



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:54 AM UTC

PDB ID : 7DOA / pdb_00007doa
Title : Crystal structure of Catabolite repressor activator from E. coli in complex with HEPES
Authors : Neetu, N.; Katiki, M.; Kumar, P.
Deposited on : 2020-12-13
Resolution : 2.70 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

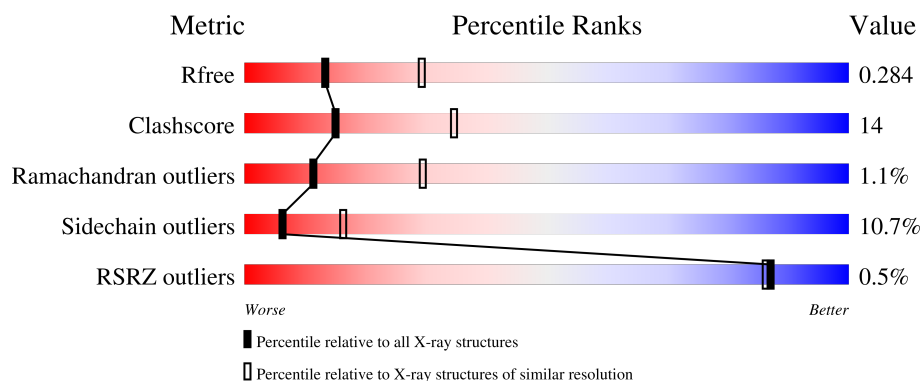
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	357	% 55% 18% • • 23%
1	B	357	49% 24% • 23%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4570 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 Catabolite repressor/activator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	274	Total	C	N	O	S	0	1	0
			2226	1407	400	412	7			
1	B	274	Total	C	N	O	S	0	1	0
			2230	1410	401	412	7			

There are 46 discrepancies between the modelled and reference sequences:

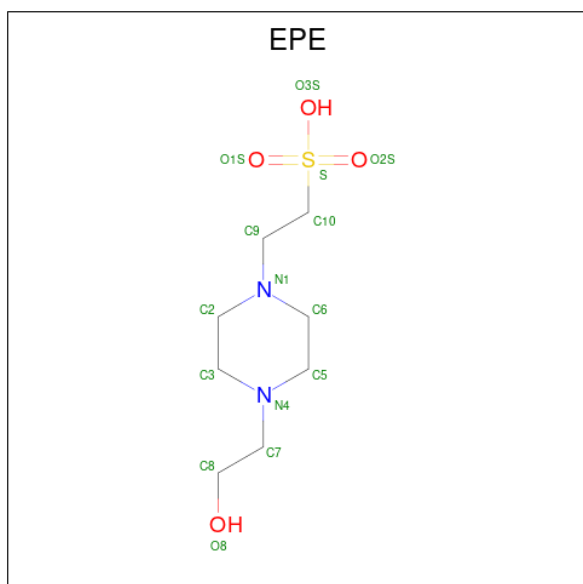
Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	HIS	-	expression tag	UNP A0A454A0X5
A	-21	HIS	-	expression tag	UNP A0A454A0X5
A	-20	HIS	-	expression tag	UNP A0A454A0X5
A	-19	HIS	-	expression tag	UNP A0A454A0X5
A	-18	HIS	-	expression tag	UNP A0A454A0X5
A	-17	HIS	-	expression tag	UNP A0A454A0X5
A	-16	ASP	-	expression tag	UNP A0A454A0X5
A	-15	TYR	-	expression tag	UNP A0A454A0X5
A	-14	ASP	-	expression tag	UNP A0A454A0X5
A	-13	ILE	-	expression tag	UNP A0A454A0X5
A	-12	PRO	-	expression tag	UNP A0A454A0X5
A	-11	THR	-	expression tag	UNP A0A454A0X5
A	-10	THR	-	expression tag	UNP A0A454A0X5
A	-9	GLU	-	expression tag	UNP A0A454A0X5
A	-8	ASN	-	expression tag	UNP A0A454A0X5
A	-7	LEU	-	expression tag	UNP A0A454A0X5
A	-6	TYR	-	expression tag	UNP A0A454A0X5
A	-5	PHE	-	expression tag	UNP A0A454A0X5
A	-4	GLN	-	expression tag	UNP A0A454A0X5
A	-3	GLY	-	expression tag	UNP A0A454A0X5
A	-2	ALA	-	expression tag	UNP A0A454A0X5
A	-1	MET	-	expression tag	UNP A0A454A0X5
A	0	ALA	-	expression tag	UNP A0A454A0X5
B	-22	HIS	-	expression tag	UNP A0A454A0X5
B	-21	HIS	-	expression tag	UNP A0A454A0X5

