



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 05:34 PM UTC

PDB ID : 5TJ9 / pdb_00005tj9
Title : 2.6 Angstrom Crystal Structure of S-adenosylhomocysteinase from *Cryptosporidium parvum* in Complex with Aristeromycin and NAD
Authors : Minasov, G.; Shuvalova, L.; Kiryukhina, O.; Dubrovskaya, I.; Bishop, B.; Kwon, K.; Anderson, W.F.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2016-10-04
Resolution : 2.60 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](#) ①) 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

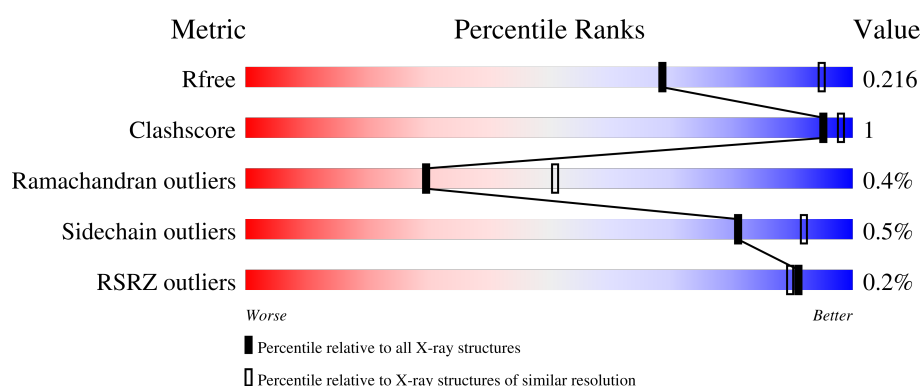
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	498	
1	B	498	
1	C	498	
1	D	498	

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 16457 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.

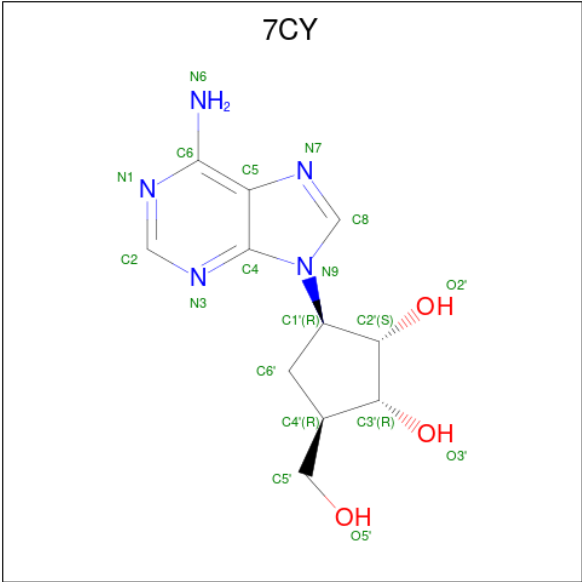
- Molecule 1 is a protein called Adenosylhomocysteinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	493	Total	C	N	O	S	0	1	0
			3902	2479	653	741	29			
1	B	494	Total	C	N	O	S	0	2	0
			3919	2488	657	745	29			
1	C	495	Total	C	N	O	S	0	2	0
			3931	2497	658	747	29			
1	D	495	Total	C	N	O	S	0	3	0
			3940	2502	659	750	29			

There are 12 discrepancies between the modelled and reference sequences:

