



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 13, 2021 – 06:12 PM JST

PDB ID : 7DOA
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 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	:	2.24
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)	:	2.24

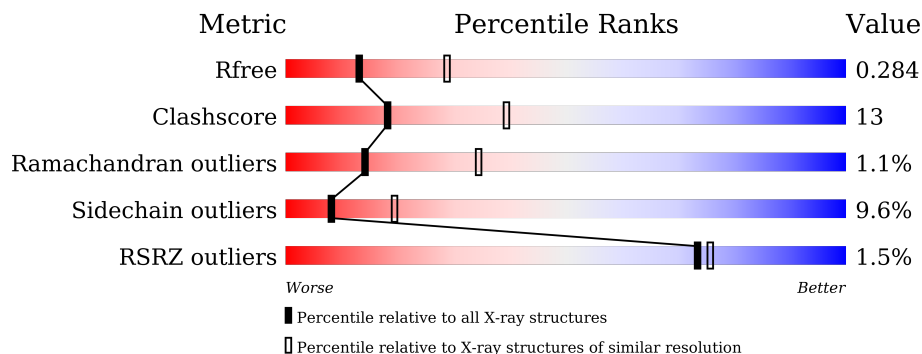
1 Overall quality at a glance

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}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (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	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 55%, yellow 17%, orange 6%, grey 23%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 55% 17% 6% 23% </div> </div>
1	B	357	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 50%, yellow 24%, orange 1%, grey 24%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 50% 24% • 23% </div> </div>

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:

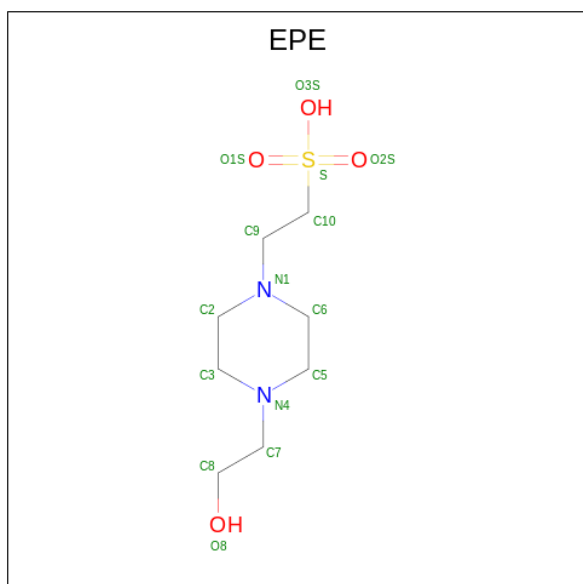
Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	HIS	-	expression tag	UNP A0A454A0X5
A	-21	HIS	-	expression tag	UNP A0A454A0X5
A	-20	HIS	-	expression tag	UNP A0A454A0X5
A	-19	HIS	-	expression tag	UNP A0A454A0X5
A	-18	HIS	-	expression tag	UNP A0A454A0X5
A	-17	HIS	-	expression tag	UNP A0A454A0X5
A	-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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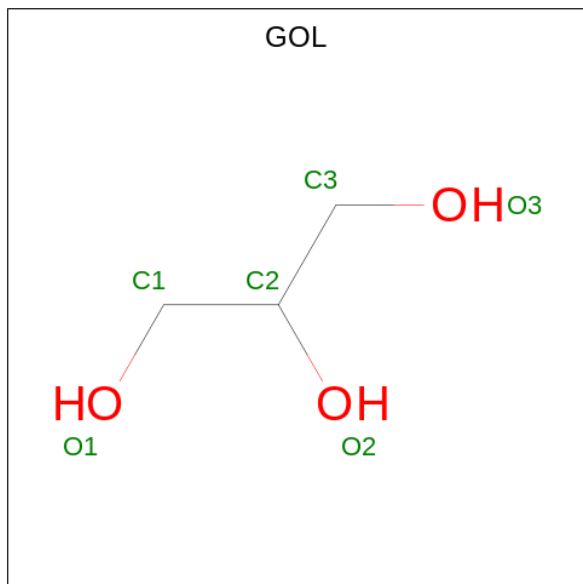
Chain	Residue	Modelled	Actual	Comment	Reference
B	-20	HIS	-	expression tag	UNP A0A454A0X5
B	-19	HIS	-	expression tag	UNP A0A454A0X5
B	-18	HIS	-	expression tag	UNP A0A454A0X5
B	-17	HIS	-	expression tag	UNP A0A454A0X5
B	-16	ASP	-	expression tag	UNP A0A454A0X5
B	-15	TYR	-	expression tag	UNP A0A454A0X5
B	-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 (three-letter code: 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 (three-letter code: 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		

