



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2020 – 11:33 PM BST

PDB ID : 5OAJ
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 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

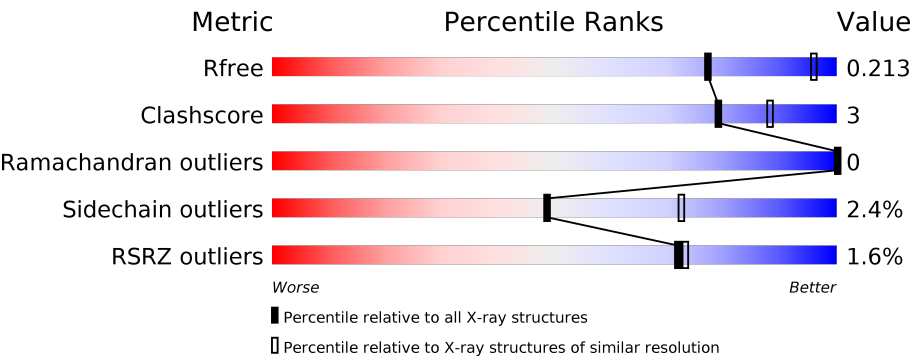
1 Overall quality at a glance i

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}	130704	5857 (2.50-2.46)
Clashscore	141614	6594 (2.50-2.46)
Ramachandran outliers	138981	6469 (2.50-2.46)
Sidechain outliers	138945	6471 (2.50-2.46)
RSRZ outliers	127900	5738 (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 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	249	<div><div></div><div>77% . . 17%</div></div>
1	B	249	<div>2%<div><div></div><div>81% 5% . 11%</div></div></div>
1	C	249	<div>%<div><div></div><div>79% . 18%</div></div></div>
1	D	249	<div>%<div><div></div><div>78% . . 17%</div></div></div>
1	E	249	<div>2%<div><div></div><div>76% 5% . 17%</div></div></div>
1	F	249	<div>2%<div><div></div><div>76% 5% . 17%</div></div></div>

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Mol	Chain	Length	Quality of chain
1	G	249	 3% 74% 6% • 18%
1	H	249	 2% 76% 5% • 17%
1	I	249	 % 77% 5% • 17%
1	J	249	 % 76% 8% • 14%

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	-
3	EDO	J	305	-	-	-	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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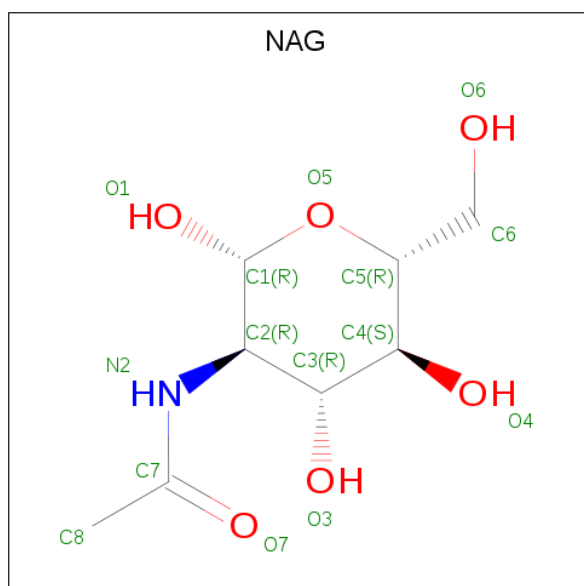
Chain	Residue	Modelled	Actual	Comment	Reference
G	245	HIS	-	expression tag	UNP Q8WSF8
G	246	HIS	-	expression tag	UNP Q8WSF8
G	247	HIS	-	expression tag	UNP Q8WSF8
G	248	HIS	-	expression tag	UNP Q8WSF8
G	249	HIS	-	expression tag	UNP Q8WSF8
H	53	PHE	THR	engineered mutation	UNP Q8WSF8
H	60	VAL	ALA	conflict	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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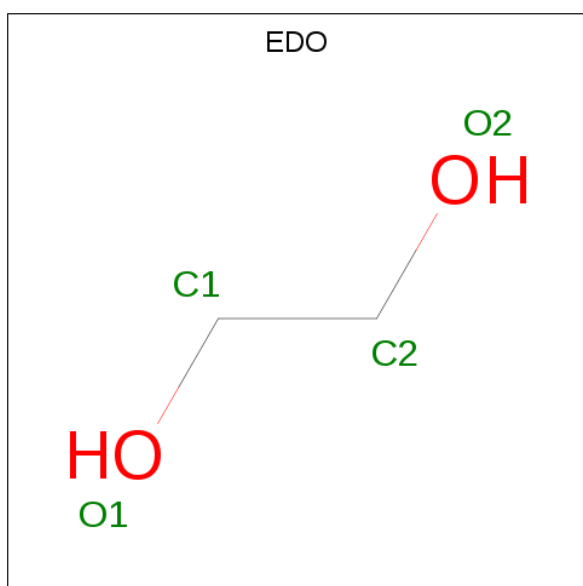
Chain	Residue	Modelled	Actual	Comment	Reference
I	247	HIS	-	expression tag	UNP Q8WSF8
I	248	HIS	-	expression tag	UNP Q8WSF8
I	249	HIS	-	expression tag	UNP Q8WSF8
J	53	PHE	THR	engineered mutation	UNP Q8WSF8
J	60	VAL	ALA	conflict	UNP Q8WSF8
J	74	ARG	GLN	engineered mutation	UNP Q8WSF8
J	110	ALA	TYR	engineered 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 (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

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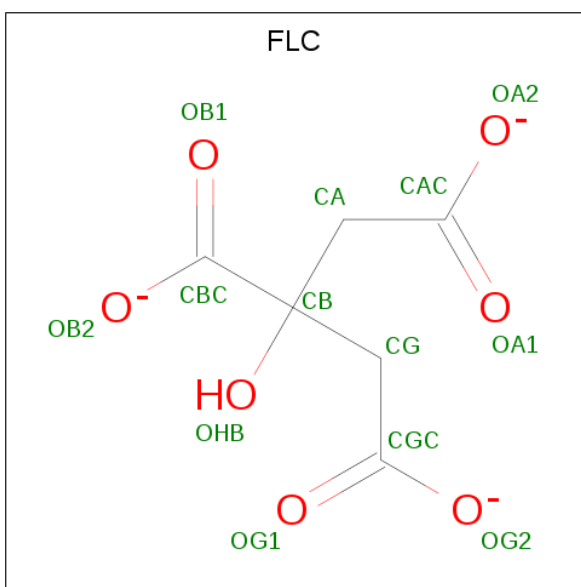
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	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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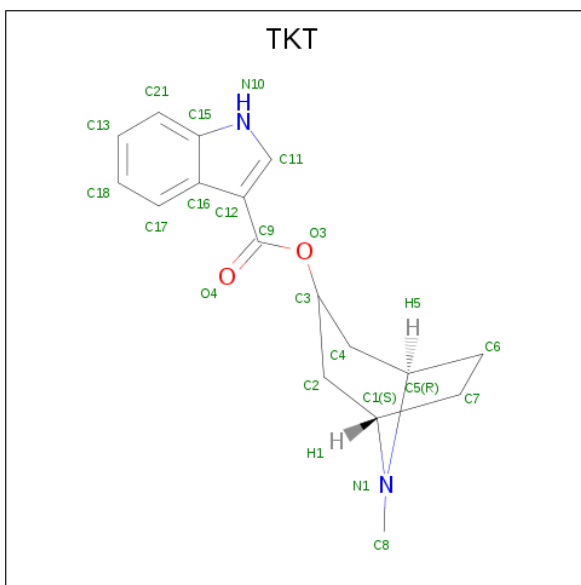
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	H	1	Total 4	C 2	O 2	0	0
3	H	1	Total 4	C 2	O 2	0	0
3	H	1	Total 4	C 2	O 2	0	0
3	H	1	Total 4	C 2	O 2	0	0
3	I	1	Total 4	C 2	O 2	0	0
3	I	1	Total 4	C 2	O 2	0	0
3	I	1	Total 4	C 2	O 2	0	0
3	I	1	Total 4	C 2	O 2	0	0
3	J	1	Total 4	C 2	O 2	0	0
3	J	1	Total 4	C 2	O 2	0	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 (three-letter code: 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 (three-letter code: TKT) (formula: $C_{17}H_{20}N_2O_2$) (labeled as "Ligand of Interest" by author).



