



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 06:07 AM UTC

PDB ID : 2X9G / pdb_00002x9g
Title : High resolution structure of TbPTR1 in complex with Pemetrexed
Authors : Dawson, A.; Barrack, K.L.; Tulloch, L.B.; Hunter, W.N.
Deposited on : 2010-03-18
Resolution : 1.10 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

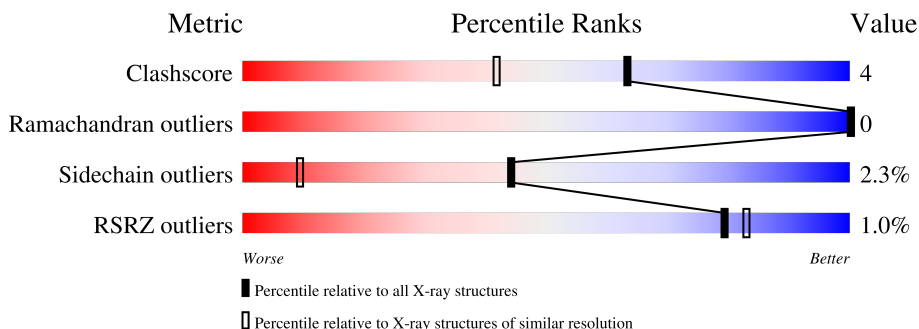
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.10 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))
Clashscore	190562	1656 (1.12-1.08)
Ramachandran outliers	187476	1616 (1.12-1.08)
Sidechain outliers	187428	1612 (1.12-1.08)
RSRZ outliers	180081	1625 (1.12-1.08)

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	288	81% 6% • 13%
1	B	288	80% 6% • 13%
1	C	288	78% 8% • 12%
1	D	288	75% 9% • 14%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 16553 atoms, of which 7199 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 PTERIDINE REDUCTASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	251	Total	C	H	N	O	S	0	9	0
			3670	1202	1766	333	357	12			
1	B	250	Total	C	H	N	O	S	0	8	0
			3654	1193	1761	331	357	12			
1	C	252	Total	C	H	N	O	S	0	8	0
			3656	1195	1751	337	362	11			
1	D	249	Total	C	H	N	O	S	0	12	0
			3685	1206	1773	332	362	12			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP O76290
A	-18	GLY	-	expression tag	UNP O76290
A	-17	SER	-	expression tag	UNP O76290
A	-16	SER	-	expression tag	UNP O76290
A	-15	HIS	-	expression tag	UNP O76290
A	-14	HIS	-	expression tag	UNP O76290
A	-13	HIS	-	expression tag	UNP O76290
A	-12	HIS	-	expression tag	UNP O76290
A	-11	HIS	-	expression tag	UNP O76290
A	-10	HIS	-	expression tag	UNP O76290
A	-9	SER	-	expression tag	UNP O76290
A	-8	SER	-	expression tag	UNP O76290
A	-7	GLY	-	expression tag	UNP O76290
A	-6	LEU	-	expression tag	UNP O76290
A	-5	VAL	-	expression tag	UNP O76290
A	-4	PRO	-	expression tag	UNP O76290
A	-3	ARG	-	expression tag	UNP O76290
A	-2	GLY	-	expression tag	UNP O76290
A	-1	SER	-	expression tag	UNP O76290
A	0	HIS	-	expression tag	UNP O76290
B	-19	MET	-	expression tag	UNP O76290

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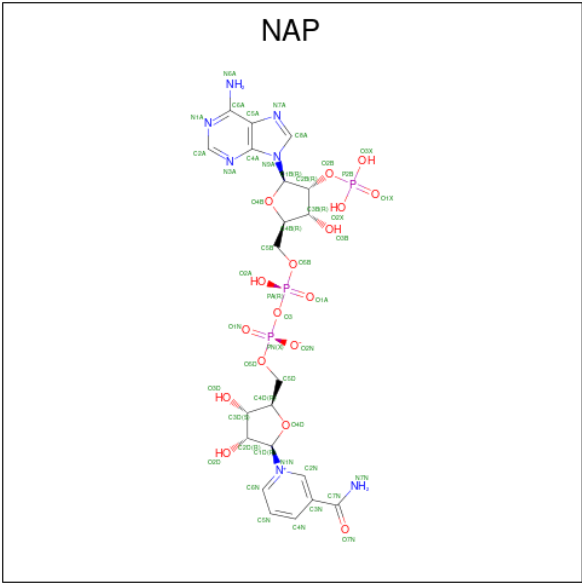
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	expression tag	UNP O76290
B	-17	SER	-	expression tag	UNP O76290
B	-16	SER	-	expression tag	UNP O76290
B	-15	HIS	-	expression tag	UNP O76290
B	-14	HIS	-	expression tag	UNP O76290
B	-13	HIS	-	expression tag	UNP O76290
B	-12	HIS	-	expression tag	UNP O76290
B	-11	HIS	-	expression tag	UNP O76290
B	-10	HIS	-	expression tag	UNP O76290
B	-9	SER	-	expression tag	UNP O76290
B	-8	SER	-	expression tag	UNP O76290
B	-7	GLY	-	expression tag	UNP O76290
B	-6	LEU	-	expression tag	UNP O76290
B	-5	VAL	-	expression tag	UNP O76290
B	-4	PRO	-	expression tag	UNP O76290
B	-3	ARG	-	expression tag	UNP O76290
B	-2	GLY	-	expression tag	UNP O76290
B	-1	SER	-	expression tag	UNP O76290
B	0	HIS	-	expression tag	UNP O76290
C	-19	MET	-	expression tag	UNP O76290
C	-18	GLY	-	expression tag	UNP O76290
C	-17	SER	-	expression tag	UNP O76290
C	-16	SER	-	expression tag	UNP O76290
C	-15	HIS	-	expression tag	UNP O76290
C	-14	HIS	-	expression tag	UNP O76290
C	-13	HIS	-	expression tag	UNP O76290
C	-12	HIS	-	expression tag	UNP O76290
C	-11	HIS	-	expression tag	UNP O76290
C	-10	HIS	-	expression tag	UNP O76290
C	-9	SER	-	expression tag	UNP O76290
C	-8	SER	-	expression tag	UNP O76290
C	-7	GLY	-	expression tag	UNP O76290
C	-6	LEU	-	expression tag	UNP O76290
C	-5	VAL	-	expression tag	UNP O76290
C	-4	PRO	-	expression tag	UNP O76290
C	-3	ARG	-	expression tag	UNP O76290
C	-2	GLY	-	expression tag	UNP O76290
C	-1	SER	-	expression tag	UNP O76290
C	0	HIS	-	expression tag	UNP O76290
D	-19	MET	-	expression tag	UNP O76290
D	-18	GLY	-	expression tag	UNP O76290
D	-17	SER	-	expression tag	UNP O76290

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	expression tag	UNP O76290
D	-15	HIS	-	expression tag	UNP O76290
D	-14	HIS	-	expression tag	UNP O76290
D	-13	HIS	-	expression tag	UNP O76290
D	-12	HIS	-	expression tag	UNP O76290
D	-11	HIS	-	expression tag	UNP O76290
D	-10	HIS	-	expression tag	UNP O76290
D	-9	SER	-	expression tag	UNP O76290
D	-8	SER	-	expression tag	UNP O76290
D	-7	GLY	-	expression tag	UNP O76290
D	-6	LEU	-	expression tag	UNP O76290
D	-5	VAL	-	expression tag	UNP O76290
D	-4	PRO	-	expression tag	UNP O76290
D	-3	ARG	-	expression tag	UNP O76290
D	-2	GLY	-	expression tag	UNP O76290
D	-1	SER	-	expression tag	UNP O76290
D	0	HIS	-	expression tag	UNP O76290

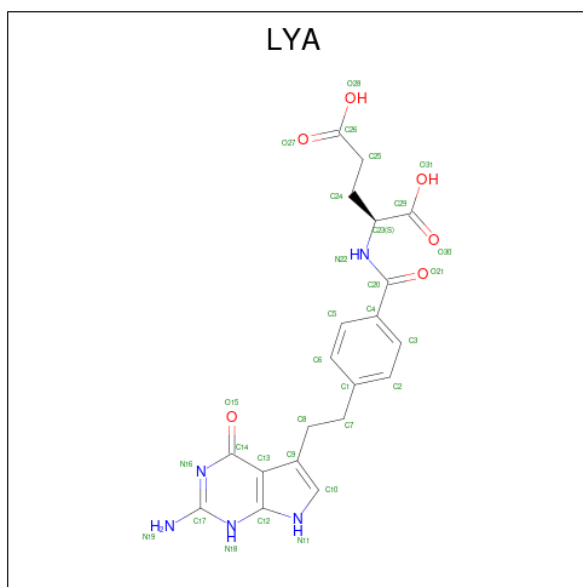
- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃).



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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	H	N	O	0	0
			66	21	18	7	17		
2	D	1	Total	C	H	N	O	0	0
			66	21	18	7	17		

- Molecule 3 is 2-{4-[2-(2-AMINO-4-OXO-4,7-DIHYDRO-3H-PYRROLO[2,3-D]PYRIMIDIN-5-YL)-ETHYL]-BENZOYLAMINO}-PENTANEDIOIC ACID (CCD ID: LYA) (formula: C₂₀H₂₁N₅O₆).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	0	1
			62	26	19	6	11		
3	B	1	Total	C	H	N	O	0	1
			62	26	19	6	11		
3	C	1	Total	C	H	N	O	0	1
			62	26	19	6	11		
3	D	1	Total	C	H	N	O	0	1
			62	26	19	6	11		

- Molecule 4 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			4	2	2		

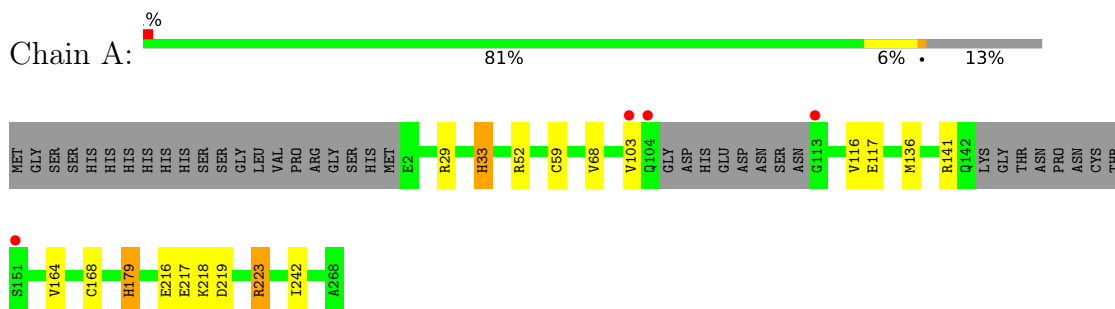
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	344	Total	O	0	0
			344	344		
5	B	380	Total	O	0	0
			380	380		
5	C	333	Total	O	0	0
			333	333		
5	D	315	Total	O	0	0
			315	315		

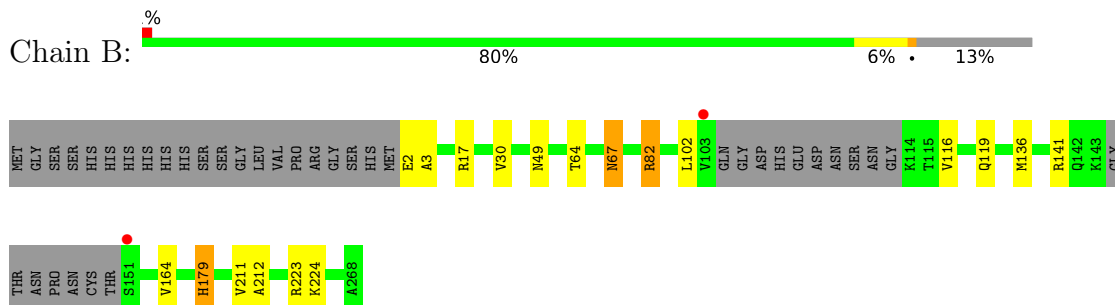
3 Residue-property plots [i](#)

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.

