



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 09:22 AM UTC

PDB ID : 2C91 / pdb_00002c91
Title : mouse succinic semialdehyde reductase, AKR7A5
Authors : Zhu, X.; Ellis, E.M.; Lapthorn, A.J.
Deposited on : 2005-12-08
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

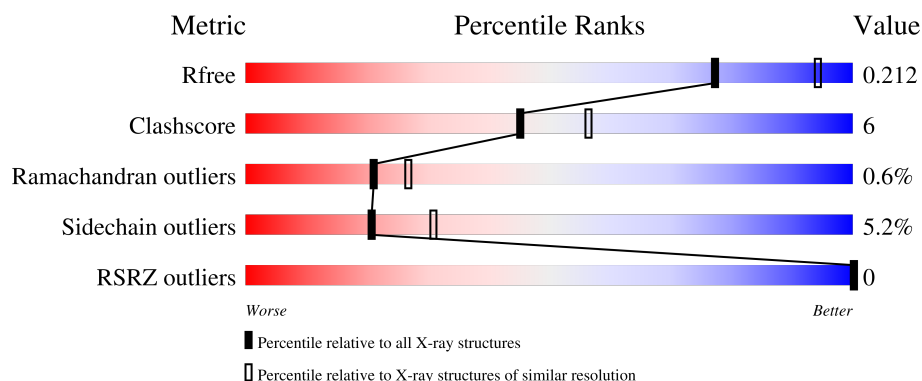
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	338	 80% 14% . .
1	B	338	 80% 13% . .
1	C	338	 83% 12% . .
1	D	338	 82% 11% . .
1	E	338	 82% 12% . .

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Mol	Chain	Length	Quality of chain
1	F	338	 82% 11% . . .
1	G	338	 75% 18% . . .
1	H	338	 82% 12% . .
1	I	338	 82% 12% . .
1	J	338	 82% 12% . .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	TLA	C	360	-	-	X	-
4	GOL	G	364	-	X	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 28440 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 AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	325	Total	C	N	O	S	0	3	0
			2569	1617	454	480	18			
1	B	324	Total	C	N	O	S	0	0	0
			2545	1603	447	477	18			
1	C	324	Total	C	N	O	S	0	1	0
			2552	1608	447	479	18			
1	D	324	Total	C	N	O	S	0	2	0
			2564	1616	453	477	18			
1	E	324	Total	C	N	O	S	0	1	0
			2556	1611	450	477	18			
1	F	324	Total	C	N	O	S	0	0	0
			2548	1606	447	477	18			
1	G	324	Total	C	N	O	S	0	1	0
			2552	1608	447	479	18			
1	H	324	Total	C	N	O	S	0	1	0
			2538	1601	440	479	18			
1	I	324	Total	C	N	O	S	0	0	0
			2548	1606	447	477	18			
1	J	325	Total	C	N	O	S	0	1	0
			2559	1613	448	480	18			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	87	ILE	VAL	conflict	UNP Q8CG76
A	122	CYS	ARG	conflict	UNP Q8CG76
B	87	ILE	VAL	conflict	UNP Q8CG76
B	122	CYS	ARG	conflict	UNP Q8CG76
C	87	ILE	VAL	conflict	UNP Q8CG76
C	122	CYS	ARG	conflict	UNP Q8CG76
D	87	ILE	VAL	conflict	UNP Q8CG76
D	122	CYS	ARG	conflict	UNP Q8CG76
E	87	ILE	VAL	conflict	UNP Q8CG76

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Chain	Residue	Modelled	Actual	Comment	Reference
E	122	CYS	ARG	conflict	UNP Q8CG76
F	87	ILE	VAL	conflict	UNP Q8CG76
F	122	CYS	ARG	conflict	UNP Q8CG76
G	87	ILE	VAL	conflict	UNP Q8CG76
G	122	CYS	ARG	conflict	UNP Q8CG76
H	87	ILE	VAL	conflict	UNP Q8CG76
H	122	CYS	ARG	conflict	UNP Q8CG76
I	87	ILE	VAL	conflict	UNP Q8CG76
I	122	CYS	ARG	conflict	UNP Q8CG76
J	87	ILE	VAL	conflict	UNP Q8CG76
J	122	CYS	ARG	conflict	UNP Q8CG76

- # NAP

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	B	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	C	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	D	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	E	1	Total 48	C 21	N 7	O 17	P 3	0	0

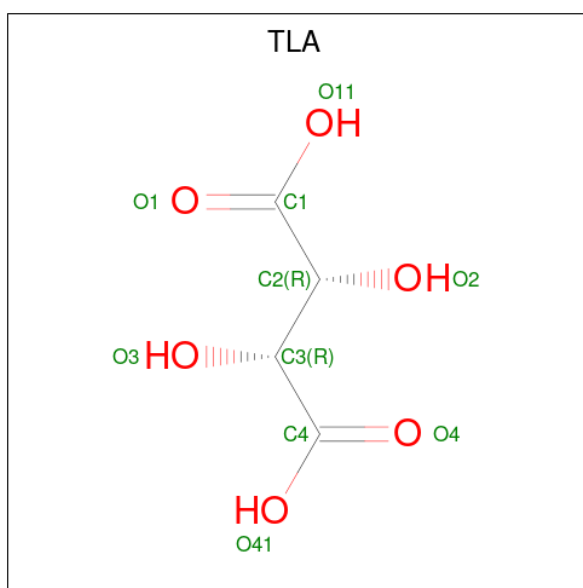


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PDB
PROTEIN DATA BANK

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	F	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	G	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	H	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	I	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	J	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 is L(+)-TARTARIC ACID (CCD ID: TLA) (formula: C₄H₆O₆).



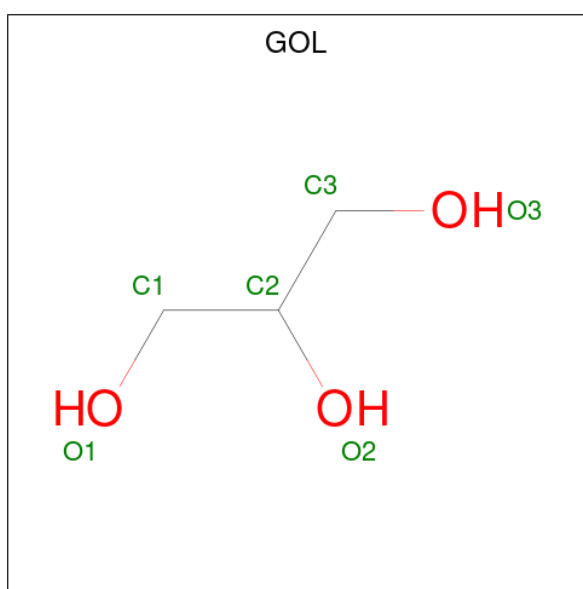
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			10	4	6		
3	B	1	Total	C	O	0	0
			10	4	6		
3	C	1	Total	C	O	0	0
			10	4	6		
3	D	1	Total	C	O	0	0
			10	4	6		
3	E	1	Total	C	O	0	0
			10	4	6		
3	F	1	Total	C	O	0	0
			10	4	6		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	G	1	Total	C	O	0	0
			10	4	6		
3	H	1	Total	C	O	0	0
			10	4	6		
3	I	1	Total	C	O	0	0
			10	4	6		
3	J	1	Total	C	O	0	0
			10	4	6		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



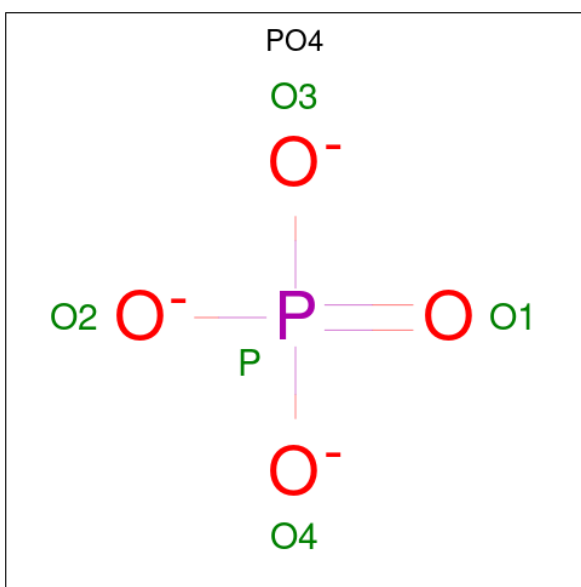
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		

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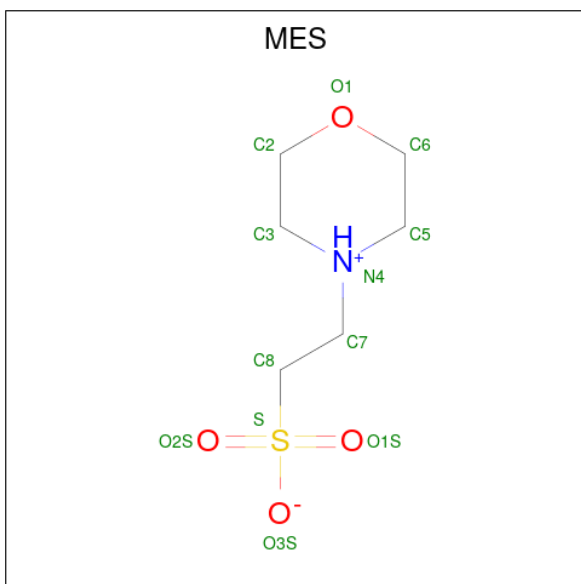
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		
4	G	1	Total	C	O	0	0
			6	3	3		
4	G	1	Total	C	O	0	0
			6	3	3		
4	G	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		
4	I	1	Total	C	O	0	0
			6	3	3		
4	I	1	Total	C	O	0	0
			6	3	3		
4	J	1	Total	C	O	0	0
			6	3	3		
4	J	1	Total	C	O	0	0
			6	3	3		
4	J	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P	0	0
			5	4	1		
5	J	1	Total	O	P	0	0
			5	4	1		

- Molecule 6 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
6	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
6	I	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
6	J	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 7 is water.

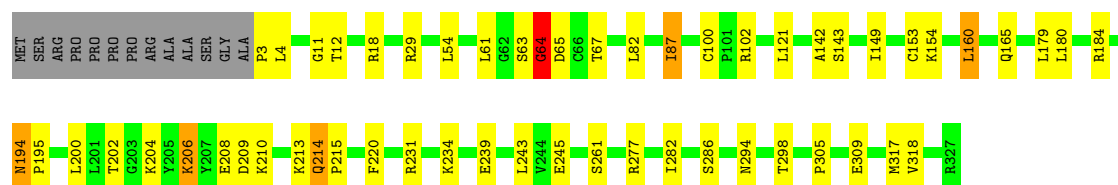
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	223	Total	O	0	0
			223	223		
7	B	131	Total	O	0	0
			131	131		
7	C	225	Total	O	0	0
			225	225		
7	D	272	Total	O	0	0
			272	272		
7	E	262	Total	O	0	0
			262	262		
7	F	214	Total	O	0	0
			214	214		
7	G	257	Total	O	0	0
			257	257		
7	H	159	Total	O	0	0
			159	159		
7	I	164	Total	O	0	0
			164	164		
7	J	202	Total	O	0	0
			202	202		

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.