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		

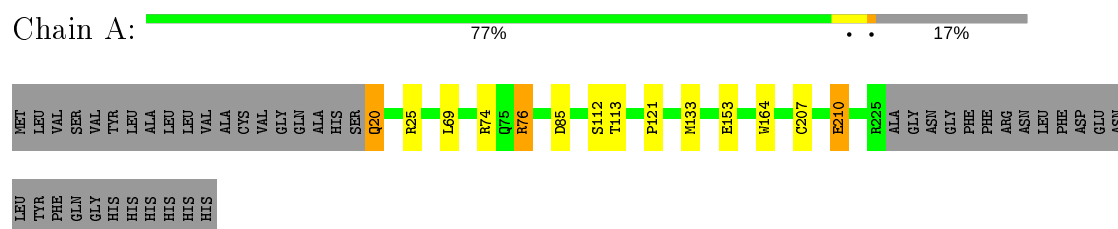
- Molecule 6 is water.

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		

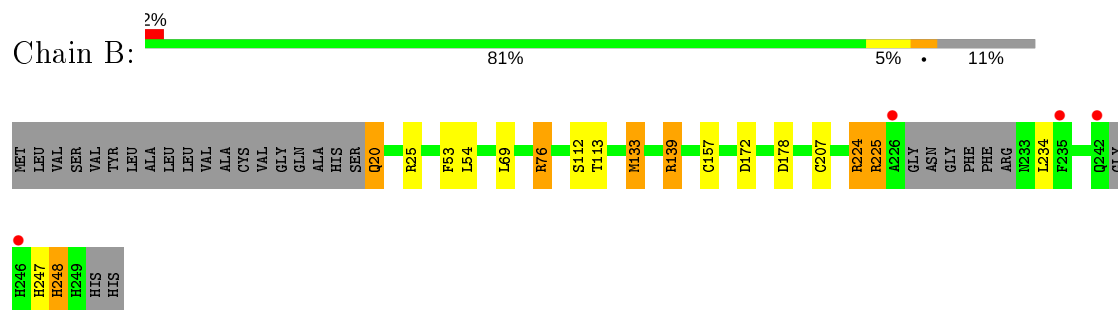
3 Residue-property plots [i](#)

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.

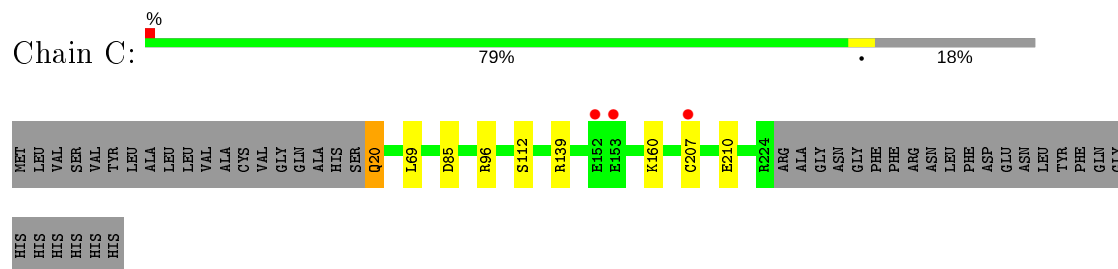
- Molecule 1: Soluble acetylcholine receptor



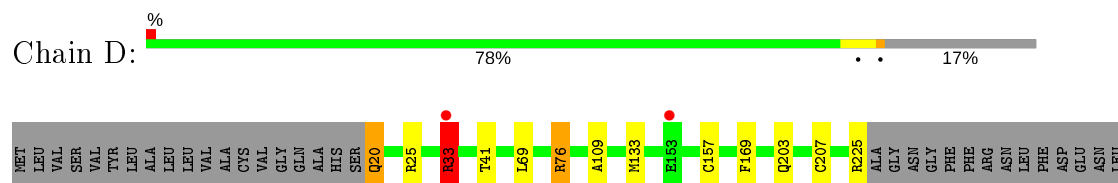
- Molecule 1: Soluble acetylcholine receptor



- Molecule 1: Soluble acetylcholine receptor

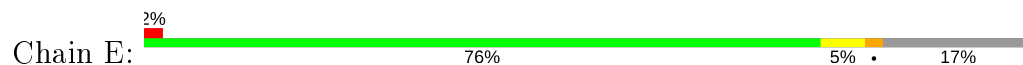


- Molecule 1: Soluble acetylcholine receptor



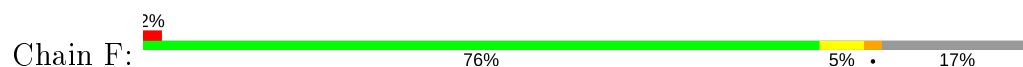
TYR
PHE
GLN
GLY
HIS
HIS
HIS
HIS

• Molecule 1: Soluble acetylcholine receptor



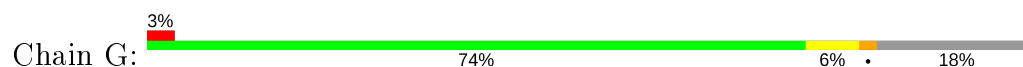
MET LEU VAL SER VAL TYR LEU ALA LEU LEU VAL ALA CYS VAL GLN TYR PHE GLN HIS SER Q20 R25 R33 L69 R74 Q75 R76 E88 N91 D106 S112 D129 M133 F134 S135 D150 S151 E152 E153 D172 L173 K174 C207 E210 I213
R225 ALA ASN PHE PHE ARG ASN PHE ASP GLU ASN TYR PHE GLN HIS SER Q20 R25 R33 L69 R74 Q75 R76 E88 N91 D106 S112 D129 M133 F134 S135 D150 S151 E152 E153 D172 L173 K174 C207 E210 I213

• Molecule 1: Soluble acetylcholine receptor



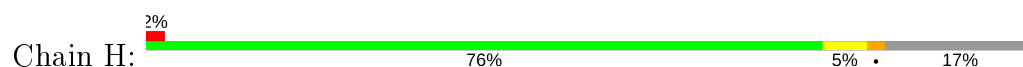
MET LEU VAL SER VAL TYR LEU ALA LEU LEU VAL ALA CYS VAL GLN TYR PHE GLN HIS SER Q20 R25 R33 L69 R74 Q75 R76 E88 N91 D106 S112 D129 M133 F134 S135 D150 S151 E152 E153 D172 L173 K174 C207 E210 I213
MET LEU VAL SER VAL TYR LEU ALA LEU LEU VAL ALA CYS VAL GLN TYR PHE GLN HIS SER Q20 R25 R33 L69 R74 Q75 R76 E88 N91 D106 S112 D129 M133 F134 S135 D150 S151 E152 E153 D172 L173 K174 C207 E210 I213
ARG ASN LEU PHE ASP GLU ASN LEU LEU VAL GLN TYR PHE GLN HIS SER Q20 R25 R33 L69 R74 Q75 R76 E88 N91 D106 S112 D129 M133 F134 S135 D150 S151 E152 E153 D172 L173 K174 C207 E210 I213

• Molecule 1: Soluble acetylcholine receptor



MET LEU VAL SER VAL TYR LEU ALA LEU LEU VAL ALA CYS VAL GLN TYR PHE GLN HIS SER Q20 R25 R33 L69 R74 Q75 R76 E88 N91 D106 S112 D129 M133 F134 S135 D150 S151 E152 E153 D172 L173 K174 C207 E210 I213
MET LEU VAL SER VAL TYR LEU ALA LEU LEU VAL ALA CYS VAL GLN TYR PHE GLN HIS SER Q20 R25 R33 L69 R74 Q75 R76 E88 N91 D106 S112 D129 M133 F134 S135 D150 S151 E152 E153 D172 L173 K174 C207 E210 I213
GLY ASN LEU PHE ASP GLU ASN LEU LEU VAL GLN TYR PHE GLN HIS SER Q20 R25 R33 L69 R74 Q75 R76 E88 N91 D106 S112 D129 M133 F134 S135 D150 S151 E152 E153 D172 L173 K174 C207 E210 I213