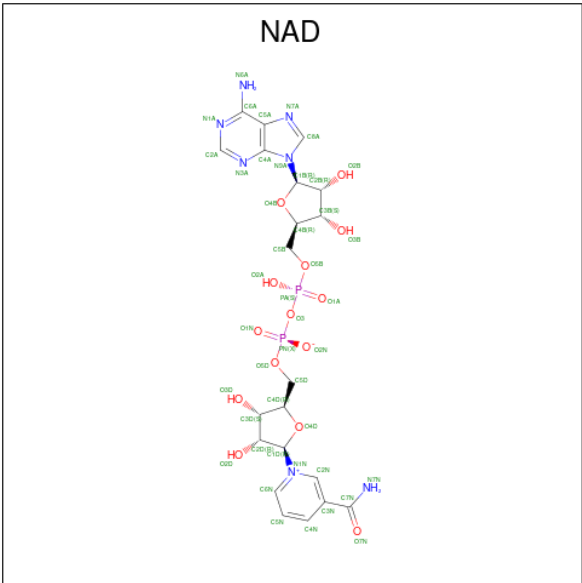
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP Q5CPH1
A	-1	ASN	-	expression tag	UNP Q5CPH1
A	0	ALA	-	expression tag	UNP Q5CPH1
B	-2	SER	-	expression tag	UNP Q5CPH1
B	-1	ASN	-	expression tag	UNP Q5CPH1
B	0	ALA	-	expression tag	UNP Q5CPH1
C	-2	SER	-	expression tag	UNP Q5CPH1
C	-1	ASN	-	expression tag	UNP Q5CPH1
C	0	ALA	-	expression tag	UNP Q5CPH1
D	-2	SER	-	expression tag	UNP Q5CPH1
D	-1	ASN	-	expression tag	UNP Q5CPH1
D	0	ALA	-	expression tag	UNP Q5CPH1

- Molecule 2 is (1R,2S,3R,5R)-3-(6-amino-9H-purin-9-yl)-5-(hydroxymethyl)cyclopentane-1,2-diol (CCD ID: 7CY) (formula: C₁₁H₁₅N₅O₃).



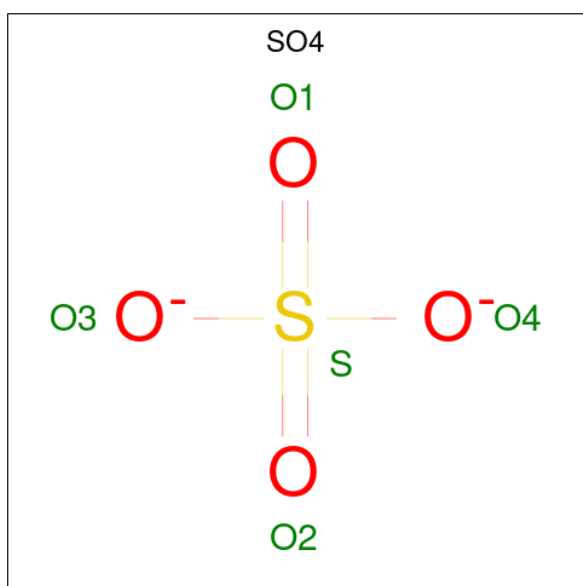
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			19	11	5	3		
2	B	1	Total	C	N	O	0	0
			19	11	5	3		
2	C	1	Total	C	N	O	0	0
			19	11	5	3		
2	D	1	Total	C	N	O	0	0
			19	11	5	3		

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



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	C	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 SULFATE ION (CCD ID: SO4) (formula: O₄S).



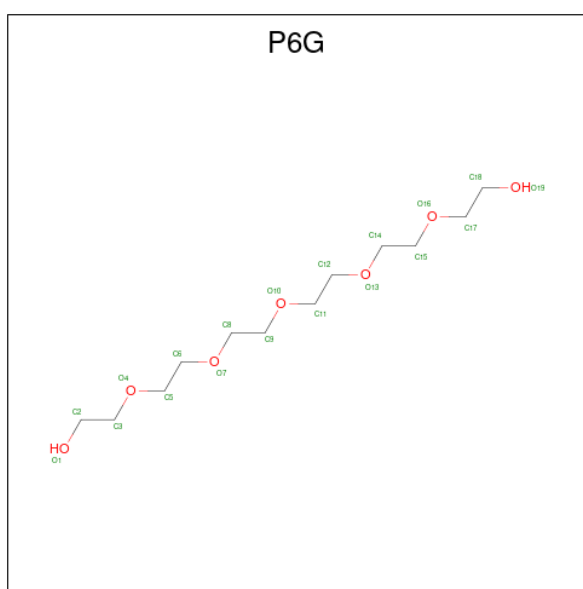
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	O S	0	0
			5 4 1			
4	A	1	Total	O S	0	0
			5 4 1			
4	A	1	Total	O S	0	0
			5 4 1			
4	B	1	Total	O S	0	0
			5 4 1			
4	B	1	Total	O S	0	0
			5 4 1			
4	B	1	Total	O S	0	0
			5 4 1			
4	B	1	Total	O S	0	0
			5 4 1			

