	C 2	O 2	0	0
3	J	1	Total 4	C 2	O 2	0	0
3	J	1	Total 4	C 2	O 2	0	0
3	J	1	Total 4	C 2	O 2	0	0
3	J	1	Total 4	C 2	O 2	0	0
3	J	1	Total 4	C 2	O 2	0	0

- Molecule 4 is CITRATE ANION (CCD ID: FLC) (formula: $\text{C}_6\text{H}_5\text{O}_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			13	6	7		
4	G	1	Total	C	O	0	0
			13	6	7		
4	I	1	Total	C	O	0	0
			13	6	7		

- Molecule 5 is (3-ENDO)-8-METHYL-8-AZABICYCLO[3.2.1]OCT-3-YL 1H-INDOLE-3-CARBOXYLATE (CCD ID: TKT) (formula: $C_{17}H_{20}N_2O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	E	1	Total	C	N	O	0	0
			21	17	2	2		
5	J	1	Total	C	N	O	0	0
			21	17	2	2		

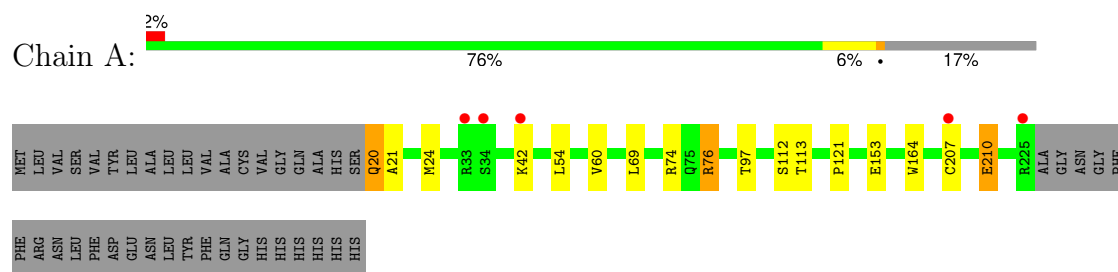
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	61	Total	O	0	0
			61	61		
6	B	62	Total	O	0	0
			62	62		
6	C	56	Total	O	0	0
			56	56		
6	D	56	Total	O	0	0
			56	56		
6	E	61	Total	O	0	0
			61	61		
6	F	51	Total	O	0	0
			51	51		
6	G	34	Total	O	0	0
			34	34		
6	H	53	Total	O	0	0
			53	53		
6	I	57	Total	O	0	0
			57	57		
6	J	50	Total	O	0	0
			50	50		

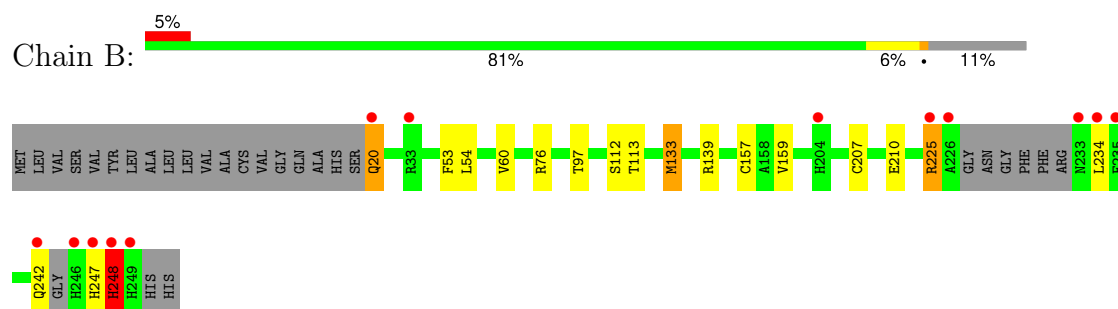
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

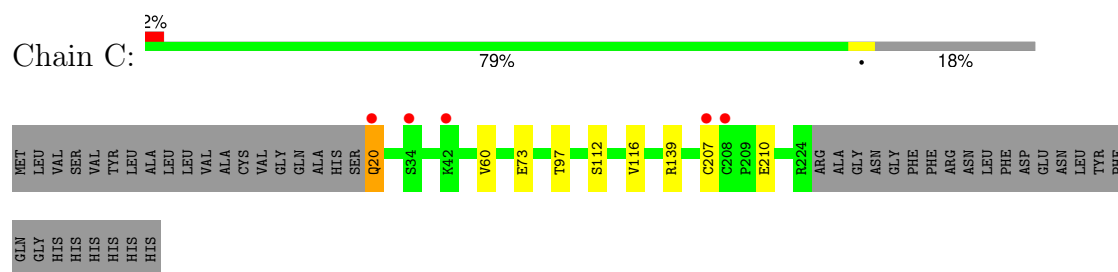
• Molecule 1: Soluble acetylcholine receptor



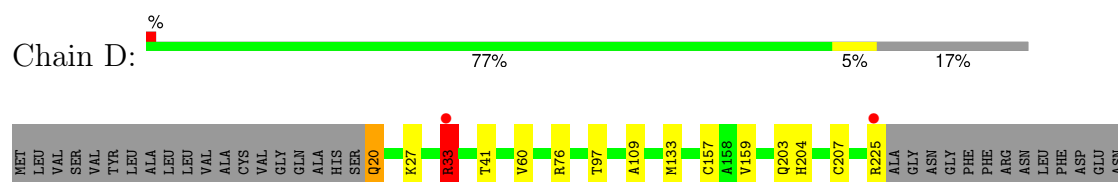
• Molecule 1: Soluble acetylcholine receptor