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 , 57.6	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	0.87	5/2275 (0.2%)	1.19	16/3090 (0.5%)
1	B	0.89	3/2279 (0.1%)	1.09	8/3094 (0.3%)
All	All	0.88	8/4554 (0.2%)	1.14	24/6184 (0.4%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	312	ARG	CD-NE	8.73	1.61	1.46
1	A	312	ARG	CD-NE	7.49	1.59	1.46
1	A	312	ARG	NE-CZ	7.14	1.42	1.33
1	B	312	ARG	NE-CZ	5.96	1.40	1.33
1	A	216	TYR	CE2-CZ	5.34	1.45	1.38
1	A	72	GLU	CD-OE2	5.12	1.31	1.25
1	A	298	GLU	CD-OE1	5.05	1.31	1.25
1	B	243	PHE	CG-CD2	5.03	1.46	1.38

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	312	ARG	NE-CZ-NH1	18.99	129.80	120.30
1	B	312	ARG	NE-CZ-NH1	16.88	128.74	120.30
1	A	90	ARG	NE-CZ-NH2	16.18	128.39	120.30
1	A	90	ARG	NE-CZ-NH1	-9.97	115.31	120.30
1	B	312	ARG	CD-NE-CZ	9.68	137.15	123.60
1	A	312	ARG	CD-NE-CZ	8.33	135.26	123.60
1	A	320	ARG	NE-CZ-NH1	7.59	124.10	120.30
1	A	95	LEU	CB-CG-CD2	-6.93	99.21	111.00
1	A	90	ARG	CD-NE-CZ	6.90	133.26	123.60
1	B	312	ARG	NE-CZ-NH2	-6.78	116.91	120.30
1	A	333	ARG	NE-CZ-NH1	6.75	123.68	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	312	ARG	NH1-CZ-NH2	-6.17	112.61	119.40
1	A	140	ASP	CB-CG-OD1	6.14	123.83	118.30
1	B	312	ARG	CG-CD-NE	6.05	124.51	111.80
1	B	165	ASP	CB-CG-OD2	5.98	123.68	118.30
1	A	60	ARG	NE-CZ-NH2	-5.97	117.31	120.30
1	B	328	ARG	NE-CZ-NH2	-5.95	117.33	120.30
1	B	163	ASP	CB-CG-OD1	5.85	123.56	118.30
1	A	144	ILE	CG1-CB-CG2	-5.72	98.81	111.40
1	A	327	ARG	NE-CZ-NH2	-5.70	117.45	120.30
1	A	312	ARG	NE-CZ-NH2	-5.48	117.56	120.30
1	A	328	ARG	NE-CZ-NH1	-5.17	117.71	120.30
1	A	208	ASP	CB-CG-OD2	5.17	122.95	118.30
1	B	259	ARG	NE-CZ-NH1	5.15	122.87	120.30

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	2226	0	2201	54	0
1	B	2230	0	2212	75	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	120	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 13.

All (120) 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: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
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: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:B:189:PRO:HG3	1:B:216:TYR:CD1	2.43	0.53
1:B:315:LYS:O	1:B:315:LYS:HD2	2.09	0.53
1:A:108:ARG:HA	1:A:111:GLU:CD	2.29	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:A:286:VAL:HG22	1:A:328:ARG:C	2.33	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: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: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: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:B:254:MET:HE1	1:B:265:PRO:HD2	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:B:109:CYS:C	1:B:113:LEU:HD12	2.39	0.42
1:A:86:GLN:HG3	1:A:301:LEU:HD23	2.00	0.42
1:A:175:ARG:C	1:A:177:PHE:H	2.23	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: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:CD2	1:B:142:PHE:C	2.94	0.40
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 [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	273/357 (76%)	254 (93%)	15 (6%)	4 (2%)	10	26
1	B	273/357 (76%)	260 (95%)	11 (4%)	2 (1%)	22	46
All	All	546/714 (76%)	514 (94%)	26 (5%)	6 (1%)	14	34

