



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 18, 2025 – 12:10 AM JST

PDB ID : 9LFY / pdb\_00009lfy  
Title : Complex crystal structure of transaldolase AprG with GalNAc from Streptococcus tenebrarius  
Authors : Xie, Z.Z.; Li, Q.R.; Zhang, L.L.; Huang, J.-W.; He, Y.T.; Chen, C.-C.; Guo, R.-T.  
Deposited on : 2025-01-09  
Resolution : 2.15 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](mailto: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>.

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

MolProbity	:	4-5-2 with Phenix2.0rc1
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.45.1

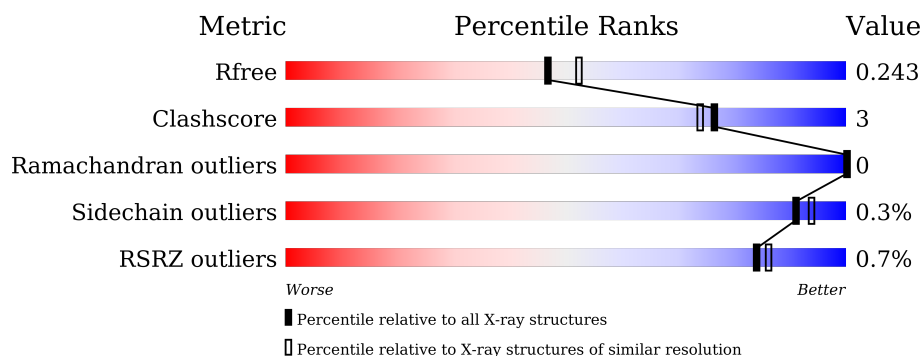
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.15 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))
$R_{free}$	164625	1881 (2.16-2.16)
Clashscore	180529	2047 (2.16-2.16)
Ramachandran outliers	177936	2027 (2.16-2.16)
Sidechain outliers	177891	2026 (2.16-2.16)
RSRZ outliers	164620	1882 (2.16-2.16)

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  $\geq 3$ , 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	345	<div> <div>%</div> <div> <div></div> <div>89%</div> <div>7%</div> <div>.</div> </div> </div>
1	B	345	<div> <div>%</div> <div> <div></div> <div>89%</div> <div>9%</div> <div>.</div> </div> </div>
1	C	345	<div> <div>%</div> <div> <div></div> <div>93%</div> <div>6%</div> <div>.</div> </div> </div>
1	D	345	<div> <div>%</div> <div> <div></div> <div>92%</div> <div>6%</div> <div>.</div> </div> </div>
1	E	345	<div> <div></div> <div> <div></div> <div>90%</div> <div>7%</div> <div>.</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	345	<div><div>%</div><div><div></div><div>86%</div><div>11%</div><div></div></div><div></div></div>

## 2 Entry composition [i](#)

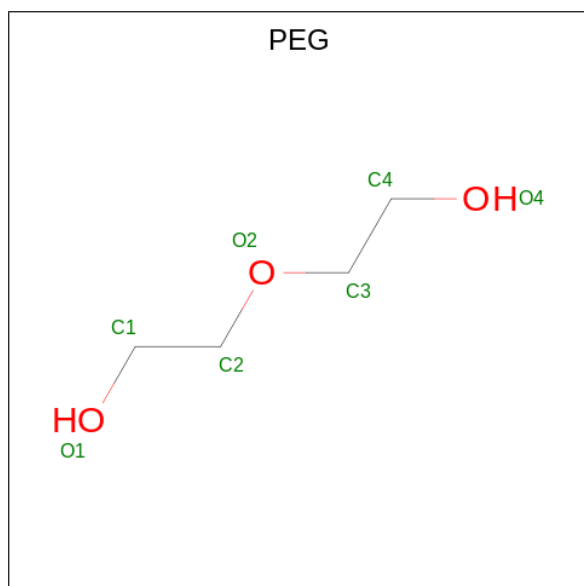
There are 3 unique types of molecules in this entry. The entry contains 16232 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 AprG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	333	Total	C	N	O	S	0	0	0
			2585	1627	446	501	11			
1	B	336	Total	C	N	O	S	0	0	0
			2599	1634	449	505	11			
1	C	341	Total	C	N	O	S	0	0	0
			2630	1654	455	510	11			
1	D	335	Total	C	N	O	S	0	0	0
			2598	1635	449	503	11			
1	E	333	Total	C	N	O	S	0	0	0
			2585	1627	446	501	11			
1	F	333	Total	C	N	O	S	0	0	0
			2585	1627	446	501	11			

- Molecule 2 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			7	4	3		
2	D	1	Total	C	O	0	0
			7	4	3		
2	E	1	Total	C	O	0	0
			7	4	3		

