



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 04:41 AM UTC

PDB ID : 7T0A / pdb_00007t0a
Title : Cryptococcus neoformans protein farnesyltransferase co-crystallized with FPP and inhibitor 2f
Authors : Wang, Y.; Shi, Y.; Beese, L.S.
Deposited on : 2021-11-29
Resolution : 2.10 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

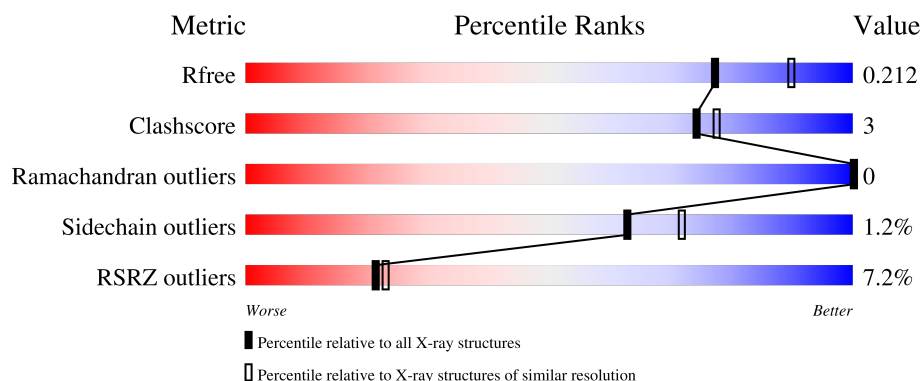
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	349	9% 86% 5% • 9%
2	B	520	5% 85% 8% 7%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7147 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 Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	318	Total	C	N	O	S	0	1	0
			2653	1711	451	480	11			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	expression tag	UNP J9VSJ6
A	-12	GLY	-	expression tag	UNP J9VSJ6
A	-11	SER	-	expression tag	UNP J9VSJ6
A	-10	SER	-	expression tag	UNP J9VSJ6
A	-9	HIS	-	expression tag	UNP J9VSJ6
A	-8	HIS	-	expression tag	UNP J9VSJ6
A	-7	HIS	-	expression tag	UNP J9VSJ6
A	-6	HIS	-	expression tag	UNP J9VSJ6
A	-5	HIS	-	expression tag	UNP J9VSJ6
A	-4	HIS	-	expression tag	UNP J9VSJ6
A	-3	SER	-	expression tag	UNP J9VSJ6
A	-2	GLN	-	expression tag	UNP J9VSJ6
A	-1	ASP	-	expression tag	UNP J9VSJ6
A	0	LEU	-	expression tag	UNP J9VSJ6

- Molecule 2 is a protein called Protein farnesyltransferase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	486	Total	C	N	O	S	0	2	0
			3750	2379	652	704	15			

- 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	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	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	A	1	Total	C	O	0	0
			4	2	2		

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

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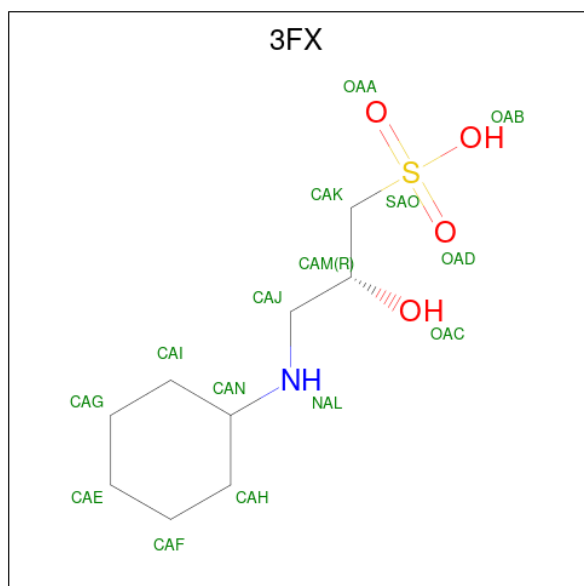
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

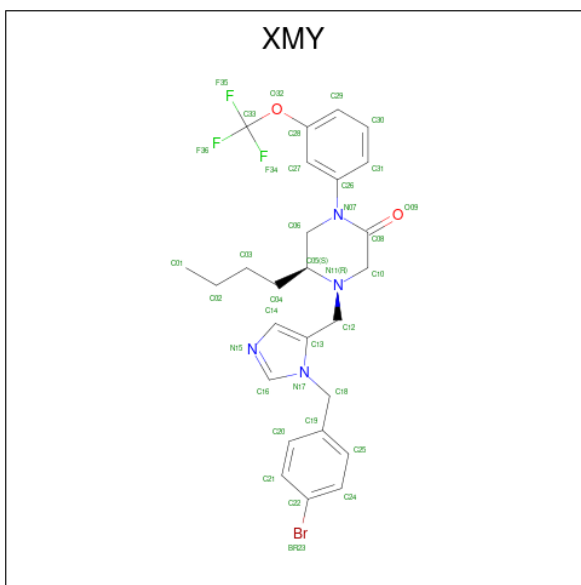
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Zn	0	0
			1	1		

- Molecule 5 is (2R)-3-(cyclohexylamino)-2-hydroxypropane-1-sulfonic acid (CCD ID: 3FX) (formula: C₉H₁₉NO₄S).