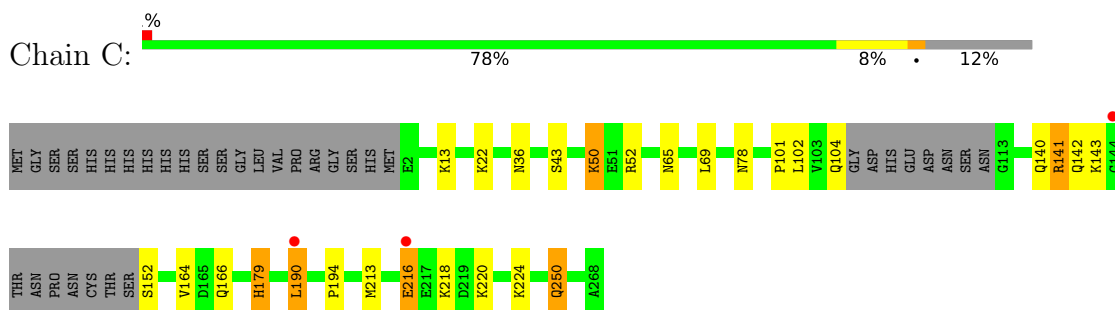
• Molecule 1: PTERIDINE REDUCTASE



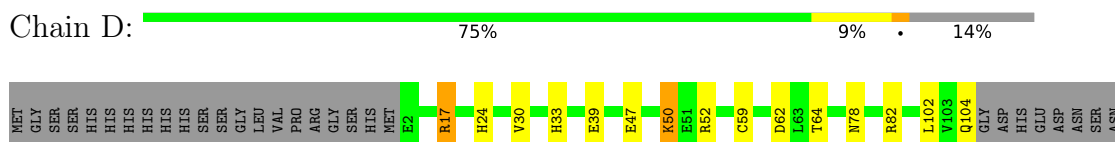
• Molecule 1: PTERIDINE REDUCTASE

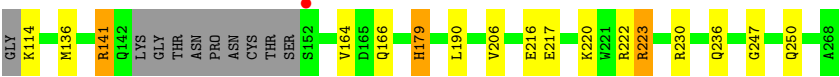


• Molecule 1: PTERIDINE REDUCTASE



• Molecule 1: PTERIDINE REDUCTASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	74.72Å 90.57Å 82.58Å 90.00° 115.61° 90.00°	Depositor
Resolution (Å)	20.00 – 1.10 20.00 – 1.10	Depositor EDS
% Data completeness (in resolution range)	94.7 (20.00-1.10) 93.1 (20.00-1.10)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.17 (at 1.10Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.121 , 0.147 0.116 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	8.2	Xtriage
Anisotropy	0.637	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 60.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.017 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	16553	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 20.67 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 8.2712e-03.*

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: NAP, ACT, LYA

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	0.86	0/1971	1.27	10/2675 (0.4%)
1	B	0.87	0/1958	1.26	12/2656 (0.5%)
1	C	0.87	0/1966	1.30	7/2664 (0.3%)
1	D	0.88	0/2002	1.31	10/2718 (0.4%)
All	All	0.87	0/7897	1.29	39/10713 (0.4%)

There are no bond length outliers.

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	230	ARG	CD-NE-CZ	18.65	150.51	124.40
1	C	141	ARG	CD-NE-CZ	12.17	141.43	124.40
1	D	223	ARG	CD-NE-CZ	-8.68	112.25	124.40
1	B	67	ASN	CA-CB-CG	7.96	120.56	112.60
1	C	216	GLU	CA-CB-CG	7.87	129.84	114.10
1	B	82	ARG	CD-NE-CZ	7.50	134.91	124.40
1	D	223	ARG	NE-CZ-NH1	-7.13	114.37	121.50
1	B	211	VAL	O-C-N	-7.07	115.01	121.87
1	B	211	VAL	CA-C-O	7.05	128.28	120.95
1	A	141	ARG	CD-NE-CZ	7.04	134.25	124.40
1	C	224	LYS	CG-CD-CE	6.94	127.27	111.30
1	C	141	ARG	NE-CZ-NH1	6.84	128.34	121.50
1	B	67	ASN	OD1-CG-ND2	-6.82	115.78	122.60
1	D	82	ARG	CD-NE-CZ	6.47	133.46	124.40
1	A	223	ARG	CD-NE-CZ	-6.44	115.39	124.40
1	A	223	ARG	CG-CD-NE	6.35	125.97	112.00
1	B	141	ARG	NE-CZ-NH2	-6.34	113.49	119.20
1	A	223	ARG	NE-CZ-NH2	6.16	124.75	119.20
1	B	211	VAL	CA-C-N	-6.14	111.26	122.38
1	B	211	VAL	C-N-CA	-6.14	111.26	122.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	223	ARG	NE-CZ-NH1	-5.85	115.65	121.50
1	C	52	ARG	NE-CZ-NH2	5.82	124.44	119.20
1	A	117	GLU	CB-CG-CD	5.71	122.31	112.60
1	A	29	ARG	CD-NE-CZ	-5.68	116.45	124.40
1	D	206	VAL	N-CA-CB	5.62	118.55	111.46
1	A	52	ARG	N-CA-CB	5.61	119.91	110.77
1	D	17	ARG	NE-CZ-NH1	-5.58	115.92	121.50
1	C	50	LYS	CA-CB-CG	5.46	125.01	114.10
1	B	141	ARG	CD-NE-CZ	5.40	131.96	124.40
1	B	17	ARG	NE-CZ-NH2	-5.32	114.42	119.20
1	D	52	ARG	NE-CZ-NH1	-5.31	116.19	121.50
1	A	33	HIS	CA-CB-CG	-5.27	108.53	113.80
1	B	82	ARG	NE-CZ-NH1	5.24	126.74	121.50
1	A	141	ARG	CG-CD-NE	5.19	123.42	112.00
1	A	141	ARG	CB-CG-CD	5.09	123.00	111.30
1	D	222	ARG	NH1-CZ-NH2	5.09	125.91	119.30
1	D	141	ARG	CG-CD-NE	5.08	123.17	112.00
1	D	24	HIS	ND1-CE1-NE2	5.06	113.46	108.40
1	C	36	ASN	OD1-CG-ND2	5.01	127.61	122.60

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	1904	1766	1932	12	0
1	B	1893	1761	1925	14	0
1	C	1905	1751	1923	16	0
1	D	1912	1773	1937	27	0
2	A	48	18	25	0	0
2	B	48	18	25	0	0
2	C	48	18	25	0	0
2	D	48	18	25	1	0
3	A	43	19	12	1	0
3	B	43	19	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	43	19	12	0	0
3	D	43	19	12	1	0
4	B	4	0	3	0	0
5	A	344	0	0	4	0
5	B	380	0	0	7	0
5	C	333	0	0	5	0
5	D	315	0	0	14	0
All	All	9354	7199	7868	64	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 (64) 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:C:250[A]:GLN:HE21	1:D:236:GLN:HE21	1.30	0.80
1:B:212:ALA:HB3	5:B:2287:HOH:O	1.86	0.76
1:A:136[B]:MET:HG3	1:C:102:LEU:O	1.86	0.75
1:C:13:LYS:HE3	5:C:2005:HOH:O	1.91	0.70
1:D:220:LYS:O	1:D:223:ARG:HG3	1.92	0.69
1:D:216[B]:GLU:HG2	1:D:217:GLU:OE2	1.94	0.67
1:D:64[B]:THR:HG21	5:D:2122:HOH:O	1.95	0.67
1:A:217:GLU:HG2	5:A:2273:HOH:O	1.95	0.66
1:D:62:ASP:OD1	1:D:64[B]:THR:HG23	1.97	0.63
1:D:190:LEU:HD23	5:D:2224:HOH:O	1.98	0.63
1:D:64[A]:THR:HG21	5:D:2121:HOH:O	2.02	0.59
1:B:164:VAL:HG22	1:B:179[B]:HIS:CD2	2.38	0.59
1:A:116[B]:VAL:HG23	5:A:2197:HOH:O	2.04	0.58
1:B:2:GLU:HG3	5:B:2003:HOH:O	2.04	0.58
1:D:164:VAL:HG22	1:D:179[B]:HIS:CD2	2.39	0.57
1:A:164:VAL:HG22	1:A:179[B]:HIS:CD2	2.40	0.56
1:B:64[A]:THR:HG21	5:B:2154:HOH:O	2.05	0.56
1:D:223:ARG:HB3	5:D:2147:HOH:O	2.07	0.55
1:D:50:LYS:HG3	5:D:2078:HOH:O	2.08	0.54
1:C:250[A]:GLN:NE2	1:D:236:GLN:HE21	2.00	0.54
1:A:103:VAL:CG1	1:C:143:LYS:HD3	2.38	0.53
1:C:190:LEU:HD21	5:C:2144:HOH:O	2.07	0.53
1:D:39:GLU:HG3	5:D:2064:HOH:O	2.09	0.53
1:C:101:PRO:HD2	5:C:2187:HOH:O	2.08	0.53
1:C:141:ARG:HG2	5:C:2206:HOH:O	2.07	0.52
1:D:250:GLN:HG2	5:D:2200:HOH:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:140:GLN:O	1:C:143:LYS:HB3	2.11	0.50
1:A:68[C]:VAL:HG13	5:A:2131:HOH:O	2.12	0.50
1:D:64[B]:THR:HG23	2:D:1269:NAP:H62A	1.77	0.50
1:B:82:ARG:HB2	5:B:2184:HOH:O	2.13	0.49
1:C:164:VAL:HG22	1:C:179:HIS:CD2	2.48	0.48
1:D:141:ARG:HG2	5:D:2190:HOH:O	2.13	0.48
1:B:2:GLU:HG2	1:B:3:ALA:N	2.29	0.47
1:A:216[A]:GLU:OE1	1:A:223:ARG:NH2	2.47	0.47
1:B:82:ARG:NH1	5:B:2186:HOH:O	2.48	0.46
1:D:17:ARG:NH2	1:D:47[B]:GLU:OE1	2.49	0.46
1:D:78[A]:ASN:OD1	1:D:141:ARG:NH1	2.48	0.46
1:A:33:HIS:HA	1:A:59:CYS:O	2.16	0.46
1:C:78[B]:ASN:OD1	1:C:141:ARG:NH2	2.49	0.46
1:D:114:LYS:NZ	5:D:2178:HOH:O	2.48	0.46
1:D:250:GLN:NE2	5:D:2287:HOH:O	2.50	0.45
1:C:220:LYS:NZ	5:C:2264:HOH:O	2.49	0.45
1:C:194:PRO:HG3	5:D:2257:HOH:O	2.17	0.45
1:D:247:GLY:O	1:D:250:GLN:HG3	2.17	0.45
1:B:49:ASN:ND2	5:B:2110:HOH:O	2.49	0.45
1:A:218:LYS:NZ	5:A:2275:HOH:O	2.49	0.43
1:A:223:ARG:HH11	1:A:223:ARG:HD2	1.61	0.43
1:B:224:LYS:NZ	5:B:2304:HOH:O	2.51	0.43
1:B:116:VAL:HA	1:B:119:GLN:HE21	1.82	0.43
1:B:136[B]:MET:HG3	1:D:102:LEU:O	2.19	0.43
1:A:168:CYS:HB3	3:A:1270[B]:LYA:C26	2.50	0.42
1:B:102:LEU:O	1:D:136[B]:MET:HG3	2.20	0.41
1:C:65:ASN:HA	1:C:69:LEU:HD22	2.03	0.41
3:D:1270[A]:LYA:O28	3:D:1270[A]:LYA:H23	2.21	0.41
1:D:190:LEU:HB3	5:D:2224:HOH:O	2.21	0.41
1:D:33:HIS:HA	1:D:59:CYS:O	2.21	0.40
1:C:213:MET:O	1:C:218:LYS:HE3	2.21	0.40
1:A:219:ASP:O	1:A:223:ARG:HG3	2.21	0.40
1:D:50:LYS:HE3	5:D:2080:HOH:O	2.21	0.40
1:D:47[B]:GLU:HG3	5:D:2068:HOH:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	255/288 (88%)	246 (96%)	9 (4%)	0	100	100
1	B	253/288 (88%)	244 (96%)	9 (4%)	0	100	100
1	C	254/288 (88%)	245 (96%)	9 (4%)	0	100	100
1	D	258/288 (90%)	250 (97%)	8 (3%)	0	100	100
All	All	1020/1152 (88%)	985 (97%)	35 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	207/231 (90%)	204 (99%)	3 (1%)	59	22
1	B	208/231 (90%)	205 (99%)	3 (1%)	59	22
1	C	207/231 (90%)	196 (95%)	11 (5%)	20	1
1	D	213/231 (92%)	208 (98%)	5 (2%)	44	9
All	All	835/924 (90%)	813 (97%)	22 (3%)	44	7