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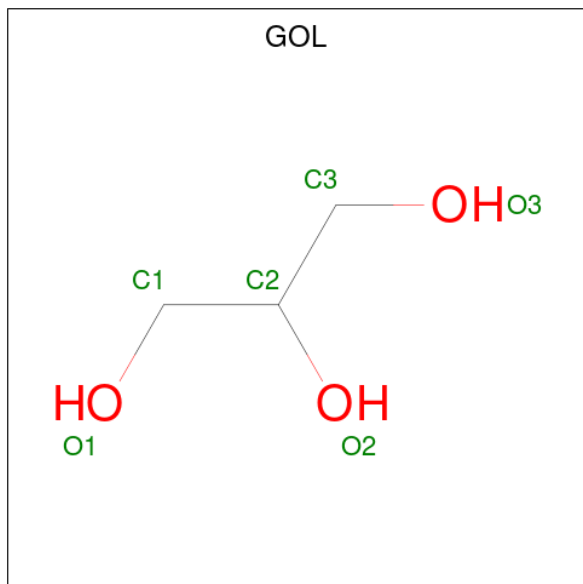
Chain	Residue	Modelled	Actual	Comment	Reference
B	-20	HIS	-	expression tag	UNP A0A454A0X5
B	-19	HIS	-	expression tag	UNP A0A454A0X5
B	-18	HIS	-	expression tag	UNP A0A454A0X5
B	-17	HIS	-	expression tag	UNP A0A454A0X5
B	-16	ASP	-	expression tag	UNP A0A454A0X5
B	-15	TYR	-	expression tag	UNP A0A454A0X5
B	-14	ASP	-	expression tag	UNP A0A454A0X5
B	-13	ILE	-	expression tag	UNP A0A454A0X5
B	-12	PRO	-	expression tag	UNP A0A454A0X5
B	-11	THR	-	expression tag	UNP A0A454A0X5
B	-10	THR	-	expression tag	UNP A0A454A0X5
B	-9	GLU	-	expression tag	UNP A0A454A0X5
B	-8	ASN	-	expression tag	UNP A0A454A0X5
B	-7	LEU	-	expression tag	UNP A0A454A0X5
B	-6	TYR	-	expression tag	UNP A0A454A0X5
B	-5	PHE	-	expression tag	UNP A0A454A0X5
B	-4	GLN	-	expression tag	UNP A0A454A0X5
B	-3	GLY	-	expression tag	UNP A0A454A0X5
B	-2	ALA	-	expression tag	UNP A0A454A0X5
B	-1	MET	-	expression tag	UNP A0A454A0X5
B	0	ALA	-	expression tag	UNP A0A454A0X5

- Molecule 2 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $C_8H_{18}N_2O_4S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
2	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
2	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			6	3	3		

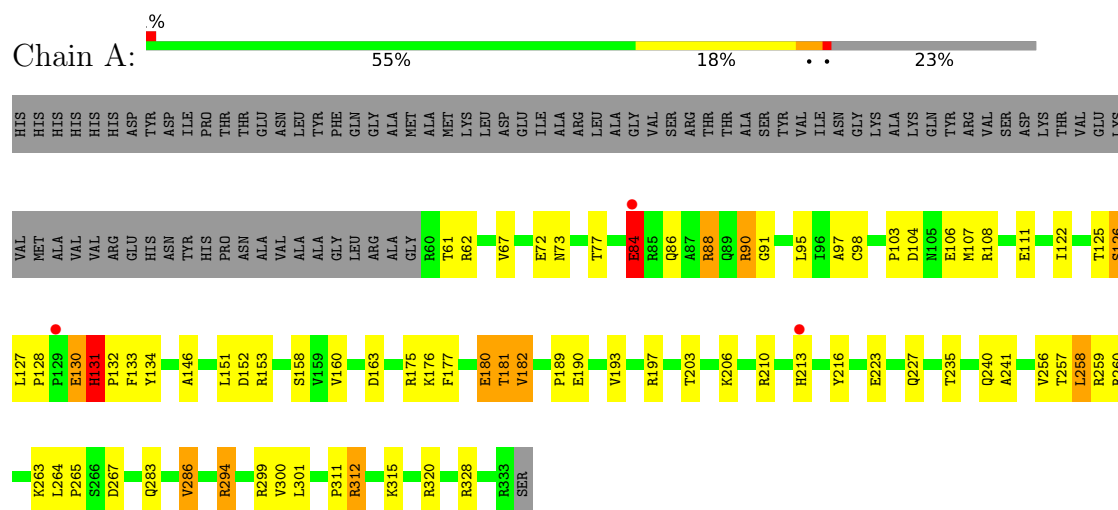
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	30	Total	O	0	0
			30	30		
4	B	33	Total	O	0	0
			33	33		

