



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 06:05 AM UTC

PDB ID : 5IXS / pdb_00005ixs
Title : Lactate Dehydrogenase in complex with hydroxylactam inhibitor compound
9: (6R)-3-[(2-chlorophenyl)sulfanyl]-4-hydroxy-6-(3-hydroxyphenyl)-6-(thiophen-3-yl)-5,6-dihydropyridin-2(1H)-one
Authors : Ultsch, M.; Eigenbrot, C.
Deposited on : 2016-03-23
Resolution : 2.05 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

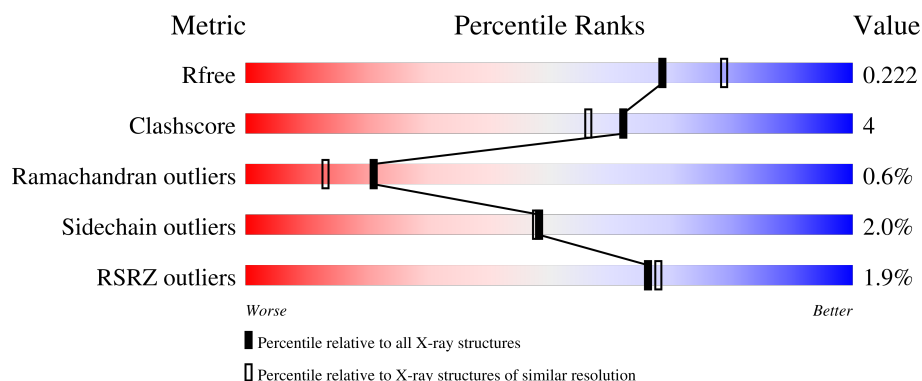
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	2260 (2.04-2.04)
Clashscore	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)
RSRZ outliers	180081	2260 (2.04-2.04)

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	331	2% 88% 9% ..
1	B	331	2% 86% 11% .
1	C	331	2% 90% 7% ..
1	D	331	2% 93% 5% .

2 Entry composition [i](#)

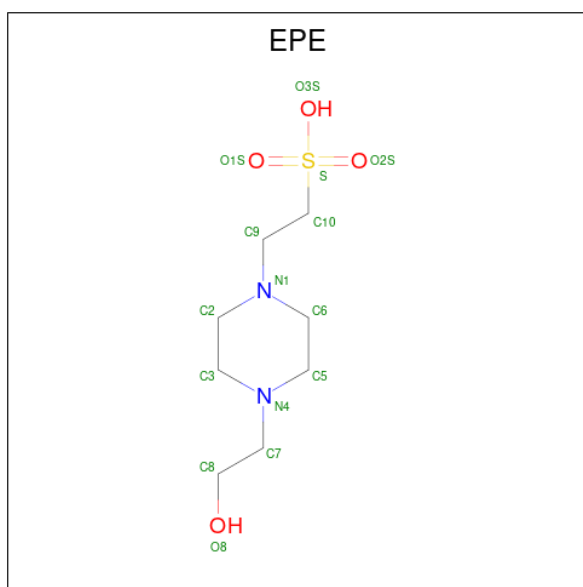
There are 7 unique types of molecules in this entry. The entry contains 11112 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 L-lactate dehydrogenase A chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	327	Total	C	N	O	S	0	4	0
			2556	1635	434	473	14			
1	B	324	Total	C	N	O	S	0	3	0
			2532	1626	430	463	13			
1	C	324	Total	C	N	O	S	0	2	0
			2522	1616	428	465	13			
1	D	330	Total	C	N	O	S	0	4	0
			2580	1650	441	475	14			

- Molecule 2 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: C₈H₁₈N₂O₄S).



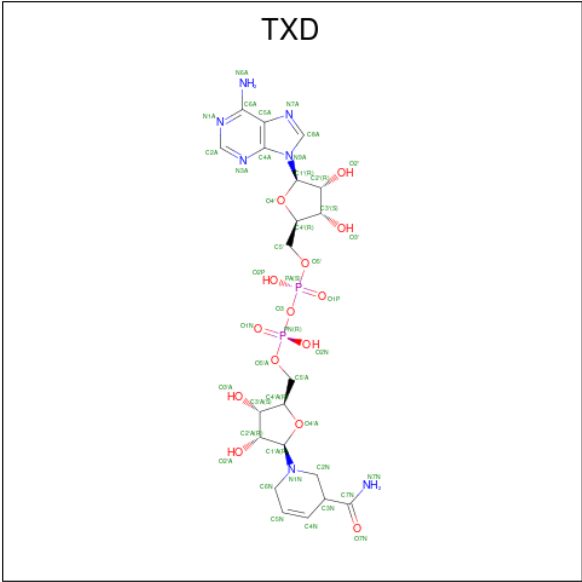
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
2	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

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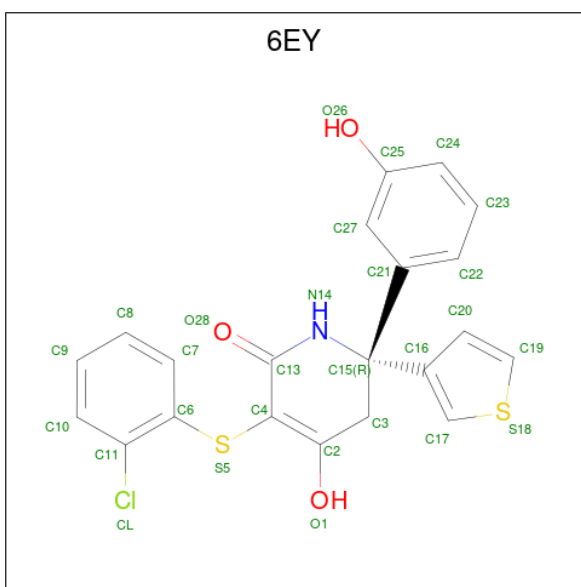
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 3 is 1,4,5,6-TETRAHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (CCD ID: TXD) (formula: C₂₁H₃₁N₇O₁₄P₂).



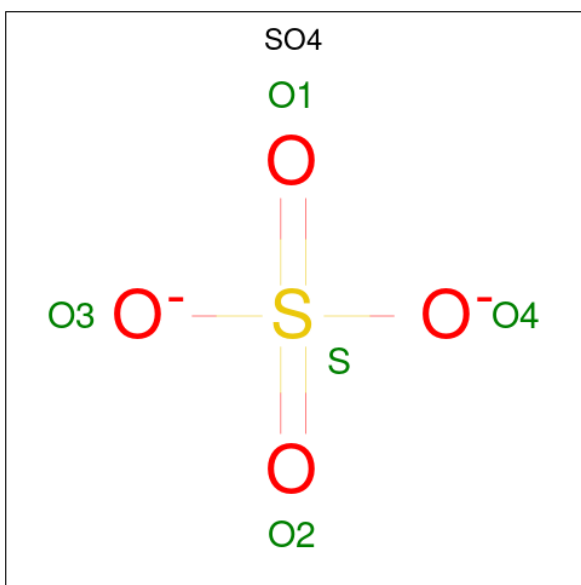
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 4 is (6R)-3-[(2-chlorophenyl)sulfanyl]-4-hydroxy-6-(3-hydroxyphenyl)-6-(thiophen-3-yl)-5,6-dihydropyridin-2(1H)-one (CCD ID: 6EY) (formula: C₂₁H₁₆ClNO₃S₂).



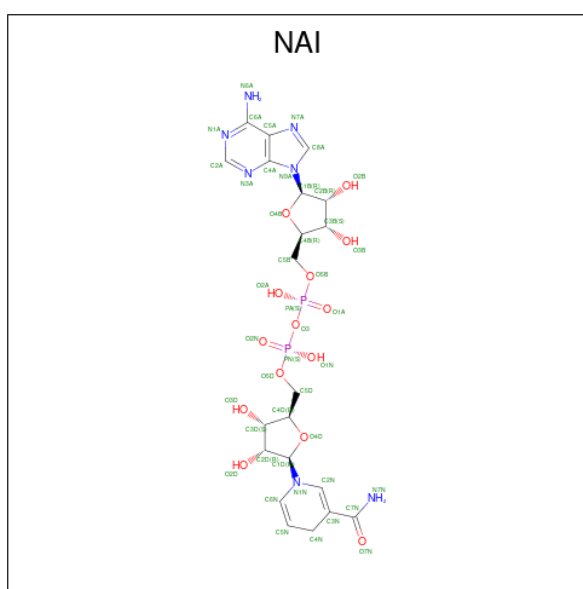
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	Cl	N	O	S	0	0
			28	21	1	1	3	2		
4	B	1	Total	C	Cl	N	O	S	0	0
			28	21	1	1	3	2		
4	C	1	Total	C	Cl	N	O	S	0	0
			28	21	1	1	3	2		
4	D	1	Total	C	Cl	N	O	S	0	0
			28	21	1	1	3	2		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 6 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (CCD ID: NAI) (formula: $C_{21}H_{29}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	C	1	Total C N O P 44 21 7 14 2	0	0

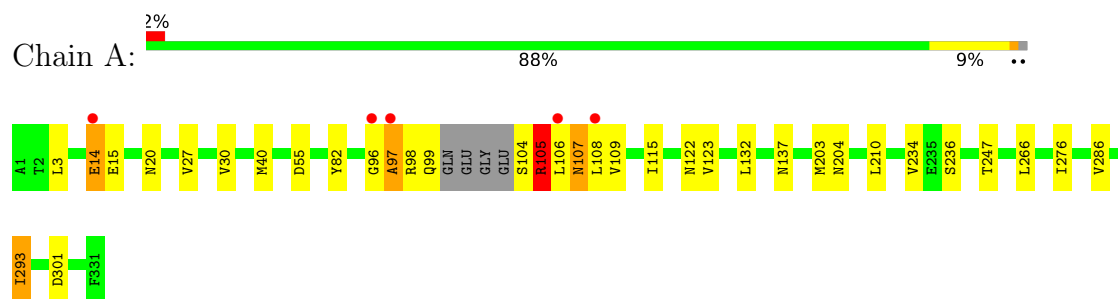
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	158	Total O 158 158	0	0
7	B	159	Total O 159 159	0	0
7	C	98	Total O 98 98	0	0
7	D	154	Total O 154 154	0	0

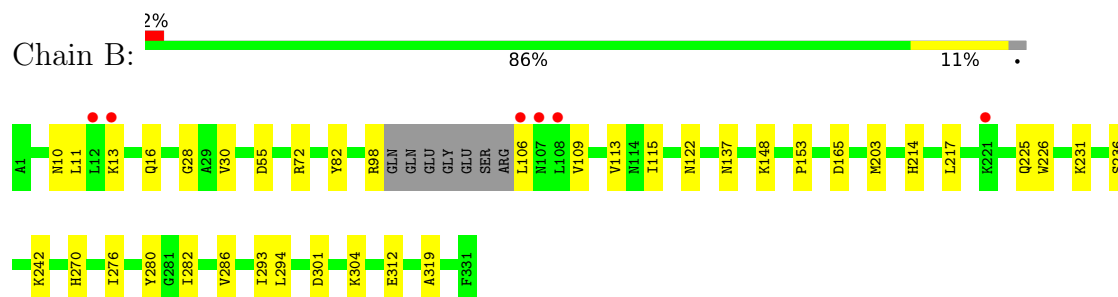
3 Residue-property plots [i](#)

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.