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	179[A]	HIS
1	A	179[B]	HIS

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Mol	Chain	Res	Type
1	A	242	ILE
1	B	67	ASN
1	B	179[A]	HIS
1	B	179[B]	HIS
1	C	22	LYS
1	C	50	LYS
1	C	104	GLN
1	C	142	GLN
1	C	152	SER
1	C	166	GLN
1	C	179	HIS
1	C	190	LEU
1	C	216	GLU
1	C	250[A]	GLN
1	C	250[B]	GLN
1	D	50	LYS
1	D	104	GLN
1	D	166	GLN
1	D	179[A]	HIS
1	D	179[B]	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	ASN
1	A	65	ASN
1	A	92	ASN
1	A	104	GLN
1	B	67	ASN
1	B	92	ASN
1	B	119	GLN
1	B	250	GLN
1	C	54	ASN
1	C	65	ASN
1	C	92	ASN
1	C	104	GLN
1	D	92	ASN
1	D	104	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 ⓘ

13 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	LYA	A	1270[A]	-	32,33,33	0.93	1 (3%)	41,46,46	1.66	10 (24%)
2	NAP	C	1269	-	50,52,52	1.14	4 (8%)	71,80,80	0.99	4 (5%)
3	LYA	C	1270[A]	-	32,33,33	1.05	1 (3%)	41,46,46	1.66	6 (14%)
3	LYA	A	1270[B]	-	32,33,33	0.97	1 (3%)	41,46,46	1.57	7 (17%)
4	ACT	B	1271	-	3,3,3	1.26	0	3,3,3	1.12	0
3	LYA	D	1270[A]	-	32,33,33	1.27	3 (9%)	41,46,46	2.03	11 (26%)
3	LYA	C	1270[B]	-	32,33,33	1.06	1 (3%)	41,46,46	1.91	12 (29%)
2	NAP	A	1269	-	50,52,52	1.10	4 (8%)	71,80,80	1.14	5 (7%)
3	LYA	D	1270[B]	-	32,33,33	1.25	3 (9%)	41,46,46	1.85	8 (19%)
3	LYA	B	1270[A]	-	32,33,33	0.94	1 (3%)	41,46,46	1.41	4 (9%)
2	NAP	D	1269	-	50,52,52	0.94	1 (2%)	71,80,80	1.13	5 (7%)
2	NAP	B	1269	-	50,52,52	1.09	3 (6%)	71,80,80	1.05	3 (4%)
3	LYA	B	1270[B]	-	32,33,33	0.98	1 (3%)	41,46,46	1.54	7 (17%)

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	LYA	A	1270[A]	-	-	3/22/22/22	0/3/3/3
2	NAP	C	1269	-	-	0/35/67/67	0/5/5/5
3	LYA	C	1270[A]	-	-	10/22/22/22	0/3/3/3
3	LYA	A	1270[B]	-	-	5/22/22/22	0/3/3/3
3	LYA	D	1270[A]	-	-	8/22/22/22	0/3/3/3
3	LYA	C	1270[B]	-	-	4/22/22/22	0/3/3/3
2	NAP	A	1269	-	-	0/35/67/67	0/5/5/5
3	LYA	D	1270[B]	-	-	4/22/22/22	0/3/3/3
3	LYA	B	1270[A]	-	-	3/22/22/22	0/3/3/3
2	NAP	D	1269	-	-	0/35/67/67	0/5/5/5
2	NAP	B	1269	-	-	0/35/67/67	0/5/5/5
3	LYA	B	1270[B]	-	-	5/22/22/22	0/3/3/3

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1269	NAP	PN-O3	4.33	1.64	1.59
2	C	1269	NAP	C2N-N1N	3.99	1.39	1.35
3	D	1270[A]	LYA	C10-C9	-3.67	1.33	1.38
3	D	1270[B]	LYA	C10-C9	-3.67	1.33	1.38
2	C	1269	NAP	PN-O3	3.52	1.63	1.59
3	C	1270[A]	LYA	C10-C9	-3.19	1.33	1.38
3	C	1270[B]	LYA	C10-C9	-3.19	1.33	1.38
2	D	1269	NAP	P2B-O2B	3.05	1.64	1.59
2	A	1269	NAP	PN-O3	2.72	1.62	1.59
2	A	1269	NAP	C2N-N1N	2.71	1.38	1.35
2	C	1269	NAP	C5A-N7A	-2.59	1.34	1.39
2	B	1269	NAP	PA-O3	2.49	1.62	1.59
2	A	1269	NAP	P2B-O2B	2.48	1.63	1.59
3	D	1270[A]	LYA	C17-N18	-2.48	1.31	1.37
3	D	1270[B]	LYA	C17-N18	-2.48	1.31	1.37
3	D	1270[B]	LYA	C23-N22	2.42	1.50	1.45
2	A	1269	NAP	C8A-N9A	-2.25	1.33	1.37
3	A	1270[A]	LYA	O15-C14	2.25	1.27	1.23
3	A	1270[B]	LYA	O15-C14	2.25	1.27	1.23
3	B	1270[A]	LYA	O15-C14	2.23	1.27	1.23
3	B	1270[B]	LYA	O15-C14	2.23	1.27	1.23
2	B	1269	NAP	C8A-N9A	-2.13	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1270[A]	LYA	O30-C29	2.10	1.28	1.22
2	C	1269	NAP	P2B-O2B	2.05	1.63	1.59

All (82) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1270[A]	LYA	C29-C23-N22	5.88	124.22	110.57
3	D	1270[A]	LYA	C14-C13-C9	5.49	137.94	129.16
3	D	1270[B]	LYA	C14-C13-C9	5.49	137.94	129.16
3	A	1270[A]	LYA	C13-C12-N18	5.06	127.54	123.46
3	A	1270[B]	LYA	C13-C12-N18	5.06	127.54	123.46
3	B	1270[A]	LYA	C13-C12-N18	4.81	127.34	123.46
3	B	1270[B]	LYA	C13-C12-N18	4.81	127.34	123.46
3	C	1270[A]	LYA	C14-C13-C9	4.78	136.80	129.16
3	C	1270[B]	LYA	C14-C13-C9	4.78	136.80	129.16
3	C	1270[A]	LYA	C13-C12-N18	4.55	127.13	123.46
3	C	1270[B]	LYA	C13-C12-N18	4.55	127.13	123.46
3	C	1270[A]	LYA	C29-C23-N22	4.19	120.29	110.57
3	C	1270[B]	LYA	O31-C29-O30	3.92	132.96	124.08
3	D	1270[B]	LYA	O30-C29-C23	-3.71	110.29	122.26
3	B	1270[A]	LYA	C14-C13-C9	3.67	135.03	129.16
3	B	1270[B]	LYA	C14-C13-C9	3.67	135.03	129.16
3	D	1270[A]	LYA	C7-C8-C9	3.56	117.27	112.61
3	D	1270[B]	LYA	C7-C8-C9	3.56	117.27	112.61
3	A	1270[A]	LYA	C14-C13-C9	3.51	134.78	129.16
3	A	1270[B]	LYA	C14-C13-C9	3.51	134.78	129.16
2	A	1269	NAP	C4A-C5A-N7A	-3.47	106.61	110.58
3	D	1270[A]	LYA	C24-C23-N22	3.30	117.44	110.91
3	A	1270[A]	LYA	O27-C26-C25	-3.19	112.99	123.09
3	D	1270[A]	LYA	O31-C29-C23	3.09	123.96	113.51
3	C	1270[B]	LYA	O30-C29-C23	-3.08	112.31	122.26
3	D	1270[B]	LYA	C24-C23-N22	-3.04	104.90	110.91
3	D	1270[A]	LYA	C25-C24-C23	3.02	118.72	113.16
3	D	1270[B]	LYA	O31-C29-O30	2.99	130.87	124.08
3	C	1270[B]	LYA	C25-C24-C23	-2.96	107.70	113.16
2	B	1269	NAP	C3N-C7N-N7N	2.96	121.38	117.74
3	D	1270[A]	LYA	O30-C29-C23	-2.96	112.72	122.26
3	B	1270[B]	LYA	C4-C20-N22	2.89	122.40	117.04
2	C	1269	NAP	C6N-N1N-C2N	-2.88	119.43	121.88
3	C	1270[B]	LYA	C24-C23-C29	-2.78	103.76	110.35
3	C	1270[B]	LYA	O28-C26-O27	2.76	130.43	123.33
3	A	1270[B]	LYA	C4-C20-N22	2.74	122.13	117.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1269	NAP	C5A-N7A-C8A	2.74	107.76	103.45
2	D	1269	NAP	N9A-C8A-N7A	-2.69	110.11	113.94
3	C	1270[B]	LYA	O27-C26-C25	-2.67	114.64	123.09
3	A	1270[A]	LYA	O21-C20-N22	2.63	127.47	122.47
2	A	1269	NAP	C5A-C4A-N3A	-2.59	123.15	126.72
2	D	1269	NAP	C4A-C5A-N7A	-2.58	107.63	110.58
3	A	1270[B]	LYA	C29-C23-N22	2.57	116.53	110.57
2	D	1269	NAP	C5A-N7A-C8A	2.53	107.42	103.45
2	C	1269	NAP	C4B-O4B-C1B	-2.53	103.89	109.47
3	D	1270[B]	LYA	O27-C26-C25	-2.50	115.16	123.09
3	C	1270[B]	LYA	C24-C23-N22	-2.50	105.96	110.91
2	C	1269	NAP	C5A-C4A-N3A	-2.49	123.29	126.72
2	B	1269	NAP	C4B-O4B-C1B	-2.48	103.99	109.47
3	B	1270[B]	LYA	C29-C23-N22	2.43	116.20	110.57
3	A	1270[B]	LYA	O28-C26-O27	2.42	129.55	123.33
3	A	1270[A]	LYA	O28-C26-C25	2.41	121.62	114.00
3	B	1270[A]	LYA	O31-C29-O30	2.33	129.38	124.08
3	B	1270[B]	LYA	O21-C20-N22	-2.26	118.18	122.47
2	A	1269	NAP	N9A-C8A-N7A	-2.25	110.74	113.94
3	C	1270[A]	LYA	C7-C8-C9	2.25	115.56	112.61
3	C	1270[B]	LYA	C7-C8-C9	2.25	115.56	112.61
2	B	1269	NAP	O7N-C7N-C3N	-2.25	116.85	119.60
2	A	1269	NAP	C4B-O4B-C1B	-2.23	104.54	109.47
2	D	1269	NAP	O3B-C3B-C2B	2.23	117.43	111.19
3	D	1270[B]	LYA	C29-C23-N22	-2.22	105.41	110.57
3	D	1270[A]	LYA	O27-C26-C25	-2.20	116.10	123.09
3	D	1270[A]	LYA	O28-C26-C25	2.20	120.94	114.00
3	C	1270[A]	LYA	C17-N18-C12	-2.11	113.72	119.75
3	C	1270[B]	LYA	C17-N18-C12	-2.11	113.72	119.75
3	A	1270[A]	LYA	C17-N18-C12	-2.11	113.73	119.75
3	A	1270[B]	LYA	C17-N18-C12	-2.11	113.73	119.75
2	D	1269	NAP	C4D-O4D-C1D	-2.10	108.01	109.92
3	D	1270[A]	LYA	O21-C20-C4	-2.09	116.75	120.90
3	A	1270[B]	LYA	O27-C26-C25	-2.08	116.49	123.09
3	C	1270[A]	LYA	C14-C13-C12	-2.07	116.28	120.34
3	C	1270[B]	LYA	C14-C13-C12	-2.07	116.28	120.34
3	A	1270[A]	LYA	O31-C29-O30	2.04	128.71	124.08
2	C	1269	NAP	N9A-C8A-N7A	-2.03	111.05	113.94
3	A	1270[A]	LYA	C29-C23-N22	-2.03	105.85	110.57
3	A	1270[A]	LYA	C4-C20-N22	-2.03	113.27	117.04
3	D	1270[A]	LYA	N19-C17-N18	2.02	121.03	116.76
3	D	1270[B]	LYA	N19-C17-N18	2.02	121.03	116.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1270[B]	LYA	O28-C26-O27	2.00	128.48	123.33
3	A	1270[A]	LYA	O30-C29-C23	-2.00	115.80	122.26
3	B	1270[A]	LYA	C17-N18-C12	-2.00	114.04	119.75
3	B	1270[B]	LYA	C17-N18-C12	-2.00	114.04	119.75

There are no chirality outliers.