• Molecule 1: Soluble acetylcholine receptor



MET LEU VAL SER VAL TYR LEU ALA LEU LEU VAL ALA CYS VAL GLN TYR PHE GLN HIS SER Q20 R25 R33 L69 R74 Q75 R76 E88 N91 D106 S112 D129 M133 F134 S135 D150 S151 E152 E153 D172 L173 K174 C207 E210 I213
MET LEU VAL SER VAL TYR LEU ALA LEU LEU VAL ALA CYS VAL GLN TYR PHE GLN HIS SER Q20 R25 R33 L69 R74 Q75 R76 E88 N91 D106 S112 D129 M133 F134 S135 D150 S151 E152 E153 D172 L173 K174 C207 E210 I213
ALA GLY ASN PHE ASP GLU ASN LEU LEU VAL GLN TYR PHE GLN HIS SER Q20 R25 R33 L69 R74 Q75 R76 E88 N91 D106 S112 D129 M133 F134 S135 D150 S151 E152 E153 D172 L173 K174 C207 E210 I213

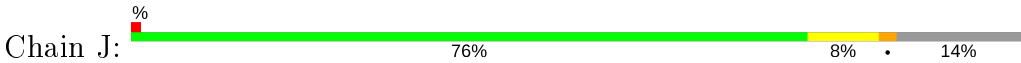
• Molecule 1: Soluble acetylcholine receptor



MET LEU VAL SER VAL TYR LEU ALA LEU LEU VAL ALA CYS VAL GLN TYR PHE GLN HIS SER Q20 R25 R33 L69 R74 Q75 R76 E88 N91 D106 S112 D129 M133 F134 S135 D150 S151 E152 E153 D172 L173 K174 C207 E210 I213
MET LEU VAL SER VAL TYR LEU ALA LEU LEU VAL ALA CYS VAL GLN TYR PHE GLN HIS SER Q20 R25 R33 L69 R74 Q75 R76 E88 N91 D106 S112 D129 M133 F134 S135 D150 S151 E152 E153 D172 L173 K174 C207 E210 I213
MET LEU VAL SER VAL TYR LEU ALA LEU LEU VAL ALA CYS VAL GLN TYR PHE GLN HIS SER Q20 R25 R33 L69 R74 Q75 R76 E88 N91 D106 S112 D129 M133 F134 S135 D150 S151 E152 E153 D172 L173 K174 C207 E210 I213

GLU
ASN
LEU
TYR
PHE
GLN
GLY
HIS
HIS
HIS
HIS
HIS

● Molecule 1: Soluble acetylcholine receptor



MET
LEU
VAL
SER
VAL
TYR
LEU
ALA
LEU
LEU
VAL
ALA
CYS
VAL
GLY
GLN
ALA
HIS
SER
Q20
R25
L54
L69
R74
Q75
R76
D85
T113
M133
F134
R139
C157
K160
D172
Q201
V202
Q203
H204
Y205
S206
C207
D214
R224
R225
ALA
GLY

ASN
GLY
PHE
ARG
ASN
LEU
F235
D236
E237
F241
GLN
GLY
HIS
HIS
HIS
HIS
HIS

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) 97.1 (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 (4.85%)	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 , 42.0	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: FLC, EDO, TKT, NAG

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	0.95	2/1689 (0.1%)	1.08	9/2302 (0.4%)
1	B	0.91	0/1825	1.05	10/2484 (0.4%)
1	C	0.91	0/1678	0.97	4/2288 (0.2%)
1	D	0.92	1/1689 (0.1%)	1.02	5/2302 (0.2%)
1	E	0.95	0/1697	1.08	11/2313 (0.5%)
1	F	0.90	2/1689 (0.1%)	1.01	6/2302 (0.3%)
1	G	0.84	0/1721	1.04	11/2348 (0.5%)
1	H	0.89	1/1689 (0.1%)	1.02	7/2302 (0.3%)
1	I	0.88	0/1689	1.02	6/2302 (0.3%)
1	J	0.89	0/1751	1.03	10/2385 (0.4%)
All	All	0.90	6/17117 (0.0%)	1.03	79/23328 (0.3%)

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

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	212	TYR	CG-CD2	6.30	1.47	1.39
1	A	153	GLU	CG-CD	6.24	1.61	1.51
1	A	210	GLU	CD-OE2	-5.48	1.19	1.25
1	D	169	PHE	CG-CD2	5.44	1.47	1.38
1	F	206	SER	CB-OG	-5.33	1.35	1.42
1	H	111	SER	CB-OG	-5.04	1.35	1.42

All (79) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	25	ARG	NE-CZ-NH2	-11.09	114.75	120.30
1	E	172	ASP	CB-CG-OD2	-10.58	108.78	118.30
1	H	76	ARG	NE-CZ-NH1	9.05	124.82	120.30
1	A	76	ARG	NE-CZ-NH1	-8.94	115.83	120.30
1	G	76	ARG	NE-CZ-NH2	8.75	124.67	120.30
1	J	54	LEU	CA-CB-CG	8.51	134.87	115.30
1	B	76	ARG	NE-CZ-NH1	8.38	124.49	120.30
1	A	25	ARG	NE-CZ-NH2	-8.03	116.28	120.30
1	F	25	ARG	NE-CZ-NH2	-7.95	116.33	120.30
1	B	157	CYS	CA-CB-SG	7.86	128.15	114.00
1	D	33	ARG	NE-CZ-NH1	7.81	124.20	120.30
1	B	178	ASP	CB-CG-OD2	-7.76	111.32	118.30
1	A	210	GLU	OE1-CD-OE2	7.67	132.50	123.30
1	E	25	ARG	NE-CZ-NH2	-7.51	116.54	120.30
1	G	83	MET	CG-SD-CE	7.46	112.13	100.20
1	F	76	ARG	NE-CZ-NH2	-7.41	116.59	120.30
1	G	224	ARG	NE-CZ-NH1	7.37	123.98	120.30
1	G	25	ARG	NE-CZ-NH1	7.28	123.94	120.30
1	I	74	ARG	NE-CZ-NH1	7.26	123.93	120.30
1	A	133	MET	CG-SD-CE	7.25	111.79	100.20
1	I	25	ARG	NE-CZ-NH2	-7.18	116.71	120.30
1	I	76	ARG	NE-CZ-NH2	7.09	123.84	120.30
1	G	69	LEU	CA-CB-CG	7.04	131.48	115.30
1	B	69	LEU	CA-CB-CG	7.03	131.48	115.30
1	C	69	LEU	CA-CB-CG	7.01	131.44	115.30
1	J	69	LEU	CA-CB-CG	6.98	131.35	115.30
1	I	69	LEU	CA-CB-CG	6.91	131.20	115.30
1	C	160	LYS	CD-CE-NZ	6.91	127.58	111.70
1	D	69	LEU	CA-CB-CG	6.85	131.04	115.30
1	F	69	LEU	CA-CB-CG	6.78	130.88	115.30
1	H	33	ARG	CG-CD-NE	-6.73	97.67	111.80
1	D	33	ARG	CG-CD-NE	6.64	125.75	111.80
1	H	25	ARG	NE-CZ-NH2	-6.61	117.00	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	76	ARG	NE-CZ-NH1	6.59	123.60	120.30
1	G	224	ARG	CG-CD-NE	6.54	125.54	111.80
1	J	76	ARG	NE-CZ-NH1	6.42	123.51	120.30
1	E	33	ARG	NE-CZ-NH2	-6.38	117.11	120.30
1	G	96	ARG	NE-CZ-NH2	-6.30	117.15	120.30
1	E	69	LEU	CA-CB-CG	6.27	129.73	115.30
1	J	224	ARG	NE-CZ-NH2	6.23	123.42	120.30
1	E	25	ARG	NE-CZ-NH1	6.21	123.40	120.30
1	B	224	ARG	NE-CZ-NH2	6.04	123.32	120.30
1	C	96	ARG	NE-CZ-NH2	-6.03	117.29	120.30
1	E	76	ARG	CG-CD-NE	-5.97	99.26	111.80
1	H	25	ARG	NE-CZ-NH1	5.94	123.27	120.30
1	A	69	LEU	CA-CB-CG	5.91	128.89	115.30
1	G	224	ARG	NE-CZ-NH2	-5.85	117.37	120.30
1	H	69	LEU	CA-CB-CG	5.84	128.74	115.30
1	J	25	ARG	NE-CZ-NH2	-5.84	117.38	120.30
1	J	160	LYS	CB-CG-CD	5.79	126.66	111.60
1	I	54	LEU	CA-CB-CG	5.79	128.61	115.30
1	A	210	GLU	CG-CD-OE1	-5.77	106.75	118.30
1	A	85	ASP	CB-CG-OD2	-5.74	113.13	118.30
1	I	225	ARG	CB-CG-CD	5.69	126.40	111.60
1	D	76	ARG	NE-CZ-NH2	-5.60	117.50	120.30
1	C	85	ASP	CB-CG-OD2	-5.54	113.32	118.30
1	G	224	ARG	CD-NE-CZ	5.44	131.21	123.60
1	B	25	ARG	NE-CZ-NH1	5.40	123.00	120.30
1	J	85	ASP	CB-CG-OD1	5.33	123.10	118.30
1	J	205	TYR	CB-CG-CD1	-5.33	117.80	121.00
1	A	76	ARG	NE-CZ-NH2	5.30	122.95	120.30
1	F	133	MET	CG-SD-CE	5.30	108.68	100.20
1	A	74	ARG	NE-CZ-NH1	5.29	122.94	120.30
1	H	74	ARG	CG-CD-NE	5.27	122.86	111.80
1	E	76	ARG	NE-CZ-NH2	-5.25	117.67	120.30
1	B	139	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	D	25	ARG	NE-CZ-NH2	-5.22	117.69	120.30
1	E	210	GLU	OE1-CD-OE2	-5.22	117.03	123.30
1	B	172	ASP	CB-CG-OD1	5.21	122.98	118.30
1	G	178	ASP	CB-CG-OD2	-5.19	113.63	118.30
1	E	129	ASP	CB-CG-OD1	5.17	122.96	118.30
1	E	174	LYS	CA-CB-CG	5.14	124.72	113.40
1	J	201	GLN	CB-CA-C	-5.13	100.13	110.40
1	G	74	ARG	CG-CD-NE	5.09	122.48	111.80
1	F	139	ARG	NE-CZ-NH1	5.08	122.84	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	76	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	F	54	LEU	CA-CB-CG	5.04	126.90	115.30
1	H	76	ARG	NE-CZ-NH2	-5.03	117.78	120.30
1	J	172	ASP	CB-CG-OD1	5.03	122.83	118.30