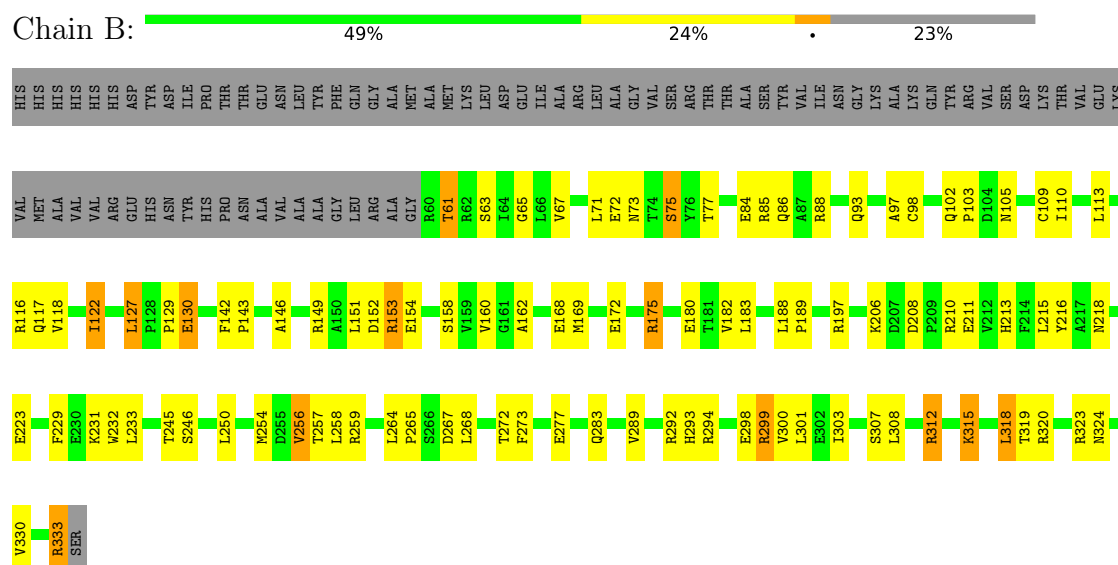
3 Residue-property plots

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: Catabolite repressor/activator



• Molecule 1: Catabolite repressor/activator



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	123.93Å 43.34Å 108.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.91 – 2.70 40.91 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.9 (40.91-2.70) 97.9 (40.91-2.70)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.02 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.217 , 0.284 0.217 , 0.284	Depositor DCC
R_{free} test set	824 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	69.7	Xtriage
Anisotropy	0.561	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 59.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4570	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.04% 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: GOL, EPE

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.07	2/2275 (0.1%)	1.20	11/3090 (0.4%)
1	B	1.08	2/2279 (0.1%)	1.16	5/3094 (0.2%)
All	All	1.08	4/4554 (0.1%)	1.18	16/6184 (0.3%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	312	ARG	CD-NE	10.74	1.61	1.46
1	A	312	ARG	CD-NE	9.23	1.59	1.46
1	A	312	ARG	NE-CZ	8.44	1.42	1.33
1	B	312	ARG	NE-CZ	7.04	1.40	1.33

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	90	ARG	NE-CZ-NH2	10.21	128.39	119.20
1	B	312	ARG	CD-NE-CZ	9.11	137.15	124.40
1	A	312	ARG	NE-CZ-NH1	8.30	129.80	121.50
1	B	130	GLU	N-CA-C	7.95	121.78	112.72
1	A	312	ARG	CD-NE-CZ	7.76	135.26	124.40
1	B	312	ARG	NE-CZ-NH1	7.24	128.74	121.50
1	A	90	ARG	CD-NE-CZ	6.33	133.26	124.40
1	A	90	ARG	NE-CZ-NH1	-6.19	115.31	121.50
1	A	131	HIS	CA-C-N	5.96	127.29	119.84
1	A	131	HIS	C-N-CA	5.96	127.29	119.84
1	A	84	GLU	CB-CA-C	-5.78	101.81	110.88
1	B	283	GLN	CA-CB-CG	-5.72	102.66	114.10
1	B	312	ARG	CG-CD-NE	5.69	124.51	112.00
1	A	312	ARG	NH1-CZ-NH2	-5.15	112.61	119.30
1	A	163	ASP	N-CA-C	5.13	117.53	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	125	THR	N-CA-C	5.08	117.67	110.50

There are no chirality outliers.

There are no planarity outliers.

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	2226	0	2201	55	0
1	B	2230	0	2212	77	1
2	A	15	0	18	1	0
2	B	30	0	36	2	0
3	B	6	0	8	0	0
4	A	30	0	0	1	0
4	B	33	0	0	4	1
All	All	4570	0	4475	123	2

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 14.