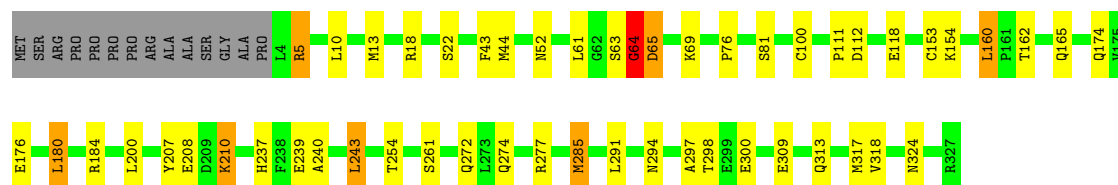
• Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2

Chain A: 



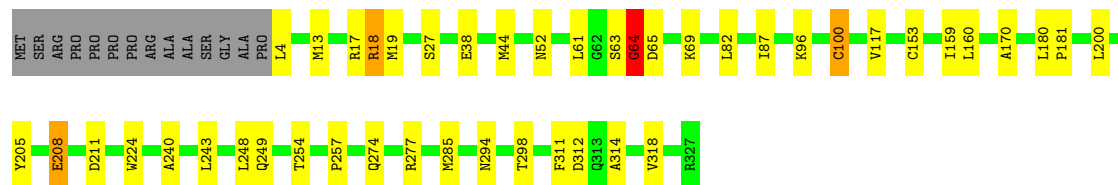
• Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2

Chain B: 



• Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2

Chain C: 



• Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2

Chain D: 





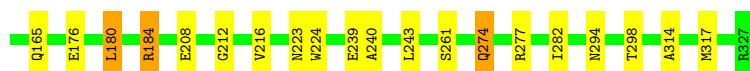
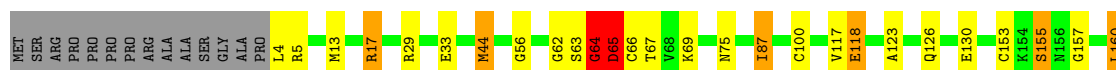
- Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2

Chain E: 82% 12% . .



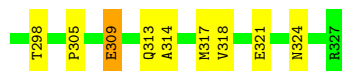
- Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2

Chain F: 82% 11% . . .



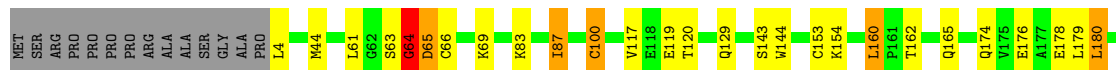
- Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2

Chain G: 75% 18% . . .



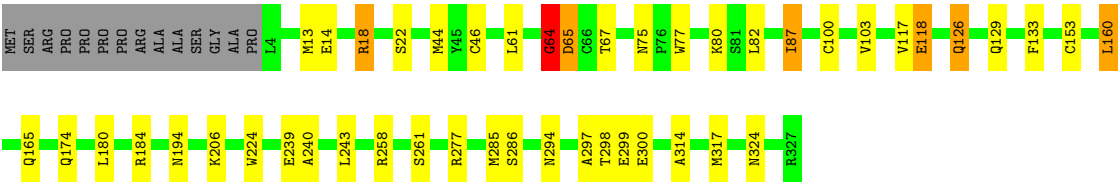
- Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2

Chain H: 82% 12% . .

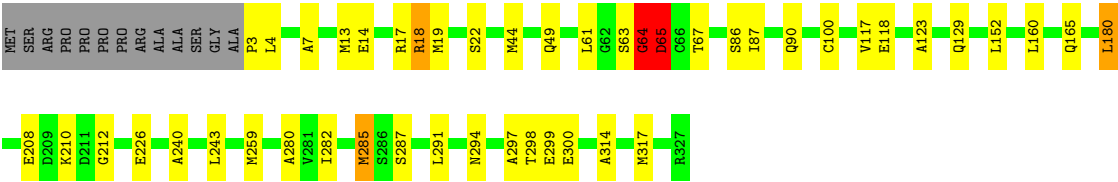
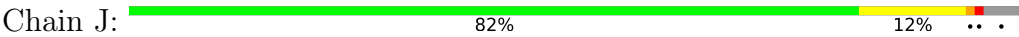


- Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2

Chain I: 82% 12% . .



● Molecule 1: AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	98.53Å 159.24Å 96.70Å 90.02° 119.40° 78.50°	Depositor
Resolution (Å)	45.00 – 2.30 45.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	89.8 (45.00-2.30) 89.7 (45.00-2.30)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.58 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.160 , 0.208 0.170 , 0.212	Depositor DCC
R_{free} test set	9982 reflections (4.51%)	wwPDB-VP
Wilson B-factor (Å ²)	29.3	Xtriage
Anisotropy	0.128	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 22.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.458 for -h-l,-k,l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	28440	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.41% 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: GOL, PO4, MES, TLA, NAP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	1.37	8/2647 (0.3%)	1.11	1/3584 (0.0%)
1	B	1.10	2/2608 (0.1%)	1.05	3/3533 (0.1%)
1	C	1.23	2/2620 (0.1%)	1.07	0/3549
1	D	1.35	11/2633 (0.4%)	1.13	3/3565 (0.1%)
1	E	1.32	6/2622 (0.2%)	1.14	3/3552 (0.1%)
1	F	1.24	3/2611 (0.1%)	1.09	4/3537 (0.1%)
1	G	1.33	5/2620 (0.2%)	1.10	5/3549 (0.1%)
1	H	1.14	1/2604 (0.0%)	1.02	2/3531 (0.1%)
1	I	1.20	2/2611 (0.1%)	1.07	1/3537 (0.0%)
1	J	1.17	2/2625 (0.1%)	1.06	4/3556 (0.1%)
All	All	1.25	42/26201 (0.2%)	1.08	26/35493 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	1
1	J	0	1
All	All	0	10

The worst 5 of 42 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	194	ASN	C-O	18.55	1.32	1.23
1	D	17	ARG	CA-C	11.04	1.59	1.52
1	A	214	GLN	C-O	-10.56	1.19	1.23
1	D	214	GLN	C-O	-8.63	1.19	1.23
1	G	214	GLN	CA-CB	7.39	1.57	1.52

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	309	GLU	CB-CA-C	10.30	127.89	110.79
1	E	216	VAL	CB-CA-C	-9.13	96.44	111.32
1	D	216	VAL	CB-CA-C	-8.44	97.56	111.32
1	A	3	PRO	N-CA-CB	7.65	111.41	103.00
1	J	3	PRO	N-CA-CB	7.47	111.21	103.00

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	64	GLY	Peptide
1	B	64	GLY	Peptide
1	C	64	GLY	Peptide
1	D	64	GLY	Peptide
1	E	64	GLY	Peptide

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	2569	0	2484	41	0
1	B	2545	0	2453	27	0
1	C	2552	0	2464	24	0
1	D	2564	0	2488	22	0
1	E	2556	0	2475	29	0
1	F	2548	0	2462	33	0
1	G	2552	0	2464	43	0
1	H	2538	0	2435	23	0
1	I	2548	0	2462	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	J	2559	0	2470	26	0
2	A	48	0	25	2	0
2	B	48	0	25	3	0
2	C	48	0	25	0	0
2	D	48	0	25	2	0
2	E	48	0	25	2	0
2	F	48	0	25	3	0
2	G	48	0	24	1	0
2	H	48	0	25	4	0
2	I	48	0	25	4	0
2	J	48	0	25	3	0
3	A	10	0	4	0	0
3	B	10	0	4	3	0
3	C	10	0	4	4	0
3	D	10	0	4	1	0
3	E	10	0	4	2	0
3	F	10	0	4	3	0
3	G	10	0	4	1	0
3	H	10	0	4	2	0
3	I	10	0	4	2	0
3	J	10	0	4	2	0
4	A	12	0	16	2	0
4	B	18	0	24	0	0
4	C	18	0	24	0	0
4	D	18	0	24	0	0
4	E	18	0	24	0	0
4	F	6	0	8	0	0
4	G	18	0	24	4	0
4	H	12	0	16	2	0
4	I	12	0	16	1	0
4	J	18	0	24	0	0
5	A	5	0	0	0	0
5	J	5	0	0	0	0
6	B	12	0	12	0	0
6	C	12	0	12	0	0
6	D	12	0	12	0	0
6	I	12	0	12	0	0
6	J	12	0	12	0	0
7	A	223	0	0	9	0
7	B	131	0	0	3	0
7	C	225	0	0	7	0
7	D	272	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	E	262	0	0	7	0
7	F	214	0	0	9	0
7	G	257	0	0	9	0
7	H	159	0	0	2	0
7	I	164	0	0	9	0
7	J	202	0	0	8	0
All	All	28440	0	25206	306	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 6.

The worst 5 of 306 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:E:100:CYS:SG	7:E:2088:HOH:O	1.95	1.23
1:C:100:CYS:SG	7:C:2071:HOH:O	2.05	1.10
1:F:44:MET:SD	7:F:2025:HOH:O	2.10	1.08
1:A:100:CYS:SG	7:A:2061:HOH:O	2.10	1.06
1:I:13:MET:HG2	7:I:2008:HOH:O	1.61	0.99

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	326/338 (96%)	320 (98%)	4 (1%)	2 (1%)	21 27
1	B	322/338 (95%)	314 (98%)	6 (2%)	2 (1%)	21 27
1	C	323/338 (96%)	314 (97%)	7 (2%)	2 (1%)	21 27
1	D	324/338 (96%)	317 (98%)	5 (2%)	2 (1%)	21 27
1	E	323/338 (96%)	316 (98%)	6 (2%)	1 (0%)	36 46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	322/338 (95%)	312 (97%)	8 (2%)	2 (1%)	21	27
1	G	323/338 (96%)	316 (98%)	5 (2%)	2 (1%)	21	27
1	H	323/338 (96%)	316 (98%)	5 (2%)	2 (1%)	21	27
1	I	322/338 (95%)	314 (98%)	6 (2%)	2 (1%)	21	27
1	J	324/338 (96%)	313 (97%)	8 (2%)	3 (1%)	14	17
All	All	3232/3380 (96%)	3152 (98%)	60 (2%)	20 (1%)	21	27

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	65	ASP
1	B	65	ASP
1	C	65	ASP
1	D	65	ASP
1	E	65	ASP

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	269/276 (98%)	259 (96%)	10 (4%)	30	45
1	B	265/276 (96%)	247 (93%)	18 (7%)	14	20
1	C	267/276 (97%)	253 (95%)	14 (5%)	21	31
1	D	268/276 (97%)	257 (96%)	11 (4%)	27	41
1	E	267/276 (97%)	254 (95%)	13 (5%)	22	34
1	F	266/276 (96%)	249 (94%)	17 (6%)	16	23
1	G	267/276 (97%)	253 (95%)	14 (5%)	21	31
1	H	264/276 (96%)	248 (94%)	16 (6%)	17	24
1	I	266/276 (96%)	250 (94%)	16 (6%)	17	25
1	J	267/276 (97%)	256 (96%)	11 (4%)	27	41
All	All	2666/2760 (97%)	2526 (95%)	140 (5%)	21	30

5 of 140 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	44	MET
1	I	126	GLN
1	J	18	ARG
1	D	184[A]	ARG
1	D	160	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 59 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	49	GLN
1	J	129	GLN
1	G	49	GLN
1	J	126	GLN
1	I	129	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