There are no chirality outliers.

All (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
1	E	207	CYS	Peptide
1	F	207	CYS	Peptide
1	G	205	TYR	Peptide
1	G	207[A]	CYS	Peptide
1	H	207	CYS	Peptide
1	I	207	CYS	Peptide
1	J	224	ARG	Peptide

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	1649	0	1580	6	0
1	B	1781	0	1687	12	0
1	C	1638	0	1569	4	0
1	D	1649	0	1582	9	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	11	0
1	I	1649	0	1581	8	0
1	J	1710	0	1628	16	0
2	A	14	0	13	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	2	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	5	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	2	0
All	All	17553	0	16338	93	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.

All (93) 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:J:133:MET:HE2	1:J:134:PHE:N	1.77	0.98
1:E:91:ASN:HD21	2:E:603:NAG:C2	1.82	0.91
1:E:91:ASN:CG	2:E:603:NAG:C1	2.47	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:208[A]:CYS:HB3	1:G:210[A]:GLU:OE2	1.82	0.79
1:D:157:CYS:HB2	6:D:456:HOH:O	1.84	0.77
1:F:74:ARG:NH1	1:F:176:ASP:OD1	2.21	0.74
1:F:74:ARG:HG3	5:J:302:TKT:C15	2.18	0.74
1:J:74:ARG:HG2	1:J:133:MET:CE	2.17	0.73
1:J:133:MET:HE2	1:J:134:PHE:H	1.53	0.72
1:F:176:ASP:HB2	6:F:724:HOH:O	1.87	0.72
1:J:74:ARG:HG2	1:J:133:MET:HE1	1.72	0.70
1:E:20:GLN:N	1:E:20:GLN:NE2	2.40	0.69
1:C:20:GLN:NE2	1:C:20:GLN:N	2.40	0.69
1:G:20:GLN:NE2	1:G:20:GLN:N	2.40	0.69
1:A:20:GLN:NE2	1:A:20:GLN:N	2.41	0.69
1:F:20:GLN:N	1:F:20:GLN:NE2	2.40	0.69
1:B:20:GLN:N	1:B:20:GLN:NE2	2.40	0.69
2:I:603:NAG:H82	2:I:603:NAG:C1	2.22	0.69
1:I:20:GLN:N	1:I:20:GLN:NE2	2.41	0.68
1:D:20:GLN:N	1:D:20:GLN:NE2	2.41	0.68
1:G:207[B]:CYS:O	1:G:208[B]:CYS:SG	2.52	0.68
1:H:20:GLN:N	1:H:20:GLN:NE2	2.41	0.68
1:J:20:GLN:N	1:J:20:GLN:NE2	2.41	0.68
1:J:157:CYS:HB2	6:J:432:HOH:O	1.94	0.67
1:D:76:ARG:HD3	6:D:432:HOH:O	1.97	0.65
1:B:225:ARG:HG2	1:B:225:ARG:HH21	1.63	0.64
1:E:74:ARG:NH2	1:E:133:MET:HE1	2.14	0.63
1:E:91:ASN:OD1	2:E:603:NAG:C1	2.47	0.62
1:H:109:ALA:O	3:H:302:EDO:H21	2.01	0.61
1:B:248:HIS:CE1	6:B:704:HOH:O	2.54	0.59
1:G:209[B]:PRO:HB2	1:G:210[B]:GLU:HG3	1.86	0.57
1:B:248:HIS:ND1	1:B:248:HIS:O	2.37	0.57
1:D:109:ALA:O	3:D:301:EDO:H12	2.05	0.56
1:F:20:GLN:N	1:F:20:GLN:HE21	2.03	0.56
1:I:109:ALA:O	3:I:604:EDO:H21	2.06	0.56
1:J:133:MET:HE2	1:J:133:MET:C	2.25	0.56
1:H:133:MET:HE3	6:H:452:HOH:O	2.06	0.55
1:B:112:SER:OG	3:B:602:EDO:H21	2.06	0.55
1:A:20:GLN:N	1:A:20:GLN:HE21	2.05	0.55
1:G:207[B]:CYS:C	1:G:208[B]:CYS:SG	2.85	0.55
1:D:20:GLN:HE21	1:D:20:GLN:N	2.04	0.55
1:E:20:GLN:N	1:E:20:GLN:HE21	2.05	0.54
1:J:203:GLN:HG3	1:J:214:ASP:OD1	2.08	0.54
1:I:20:GLN:N	1:I:20:GLN:HE21	2.05	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:25:ARG:NH2	1:G:88:GLU:O	2.35	0.53
1:H:113:THR:O	1:I:139:ARG:HD2	2.09	0.53
1:J:20:GLN:N	1:J:20:GLN:HE21	2.05	0.53
1:I:201:GLN:NE2	1:J:235:PHE:O	2.33	0.53
1:J:203:GLN:CG	1:J:214:ASP:OD1	2.58	0.52
1:E:91:ASN:ND2	2:E:603:NAG:O5	2.38	0.52
1:C:112:SER:OG	3:C:602:EDO:H21	2.10	0.51
1:G:20:GLN:HE21	1:G:20:GLN:N	2.09	0.51
1:F:112:SER:OG	3:F:602:EDO:H12	2.12	0.50
1:D:33:ARG:HD2	6:D:404:HOH:O	2.10	0.49
1:B:20:GLN:N	1:B:20:GLN:HE21	2.07	0.49
1:D:33:ARG:NE	6:D:404:HOH:O	2.46	0.49
1:E:172:ASP:HA	1:E:213:ILE:HD12	1.93	0.49
1:H:20:GLN:N	1:H:20:GLN:HE21	2.07	0.48
1:C:20:GLN:HE21	1:C:20:GLN:N	2.08	0.48
1:E:112:SER:OG	3:E:604:EDO:H21	2.14	0.48
1:E:25:ARG:NH2	1:E:88:GLU:O	2.38	0.48
1:B:133:MET:HE3	6:B:734:HOH:O	2.14	0.47
1:A:113:THR:O	1:B:139:ARG:HD2	2.14	0.47
1:J:202:VAL:HG12	1:J:204:HIS:CE1	2.50	0.47
1:F:139:ARG:HD2	1:J:113:THR:O	2.16	0.46
1:H:29:ASP:OD1	1:H:33:ARG:CZ	2.63	0.46
1:F:20:GLN:N	3:F:605:EDO:HO1	2.13	0.46
1:B:53:PHE:CE2	1:B:247:HIS:HB3	2.50	0.45
1:I:113:THR:O	1:J:139:ARG:HD2	2.16	0.45
1:J:157:CYS:CB	6:J:432:HOH:O	2.59	0.45
1:A:164:TRP:CE3	1:B:248:HIS:HD2	2.35	0.44
1:D:41:THR:HB	6:D:449:HOH:O	2.18	0.44
1:G:160:LYS:HE2	1:G:160:LYS:HB2	1.82	0.43
1:H:106:ASP:HB2	1:I:121:PRO:HG2	2.00	0.43
1:H:174:LYS:HD3	6:H:421:HOH:O	2.17	0.43
1:G:113:THR:O	1:H:139:ARG:HD2	2.19	0.43
1:F:74:ARG:HG3	5:J:302:TKT:C21	2.49	0.43
1:B:225:ARG:CG	1:B:225:ARG:HH21	2.28	0.42
1:A:121:PRO:HG2	1:E:106:ASP:HB2	2.00	0.42
1:J:207:CYS:HB2	5:J:302:TKT:C15	2.50	0.42
1:D:203:GLN:HE21	1:D:203:GLN:HB3	1.76	0.42
1:B:113:THR:O	1:C:139:ARG:HD2	2.19	0.42
1:E:133:MET:HE1	1:E:135:SER:OG	2.19	0.42
1:F:113:THR:O	1:G:139:ARG:HD2	2.20	0.41
1:H:203:GLN:NE2	6:H:407:HOH:O	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:34:SER:N	6:I:708:HOH:O	2.52	0.41
3:G:605:EDO:C2	6:G:734:HOH:O	2.68	0.41
1:E:91:ASN:ND2	2:E:603:NAG:C2	2.60	0.41
1:H:29:ASP:OD1	1:H:33:ARG:NE	2.54	0.41
1:E:133:MET:CE	1:E:135:SER:OG	2.70	0.40
1:A:112:SER:OG	3:A:302:EDO:H21	2.22	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	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 ⓘ