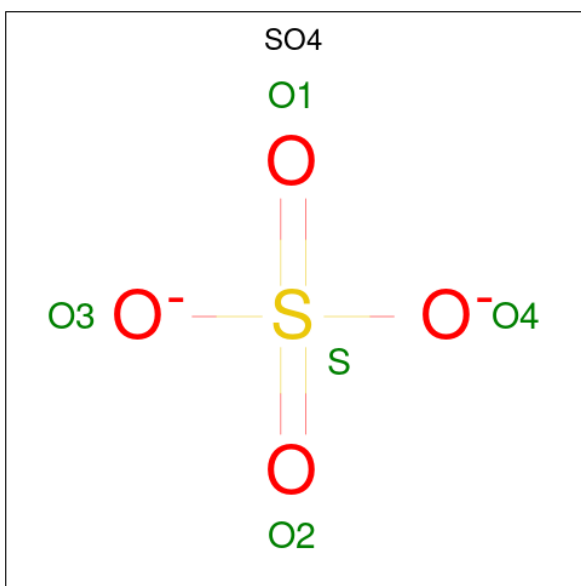
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	S	0	0
			15	9	1	4	1		
5	B	1	Total	C	N	O	S	0	0
			15	9	1	4	1		
5	B	1	Total	C	N	O	S	0	0
			15	9	1	4	1		

- Molecule 6 is (5S)-4-({1-[(4-bromophenyl)methyl]-1H-imidazol-5-yl}methyl)-5-butyl-1-[3-(trifluoromethoxy)phenyl]piperazin-2-one (CCD ID: XMY) (formula: C₂₆H₂₈BrF₃N₄O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	B	1	Total	Br	C	F	N	O	0	0
			36	1	26	3	4	2		

- Molecule 7 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	141	Total 141	O 141	0	0
8	B	280	Total 280	O 280	0	0

- Molecule 1: Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	141.21Å 141.21Å 129.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.93 – 2.10 49.93 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.93-2.10) 91.0 (49.93-2.10)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.187 , 0.213 0.187 , 0.212	Depositor DCC
R_{free} test set	1998 reflections (2.60%)	wwPDB-VP
Wilson B-factor (Å ²)	29.1	Xtriage
Anisotropy	0.583	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 43.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7147	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, SO4, XMY, 3FX, ZN

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	0.18	0/2737	0.32	1/3728 (0.0%)
2	B	0.23	2/3845 (0.1%)	0.36	0/5222
All	All	0.21	2/6582 (0.0%)	0.34	1/8950 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	23	PRO	C-O	-5.46	1.17	1.23
2	B	22	ARG	C-O	-5.13	1.18	1.24

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	278	PRO	N-CA-C	-5.84	100.45	112.47