52 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
4	GOL	G	363	-	5,5,5	0.64	0	5,5,5	1.24	1 (20%)
4	GOL	B	362	-	5,5,5	0.81	0	5,5,5	1.35	1 (20%)
2	NAP	J	350	-	50,52,52	1.86	8 (16%)	71,80,80	1.68	15 (21%)
4	GOL	D	362	-	5,5,5	0.56	0	5,5,5	0.82	0
4	GOL	F	361	-	5,5,5	0.76	0	5,5,5	1.59	2 (40%)
3	TLA	C	360	-	9,9,9	1.67	2 (22%)	12,12,12	1.73	4 (33%)
4	GOL	C	361	-	5,5,5	0.71	0	5,5,5	1.42	0
4	GOL	I	362	-	5,5,5	0.73	0	5,5,5	1.45	1 (20%)
2	NAP	B	350	-	50,52,52	1.84	10 (20%)	71,80,80	1.79	16 (22%)
4	GOL	D	361	-	5,5,5	0.65	0	5,5,5	0.38	0
4	GOL	G	364	-	5,5,5	1.02	0	5,5,5	1.65	2 (40%)
4	GOL	H	361	-	5,5,5	0.44	0	5,5,5	0.63	0
3	TLA	H	360	-	9,9,9	1.69	3 (33%)	12,12,12	0.80	0
3	TLA	F	360	-	9,9,9	1.03	1 (11%)	12,12,12	1.93	3 (25%)
6	MES	J	368	-	12,12,12	1.79	3 (25%)	15,16,16	2.38	5 (33%)
5	PO4	J	367	-	4,4,4	1.01	0	6,6,6	0.63	0
2	NAP	G	350	-	50,52,52	1.94	12 (24%)	71,80,80	1.58	15 (21%)
4	GOL	J	363	-	5,5,5	0.46	0	5,5,5	1.11	0
3	TLA	I	360	-	9,9,9	1.86	2 (22%)	12,12,12	1.51	2 (16%)
4	GOL	J	366	-	5,5,5	0.94	0	5,5,5	0.97	0
2	NAP	F	350	-	50,52,52	1.95	6 (12%)	71,80,80	1.61	16 (22%)
4	GOL	H	362	-	5,5,5	0.76	0	5,5,5	1.13	0
3	TLA	G	360	-	9,9,9	1.79	5 (55%)	12,12,12	1.16	1 (8%)
6	MES	B	364	-	12,12,12	2.10	1 (8%)	15,16,16	3.10	10 (66%)
6	MES	D	364	-	12,12,12	1.87	1 (8%)	15,16,16	2.77	7 (46%)
4	GOL	B	363	-	5,5,5	0.73	0	5,5,5	0.98	0
4	GOL	C	363	-	5,5,5	0.86	0	5,5,5	1.45	1 (20%)
4	GOL	G	362	-	5,5,5	0.67	0	5,5,5	1.32	1 (20%)
2	NAP	H	350	-	50,52,52	2.05	9 (18%)	71,80,80	2.02	22 (30%)
4	GOL	E	362	-	5,5,5	0.69	0	5,5,5	0.69	0
4	GOL	I	361	-	5,5,5	0.56	0	5,5,5	0.91	0
5	PO4	A	364	-	4,4,4	0.82	0	6,6,6	2.48	3 (50%)
4	GOL	E	363	-	5,5,5	0.82	0	5,5,5	1.00	0
3	TLA	D	360	-	9,9,9	1.91	3 (33%)	12,12,12	1.98	4 (33%)
4	GOL	J	364	-	5,5,5	0.59	0	5,5,5	0.76	0
2	NAP	D	350	-	50,52,52	1.79	7 (14%)	71,80,80	1.50	11 (15%)
6	MES	C	364	-	12,12,12	2.11	1 (8%)	15,16,16	2.41	6 (40%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAP	C	350	-	50,52,52	1.91	7 (14%)	71,80,80	1.54	13 (18%)
3	TLA	J	360	-	9,9,9	1.69	3 (33%)	12,12,12	0.92	1 (8%)
3	TLA	A	360	-	9,9,9	1.18	1 (11%)	12,12,12	1.69	4 (33%)
4	GOL	A	361	-	5,5,5	0.56	0	5,5,5	0.74	0
6	MES	I	363	-	12,12,12	2.13	3 (25%)	15,16,16	2.56	5 (33%)
4	GOL	D	363	-	5,5,5	1.52	0	5,5,5	1.82	1 (20%)
2	NAP	I	350	-	50,52,52	1.80	5 (10%)	71,80,80	1.67	15 (21%)
4	GOL	B	361	-	5,5,5	0.56	0	5,5,5	0.57	0
2	NAP	A	350	-	50,52,52	1.87	9 (18%)	71,80,80	1.57	14 (19%)
4	GOL	E	361	-	5,5,5	0.59	0	5,5,5	0.97	0
2	NAP	E	350	-	50,52,52	2.07	5 (10%)	71,80,80	1.66	13 (18%)
4	GOL	A	363	-	5,5,5	0.87	0	5,5,5	0.96	0
4	GOL	C	362	-	5,5,5	0.58	0	5,5,5	1.22	1 (20%)
3	TLA	B	360	-	9,9,9	2.18	2 (22%)	12,12,12	1.24	2 (16%)
3	TLA	E	360	-	9,9,9	1.70	3 (33%)	12,12,12	1.32	1 (8%)

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
4	GOL	G	363	-	-	2/4/4/4	-
4	GOL	B	362	-	-	2/4/4/4	-
2	NAP	J	350	-	-	4/35/67/67	0/5/5/5
4	GOL	D	362	-	-	0/4/4/4	-
4	GOL	F	361	-	-	2/4/4/4	-
3	TLA	C	360	-	-	6/12/12/12	-
4	GOL	C	361	-	-	1/4/4/4	-
4	GOL	I	362	-	-	2/4/4/4	-
2	NAP	B	350	-	-	3/35/67/67	0/5/5/5
4	GOL	D	361	-	-	0/4/4/4	-
4	GOL	G	364	-	-	4/4/4/4	-
4	GOL	H	361	-	-	2/4/4/4	-
3	TLA	H	360	-	-	4/12/12/12	-
3	TLA	F	360	-	-	6/12/12/12	-
6	MES	J	368	-	-	4/6/14/14	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAP	G	350	-	-	5/35/67/67	0/5/5/5
4	GOL	J	363	-	-	0/4/4/4	-
3	TLA	I	360	-	-	6/12/12/12	-
4	GOL	J	366	-	-	3/4/4/4	-
2	NAP	F	350	-	-	4/35/67/67	0/5/5/5
4	GOL	H	362	-	-	3/4/4/4	-
3	TLA	G	360	-	-	6/12/12/12	-
6	MES	B	364	-	-	4/6/14/14	0/1/1/1
6	MES	D	364	-	-	4/6/14/14	0/1/1/1
4	GOL	B	363	-	-	0/4/4/4	-
4	GOL	C	363	-	-	4/4/4/4	-
4	GOL	G	362	-	-	4/4/4/4	-
2	NAP	H	350	-	-	4/35/67/67	0/5/5/5
4	GOL	E	362	-	-	2/4/4/4	-
4	GOL	I	361	-	-	2/4/4/4	-
4	GOL	E	363	-	-	0/4/4/4	-
3	TLA	D	360	-	-	6/12/12/12	-
4	GOL	J	364	-	-	2/4/4/4	-
2	NAP	D	350	-	-	1/35/67/67	0/5/5/5
6	MES	C	364	-	-	4/6/14/14	0/1/1/1
2	NAP	C	350	-	-	2/35/67/67	0/5/5/5
3	TLA	J	360	-	-	4/12/12/12	-
3	TLA	A	360	-	-	6/12/12/12	-
4	GOL	A	361	-	-	2/4/4/4	-
6	MES	I	363	-	-	4/6/14/14	0/1/1/1
4	GOL	D	363	-	-	4/4/4/4	-
2	NAP	I	350	-	-	3/35/67/67	0/5/5/5
4	GOL	B	361	-	-	0/4/4/4	-
2	NAP	A	350	-	-	1/35/67/67	0/5/5/5
4	GOL	E	361	-	-	3/4/4/4	-
2	NAP	E	350	-	-	5/35/67/67	0/5/5/5
4	GOL	A	363	-	-	0/4/4/4	-
4	GOL	C	362	-	-	0/4/4/4	-
3	TLA	B	360	-	-	4/12/12/12	-
3	TLA	E	360	-	-	6/12/12/12	-

The worst 5 of 112 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	350	NAP	O7N-C7N	9.24	1.41	1.24
2	A	350	NAP	O7N-C7N	8.95	1.40	1.24
2	H	350	NAP	O7N-C7N	8.91	1.40	1.24
2	D	350	NAP	O7N-C7N	8.51	1.40	1.24
2	E	350	NAP	O7N-C7N	7.91	1.38	1.24

The worst 5 of 219 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	368	MES	C5-N4-C3	7.31	124.58	108.84
6	D	364	MES	C5-N4-C3	7.28	124.52	108.84
2	B	350	NAP	N3A-C2A-N1A	-7.20	117.69	128.58
2	E	350	NAP	N3A-C2A-N1A	-7.15	117.76	128.58
6	B	364	MES	C5-N4-C3	6.60	123.05	108.84

There are no chirality outliers.

5 of 150 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	350	NAP	O4D-C1D-N1N-C2N
2	B	350	NAP	O4D-C1D-N1N-C6N
2	E	350	NAP	O4D-C1D-N1N-C6N
2	G	350	NAP	O4D-C1D-N1N-C6N
2	H	350	NAP	O4D-C1D-N1N-C6N

There are no ring outliers.

22 monomers are involved in 47 short contacts:

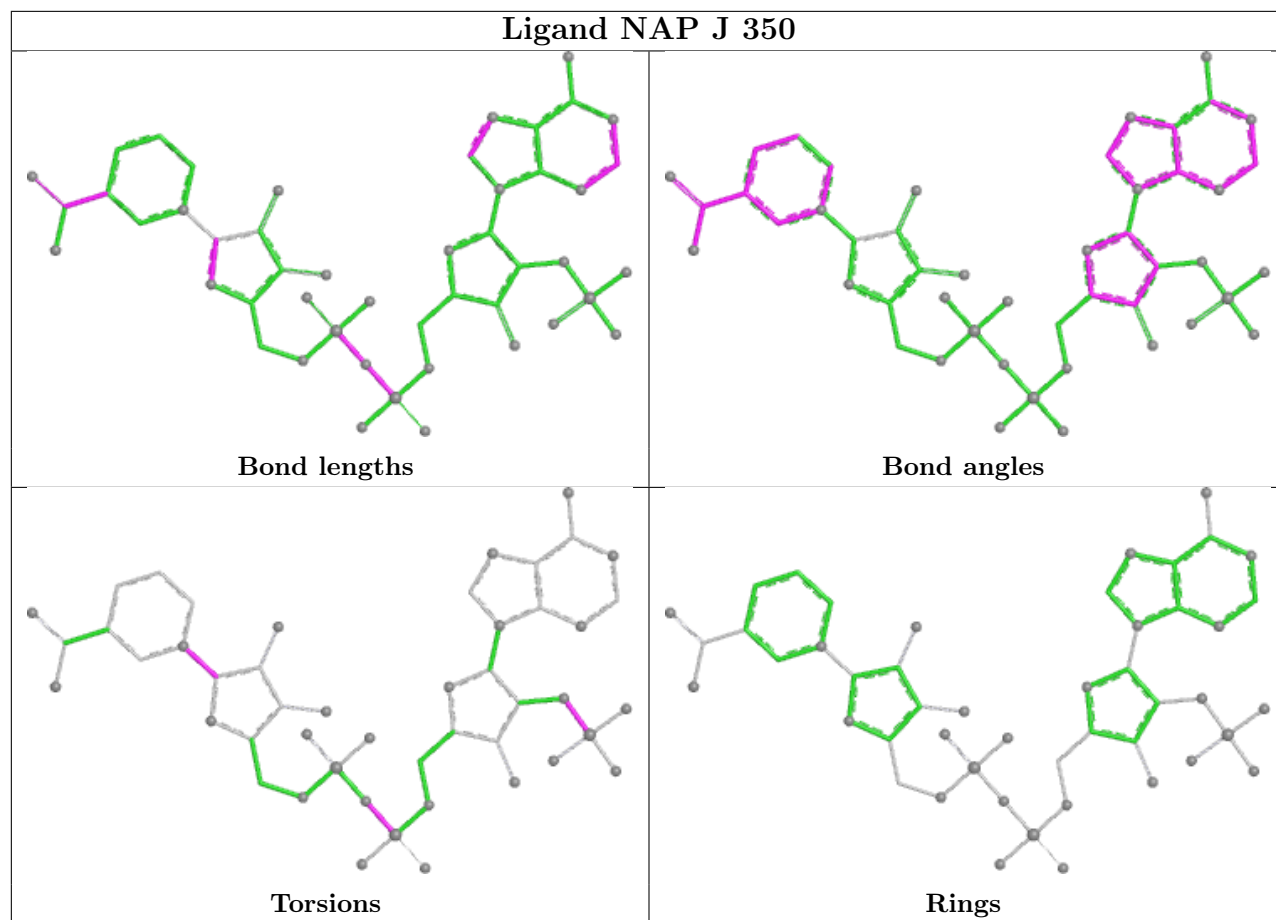
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	J	350	NAP	3	0
3	C	360	TLA	4	0
4	I	362	GOL	1	0
2	B	350	NAP	3	0
4	G	364	GOL	4	0
4	H	361	GOL	2	0
3	H	360	TLA	2	0
3	F	360	TLA	3	0
2	G	350	NAP	1	0
3	I	360	TLA	2	0
2	F	350	NAP	3	0
3	G	360	TLA	1	0
2	H	350	NAP	4	0