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%)	186 (98%)	3 (2%)	62	82
1	B	202/224 (90%)	194 (96%)	8 (4%)	31	53
1	C	188/224 (84%)	187 (100%)	1 (0%)	88	95
1	D	189/224 (84%)	185 (98%)	4 (2%)	53	76
1	E	190/224 (85%)	187 (98%)	3 (2%)	62	82
1	F	189/224 (84%)	184 (97%)	5 (3%)	46	70
1	G	194/224 (87%)	187 (96%)	7 (4%)	35	58
1	H	189/224 (84%)	183 (97%)	6 (3%)	39	63
1	I	189/224 (84%)	185 (98%)	4 (2%)	53	76
1	J	195/224 (87%)	190 (97%)	5 (3%)	46	70
All	All	1914/2240 (85%)	1868 (98%)	46 (2%)	49	72

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	76	ARG
1	A	210	GLU
1	B	20	GLN
1	B	54	LEU
1	B	76	ARG
1	B	133	MET
1	B	224	ARG
1	B	225	ARG
1	B	234	LEU
1	B	248	HIS
1	C	20	GLN
1	D	20	GLN
1	D	33	ARG
1	D	133	MET
1	D	225	ARG

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Mol	Chain	Res	Type
1	E	20	GLN
1	E	76	ARG
1	E	210	GLU
1	F	20	GLN
1	F	76	ARG
1	F	133	MET
1	F	203	GLN
1	F	210	GLU
1	G	20	GLN
1	G	42	LYS
1	G	153	GLU
1	G	160	LYS
1	G	210[A]	GLU
1	G	210[B]	GLU
1	G	224	ARG
1	H	20	GLN
1	H	74	ARG
1	H	76	ARG
1	H	190	LYS
1	H	203	GLN
1	H	210	GLU
1	I	20	GLN
1	I	54	LEU
1	I	153	GLU
1	I	225	ARG
1	J	20	GLN
1	J	54	LEU
1	J	133	MET
1	J	203	GLN
1	J	237	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	80	ASN
1	A	87	ASN
1	A	216	ASN
1	B	20	GLN
1	B	80	ASN
1	B	87	ASN
1	B	216	ASN

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Mol	Chain	Res	Type
1	B	248	HIS
1	C	20	GLN
1	C	80	ASN
1	D	20	GLN
1	D	80	ASN
1	D	203	GLN
1	D	216	ASN
1	E	20	GLN
1	E	55	GLN
1	E	80	ASN
1	E	91	ASN
1	E	216	ASN
1	F	20	GLN
1	F	80	ASN
1	F	87	ASN
1	F	203	GLN
1	F	216	ASN
1	G	20	GLN
1	G	80	ASN
1	G	216	ASN
1	H	20	GLN
1	H	80	ASN
1	H	203	GLN
1	H	216	ASN
1	I	20	GLN
1	I	80	ASN
1	I	216	ASN
1	J	20	GLN
1	J	55	GLN
1	J	80	ASN
1	J	204	HIS
1	J	216	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides 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	305	-	3,3,3	0.81	0	2,2,2	0.10	0
3	EDO	E	604	-	3,3,3	0.76	0	2,2,2	1.28	0
3	EDO	A	302	-	3,3,3	0.38	0	2,2,2	1.44	0
3	EDO	D	301	-	3,3,3	0.59	0	2,2,2	1.39	0
3	EDO	A	303	-	3,3,3	0.78	0	2,2,2	0.43	0
3	EDO	J	303	-	3,3,3	0.49	0	2,2,2	0.33	0
5	TKT	J	302	-	23,24,24	1.12	2 (8%)	33,35,35	0.87	1 (3%)
3	EDO	H	302	-	3,3,3	0.97	0	2,2,2	1.50	0
3	EDO	D	303	-	3,3,3	0.62	0	2,2,2	0.20	0
3	EDO	B	604	-	3,3,3	0.40	0	2,2,2	0.54	0
3	EDO	C	605	-	3,3,3	0.65	0	2,2,2	0.48	0
3	EDO	I	605	-	3,3,3	0.64	0	2,2,2	0.66	0
3	EDO	F	601	-	3,3,3	0.70	0	2,2,2	0.44	0
3	EDO	H	304	-	3,3,3	0.34	0	2,2,2	0.60	0
3	EDO	I	604	-	3,3,3	0.49	0	2,2,2	0.68	0
3	EDO	A	304	-	3,3,3	0.55	0	2,2,2	0.70	0
3	EDO	D	304	-	3,3,3	0.81	0	2,2,2	0.24	0
3	EDO	E	605	-	3,3,3	1.05	0	2,2,2	1.32	0
3	EDO	G	605	-	3,3,3	0.71	0	2,2,2	0.05	0
3	EDO	F	603	-	3,3,3	0.72	0	2,2,2	0.20	0
3	EDO	H	305	-	3,3,3	1.11	0	2,2,2	0.60	0
3	EDO	F	605	-	3,3,3	0.79	0	2,2,2	0.32	0
2	NAG	E	603	-	14,14,15	0.30	0	17,19,21	0.61	0
3	EDO	C	603	-	3,3,3	0.58	0	2,2,2	0.63	0
3	EDO	B	605	-	3,3,3	0.92	0	2,2,2	0.26	0
2	NAG	H	301	1	14,14,15	0.30	0	17,19,21	0.62	0
3	EDO	E	606	-	3,3,3	0.91	0	2,2,2	0.85	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	E	602	-	3,3,3	0.51	0	2,2,2	0.34	0
3	EDO	C	602	-	3,3,3	0.89	0	2,2,2	0.77	0
3	EDO	J	304	-	3,3,3	0.54	0	2,2,2	0.46	0
3	EDO	H	303	-	3,3,3	0.77	0	2,2,2	0.76	0
3	EDO	G	602	-	3,3,3	0.71	0	2,2,2	0.62	0
3	EDO	I	606	-	3,3,3	0.83	0	2,2,2	0.21	0
2	NAG	I	603	1	14,14,15	0.29	0	17,19,21	0.61	0
3	EDO	B	603	-	3,3,3	0.49	0	2,2,2	1.10	0
3	EDO	J	306	-	3,3,3	0.73	0	2,2,2	0.31	0
3	EDO	D	302	-	3,3,3	0.74	0	2,2,2	0.38	0
3	EDO	C	604	-	3,3,3	0.63	0	2,2,2	0.28	0
3	EDO	F	604	-	3,3,3	0.91	0	2,2,2	0.72	0
3	EDO	B	601	-	3,3,3	1.01	0	2,2,2	0.03	0
3	EDO	J	301	-	3,3,3	0.52	0	2,2,2	0.64	0
2	NAG	A	301	1	14,14,15	0.28	0	17,19,21	0.61	0
3	EDO	G	603	-	3,3,3	1.27	0	2,2,2	0.66	0
4	FLC	I	601	-	3,12,12	1.65	1 (33%)	3,17,17	5.79	2 (66%)
3	EDO	B	602	-	3,3,3	1.04	0	2,2,2	1.72	1 (50%)
3	EDO	F	602	-	3,3,3	0.48	0	2,2,2	1.28	0
3	EDO	I	602	-	3,3,3	0.60	0	2,2,2	0.20	0
4	FLC	G	601	-	3,12,12	2.16	1 (33%)	3,17,17	3.42	2 (66%)
5	TKT	E	601	-	23,24,24	1.05	1 (4%)	33,35,35	1.04	2 (6%)
3	EDO	G	604	-	3,3,3	0.68	0	2,2,2	0.32	0
4	FLC	C	601	-	3,12,12	1.48	1 (33%)	3,17,17	3.41	2 (66%)