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2653	0	2567	12	0
2	B	3750	0	3669	29	0
3	A	104	0	156	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	132	0	198	12	0
4	B	1	0	0	0	0
5	B	45	0	57	1	0
6	B	36	0	0	0	0
7	B	5	0	0	0	0
8	A	141	0	0	1	0
8	B	280	0	0	0	0
All	All	7147	0	6647	41	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 (41) 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:A:277:ASP:HB3	1:A:278:PRO:HD3	1.35	1.08
1:A:277:ASP:HB3	1:A:278:PRO:CD	2.09	0.82
1:A:145:TYR:H	3:A:426:EDO:H22	1.63	0.63
2:B:178:ARG:HE	3:B:631:EDO:H22	1.63	0.63
2:B:323:ASP:HB3	2:B:326:TYR:CD2	2.37	0.60
1:A:296:ASP:OD1	1:A:329:ARG:NH2	2.37	0.58
2:B:457:TRP:H	3:B:615:EDO:H12	1.71	0.55
1:A:184:GLY:HA3	3:A:403:EDO:H12	1.88	0.54
2:B:424:LYS:HA	3:B:617:EDO:H11	1.89	0.54
2:B:84:LEU:HD13	2:B:91:LEU:HD21	1.89	0.54
1:A:183:ASP:HB3	3:A:414:EDO:H22	1.90	0.53
2:B:214:PRO:O	3:B:616:EDO:O2	2.24	0.53
2:B:323:ASP:HB3	2:B:326:TYR:HD2	1.74	0.52
1:A:125[A]:GLN:NE2	8:A:509:HOH:O	2.42	0.52
2:B:139:HIS:HB3	2:B:142:PRO:HD2	1.93	0.51
2:B:464:GLN:HG3	3:B:635:EDO:H22	1.94	0.50
2:B:491:ASP:OD2	5:B:602:3FX:NAL	2.42	0.50
3:A:419:EDO:H21	2:B:82:VAL:HG11	1.94	0.49
2:B:285:LEU:HD13	3:B:616:EDO:H21	1.95	0.49
2:B:139:HIS:CE1	2:B:188:VAL:HB	2.48	0.48
2:B:344:GLU:HG2	3:B:632:EDO:H12	1.95	0.48
1:A:162:GLY:HA2	3:A:412:EDO:H21	1.96	0.48
2:B:50:LEU:H	2:B:50:LEU:HG	1.31	0.48
2:B:89:PRO:HG2	2:B:142:PRO:HB3	1.96	0.47
2:B:328:TRP:CZ2	2:B:502:ASN:HB2	2.49	0.47
2:B:239:PHE:HB2	2:B:262[B]:MET:SD	2.55	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:440:ASP:OD2	2:B:442:SER:OG	2.31	0.46
2:B:310:GLU:OE1	2:B:315:ARG:NH2	2.48	0.46
1:A:66:ILE:HG21	1:A:76:VAL:HG21	1.98	0.45
2:B:445:LEU:HA	3:B:637:EDO:H22	1.99	0.44
1:A:113:HIS:HD2	3:A:413:EDO:H11	1.83	0.43
2:B:296:ALA:HB1	3:B:628:EDO:H22	2.00	0.43
2:B:228:GLN:HG2	3:B:627:EDO:H22	2.01	0.43
1:A:195:TYR:HA	1:A:199:SER:OG	2.19	0.42
1:A:13:ARG:HE	1:A:13:ARG:H	1.67	0.41
2:B:300:TRP:O	2:B:304:GLN:HG2	2.19	0.41
2:B:29:GLU:OE1	3:B:626:EDO:O2	2.26	0.41
2:B:457:TRP:HD1	3:B:615:EDO:H22	1.85	0.41
2:B:325:CYS:HB3	2:B:410:HIS:CD2	2.55	0.41
2:B:407:ASP:CG	2:B:410:HIS:HD1	2.28	0.41
2:B:509:LYS:HB3	2:B:510:PRO:HD3	2.02	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	315/349 (90%)	306 (97%)	9 (3%)	0	100	100
2	B	482/520 (93%)	474 (98%)	8 (2%)	0	100	100
All	All	797/869 (92%)	780 (98%)	17 (2%)	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	288/316 (91%)	284 (99%)	4 (1%)	59	67
2	B	406/436 (93%)	402 (99%)	4 (1%)	68	76
All	All	694/752 (92%)	686 (99%)	8 (1%)	63	72