All (123) 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:107:MET:SD	1:A:133:PHE:CD1	2.52	1.01
1:A:88:ARG:NH2	1:B:98:CYS:HB2	1.87	0.89
1:A:107:MET:SD	1:A:133:PHE:CE1	2.66	0.88
1:A:294:ARG:HH11	1:A:294:ARG:HG3	1.44	0.82
1:B:254:MET:HE1	1:B:265:PRO:HD2	1.64	0.80
1:B:246:SER:HB2	2:B:401:EPE:H32	1.62	0.80
1:A:130:GLU:HG3	1:A:131:HIS:H	1.52	0.75
1:B:153:ARG:HE	1:B:318:LEU:HD22	1.52	0.72
1:A:84:GLU:OE2	1:B:71:LEU:HD12	1.89	0.72
1:A:88:ARG:HH22	1:B:98:CYS:HB2	1.55	0.71
1:A:180:GLU:N	1:A:240:GLN:OE1	2.24	0.70
1:A:107:MET:HB3	1:A:133:PHE:CE1	2.27	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:286:VAL:CG2	1:A:328:ARG:HB2	2.23	0.69
1:A:95:LEU:CD2	1:B:93:GLN:HG2	2.23	0.69
1:B:109:CYS:O	1:B:113:LEU:HD12	1.94	0.67
1:B:299:ARG:HH11	1:B:299:ARG:HB2	1.58	0.66
1:A:107:MET:HB3	1:A:133:PHE:CZ	2.31	0.66
1:A:130:GLU:CG	1:A:131:HIS:H	2.09	0.64
1:A:213[A]:HIS:NE2	4:A:501:HOH:O	2.19	0.61
1:A:259:ARG:HH22	1:B:333:ARG:HB3	1.64	0.61
1:B:272:THR:HG22	1:B:273:PHE:O	2.00	0.60
1:A:106:GLU:OE2	1:A:126:SER:HB2	2.01	0.59
1:A:95:LEU:HD23	1:B:93:GLN:CG	2.33	0.59
1:B:289:VAL:HG22	1:B:323:ARG:HB3	1.84	0.59
1:A:62:ARG:HD3	1:A:91:GLY:O	2.03	0.59
1:A:103:PRO:O	1:A:107:MET:HG3	2.03	0.59
1:B:197:ARG:HH12	2:B:401:EPE:H52	1.69	0.58
1:B:197:ARG:HD3	1:B:245:THR:HG23	1.87	0.57
1:A:108:ARG:HA	1:A:111:GLU:CD	2.29	0.57
1:B:61:THR:HB	1:B:63:SER:OG	2.05	0.57
1:A:61:THR:O	1:B:116:ARG:NH1	2.38	0.56
1:B:175:ARG:CZ	1:B:208:ASP:HB2	2.36	0.56
1:A:197:ARG:HH12	2:A:401:EPE:H32	1.71	0.55
1:B:65:GLY:HA3	1:B:113:LEU:HD22	1.90	0.54
1:B:102:GLN:HB2	1:B:105:ASN:ND2	2.23	0.54
1:A:286:VAL:HG22	1:A:328:ARG:C	2.33	0.53
1:B:189:PRO:HG3	1:B:216:TYR:CD1	2.43	0.53
1:B:254:MET:HE3	1:B:264:LEU:HD13	1.90	0.53
1:B:315:LYS:O	1:B:315:LYS:HD2	2.09	0.53
1:A:311:PRO:O	1:A:312:ARG:CB	2.57	0.52
1:A:84:GLU:OE2	1:B:71:LEU:CD1	2.57	0.52
1:B:117:GLN:CG	1:B:117:GLN:O	2.58	0.52
1:A:203:THR:HA	1:A:206:LYS:HE2	1.91	0.52
1:B:258:LEU:HB2	1:B:264:LEU:HD23	1.91	0.52
1:B:299:ARG:HB2	1:B:299:ARG:NH1	2.23	0.52
1:A:175:ARG:HG3	1:A:210:ARG:NH2	2.25	0.52
1:B:257:THR:HG21	1:B:265:PRO:HG3	1.92	0.51
1:A:182:VAL:HB	1:A:241:ALA:HB3	1.93	0.51
1:B:143:PRO:HB3	1:B:307:SER:OG	2.11	0.51
1:B:162:ALA:HA	1:B:320:ARG:CZ	2.41	0.51
1:B:160:VAL:O	1:B:320:ARG:HA	2.12	0.50
1:B:320:ARG:NH1	4:B:503:HOH:O	2.44	0.50
1:A:189:PRO:HG3	1:A:216:TYR:CD1	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:229:PHE:HD2	1:B:256:VAL:CG2	2.25	0.50
1:A:146:ALA:HB3	1:A:158:SER:OG	2.12	0.50
1:B:188:LEU:HD11	1:B:218:ASN:O	2.12	0.50
1:A:181:THR:HG22	1:A:240:GLN:NE2	2.27	0.49
1:A:223:GLU:O	1:A:227:GLN:HG3	2.12	0.49
1:B:229:PHE:O	1:B:233:LEU:HD13	2.12	0.49
1:A:256:VAL:O	1:A:260:ARG:HB3	2.13	0.49
1:A:257:THR:HG21	1:A:265:PRO:HG3	1.94	0.49
1:B:172:GLU:HB2	4:B:514:HOH:O	2.12	0.49
1:B:86:GLN:HG3	1:B:301:LEU:HD23	1.94	0.48
1:B:229:PHE:CD2	1:B:256:VAL:CG2	2.96	0.48
1:B:175:ARG:NH1	1:B:208:ASP:HB2	2.28	0.48
1:B:122:ILE:HD13	1:B:300:VAL:HG12	1.95	0.48
1:A:128:PRO:O	1:A:131:HIS:HB3	2.13	0.48
1:A:106:GLU:OE2	1:A:126:SER:N	2.46	0.47
1:B:109:CYS:C	1:B:113:LEU:HD12	2.39	0.47
1:B:188:LEU:N	1:B:188:LEU:HD12	2.29	0.47
1:A:267:ASP:OD1	1:A:267:ASP:N	2.45	0.47
1:A:175:ARG:C	1:A:177:PHE:H	2.23	0.47
1:B:229:PHE:CZ	1:B:233:LEU:HD11	2.49	0.47
1:B:250:LEU:HD22	1:B:272:THR:OG1	2.15	0.47
1:A:294:ARG:HH11	1:A:294:ARG:CG	2.20	0.46
1:B:158:SER:HB2	1:B:318:LEU:HD12	1.97	0.46
1:A:311:PRO:O	1:A:312:ARG:HB3	2.16	0.46
1:B:122:ILE:HD13	1:B:300:VAL:CG1	2.46	0.46
1:B:197:ARG:CD	1:B:245:THR:HG23	2.44	0.46
1:B:102:GLN:HB2	1:B:105:ASN:HD22	1.81	0.46
1:A:294:ARG:HG3	1:A:294:ARG:NH1	2.20	0.45
1:B:85:ARG:HH11	1:B:294:ARG:NH1	2.15	0.45
1:B:142:PHE:CD2	1:B:142:PHE:C	2.94	0.45
1:A:134:TYR:CD2	1:A:151:LEU:HD21	2.51	0.45
1:A:258:LEU:HD12	1:A:264:LEU:HD12	1.99	0.45
1:A:286:VAL:HG22	1:A:328:ARG:HB2	1.99	0.44
1:B:180:GLU:HA	1:B:210:ARG:HD2	1.99	0.44
1:B:188:LEU:HD11	1:B:218:ASN:C	2.42	0.44
1:B:229:PHE:CD2	1:B:256:VAL:HG21	2.53	0.44
1:B:67:VAL:HA	1:B:97:ALA:O	2.18	0.44
1:B:61:THR:HG21	4:B:505:HOH:O	2.18	0.43
1:B:146:ALA:HB3	1:B:158:SER:OG	2.18	0.43
1:A:73:ASN:O	1:A:77:THR:HG23	2.18	0.43
1:A:104:ASP:O	1:A:108:ARG:HG2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:67:VAL:HA	1:A:97:ALA:O	2.18	0.43
1:A:160:VAL:O	1:A:320:ARG:HA	2.18	0.43
1:A:175:ARG:CG	1:A:210:ARG:NH2	2.82	0.43
1:B:162:ALA:HA	1:B:320:ARG:NE	2.34	0.43
1:B:183:LEU:HD11	1:B:215:LEU:HB2	2.01	0.43
1:B:245:THR:HG22	1:B:245:THR:O	2.19	0.43
1:B:294:ARG:O	1:B:298:GLU:HG3	2.18	0.43
1:A:86:GLN:HG3	1:A:301:LEU:HD23	2.00	0.42
1:B:206:LYS:HE3	1:B:206:LYS:HB3	1.45	0.42
1:B:153:ARG:HG3	1:B:318:LEU:HD13	1.99	0.42
1:B:267:ASP:OD1	1:B:267:ASP:N	2.53	0.42
1:A:98:CYS:HB2	1:B:84:GLU:OE1	2.19	0.42
1:B:292:ARG:HD3	1:B:324:ASN:OD1	2.20	0.42
1:B:189:PRO:HG3	1:B:216:TYR:CG	2.55	0.42
1:B:75:SER:OG	1:B:293:HIS:HE1	2.02	0.42
1:B:102:GLN:NE2	4:B:504:HOH:O	2.50	0.41
1:B:259:ARG:HD2	1:B:259:ARG:HA	1.81	0.41
1:A:294:ARG:CG	1:A:294:ARG:NH1	2.81	0.41
1:A:122:ILE:HG21	1:A:300:VAL:HG11	2.02	0.41
1:B:168:GLU:O	1:B:172:GLU:OE2	2.39	0.41
1:B:232:TRP:HE3	1:B:233:LEU:HD12	1.86	0.41
1:A:152:ASP:OD1	1:A:152:ASP:C	2.63	0.41
1:B:73:ASN:O	1:B:77:THR:HG23	2.21	0.41
1:B:103:PRO:HB3	1:B:127:LEU:HD11	2.02	0.41
1:B:142:PHE:HA	1:B:143:PRO:HD3	1.87	0.40
1:B:229:PHE:HD2	1:B:256:VAL:HG21	1.86	0.40
1:A:128:PRO:HB2	1:A:130:GLU:CG	2.51	0.40
1:B:272:THR:O	1:B:289:VAL:HG12	2.22	0.40
1:B:85:ARG:HH11	1:B:294:ARG:HH12	1.69	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:130:GLU:OE1	1:B:130:GLU:OE1[2_555]	2.00	0.20
4:B:529:HOH:O	4:B:530:HOH:O[1_545]	2.18	0.02