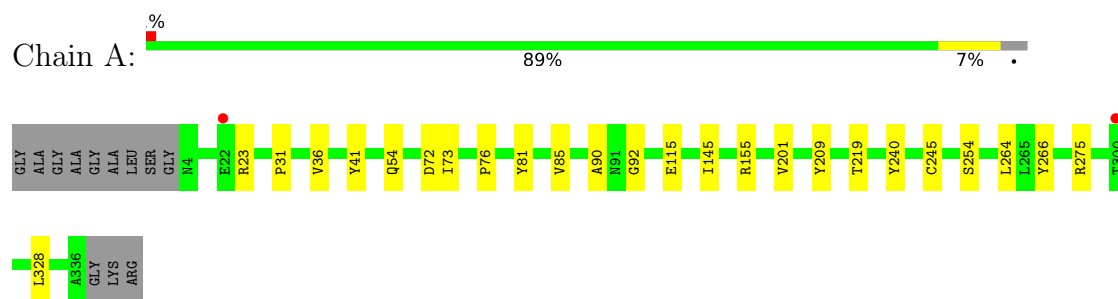
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	106	Total	O	0	0
			106	106		
3	B	127	Total	O	0	0
			127	127		
3	C	98	Total	O	0	0
			98	98		
3	D	102	Total	O	0	0
			102	102		
3	E	117	Total	O	0	0
			117	117		
3	F	79	Total	O	0	0
			79	79		

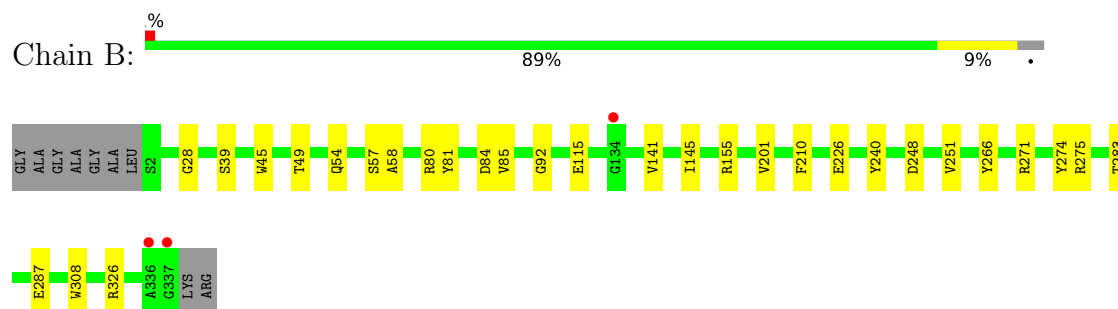
### 3 Residue-property plots [i](#)

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.