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 [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	239/306 (78%)	219 (92%)	20 (8%)	11	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	240/306 (78%)	213 (89%)	27 (11%)	6	13
All	All	479/612 (78%)	432 (90%)	47 (10%)	8	18

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	ARG
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	258	LEU
1	A	259	ARG
1	A	263	LYS
1	A	283	GLN
1	A	286	VAL
1	A	294	ARG
1	A	315	LYS
1	B	61	THR
1	B	75	SER
1	B	88	ARG
1	B	90	ARG
1	B	127	LEU
1	B	129	PRO
1	B	149	ARG
1	B	154	GLU
1	B	175	ARG
1	B	182	VAL
1	B	184	TYR
1	B	206	LYS
1	B	211	GLU
1	B	213[A]	HIS
1	B	213[B]	HIS
1	B	223	GLU

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Mol	Chain	Res	Type
1	B	231	LYS
1	B	246	SER
1	B	268	LEU
1	B	277	GLU
1	B	299	ARG
1	B	308	LEU
1	B	312	ARG
1	B	315	LYS
1	B	318	LEU
1	B	319	THR
1	B	333	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
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 monosaccharides 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
2	EPE	A	401	-	15,15,15	2.13	1 (6%)	18,20,20	1.99	7 (38%)
3	GOL	B	403	-	5,5,5	0.53	0	5,5,5	0.50	0
2	EPE	B	402	-	15,15,15	1.95	1 (6%)	18,20,20	2.02	7 (38%)
2	EPE	B	401	-	15,15,15	2.00	3 (20%)	18,20,20	1.86	6 (33%)

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	EPE	A	401	-	-	5/9/19/19	0/1/1/1
3	GOL	B	403	-	-	2/4/4/4	-
2	EPE	B	402	-	-	6/9/19/19	0/1/1/1
2	EPE	B	401	-	-	5/9/19/19	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	-7.04	1.67	1.77
2	A	401	EPE	C10-S	-6.92	1.67	1.77
2	B	401	EPE	C10-S	-5.84	1.69	1.77
2	B	401	EPE	O2S-S	2.21	1.51	1.45
2	B	401	EPE	C7-N4	2.08	1.52	1.47

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	EPE	O2S-S-C10	4.37	112.17	106.92
2	B	401	EPE	O3S-S-C10	3.74	111.82	105.77
2	B	402	EPE	O2S-S-C10	3.67	111.34	106.92
2	B	402	EPE	O1S-S-C10	3.32	110.91	106.92
2	B	402	EPE	C6-C5-N4	3.18	117.17	110.64
2	A	401	EPE	C6-N1-C2	3.18	115.98	108.83
2	B	401	EPE	C5-N4-C3	3.10	115.81	108.83
2	A	401	EPE	C7-N4-C3	2.65	118.02	111.23
2	A	401	EPE	C3-C2-N1	2.59	115.96	110.64
2	B	401	EPE	O3S-S-O1S	-2.57	105.01	111.27
2	B	402	EPE	C9-N1-C2	-2.48	104.90	111.23
2	B	401	EPE	C6-N1-C2	2.48	114.40	108.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	EPE	C2-C3-N4	2.47	115.72	110.64
2	B	402	EPE	C7-N4-C5	2.40	117.38	111.23
2	B	401	EPE	C6-C5-N4	2.39	115.55	110.64
2	A	401	EPE	C5-C6-N1	2.38	115.52	110.64
2	A	401	EPE	O3S-S-C10	2.22	109.37	105.77
2	B	402	EPE	C5-N4-C3	2.18	113.74	108.83
2	A	401	EPE	O2S-S-O1S	-2.07	106.80	113.95
2	B	402	EPE	C3-C2-N1	2.01	114.76	110.64

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	401	EPE	C8-C7-N4-C5
2	B	401	EPE	N4-C7-C8-O8
2	B	402	EPE	C8-C7-N4-C5
2	B	402	EPE	S-C10-C9-N1
2	B	402	EPE	C9-C10-S-O1S
2	B	402	EPE	C9-C10-S-O3S
3	B	403	GOL	C1-C2-C3-O3
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	A	401	EPE	C10-C9-N1-C6
2	B	402	EPE	C10-C9-N1-C6
2	B	401	EPE	S-C10-C9-N1