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	305	-	-	1/1/1/1	-
3	EDO	E	604	-	-	1/1/1/1	-
3	EDO	A	302	-	-	1/1/1/1	-
3	EDO	D	301	-	-	1/1/1/1	-
3	EDO	A	303	-	-	0/1/1/1	-
3	EDO	J	303	-	-	1/1/1/1	-
5	TKT	J	302	-	-	0/8/29/29	0/5/4/4
3	EDO	H	302	-	-	1/1/1/1	-
3	EDO	D	303	-	-	0/1/1/1	-
3	EDO	B	604	-	-	1/1/1/1	-

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

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	J	302	TKT	C12-C16	3.97	1.45	1.42
5	E	601	TKT	C12-C9	-3.70	1.42	1.50
4	G	601	FLC	CG-CB	3.21	1.59	1.54
4	C	601	FLC	CG-CB	2.56	1.58	1.54
4	I	601	FLC	OHB-CB	2.46	1.47	1.43
5	J	302	TKT	O3-C9	2.22	1.39	1.34

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	601	FLC	CB-CA-CAC	-9.34	100.03	114.98
4	G	601	FLC	CB-CG-CGC	5.17	123.26	114.98
4	C	601	FLC	CB-CA-CAC	-4.65	107.54	114.98
4	I	601	FLC	CB-CG-CGC	-3.58	109.25	114.98
4	C	601	FLC	CB-CG-CGC	3.55	120.67	114.98
5	E	601	TKT	O3-C9-C12	-3.48	107.75	111.63
5	E	601	TKT	O3-C9-O4	2.89	128.25	123.53
5	J	302	TKT	C11-C12-C9	-2.32	124.33	127.78
4	G	601	FLC	CB-CA-CAC	-2.19	111.47	114.98
3	B	602	EDO	O1-C1-C2	-2.11	96.70	111.91

There are no chirality outliers.

All (44) 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
4	G	601	FLC	CAC-CA-CB-CBC
4	G	601	FLC	CAC-CA-CB-CG
4	G	601	FLC	CAC-CA-CB-OHB
4	G	601	FLC	CBC-CB-CG-CGC
2	E	603	NAG	O5-C5-C6-O6
2	E	603	NAG	C4-C5-C6-O6
3	E	604	EDO	O1-C1-C2-O2
3	A	302	EDO	O1-C1-C2-O2
3	H	302	EDO	O1-C1-C2-O2
3	I	604	EDO	O1-C1-C2-O2
3	E	606	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
3	C	602	EDO	O1-C1-C2-O2
3	B	602	EDO	O1-C1-C2-O2
3	F	602	EDO	O1-C1-C2-O2
3	D	301	EDO	O1-C1-C2-O2
3	C	605	EDO	O1-C1-C2-O2
3	F	601	EDO	O1-C1-C2-O2
3	F	603	EDO	O1-C1-C2-O2
3	J	306	EDO	O1-C1-C2-O2
3	F	604	EDO	O1-C1-C2-O2
4	G	601	FLC	CA-CB-CG-CGC
4	G	601	FLC	OHB-CB-CG-CGC
3	C	604	EDO	O1-C1-C2-O2
3	F	605	EDO	O1-C1-C2-O2
3	E	602	EDO	O1-C1-C2-O2
3	J	301	EDO	O1-C1-C2-O2
2	I	603	NAG	C4-C5-C6-O6
3	J	303	EDO	O1-C1-C2-O2
3	B	605	EDO	O1-C1-C2-O2
3	C	603	EDO	O1-C1-C2-O2
3	G	602	EDO	O1-C1-C2-O2
3	I	602	EDO	O1-C1-C2-O2
4	C	601	FLC	CAC-CA-CB-OHB
3	B	604	EDO	O1-C1-C2-O2
3	H	304	EDO	O1-C1-C2-O2
3	D	304	EDO	O1-C1-C2-O2
2	I	603	NAG	O5-C5-C6-O6
3	J	305	EDO	O1-C1-C2-O2
3	J	304	EDO	O1-C1-C2-O2

There are no ring outliers.

13 monomers are involved in 21 short contacts:

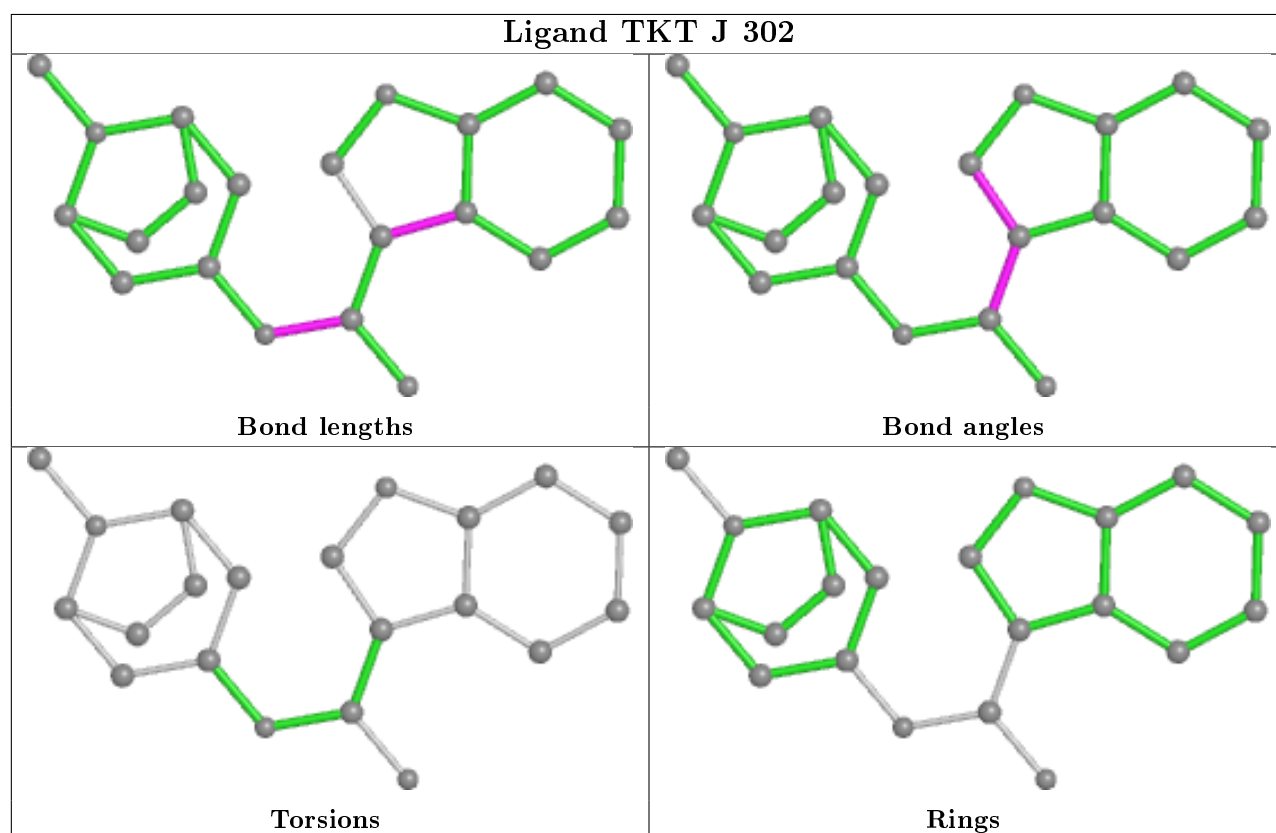
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	604	EDO	1	0
3	A	302	EDO	1	0
3	D	301	EDO	1	0
5	J	302	TKT	3	0
3	H	302	EDO	1	0
3	I	604	EDO	1	0
3	G	605	EDO	1	0
3	F	605	EDO	1	0
2	E	603	NAG	7	0

