



Full wwPDB X-ray Structure Validation Report ⓘ

May 23, 2020 – 11:20 pm BST

PDB ID : 6O3F
Title : Crystal Structure of Lysyl-tRNA Synthetase from Chlamydia trachomatis with complexed with L-lysine and a difluoro cyclohexyl chromone ligand
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2019-02-26
Resolution : 2.40 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	:	2.11
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)	:	2.11

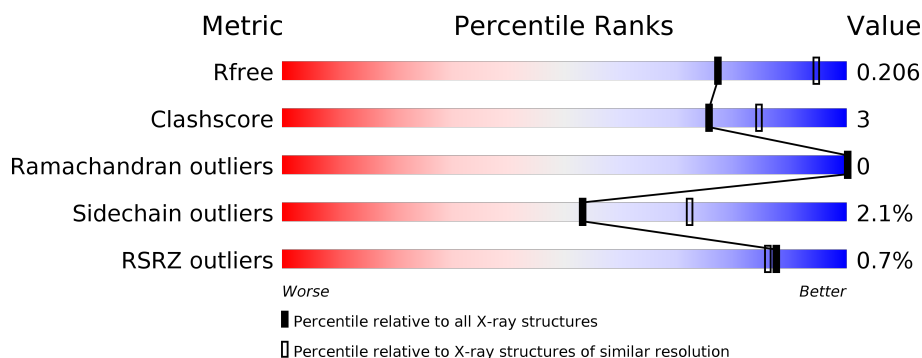
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	529	<div> <div>%</div> <div> <div></div> <div>89%</div> <div>9%</div> <div>.</div> </div> </div>
1	B	529	<div> <div>%</div> <div> <div></div> <div>90%</div> <div>7%</div> <div>..</div> </div> </div>

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 8795 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.

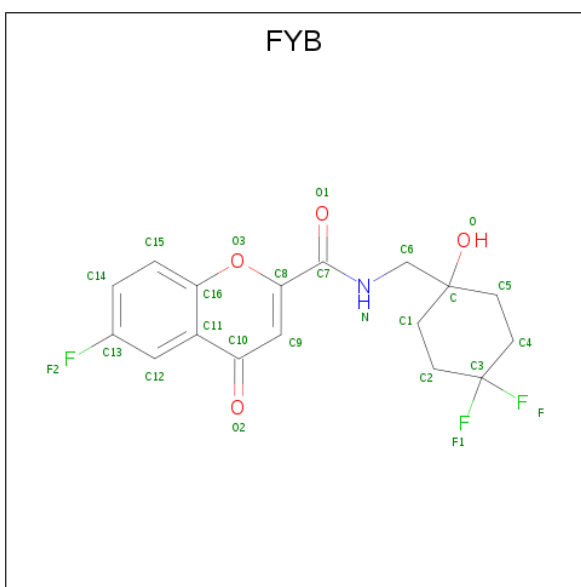
- Molecule 1 is a protein called Lysine-tRNA ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	517	Total	C	N	O	S	0	2	0
			4084	2605	685	772	22			
1	B	517	Total	C	N	O	S	0	3	0
			4086	2608	686	770	22			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	UNP B0BAN6
A	-6	ALA	-	expression tag	UNP B0BAN6
A	-5	HIS	-	expression tag	UNP B0BAN6
A	-4	HIS	-	expression tag	UNP B0BAN6
A	-3	HIS	-	expression tag	UNP B0BAN6
A	-2	HIS	-	expression tag	UNP B0BAN6
A	-1	HIS	-	expression tag	UNP B0BAN6
A	0	HIS	-	expression tag	UNP B0BAN6
B	-7	MET	-	initiating methionine	UNP B0BAN6
B	-6	ALA	-	expression tag	UNP B0BAN6
B	-5	HIS	-	expression tag	UNP B0BAN6
B	-4	HIS	-	expression tag	UNP B0BAN6
B	-3	HIS	-	expression tag	UNP B0BAN6
B	-2	HIS	-	expression tag	UNP B0BAN6
B	-1	HIS	-	expression tag	UNP B0BAN6
B	0	HIS	-	expression tag	UNP B0BAN6

- Molecule 2 is {N}-[[4,4-bis(fluoranyl)-1-oxidanyl-cyclohexyl]methyl]-6-fluoranyl-4-oxidanylidene-chromene-2-carboxamide (three-letter code: FYB) (formula: C₁₇H₁₆F₃NO₄).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			25	17	3	1	4		
2	B	1	Total	C	F	N	O	0	0
			25	17	3	1	4		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: 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		

Continued on next page...

Continued from previous page...

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	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
3	B	1	Total 4	C 2	O 2	0	0

Continued on next page...

Continued from previous page...

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		
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 SULFATE ION (three-letter code: SO4) (formula: O₄S).