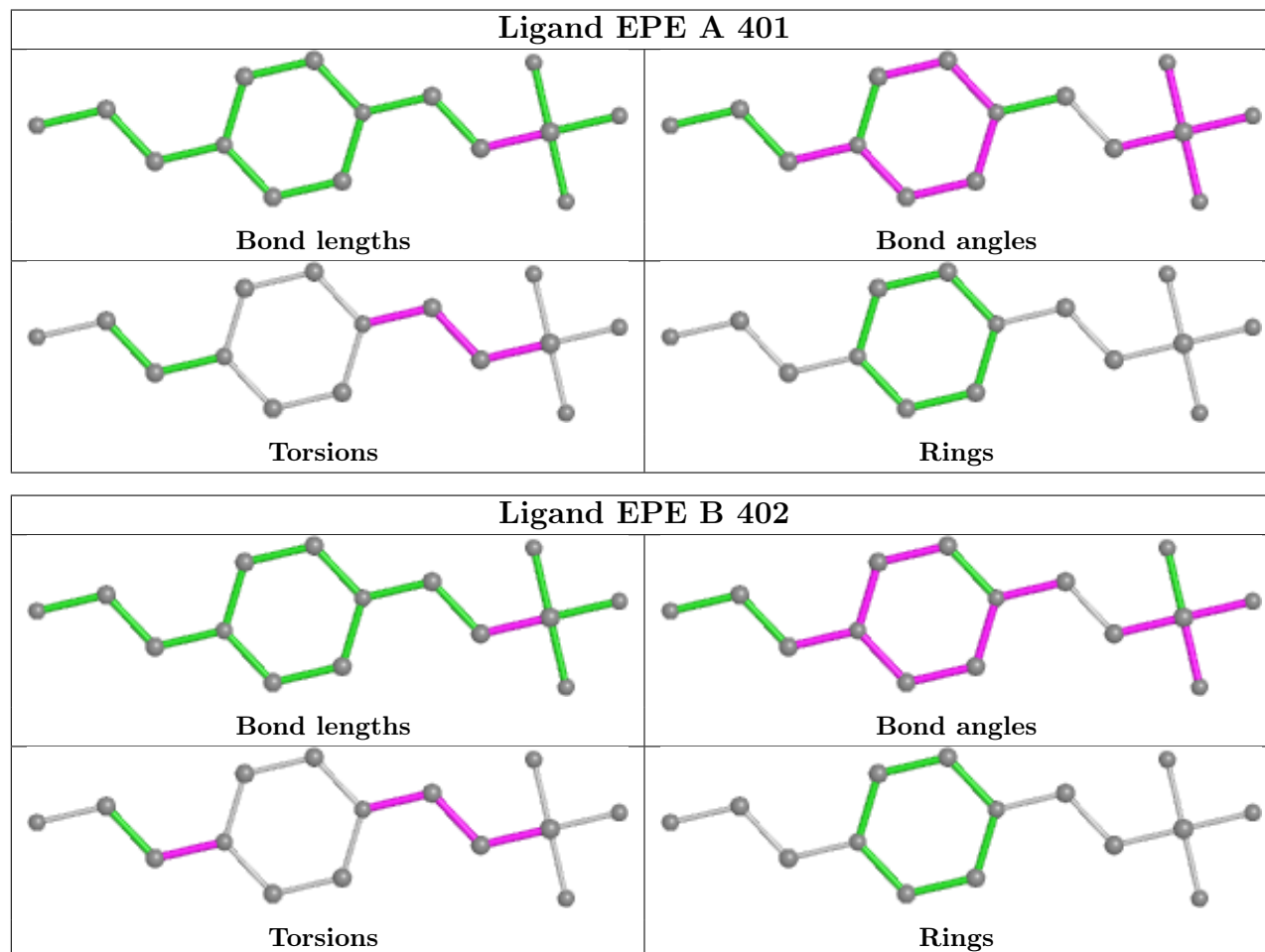
There are no ring outliers.