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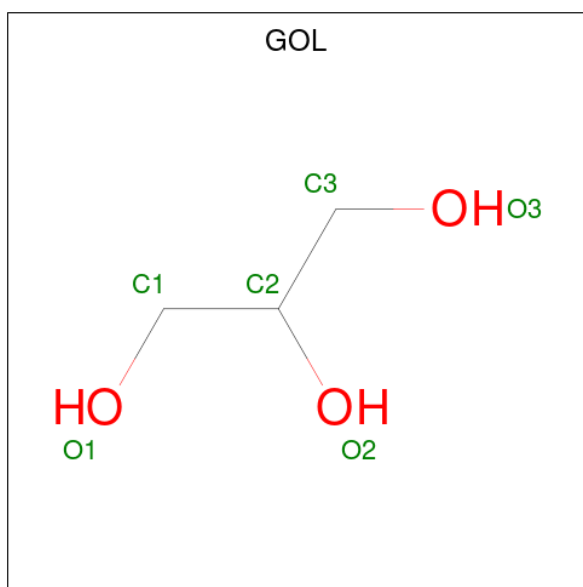
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is HEXAETHYLENE GLYCOL (CCD ID: P6G) (formula: $C_{12}H_{26}O_7$).



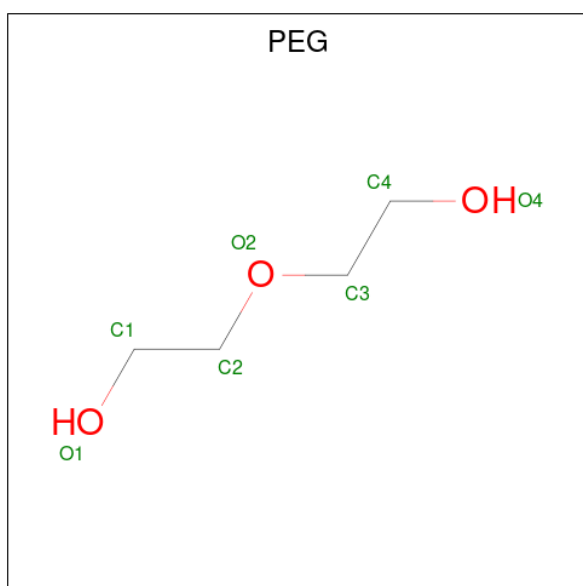
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			19	12	7		
5	B	1	Total	C	O	0	0
			19	12	7		

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 7 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	D	1	Total	C	O	0	0
			7	4	3		
7	D	1	Total	C	O	0	0
			7	4	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	D	1	Total	C	O	0	0
			7	4	3		

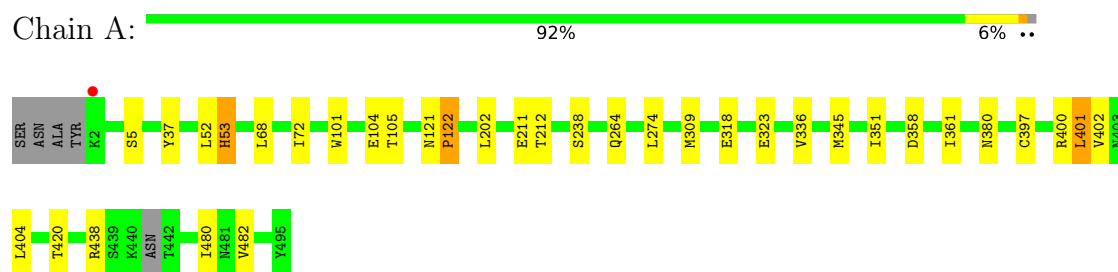
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	92	Total	O	0	1
			93	93		
8	B	98	Total	O	0	0
			98	98		
8	C	81	Total	O	0	0
			81	81		
8	D	110	Total	O	0	0
			110	110		

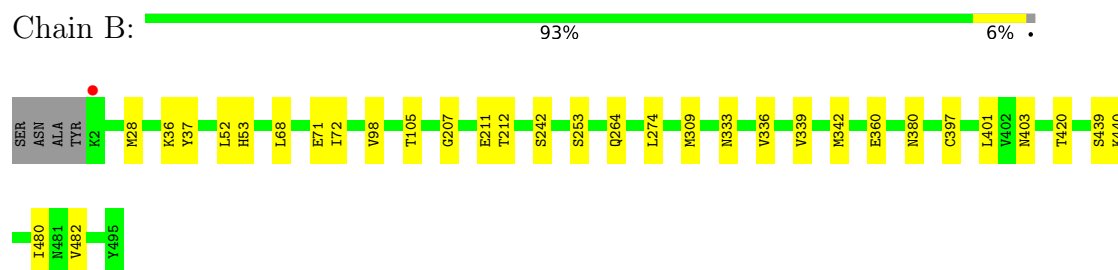
3 Residue-property plots [i](#)

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.