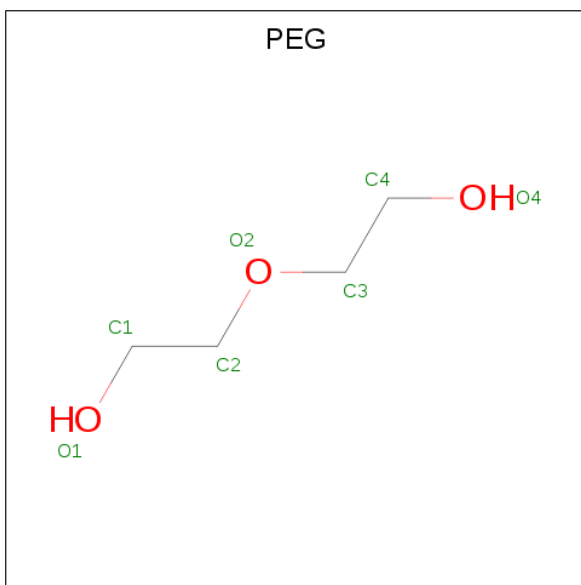
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		

Continued on next page...

Continued from previous page...

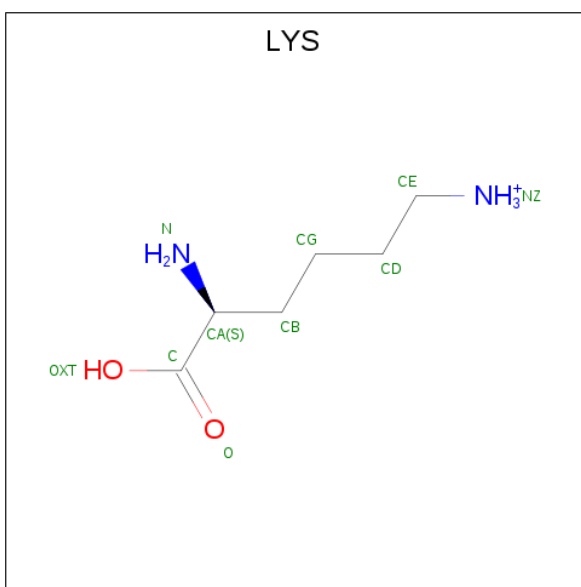
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



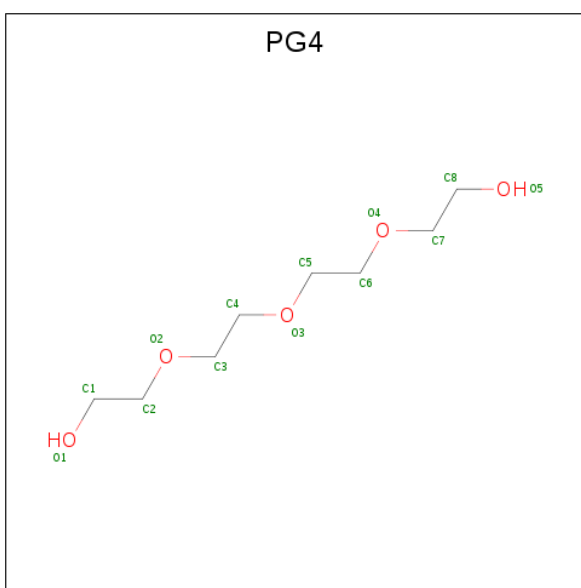
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is LYSINE (three-letter code: LYS) (formula: $C_6H_{15}N_2O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			10	6	2	2		
6	B	1	Total	C	N	O	0	0
			10	6	2	2		

- Molecule 7 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C₈H₁₈O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			13	8	5		

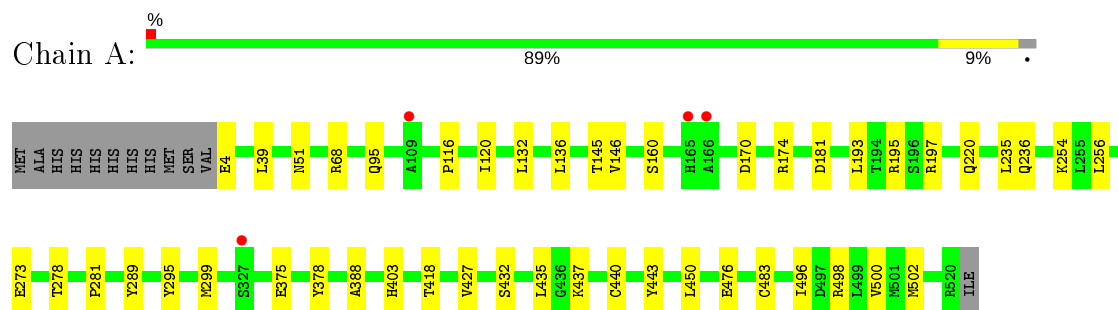
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	193	Total 195	O 195	0	2
8	B	176	Total 178	O 178	0	2