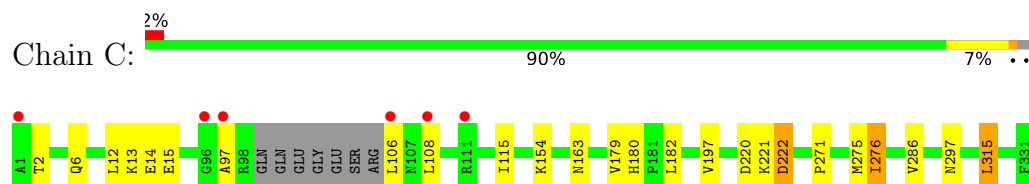
- Molecule 1: L-lactate dehydrogenase A chain



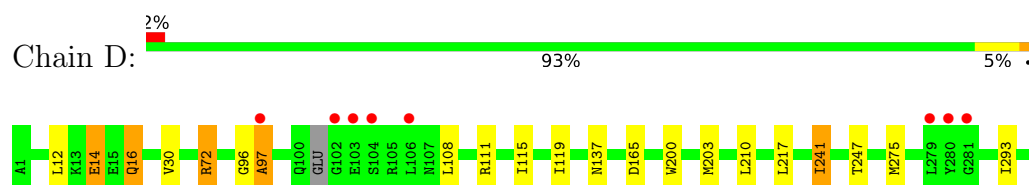
- Molecule 1: L-lactate dehydrogenase A chain



- Molecule 1: L-lactate dehydrogenase A chain



- Molecule 1: L-lactate dehydrogenase A chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	74.62Å 81.23Å 104.80Å 90.00° 97.56° 90.00°	Depositor
Resolution (Å)	37.80 – 2.05 37.80 – 2.05	Depositor EDS
% Data completeness (in resolution range)	98.0 (37.80-2.05) 98.0 (37.80-2.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 2.05Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.174 , 0.221 0.178 , 0.222	Depositor DCC
R_{free} test set	1571 reflections (2.02%)	wwPDB-VP
Wilson B-factor (Å ²)	32.7	Xtriage
Anisotropy	0.020	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 32.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11112	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TXD, NAI, SO4, 6EY, 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	0.58	0/2611	0.80	0/3529
1	B	0.56	0/2585	0.79	0/3495
1	C	0.53	0/2571	0.78	0/3476
1	D	0.56	0/2635	0.78	0/3560
All	All	0.56	0/10402	0.79	0/14060

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	2556	0	2656	33	0
1	B	2532	0	2639	29	0
1	C	2522	0	2623	18	0
1	D	2580	0	2687	16	0
2	A	15	0	17	0	0
2	B	15	0	17	1	0
2	C	15	0	18	0	0
3	A	44	0	27	6	0
3	B	44	0	27	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	44	0	27	2	0
4	A	28	0	0	2	0
4	B	28	0	0	2	0
4	C	28	0	0	0	0
4	D	28	0	0	0	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
5	C	5	0	0	0	0
5	D	5	0	0	0	0
6	C	44	0	26	1	0
7	A	158	0	0	2	0
7	B	159	0	0	5	0
7	C	98	0	0	1	0
7	D	154	0	0	0	0
All	All	11112	0	10764	88	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 4.

All (88) 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:105:ARG:HG2	1:A:105:ARG:HH11	1.23	0.97
1:A:20:ASN:OD1	7:A:501:HOH:O	2.01	0.78
1:B:98:ARG:HG3	4:B:403:6EY:C24	2.16	0.76
1:B:276:ILE:HD11	1:B:286:VAL:HG23	1.66	0.76
1:A:14:GLU:HB3	1:A:15:GLU:HB2	1.69	0.74
1:B:203:MET:HB2	7:B:654:HOH:O	1.91	0.70
1:B:30:VAL:HG21	3:B:402:TXD:H6N1	1.71	0.70
1:A:105:ARG:HG2	1:A:105:ARG:NH1	1.93	0.69
1:B:203:MET:SD	7:B:654:HOH:O	2.52	0.67
1:A:247:THR:HG23	3:A:402:TXD:H5N	1.78	0.66
1:A:293:ILE:CD1	1:C:179:VAL:HG22	2.25	0.65
1:B:10:ASN:OD1	1:B:13:LYS:HG2	1.97	0.64
1:A:99:GLN:HG2	1:A:108:LEU:HD22	1.82	0.62
1:B:72[A]:ARG:NH1	7:B:502:HOH:O	2.32	0.61
1:A:247:THR:CG2	3:A:402:TXD:H5N	2.30	0.61
1:D:203[A]:MET:HE2	1:D:217:LEU:HD21	1.84	0.60
1:D:96:GLY:O	1:D:111:ARG:NH1	2.36	0.59
1:A:3:LEU:HD13	1:B:214:HIS:HB2	1.84	0.59
1:D:203[A]:MET:HG2	1:D:210:LEU:HD22	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:137:ASN:ND2	3:B:402:TXD:H2N1	2.18	0.58
1:A:105:ARG:HG3	1:A:106:LEU:N	2.19	0.57
1:C:13:LYS:O	1:C:15:GLU:N	2.37	0.57
4:A:403:6EY:O26	7:A:502:HOH:O	2.17	0.56
1:B:98:ARG:CG	4:B:403:6EY:C24	2.84	0.56
1:B:276:ILE:HD13	1:B:282:ILE:HD13	1.87	0.56
1:B:225:GLN:NE2	7:B:503:HOH:O	2.38	0.56
1:C:276:ILE:HD11	1:C:286:VAL:HG23	1.88	0.56
1:A:293:ILE:HD12	1:C:179:VAL:HG22	1.87	0.55
1:A:14:GLU:HB3	1:A:15:GLU:CB	2.35	0.55
1:A:105:ARG:HH11	1:A:105:ARG:CG	2.08	0.55
1:A:30:VAL:HG21	3:A:402:TXD:H6N1	1.89	0.54
1:A:204:ASN:HA	1:A:210:LEU:HD13	1.90	0.54
1:D:30:VAL:HG21	3:D:801:TXD:H6N1	1.89	0.53
1:C:154[B]:LYS:HE2	1:C:275:MET:SD	2.49	0.52
1:C:182:LEU:HD11	1:D:72[B]:ARG:NH2	2.24	0.52
1:D:203[A]:MET:CE	1:D:217:LEU:HD21	2.40	0.52
1:D:115:ILE:HG22	1:D:119:ILE:HD12	1.93	0.51
1:D:200:TRP:CE3	1:D:203[B]:MET:SD	3.04	0.51
1:A:104:SER:O	1:A:105:ARG:HB3	2.11	0.50
1:A:293:ILE:HG13	1:A:301:ASP:HB2	1.93	0.50
1:A:97:ALA:HA	3:A:402:TXD:O2P	2.12	0.50
1:A:104:SER:HB2	1:A:107:ASN:HB2	1.92	0.50
1:A:98:ARG:O	1:A:99:GLN:C	2.54	0.49
1:C:115:ILE:HG23	6:C:402:NAI:N6A	2.27	0.49
1:A:96:GLY:O	1:A:97:ALA:CB	2.61	0.49
1:A:96:GLY:O	1:A:97:ALA:HB3	2.13	0.49
1:B:153:PRO:HA	2:B:401:EPE:H92	1.96	0.48
1:A:115:ILE:HG23	3:A:402:TXD:N6A	2.29	0.48
1:D:97:ALA:HB3	1:D:111:ARG:HH12	1.80	0.47
1:D:293[A]:ILE:HD12	1:D:301:ASP:HB2	1.96	0.47
1:A:82:TYR:CG	1:A:122:ASN:HB3	2.49	0.47
1:A:203:MET:HG2	1:A:210:LEU:HD22	1.96	0.47
1:C:221:LYS:O	1:C:222:ASP:C	2.58	0.47
1:D:137:ASN:ND2	3:D:801:TXD:H2N1	2.29	0.47
1:C:182:LEU:HD11	1:D:72[B]:ARG:CZ	2.46	0.46
1:C:197:VAL:HG21	1:C:315:LEU:HD23	1.96	0.46
1:B:109:VAL:O	1:B:113:VAL:HG23	2.15	0.46
1:D:12:LEU:HD22	1:D:14:GLU:HG2	1.96	0.46
1:C:154[B]:LYS:HE3	7:C:515:HOH:O	2.15	0.46
1:B:293:ILE:HD12	1:B:301:ASP:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:98:ARG:NH2	3:B:402:TXD:O1P	2.49	0.45
1:B:270:HIS:CD2	1:B:294:LEU:HD12	2.52	0.45
1:D:108:LEU:HD12	1:D:111:ARG:HH21	1.82	0.45
1:D:241:ILE:CD1	1:D:247:THR:HG23	2.47	0.45
1:B:16:GLN:HE21	1:C:297:ASN:HD22	1.65	0.44
1:B:115:ILE:HG23	3:B:402:TXD:N6A	2.33	0.44
1:A:98:ARG:HG2	4:A:403:6EY:O26	2.17	0.44
1:A:137:ASN:ND2	3:A:402:TXD:H2N1	2.33	0.43
1:B:82:TYR:CG	1:B:122:ASN:HB3	2.53	0.43
1:A:14:GLU:HB3	1:A:15:GLU:CA	2.48	0.43
1:B:231:LYS:HA	1:B:231:LYS:HD3	1.89	0.43
1:B:137:ASN:HD21	3:B:402:TXD:H2N1	1.81	0.43
1:A:123:VAL:HG11	1:A:132:LEU:HD21	2.01	0.42
1:A:276:ILE:HG22	1:A:286:VAL:HG23	2.01	0.42
1:B:28:GLY:HA3	3:B:402:TXD:O5'	2.19	0.42
1:B:242:LYS:NZ	7:B:509:HOH:O	2.52	0.42
1:B:280:TYR:HB3	1:B:312:GLU:HG3	2.00	0.42
1:C:163:ASN:HA	1:C:271:PRO:HG2	2.01	0.42
1:A:266:LEU:O	1:C:180:HIS:HB2	2.20	0.41
1:A:105:ARG:O	1:A:109:VAL:N	2.48	0.41
1:B:304:LYS:HE3	1:C:6:GLN:O	2.21	0.41
1:B:217:LEU:HD12	1:B:226:TRP:HB2	2.03	0.41
1:B:286:VAL:HG21	1:B:319:ALA:HB1	2.03	0.41
1:C:2:THR:O	1:C:6:GLN:HG3	2.21	0.41
1:D:203[A]:MET:HE1	1:D:217:LEU:HD11	2.03	0.41
1:C:12:LEU:HD12	1:C:12:LEU:O	2.20	0.40
1:B:11:LEU:HD23	1:C:154[A]:LYS:HG3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	327/331 (99%)	315 (96%)	9 (3%)	3 (1%)	14	7
1	B	323/331 (98%)	317 (98%)	6 (2%)	0	100	100
1	C	322/331 (97%)	312 (97%)	7 (2%)	3 (1%)	14	7
1	D	330/331 (100%)	322 (98%)	6 (2%)	2 (1%)	21	13
All	All	1302/1324 (98%)	1266 (97%)	28 (2%)	8 (1%)	21	13

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	105	ARG
1	C	14	GLU
1	A	97	ALA
1	D	97	ALA
1	C	222	ASP
1	C	97	ALA
1	D	16	GLN
1	A	27	VAL