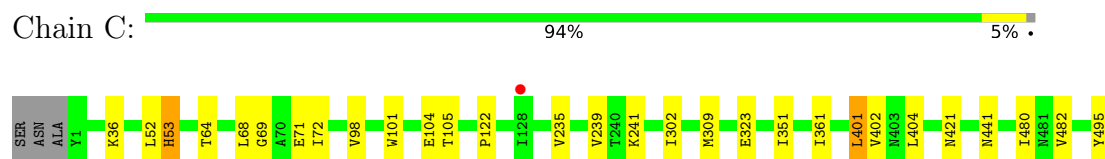
• Molecule 1: Adenosylhomocysteinase



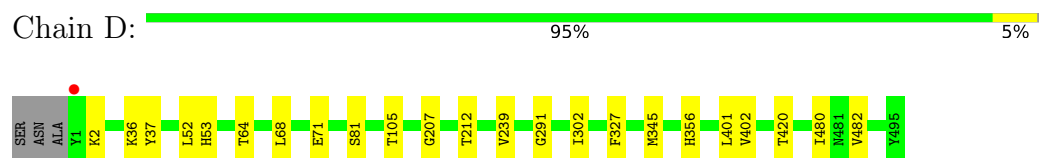
• Molecule 1: Adenosylhomocysteinase



• Molecule 1: Adenosylhomocysteinase



• Molecule 1: Adenosylhomocysteinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	66.33Å 184.90Å 102.51Å 90.00° 107.80° 90.00°	Depositor
Resolution (Å)	29.88 – 2.60 29.88 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (29.88-2.60) 99.9 (29.88-2.60)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.65 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.168 , 0.218 0.169 , 0.216	Depositor DCC
R_{free} test set	3741 reflections (5.19%)	wwPDB-VP
Wilson B-factor (Å ²)	49.2	Xtriage
Anisotropy	0.063	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 23.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.022 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	16457	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.71% 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: PEG, 7CY, NAD, P6G, GOL, SO4

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	0.60	0/3965	0.94	11/5344 (0.2%)
1	B	0.60	0/3983	0.93	11/5370 (0.2%)
1	C	0.58	0/3996	0.93	7/5388 (0.1%)
1	D	0.59	1/4005 (0.0%)	0.93	10/5400 (0.2%)
All	All	0.59	1/15949 (0.0%)	0.93	39/21502 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	2	LYS	CA-C	5.29	1.55	1.52