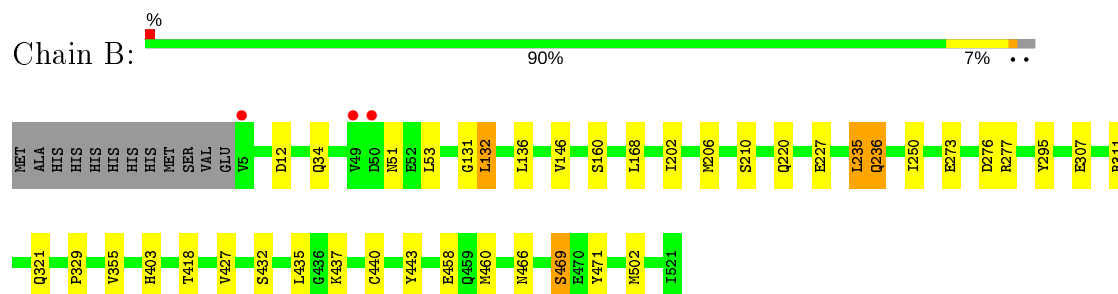
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Lysine-tRNA ligase



• Molecule 1: Lysine-tRNA ligase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	95.49 Å 57.28 Å 138.19 Å 90.00° 95.19° 90.00°	Depositor
Resolution (Å)	45.55 – 2.40 49.07 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.8 (45.55-2.40) 99.8 (49.07-2.40)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.33 (at 2.39 Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.163 , 0.205 0.163 , 0.206	Depositor DCC
R_{free} test set	1969 reflections (3.35%)	wwPDB-VP
Wilson B-factor (Å ²)	36.2	Xtriage
Anisotropy	0.469	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 59.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8795	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.04% 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: FYB, PG4, PEG, EDO, SO4

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	0.40	0/4171	0.56	0/5653
1	B	0.40	0/4176	0.58	2/5658 (0.0%)
All	All	0.40	0/8347	0.57	2/11311 (0.0%)

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
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	132	LEU	CA-CB-CG	-5.76	102.04	115.30
1	B	471	TYR	C-N-CA	-5.09	108.96	121.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	443	TYR	Peptide
1	B	443	TYR	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	4084	0	4001	28	0
1	B	4086	0	4022	23	0
2	A	25	0	0	0	0
2	B	25	0	0	0	0
3	A	52	0	77	10	0
3	B	68	0	102	8	0
4	A	20	0	0	1	0
4	B	15	0	0	1	0
5	A	7	0	10	0	0
5	B	7	0	10	0	0
6	A	10	0	12	0	0
6	B	10	0	12	0	0
7	B	13	0	18	2	0
8	A	195	0	0	1	0
8	B	178	0	0	2	0
All	All	8795	0	8264	51	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 (51) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:160[A]:SER:H	3:B:719:EDO:H21	1.45	0.82
1:B:160[B]:SER:H	3:B:719:EDO:H21	1.45	0.82
1:B:307:GLU:OE1	1:B:311:ARG:NH1	2.21	0.73
1:A:476:GLU:HB2	3:A:706:EDO:H21	1.75	0.67
1:B:236:GLN:NE2	8:B:803:HOH:O	2.34	0.61
1:A:197[B]:ARG:HD2	3:A:719:EDO:H11	1.84	0.59
1:A:450:LEU:HD23	3:A:712:EDO:H11	1.84	0.59
1:B:432:SER:HB2	1:B:440:CYS:HB3	1.85	0.57
1:A:483:CYS:SG	3:A:712:EDO:H22	2.44	0.57