• Molecule 1: Soluble acetylcholine receptor

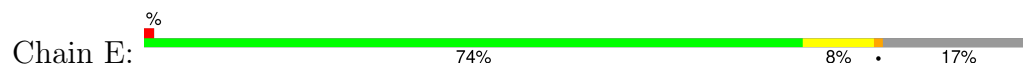


• Molecule 1: Soluble acetylcholine receptor



LEU
TYR
PHE
GLN
GLY
HIS
HIS
HIS
HIS

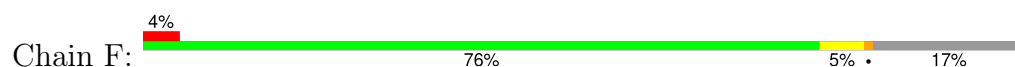
• Molecule 1: Soluble acetylcholine receptor



MET LEU VAL SER VAL TYR LEU ALA LEU LEU VAL ALA CYS VAL GLN GLN ALA HIS SER Q20 R25 R33 V60 L69 R74 Q75 R76 E88 N91 T97 D106 S112 S120 M133 F134 S135 V159 D172 L173 K174 H204 C207 E210

I213 R225 ALA GLY ASN PHE PHE ARG VAL LEU PHE ASP GLN ALA ASN LEU TYR PHE GLN GLY HIS HIS HIS HIS

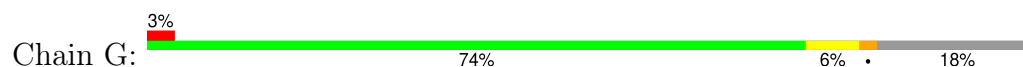
• Molecule 1: Soluble acetylcholine receptor



MET LEU VAL SER VAL TYR LEU ALA LEU LEU VAL ALA CYS VAL GLN GLN ALA HIS SER Q20 N32 R33 S34 P35 K59 V60 R74 Q75 R76 T97 S112 T113 M133 R139 D176 Q203 H204 Y205 S206 C207 C208 P209 E210 R225 ALA GLY ASN GLY PHE

ARG ASN LEU PHE ASP GLU ASN LEU TYR PHE VAL HIS HIS HIS HIS HIS HIS

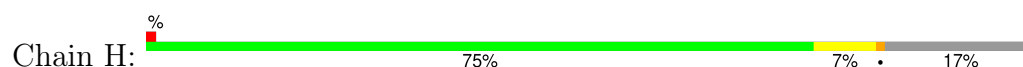
• Molecule 1: Soluble acetylcholine receptor



MET LEU VAL SER VAL TYR LEU ALA LEU LEU VAL ALA CYS VAL GLN GLN ALA HIS SER Q20 R25 R33 K42 K59 V60 R76 M83 E88 T97 T113 R139 E153 V159 K160 F169 Y205 S206 C207 C208 P209 E210 R224 ARG ALA GLY

ASN GLY PHE PHE ARG ASN LEU PHE ASP GLU ASN LEU TYR PHE VAL HIS HIS HIS HIS HIS HIS

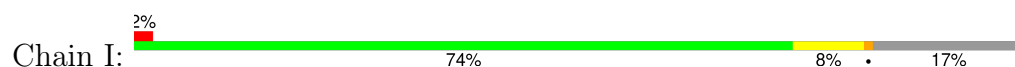
• Molecule 1: Soluble acetylcholine receptor



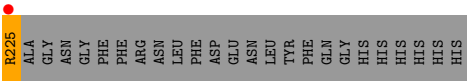
MET LEU VAL SER VAL TYR LEU ALA LEU LEU VAL ALA CYS VAL GLN GLN ALA HIS SER Q20 A21 M24 D29 R33 S34 L54 K59 R74 Q75 R76 T97 D106 A109 T113 M133 R139 K160 K174 Q203 C207 E210 R225

ALA GLY ASN GLY PHE PHE ARG ASN LEU TYR PHE VAL HIS HIS HIS HIS HIS HIS

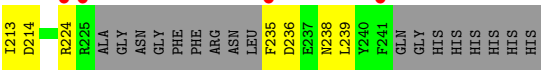
• Molecule 1: Soluble acetylcholine receptor



MET LEU VAL SER VAL TYR LEU ALA LEU LEU VAL ALA CYS VAL GLN GLN ALA HIS SER Q20 A21 M24 R33 S34 L54 K59 V60 R74 Q75 R76 T97 A109 T113 P121 M133 R139 E153 V159 Q201 S206 C207 E210 R224



● Molecule 1: Soluble acetylcholine receptor



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	100.24Å 137.47Å 103.67Å 90.00° 90.79° 90.00°	Depositor
Resolution (Å)	42.66 – 2.47 42.66 – 2.47	Depositor EDS
% Data completeness (in resolution range)	97.0 (42.66-2.47) 97.0 (42.66-2.47)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.15 (at 2.48Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.173 , 0.208 0.179 , 0.213	Depositor DCC
R_{free} test set	4739 reflections (4.71%)	wwPDB-VP
Wilson B-factor (Å ²)	37.0	Xtriage
Anisotropy	0.263	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 38.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.004 for l,k,-h 0.022 for h,-k,-l 0.017 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	17553	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.49% 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: NAG, EDO, TKT, FLC