All (42) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1270[A]	LYA	C1-C7-C8-C9
3	A	1270[B]	LYA	C1-C7-C8-C9
3	B	1270[A]	LYA	C1-C7-C8-C9
3	B	1270[B]	LYA	C1-C7-C8-C9
3	C	1270[A]	LYA	N22-C23-C24-C25
3	D	1270[A]	LYA	N22-C23-C24-C25
3	D	1270[A]	LYA	C23-C24-C25-C26
3	A	1270[B]	LYA	C29-C23-N22-C20
3	B	1270[B]	LYA	C29-C23-N22-C20
3	C	1270[A]	LYA	C23-C24-C25-C26
3	C	1270[A]	LYA	C29-C23-C24-C25
3	D	1270[A]	LYA	C29-C23-C24-C25
3	B	1270[B]	LYA	C23-C24-C25-C26
3	D	1270[B]	LYA	C23-C24-C25-C26
3	A	1270[B]	LYA	C23-C24-C25-C26
3	C	1270[A]	LYA	C1-C7-C8-C9
3	C	1270[B]	LYA	C1-C7-C8-C9
3	C	1270[B]	LYA	C23-C24-C25-C26
3	D	1270[A]	LYA	C1-C7-C8-C9
3	D	1270[B]	LYA	C1-C7-C8-C9
3	C	1270[A]	LYA	C24-C23-N22-C20
3	D	1270[A]	LYA	C24-C23-C29-O31
3	D	1270[A]	LYA	C24-C23-C29-O30
3	C	1270[A]	LYA	C6-C1-C7-C8
3	C	1270[B]	LYA	C6-C1-C7-C8
3	D	1270[A]	LYA	C6-C1-C7-C8
3	D	1270[B]	LYA	C6-C1-C7-C8
3	C	1270[A]	LYA	C2-C1-C7-C8
3	C	1270[B]	LYA	C2-C1-C7-C8
3	D	1270[A]	LYA	C2-C1-C7-C8
3	D	1270[B]	LYA	C2-C1-C7-C8
3	C	1270[A]	LYA	C24-C23-C29-O30
3	C	1270[A]	LYA	C24-C23-C29-O31

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Mol	Chain	Res	Type	Atoms
3	B	1270[A]	LYA	C2-C1-C7-C8
3	B	1270[B]	LYA	C2-C1-C7-C8
3	A	1270[A]	LYA	C2-C1-C7-C8
3	A	1270[B]	LYA	C2-C1-C7-C8
3	A	1270[A]	LYA	C6-C1-C7-C8
3	A	1270[B]	LYA	C6-C1-C7-C8
3	B	1270[A]	LYA	C6-C1-C7-C8
3	B	1270[B]	LYA	C6-C1-C7-C8
3	C	1270[A]	LYA	C24-C25-C26-O28

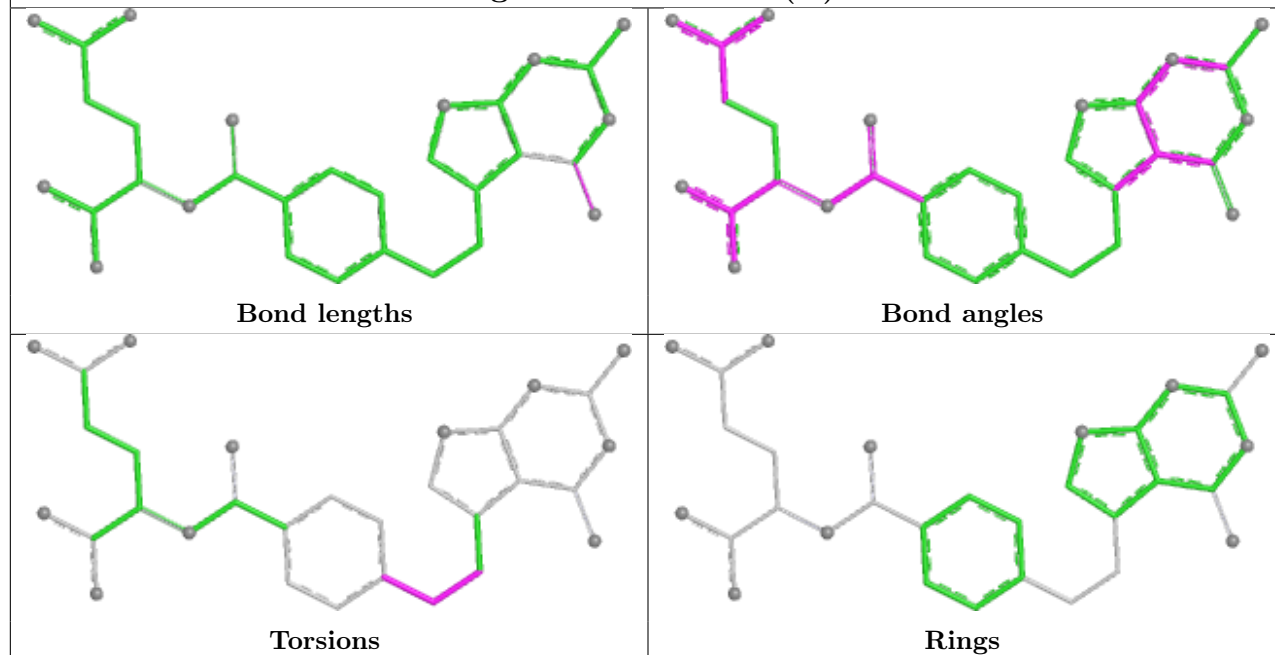
There are no ring outliers.

3 monomers are involved in 3 short contacts:

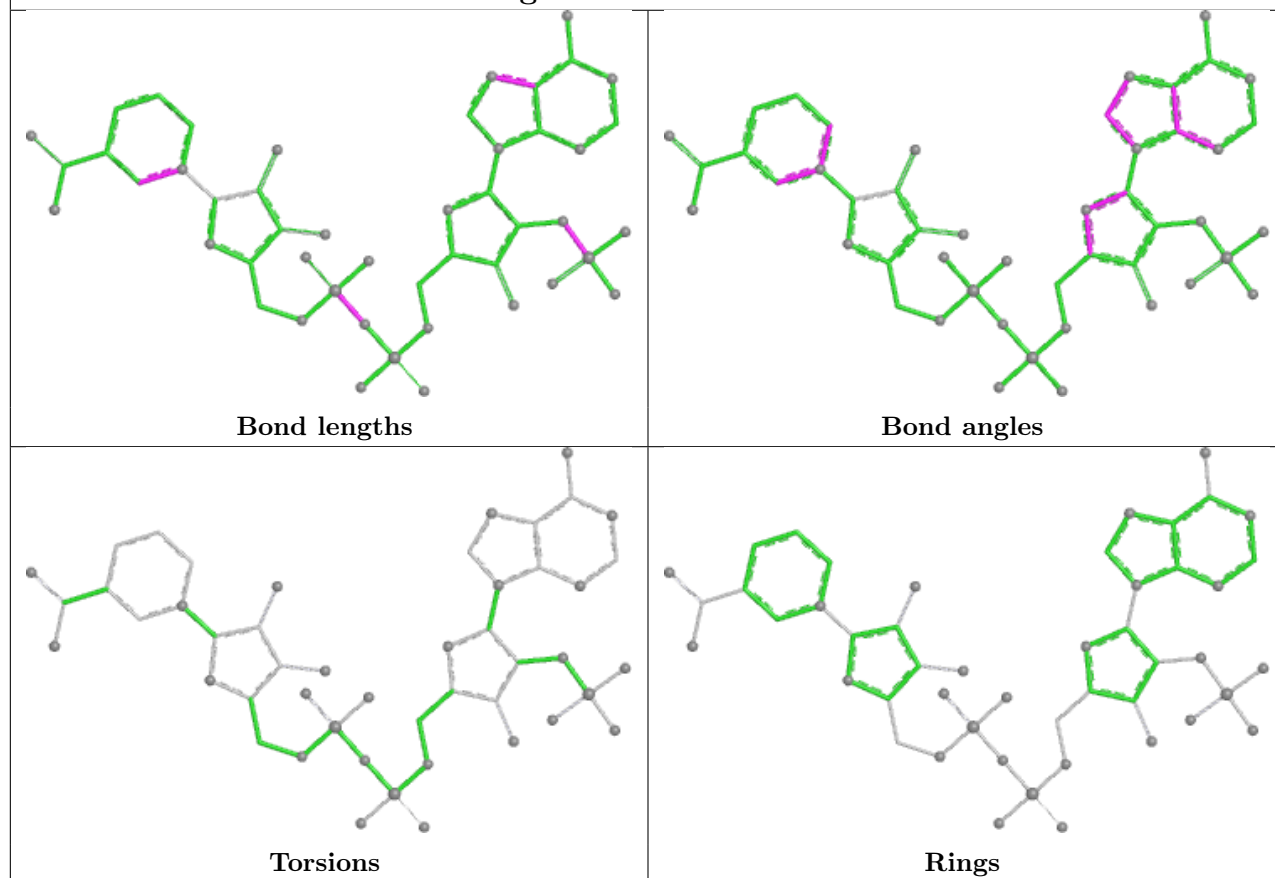
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1270[B]	LYA	1	0
3	D	1270[A]	LYA	1	0
2	D	1269	NAP	1	0