1:A:136:LEU:HD23	1:A:146:VAL:HG22	1.87	0.56
1:B:12:ASP:HB3	3:B:719:EDO:O2	2.06	0.55
1:A:4:GLU:N	8:A:806:HOH:O	2.42	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:277:ARG:HG3	3:B:714:EDO:H21	1.91	0.52
1:A:95:GLN:HG2	1:A:145:THR:HG23	1.91	0.52
1:A:68:ARG:HG3	3:A:714:EDO:H12	1.90	0.52
1:B:220:GLN:HA	3:B:707:EDO:H12	1.92	0.52
1:B:466:ASN:HB3	1:B:469:SER:HB2	1.93	0.51
1:A:256:LEU:HD11	1:A:289:TYR:HB3	1.92	0.50
1:A:116:PRO:O	1:A:120:ILE:HG13	2.12	0.49
1:A:435:LEU:HD12	1:A:502:MET:HG2	1.94	0.49
1:B:321:GLN:HE21	1:B:329:PRO:HB3	1.78	0.48
1:B:136:LEU:HD23	1:B:146:VAL:HG22	1.95	0.48
3:B:706:EDO:H22	8:B:893:HOH:O	2.14	0.48
1:A:299:MET:SD	3:A:709:EDO:H21	2.54	0.47
1:A:278:THR:HG21	1:A:437:LYS:HD2	1.97	0.46
1:A:496:ILE:O	1:A:500:VAL:HG23	2.15	0.46
1:B:403:HIS:O	1:B:432:SER:HA	2.16	0.46
1:A:388:ALA:HB1	3:A:707:EDO:H21	1.98	0.46
1:A:403:HIS:O	1:A:432:SER:HA	2.16	0.46
1:B:34:GLN:HG2	3:B:720:EDO:H12	1.98	0.44
1:A:498:ARG:NH1	4:A:711:SO4:O1	2.50	0.44
1:B:276:ASP:C	3:B:714:EDO:H12	2.38	0.44
1:B:168:LEU:N	4:B:712:SO4:O4	2.36	0.44
1:A:39:LEU:HA	1:A:39:LEU:HD23	1.66	0.44
1:A:254:LYS:NZ	3:A:718:EDO:H11	2.33	0.44
1:A:281:PRO:HG2	1:B:235:LEU:HD11	1.99	0.44
1:B:435:LEU:HD12	1:B:502:MET:HG2	2.00	0.43
1:A:195:ARG:HG3	1:A:500:VAL:HG21	1.99	0.43
1:A:432:SER:HB2	1:A:440:CYS:HB3	2.00	0.43
1:A:418:THR:HA	1:A:427:VAL:HA	1.99	0.43
1:A:160:SER:OG	3:A:716:EDO:H21	2.19	0.43
1:A:375:GLU:HA	1:A:378:TYR:CE2	2.54	0.42
1:B:250:ILE:HD11	7:B:715:PG4:H21	2.01	0.42
1:B:437:LYS:HA	1:B:437:LYS:HD3	1.82	0.41
1:A:220:GLN:HG2	3:A:705:EDO:H12	2.03	0.41
1:B:418:THR:HA	1:B:427:VAL:HA	2.03	0.41
1:A:193:LEU:O	1:A:197[A]:ARG:HG3	2.20	0.41
1:B:227:GLU:HG2	7:B:715:PG4:H62	2.03	0.41
1:B:202:ILE:O	1:B:206:MET:HG2	2.20	0.41
1:B:131:GLY:C	1:B:132:LEU:HG	2.41	0.40
1:A:170:ASP:O	1:A:174:ARG:HG3	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	517/529 (98%)	508 (98%)	9 (2%)	0	100	100
1	B	518/529 (98%)	511 (99%)	7 (1%)	0	100	100
All	All	1035/1058 (98%)	1019 (98%)	16 (2%)	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	436/465 (94%)	429 (98%)	7 (2%)	62	79
1	B	438/465 (94%)	427 (98%)	11 (2%)	47	67
All	All	874/930 (94%)	856 (98%)	18 (2%)	53	72