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	72	ILE	N-CA-C	6.88	118.71	108.46
1	B	207	GLY	N-CA-C	6.67	119.96	111.09
1	D	207	GLY	N-CA-C	6.60	120.20	110.63
1	A	5	SER	N-CA-C	6.55	119.52	110.35
1	D	105	THR	N-CA-C	-6.33	102.01	110.55
1	D	71	GLU	N-CA-C	-6.29	99.45	109.76
1	C	98	VAL	N-CA-C	6.23	117.45	108.48
1	C	71	GLU	N-CA-C	-6.09	99.73	109.96
1	C	105	THR	N-CA-C	-6.00	102.44	110.55
1	A	402	VAL	N-CA-C	6.00	116.74	110.62
1	B	212	THR	N-CA-C	5.95	119.25	109.85
1	D	402	VAL	N-CA-C	5.93	116.67	110.62
1	C	402	VAL	N-CA-C	5.84	116.58	110.62
1	C	72	ILE	N-CA-C	5.84	117.16	108.46
1	A	211	GLU	N-CA-C	5.81	118.84	111.69
1	B	98	VAL	N-CA-C	5.76	116.89	108.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	121	ASN	CA-C-N	5.67	126.92	119.84
1	A	121	ASN	C-N-CA	5.67	126.92	119.84
1	A	264	GLN	N-CA-C	5.65	118.18	110.55
1	A	72	ILE	N-CA-C	5.61	118.00	108.86
1	A	105	THR	N-CA-C	-5.58	102.25	110.52
1	B	105	THR	N-CA-C	-5.48	102.38	110.48
1	B	242	SER	N-CA-C	5.38	116.83	111.07
1	C	69	GLY	N-CA-C	5.26	122.58	115.00
1	D	36	LYS	N-CA-C	5.22	116.77	111.14
1	A	420	THR	N-CA-C	-5.16	105.73	111.36
1	B	211	GLU	N-CA-C	5.15	117.69	111.40
1	D	81	SER	N-CA-C	5.14	119.27	112.89
1	A	212	THR	N-CA-C	5.13	117.96	109.85
1	D	291	GLY	N-CA-C	5.13	122.43	115.30
1	D	212	THR	N-CA-C	5.12	118.08	110.14
1	D	356	HIS	N-CA-C	5.12	116.86	111.28
1	B	71	GLU	N-CA-C	-5.11	101.38	109.76
1	B	264	GLN	N-CA-C	5.11	117.44	110.55
1	B	420	THR	N-CA-C	-5.09	105.92	111.82
1	B	36	LYS	N-CA-C	5.07	116.89	111.36
1	A	238	SER	N-CA-C	-5.06	103.36	110.50
1	D	420	THR	N-CA-C	-5.02	106.00	111.82
1	C	36	LYS	N-CA-C	5.01	116.82	111.36

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	3902	0	3962	13	0
1	B	3919	0	3976	9	0
1	C	3931	0	3988	12	0
1	D	3940	0	3993	7	0
2	A	19	0	0	0	0
2	B	19	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	19	0	0	0	0
2	D	19	0	0	0	0
3	A	44	0	26	0	0
3	B	44	0	26	0	0
3	C	44	0	26	0	0
3	D	44	0	26	0	0
4	A	15	0	0	0	0
4	B	25	0	0	0	0
4	C	5	0	0	0	0
4	D	15	0	0	0	0
5	A	19	0	26	0	0
5	B	19	0	26	0	0
6	A	6	0	8	0	0
6	C	6	0	8	0	0
7	D	21	0	30	0	0
8	A	93	0	0	0	0
8	B	98	0	0	0	0
8	C	81	0	0	0	0
8	D	110	0	0	0	0
All	All	16457	0	16121	39	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 1.