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	288/287 (100%)	280 (97%)	8 (3%)	38	34
1	B	284/287 (99%)	279 (98%)	5 (2%)	51	51
1	C	283/287 (99%)	278 (98%)	5 (2%)	51	51
1	D	290/287 (101%)	283 (98%)	7 (2%)	43	40
All	All	1145/1148 (100%)	1120 (98%)	25 (2%)	48	44

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	GLU
1	A	55[A]	ASP
1	A	55[B]	ASP

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Mol	Chain	Res	Type
1	A	105	ARG
1	A	107	ASN
1	A	234	VAL
1	A	236	SER
1	A	293	ILE
1	B	55	ASP
1	B	106	LEU
1	B	148	LYS
1	B	165	ASP
1	B	236	SER
1	C	106	LEU
1	C	108	LEU
1	C	220	ASP
1	C	276	ILE
1	C	315	LEU
1	D	14	GLU
1	D	16	GLN
1	D	72[A]	ARG
1	D	72[B]	ARG
1	D	165	ASP
1	D	241	ILE
1	D	275	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	20	ASN
1	A	99	GLN
1	B	16	GLN
1	B	296	GLN
1	B	326	GLN
1	B	330	GLN
1	C	6	GLN
1	C	19	GLN
1	C	296	GLN
1	D	10	ASN
1	D	19	GLN
1	D	20	ASN
1	D	100	GLN
1	D	330	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

15 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	B	401	-	15,15,15	1.70	1 (6%)	19,20,20	4.29	13 (68%)
4	6EY	D	802	-	30,31,31	0.88	1 (3%)	32,45,45	1.49	4 (12%)
3	TXD	B	402	-	47,48,48	2.33	13 (27%)	66,73,73	2.24	18 (27%)
5	SO4	B	404	-	4,4,4	0.33	0	6,6,6	0.13	0
4	6EY	B	403	-	30,31,31	0.90	1 (3%)	32,45,45	1.74	4 (12%)
5	SO4	D	803	-	4,4,4	0.41	0	6,6,6	0.16	0
5	SO4	C	404	-	4,4,4	0.44	0	6,6,6	0.29	0
5	SO4	A	404	-	4,4,4	0.26	0	6,6,6	0.13	0
4	6EY	C	403	-	30,31,31	0.89	2 (6%)	32,45,45	1.42	2 (6%)
2	EPE	A	401	-	15,15,15	1.85	1 (6%)	19,20,20	4.10	10 (52%)
4	6EY	A	403	-	30,31,31	0.90	2 (6%)	32,45,45	1.45	5 (15%)
2	EPE	C	401	-	15,15,15	1.77	1 (6%)	19,20,20	4.28	10 (52%)
3	TXD	D	801	-	47,48,48	2.25	12 (25%)	66,73,73	2.44	22 (33%)
3	TXD	A	402	-	47,48,48	2.21	14 (29%)	66,73,73	2.38	22 (33%)
6	NAI	C	402	-	47,48,48	2.08	15 (31%)	64,73,73	2.23	13 (20%)

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	B	401	-	-	6/9/19/19	0/1/1/1
4	6EY	D	802	-	-	0/10/34/34	0/4/4/4
3	TXD	B	402	-	-	4/30/72/72	0/5/5/5
4	6EY	B	403	-	-	0/10/34/34	0/4/4/4
4	6EY	C	403	-	-	0/10/34/34	0/4/4/4
2	EPE	A	401	-	-	8/9/19/19	0/1/1/1
4	6EY	A	403	-	-	0/10/34/34	0/4/4/4
2	EPE	C	401	-	-	6/9/19/19	0/1/1/1
3	TXD	D	801	-	-	5/30/72/72	0/5/5/5
3	TXD	A	402	-	-	4/30/72/72	0/5/5/5
6	NAI	C	402	-	-	1/29/72/72	0/5/5/5

All (63) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	402	TXD	C4N-C5N	7.67	1.50	1.32
3	A	402	TXD	C4N-C5N	7.51	1.50	1.32
3	D	801	TXD	C4N-C5N	7.51	1.50	1.32
2	A	401	EPE	C10-S	-6.54	1.68	1.77
2	C	401	EPE	C10-S	-6.10	1.69	1.77
2	B	401	EPE	C10-S	-5.88	1.69	1.77
6	C	402	NAI	C6N-C5N	5.58	1.50	1.33
3	B	402	TXD	C2N-C3N	-5.07	1.47	1.53
6	C	402	NAI	C2N-C3N	4.92	1.48	1.35
3	D	801	TXD	C2'-C3'	-4.64	1.40	1.53
3	D	801	TXD	C7N-N7N	4.54	1.43	1.32
3	B	402	TXD	C7N-N7N	4.52	1.43	1.32
3	B	402	TXD	C2'-C3'	-4.50	1.41	1.53
3	B	402	TXD	C6A-N6A	4.47	1.45	1.34
3	A	402	TXD	C2'-C3'	-4.47	1.41	1.53
6	C	402	NAI	C6A-N6A	4.46	1.45	1.34
3	D	801	TXD	C2N-N1N	-4.34	1.40	1.47
3	B	402	TXD	C2N-N1N	-4.34	1.40	1.47
6	C	402	NAI	C2B-C3B	-4.20	1.42	1.53
3	D	801	TXD	C6A-N6A	4.19	1.44	1.34
3	A	402	TXD	C6A-N6A	4.15	1.44	1.34
3	A	402	TXD	C2N-C3N	-4.11	1.48	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	402	TXD	C7N-N7N	4.11	1.42	1.32
3	D	801	TXD	C2N-C3N	-3.78	1.48	1.53
3	D	801	TXD	O2'A-C2'A	-3.65	1.33	1.43
3	A	402	TXD	PA-O3	3.64	1.63	1.59
3	A	402	TXD	C2N-N1N	-3.53	1.41	1.47
6	C	402	NAI	C7N-N7N	3.51	1.43	1.33
6	C	402	NAI	O2D-C2D	-3.24	1.34	1.43
3	B	402	TXD	O2'A-C2'A	-3.20	1.35	1.43
3	B	402	TXD	PA-O3	3.18	1.62	1.59
6	C	402	NAI	C6N-N1N	2.97	1.44	1.37
6	C	402	NAI	PA-O3	2.94	1.62	1.59
6	C	402	NAI	C5D-C4D	-2.93	1.42	1.51
3	D	801	TXD	C5A-N7A	-2.91	1.33	1.39
3	A	402	TXD	C5'A-C4'A	-2.91	1.42	1.51
3	A	402	TXD	PN-O3	2.86	1.62	1.59
3	D	801	TXD	C5'A-C4'A	-2.81	1.43	1.51
3	D	801	TXD	C3N-C7N	-2.79	1.49	1.53
6	C	402	NAI	PN-O3	2.75	1.62	1.59
3	A	402	TXD	O2'A-C2'A	-2.59	1.36	1.43
3	B	402	TXD	C3N-C7N	-2.55	1.50	1.53
4	B	403	6EY	C17-S18	2.53	1.77	1.70
3	B	402	TXD	C5'A-C4'A	-2.46	1.44	1.51
3	D	801	TXD	C3'A-C2'A	-2.44	1.46	1.53
4	C	403	6EY	C17-S18	2.40	1.77	1.70
3	B	402	TXD	C5A-N7A	-2.40	1.34	1.39
3	A	402	TXD	C5A-N7A	-2.39	1.34	1.39
4	D	802	6EY	C15-C21	-2.31	1.51	1.53
4	A	403	6EY	C17-S18	2.25	1.76	1.70
6	C	402	NAI	C8A-N7A	2.24	1.36	1.31
3	D	801	TXD	C8A-N7A	2.20	1.35	1.31
6	C	402	NAI	C2D-C3D	-2.17	1.47	1.53
6	C	402	NAI	O3D-C3D	-2.16	1.37	1.43
3	B	402	TXD	C5'-C4'	-2.13	1.45	1.51
3	A	402	TXD	C3N-C7N	-2.08	1.50	1.53
3	A	402	TXD	C3'A-C2'A	-2.07	1.47	1.53
6	C	402	NAI	O4B-C4B	-2.07	1.40	1.45
4	A	403	6EY	C15-C21	-2.07	1.51	1.53
4	C	403	6EY	C20-C16	-2.04	1.39	1.44
6	C	402	NAI	C5A-N7A	-2.01	1.35	1.39
3	B	402	TXD	O4'-C4'	-2.01	1.40	1.45
3	A	402	TXD	C5'-C4'	-2.00	1.45	1.51