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

Mol	Chain	Res	Type
1	A	51	ASN
1	A	132	LEU
1	A	181	ASP
1	A	235	LEU
1	A	236	GLN
1	A	273	GLU
1	A	295	TYR
1	B	51	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	53	LEU
1	B	210	SER
1	B	235	LEU
1	B	236	GLN
1	B	273	GLU
1	B	295	TYR
1	B	355	VAL
1	B	458	GLU
1	B	460	MET
1	B	469	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	51	ASN
1	B	321	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

44 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
4	SO4	B	716	-	4,4,4	0.13	0	6,6,6	0.11	0
3	EDO	A	708	-	3,3,3	0.65	0	2,2,2	0.04	0
4	SO4	B	712	-	4,4,4	0.15	0	6,6,6	0.50	0
4	SO4	A	717	-	4,4,4	0.14	0	6,6,6	0.09	0
3	EDO	B	711	-	3,3,3	0.44	0	2,2,2	0.47	0
3	EDO	A	702	-	3,3,3	0.77	0	2,2,2	0.21	0
3	EDO	B	703	-	3,3,3	0.49	0	2,2,2	0.09	0
3	EDO	A	718	-	3,3,3	0.51	0	2,2,2	0.28	0
5	PEG	A	713	-	6,6,6	0.22	0	5,5,5	0.23	0
3	EDO	A	714	-	3,3,3	0.42	0	2,2,2	0.46	0
3	EDO	B	705	-	3,3,3	0.52	0	2,2,2	0.58	0
3	EDO	B	708	-	3,3,3	0.37	0	2,2,2	0.57	0
3	EDO	A	719	-	3,3,3	0.53	0	2,2,2	0.26	0
3	EDO	B	707	-	3,3,3	0.35	0	2,2,2	0.75	0
3	EDO	A	716	-	3,3,3	0.47	0	2,2,2	0.22	0
4	SO4	A	715	-	4,4,4	0.13	0	6,6,6	0.16	0
3	EDO	A	704	-	3,3,3	0.45	0	2,2,2	0.33	0
4	SO4	A	711	-	4,4,4	0.13	0	6,6,6	0.12	0
3	EDO	B	704	-	3,3,3	0.37	0	2,2,2	0.73	0
2	FYB	B	702	-	23,27,27	0.97	1 (4%)	25,41,41	2.78	5 (20%)
7	PG4	B	715	-	12,12,12	0.17	0	11,11,11	0.17	0
3	EDO	B	723	-	3,3,3	0.50	0	2,2,2	0.28	0
3	EDO	B	713	-	3,3,3	0.45	0	2,2,2	0.26	0
4	SO4	B	709	-	4,4,4	0.16	0	6,6,6	0.11	0
3	EDO	B	706	-	3,3,3	0.74	0	2,2,2	0.46	0
4	SO4	A	710	-	4,4,4	0.14	0	6,6,6	0.20	0
3	EDO	A	709	-	3,3,3	0.59	0	2,2,2	0.06	0
3	EDO	B	710	-	3,3,3	0.52	0	2,2,2	0.38	0
3	EDO	B	722	-	3,3,3	0.49	0	2,2,2	0.21	0
5	PEG	B	718	-	6,6,6	0.21	0	5,5,5	0.12	0
3	EDO	A	707	-	3,3,3	0.45	0	2,2,2	0.46	0
3	EDO	B	719	-	3,3,3	0.48	0	2,2,2	0.20	0
3	EDO	B	720	-	3,3,3	0.49	0	2,2,2	0.28	0
3	EDO	B	701	-	3,3,3	0.33	0	2,2,2	0.62	0
3	EDO	B	721	-	3,3,3	0.47	0	2,2,2	0.47	0
3	EDO	A	706	-	3,3,3	0.45	0	2,2,2	0.41	0
3	EDO	B	714	-	3,3,3	0.51	0	2,2,2	0.22	0
3	EDO	A	705	-	3,3,3	0.54	0	2,2,2	0.20	0
2	FYB	A	701	-	23,27,27	0.97	1 (4%)	25,41,41	1.99	4 (16%)
3	EDO	A	712	-	3,3,3	0.30	0	2,2,2	0.82	0
3	EDO	A	703	-	3,3,3	0.44	0	2,2,2	0.58	0
3	EDO	B	717	-	3,3,3	0.43	0	2,2,2	0.61	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	A	708	-	-	1/1/1/1	-
3	EDO	B	711	-	-	0/1/1/1	-
3	EDO	A	702	-	-	0/1/1/1	-
3	EDO	B	703	-	-	0/1/1/1	-
3	EDO	A	718	-	-	0/1/1/1	-
5	PEG	B	718	-	-	0/4/4/4	-
3	EDO	A	714	-	-	0/1/1/1	-
3	EDO	B	705	-	-	1/1/1/1	-
3	EDO	A	703	-	-	1/1/1/1	-
3	EDO	A	719	-	-	1/1/1/1	-
3	EDO	B	707	-	-	0/1/1/1	-
3	EDO	A	716	-	-	0/1/1/1	-
3	EDO	A	704	-	-	0/1/1/1	-
3	EDO	B	704	-	-	1/1/1/1	-
2	FYB	B	702	-	-	0/8/24/24	0/3/3/3
7	PG4	B	715	-	-	3/10/10/10	-
3	EDO	B	723	-	-	1/1/1/1	-
3	EDO	B	713	-	-	0/1/1/1	-
3	EDO	B	706	-	-	0/1/1/1	-
3	EDO	A	709	-	-	0/1/1/1	-
3	EDO	B	710	-	-	0/1/1/1	-
3	EDO	B	722	-	-	1/1/1/1	-
5	PEG	A	713	-	-	2/4/4/4	-
3	EDO	A	707	-	-	0/1/1/1	-
3	EDO	B	719	-	-	0/1/1/1	-
3	EDO	B	720	-	-	0/1/1/1	-
3	EDO	B	701	-	-	1/1/1/1	-
3	EDO	B	721	-	-	1/1/1/1	-
3	EDO	A	706	-	-	1/1/1/1	-
3	EDO	B	714	-	-	1/1/1/1	-
3	EDO	A	705	-	-	1/1/1/1	-
2	FYB	A	701	-	-	0/8/24/24	0/3/3/3
3	EDO	A	712	-	-	0/1/1/1	-
3	EDO	B	708	-	-	1/1/1/1	-
3	EDO	B	717	-	-	0/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	702	FYB	C9-C10	3.25	1.44	1.37
2	A	701	FYB	C9-C10	3.23	1.44	1.37

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	702	FYB	C1-C2-C3	-8.83	105.69	110.93
2	A	701	FYB	C9-C10-C11	-7.05	115.24	123.05
2	B	702	FYB	C9-C10-C11	-6.91	115.40	123.05
2	B	702	FYB	C5-C4-C3	-6.75	106.93	110.93
2	A	701	FYB	C1-C2-C3	-5.04	107.94	110.93
2	A	701	FYB	O3-C8-C9	3.41	123.40	119.15
2	B	702	FYB	O3-C8-C9	3.25	123.20	119.15
2	A	701	FYB	C12-C11-C16	2.24	118.91	116.39
2	B	702	FYB	C12-C11-C16	2.07	118.72	116.39

There are no chirality outliers.