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	1.15	0/1689	1.06	3/2302 (0.1%)
1	B	1.16	1/1825 (0.1%)	1.07	1/2484 (0.0%)
1	C	1.17	2/1678 (0.1%)	1.02	0/2288
1	D	1.16	1/1689 (0.1%)	1.02	1/2302 (0.0%)
1	E	1.22	3/1697 (0.2%)	1.06	2/2313 (0.1%)
1	F	1.14	1/1689 (0.1%)	1.04	2/2302 (0.1%)
1	G	1.08	0/1721	1.03	4/2348 (0.2%)
1	H	1.14	1/1689 (0.1%)	1.03	3/2302 (0.1%)
1	I	1.13	0/1689	1.03	3/2302 (0.1%)
1	J	1.16	4/1751 (0.2%)	1.06	5/2385 (0.2%)
All	All	1.15	13/17117 (0.1%)	1.04	24/23328 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	2
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	2
1	H	0	1
1	I	0	1
1	J	0	1
All	All	0	12

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	120	SER	C-O	-6.56	1.17	1.24
1	J	213	ILE	N-CA	6.54	1.53	1.46
1	J	213	ILE	CA-CB	-6.50	1.46	1.54
1	E	173	LEU	CA-C	-6.23	1.45	1.52
1	J	107	ILE	C-O	-6.03	1.17	1.24

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	153	GLU	CB-CG-CD	7.46	125.28	112.60
1	J	33	ARG	N-CA-C	6.85	118.83	111.36
1	J	160	LYS	CB-CG-CD	6.68	126.66	111.30
1	I	225	ARG	CB-CG-CD	6.56	126.40	111.30
1	H	33	ARG	CG-CD-NE	-6.51	97.67	112.00

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	207	CYS	Peptide
1	B	207	CYS	Peptide
1	C	207	CYS	Peptide
1	C	210	GLU	Sidechain
1	D	207	CYS	Peptide

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	1649	0	1580	7	0
1	B	1781	0	1687	13	0
1	C	1638	0	1569	4	0
1	D	1649	0	1582	10	0
1	E	1654	0	1588	16	0
1	F	1649	0	1582	10	0
1	G	1679	0	1601	10	0
1	H	1649	0	1581	12	0
1	I	1649	0	1581	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	J	1710	0	1628	21	0
2	A	14	0	13	0	0
2	E	14	0	13	7	0
2	H	14	0	13	0	0
2	I	14	0	13	1	0
3	A	12	0	18	1	0
3	B	20	0	30	1	0
3	C	16	0	24	1	0
3	D	16	0	24	1	0
3	E	16	0	24	1	0
3	F	20	0	30	1	0
3	G	16	0	24	1	0
3	H	16	0	24	1	0
3	I	16	0	24	1	0
3	J	20	0	30	0	0
4	C	13	0	5	0	0
4	G	13	0	5	0	0
4	I	13	0	5	0	0
5	E	21	0	20	0	0
5	J	21	0	20	3	0
6	A	61	0	0	0	0
6	B	62	0	0	2	0
6	C	56	0	0	0	0
6	D	56	0	0	6	0
6	E	61	0	0	0	0
6	F	51	0	0	1	0
6	G	34	0	0	1	0
6	H	53	0	0	3	0
6	I	57	0	0	1	0
6	J	50	0	0	3	0
All	All	17553	0	16338	103	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 3.

The worst 5 of 103 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:E:91:ASN:HD21	2:E:603:NAG:C1	1.00	1.59
1:E:91:ASN:ND2	2:E:603:NAG:C1	1.79	1.43
1:E:91:ASN:HD21	2:E:603:NAG:C2	1.82	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:91:ASN:CG	2:E:603:NAG:C1	2.47	0.88
1:J:74:ARG:HG2	1:J:133:MET:HE3	1.59	0.85

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	204/249 (82%)	202 (99%)	2 (1%)	0	100	100
1	B	215/249 (86%)	212 (99%)	3 (1%)	0	100	100
1	C	203/249 (82%)	201 (99%)	2 (1%)	0	100	100
1	D	204/249 (82%)	202 (99%)	2 (1%)	0	100	100
1	E	205/249 (82%)	204 (100%)	1 (0%)	0	100	100
1	F	204/249 (82%)	202 (99%)	2 (1%)	0	100	100
1	G	209/249 (84%)	204 (98%)	5 (2%)	0	100	100
1	H	204/249 (82%)	202 (99%)	2 (1%)	0	100	100
1	I	204/249 (82%)	202 (99%)	2 (1%)	0	100	100
1	J	209/249 (84%)	207 (99%)	2 (1%)	0	100	100
All	All	2061/2490 (83%)	2038 (99%)	23 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	189/224 (84%)	180 (95%)	9 (5%)	23	43
1	B	202/224 (90%)	190 (94%)	12 (6%)	18	34
1	C	188/224 (84%)	185 (98%)	3 (2%)	55	77
1	D	189/224 (84%)	182 (96%)	7 (4%)	30	54
1	E	190/224 (85%)	182 (96%)	8 (4%)	26	49
1	F	189/224 (84%)	181 (96%)	8 (4%)	26	49
1	G	194/224 (87%)	184 (95%)	10 (5%)	21	39
1	H	189/224 (84%)	182 (96%)	7 (4%)	30	54
1	I	189/224 (84%)	179 (95%)	10 (5%)	20	39
1	J	195/224 (87%)	187 (96%)	8 (4%)	27	50
All	All	1914/2240 (85%)	1832 (96%)	82 (4%)	26	48