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ARG
1	A	107	LYS
1	A	270	PHE
1	A	276	SER
2	B	50	LEU
2	B	51	VAL
2	B	374	ILE
2	B	448	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	146	HIS
1	A	168	GLN
1	A	187	ASN
1	A	227	ASN
2	B	108	GLN
2	B	319	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 65 ligands modelled in this entry, 1 is monoatomic - leaving 64 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	EDO	B	621	-	3,3,3	0.42	0	2,2,2	0.38	0
3	EDO	A	401	-	3,3,3	0.42	0	2,2,2	0.35	0
3	EDO	B	622	-	3,3,3	0.41	0	2,2,2	0.38	0
3	EDO	B	633	-	3,3,3	0.43	0	2,2,2	0.31	0
3	EDO	B	639	-	3,3,3	0.43	0	2,2,2	0.36	0
3	EDO	B	613	-	3,3,3	0.42	0	2,2,2	0.38	0
3	EDO	A	403	-	3,3,3	0.42	0	2,2,2	0.39	0
3	EDO	A	413	-	3,3,3	0.43	0	2,2,2	0.36	0
3	EDO	A	417	-	3,3,3	0.43	0	2,2,2	0.36	0
3	EDO	B	610	-	3,3,3	0.42	0	2,2,2	0.39	0
3	EDO	B	616	-	3,3,3	0.42	0	2,2,2	0.39	0
3	EDO	B	638	-	3,3,3	0.43	0	2,2,2	0.39	0
3	EDO	B	631	-	3,3,3	0.43	0	2,2,2	0.35	0
3	EDO	A	406	-	3,3,3	0.42	0	2,2,2	0.38	0
3	EDO	B	612	-	3,3,3	0.43	0	2,2,2	0.37	0
3	EDO	B	624	-	3,3,3	0.43	0	2,2,2	0.36	0
3	EDO	B	626	-	3,3,3	0.42	0	2,2,2	0.35	0
3	EDO	A	419	-	3,3,3	0.43	0	2,2,2	0.36	0
3	EDO	A	409	-	3,3,3	0.43	0	2,2,2	0.38	0
3	EDO	B	635	-	3,3,3	0.42	0	2,2,2	0.40	0
3	EDO	B	637	-	3,3,3	0.43	0	2,2,2	0.38	0
3	EDO	A	424	-	3,3,3	0.43	0	2,2,2	0.38	0
3	EDO	B	623	-	3,3,3	0.42	0	2,2,2	0.37	0
3	EDO	B	634	-	3,3,3	0.42	0	2,2,2	0.39	0
5	3FX	B	603	-	14,15,15	1.03	2 (14%)	16,20,20	1.64	3 (18%)
3	EDO	A	414	-	3,3,3	0.42	0	2,2,2	0.29	0
3	EDO	A	415	-	3,3,3	0.43	0	2,2,2	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	B	609	-	3,3,3	0.42	0	2,2,2	0.40	0
3	EDO	A	408	-	3,3,3	0.42	0	2,2,2	0.34	0
3	EDO	B	608	-	3,3,3	0.43	0	2,2,2	0.40	0
3	EDO	A	421	-	3,3,3	0.43	0	2,2,2	0.36	0
3	EDO	B	617	-	3,3,3	0.43	0	2,2,2	0.35	0
3	EDO	B	607	-	3,3,3	0.42	0	2,2,2	0.39	0
3	EDO	A	426	-	3,3,3	0.42	0	2,2,2	0.36	0
3	EDO	B	628	-	3,3,3	0.41	0	2,2,2	0.39	0
3	EDO	A	410	-	3,3,3	0.43	0	2,2,2	0.30	0
3	EDO	A	411	-	3,3,3	0.41	0	2,2,2	0.47	0
3	EDO	A	407	-	3,3,3	0.43	0	2,2,2	0.38	0
3	EDO	A	423	-	3,3,3	0.42	0	2,2,2	0.36	0
3	EDO	B	636	-	3,3,3	0.43	0	2,2,2	0.36	0
3	EDO	A	402	-	3,3,3	0.42	0	2,2,2	0.41	0
3	EDO	A	412	-	3,3,3	0.44	0	2,2,2	0.29	0
3	EDO	A	425	-	3,3,3	0.42	0	2,2,2	0.39	0
3	EDO	B	627	-	3,3,3	0.42	0	2,2,2	0.37	0
5	3FX	B	604	-	14,15,15	1.04	2 (14%)	16,20,20	1.57	4 (25%)
3	EDO	B	625	-	3,3,3	0.41	0	2,2,2	0.40	0
3	EDO	A	404	-	3,3,3	0.42	0	2,2,2	0.37	0
3	EDO	B	620	-	3,3,3	0.41	0	2,2,2	0.33	0
3	EDO	B	618	-	3,3,3	0.43	0	2,2,2	0.37	0
3	EDO	A	420	-	3,3,3	0.44	0	2,2,2	0.28	0
3	EDO	B	614	-	3,3,3	0.44	0	2,2,2	0.34	0
5	3FX	B	602	-	14,15,15	1.04	2 (14%)	16,20,20	1.60	4 (25%)
3	EDO	B	632	-	3,3,3	0.43	0	2,2,2	0.34	0
3	EDO	A	422	-	3,3,3	0.43	0	2,2,2	0.40	0
3	EDO	B	611	-	3,3,3	0.43	0	2,2,2	0.37	0
3	EDO	B	615	-	3,3,3	0.43	0	2,2,2	0.32	0
3	EDO	B	619	-	3,3,3	0.42	0	2,2,2	0.39	0
6	XMY	B	605	4	39,39,39	2.73	14 (35%)	45,55,55	1.24	4 (8%)
3	EDO	B	630	-	3,3,3	0.42	0	2,2,2	0.38	0
7	SO4	B	606	-	4,4,4	0.23	0	6,6,6	0.09	0
3	EDO	A	405	-	3,3,3	0.43	0	2,2,2	0.35	0
3	EDO	A	418	-	3,3,3	0.41	0	2,2,2	0.45	0
3	EDO	B	629	-	3,3,3	0.44	0	2,2,2	0.29	0
3	EDO	A	416	-	3,3,3	0.43	0	2,2,2	0.39	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	B	621	-	-	0/1/1/1	-
3	EDO	A	401	-	-	0/1/1/1	-
3	EDO	B	622	-	-	0/1/1/1	-
3	EDO	B	633	-	-	0/1/1/1	-
3	EDO	B	639	-	-	0/1/1/1	-
3	EDO	B	613	-	-	0/1/1/1	-
3	EDO	A	403	-	-	1/1/1/1	-
3	EDO	A	413	-	-	0/1/1/1	-
3	EDO	A	417	-	-	0/1/1/1	-
3	EDO	B	610	-	-	0/1/1/1	-
3	EDO	B	616	-	-	1/1/1/1	-
3	EDO	B	638	-	-	0/1/1/1	-
3	EDO	B	631	-	-	0/1/1/1	-
3	EDO	A	406	-	-	0/1/1/1	-
3	EDO	B	612	-	-	0/1/1/1	-
3	EDO	B	624	-	-	0/1/1/1	-
3	EDO	B	626	-	-	0/1/1/1	-
3	EDO	A	419	-	-	0/1/1/1	-
3	EDO	A	409	-	-	0/1/1/1	-
3	EDO	B	635	-	-	1/1/1/1	-
3	EDO	B	637	-	-	0/1/1/1	-
3	EDO	A	424	-	-	0/1/1/1	-
3	EDO	B	623	-	-	0/1/1/1	-
3	EDO	B	634	-	-	0/1/1/1	-
5	3FX	B	603	-	-	5/10/18/18	0/1/1/1
3	EDO	A	414	-	-	0/1/1/1	-
3	EDO	A	415	-	-	0/1/1/1	-
3	EDO	B	609	-	-	0/1/1/1	-
3	EDO	A	408	-	-	0/1/1/1	-
3	EDO	B	608	-	-	0/1/1/1	-
3	EDO	A	421	-	-	0/1/1/1	-
3	EDO	B	617	-	-	0/1/1/1	-
3	EDO	B	607	-	-	0/1/1/1	-
3	EDO	A	426	-	-	1/1/1/1	-
3	EDO	B	628	-	-	0/1/1/1	-
3	EDO	A	410	-	-	0/1/1/1	-
3	EDO	A	411	-	-	0/1/1/1	-
3	EDO	A	407	-	-	0/1/1/1	-
3	EDO	A	423	-	-	0/1/1/1	-
3	EDO	B	636	-	-	0/1/1/1	-
3	EDO	A	402	-	-	0/1/1/1	-
3	EDO	A	412	-	-	0/1/1/1	-
3	EDO	A	425	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	B	627	-	-	0/1/1/1	-
5	3FX	B	604	-	-	2/10/18/18	0/1/1/1
3	EDO	B	625	-	-	1/1/1/1	-
3	EDO	A	404	-	-	0/1/1/1	-
3	EDO	B	620	-	-	0/1/1/1	-
3	EDO	B	618	-	-	0/1/1/1	-
3	EDO	A	420	-	-	0/1/1/1	-
3	EDO	B	614	-	-	0/1/1/1	-
5	3FX	B	602	-	-	4/10/18/18	0/1/1/1
3	EDO	B	632	-	-	0/1/1/1	-
3	EDO	A	422	-	-	0/1/1/1	-
3	EDO	B	611	-	-	1/1/1/1	-
3	EDO	B	615	-	-	0/1/1/1	-
3	EDO	B	619	-	-	0/1/1/1	-
6	XMY	B	605	4	-	5/21/37/37	0/4/4/4
3	EDO	B	630	-	-	0/1/1/1	-
3	EDO	A	405	-	-	0/1/1/1	-
3	EDO	A	418	-	-	0/1/1/1	-
3	EDO	B	629	-	-	0/1/1/1	-
3	EDO	A	416	-	-	0/1/1/1	-