All (18) torsion outliers are listed below:

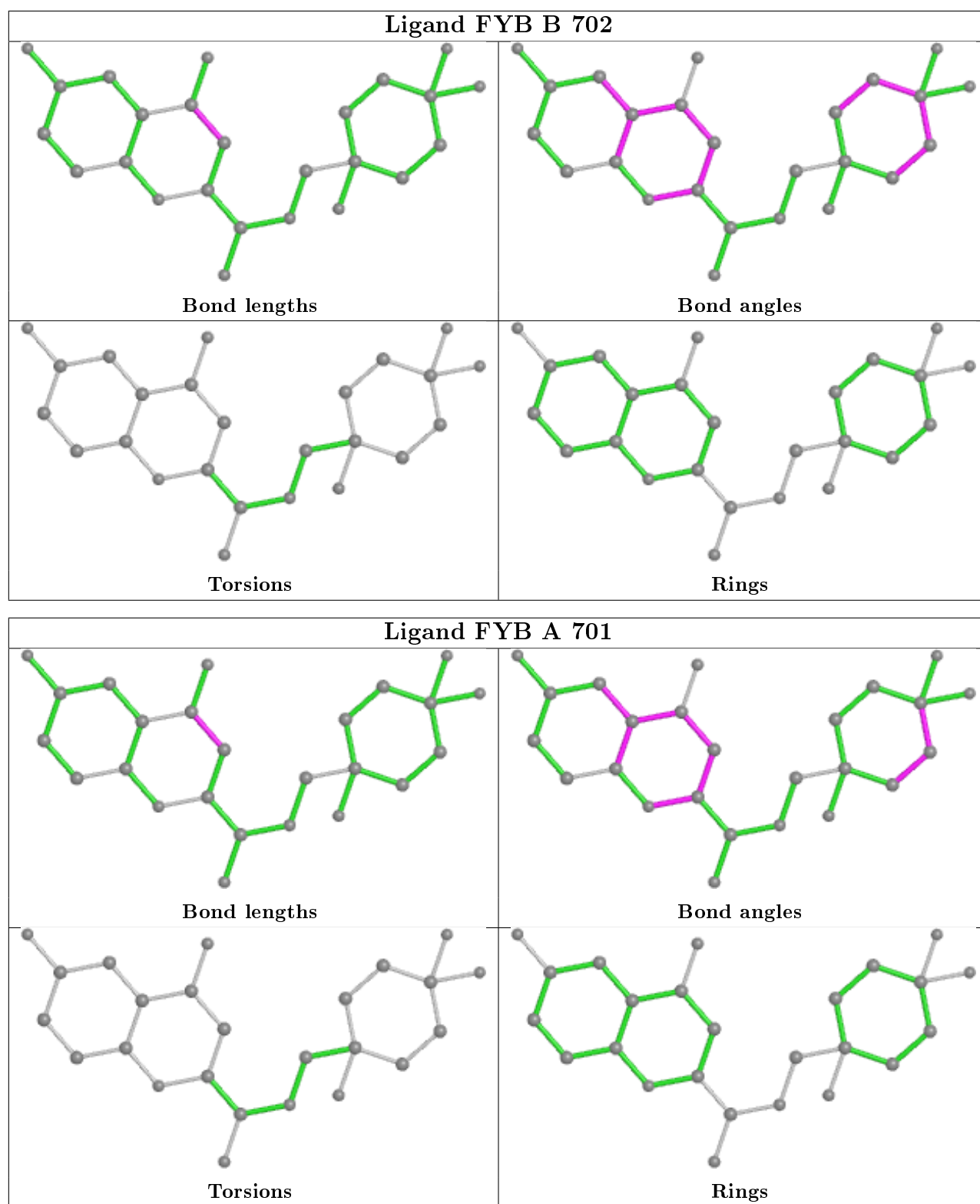
Mol	Chain	Res	Type	Atoms
3	B	701	EDO	O1-C1-C2-O2
3	A	706	EDO	O1-C1-C2-O2
3	A	708	EDO	O1-C1-C2-O2
3	B	705	EDO	O1-C1-C2-O2
3	B	722	EDO	O1-C1-C2-O2
3	B	714	EDO	O1-C1-C2-O2
3	A	719	EDO	O1-C1-C2-O2
3	A	705	EDO	O1-C1-C2-O2
7	B	715	PG4	C1-C2-O2-C3
5	A	713	PEG	O2-C3-C4-O4
5	A	713	PEG	C4-C3-O2-C2
3	A	703	EDO	O1-C1-C2-O2
3	B	723	EDO	O1-C1-C2-O2
3	B	708	EDO	O1-C1-C2-O2
7	B	715	PG4	O3-C5-C6-O4
3	B	704	EDO	O1-C1-C2-O2
7	B	715	PG4	O2-C3-C4-O3
3	B	721	EDO	O1-C1-C2-O2

There are no ring outliers.