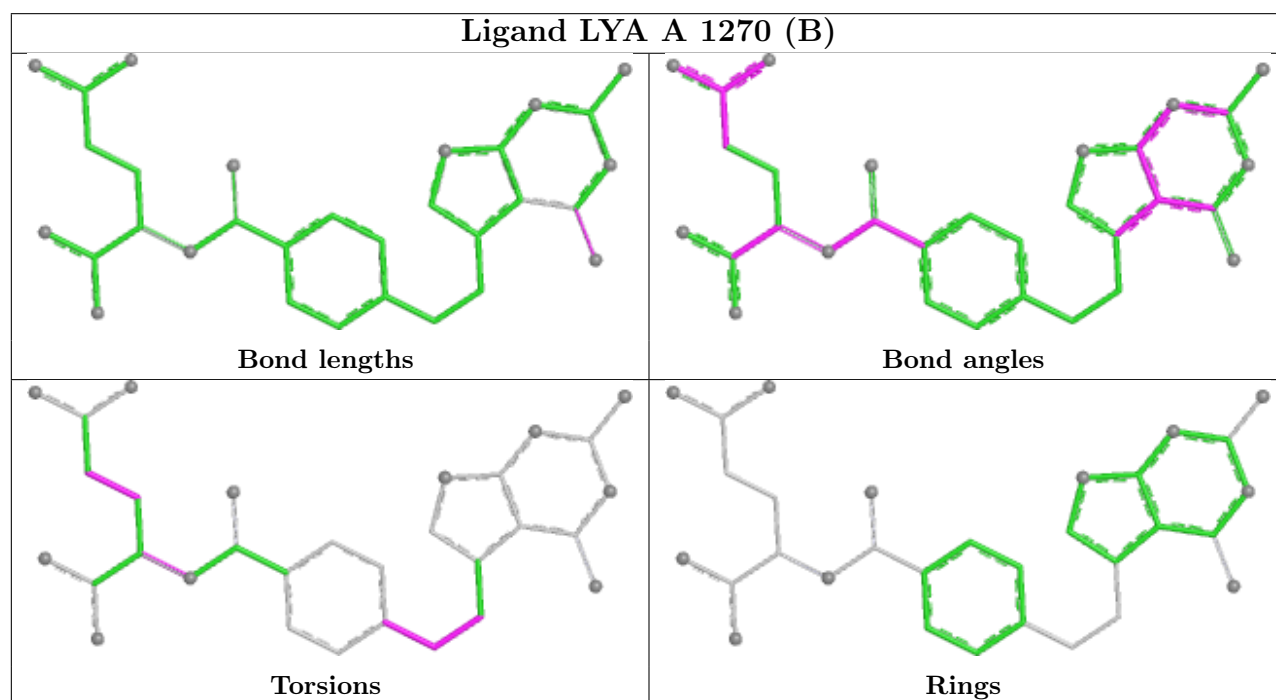
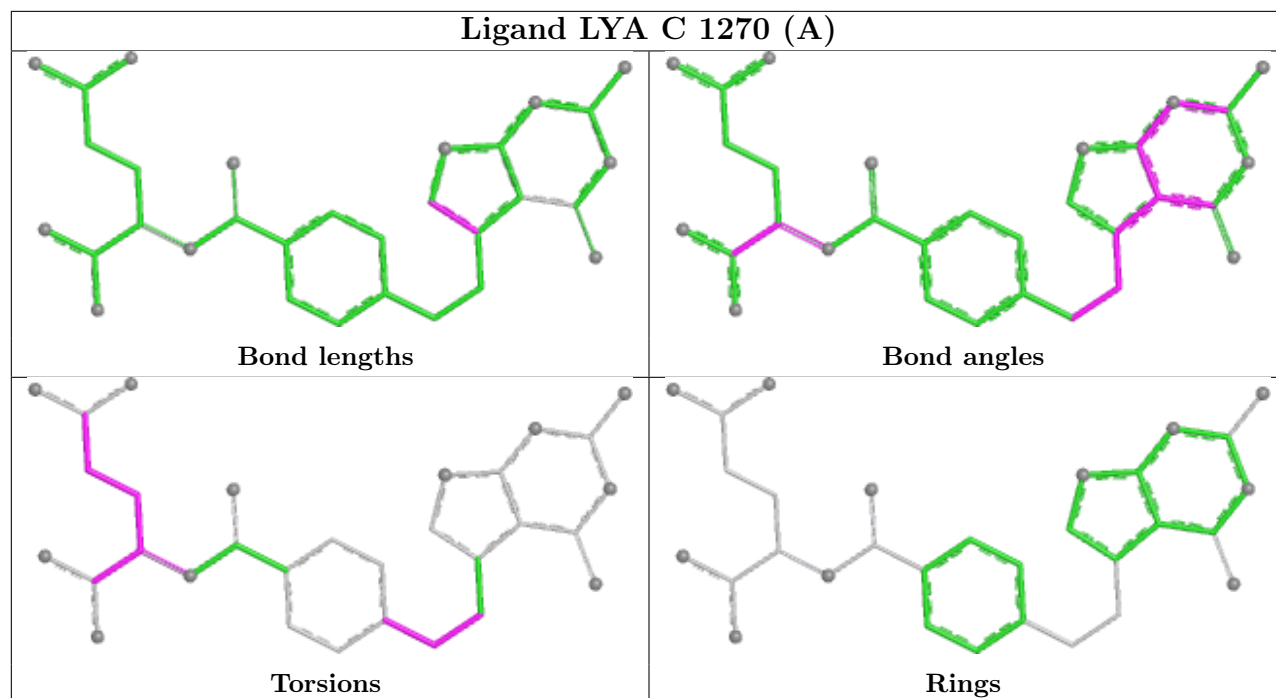
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 LYA A 1270 (A)

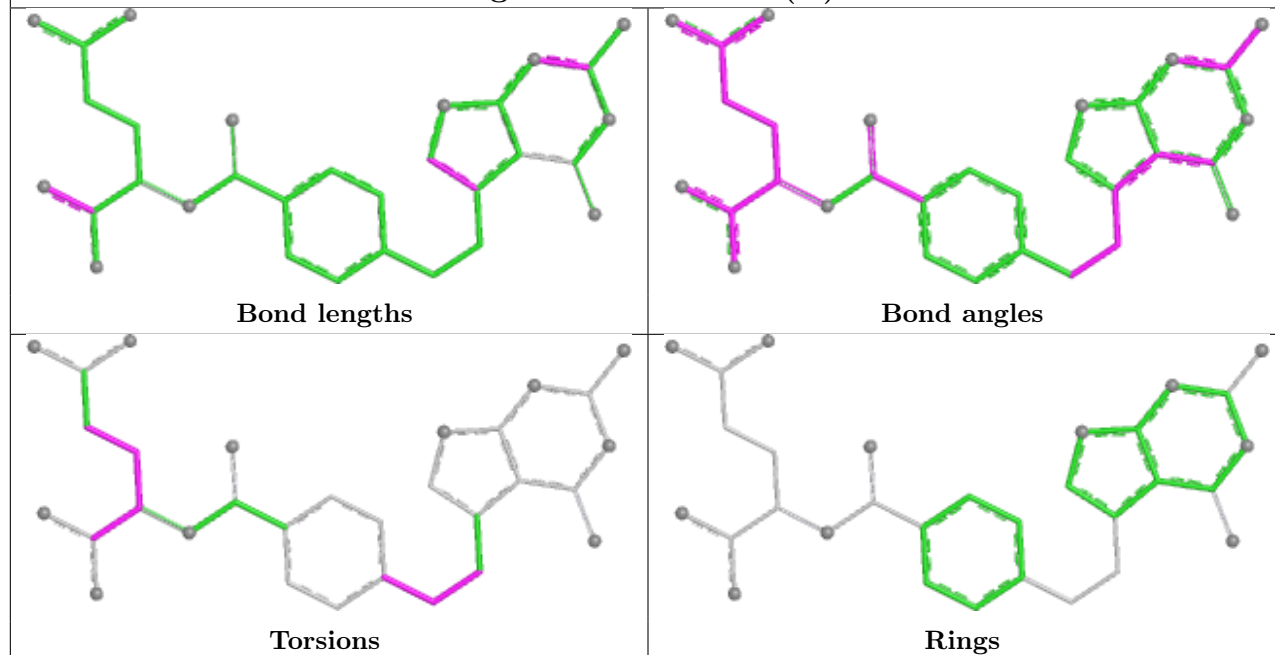


Ligand NAP C 1269

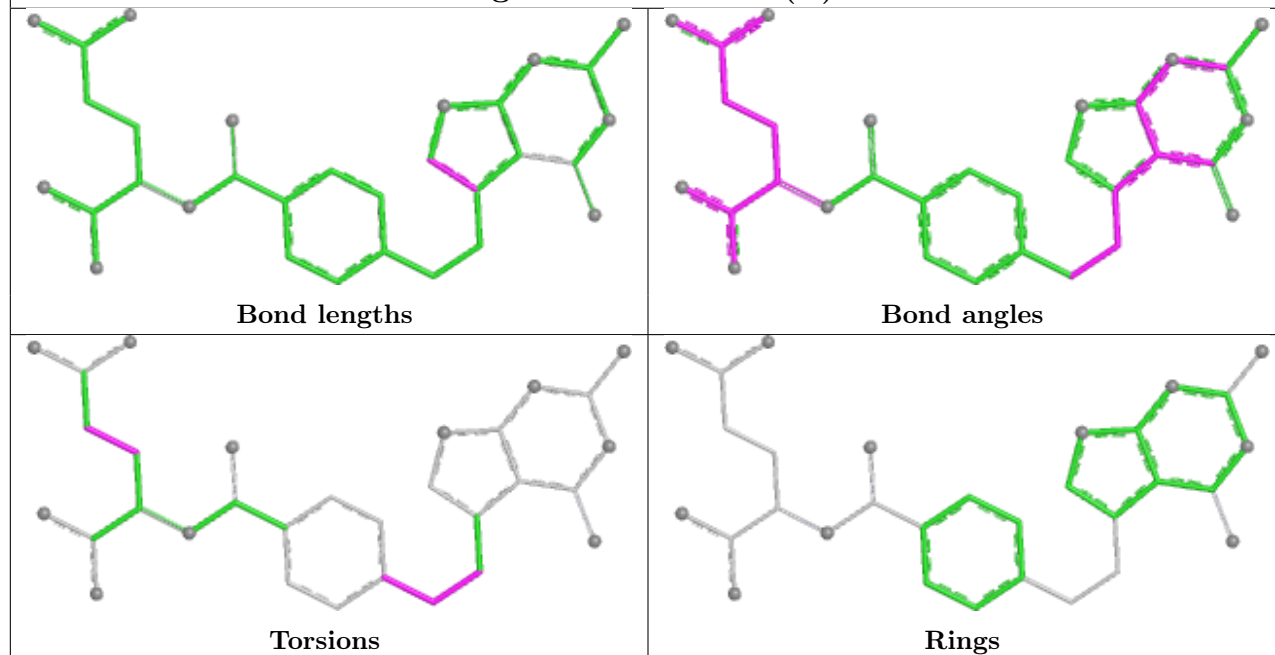




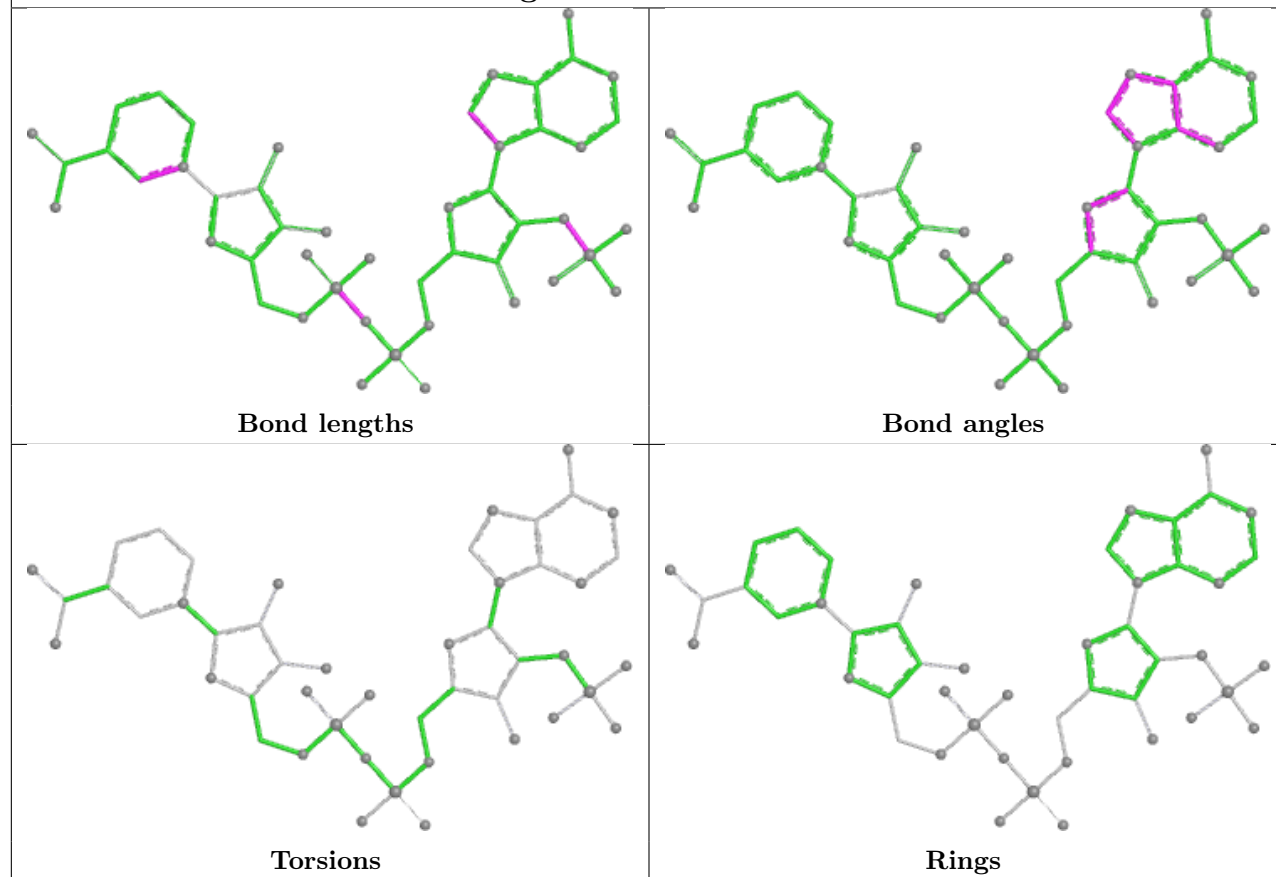
Ligand LYA D 1270 (A)