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	605	XMY	C12-N11	-7.75	1.28	1.47
6	B	605	XMY	C08-N07	5.96	1.47	1.36
6	B	605	XMY	C12-C13	5.47	1.57	1.50
6	B	605	XMY	C05-N11	-5.45	1.39	1.48
6	B	605	XMY	C10-C08	4.66	1.60	1.51
6	B	605	XMY	C10-N11	-4.56	1.36	1.47
6	B	605	XMY	O09-C08	-3.72	1.14	1.23
6	B	605	XMY	BR23-C22	3.24	1.96	1.90
6	B	605	XMY	C13-N17	-3.18	1.34	1.38
6	B	605	XMY	C26-N07	2.87	1.49	1.43
6	B	605	XMY	C27-C26	2.62	1.44	1.39
6	B	605	XMY	O32-C33	2.48	1.44	1.31
6	B	605	XMY	C18-C19	2.43	1.55	1.51
6	B	605	XMY	C04-C05	2.42	1.62	1.52
5	B	604	3FX	OAD-SAO	2.29	1.51	1.45
5	B	604	3FX	OAA-SAO	2.25	1.51	1.45
5	B	602	3FX	OAD-SAO	2.25	1.51	1.45
5	B	603	3FX	OAD-SAO	2.25	1.51	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	602	3FX	OAA-SAO	2.23	1.51	1.45
5	B	603	3FX	OAA-SAO	2.20	1.51	1.45

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	605	XMY	C14-C13-N17	4.70	107.90	105.08
5	B	603	3FX	OAD-SAO-OAA	-3.90	101.16	113.82
5	B	604	3FX	OAD-SAO-OAA	-3.85	101.30	113.82
5	B	602	3FX	OAD-SAO-OAA	-3.78	101.51	113.82
5	B	603	3FX	OAD-SAO-CAK	3.64	112.19	106.76
5	B	602	3FX	OAD-SAO-CAK	3.38	111.80	106.76
6	B	605	XMY	C06-N07-C08	-3.23	117.57	122.27
5	B	604	3FX	OAD-SAO-CAK	3.06	111.32	106.76
5	B	604	3FX	OAA-SAO-CAK	2.94	111.15	106.76
5	B	602	3FX	OAA-SAO-CAK	2.81	110.96	106.76
5	B	603	3FX	OAA-SAO-CAK	2.77	110.89	106.76
6	B	605	XMY	C13-C12-N11	-2.43	106.92	112.69
5	B	604	3FX	OAB-SAO-CAK	2.24	110.31	105.97
5	B	602	3FX	OAB-SAO-CAK	2.21	110.25	105.97
6	B	605	XMY	C14-N15-C16	2.07	107.94	105.24