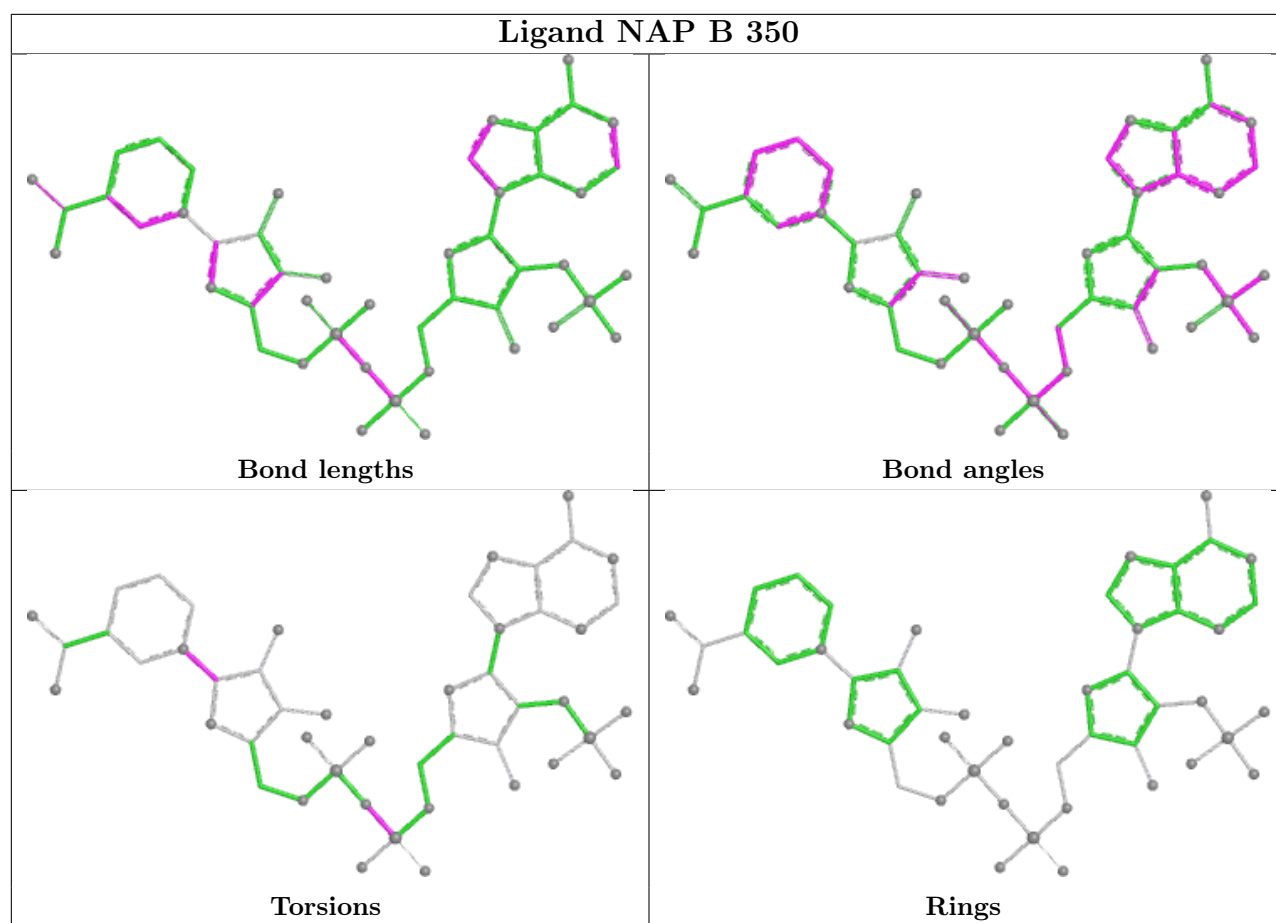
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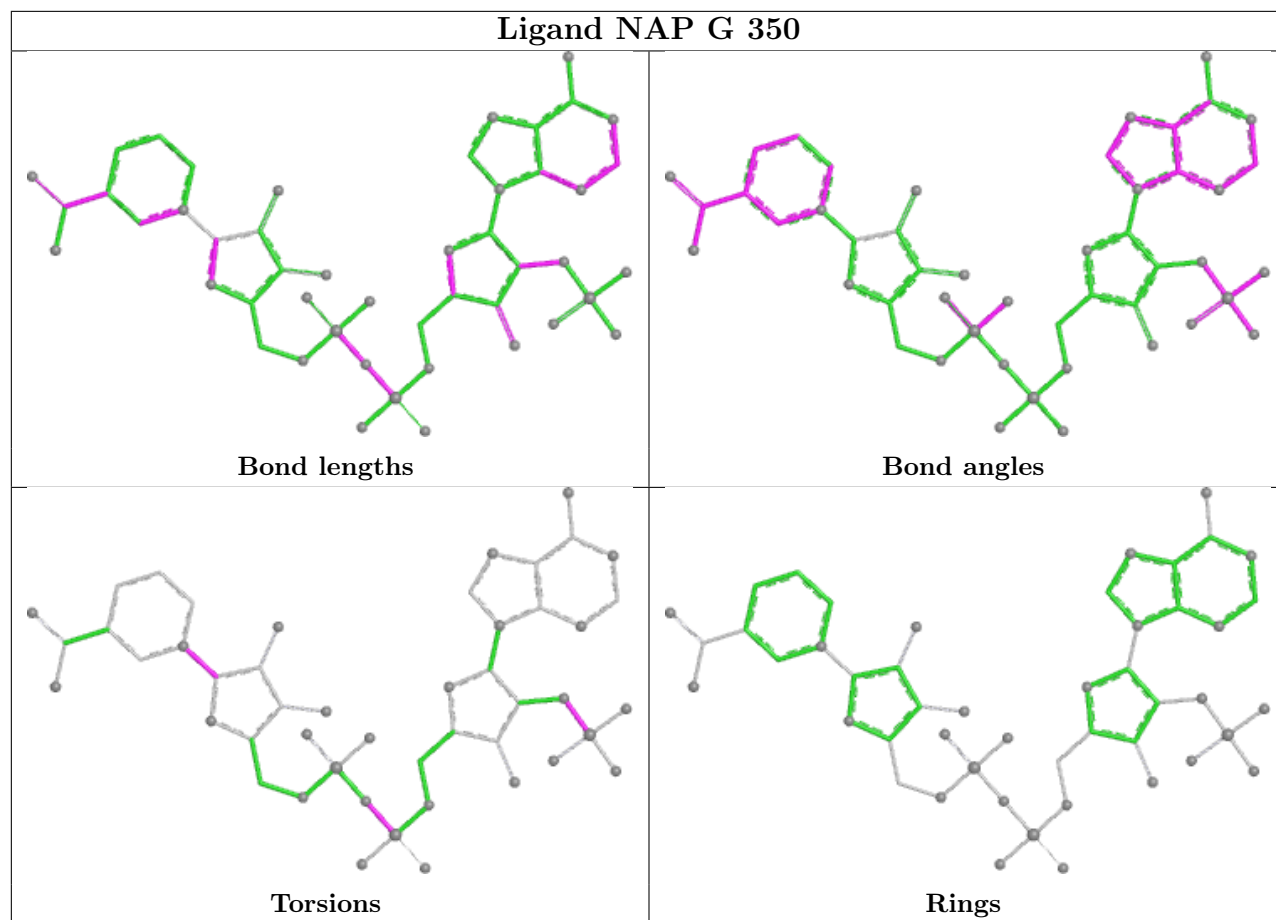
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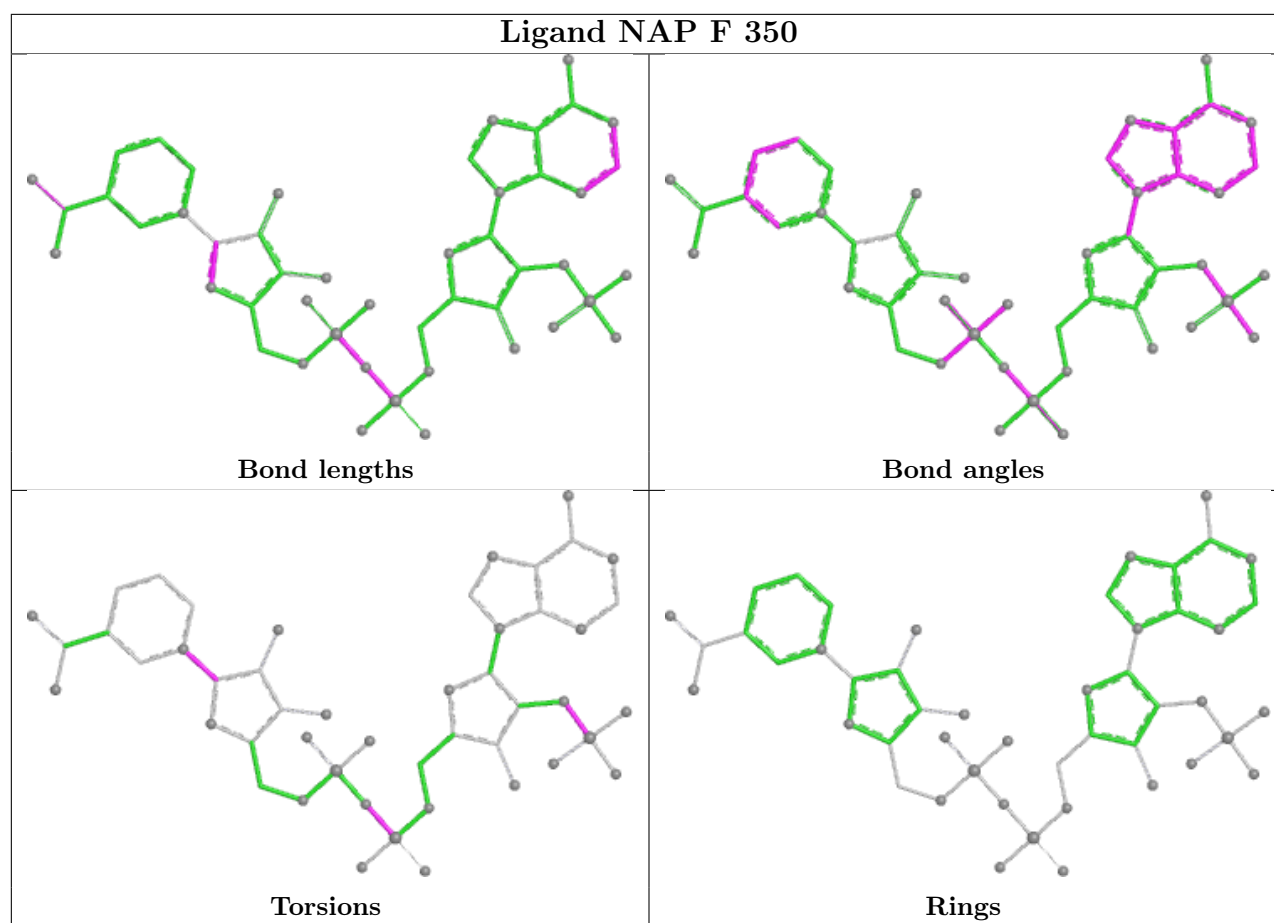
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	360	TLA	1	0
2	D	350	NAP	2	0
3	J	360	TLA	2	0
4	A	361	GOL	2	0
2	I	350	NAP	4	0
2	A	350	NAP	2	0
2	E	350	NAP	2	0
3	B	360	TLA	3	0
3	E	360	TLA	2	0