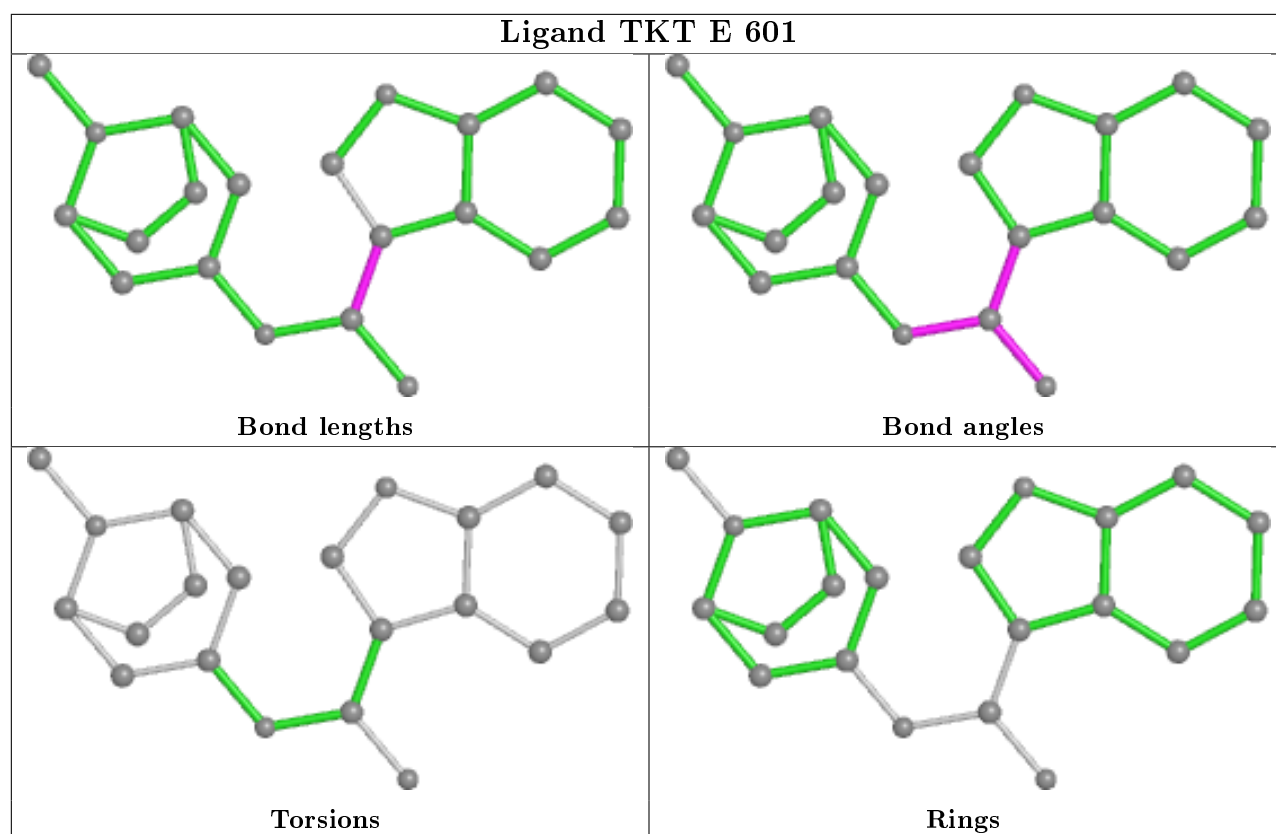
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	602	EDO	1	0
2	I	603	NAG	1	0
3	B	602	EDO	1	0
3	F	602	EDO	1	0

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%)	-0.35	0 100 100	22, 33, 62, 85	0
1	B	221/249 (88%)	-0.21	4 (1%) 68 70	21, 35, 71, 100	0
1	C	205/249 (82%)	-0.23	3 (1%) 73 75	21, 33, 63, 103	0
1	D	206/249 (82%)	-0.24	2 (0%) 82 84	22, 34, 58, 91	0
1	E	206/249 (82%)	-0.31	4 (1%) 66 68	21, 32, 56, 102	0
1	F	206/249 (82%)	-0.15	6 (2%) 51 54	26, 38, 75, 105	0
1	G	205/249 (82%)	0.00	7 (3%) 45 47	26, 43, 75, 104	0
1	H	206/249 (82%)	-0.17	5 (2%) 59 61	26, 39, 65, 97	0
1	I	206/249 (82%)	-0.32	1 (0%) 91 91	23, 37, 72, 93	0
1	J	213/249 (85%)	-0.13	2 (0%) 84 86	25, 40, 74, 100	0
All	All	2080/2490 (83%)	-0.21	34 (1%) 72 73	21, 36, 70, 105	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	207	CYS	4.7
1	F	225	ARG	4.2
1	E	225	ARG	3.8
1	G	207[A]	CYS	3.3
1	F	206	SER	3.3
1	G	208[A]	CYS	3.2
1	F	208	CYS	3.1
1	B	235	PHE	3.0
1	C	207	CYS	2.9
1	H	152	GLU	2.8
1	B	226	ALA	2.7
1	H	153	GLU	2.7
1	H	225	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
1	J	235	PHE	2.6
1	G	206[A]	SER	2.6
1	E	152	GLU	2.6
1	I	224	ARG	2.5
1	E	150	ASP	2.5
1	G	153	GLU	2.5
1	C	153	GLU	2.5
1	G	152	GLU	2.5
1	B	246	HIS	2.4
1	H	33	ARG	2.4
1	F	224	ARG	2.4
1	C	152	GLU	2.1
1	E	153	GLU	2.1
1	B	242	GLN	2.1
1	G	209[A]	PRO	2.1
1	D	33	ARG	2.1
1	G	150	ASP	2.1
1	H	151	SER	2.0
1	J	225	ARG	2.0
1	D	153	GLU	2.0
1	F	43	ASP	2.0

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 monosaccharides 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(\AA^2)	Q<0.9
3	EDO	J	305	4/4	0.63	0.48	66,73,80,83	0
3	EDO	D	304	4/4	0.67	0.20	64,65,72,73	0