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	604	3FX	SAO-CAK-CAM-OAC
5	B	604	3FX	SAO-CAK-CAM-CAJ
5	B	603	3FX	CAI-CAN-NAL-CAJ
6	B	605	XMY	C13-C12-N11-C10
3	A	426	EDO	O1-C1-C2-O2
6	B	605	XMY	C03-C04-C05-C06
5	B	602	3FX	SAO-CAK-CAM-OAC
5	B	602	3FX	CAM-CAK-SAO-OAA
5	B	603	3FX	NAL-CAJ-CAM-CAK
3	B	625	EDO	O1-C1-C2-O2
5	B	603	3FX	NAL-CAJ-CAM-OAC
5	B	602	3FX	SAO-CAK-CAM-CAJ
5	B	603	3FX	CAH-CAN-NAL-CAJ
3	A	403	EDO	O1-C1-C2-O2
3	B	611	EDO	O1-C1-C2-O2
3	B	616	EDO	O1-C1-C2-O2

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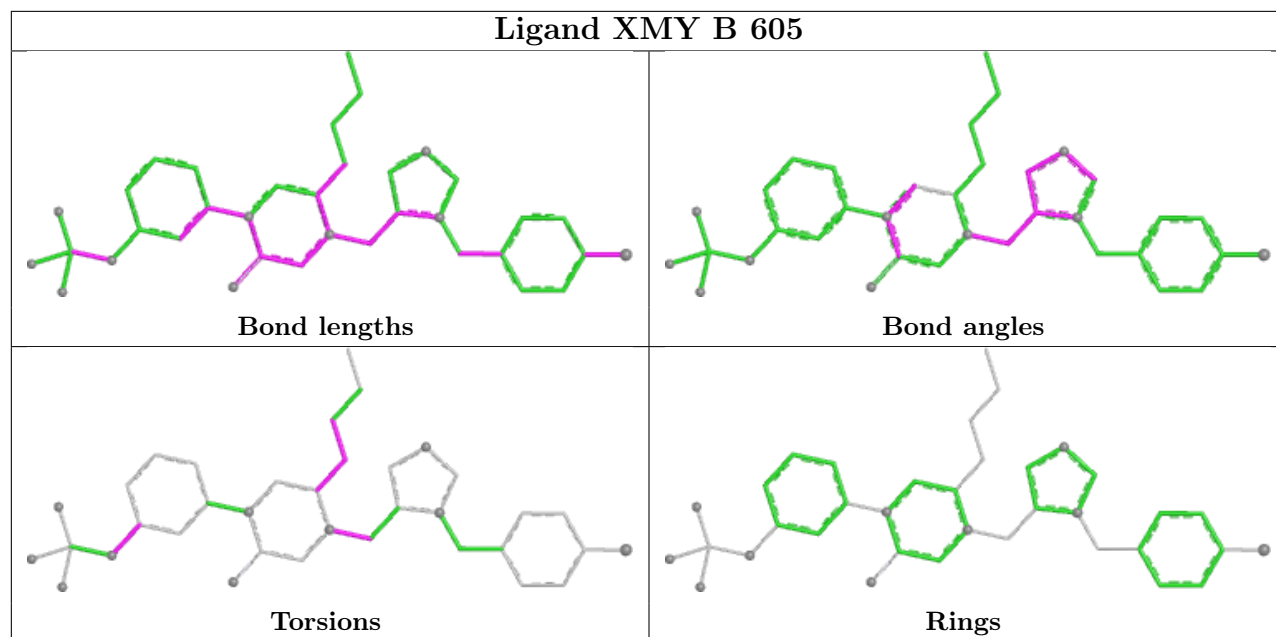
Mol	Chain	Res	Type	Atoms
3	B	635	EDO	O1-C1-C2-O2
5	B	602	3FX	CAM-CAK-SAO-OAB
5	B	603	3FX	SAO-CAK-CAM-OAC
6	B	605	XMY	C29-C28-O32-C33
6	B	605	XMY	C27-C28-O32-C33
6	B	605	XMY	C02-C03-C04-C05

There are no ring outliers.