All (123) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	EPE	O1S-S-C10	-11.20	89.81	106.73
2	C	401	EPE	O2S-S-C10	-11.05	90.04	106.73
2	A	401	EPE	O1S-S-C10	-9.92	91.75	106.73
2	C	401	EPE	O3S-S-C10	-8.76	88.87	106.00
6	C	402	NAI	C1D-N1N-C2N	8.59	135.30	121.14
2	C	401	EPE	O1S-S-C10	-7.67	95.13	106.73
2	A	401	EPE	O2S-S-C10	-7.35	95.62	106.73
6	C	402	NAI	C1D-N1N-C6N	-7.28	105.38	120.77
4	B	403	6EY	C15-N14-C13	7.25	122.73	117.33
3	B	402	TXD	O4'A-C1'A-N1N	7.20	119.83	109.47
2	A	401	EPE	O3S-S-C10	-6.96	92.38	106.00
3	D	801	TXD	C2N-C3N-C4N	6.64	118.11	108.63
3	A	402	TXD	C6N-N1N-C2N	6.62	119.62	109.43
3	A	402	TXD	C2N-C3N-C4N	6.45	117.84	108.63
3	D	801	TXD	O4'A-C1'A-N1N	6.42	118.72	109.47
3	B	402	TXD	C3N-C4N-C5N	-6.34	112.54	123.33
3	D	801	TXD	C6N-N1N-C2N	6.26	119.06	109.43
3	D	801	TXD	C5A-C4A-N3A	-6.21	118.16	126.72
2	B	401	EPE	O2S-S-C10	-6.13	97.46	106.73
3	D	801	TXD	C3N-C4N-C5N	-5.94	113.22	123.33
4	C	403	6EY	C15-N14-C13	5.91	121.73	117.33
3	A	402	TXD	C3N-C4N-C5N	-5.89	113.31	123.33
6	C	402	NAI	O4D-C1D-N1N	5.39	118.37	108.08
3	A	402	TXD	O4'A-C1'A-N1N	5.38	117.21	109.47
2	A	401	EPE	C6-N1-C2	5.30	120.26	108.84
2	C	401	EPE	C6-N1-C2	5.20	120.04	108.84
3	B	402	TXD	C4N-C3N-C7N	5.15	124.25	109.80
3	A	402	TXD	C5A-C4A-N3A	-5.13	119.66	126.72
2	B	401	EPE	O3S-S-C10	-5.08	96.07	106.00
6	C	402	NAI	C5A-C4A-N3A	-5.04	119.78	126.72
4	A	403	6EY	C15-N14-C13	4.96	121.02	117.33
2	B	401	EPE	C6-N1-C2	4.93	119.47	108.84
3	B	402	TXD	C5A-C4A-N3A	-4.93	119.93	126.72
2	A	401	EPE	C6-C5-N4	-4.84	100.90	110.65
3	B	402	TXD	C2N-C3N-C4N	4.83	115.52	108.63
3	A	402	TXD	N1A-C2A-N3A	-4.76	121.38	128.58
3	B	402	TXD	C6N-N1N-C2N	4.73	116.70	109.43
2	B	401	EPE	C6-C5-N4	4.72	120.16	110.65
2	B	401	EPE	C5-C6-N1	4.67	120.06	110.65
2	B	401	EPE	C5-N4-C3	4.56	118.66	108.84
6	C	402	NAI	N3A-C2A-N1A	-4.53	121.73	128.58
2	B	401	EPE	C2-C3-N4	4.51	119.74	110.65
3	A	402	TXD	C4N-C3N-C7N	4.27	121.77	109.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	EPE	O3S-S-O1S	4.25	122.02	111.40
4	D	802	6EY	C15-N14-C13	4.17	120.43	117.33
3	B	402	TXD	N1A-C2A-N3A	-4.15	122.29	128.58
2	B	401	EPE	C3-C2-N1	4.07	118.86	110.65
3	D	801	TXD	N1A-C2A-N3A	-4.04	122.47	128.58
3	D	801	TXD	N3A-C4A-N9A	3.96	133.89	127.17
3	D	801	TXD	C2A-N3A-C4A	3.89	121.34	111.83
3	D	801	TXD	C4N-C3N-C7N	3.86	120.64	109.80
3	A	402	TXD	C2A-N3A-C4A	3.82	121.15	111.83
6	C	402	NAI	C2A-N3A-C4A	3.62	120.68	111.83
2	C	401	EPE	O3S-S-O2S	3.59	120.38	111.40
3	B	402	TXD	C5N-C6N-N1N	3.57	119.49	110.94
3	D	801	TXD	C4A-C5A-N7A	-3.54	106.54	110.58
3	B	402	TXD	N3A-C4A-N9A	3.52	133.16	127.17
3	D	801	TXD	C5N-C6N-N1N	3.52	119.38	110.94
3	A	402	TXD	N3A-C4A-N9A	3.49	133.10	127.17
4	D	802	6EY	C6-S5-C4	3.40	107.13	102.81
6	C	402	NAI	N3A-C4A-N9A	3.39	132.93	127.17
3	A	402	TXD	N9A-C8A-N7A	-3.37	109.15	113.94
3	D	801	TXD	C5A-N7A-C8A	3.34	108.70	103.45
4	A	403	6EY	C3-C15-N14	3.30	112.08	108.09
2	A	401	EPE	O3S-S-O2S	3.28	119.61	111.40
2	A	401	EPE	C7-N4-C5	3.28	119.98	111.24
3	B	402	TXD	C2A-N3A-C4A	3.28	119.83	111.83
2	A	401	EPE	C3-C2-N1	3.26	117.23	110.65
3	D	801	TXD	O4'-C1'-N9A	3.22	114.27	108.09
2	C	401	EPE	C5-C6-N1	3.21	117.11	110.65
2	A	401	EPE	C10-C9-N1	-3.17	100.36	112.36
3	B	402	TXD	N9A-C8A-N7A	-3.15	109.47	113.94
4	D	802	6EY	C4-C13-N14	3.14	120.09	113.96
4	C	403	6EY	C4-C13-N14	3.14	120.08	113.96
2	C	401	EPE	O3S-S-O1S	3.13	119.22	111.40
3	A	402	TXD	C5A-N7A-C8A	3.09	108.31	103.45
3	A	402	TXD	C6N-N1N-C1'A	-3.05	104.08	112.93
6	C	402	NAI	N9A-C8A-N7A	-2.98	109.71	113.94
6	C	402	NAI	C4A-C5A-N7A	-2.97	107.19	110.58
6	C	402	NAI	C4D-O4D-C1D	-2.94	102.97	109.47
3	A	402	TXD	C5N-C6N-N1N	2.93	117.96	110.94
3	A	402	TXD	C4'A-O4'A-C1'A	-2.90	103.05	109.47
3	D	801	TXD	N9A-C8A-N7A	-2.90	109.82	113.94
2	C	401	EPE	C2-C3-N4	-2.89	104.81	110.65
3	A	402	TXD	O2N-PN-O3	2.89	115.08	107.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402	TXD	C4A-C5A-N7A	-2.87	107.30	110.58
6	C	402	NAI	C5A-N7A-C8A	2.83	107.90	103.45
2	B	401	EPE	O2S-S-O1S	2.80	122.94	113.82
3	A	402	TXD	C3N-C7N-N7N	2.80	119.70	116.80
3	D	801	TXD	C4'A-O4'A-C1'A	-2.77	103.35	109.47
3	D	801	TXD	C6N-N1N-C1'A	-2.76	104.91	112.93
3	B	402	TXD	C5A-N7A-C8A	2.76	107.79	103.45
4	B	403	6EY	C4-C13-N14	2.68	119.19	113.96
2	B	401	EPE	O3S-S-O1S	2.67	118.07	111.40
3	B	402	TXD	C4A-C5A-N7A	-2.65	107.56	110.58
3	D	801	TXD	C4'-O4'-C1'	-2.64	103.64	109.47
3	D	801	TXD	C3N-C7N-N7N	2.62	119.52	116.80
3	A	402	TXD	O4'-C1'-N9A	2.53	112.94	108.09
4	B	403	6EY	C24-C25-C27	-2.51	117.44	120.19
2	C	401	EPE	C7-N4-C3	2.50	117.90	111.24
4	D	802	6EY	C3-C15-N14	2.44	111.04	108.09
6	C	402	NAI	O4B-C1B-N9A	2.44	112.77	108.09
4	A	403	6EY	C4-C13-N14	2.43	118.71	113.96
3	B	402	TXD	C4A-N9A-C8A	2.41	108.27	105.74
3	B	402	TXD	C4'-O4'-C1'	-2.39	104.19	109.47
4	A	403	6EY	C15-C16-C17	-2.39	123.16	126.64
3	B	402	TXD	O5'A-C5'A-C4'A	2.38	117.08	108.99
2	C	401	EPE	C10-C9-N1	-2.37	103.38	112.36
3	D	801	TXD	O2N-PN-O3	2.36	113.64	107.27
3	A	402	TXD	O7N-C7N-N7N	-2.35	118.90	123.04
2	B	401	EPE	O3S-S-O2S	2.33	117.23	111.40
3	D	801	TXD	O5'-C5'-C4'	2.31	116.84	108.99
2	B	401	EPE	C10-C9-N1	-2.30	103.67	112.36
3	B	402	TXD	C6N-N1N-C1'A	-2.30	106.26	112.93
4	B	403	6EY	C3-C15-N14	2.24	110.80	108.09
3	A	402	TXD	C4'-O4'-C1'	-2.22	104.56	109.47
3	B	402	TXD	C4'A-O4'A-C1'A	-2.22	104.56	109.47
3	D	801	TXD	O4'-C1'-C2'	-2.22	101.87	106.62
3	A	402	TXD	C4A-N9A-C8A	2.16	108.00	105.74
4	A	403	6EY	C6-S5-C4	2.11	105.48	102.81
3	A	402	TXD	C3'A-C2'A-C1'A	-2.10	97.50	101.46
6	C	402	NAI	C4A-N9A-C8A	2.07	107.91	105.74
3	D	801	TXD	O5'A-C5'A-C4'A	2.03	115.91	108.99

There are no chirality outliers.

All (34) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	EPE	C9-C10-S-O1S
2	A	401	EPE	C9-C10-S-O3S
2	B	401	EPE	C10-C9-N1-C6
2	C	401	EPE	C8-C7-N4-C3
3	A	402	TXD	O4'A-C1'A-N1N-C2N
3	B	402	TXD	O4'A-C1'A-N1N-C2N
3	D	801	TXD	O4'A-C1'A-N1N-C2N
2	A	401	EPE	C8-C7-N4-C5
2	B	401	EPE	C9-C10-S-O3S
2	C	401	EPE	C9-C10-S-O3S
3	A	402	TXD	C2N-C3N-C7N-N7N
3	B	402	TXD	C2N-C3N-C7N-N7N
3	D	801	TXD	C2N-C3N-C7N-N7N
3	A	402	TXD	C2N-C3N-C7N-O7N
3	D	801	TXD	C2N-C3N-C7N-O7N
2	A	401	EPE	S-C10-C9-N1
2	A	401	EPE	C10-C9-N1-C2
2	A	401	EPE	C10-C9-N1-C6
3	B	402	TXD	C2N-C3N-C7N-O7N
2	C	401	EPE	C8-C7-N4-C5
2	A	401	EPE	C9-C10-S-O2S
2	B	401	EPE	C9-C10-S-O1S
2	B	401	EPE	C9-C10-S-O2S
2	C	401	EPE	C9-C10-S-O1S
2	C	401	EPE	C9-C10-S-O2S
3	A	402	TXD	C2'A-C1'A-N1N-C2N
3	D	801	TXD	C2'A-C1'A-N1N-C2N
2	B	401	EPE	N4-C7-C8-O8
2	B	401	EPE	C10-C9-N1-C2
2	C	401	EPE	C10-C9-N1-C6
2	A	401	EPE	C8-C7-N4-C3
6	C	402	NAI	O4D-C1D-N1N-C2N
3	B	402	TXD	C4N-C3N-C7N-N7N
3	D	801	TXD	O4'-C4'-C5'-O5'

There are no ring outliers.

7 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	EPE	1	0
3	B	402	TXD	6	0
4	B	403	6EY	2	0
4	A	403	6EY	2	0

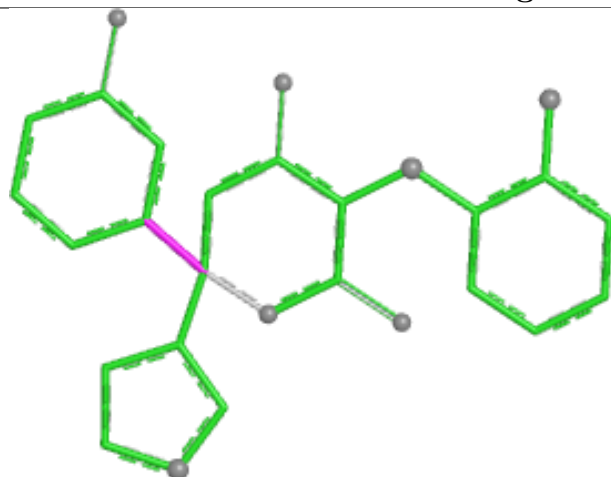
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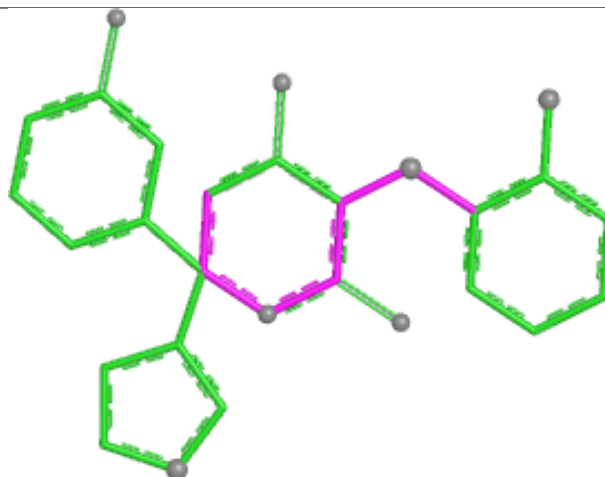
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	801	TXD	2	0
3	A	402	TXD	6	0
6	C	402	NAI	1	0

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.