5 of 82 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	20	GLN
1	I	159	VAL
1	H	74	ARG
1	I	54	LEU
1	J	54	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	20	GLN
1	H	203	GLN
1	G	55	GLN
1	G	216	ASN
1	H	216	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

51 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	EDO	J	304	-	3,3,3	0.49	0	2,2,2	0.49	0
3	EDO	C	603	-	3,3,3	0.58	0	2,2,2	0.61	0
3	EDO	G	604	-	3,3,3	0.63	0	2,2,2	0.35	0
3	EDO	G	602	-	3,3,3	0.69	0	2,2,2	0.64	0
3	EDO	G	603	-	3,3,3	1.25	0	2,2,2	0.61	0
3	EDO	I	604	-	3,3,3	0.48	0	2,2,2	0.71	0
3	EDO	A	304	-	3,3,3	0.52	0	2,2,2	0.72	0
4	FLC	G	601	-	12,12,12	2.12	2 (16%)	17,17,17	2.77	9 (52%)
3	EDO	H	302	-	3,3,3	0.98	0	2,2,2	1.48	0
3	EDO	J	306	-	3,3,3	0.70	0	2,2,2	0.23	0
3	EDO	I	602	-	3,3,3	0.55	0	2,2,2	0.24	0
3	EDO	F	604	-	3,3,3	0.90	0	2,2,2	0.67	0
5	TKT	E	601	-	24,24,24	0.71	1 (4%)	35,35,35	0.86	2 (5%)
4	FLC	C	601	-	12,12,12	1.57	2 (16%)	17,17,17	2.57	8 (47%)
3	EDO	C	604	-	3,3,3	0.60	0	2,2,2	0.32	0
3	EDO	B	601	-	3,3,3	0.99	0	2,2,2	0.09	0
5	TKT	J	302	-	24,24,24	0.61	1 (4%)	35,35,35	0.65	0
3	EDO	J	301	-	3,3,3	0.49	0	2,2,2	0.63	0
3	EDO	B	602	-	3,3,3	1.05	0	2,2,2	1.69	1 (50%)
3	EDO	H	305	-	3,3,3	1.08	0	2,2,2	0.51	0
3	EDO	A	303	-	3,3,3	0.75	0	2,2,2	0.43	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	F	603	-	3,3,3	0.69	0	2,2,2	0.24	0
3	EDO	F	601	-	3,3,3	0.66	0	2,2,2	0.45	0
3	EDO	B	603	-	3,3,3	0.47	0	2,2,2	1.08	0
3	EDO	D	301	-	3,3,3	0.60	0	2,2,2	1.37	0
3	EDO	D	302	-	3,3,3	0.69	0	2,2,2	0.41	0
3	EDO	D	304	-	3,3,3	0.79	0	2,2,2	0.19	0
3	EDO	I	605	-	3,3,3	0.61	0	2,2,2	0.67	0
3	EDO	G	605	-	3,3,3	0.66	0	2,2,2	0.11	0
4	FLC	I	601	-	12,12,12	1.47	1 (8%)	17,17,17	1.60	2 (11%)
3	EDO	D	303	-	3,3,3	0.60	0	2,2,2	0.23	0
3	EDO	H	303	-	3,3,3	0.73	0	2,2,2	0.75	0
3	EDO	I	606	-	3,3,3	0.79	0	2,2,2	0.20	0
3	EDO	F	605	-	3,3,3	0.75	0	2,2,2	0.27	0
2	NAG	E	603	-	14,14,15	0.30	0	17,19,21	0.56	0
2	NAG	I	603	1	14,14,15	0.29	0	17,19,21	0.56	0
3	EDO	E	605	-	3,3,3	1.01	0	2,2,2	1.27	0
3	EDO	B	605	-	3,3,3	0.88	0	2,2,2	0.31	0
3	EDO	C	605	-	3,3,3	0.61	0	2,2,2	0.50	0
3	EDO	E	604	-	3,3,3	0.77	0	2,2,2	1.27	0
3	EDO	E	606	-	3,3,3	0.88	0	2,2,2	0.84	0
3	EDO	F	602	-	3,3,3	0.49	0	2,2,2	1.27	0
3	EDO	B	604	-	3,3,3	0.37	0	2,2,2	0.56	0
2	NAG	A	301	1	14,14,15	0.28	0	17,19,21	0.56	0
3	EDO	E	602	-	3,3,3	0.50	0	2,2,2	0.30	0
3	EDO	J	303	-	3,3,3	0.48	0	2,2,2	0.34	0
3	EDO	C	602	-	3,3,3	0.90	0	2,2,2	0.79	0
3	EDO	J	305	-	3,3,3	0.77	0	2,2,2	0.15	0
2	NAG	H	301	1	14,14,15	0.30	0	17,19,21	0.57	0
3	EDO	H	304	-	3,3,3	0.32	0	2,2,2	0.62	0
3	EDO	A	302	-	3,3,3	0.38	0	2,2,2	1.42	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
3	EDO	J	304	-	-	1/1/1/1	-
3	EDO	C	603	-	-	1/1/1/1	-
3	EDO	G	604	-	-	0/1/1/1	-
3	EDO	G	602	-	-	1/1/1/1	-
3	EDO	G	603	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	I	604	-	-	1/1/1/1	-
3	EDO	A	304	-	-	0/1/1/1	-
4	FLC	G	601	-	-	12/16/16/16	-
3	EDO	H	302	-	-	1/1/1/1	-
3	EDO	J	306	-	-	1/1/1/1	-
3	EDO	I	602	-	-	1/1/1/1	-
3	EDO	F	604	-	-	1/1/1/1	-
5	TKT	E	601	-	-	0/8/29/29	0/5/4/4
4	FLC	C	601	-	-	7/16/16/16	-
3	EDO	C	604	-	-	1/1/1/1	-
3	EDO	B	601	-	-	0/1/1/1	-
5	TKT	J	302	-	-	0/8/29/29	0/5/4/4
3	EDO	J	301	-	-	1/1/1/1	-
3	EDO	B	602	-	-	1/1/1/1	-
3	EDO	H	305	-	-	0/1/1/1	-
3	EDO	A	303	-	-	0/1/1/1	-
3	EDO	F	603	-	-	1/1/1/1	-
3	EDO	F	601	-	-	1/1/1/1	-
3	EDO	B	603	-	-	0/1/1/1	-
3	EDO	D	301	-	-	1/1/1/1	-
3	EDO	D	302	-	-	0/1/1/1	-
3	EDO	D	304	-	-	1/1/1/1	-
3	EDO	I	605	-	-	0/1/1/1	-
3	EDO	G	605	-	-	0/1/1/1	-
4	FLC	I	601	-	-	4/16/16/16	-
3	EDO	D	303	-	-	0/1/1/1	-
3	EDO	H	303	-	-	0/1/1/1	-
3	EDO	I	606	-	-	0/1/1/1	-
3	EDO	F	605	-	-	1/1/1/1	-
2	NAG	E	603	-	-	2/6/23/26	0/1/1/1
2	NAG	I	603	1	-	5/6/23/26	0/1/1/1
3	EDO	E	605	-	-	0/1/1/1	-
3	EDO	B	605	-	-	1/1/1/1	-
3	EDO	C	605	-	-	1/1/1/1	-
3	EDO	E	604	-	-	1/1/1/1	-
3	EDO	E	606	-	-	1/1/1/1	-
3	EDO	F	602	-	-	1/1/1/1	-
3	EDO	B	604	-	-	1/1/1/1	-
2	NAG	A	301	1	-	0/6/23/26	0/1/1/1
3	EDO	E	602	-	-	1/1/1/1	-
3	EDO	J	303	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	C	602	-	-	1/1/1/1	-
3	EDO	J	305	-	-	1/1/1/1	-
2	NAG	H	301	1	-	2/6/23/26	0/1/1/1
3	EDO	H	304	-	-	1/1/1/1	-
3	EDO	A	302	-	-	1/1/1/1	-