17 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	403	EDO	1	0
3	A	413	EDO	1	0
3	B	616	EDO	2	0
3	B	631	EDO	1	0
3	B	626	EDO	1	0
3	A	419	EDO	1	0
3	B	635	EDO	1	0
3	B	637	EDO	1	0
3	A	414	EDO	1	0
3	B	617	EDO	1	0
3	A	426	EDO	1	0
3	B	628	EDO	1	0
3	A	412	EDO	1	0
3	B	627	EDO	1	0
5	B	602	3FX	1	0
3	B	632	EDO	1	0
3	B	615	EDO	2	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	318/349 (91%)	0.70	32 (10%)	12 13	18, 42, 72, 105	1 (0%)
2	B	486/520 (93%)	0.24	26 (5%)	32 34	15, 33, 62, 101	2 (0%)
All	All	804/869 (92%)	0.42	58 (7%)	21 23	15, 36, 66, 105	3 (0%)

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	75[A]	PHE	9.5
2	B	371	ILE	5.6
2	B	2	ALA	5.4
1	A	102	ALA	5.3
2	B	50	LEU	5.1
2	B	51	VAL	4.8
2	B	77	LEU	4.7
2	B	74	PHE	4.7
2	B	243	SER	4.7
1	A	139	LEU	4.6
2	B	73	SER	4.5
2	B	349	VAL	4.4
1	A	107	LYS	4.3
1	A	334	ALA	3.9
1	A	109	TYR	3.7
1	A	103	VAL	3.5
1	A	248	ILE	3.5
2	B	393	GLY	3.5
1	A	5	THR	3.5
1	A	270	PHE	3.2
1	A	25	ASP	3.1
1	A	106	LEU	3.1
1	A	271	GLY	3.1
2	B	72	SER	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	140	PRO	3.0
2	B	81	PHE	3.0
1	A	278	PRO	3.0
1	A	11	GLN	3.0
2	B	52	SER	3.0
1	A	257	ALA	2.9
1	A	105	ASN	2.8
2	B	54	HIS	2.8
1	A	8	PRO	2.8
2	B	76	GLN	2.7
2	B	80	LYS	2.6
2	B	4	GLU	2.6
1	A	16	ALA	2.5
2	B	348	LYS	2.5
1	A	26	GLY	2.4
1	A	13	ARG	2.4
1	A	302	ASN	2.4
1	A	279	LEU	2.4
2	B	452	ALA	2.3
1	A	125[A]	GLN	2.3
2	B	347	ARG	2.3
2	B	3	THR	2.3
1	A	249	LEU	2.3
1	A	276	SER	2.3
1	A	246	VAL	2.3
1	A	101	PHE	2.3
2	B	36	LEU	2.2
2	B	451	VAL	2.2
1	A	100	GLU	2.1
1	A	272	PHE	2.1
2	B	287	SER	2.1
1	A	108	SER	2.1
2	B	255	GLU	2.0
1	A	34	MET	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 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
3	EDO	A	420	4/4	0.64	0.29	51,51,62,75	0
3	EDO	A	423	4/4	0.70	0.25	59,62,68,71	0
3	EDO	A	417	4/4	0.71	0.24	52,57,63,69	0
3	EDO	B	625	4/4	0.72	0.26	43,55,63,69	0
5	3FX	B	604	15/15	0.72	0.19	45,70,102,107	0
3	EDO	B	639	4/4	0.73	0.23	67,73,73,74	0
3	EDO	B	632	4/4	0.74	0.25	48,52,56,61	0
3	EDO	B	637	4/4	0.77	0.19	59,60,65,68	0
3	EDO	B	615	4/4	0.78	0.22	53,53,54,67	0
3	EDO	A	424	4/4	0.79	0.19	44,53,61,70	0
3	EDO	B	620	4/4	0.80	0.19	46,52,55,59	0
3	EDO	B	633	4/4	0.81	0.23	51,54,65,69	0
3	EDO	B	629	4/4	0.81	0.24	52,63,66,68	0
3	EDO	A	414	4/4	0.82	0.24	40,44,59,66	0
3	EDO	B	624	4/4	0.83	0.16	54,54,57,61	0
3	EDO	B	617	4/4	0.83	0.22	36,48,50,65	0
3	EDO	B	618	4/4	0.83	0.17	49,54,59,72	0
3	EDO	A	421	4/4	0.83	0.19	56,65,65,68	0
3	EDO	A	413	4/4	0.84	0.19	46,47,50,62	0
3	EDO	A	418	4/4	0.84	0.15	45,52,52,55	0
3	EDO	A	422	4/4	0.84	0.19	46,49,52,57	0
3	EDO	A	419	4/4	0.84	0.18	47,55,55,65	0
3	EDO	B	631	4/4	0.84	0.21	48,53,59,62	0
3	EDO	B	634	4/4	0.85	0.18	47,49,62,66	0
3	EDO	A	407	4/4	0.85	0.21	45,54,62,66	0
3	EDO	B	638	4/4	0.85	0.16	53,66,67,69	0
3	EDO	A	415	4/4	0.85	0.16	53,54,58,62	0
3	EDO	B	623	4/4	0.85	0.16	41,61,69,73	0
3	EDO	A	402	4/4	0.86	0.15	39,42,45,55	0
3	EDO	B	636	4/4	0.86	0.15	52,57,66,67	0
3	EDO	B	628	4/4	0.86	0.19	52,55,55,65	0
3	EDO	B	622	4/4	0.87	0.18	40,41,45,69	0