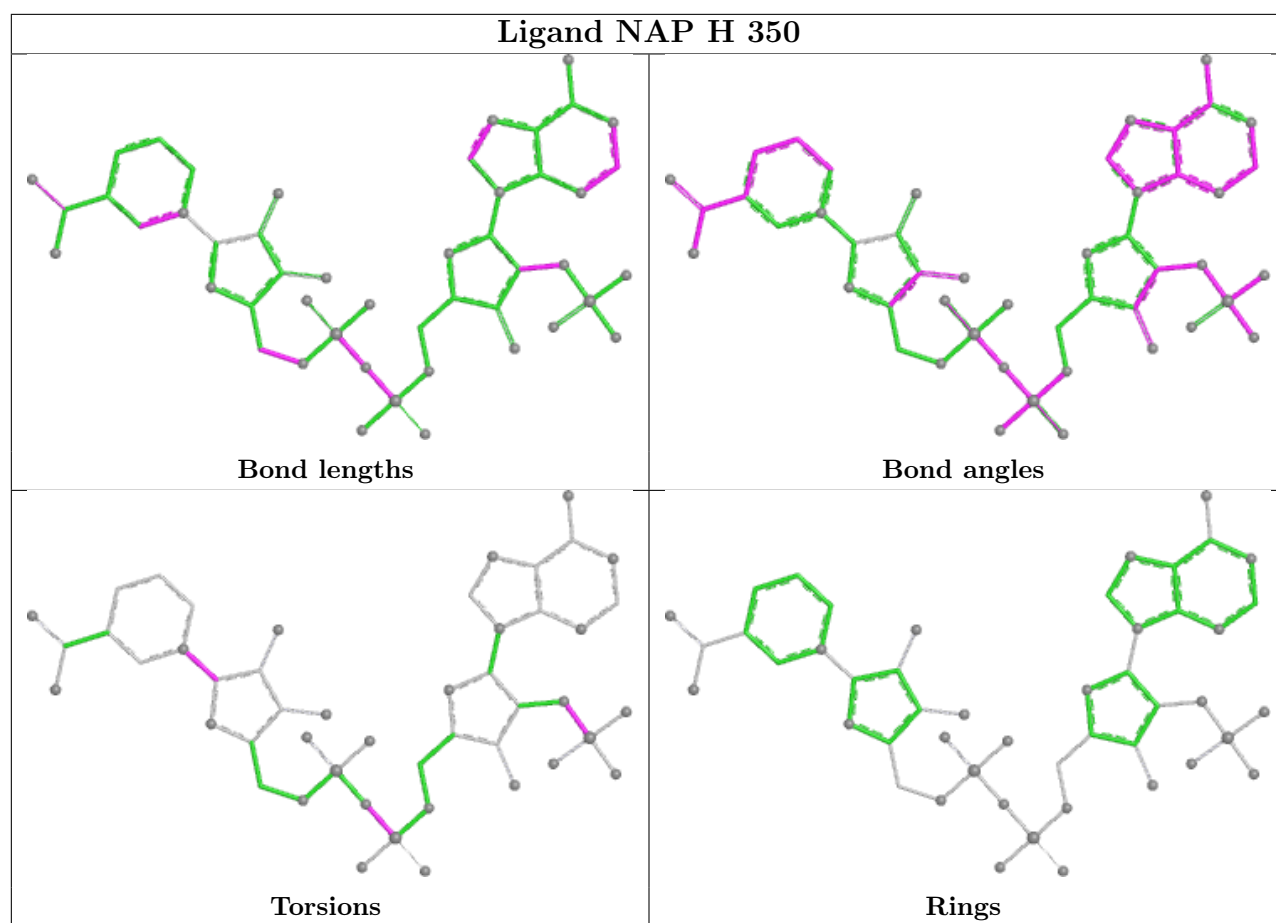
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