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	601	FLC	CB-CBC	4.62	1.58	1.53
4	G	601	FLC	CG-CB	4.42	1.59	1.54
4	C	601	FLC	CG-CB	3.68	1.58	1.54
4	C	601	FLC	CG-CGC	2.49	1.58	1.50
5	E	601	TKT	C12-C9	-2.34	1.42	1.48

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	601	FLC	OHB-CB-CBC	-6.19	100.18	108.96
4	G	601	FLC	OB2-CBC-CB	6.11	124.87	113.14
4	I	601	FLC	CB-CA-CAC	-5.08	100.03	113.92
4	C	601	FLC	CG-CB-CBC	4.01	118.90	110.03
4	G	601	FLC	CA-CB-CBC	-3.64	101.99	110.03

There are no chirality outliers.

5 of 60 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	H	301	NAG	C8-C7-N2-C2
2	H	301	NAG	O7-C7-N2-C2
2	I	603	NAG	C1-C2-N2-C7
2	I	603	NAG	C8-C7-N2-C2
2	I	603	NAG	O7-C7-N2-C2

There are no ring outliers.

12 monomers are involved in 20 short contacts:

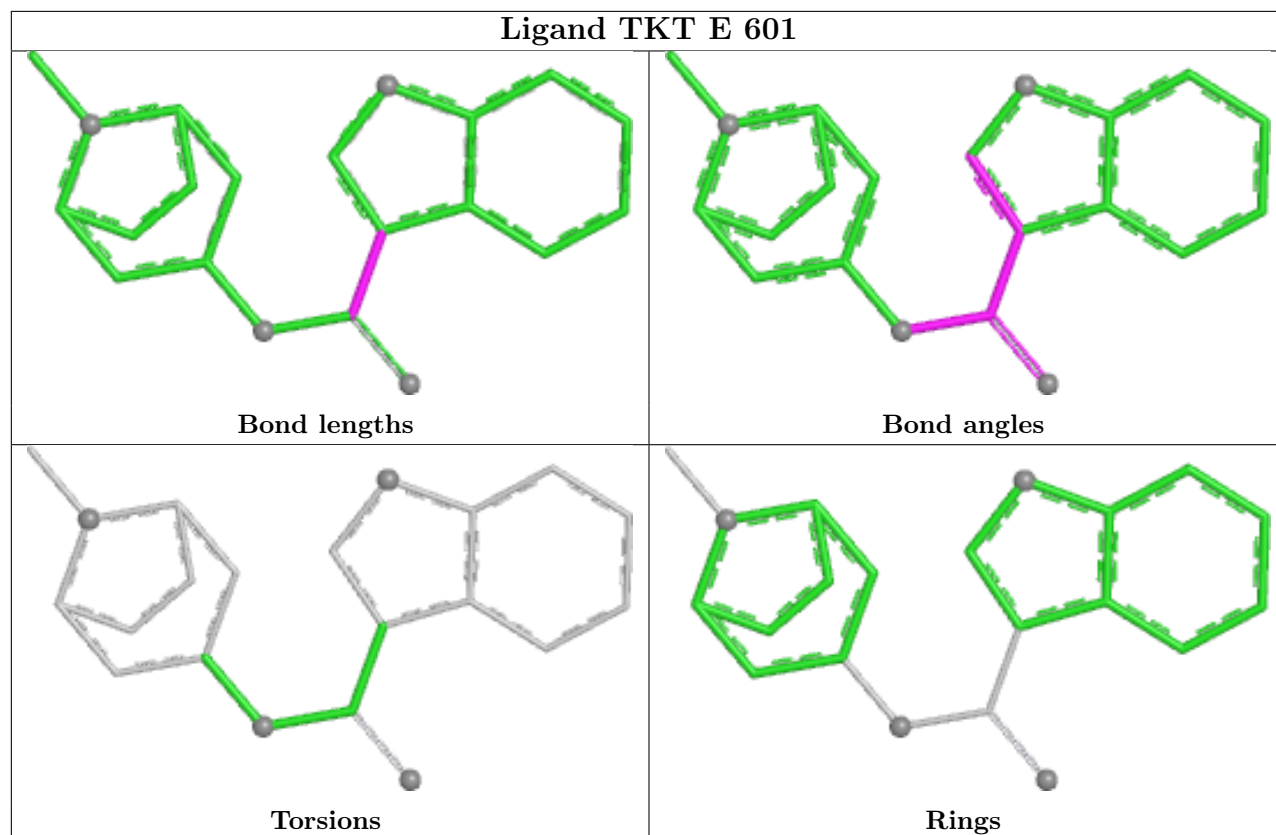
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	604	EDO	1	0
3	H	302	EDO	1	0
5	J	302	TKT	3	0

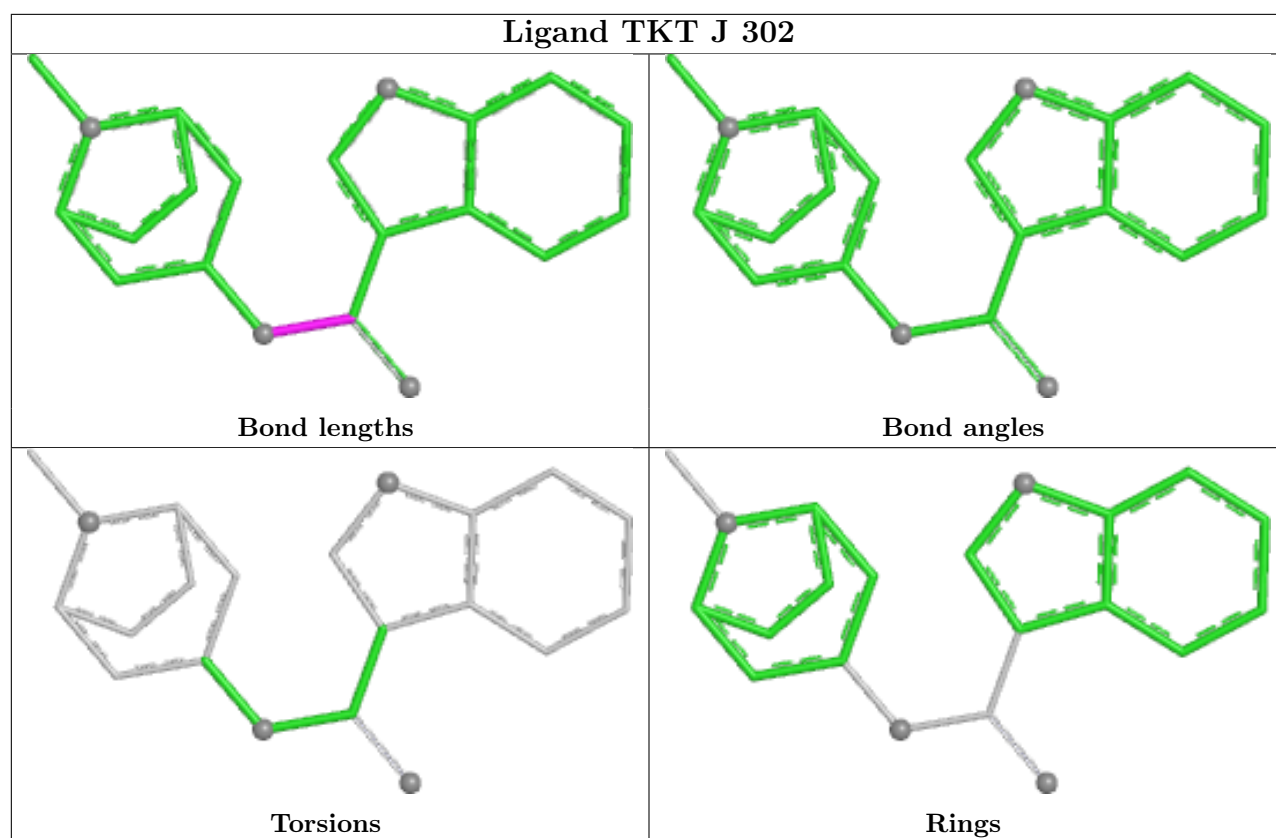
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	602	EDO	1	0
3	D	301	EDO	1	0
3	G	605	EDO	1	0
2	E	603	NAG	7	0
2	I	603	NAG	1	0
3	E	604	EDO	1	0
3	F	602	EDO	1	0
3	C	602	EDO	1	0
3	A	302	EDO	1	0