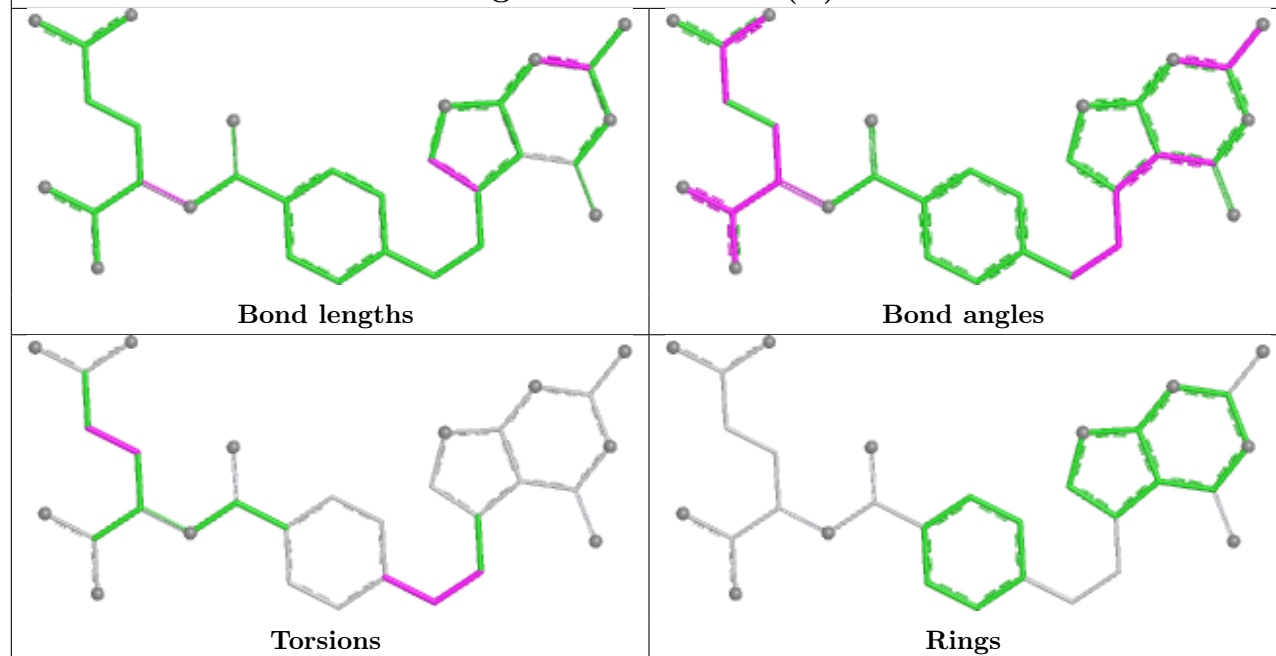
Ligand LYA C 1270 (B)



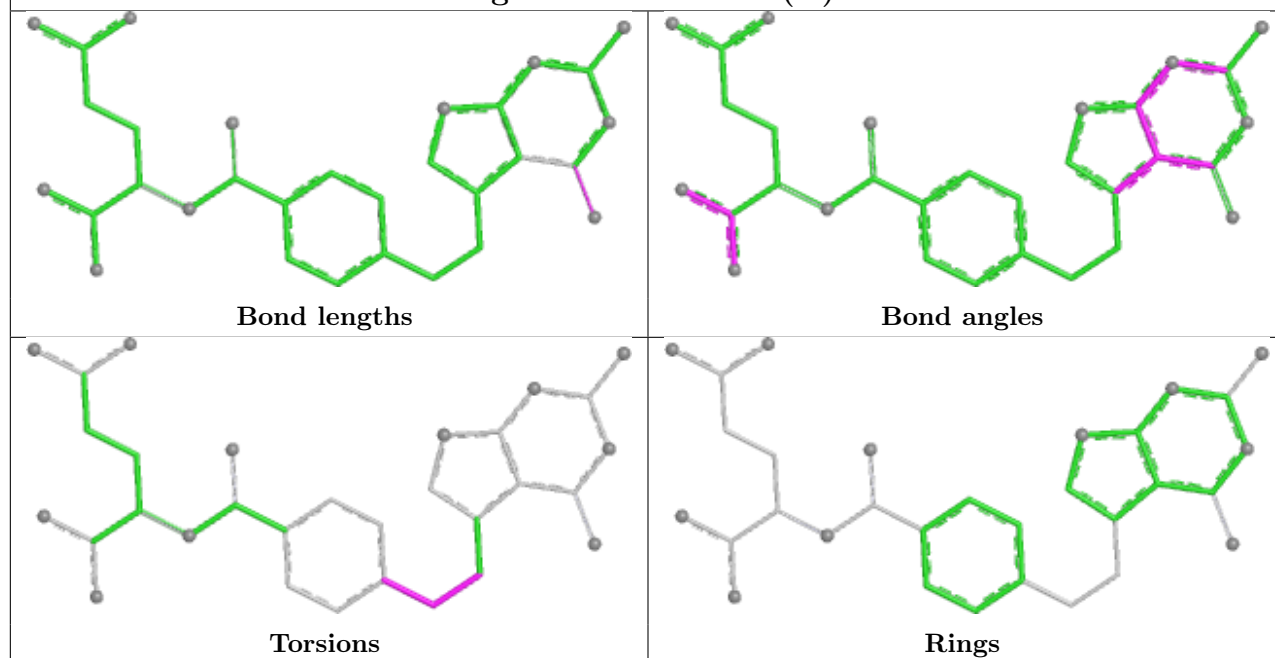
Ligand NAP A 1269



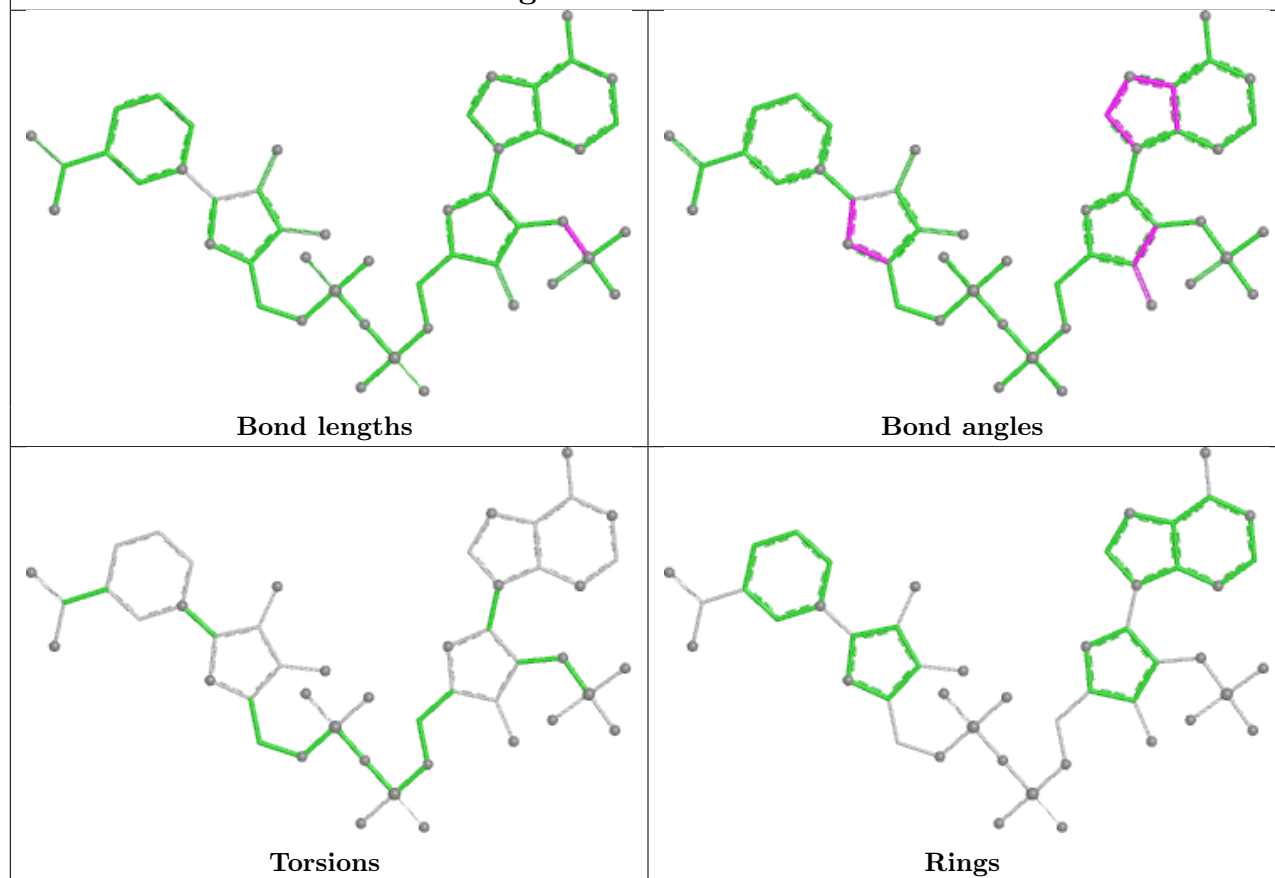
Ligand LYA D 1270 (B)

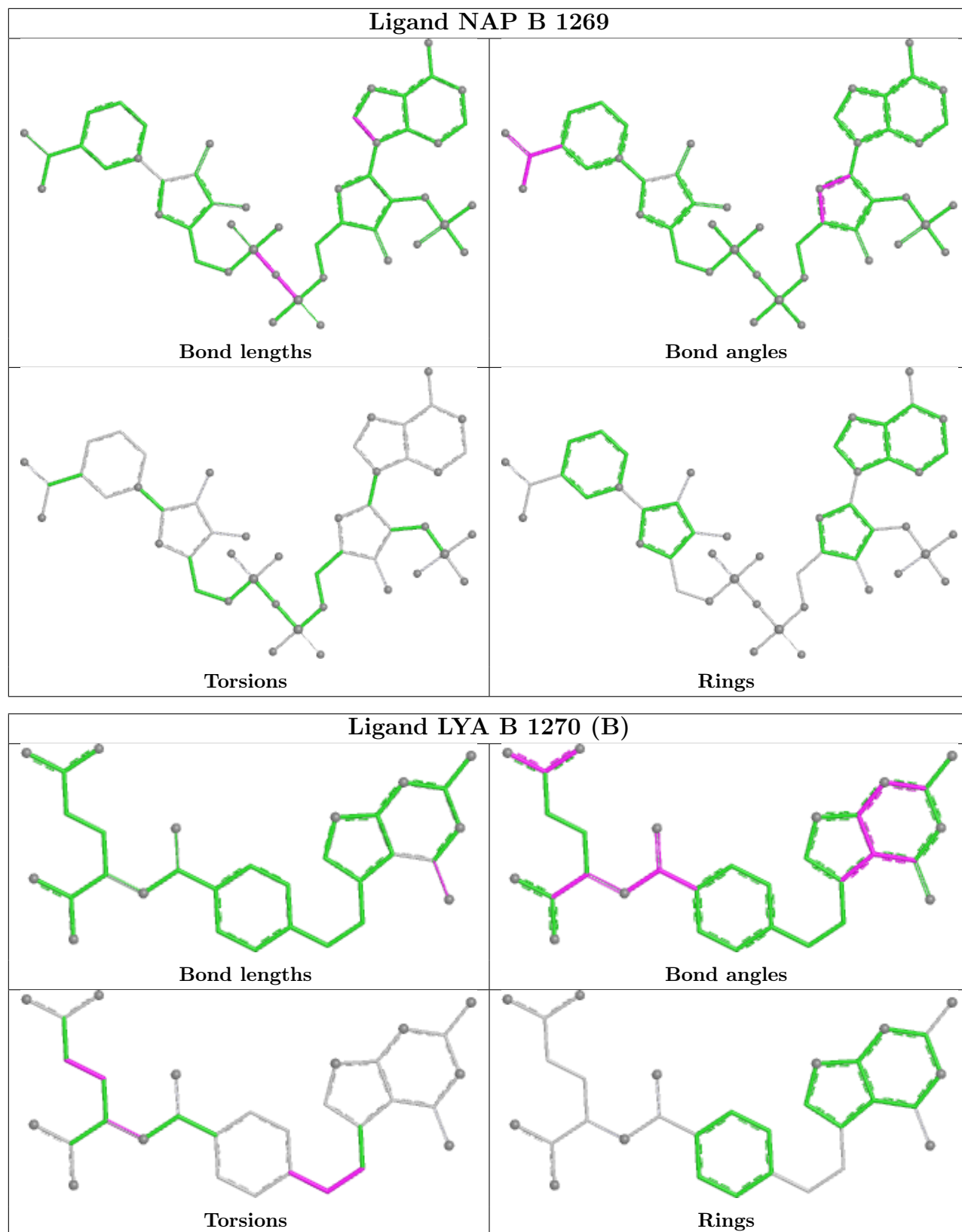


Ligand LYA B 1270 (A)