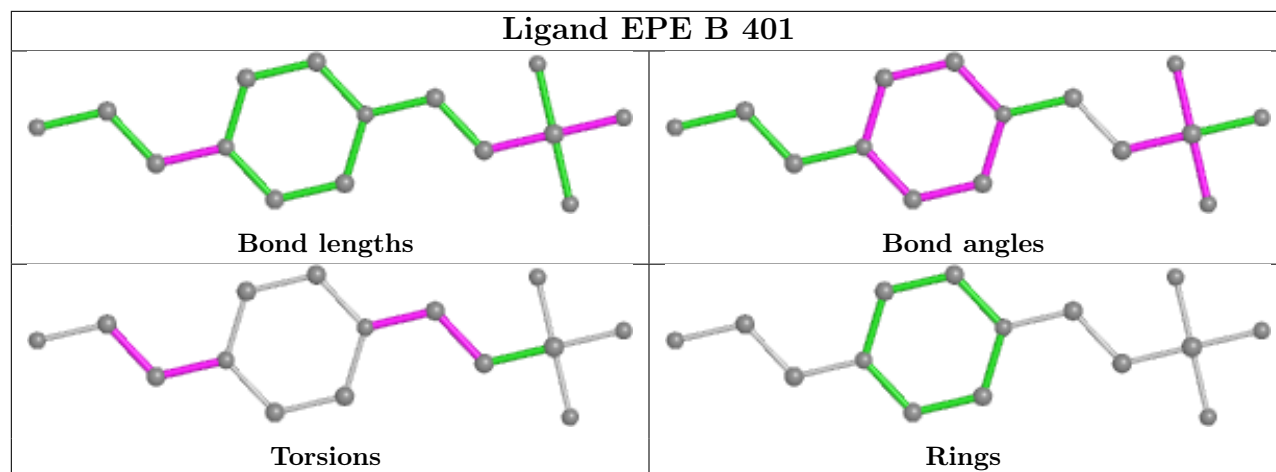
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	EPE	1	0
2	B	401	EPE	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 [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%)	0.06	3 (1%) 80 82	44, 70, 102, 120	0
1	B	274/357 (76%)	0.16	5 (1%) 68 70	47, 71, 105, 126	0
All	All	548/714 (76%)	0.11	8 (1%) 73 76	44, 71, 105, 126	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	333	ARG	3.4
1	A	129	PRO	3.3
1	A	260	ARG	3.0
1	B	235	THR	2.9
1	A	301	LEU	2.6
1	B	309	ASP	2.5
1	B	211	GLU	2.3
1	B	209	PRO	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 monosaccharides 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,

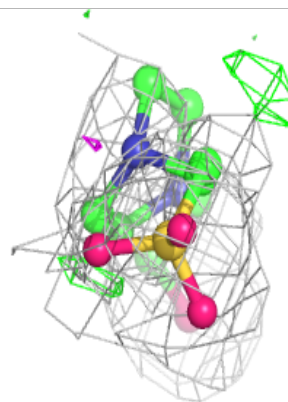
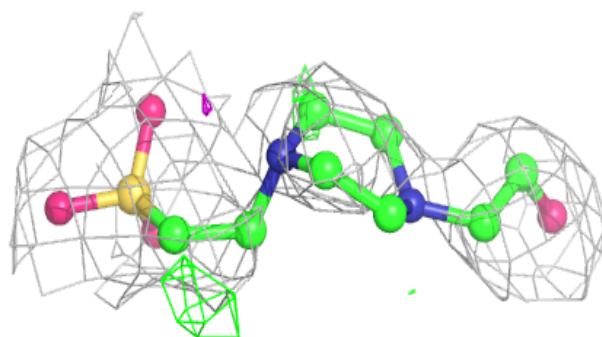
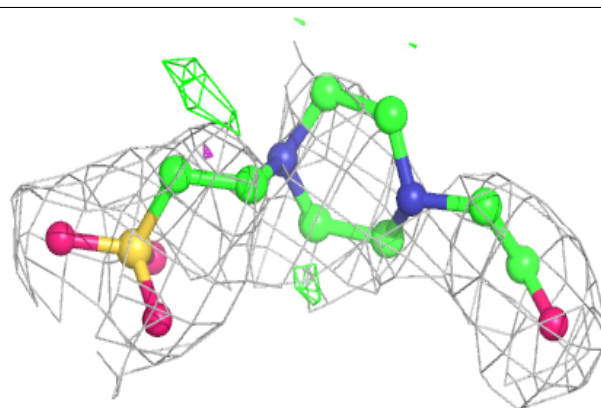
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	EPE	B	401	15/15	0.82	0.27	70,98,106,107	0
3	GOL	B	403	6/6	0.83	0.26	79,81,98,101	0
2	EPE	A	401	15/15	0.92	0.17	70,88,104,104	0
2	EPE	B	402	15/15	0.94	0.21	76,80,85,87	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.