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	206/249 (82%)	-0.26	5 (2%) 59 56	22, 33, 62, 85	0
1	B	221/249 (88%)	0.01	13 (5%) 28 25	21, 35, 71, 100	0
1	C	205/249 (82%)	-0.25	5 (2%) 59 56	21, 33, 63, 103	0
1	D	206/249 (82%)	-0.25	2 (0%) 79 77	22, 34, 58, 91	0
1	E	206/249 (82%)	-0.31	2 (0%) 79 77	21, 32, 56, 102	1 (0%)
1	F	206/249 (82%)	-0.05	10 (4%) 35 31	26, 38, 74, 105	0
1	G	205/249 (82%)	0.12	8 (3%) 43 39	26, 43, 71, 89	6 (2%)
1	H	206/249 (82%)	-0.08	3 (1%) 72 69	26, 39, 65, 97	0
1	I	206/249 (82%)	-0.17	5 (2%) 59 56	23, 37, 72, 93	0
1	J	213/249 (85%)	0.09	6 (2%) 55 51	25, 40, 74, 100	0
All	All	2080/2490 (83%)	-0.11	59 (2%) 55 51	21, 36, 69, 105	7 (0%)

The worst 5 of 59 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	209[A]	PRO	9.0
1	J	235	PHE	6.2
1	B	226	ALA	5.5
1	B	235	PHE	4.9
1	G	206[A]	SER	4.6

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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	I	603	14/15	0.37	0.21	72,98,112,119	0
3	EDO	H	305	4/4	0.57	0.34	61,61,71,73	0
2	NAG	H	301	14/15	0.62	0.19	72,99,106,114	0
2	NAG	E	603	14/15	0.64	0.19	66,86,92,92	0
3	EDO	D	304	4/4	0.65	0.35	64,65,72,73	0
2	NAG	A	301	14/15	0.65	0.19	62,93,104,124	0
3	EDO	J	305	4/4	0.72	0.28	66,73,80,83	0
3	EDO	J	306	4/4	0.74	0.33	54,66,68,70	0
3	EDO	F	605	4/4	0.75	0.19	43,58,65,71	0
3	EDO	H	303	4/4	0.76	0.19	42,47,49,54	0
3	EDO	J	301	4/4	0.76	0.26	66,78,86,87	0
3	EDO	I	606	4/4	0.77	0.21	46,60,60,66	0
3	EDO	I	602	4/4	0.78	0.26	57,61,62,62	0
3	EDO	C	605	4/4	0.79	0.25	55,61,61,66	0
3	EDO	G	603	4/4	0.79	0.21	42,48,48,51	0
3	EDO	B	605	4/4	0.79	0.22	44,54,58,62	0
4	FLC	G	601	13/13	0.79	0.19	70,82,92,98	0
3	EDO	B	603	4/4	0.80	0.21	40,45,45,58	0
3	EDO	F	601	4/4	0.82	0.27	48,54,55,55	0
3	EDO	J	304	4/4	0.83	0.18	46,51,52,55	0
3	EDO	A	303	4/4	0.83	0.23	43,53,58,69	0
3	EDO	B	601	4/4	0.84	0.22	50,52,53,53	0
3	EDO	C	604	4/4	0.84	0.17	53,59,62,64	0
4	FLC	I	601	13/13	0.84	0.15	56,77,112,123	0
3	EDO	D	303	4/4	0.85	0.17	46,49,52,53	0
4	FLC	C	601	13/13	0.85	0.19	60,92,105,114	0
3	EDO	E	606	4/4	0.86	0.15	38,52,54,62	0
3	EDO	C	603	4/4	0.87	0.16	42,49,49,53	0
3	EDO	F	604	4/4	0.87	0.18	54,59,59,63	0
3	EDO	B	604	4/4	0.87	0.16	58,61,64,66	0
3	EDO	E	602	4/4	0.88	0.23	43,45,46,56	0
3	EDO	E	605	4/4	0.88	0.13	35,36,39,39	0