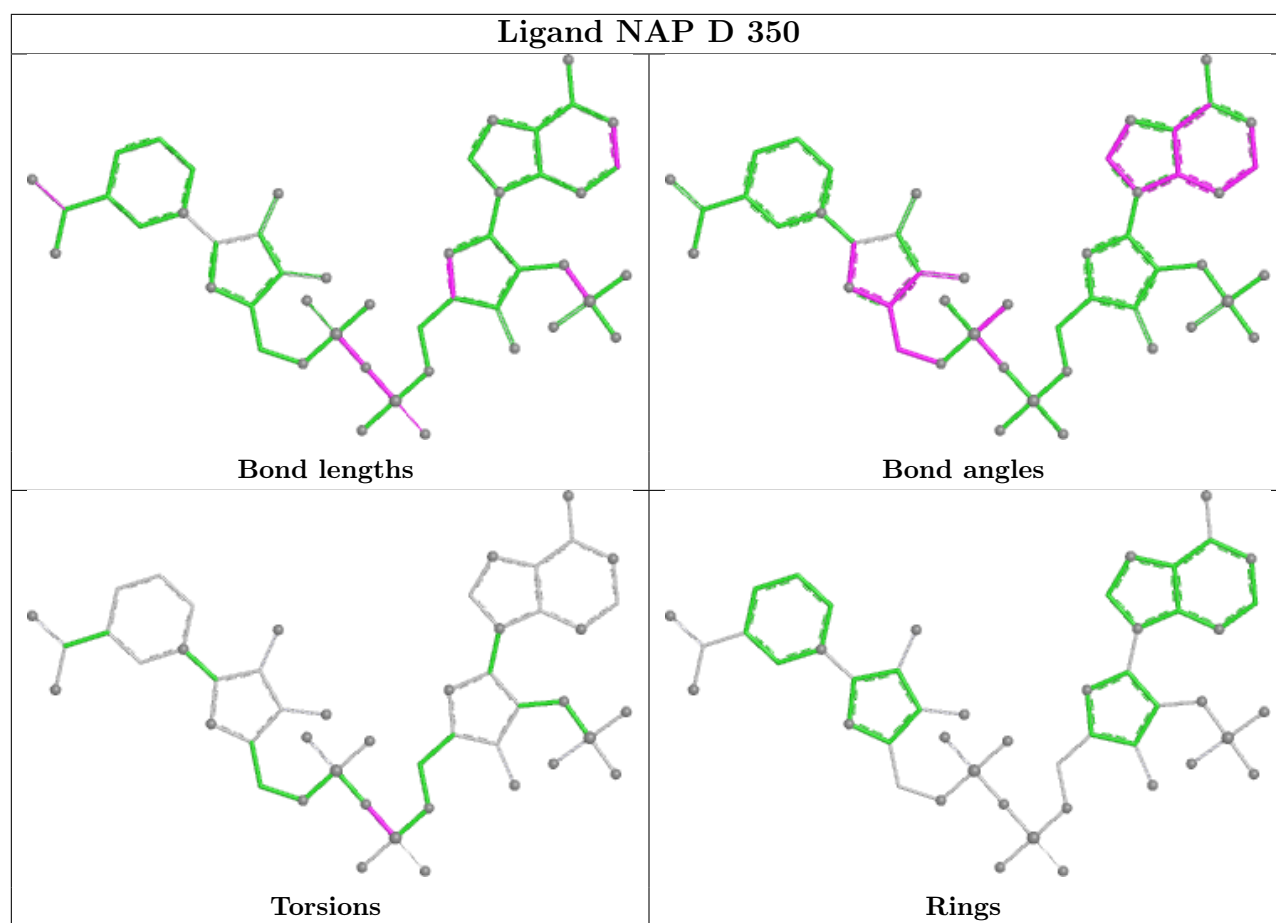


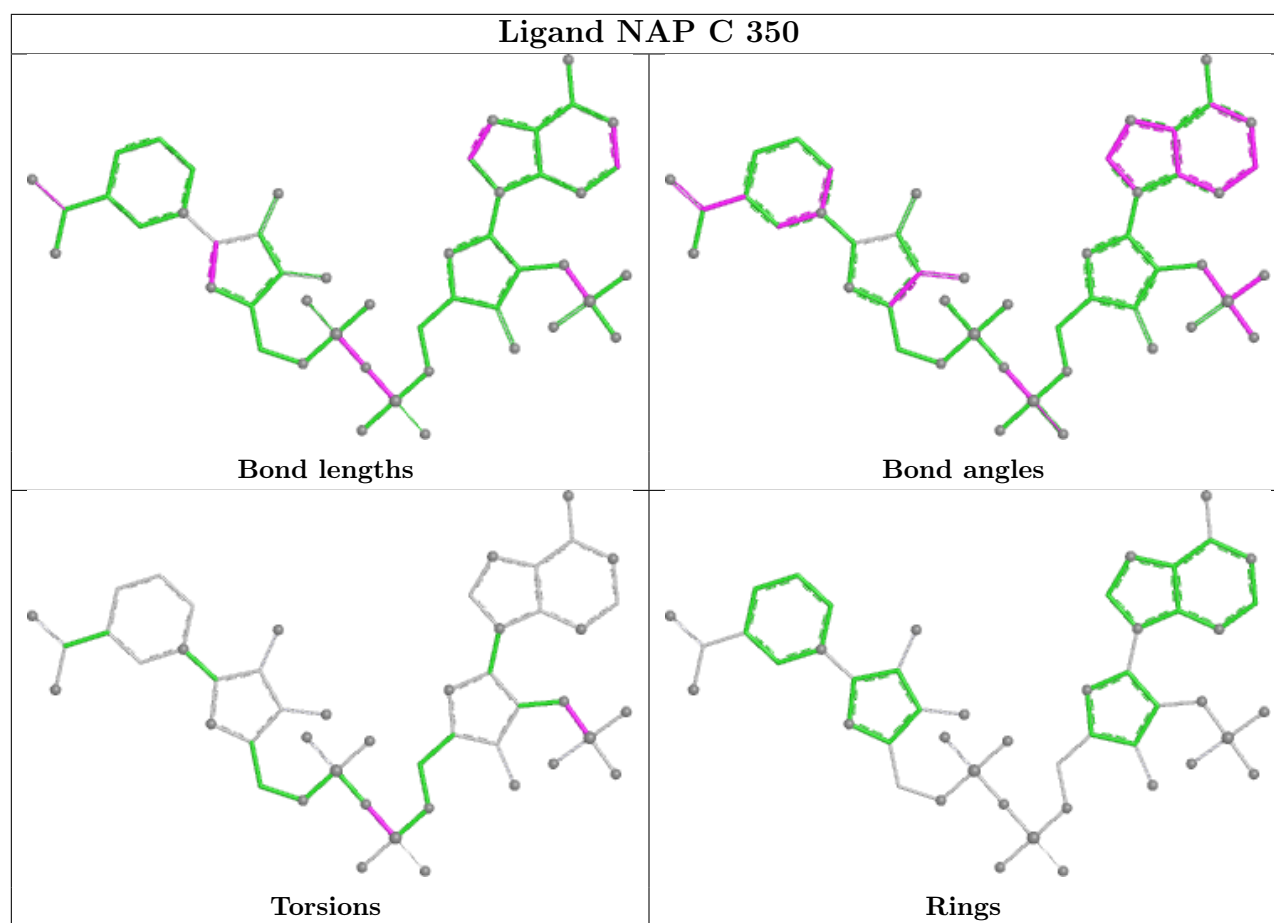


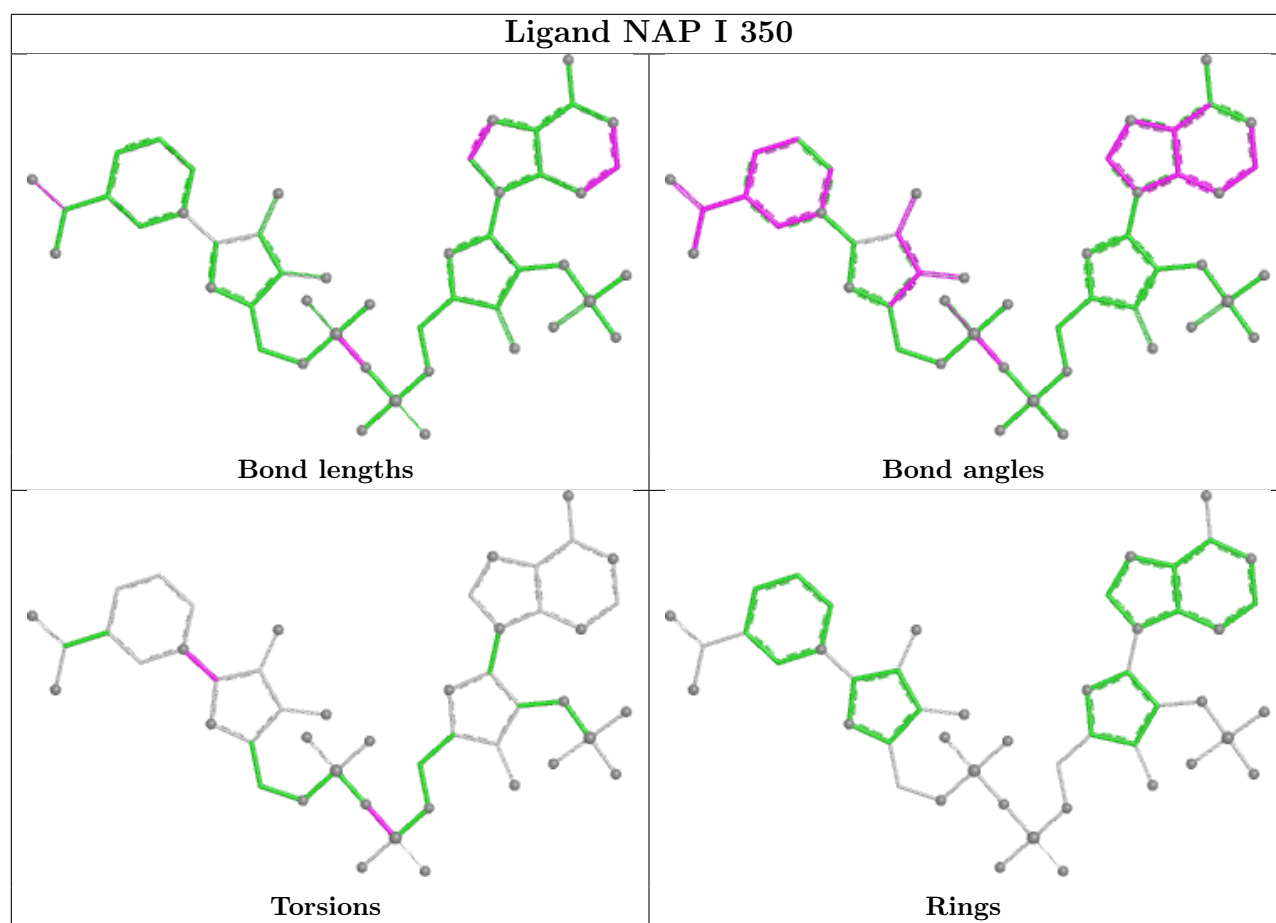


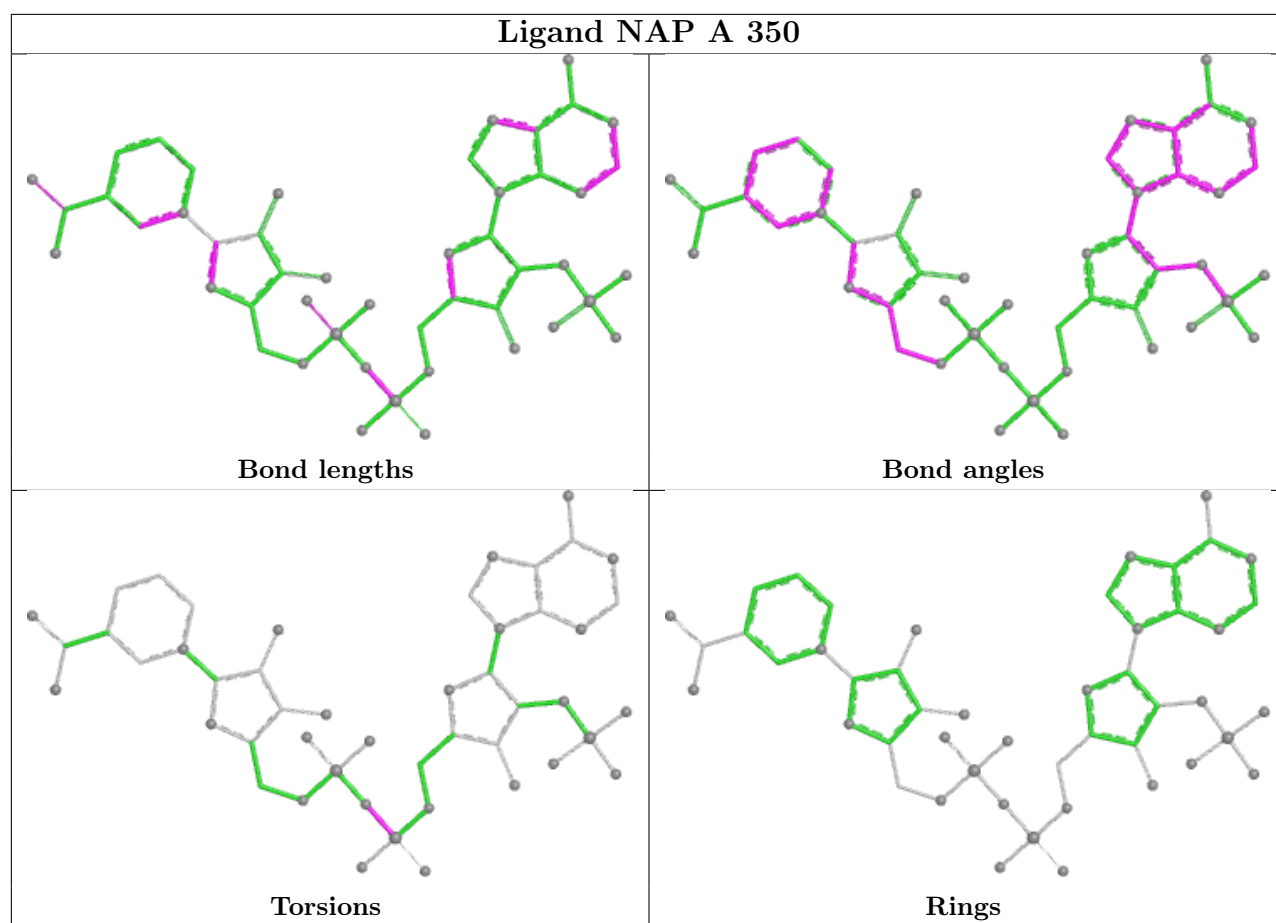


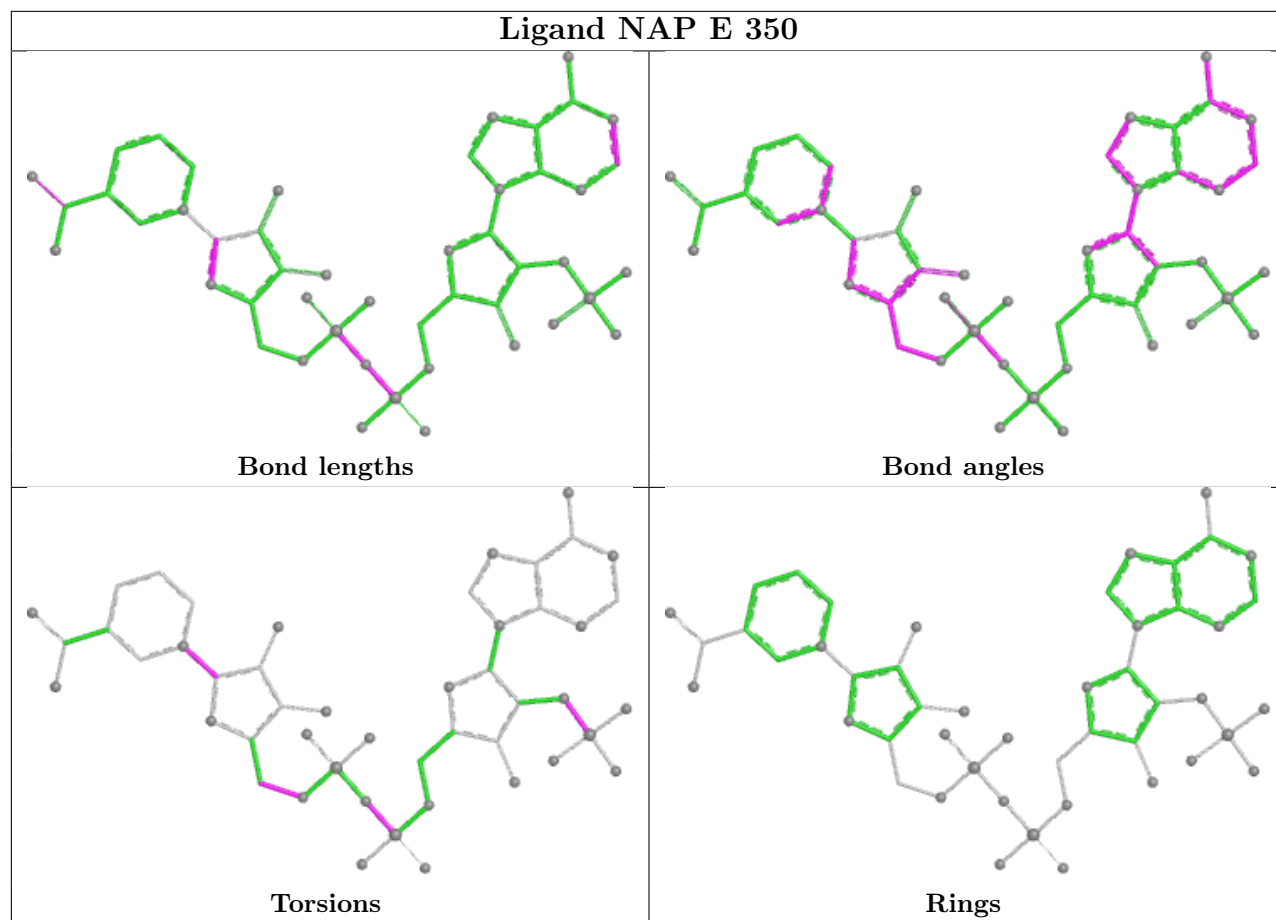












5.7 Other polymers [i](#)

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	325/338 (96%)	-1.52	0 100 100	22, 36, 47, 72	3 (0%)
1	B	324/338 (95%)	-1.46	0 100 100	29, 36, 47, 71	0
1	C	324/338 (95%)	-1.52	0 100 100	25, 36, 47, 72	1 (0%)
1	D	324/338 (95%)	-1.53	0 100 100	19, 36, 47, 73	2 (0%)
1	E	324/338 (95%)	-1.52	0 100 100	25, 36, 47, 72	1 (0%)
1	F	324/338 (95%)	-1.51	0 100 100	30, 36, 47, 72	0
1	G	324/338 (95%)	-1.51	0 100 100	25, 36, 47, 72	1 (0%)
1	H	324/338 (95%)	-1.49	0 100 100	22, 36, 46, 71	1 (0%)
1	I	324/338 (95%)	-1.50	0 100 100	29, 36, 47, 72	0
1	J	325/338 (96%)	-1.51	0 100 100	22, 36, 47, 72	1 (0%)
All	All	3242/3380 (95%)	-1.51	0 100 100	19, 36, 47, 73	10 (0%)