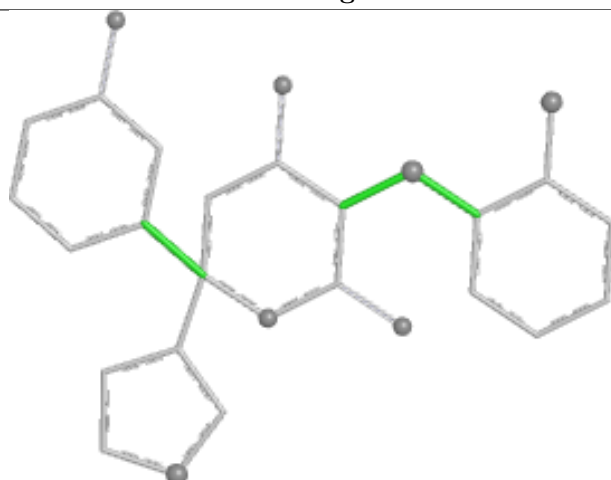
Ligand 6EY D 802



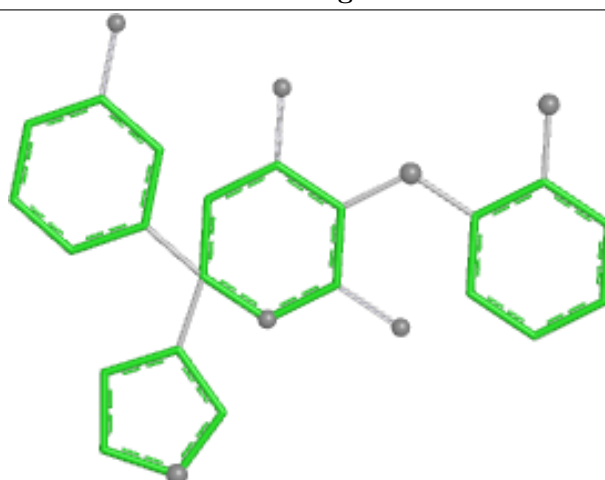
Bond lengths



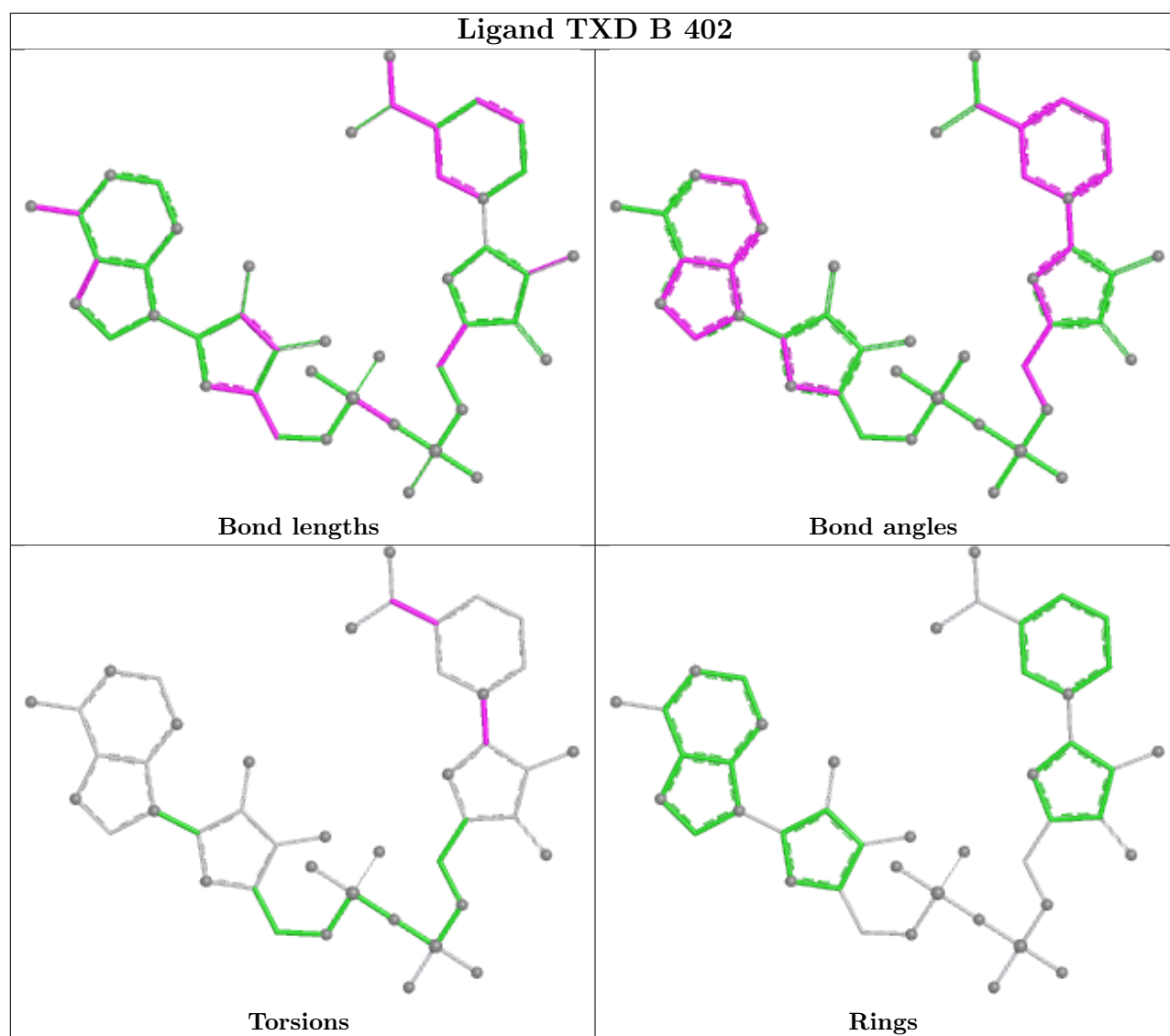
Bond angles



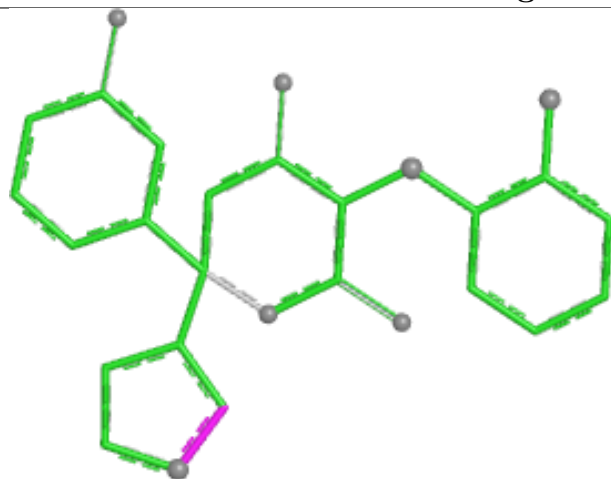
Torsions



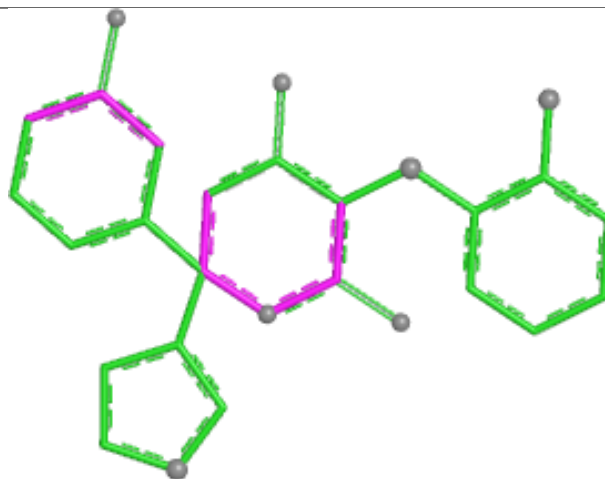
Rings



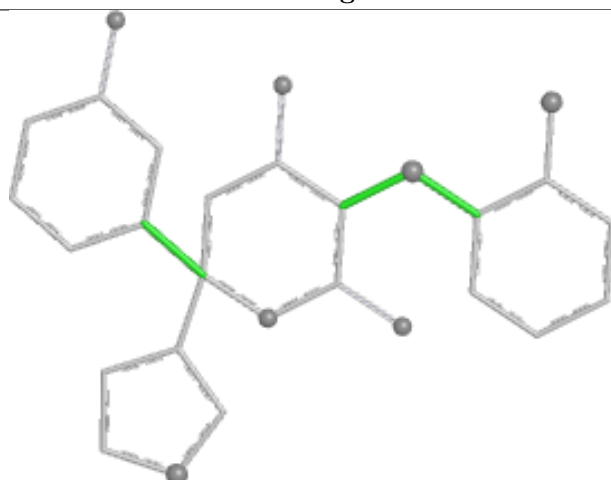
Ligand 6EY B 403



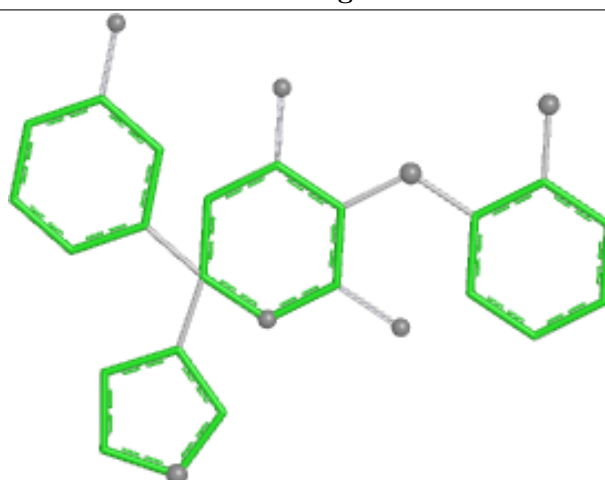
Bond lengths



Bond angles

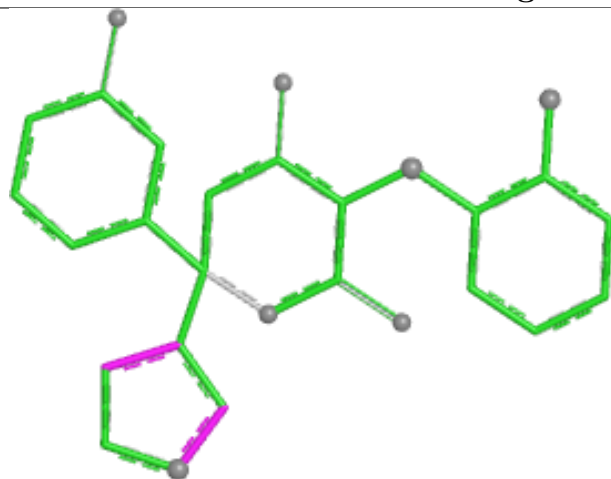


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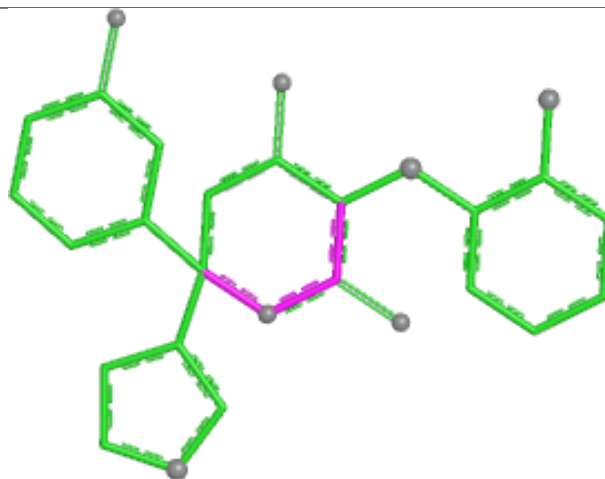