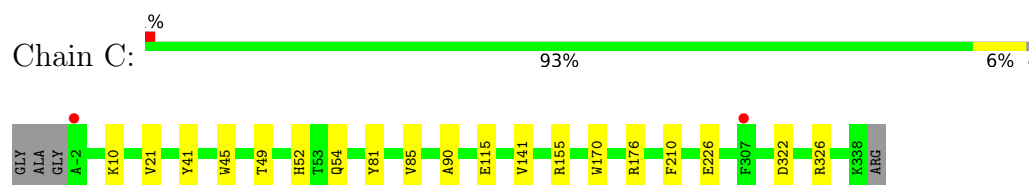
#### • Molecule 1: AprG



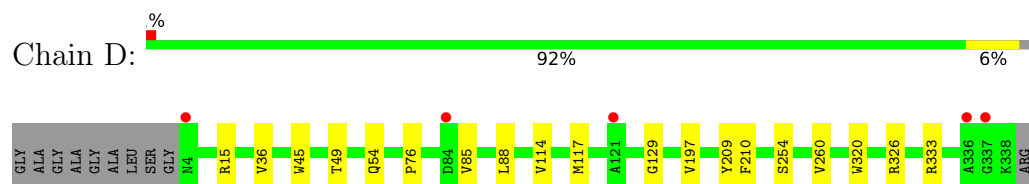
#### • Molecule 1: AprG



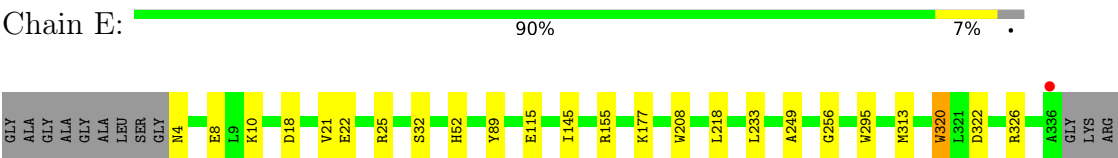
#### • Molecule 1: AprG



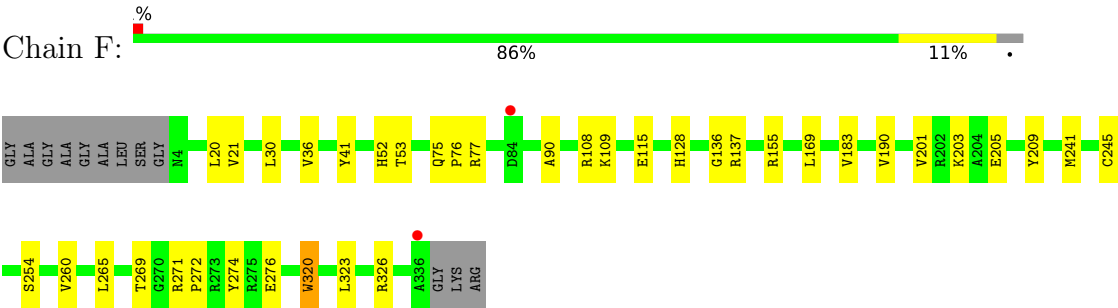
#### • Molecule 1: AprG



#### • Molecule 1: AprG



● Molecule 1: AprG



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.89Å 141.23Å 129.33Å 90.00° 101.49° 90.00°	Depositor
Resolution (Å)	31.68 – 2.15 31.68 – 2.15	Depositor EDS
% Data completeness (in resolution range)	93.3 (31.68-2.15) 93.3 (31.68-2.15)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.63 (at 2.16Å)	Xtriage
Refinement program	PHENIX (1.21.1_5286: ???)	Depositor
R, $R_{free}$	0.206 , 0.243 0.206 , 0.243	Depositor DCC
$R_{free}$ test set	5080 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.7	Xtriage
Anisotropy	0.192	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 37.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.105 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	16232	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PEG, A1EJZ

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	0.10	0/2623	0.27	0/3570
1	B	0.12	0/2637	0.27	0/3588
1	C	0.11	0/2668	0.26	0/3629
1	D	0.11	0/2636	0.27	0/3586
1	E	0.11	0/2623	0.27	0/3570
1	F	0.12	0/2623	0.28	0/3570
All	All	0.11	0/15810	0.27	0/21513