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

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

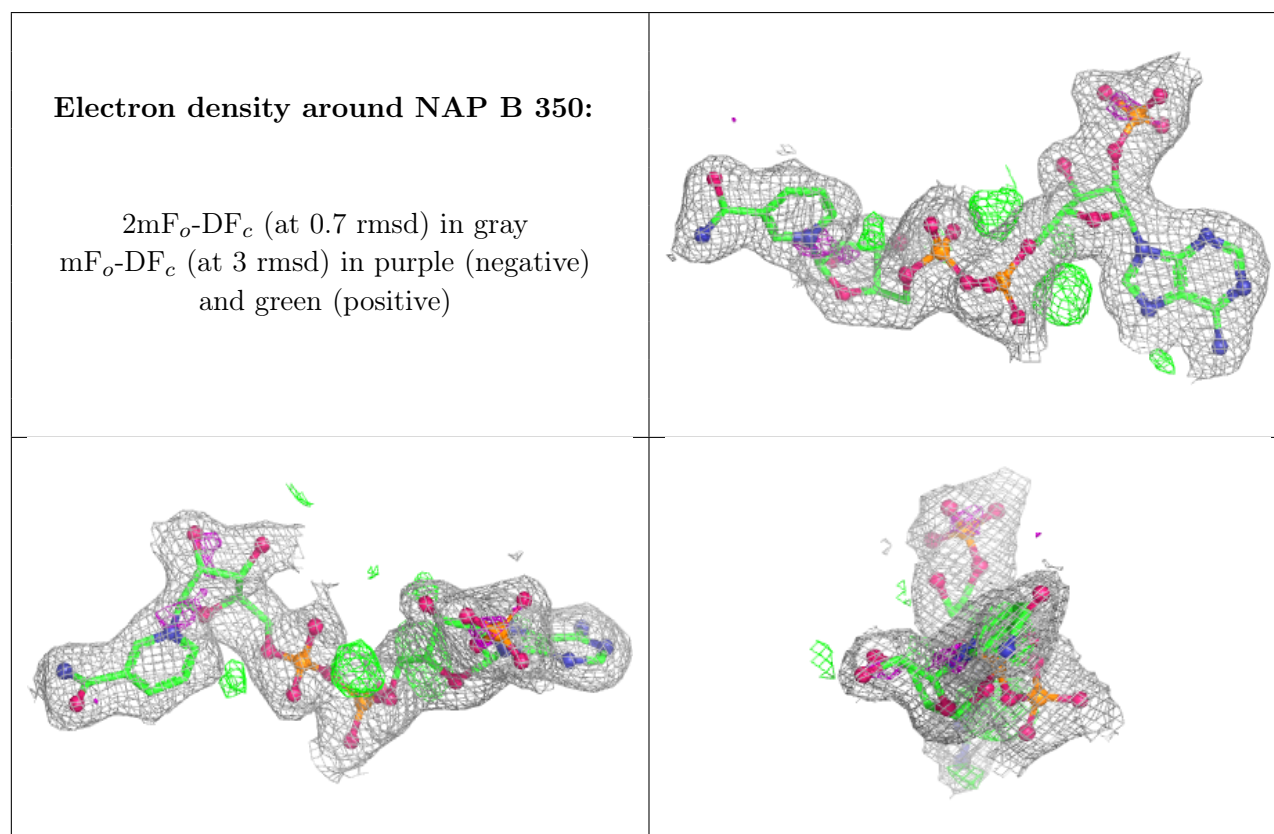
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAP	B	350	48/48	0.99	0.03	27,32,38,43	0
2	NAP	H	350	48/48	0.99	0.03	24,33,37,43	0
3	TLA	A	360	10/10	0.99	0.03	28,33,35,35	0
3	TLA	B	360	10/10	0.99	0.04	34,37,41,42	0
3	TLA	C	360	10/10	0.99	0.04	29,33,38,41	0
3	TLA	D	360	10/10	0.99	0.04	25,31,34,36	0
3	TLA	F	360	10/10	0.99	0.04	31,36,39,39	0
4	GOL	A	361	6/6	0.99	0.05	37,40,45,46	0
4	GOL	A	363	6/6	0.99	0.05	39,42,42,43	0
4	GOL	B	361	6/6	0.99	0.04	33,40,42,42	0
4	GOL	B	362	6/6	0.99	0.05	57,61,62,63	0
4	GOL	B	363	6/6	0.99	0.03	30,33,34,35	0
4	GOL	C	361	6/6	0.99	0.03	38,45,47,50	0
4	GOL	C	362	6/6	0.99	0.04	33,36,39,39	0
4	GOL	C	363	6/6	0.99	0.06	49,60,61,62	0
4	GOL	D	361	6/6	0.99	0.04	29,29,33,33	0
4	GOL	D	362	6/6	0.99	0.03	33,34,35,36	0
4	GOL	D	363	6/6	0.99	0.06	48,53,55,55	0
4	GOL	E	362	6/6	0.99	0.04	31,33,36,36	0
4	GOL	F	361	6/6	0.99	0.04	36,39,41,42	0
4	GOL	G	362	6/6	0.99	0.03	31,36,37,39	0
4	GOL	G	363	6/6	0.99	0.05	34,36,36,38	0
4	GOL	G	364	6/6	0.99	0.05	58,62,62,64	0
4	GOL	H	361	6/6	0.99	0.04	37,44,45,46	0
4	GOL	H	362	6/6	0.99	0.05	30,34,36,36	0
4	GOL	I	361	6/6	0.99	0.05	44,47,48,48	0
4	GOL	I	362	6/6	0.99	0.04	33,34,36,39	0
4	GOL	J	363	6/6	0.99	0.04	39,42,42,46	0
4	GOL	J	364	6/6	0.99	0.04	45,48,49,50	0
4	GOL	J	366	6/6	0.99	0.07	51,53,53,54	0
5	PO4	A	364	5/5	0.99	0.04	59,59,63,65	0
5	PO4	J	367	5/5	0.99	0.04	60,60,65,67	0
6	MES	B	364	12/12	0.99	0.04	50,61,65,65	0
6	MES	C	364	12/12	0.99	0.04	57,62,64,64	0
6	MES	D	364	12/12	0.99	0.05	48,62,66,67	0
6	MES	I	363	12/12	0.99	0.04	55,60,61,61	0
6	MES	J	368	12/12	0.99	0.04	53,57,59,60	0
2	NAP	J	350	48/48	1.00	0.03	23,30,35,40	0
2	NAP	C	350	48/48	1.00	0.03	23,29,35,37	0
2	NAP	D	350	48/48	1.00	0.02	20,25,32,37	0
2	NAP	E	350	48/48	1.00	0.02	20,27,31,36	0

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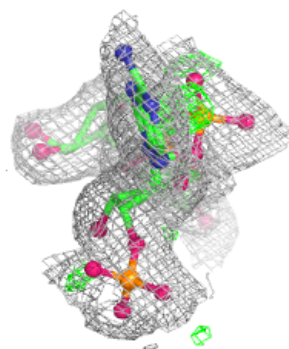
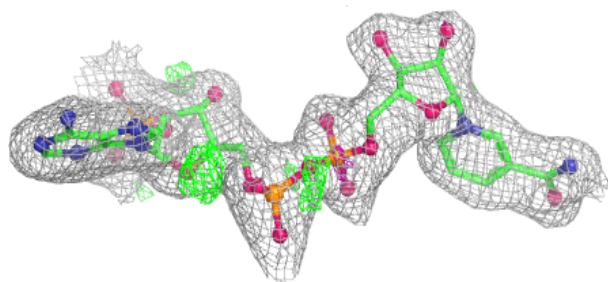
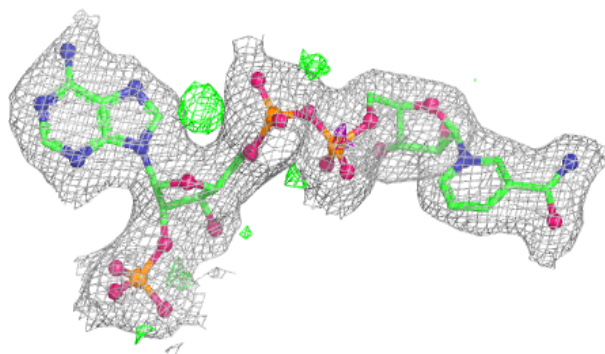
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAP	F	350	48/48	1.00	0.03	23,29,34,36	0
3	TLA	E	360	10/10	1.00	0.03	26,31,35,35	0
2	NAP	G	350	48/48	1.00	0.02	19,27,31,35	0
3	TLA	G	360	10/10	1.00	0.03	31,33,35,35	0
3	TLA	H	360	10/10	1.00	0.05	30,36,41,43	0
4	GOL	E	361	6/6	1.00	0.02	33,36,36,37	0
3	TLA	I	360	10/10	1.00	0.03	27,35,37,40	0
4	GOL	E	363	6/6	1.00	0.05	28,31,31,32	0
3	TLA	J	360	10/10	1.00	0.04	29,33,34,37	0
2	NAP	A	350	48/48	1.00	0.02	21,26,31,35	0
2	NAP	I	350	48/48	1.00	0.03	22,31,35,36	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.