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	273/357 (76%)	254 (93%)	15 (6%)	4 (2%)	8	22
1	B	273/357 (76%)	260 (95%)	11 (4%)	2 (1%)	18	41
All	All	546/714 (76%)	514 (94%)	26 (5%)	6 (1%)	11	29

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	153	ARG
1	A	176	LYS
1	A	132	PRO
1	A	131	HIS
1	B	152	ASP
1	B	153	ARG

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	239/306 (78%)	219 (92%)	20 (8%)	10	26
1	B	240/306 (78%)	208 (87%)	32 (13%)	4	10
All	All	479/612 (78%)	427 (89%)	52 (11%)	6	16

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	GLU
1	A	84	GLU
1	A	88	ARG
1	A	90	ARG
1	A	126	SER
1	A	127	LEU
1	A	130	GLU
1	A	180	GLU
1	A	181	THR
1	A	182	VAL
1	A	190	GLU
1	A	193	VAL
1	A	235	THR
1	A	258	LEU
1	A	263	LYS
1	A	283	GLN
1	A	286	VAL
1	A	294	ARG
1	A	299	ARG
1	A	315	LYS
1	B	61	THR
1	B	72	GLU
1	B	75	SER
1	B	88	ARG
1	B	110	ILE
1	B	118	VAL
1	B	122	ILE
1	B	127	LEU
1	B	129	PRO
1	B	149	ARG
1	B	151	LEU
1	B	154	GLU
1	B	169	MET
1	B	175	ARG
1	B	182	VAL
1	B	211	GLU
1	B	213[A]	HIS
1	B	213[B]	HIS
1	B	223	GLU
1	B	231	LYS
1	B	256	VAL
1	B	268	LEU
1	B	277	GLU