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [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	2585	0	2438	15	0
1	B	2599	0	2449	16	0
1	C	2630	0	2489	13	0
1	D	2598	0	2454	13	0
1	E	2585	0	2438	13	0
1	F	2585	0	2438	22	0
2	B	7	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	7	0	10	0	0
2	E	7	0	10	0	0
3	A	106	0	0	0	0
3	B	127	0	0	0	0
3	C	98	0	0	0	0
3	D	102	0	0	2	0
3	E	117	0	0	0	0
3	F	79	0	0	0	0
All	All	16232	0	14736	84	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 (84) 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:F:128:HIS:HE1	1:F:136:GLY:H	1.31	0.76
1:F:36:VAL:HA	1:F:76:PRO:HB2	1.69	0.74
1:B:248:ASP:HA	1:B:251:VAL:HG22	1.72	0.71
1:D:15:ARG:NH2	3:D:501:HOH:O	2.29	0.66
1:C:326:ARG:HD2	1:F:53:THR:HB	1.81	0.63
1:C:170:TRP:O	1:C:176:ARG:NH2	2.37	0.58
1:F:20:LEU:HD22	1:F:30:LEU:HD13	1.88	0.56
1:C:226:GLU:OE1	1:F:109:LYS:NZ	2.28	0.55
1:F:241:MET:HA	1:F:245:CYS:SG	2.47	0.54
1:F:269:THR:HB	1:F:271:ARG:HH11	1.72	0.53
1:E:295:TRP:HB3	1:E:313:MET:HE3	1.90	0.53
1:A:219:THR:HG22	1:A:264:LEU:HD22	1.92	0.52
1:D:333:ARG:NH2	3:D:504:HOH:O	2.42	0.52
1:F:137:ARG:HD3	1:F:183:VAL:HG11	1.91	0.51
1:F:75:GLN:OE1	1:F:77:ARG:N	2.32	0.51
1:B:45:TRP:O	1:B:49:THR:HG23	2.10	0.51
1:B:54:GLN:HG2	1:D:326:ARG:HA	1.93	0.51
1:B:283:THR:O	1:B:287:GLU:HG3	2.12	0.50
1:B:326:ARG:HA	1:D:54:GLN:HG2	1.95	0.49
1:A:54:GLN:HG2	1:E:326:ARG:HA	1.95	0.49
1:C:115:GLU:OE2	1:C:155:ARG:NH2	2.45	0.49
1:A:209:TYR:HB3	1:A:254:SER:HB2	1.94	0.48
1:C:54:GLN:HG2	1:F:326:ARG:HA	1.95	0.48
1:E:4:ASN:HB3	1:E:8:GLU:HB2	1.95	0.48
1:E:10:LYS:NZ	1:E:322:ASP:OD2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:VAL:HG21	1:A:240:TYR:OH	2.13	0.48
1:D:88:LEU:HD22	1:D:114:VAL:HG22	1.95	0.48
1:B:39:SER:HB3	1:B:308:TRP:HB2	1.96	0.47
1:C:41:TYR:CD2	1:C:90:ALA:HA	2.49	0.47
1:A:36:VAL:HA	1:A:76:PRO:HG2	1.95	0.47
1:C:81:TYR:HA	1:C:85:VAL:HB	1.97	0.47
1:E:25:ARG:NH2	1:E:32:SER:O	2.47	0.47
1:A:266:TYR:CZ	1:A:275:ARG:HD3	2.50	0.47
1:B:141:VAL:HG23	1:B:210:PHE:HA	1.96	0.47
1:D:117:MET:HE1	1:D:129:GLY:HA2	1.98	0.46
1:C:326:ARG:CD	1:F:53:THR:HB	2.45	0.46
1:D:85:VAL:HG13	1:D:197:VAL:HG21	1.98	0.46
1:B:28:GLY:HA2	1:B:58:ALA:HB1	1.97	0.46
1:B:80:ARG:HD2	1:B:84:ASP:OD1	2.16	0.46
1:E:18:ASP:O	1:E:22:GLU:HG2	2.16	0.46
1:E:115:GLU:OE1	1:E:155:ARG:HD3	2.16	0.45
1:F:203:LYS:HB3	1:F:205:GLU:HG3	1.97	0.45
1:B:115:GLU:OE1	1:B:155:ARG:NH1	2.49	0.45
1:C:21:VAL:HG21	1:C:52:HIS:CG	2.52	0.45
1:A:275:ARG:HG3	1:A:328:LEU:HD22	1.98	0.45
1:C:45:TRP:O	1:C:49:THR:HG23	2.17	0.45
1:F:128:HIS:CE1	1:F:136:GLY:H	2.22	0.45
1:D:45:TRP:O	1:D:49:THR:HG23	2.17	0.44
1:E:89:TYR:HA	1:E:145:ILE:HG21	2.00	0.44
1:A:266:TYR:CD2	1:A:275:ARG:HB2	2.53	0.44
1:C:141:VAL:HG23	1:C:210:PHE:HA	1.98	0.44
1:F:108:ARG:NH2	1:F:109:LYS:HE3	2.32	0.44
1:A:201:VAL:HG13	1:A:245:CYS:HA	1.99	0.44
1:A:72:ASP:OD1	1:A:73:ILE:N	2.50	0.43
1:F:21:VAL:HG21	1:F:52:HIS:CG	2.53	0.43
1:C:10:LYS:NZ	1:C:322:ASP:OD2	2.43	0.43
1:E:177:LYS:HA	1:E:177:LYS:HD3	1.87	0.43
1:D:209:TYR:HB3	1:D:254:SER:HB2	2.00	0.43
1:E:256:GLY:HA3	1:E:320:TRP:CD1	2.54	0.43
1:B:201:VAL:HG11	1:B:240:TYR:OH	2.19	0.43
1:A:81:TYR:HA	1:A:85:VAL:HB	2.01	0.42
1:F:169:LEU:HD12	1:F:190:VAL:HG22	2.00	0.42
1:E:21:VAL:HG21	1:E:52:HIS:CG	2.55	0.42
1:E:208:TRP:CG	1:E:249:ALA:HA	2.55	0.42
1:F:272:PRO:O	1:F:276:GLU:HG3	2.20	0.42
1:F:115:GLU:HG3	1:F:155:ARG:NH1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:271:ARG:HB2	1:B:274:TYR:CD2	2.55	0.42
1:A:92:GLY:HA3	1:A:145:ILE:HG13	2.01	0.42
1:F:41:TYR:CD2	1:F:90:ALA:HA	2.55	0.42
1:A:41:TYR:CD2	1:A:90:ALA:HA	2.55	0.42
1:D:260:VAL:HG21	1:D:320:TRP:CE3	2.55	0.42
1:F:209:TYR:HB3	1:F:254:SER:HB2	2.02	0.42
1:B:81:TYR:HA	1:B:85:VAL:HB	2.01	0.41
1:E:218:LEU:HD13	1:E:233:LEU:HG	2.02	0.41
1:B:92:GLY:HA3	1:B:145:ILE:HG13	2.02	0.41
1:B:57:SER:OG	1:D:326:ARG:HG3	2.21	0.41
1:B:266:TYR:CD1	1:B:275:ARG:HB2	2.55	0.41
1:D:36:VAL:HA	1:D:76:PRO:HG2	2.02	0.41
1:F:260:VAL:HG21	1:F:320:TRP:CE3	2.56	0.40
1:C:322:ASP:O	1:C:326:ARG:HB2	2.20	0.40
1:F:265:LEU:HB3	1:F:274:TYR:CD2	2.56	0.40
1:A:23:ARG:HB2	1:A:31:PRO:HG3	2.02	0.40
1:D:197:VAL:HG11	1:D:210:PHE:CZ	2.57	0.40
1:A:115:GLU:HG3	1:A:155:ARG:HH11	1.86	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	330/345 (96%)	320 (97%)	10 (3%)	0	100	100
1	B	333/345 (96%)	329 (99%)	4 (1%)	0	100	100
1	C	338/345 (98%)	328 (97%)	10 (3%)	0	100	100
1	D	332/345 (96%)	323 (97%)	9 (3%)	0	100	100
1	E	330/345 (96%)	323 (98%)	7 (2%)	0	100	100
1	F	330/345 (96%)	322 (98%)	8 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1993/2070 (96%)	1945 (98%)	48 (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	259/263 (98%)	259 (100%)	0	100	100
1	B	260/263 (99%)	259 (100%)	1 (0%)	89	92
1	C	262/263 (100%)	262 (100%)	0	100	100
1	D	260/263 (99%)	260 (100%)	0	100	100
1	E	259/263 (98%)	258 (100%)	1 (0%)	89	92
1	F	259/263 (98%)	256 (99%)	3 (1%)	67	73
All	All	1559/1578 (99%)	1554 (100%)	5 (0%)	91	94