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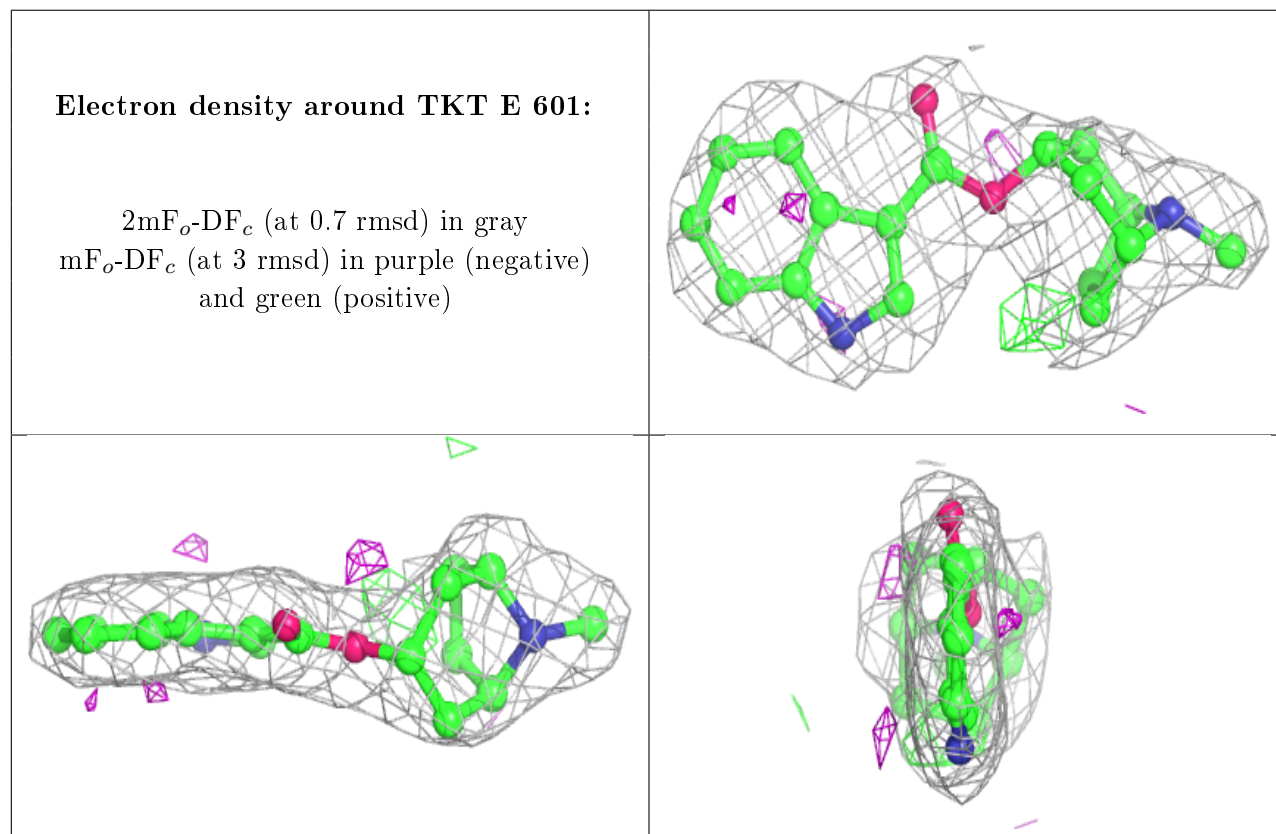
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	EDO	H	305	4/4	0.70	0.20	61,61,71,73	0
2	NAG	I	603	14/15	0.71	0.37	72,98,112,119	0
2	NAG	E	603	14/15	0.74	0.21	66,86,92,92	0
4	FLC	G	601	13/13	0.78	0.24	70,82,92,98	0
4	FLC	C	601	13/13	0.79	0.28	60,92,105,114	0
2	NAG	H	301	14/15	0.80	0.26	72,99,106,114	0
3	EDO	J	301	4/4	0.81	0.25	66,78,86,87	0
3	EDO	H	304	4/4	0.83	0.29	56,57,59,68	0
2	NAG	A	301	14/15	0.83	0.35	62,93,104,124	0
3	EDO	I	606	4/4	0.83	0.20	46,60,60,66	0
3	EDO	B	605	4/4	0.83	0.16	44,54,58,62	0
3	EDO	F	605	4/4	0.84	0.19	43,58,65,71	0
3	EDO	G	603	4/4	0.84	0.19	42,48,48,51	0
3	EDO	H	303	4/4	0.85	0.15	42,47,49,54	0
3	EDO	C	605	4/4	0.85	0.12	55,61,61,66	0
4	FLC	I	601	13/13	0.86	0.22	56,77,112,123	0
3	EDO	J	306	4/4	0.86	0.17	54,66,68,70	0
3	EDO	A	303	4/4	0.86	0.17	43,53,58,69	0
3	EDO	B	603	4/4	0.87	0.17	40,45,45,58	0
3	EDO	C	604	4/4	0.87	0.18	53,59,62,64	0
3	EDO	B	601	4/4	0.88	0.20	50,52,53,53	0
3	EDO	E	602	4/4	0.89	0.30	43,45,46,56	0
3	EDO	A	304	4/4	0.90	0.19	50,56,59,68	0
3	EDO	F	604	4/4	0.91	0.16	54,59,59,63	0
3	EDO	D	303	4/4	0.91	0.28	46,49,52,53	0
3	EDO	F	603	4/4	0.91	0.18	42,47,47,54	0
3	EDO	G	604	4/4	0.91	0.20	50,64,64,67	0
3	EDO	J	304	4/4	0.91	0.15	46,51,52,55	0
3	EDO	I	605	4/4	0.92	0.16	42,44,46,50	0
5	TKT	E	601	21/21	0.92	0.16	33,43,57,57	0
3	EDO	D	302	4/4	0.93	0.13	35,46,53,58	0
3	EDO	G	602	4/4	0.93	0.21	44,49,53,57	0
3	EDO	E	606	4/4	0.93	0.21	38,52,54,62	0
3	EDO	F	601	4/4	0.93	0.22	48,54,55,55	0
3	EDO	B	604	4/4	0.93	0.27	58,61,64,66	0
3	EDO	E	605	4/4	0.93	0.13	35,36,39,39	0
3	EDO	G	605	4/4	0.94	0.12	50,59,63,64	0
3	EDO	C	603	4/4	0.94	0.17	42,49,49,53	0
3	EDO	C	602	4/4	0.94	0.24	32,34,35,45	0
3	EDO	I	602	4/4	0.94	0.34	57,61,62,62	0
3	EDO	J	303	4/4	0.95	0.28	53,54,57,63	0
3	EDO	I	604	4/4	0.95	0.21	41,44,46,51	0

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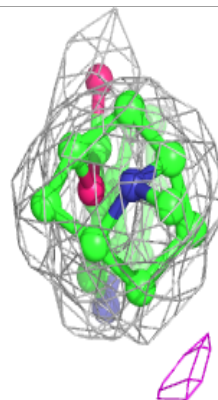
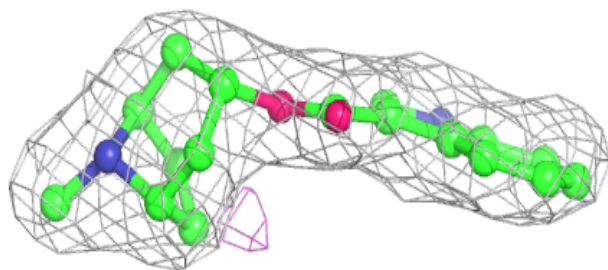
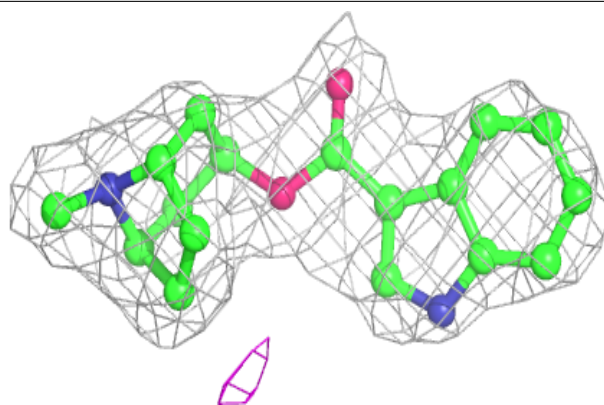
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	EDO	A	302	4/4	0.96	0.16	32,32,36,39	0
5	TKT	J	302	21/21	0.96	0.13	29,45,62,67	0
3	EDO	B	602	4/4	0.96	0.21	32,36,39,41	0
3	EDO	E	604	4/4	0.96	0.19	30,30,33,36	0
3	EDO	F	602	4/4	0.97	0.21	33,36,39,44	0
3	EDO	H	302	4/4	0.98	0.18	22,22,24,29	0
3	EDO	D	301	4/4	0.99	0.19	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 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.