Ligand NAP D 1269





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	251/288 (87%)	-0.64	4 (1%) 70 74	5, 12, 29, 61	9 (3%)
1	B	250/288 (86%)	-0.71	2 (0%) 82 86	5, 11, 25, 59	8 (3%)
1	C	252/288 (87%)	-0.60	3 (1%) 76 81	6, 12, 31, 72	8 (3%)
1	D	249/288 (86%)	-0.66	1 (0%) 88 90	5, 11, 27, 56	12 (4%)
All	All	1002/1152 (86%)	-0.65	10 (0%) 79 83	5, 12, 29, 72	37 (3%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	144	GLY	6.1
1	D	152	SER	3.6
1	A	151	SER	2.9
1	B	103	VAL	2.8
1	A	103	VAL	2.6
1	C	216	GLU	2.4
1	A	113	GLY	2.3
1	A	104	GLN	2.3
1	C	190	LEU	2.3
1	B	151	SER	2.2

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

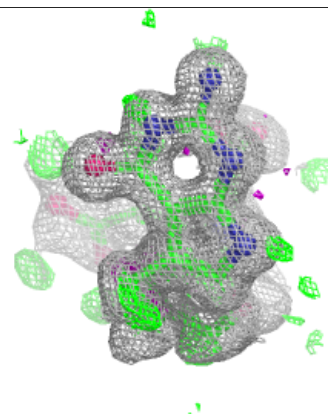
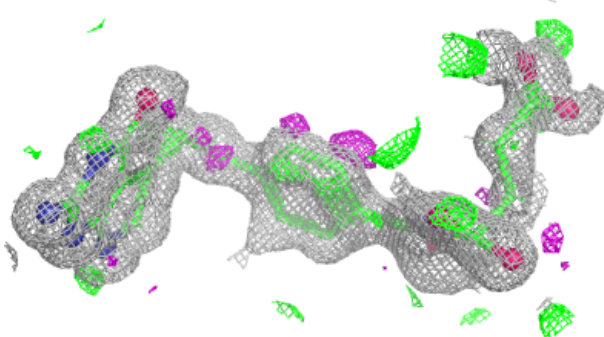
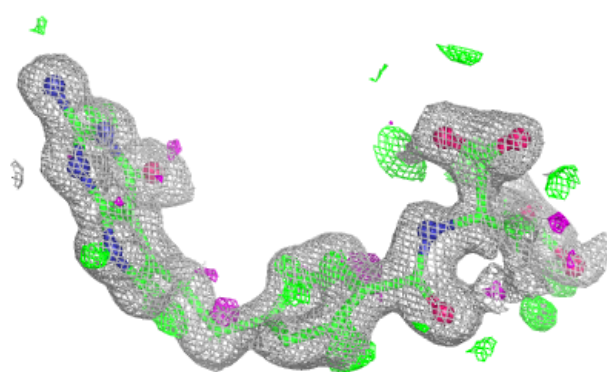
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	LYA	A	1270[A]	31/31	0.97	0.07	8,16,26,34	17
3	LYA	A	1270[B]	31/31	0.97	0.07	8,16,23,31	17
3	LYA	D	1270[A]	31/31	0.97	0.09	8,16,32,37	17
3	LYA	D	1270[B]	31/31	0.97	0.09	8,16,24,32	17
3	LYA	C	1270[A]	31/31	0.98	0.08	7,17,32,35	17
3	LYA	C	1270[B]	31/31	0.98	0.08	7,15,24,31	17
3	LYA	B	1270[A]	31/31	0.98	0.06	6,13,19,21	17
3	LYA	B	1270[B]	31/31	0.98	0.06	6,13,19,23	17
4	ACT	B	1271	4/4	0.99	0.04	12,13,13,14	0
2	NAP	B	1269	48/48	1.00	0.02	5,7,9,10	0
2	NAP	C	1269	48/48	1.00	0.02	5,7,9,10	0
2	NAP	D	1269	48/48	1.00	0.02	6,8,10,12	0
2	NAP	A	1269	48/48	1.00	0.03	6,8,11,14	0

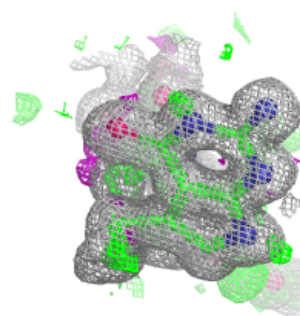
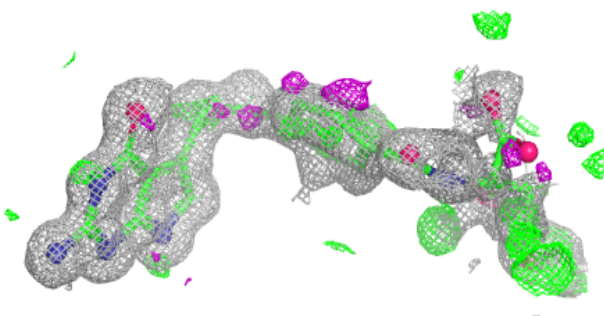
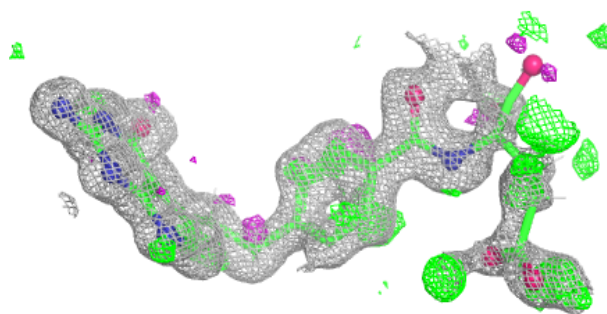
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around LYA A 1270 (A):

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

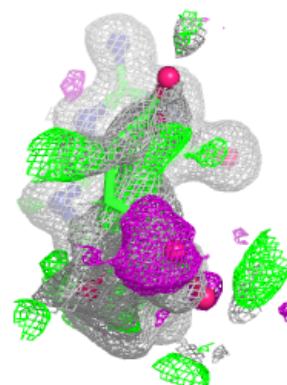
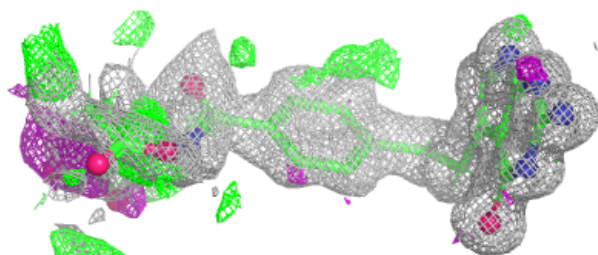
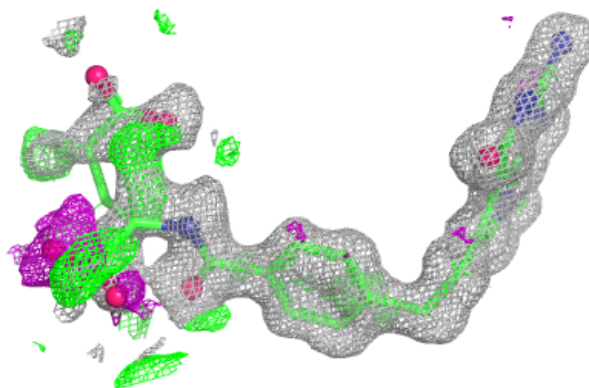
**Electron density around LYA A 1270 (B):**

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

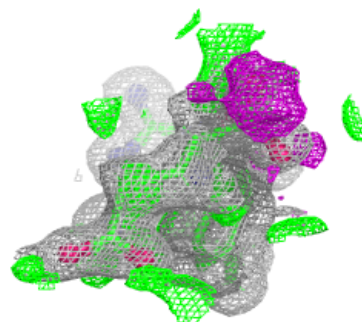
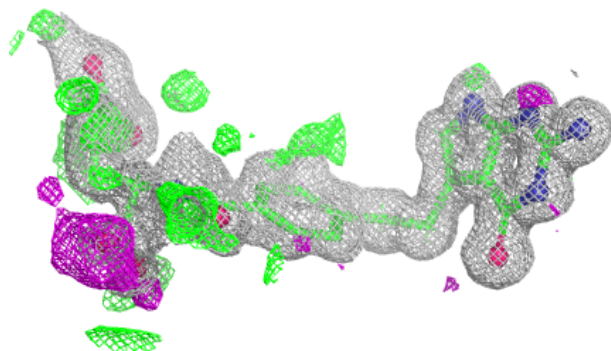
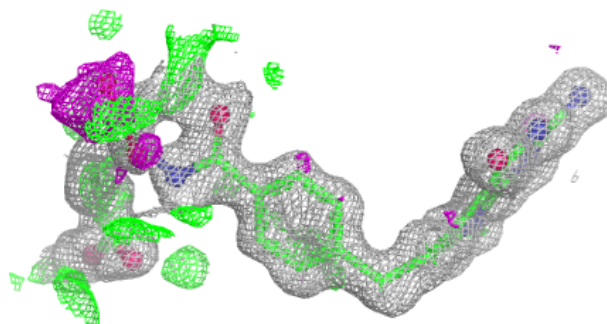


Electron density around LYA D 1270 (A):

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

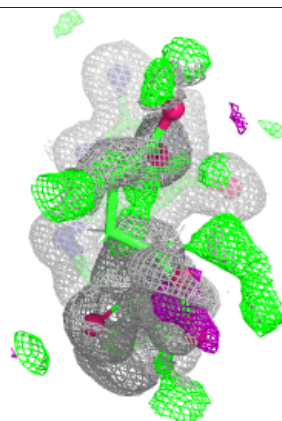
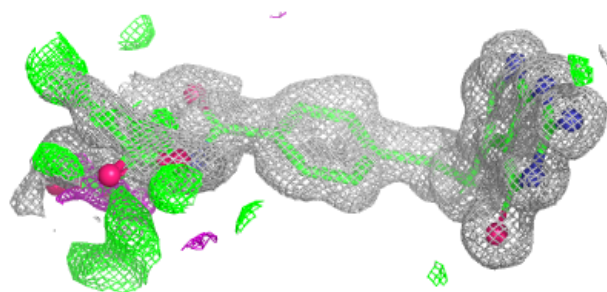
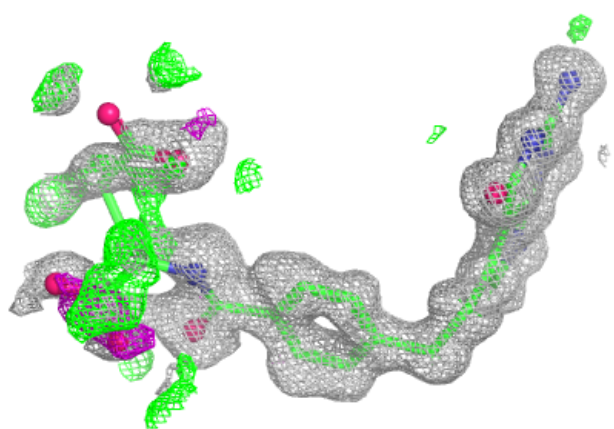
**Electron density around LYA D 1270 (B):**