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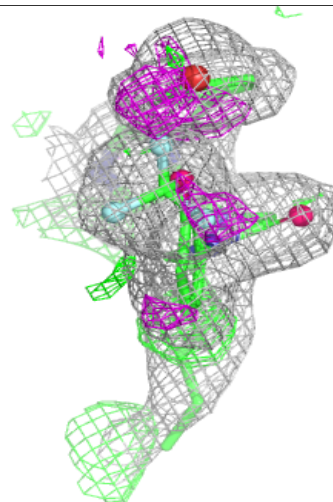
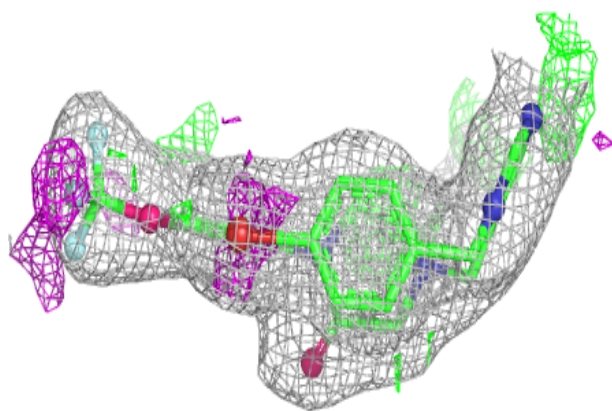
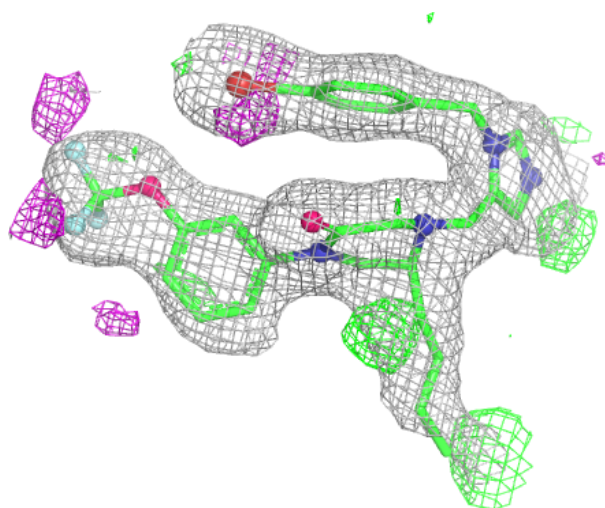
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	EDO	A	416	4/4	0.87	0.17	46,53,66,66	0
3	EDO	B	630	4/4	0.87	0.14	55,61,67,73	0
3	EDO	B	611	4/4	0.87	0.17	38,39,45,53	0
3	EDO	A	412	4/4	0.87	0.17	34,43,45,53	0
3	EDO	B	626	4/4	0.87	0.19	41,46,57,59	0
3	EDO	A	411	4/4	0.88	0.14	46,51,57,59	0
3	EDO	B	616	4/4	0.89	0.15	48,50,52,54	0
3	EDO	B	609	4/4	0.89	0.14	33,44,46,54	0
3	EDO	A	409	4/4	0.89	0.15	43,46,47,51	0
3	EDO	A	425	4/4	0.89	0.17	45,53,57,58	0
3	EDO	B	635	4/4	0.89	0.15	60,61,63,65	0
3	EDO	B	627	4/4	0.90	0.13	46,47,47,57	0
3	EDO	A	406	4/4	0.90	0.14	45,47,50,63	0
3	EDO	A	401	4/4	0.91	0.14	40,49,54,57	0
3	EDO	B	621	4/4	0.91	0.13	44,51,52,54	0
3	EDO	A	426	4/4	0.91	0.14	29,42,53,60	0
3	EDO	B	619	4/4	0.92	0.17	35,38,48,53	0
5	3FX	B	603	15/15	0.92	0.15	36,56,71,76	0
3	EDO	A	410	4/4	0.92	0.14	44,50,54,55	0
3	EDO	B	610	4/4	0.93	0.11	32,41,42,47	0
3	EDO	A	403	4/4	0.93	0.11	42,45,47,50	0
3	EDO	B	612	4/4	0.93	0.12	42,43,46,48	0
3	EDO	B	607	4/4	0.94	0.12	42,43,44,47	0
3	EDO	B	613	4/4	0.94	0.09	36,41,44,47	0
3	EDO	B	614	4/4	0.94	0.15	42,43,49,49	0
3	EDO	A	404	4/4	0.94	0.11	46,48,49,52	0
3	EDO	A	405	4/4	0.94	0.10	39,41,42,51	0
3	EDO	A	408	4/4	0.94	0.09	36,39,41,43	0
6	XMY	B	605	36/36	0.94	0.11	27,38,52,57	0
5	3FX	B	602	15/15	0.95	0.09	23,32,35,38	0
3	EDO	B	608	4/4	0.97	0.07	29,31,33,36	0
7	SO4	B	606	5/5	0.98	0.06	35,39,42,49	0
4	ZN	B	601	1/1	0.99	0.02	30,30,30,30	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 XMY B 605:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.