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Mol	Chain	Res	Type
1	B	299	ARG
1	B	303	ILE
1	B	308	LEU
1	B	312	ARG
1	B	315	LYS
1	B	318	LEU
1	B	319	THR
1	B	330	VAL
1	B	333	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	199	GLN
1	B	199	GLN
1	B	293	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	GOL	B	403	-	5,5,5	0.55	0	5,5,5	0.51	0
2	EPE	B	401	-	15,15,15	2.05	3 (20%)	19,20,20	1.76	6 (31%)
2	EPE	A	401	-	15,15,15	2.18	1 (6%)	19,20,20	1.83	6 (31%)
2	EPE	B	402	-	15,15,15	2.00	1 (6%)	19,20,20	1.86	7 (36%)

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	GOL	B	403	-	-	2/4/4/4	-
2	EPE	B	401	-	-	5/9/19/19	0/1/1/1
2	EPE	A	401	-	-	5/9/19/19	0/1/1/1
2	EPE	B	402	-	-	6/9/19/19	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	402	EPE	C10-S	-7.20	1.67	1.77
2	A	401	EPE	C10-S	-7.07	1.67	1.77
2	B	401	EPE	C10-S	-5.98	1.69	1.77
2	B	401	EPE	O2S-S	2.28	1.51	1.45
2	B	401	EPE	C7-N4	2.10	1.52	1.47

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	EPE	O2S-S-C10	3.60	112.17	106.73
2	A	401	EPE	C6-N1-C2	3.32	115.98	108.84
2	B	401	EPE	C5-N4-C3	3.24	115.81	108.84
2	B	402	EPE	C6-C5-N4	3.23	117.17	110.65
2	B	402	EPE	O2S-S-C10	3.05	111.34	106.73
2	B	401	EPE	O3S-S-C10	2.97	111.82	106.00
2	B	402	EPE	O1S-S-C10	2.77	110.91	106.73
2	A	401	EPE	C3-C2-N1	2.63	115.96	110.65
2	B	401	EPE	C6-N1-C2	2.58	114.40	108.84
2	B	401	EPE	O3S-S-O1S	-2.56	105.01	111.40
2	A	401	EPE	C7-N4-C3	2.54	118.02	111.24
2	B	401	EPE	C2-C3-N4	2.51	115.72	110.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	EPE	C6-C5-N4	2.43	115.55	110.65
2	A	401	EPE	C5-C6-N1	2.41	115.52	110.65
2	B	402	EPE	C9-N1-C2	-2.38	104.90	111.24
2	B	402	EPE	C7-N4-C5	2.30	117.38	111.24
2	B	402	EPE	C5-N4-C3	2.28	113.74	108.84
2	A	401	EPE	O2S-S-O1S	-2.16	106.80	113.82
2	B	402	EPE	C3-C2-N1	2.04	114.76	110.65

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	401	EPE	C10-C9-N1-C6
2	B	402	EPE	C8-C7-N4-C5
2	B	402	EPE	C9-C10-S-O1S
2	B	402	EPE	C9-C10-S-O3S
3	B	403	GOL	C1-C2-C3-O3
2	B	401	EPE	N4-C7-C8-O8
2	B	401	EPE	C8-C7-N4-C5
3	B	403	GOL	O2-C2-C3-O3
2	A	401	EPE	S-C10-C9-N1
2	B	401	EPE	C10-C9-N1-C2
2	A	401	EPE	C9-C10-S-O3S
2	A	401	EPE	C9-C10-S-O1S
2	A	401	EPE	C9-C10-S-O2S
2	B	402	EPE	C9-C10-S-O2S
2	B	402	EPE	S-C10-C9-N1
2	A	401	EPE	C10-C9-N1-C6
2	B	402	EPE	C10-C9-N1-C6
2	B	401	EPE	S-C10-C9-N1