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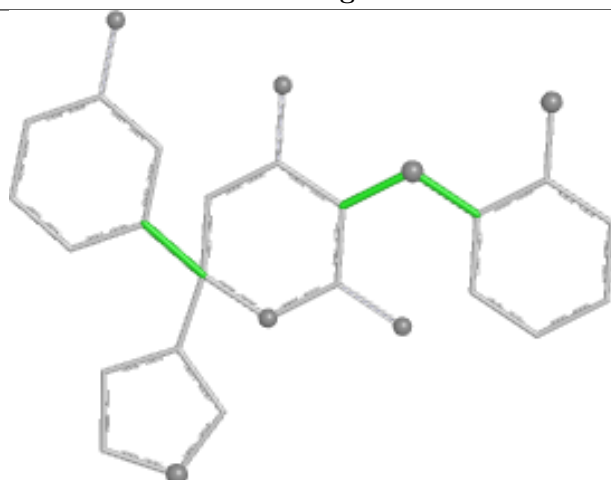
Ligand 6EY C 403



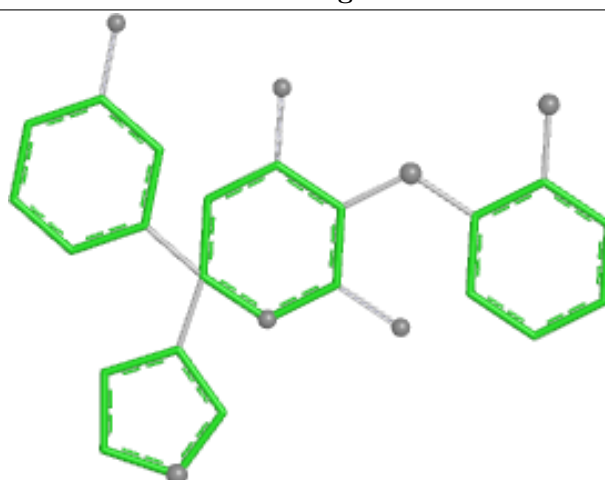
Bond lengths



Bond angles

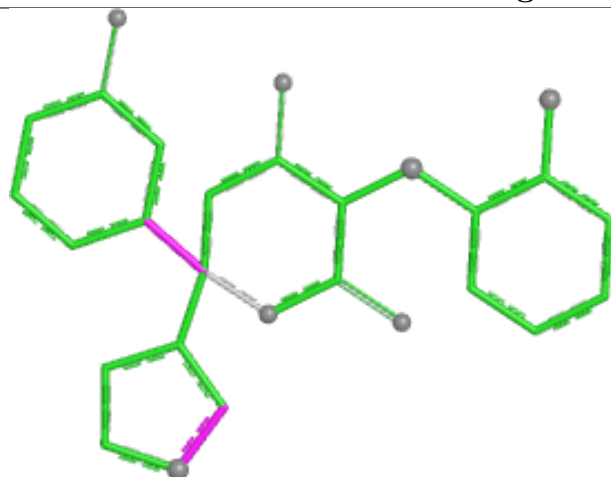


Torsions

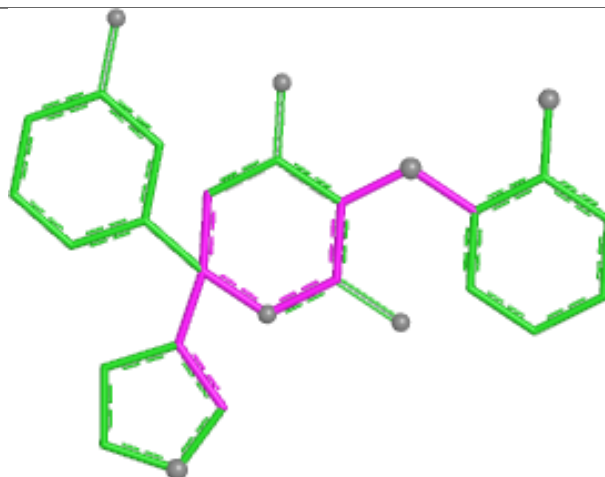


Rings

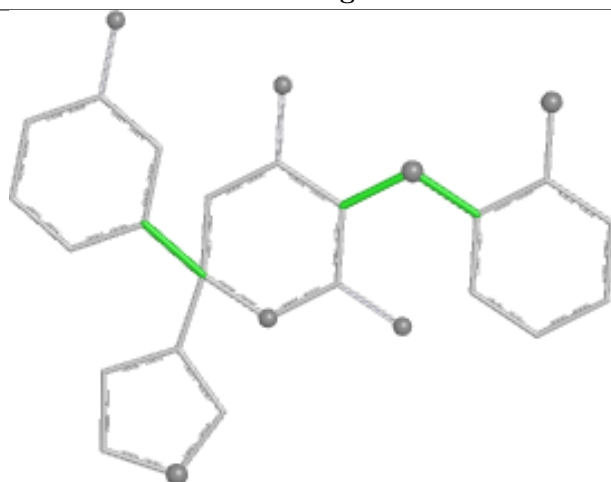
Ligand 6EY A 403



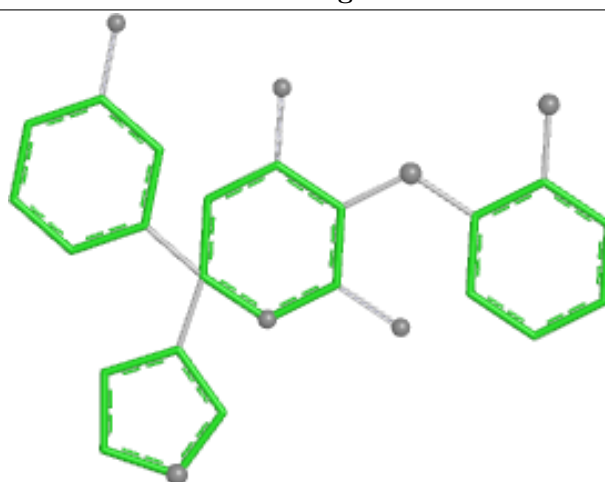
Bond lengths



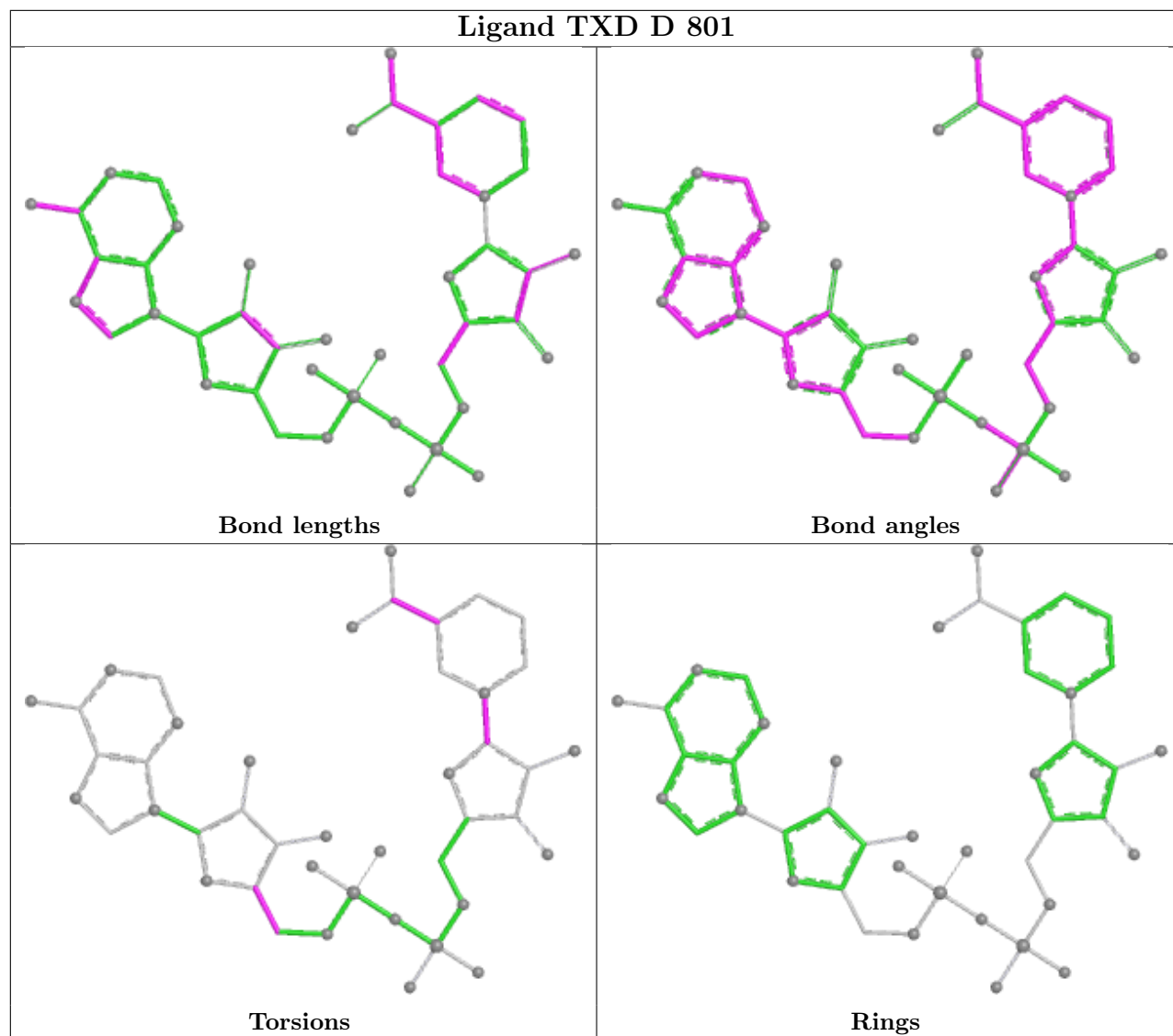
Bond angles

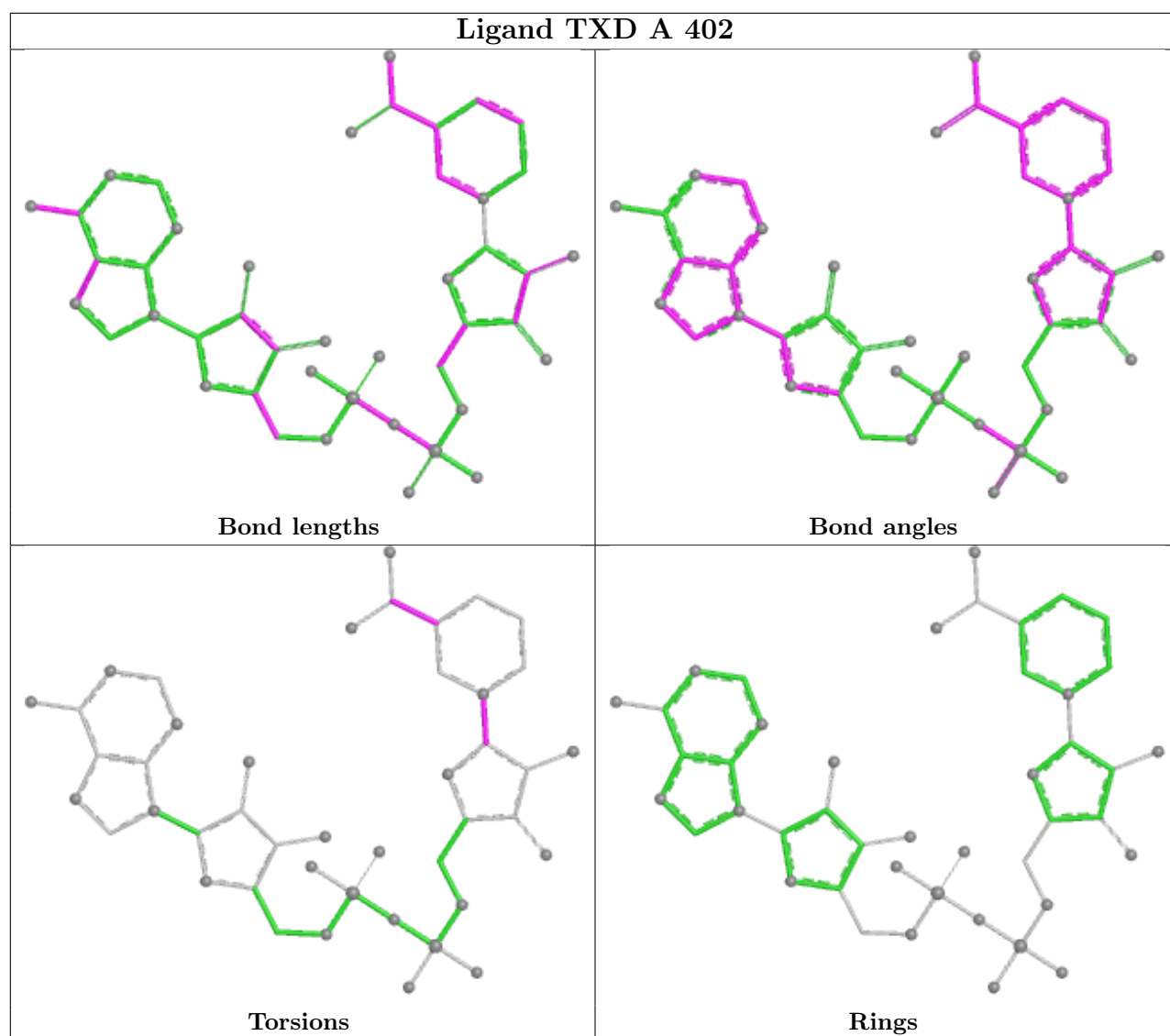


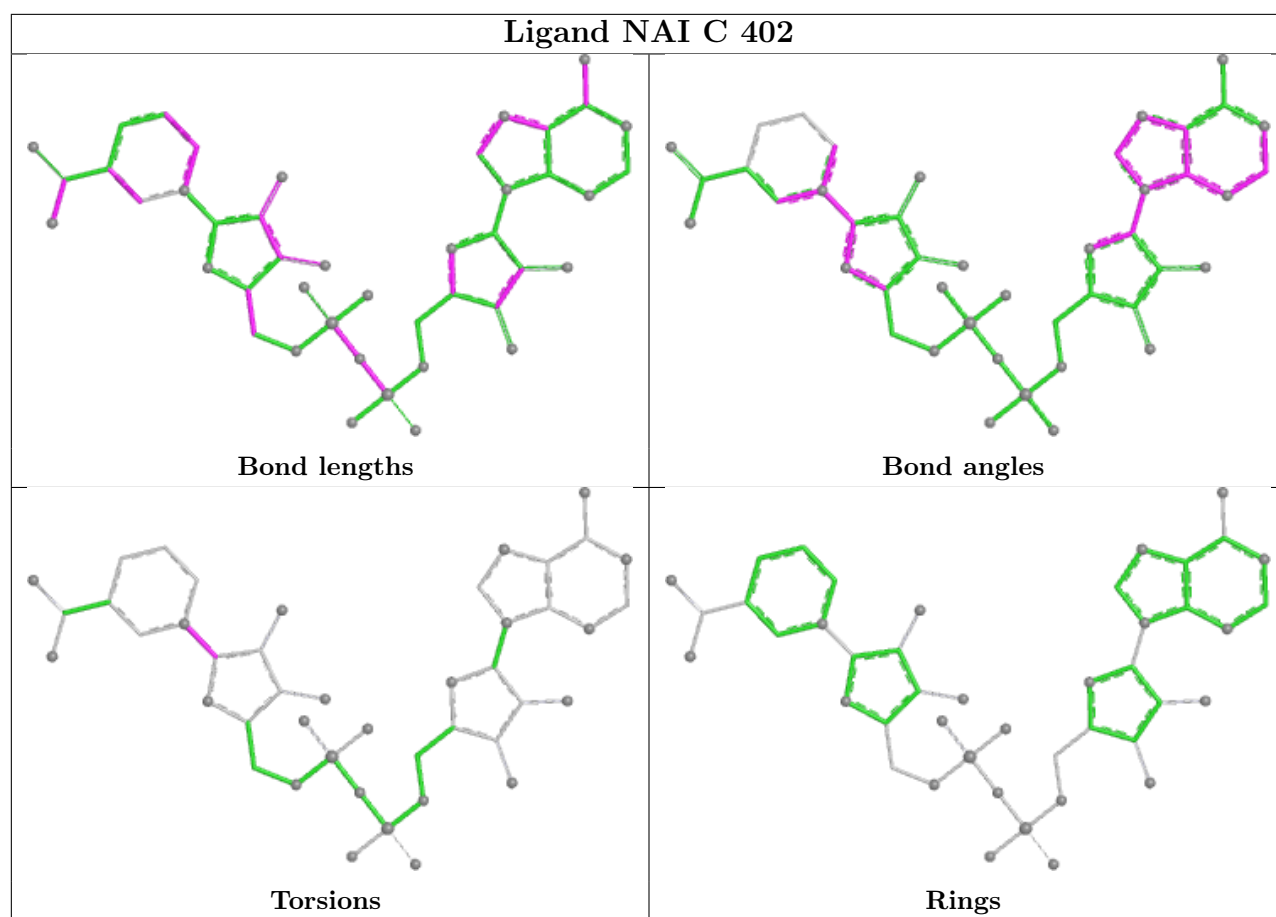
Torsions



Rings







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	327/331 (98%)	-0.34	5 (1%) 72 73	13, 30, 59, 88	4 (1%)
1	B	324/331 (97%)	-0.33	6 (1%) 66 68	18, 30, 60, 108	3 (0%)
1	C	324/331 (97%)	-0.06	6 (1%) 66 68	21, 38, 82, 135	2 (0%)
1	D	330/331 (99%)	-0.32	8 (2%) 59 61	15, 30, 68, 119	4 (1%)
All	All	1305/1324 (98%)	-0.26	25 (1%) 66 68	13, 32, 71, 135	13 (0%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	106	LEU	4.7
1	B	108	LEU	3.9
1	A	106	LEU	3.5
1	C	106	LEU	3.3
1	A	97	ALA	3.2
1	B	106	LEU	3.2
1	C	97	ALA	3.1
1	C	108	LEU	3.1
1	D	102	GLY	3.1
1	A	14	GLU	3.0
1	D	104	SER	2.9
1	C	1	ALA	2.7
1	A	96	GLY	2.7
1	D	97	ALA	2.6
1	B	221	LYS	2.4
1	C	111	ARG	2.3