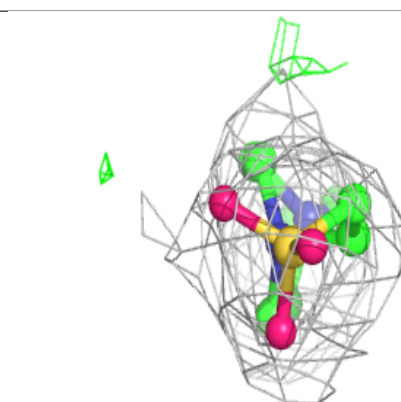
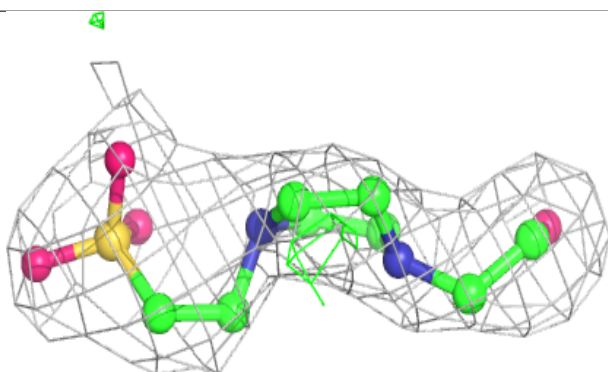
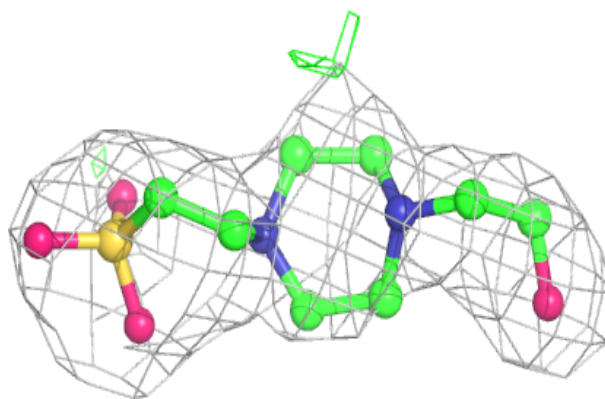
Electron density around EPE B 401:

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

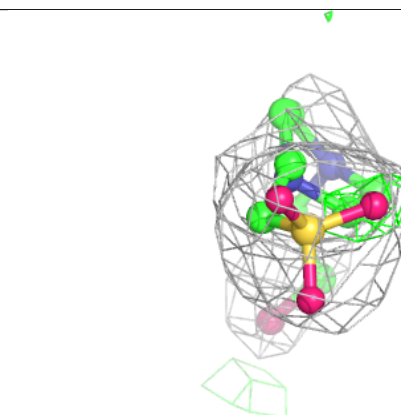
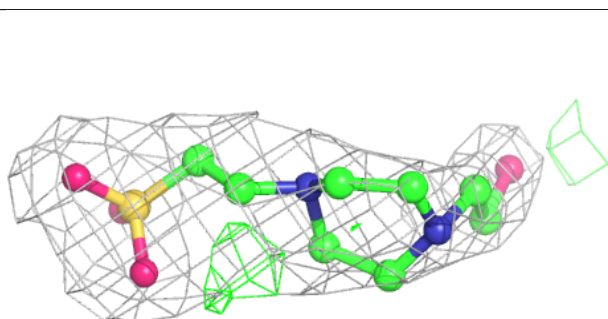
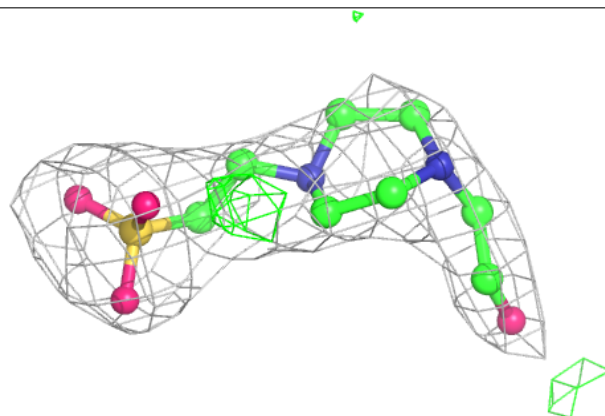


Electron density around EPE A 401:

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

**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)



6.5 Other polymers [i](#)

There are no such residues in this entry.