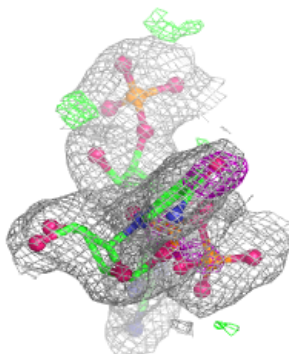
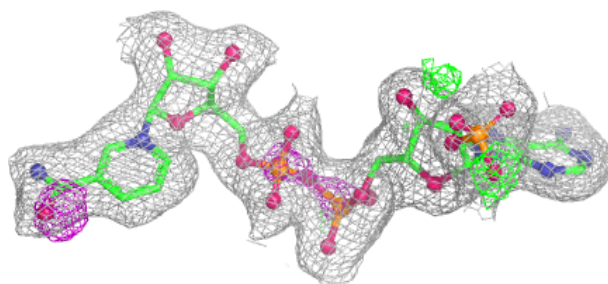
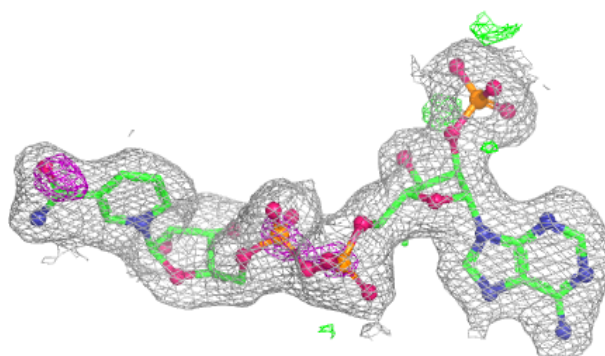


Electron density around NAP H 350:

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

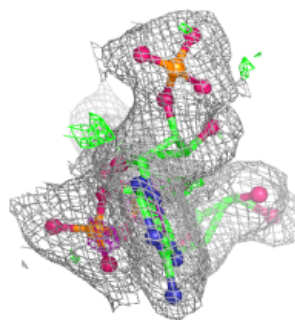
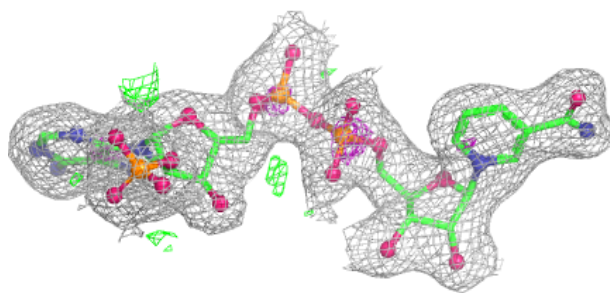
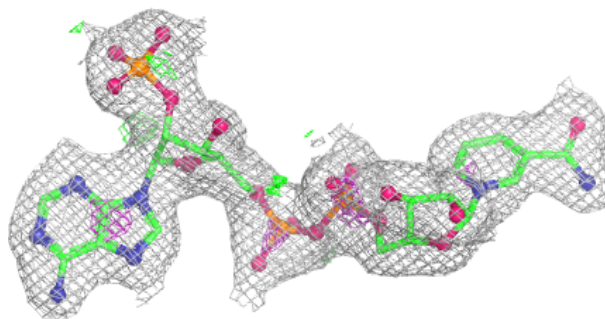
**Electron density around NAP J 350:**

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

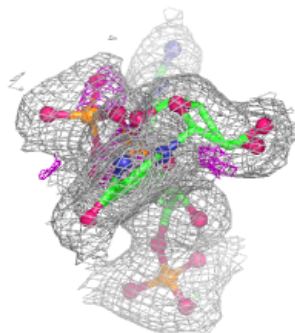
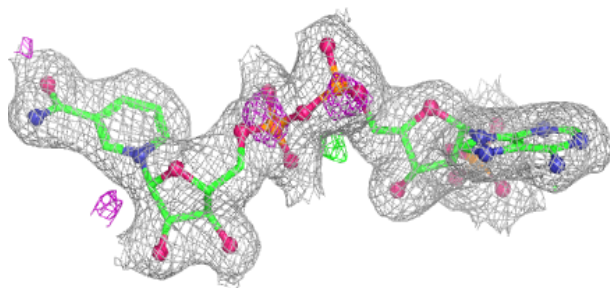
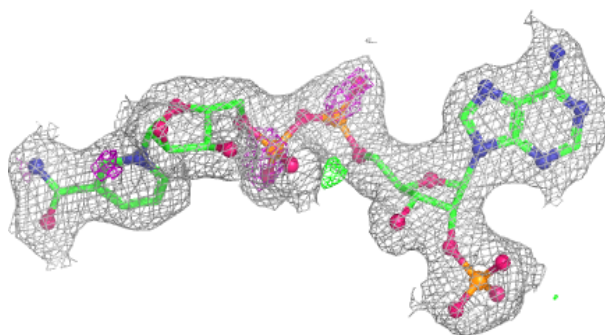


Electron density around NAP C 350:

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

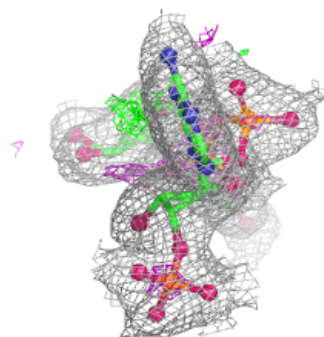
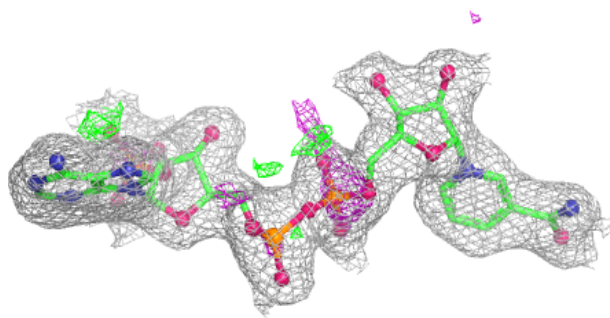
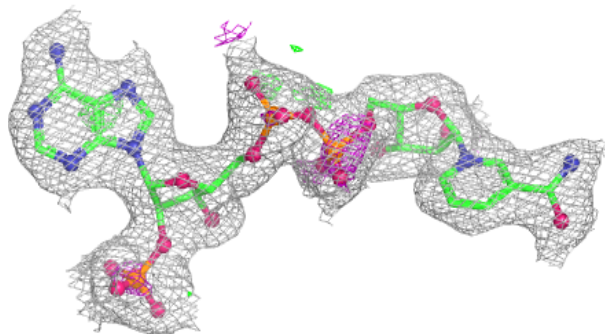
**Electron density around NAP D 350:**

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

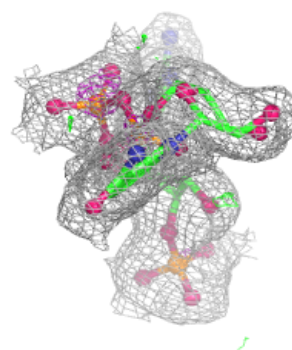
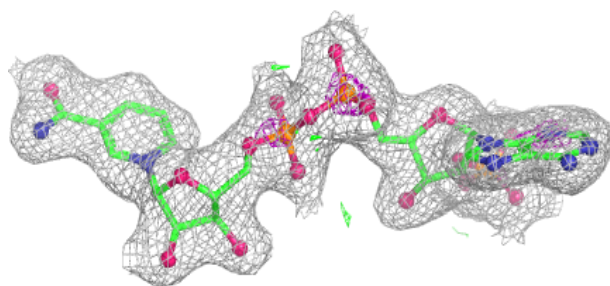
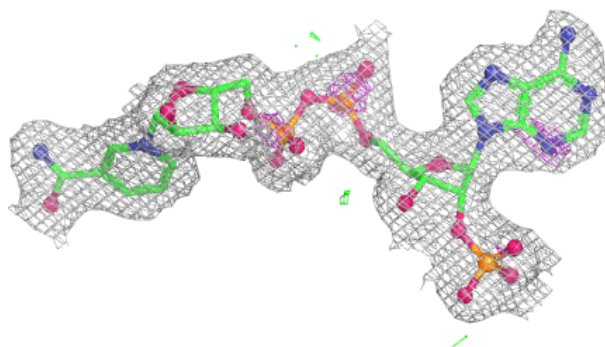


Electron density around NAP E 350:

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

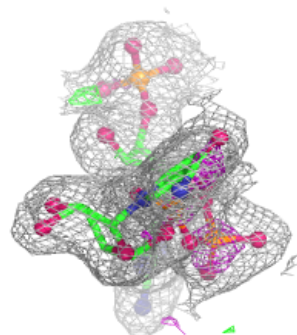
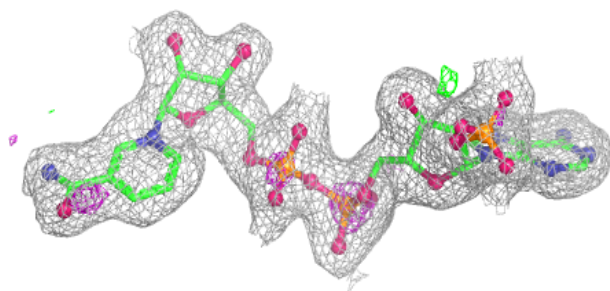
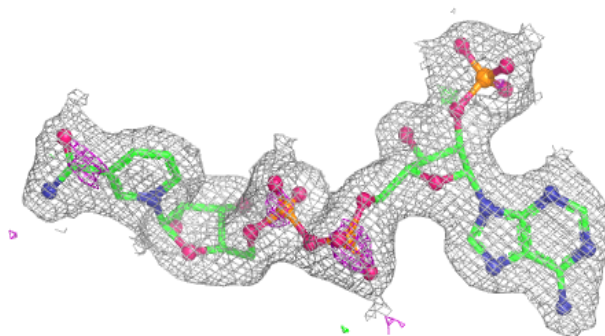
**Electron density around NAP F 350:**

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

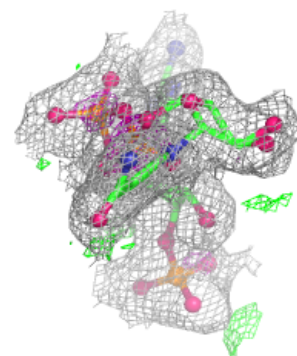
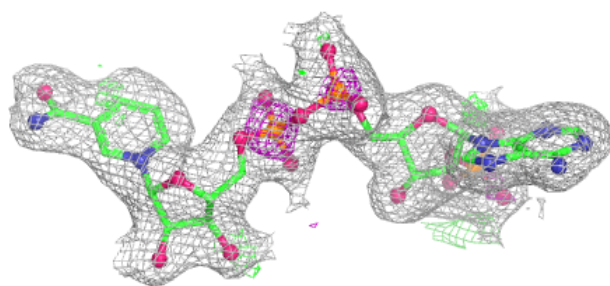
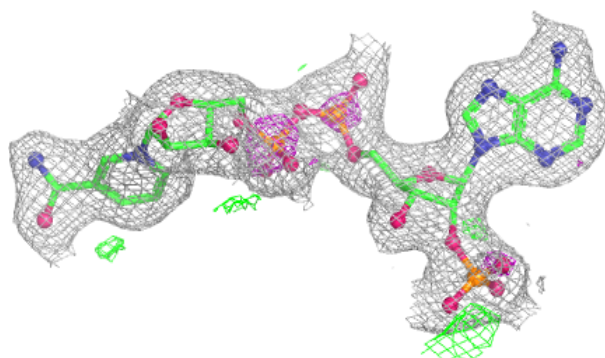


Electron density around NAP G 350:

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

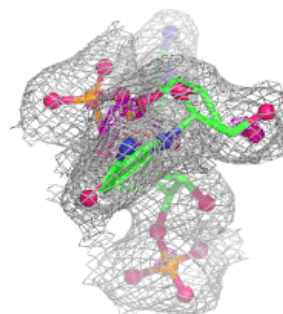
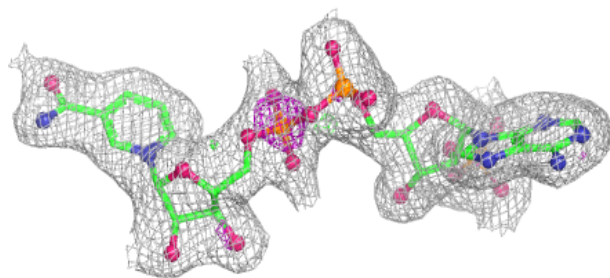
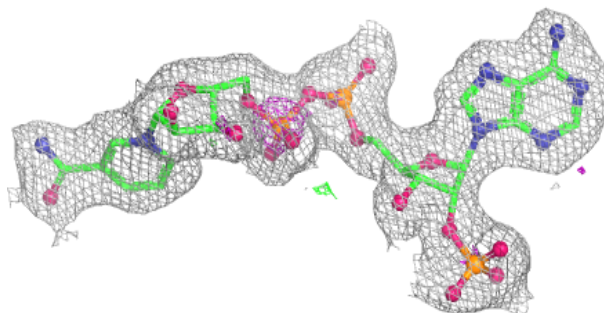
**Electron density around NAP A 350:**

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



Electron density around NAP I 350:

$2mF_o-DF_c$ (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.