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	226	GLU
1	E	320	TRP
1	F	201	VAL
1	F	320	TRP
1	F	323	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	ASN
1	B	200	GLN
1	C	7	HIS
1	C	48	HIS

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Mol	Chain	Res	Type
1	D	68	GLN
1	D	200	GLN
1	F	11	ASN
1	F	54	GLN
1	F	128	HIS
1	F	200	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 non-standard protein/DNA/RNA residues 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
1	A1EJZ	E	257	1	20,22,23	0.49	0	18,27,29	0.29	0
1	A1EJZ	F	257	1	20,22,23	0.49	0	18,27,29	0.27	0
1	A1EJZ	B	257	1	20,22,23	0.44	0	18,27,29	0.44	0
1	A1EJZ	D	257	1	20,22,23	0.43	0	18,27,29	0.45	0
1	A1EJZ	A	257	1	20,22,23	0.44	0	18,27,29	0.29	0
1	A1EJZ	C	257	1	20,22,23	0.43	0	18,27,29	0.37	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
1	A1EJZ	E	257	1	-	1/26/29/31	-
1	A1EJZ	F	257	1	-	1/26/29/31	-
1	A1EJZ	B	257	1	-	1/26/29/31	-
1	A1EJZ	D	257	1	-	1/26/29/31	-

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	A1EJZ	A	257	1	-	1/26/29/31	-
1	A1EJZ	C	257	1	-	1/26/29/31	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	257	A1EJZ	C14-C17-NZ-CE
1	B	257	A1EJZ	C14-C17-NZ-CE
1	C	257	A1EJZ	C14-C17-NZ-CE
1	D	257	A1EJZ	C14-C17-NZ-CE
1	E	257	A1EJZ	C14-C17-NZ-CE
1	F	257	A1EJZ	C14-C17-NZ-CE

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

3 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	$\# Z  > 2$
2	PEG	D	401	-	6,6,6	0.24	0	5,5,5	0.21	0
2	PEG	B	401	-	6,6,6	0.24	0	5,5,5	0.22	0
2	PEG	E	401	-	6,6,6	0.24	0	5,5,5	0.25	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PEG	D	401	-	-	2/4/4/4	-
2	PEG	B	401	-	-	3/4/4/4	-
2	PEG	E	401	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