17 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	712	SO4	1	0
3	A	718	EDO	1	0
3	A	714	EDO	1	0
3	A	719	EDO	1	0
3	B	707	EDO	1	0
3	A	716	EDO	1	0
4	A	711	SO4	1	0
7	B	715	PG4	2	0
3	B	706	EDO	1	0
3	A	709	EDO	1	0
3	A	707	EDO	1	0
3	B	719	EDO	3	0
3	B	720	EDO	1	0
3	A	706	EDO	1	0
3	B	714	EDO	2	0
3	A	705	EDO	1	0
3	A	712	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	517/529 (97%)	-0.55	4 (0%) 86 84	22, 39, 71, 108	0
1	B	517/529 (97%)	-0.44	3 (0%) 89 88	27, 40, 67, 114	0
All	All	1034/1058 (97%)	-0.49	7 (0%) 87 86	22, 39, 69, 114	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	49	VAL	3.1
1	B	5	VAL	3.1
1	B	50	ASP	2.5
1	A	327	SER	2.4
1	A	166	ALA	2.1
1	A	109	ALA	2.1
1	A	165	HIS	2.1

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	EDO	A	709	4/4	0.61	0.26	63,65,68,68	0
3	EDO	A	702	4/4	0.75	0.26	41,48,52,54	0
4	SO4	A	717	5/5	0.81	0.33	155,157,157,158	0
3	EDO	B	711	4/4	0.81	0.25	68,68,69,70	0
3	EDO	B	710	4/4	0.83	0.22	56,60,64,65	0
3	EDO	A	705	4/4	0.83	0.27	56,56,57,57	0
3	EDO	B	722	4/4	0.84	0.41	59,61,65,68	0
3	EDO	A	714	4/4	0.84	0.19	71,72,72,75	0
3	EDO	A	708	4/4	0.85	0.29	50,57,63,64	0
3	EDO	B	721	4/4	0.86	0.29	69,72,74,74	0
3	EDO	A	719	4/4	0.86	0.21	48,50,58,63	0
3	EDO	B	706	4/4	0.87	0.17	35,38,45,56	0
3	EDO	B	705	4/4	0.87	0.15	39,41,43,50	0
5	PEG	B	718	7/7	0.87	0.19	54,59,72,74	0
3	EDO	B	714	4/4	0.88	0.23	47,55,57,60	0
3	EDO	B	708	4/4	0.88	0.22	57,60,65,71	0
3	EDO	B	719	4/4	0.89	0.34	60,66,77,83	0
3	EDO	A	707	4/4	0.89	0.14	55,59,67,67	0
3	EDO	A	706	4/4	0.89	0.20	70,71,71,72	0
3	EDO	B	723	4/4	0.90	0.21	53,57,58,61	0
4	SO4	B	709	5/5	0.90	0.17	120,121,122,123	0
4	SO4	A	715	5/5	0.90	0.31	135,138,139,139	0
4	SO4	A	711	5/5	0.90	0.19	128,129,131,131	0
3	EDO	B	720	4/4	0.90	0.23	56,64,69,71	0
3	EDO	B	717	4/4	0.90	0.11	67,67,68,70	0
7	PG4	B	715	13/13	0.91	0.15	55,62,70,70	0
3	EDO	A	718	4/4	0.91	0.21	38,40,49,54	0
3	EDO	B	707	4/4	0.92	0.25	59,63,68,79	0
3	EDO	B	713	4/4	0.93	0.25	59,62,66,69	0
3	EDO	A	704	4/4	0.93	0.30	54,57,65,68	0
3	EDO	A	716	4/4	0.93	0.18	56,59,60,62	0
4	SO4	A	710	5/5	0.93	0.31	85,91,96,98	0
5	PEG	A	713	7/7	0.94	0.18	47,55,62,63	0
4	SO4	B	716	5/5	0.94	0.35	96,97,103,105	0
3	EDO	B	701	4/4	0.94	0.19	42,43,49,62	0
3	EDO	B	704	4/4	0.95	0.22	42,47,51,63	0
3	EDO	A	703	4/4	0.96	0.16	26,35,38,48	0
3	EDO	B	703	4/4	0.97	0.20	46,47,49,52	0
3	EDO	A	712	4/4	0.97	0.12	50,51,52,55	0
2	FYB	B	702	25/25	0.97	0.13	29,37,42,44	0
6	LYS	B	724	10/10	0.97	0.14	29,29,33,35	0
6	LYS	A	720	10/10	0.98	0.11	21,26,29,34	0
4	SO4	B	712	5/5	0.98	0.24	37,50,56,57	0

Continued on next page...