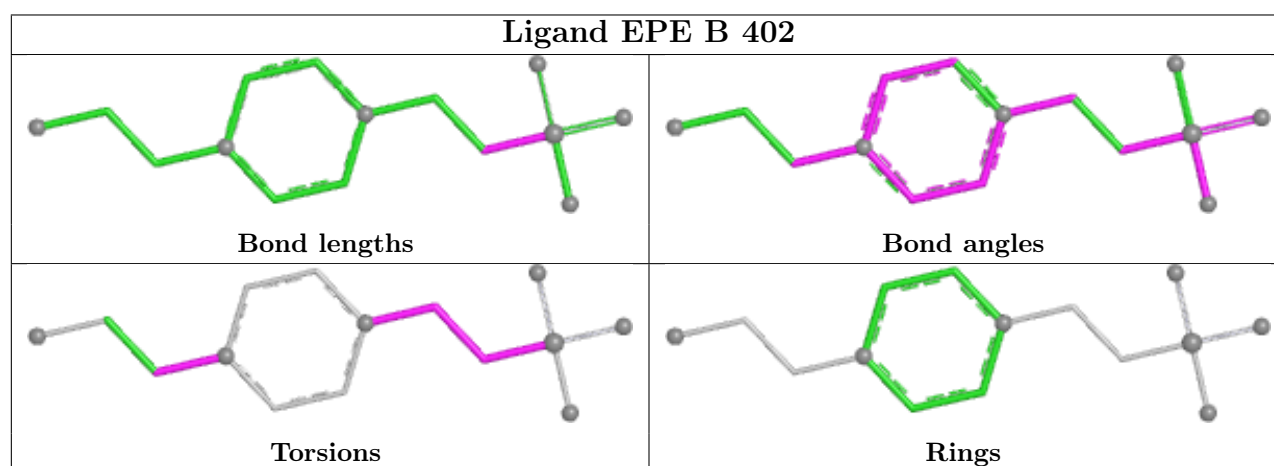
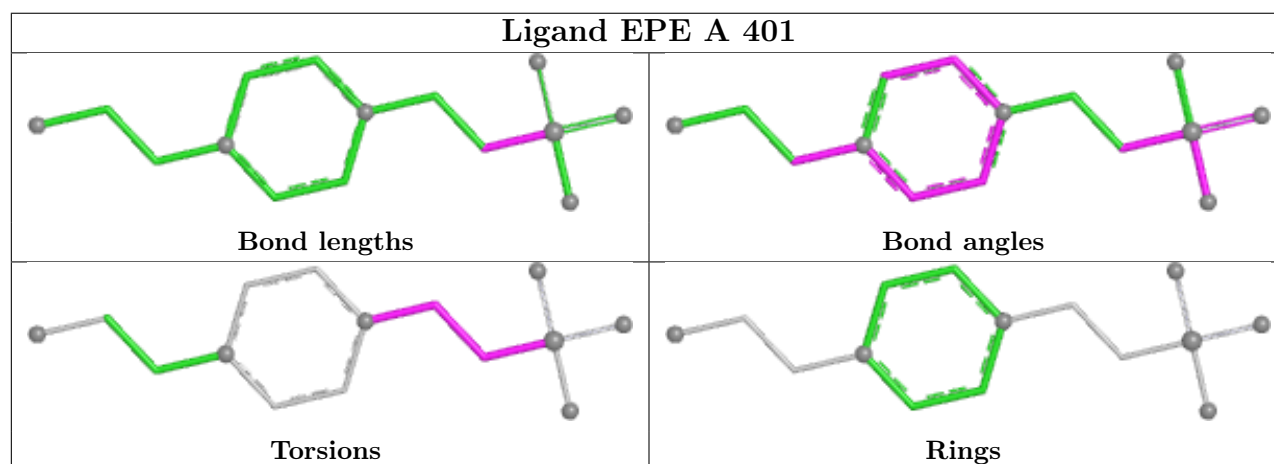
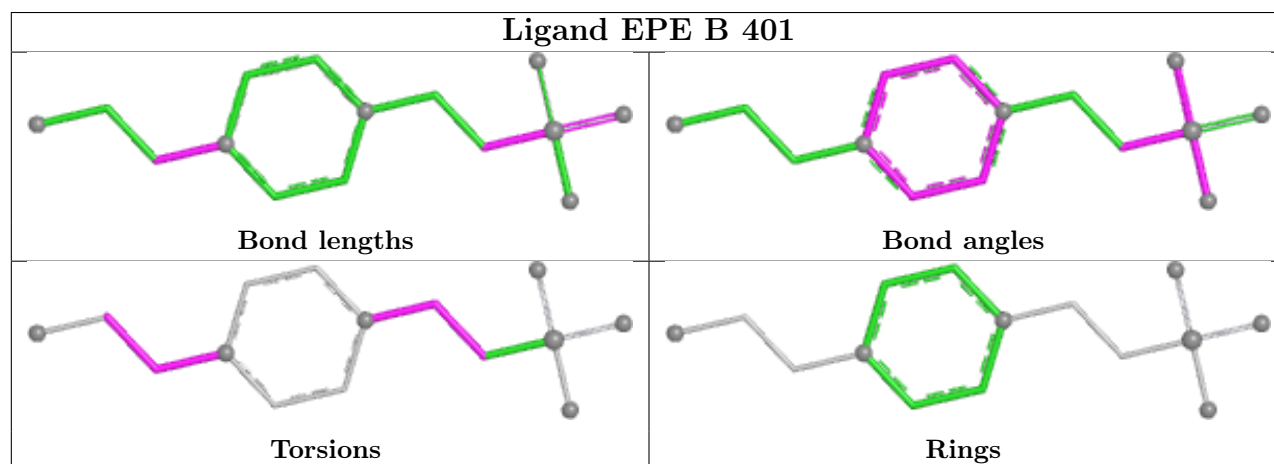
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	EPE	2	0
2	A	401	EPE	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 [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	274/357 (76%)	-0.10	3 (1%) 78 76	36, 70, 102, 120	1 (0%)
1	B	274/357 (76%)	-0.08	0 100 100	45, 71, 105, 126	1 (0%)
All	All	548/714 (76%)	-0.09	3 (0%) 87 86	36, 71, 105, 126	2 (0%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	84	GLU	4.8
1	A	129	PRO	3.2
1	A	213[A]	HIS	2.8

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 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, 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	GOL	B	403	6/6	0.74	0.15	79,81,98,101	0
2	EPE	B	401	15/15	0.83	0.14	70,98,106,107	0