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

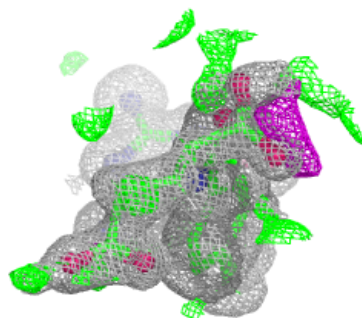
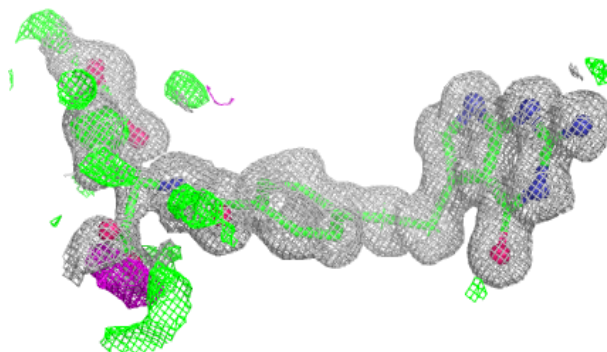
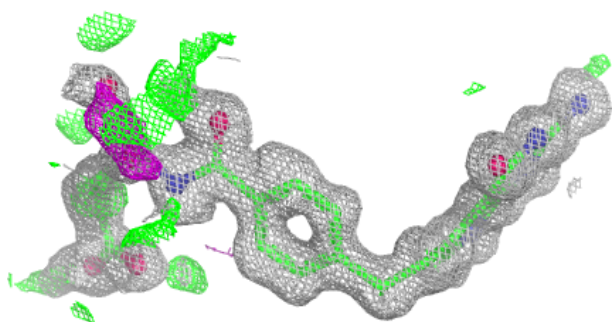


Electron density around LYA C 1270 (A):

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

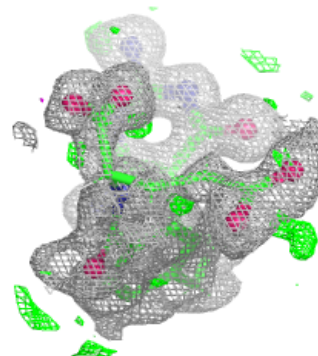
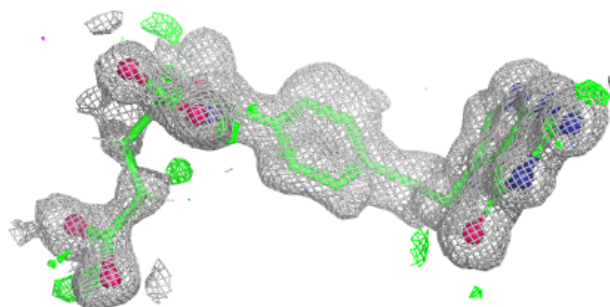
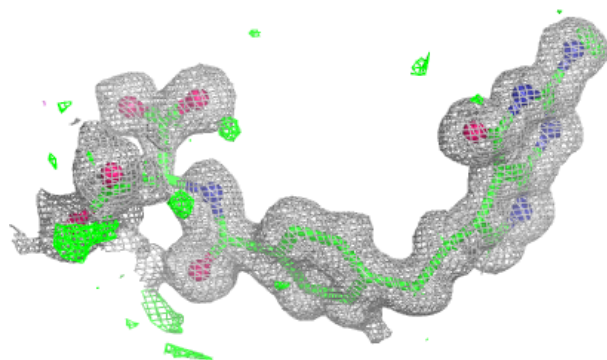
**Electron density around LYA C 1270 (B):**

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

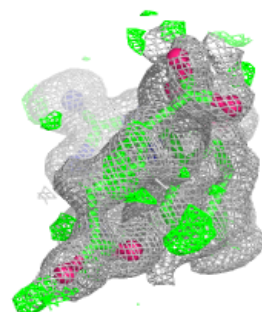
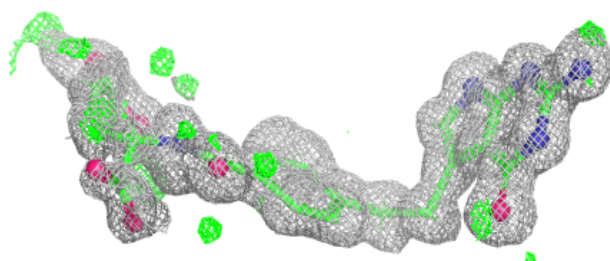
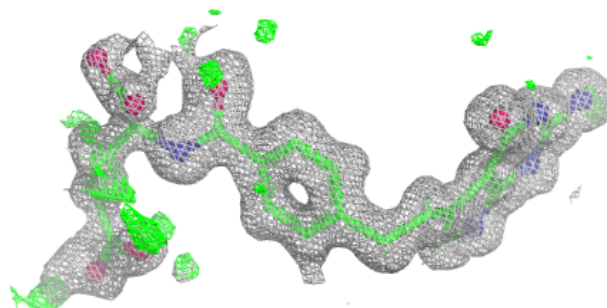


Electron density around LYA B 1270 (A):

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

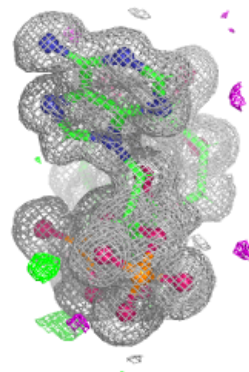
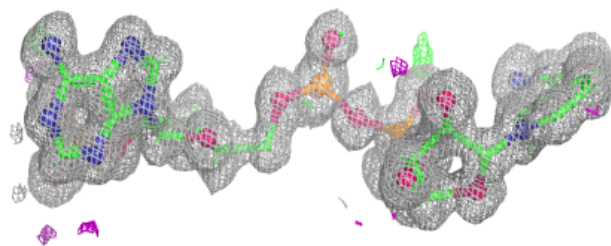
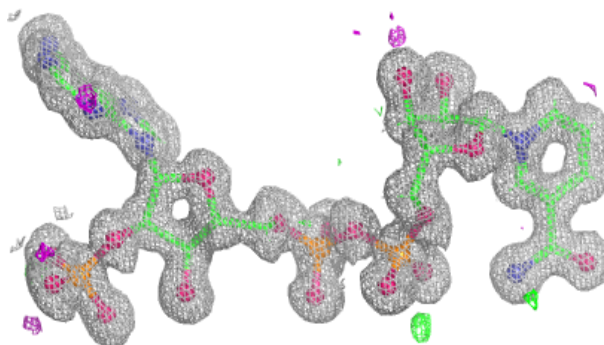
**Electron density around LYA B 1270 (B):**

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and green (positive)

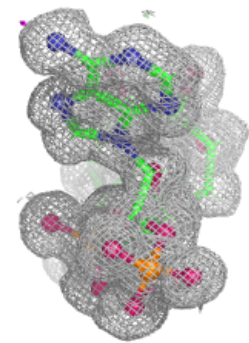
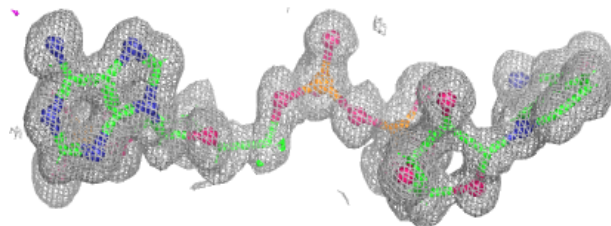
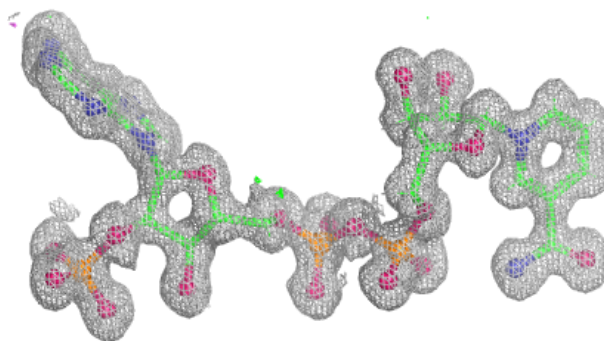


Electron density around NAP B 1269:

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

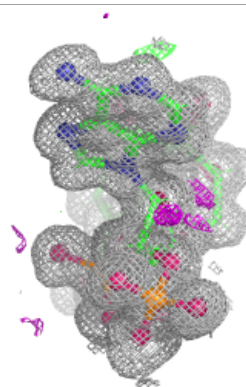
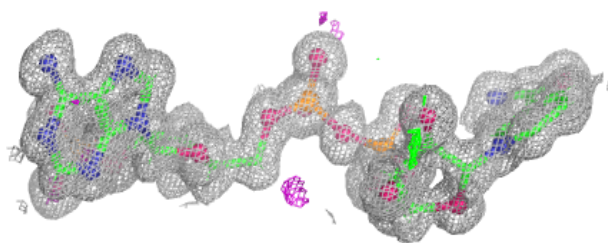
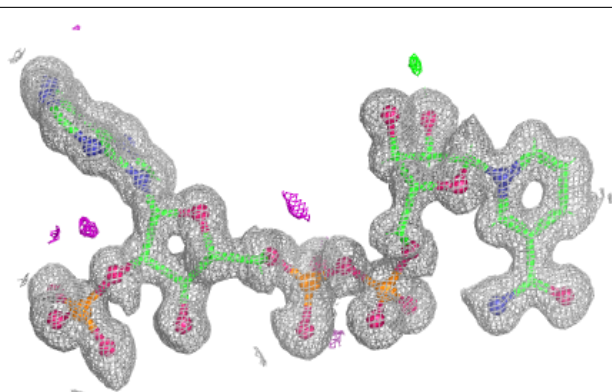
**Electron density around NAP C 1269:**

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

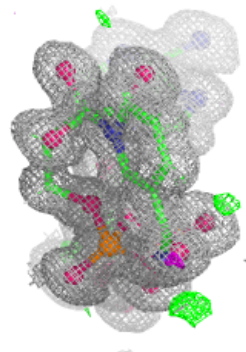
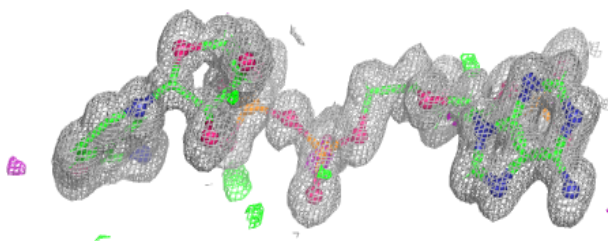
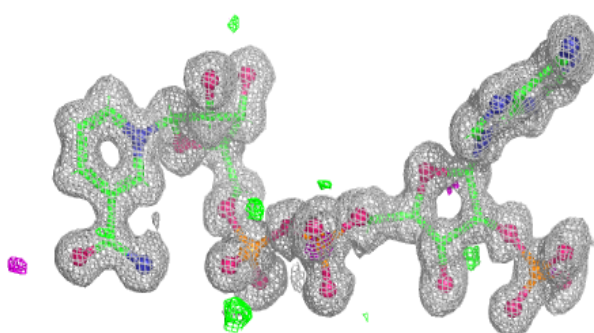


Electron density around NAP D 1269:

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

**Electron density around NAP A 1269:**

$2mF_o-DF_c$ (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.