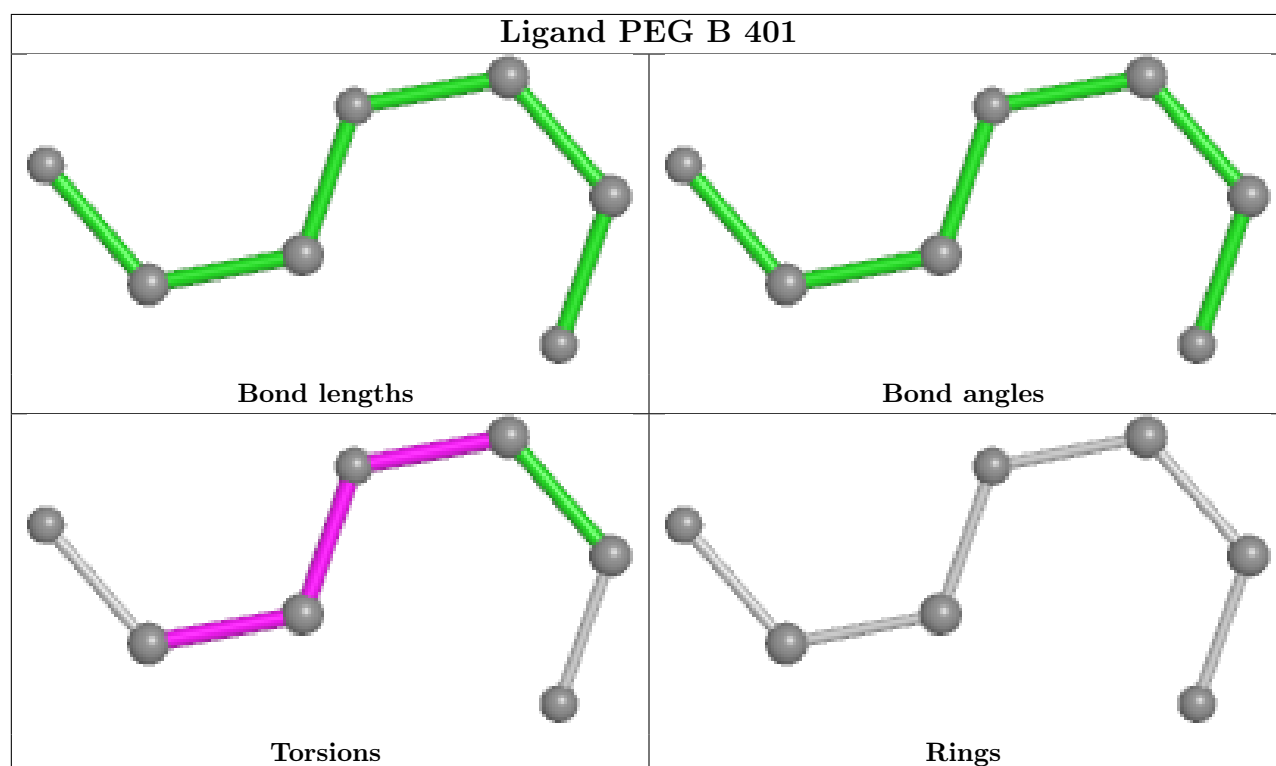
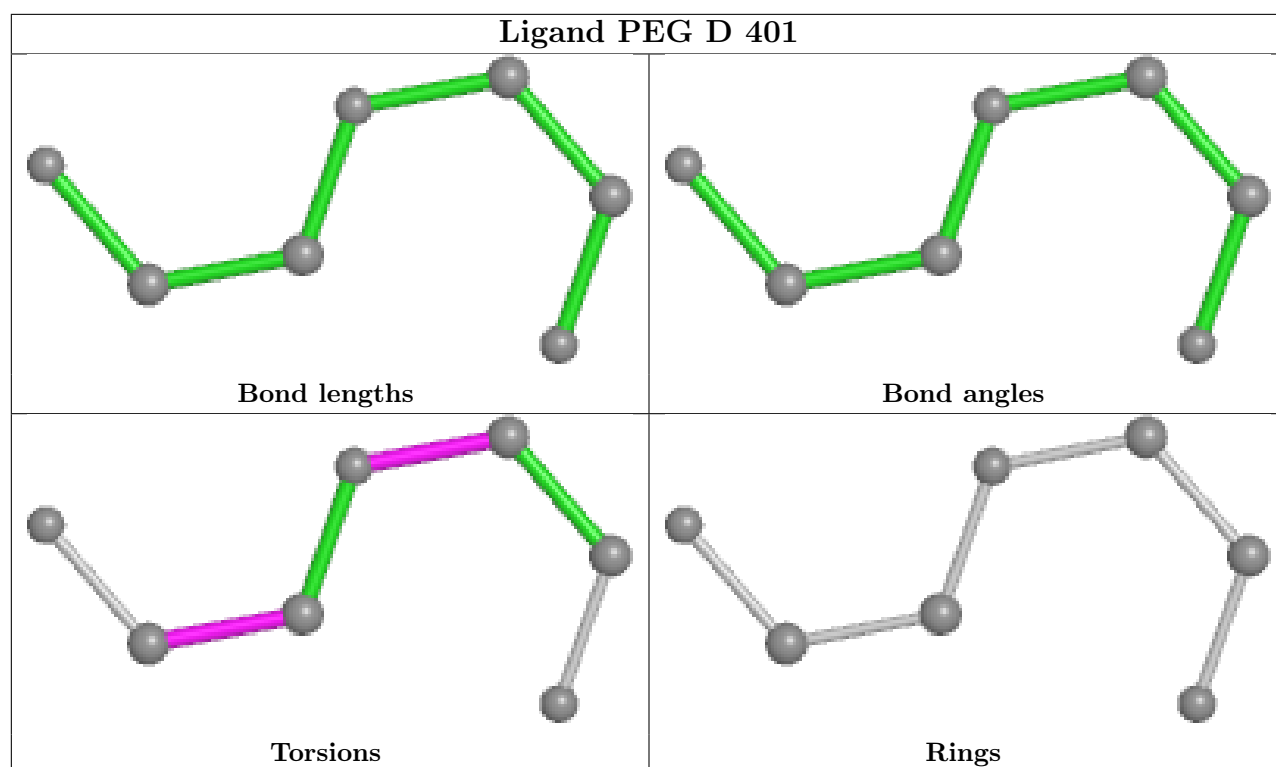
Mol	Chain	Res	Type	Atoms
2	D	401	PEG	O1-C1-C2-O2
2	B	401	PEG	O1-C1-C2-O2
2	B	401	PEG	C4-C3-O2-C2
2	B	401	PEG	C1-C2-O2-C3
2	D	401	PEG	C4-C3-O2-C2