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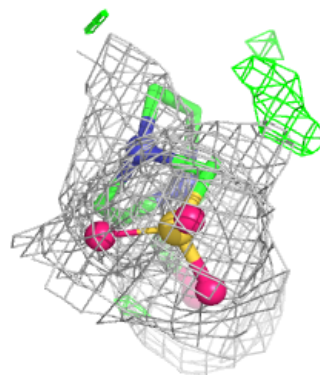
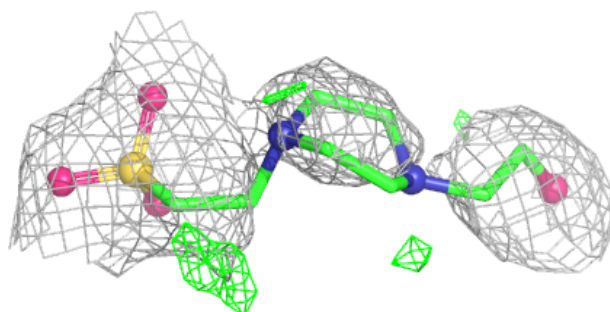
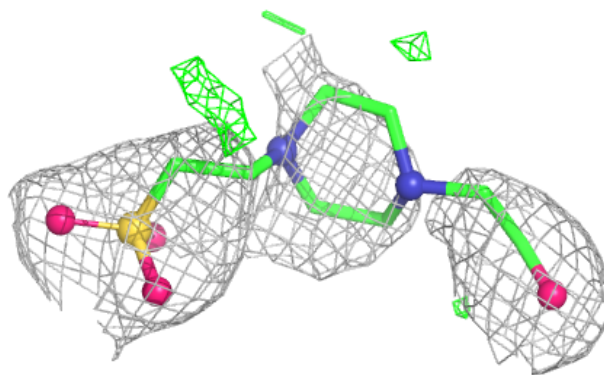
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	EPE	B	402	15/15	0.92	0.10	76,80,85,87	0
2	EPE	A	401	15/15	0.92	0.10	70,88,104,104	0

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.

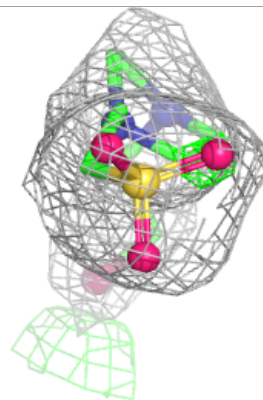
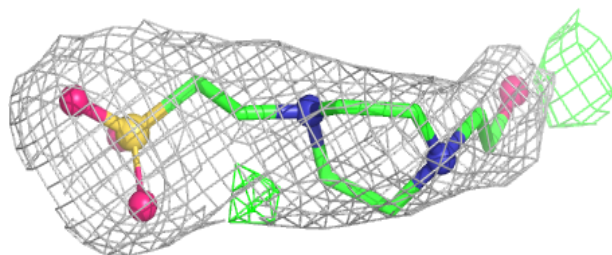
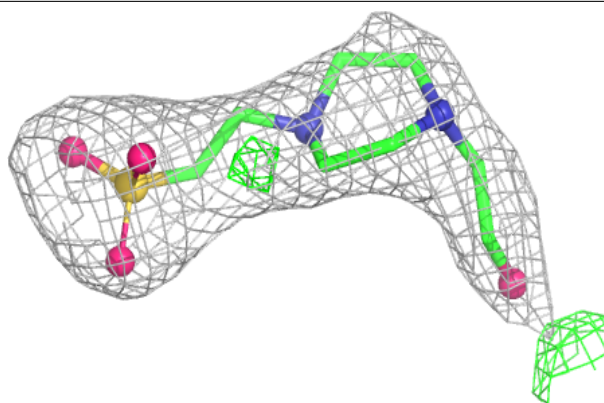
Electron density around EPE B 401:

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

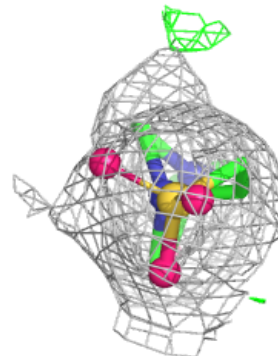
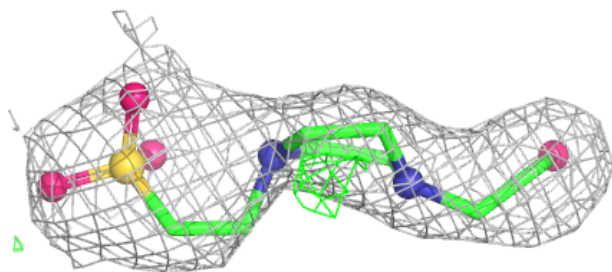
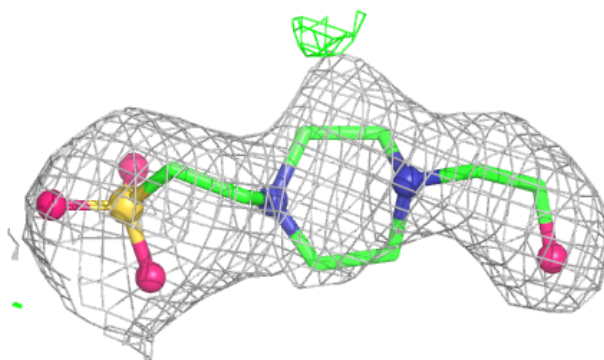


Electron density around EPE B 402:

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

**Electron density around EPE A 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 [i](#)

There are no such residues in this entry.