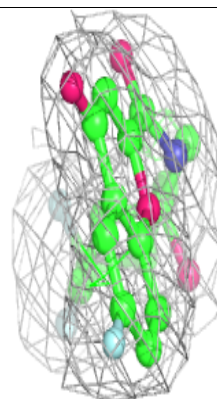
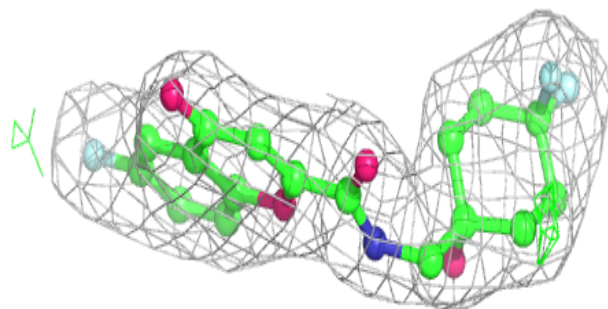
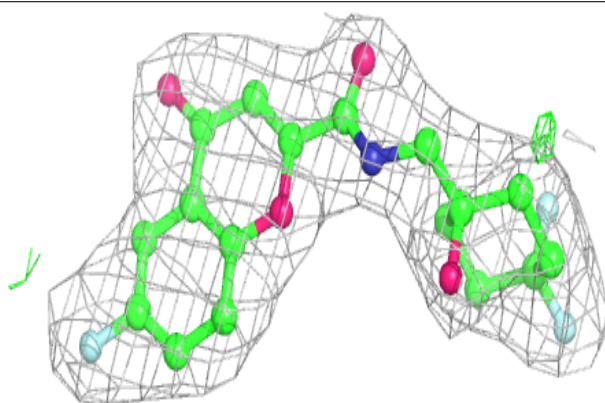
Continued from previous page...

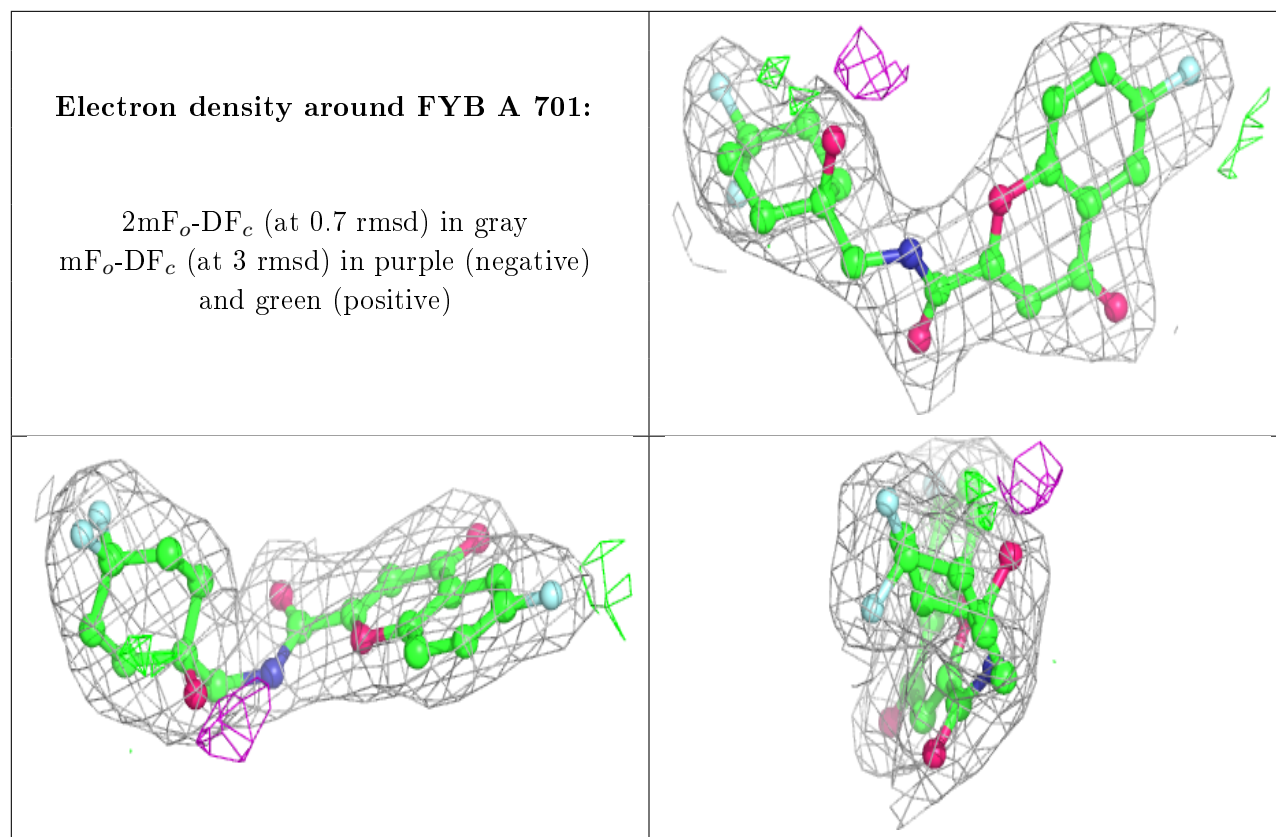
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	FYB	A	701	25/25	0.98	0.10	27,34,40,42	0

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 FYB B 702:

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.