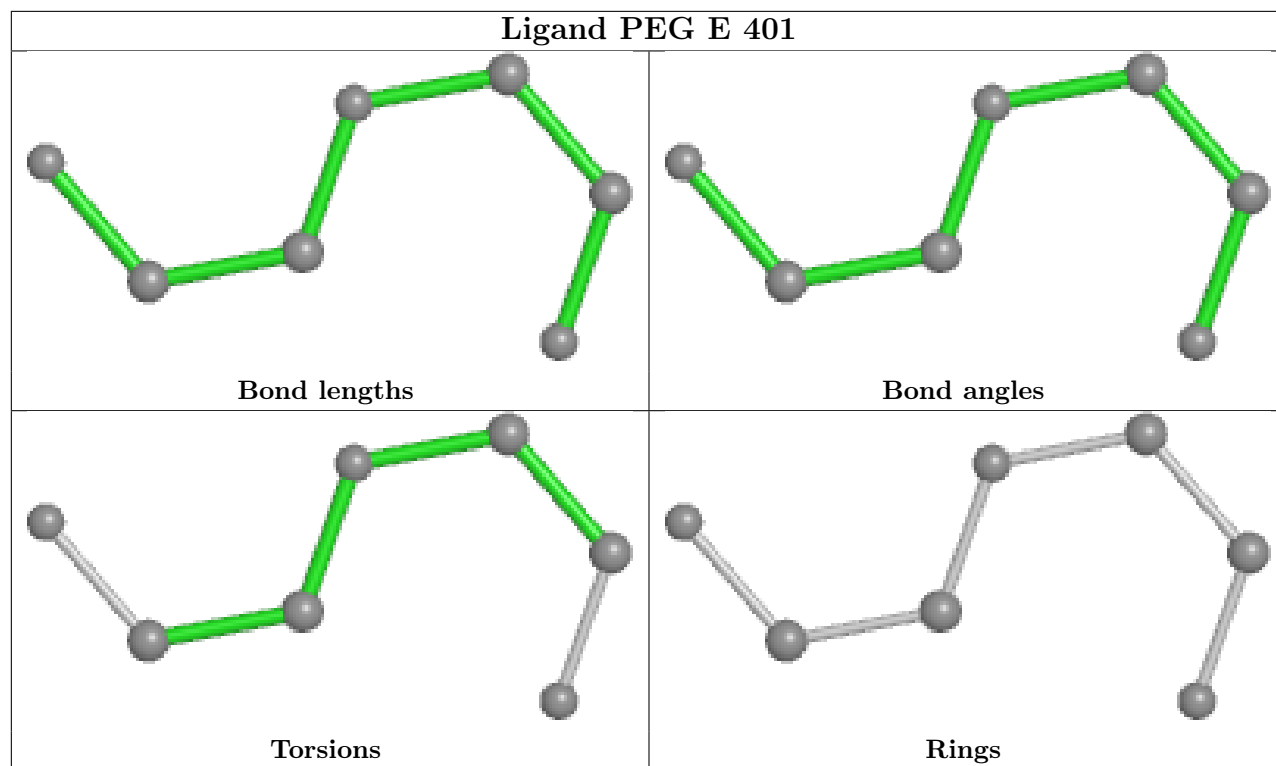
There are no ring outliers.

No monomer is involved in short contacts.

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	332/345 (96%)	0.14	2 (0%) 85 87	22, 33, 48, 61	0
1	B	335/345 (97%)	-0.03	3 (0%) 81 83	21, 30, 42, 61	0
1	C	340/345 (98%)	0.03	2 (0%) 85 87	22, 33, 44, 59	0
1	D	334/345 (96%)	0.15	5 (1%) 71 75	24, 33, 46, 58	0
1	E	332/345 (96%)	-0.01	1 (0%) 90 92	21, 31, 46, 55	0
1	F	332/345 (96%)	0.35	2 (0%) 85 87	27, 37, 50, 59	0
All	All	2005/2070 (96%)	0.11	15 (0%) 84 86	21, 33, 47, 61	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	336	ALA	3.7
1	B	337	GLY	3.2
1	B	134	GLY	2.7
1	D	336	ALA	2.7
1	C	-2	ALA	2.6
1	F	84	ASP	2.6
1	B	336	ALA	2.4
1	D	4	ASN	2.3
1	A	300	THR	2.3
1	C	307	PHE	2.2
1	E	336	ALA	2.2
1	D	84	ASP	2.2
1	D	337	GLY	2.1
1	A	22	GLU	2.1
1	D	121	ALA	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
1	A1EJZ	A	257	23/24	0.87	0.10	30,36,42,44	0
1	A1EJZ	F	257	23/24	0.88	0.09	30,35,42,51	0
1	A1EJZ	E	257	23/24	0.89	0.09	25,31,38,40	0
1	A1EJZ	D	257	23/24	0.89	0.09	30,35,43,47	0
1	A1EJZ	B	257	23/24	0.90	0.09	20,33,45,45	0
1	A1EJZ	C	257	23/24	0.92	0.07	23,32,40,40	0