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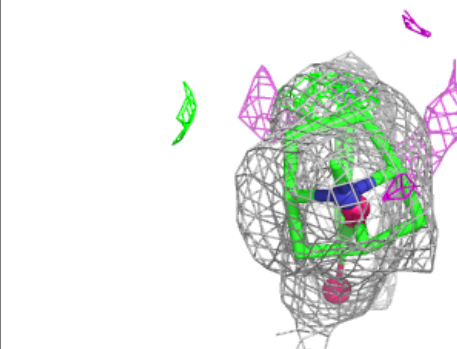
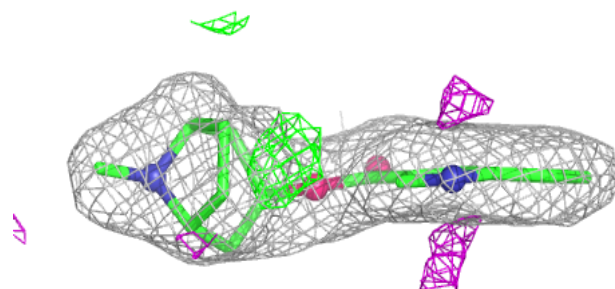
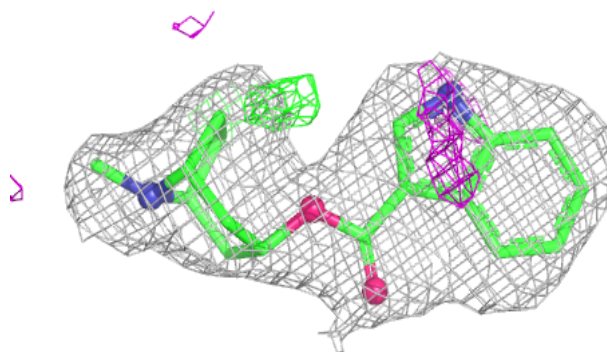
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	EDO	D	302	4/4	0.88	0.18	35,46,53,58	0
3	EDO	G	605	4/4	0.89	0.17	50,59,63,64	0
3	EDO	F	603	4/4	0.90	0.17	42,47,47,54	0
3	EDO	G	604	4/4	0.90	0.17	50,64,64,67	0
3	EDO	H	304	4/4	0.91	0.14	56,57,59,68	0
3	EDO	A	304	4/4	0.91	0.16	50,56,59,68	0
3	EDO	G	602	4/4	0.91	0.12	44,49,53,57	0
3	EDO	I	605	4/4	0.91	0.15	42,44,46,50	0
5	TKT	E	601	21/21	0.91	0.11	33,43,57,57	0
3	EDO	B	602	4/4	0.92	0.12	32,36,39,41	0
3	EDO	I	604	4/4	0.92	0.13	41,44,46,51	0
3	EDO	J	303	4/4	0.93	0.18	53,54,57,63	0
3	EDO	F	602	4/4	0.94	0.11	33,36,39,44	0
3	EDO	C	602	4/4	0.94	0.12	32,34,35,45	0
3	EDO	A	302	4/4	0.94	0.09	32,32,36,39	0
3	EDO	E	604	4/4	0.94	0.10	30,30,33,36	0
5	TKT	J	302	21/21	0.94	0.09	29,45,62,67	0
3	EDO	H	302	4/4	0.96	0.08	22,22,24,29	0
3	EDO	D	301	4/4	0.96	0.09	29,29,30,32	0

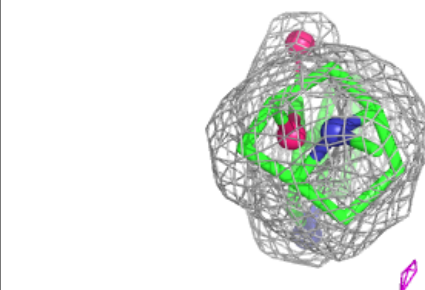
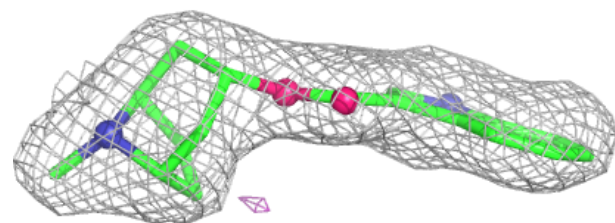
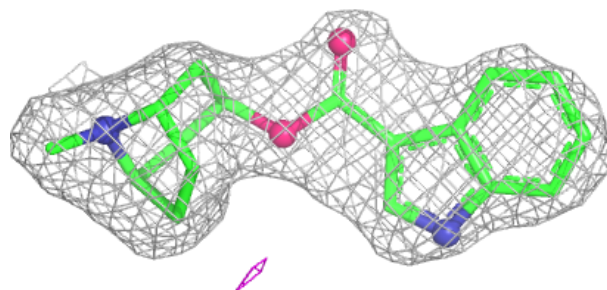
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around TKT E 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 TKT J 302:**

$2mF_o-DF_c$ (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.