1	C	96	GLY	2.2
1	D	103	GLU	2.2
1	B	107	ASN	2.2
1	A	108	LEU	2.2
1	B	12	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	281	GLY	2.1
1	B	13	LYS	2.1
1	D	279	LEU	2.1
1	D	280	TYR	2.0

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](#)

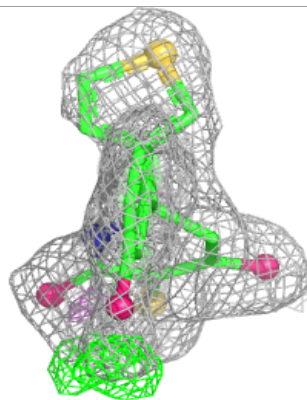
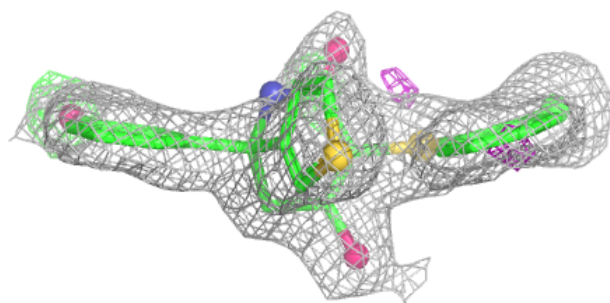
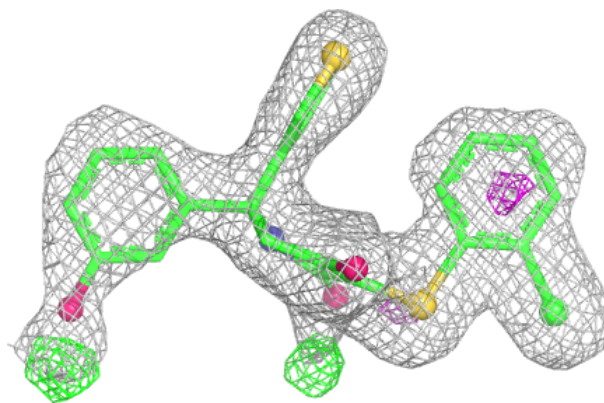
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	EPE	C	401	15/15	0.72	0.20	49,76,92,95	15
2	EPE	A	401	15/15	0.81	0.17	34,57,65,67	15
2	EPE	B	401	15/15	0.86	0.14	43,57,81,94	15
4	6EY	B	403	28/28	0.92	0.11	34,57,72,83	0
6	NAI	C	402	44/44	0.92	0.08	34,50,60,68	0
4	6EY	C	403	28/28	0.94	0.08	26,51,71,84	0
4	6EY	A	403	28/28	0.96	0.07	26,37,47,57	0
4	6EY	D	802	28/28	0.96	0.07	31,38,59,71	0
3	TXD	B	402	44/44	0.96	0.06	24,34,40,45	0
3	TXD	D	801	44/44	0.97	0.06	22,34,40,53	0
3	TXD	A	402	44/44	0.97	0.05	21,30,38,44	0
5	SO4	D	803	5/5	0.98	0.06	21,23,26,32	4
5	SO4	C	404	5/5	0.99	0.04	24,24,31,36	4
5	SO4	A	404	5/5	0.99	0.06	23,24,29,35	4
5	SO4	B	404	5/5	0.99	0.05	20,24,26,32	4

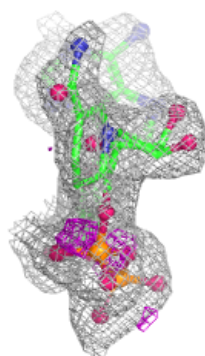
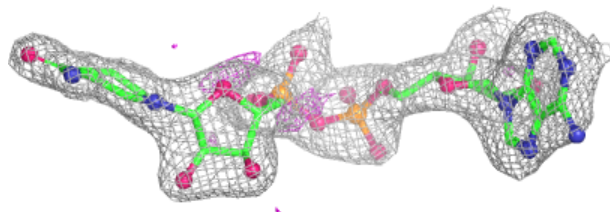
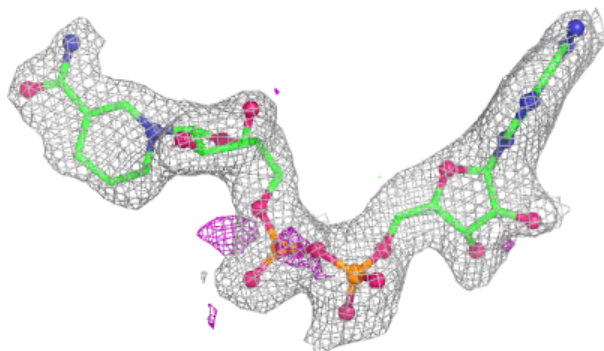
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 6EY B 403:

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

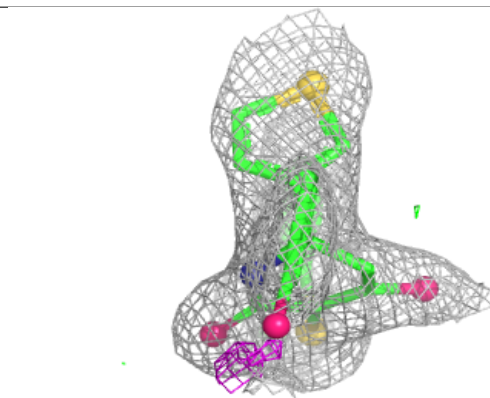
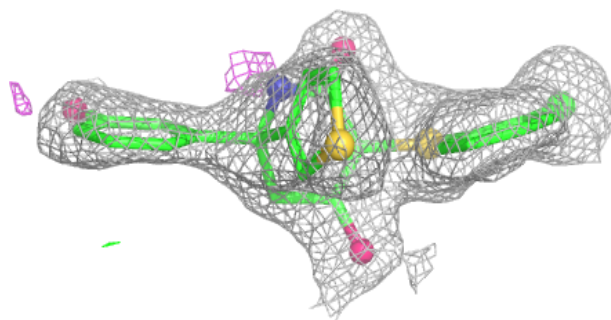
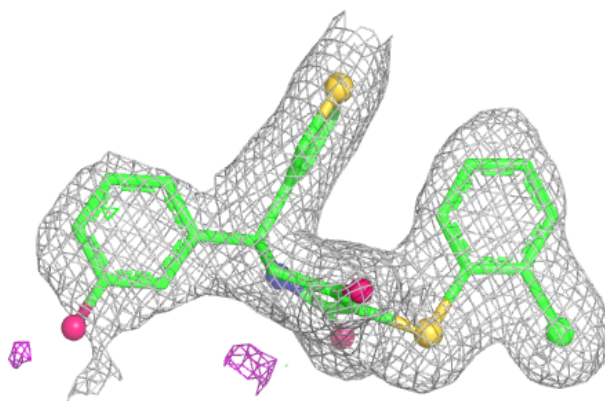
**Electron density around NAI C 402:**

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

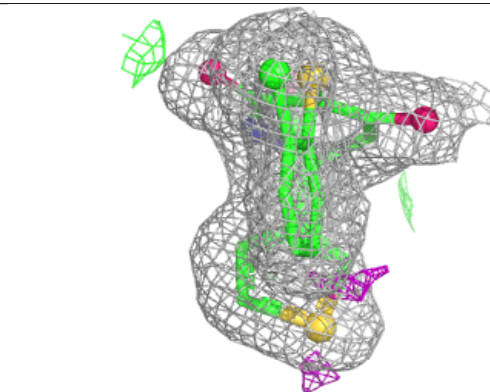
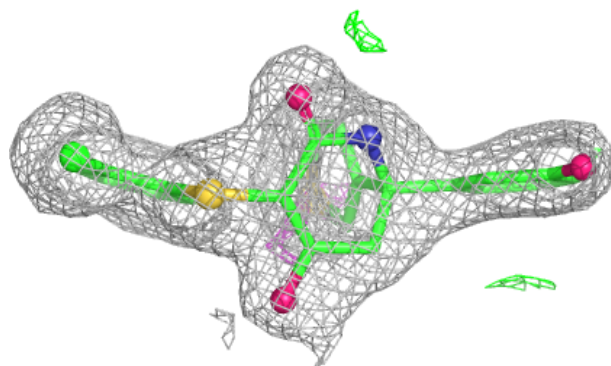
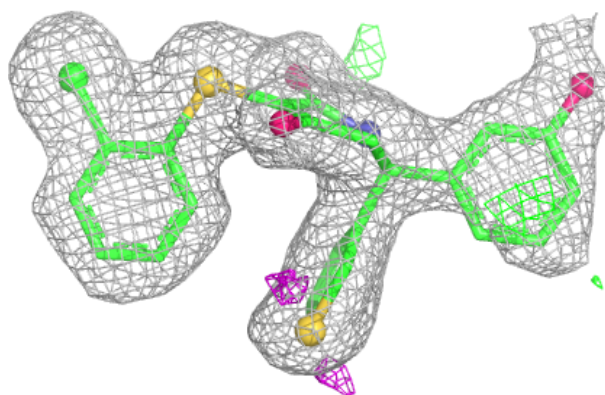


Electron density around 6EY C 403:

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

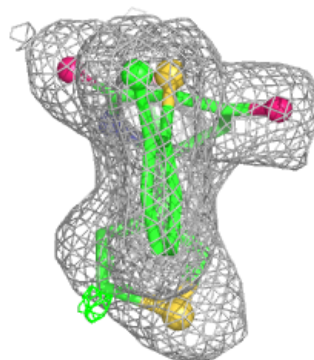
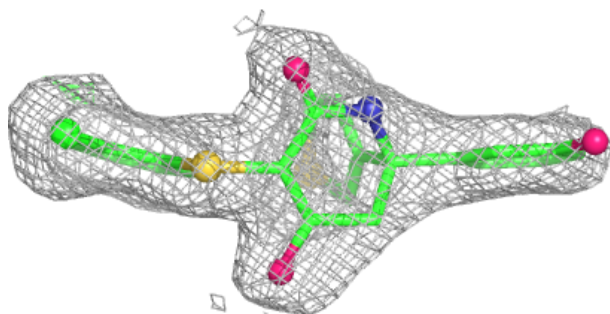
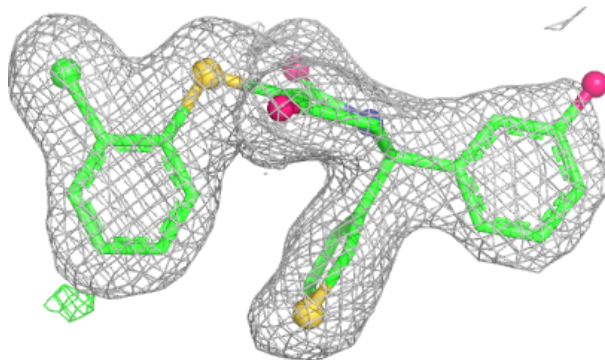
**Electron density around 6EY A 403:**

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

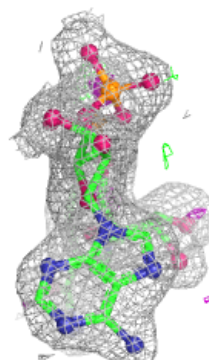
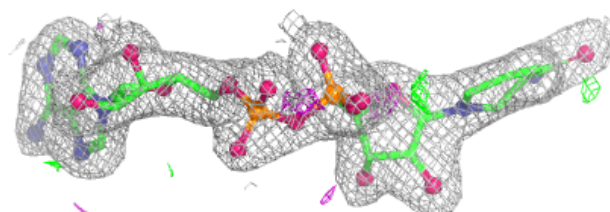
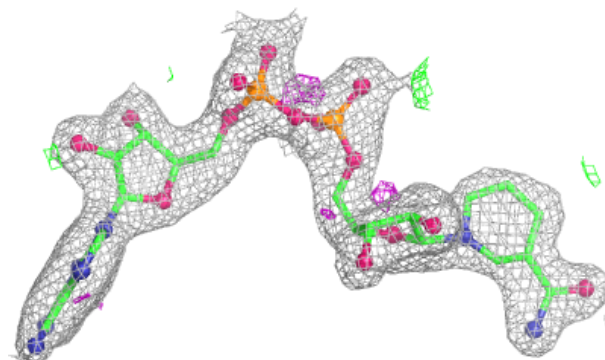


Electron density around 6EY D 802:

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and green (positive)

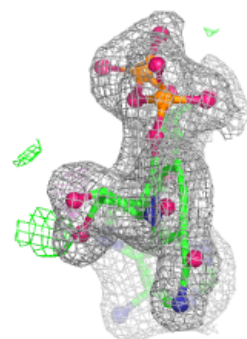
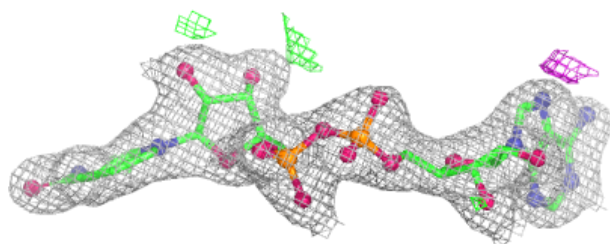
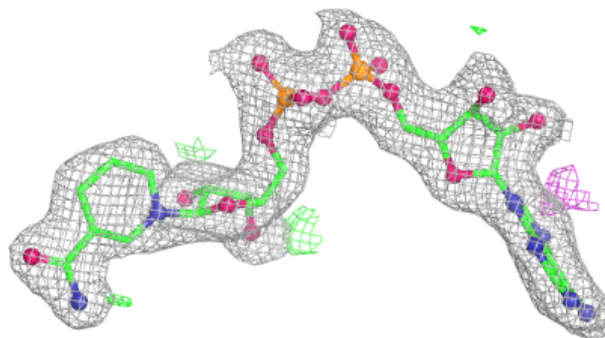
**Electron density around TXD B 402:**

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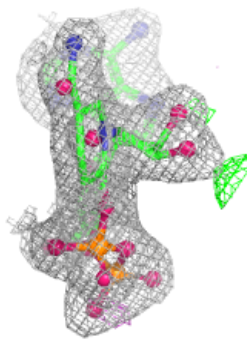
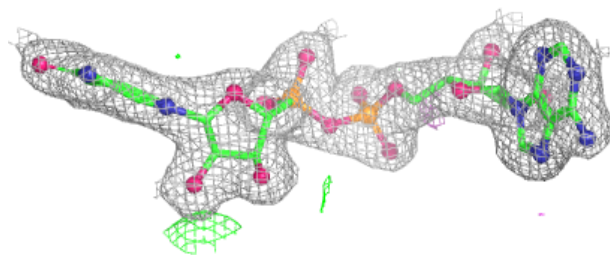
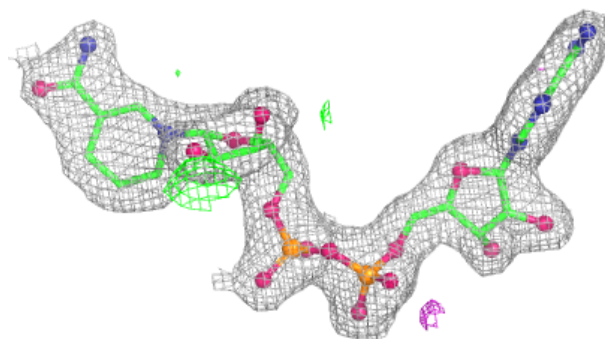


Electron density around TXD D 801:

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and green (positive)

**Electron density around TXD A 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.