## 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 6.4 Ligands [i](#)

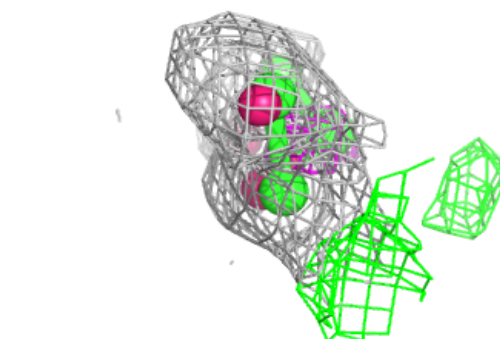
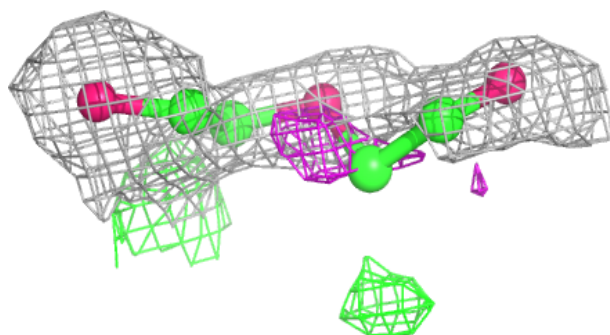
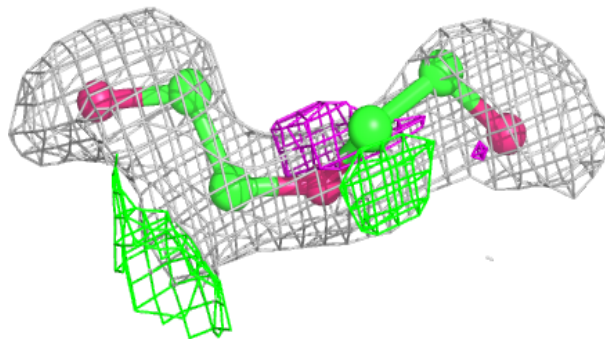
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PEG	B	401	7/7	0.61	0.20	39,42,51,51	0
2	PEG	D	401	7/7	0.80	0.13	46,51,53,57	0
2	PEG	E	401	7/7	0.82	0.12	40,46,52,56	0

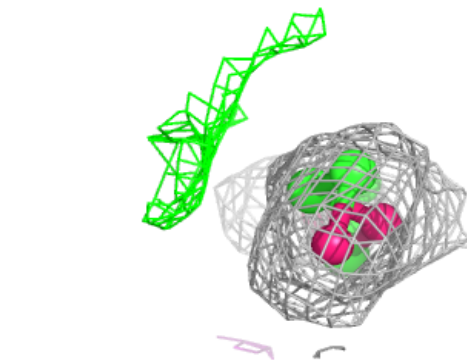
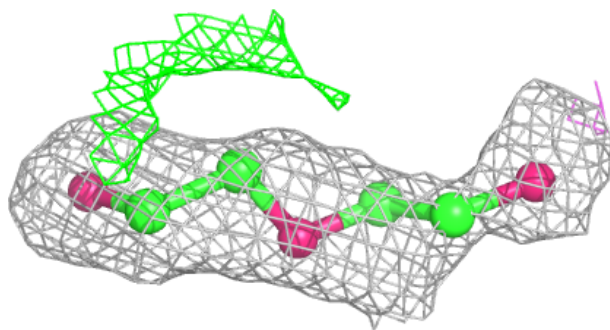
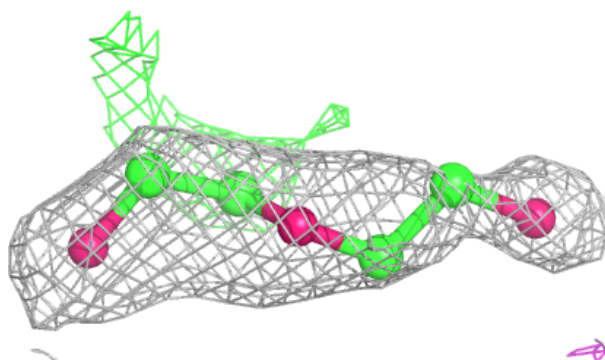
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around PEG B 401:**

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

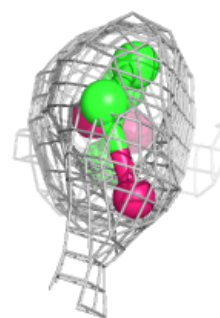
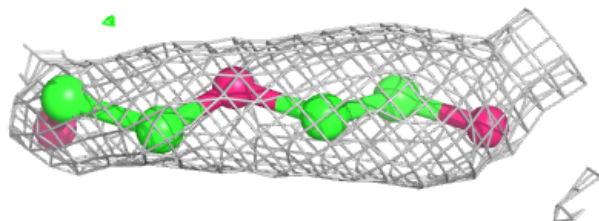
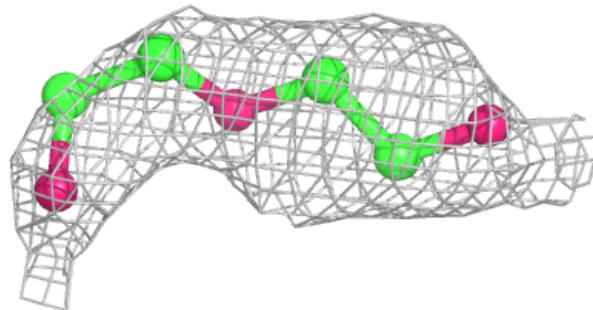
**Electron density around PEG D 401:**

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



**Electron density around PEG E 401:**

$2mF_o-DF_c$  (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.