All (39) 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:309:MET:HA	1:A:309:MET:HE2	1.82	0.62
1:B:274:LEU:HD22	1:B:336:VAL:HG12	1.86	0.58
1:C:401:LEU:HD13	1:C:404:LEU:HB2	1.89	0.54
1:D:37:TYR:HB2	1:D:68:LEU:HD22	1.92	0.51
1:A:401:LEU:HD13	1:A:404:LEU:HB2	1.95	0.48
1:C:302:ILE:HG21	1:D:239:VAL:HG11	1.96	0.47
1:B:380:ASN:HB3	1:B:397:CYS:HB3	1.97	0.46
1:A:37:TYR:HB2	1:A:68:LEU:HD22	1.97	0.46
1:C:351:ILE:HG22	1:C:361:ILE:HD13	1.98	0.46
1:B:253:SER:HB2	1:B:403:ASN:HB2	1.98	0.45
1:C:309:MET:HA	1:C:309:MET:HE2	1.97	0.45
1:D:480:ILE:HG13	1:D:482:VAL:HG22	1.97	0.45
1:C:239:VAL:HG21	1:C:495:TYR:CE2	2.52	0.45
1:D:64:THR:O	1:D:68:LEU:HG	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:LEU:HD22	1:A:336:VAL:HG12	1.99	0.45
1:C:235:VAL:HG13	1:C:421:ASN:HB3	1.99	0.45
1:C:480:ILE:HG13	1:C:482:VAL:HG22	1.99	0.44
1:A:358:ASP:HB3	1:A:400:ARG:HG3	1.98	0.44
1:D:52:LEU:O	1:D:53:HIS:C	2.60	0.44
1:A:202:LEU:O	1:A:438:ARG:NE	2.50	0.44
1:A:274:LEU:N	1:A:274:LEU:HD12	2.34	0.43
1:B:309:MET:HE2	1:B:309:MET:HA	2.00	0.42
1:B:37:TYR:HB2	1:B:68:LEU:HD22	2.01	0.42
1:A:380:ASN:HB3	1:A:397:CYS:HB3	2.01	0.42
1:B:333:ASN:O	1:B:360:GLU:HG2	2.20	0.42
1:C:239:VAL:HG11	1:D:302:ILE:HG21	2.02	0.42
1:C:241:LYS:C	1:C:241:LYS:HD3	2.45	0.41
1:C:52:LEU:O	1:C:53:HIS:C	2.62	0.41
1:B:52:LEU:O	1:B:53:HIS:C	2.64	0.41
1:A:345:MET:SD	1:A:351:ILE:HD11	2.61	0.41
1:C:64:THR:O	1:C:68:LEU:HG	2.19	0.41
1:C:101:TRP:O	1:C:104:GLU:HG3	2.21	0.41
1:B:480:ILE:HG13	1:B:482:VAL:HG22	2.02	0.40
1:A:351:ILE:HG22	1:A:361:ILE:HD13	2.02	0.40
1:D:327:PHE:CE1	1:D:345:MET:HE2	2.56	0.40
1:A:480:ILE:HG13	1:A:482:VAL:HG22	2.03	0.40
1:A:101:TRP:O	1:A:104:GLU:HG3	2.21	0.40
1:A:52:LEU:O	1:A:53:HIS:C	2.64	0.40
1:B:339:VAL:HA	1:B:342:MET:HE3	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	490/498 (98%)	465 (95%)	23 (5%)	2 (0%)	30 51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	494/498 (99%)	472 (96%)	20 (4%)	2 (0%)	30	51
1	C	495/498 (99%)	471 (95%)	21 (4%)	3 (1%)	21	42
1	D	496/498 (100%)	479 (97%)	17 (3%)	0	100	100
All	All	1975/1992 (99%)	1887 (96%)	81 (4%)	7 (0%)	30	51

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	122	PRO
1	C	122	PRO
1	A	53	HIS
1	C	53	HIS
1	C	441	ASN
1	B	439	SER
1	B	440	LYS

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	432/435 (99%)	428 (99%)	4 (1%)	70	87
1	B	434/435 (100%)	431 (99%)	3 (1%)	76	89
1	C	435/435 (100%)	433 (100%)	2 (0%)	81	92
1	D	436/435 (100%)	435 (100%)	1 (0%)	87	95
All	All	1737/1740 (100%)	1727 (99%)	10 (1%)	81	91

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	122	PRO
1	A	318	GLU
1	A	323	GLU
1	A	401	LEU

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Mol	Chain	Res	Type
1	B	28[A]	MET
1	B	28[B]	MET
1	B	401	LEU
1	C	323	GLU
1	C	401	LEU
1	D	401	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	421	ASN
1	B	114	ASN
1	B	368	ASN
1	B	421	ASN
1	C	114	ASN
1	C	194	ASN
1	C	368	ASN
1	C	379	GLN
1	C	481	ASN
1	D	103	ASN
1	D	368	ASN
1	D	379	GLN
1	D	380	ASN

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](#)

27 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	SO4	A	505	-	4,4,4	0.44	0	6,6,6	0.12	0
3	NAD	A	502	-	46,48,48	1.27	7 (15%)	64,73,73	1.59	12 (18%)
5	P6G	B	508	-	18,18,18	0.53	0	17,17,17	0.25	0
5	P6G	A	506	-	18,18,18	0.50	0	17,17,17	0.23	0
4	SO4	B	505	-	4,4,4	0.43	0	6,6,6	0.10	0
4	SO4	D	504	-	4,4,4	0.44	0	6,6,6	0.13	0
4	SO4	B	503	-	4,4,4	0.43	0	6,6,6	0.05	0
4	SO4	C	503	-	4,4,4	0.43	0	6,6,6	0.07	0
7	PEG	D	506	-	6,6,6	0.43	0	5,5,5	0.31	0
7	PEG	D	507	-	6,6,6	0.50	0	5,5,5	0.26	0
2	7CY	B	501	-	21,21,21	1.63	6 (28%)	30,31,31	2.10	11 (36%)
2	7CY	C	501	-	21,21,21	1.68	6 (28%)	30,31,31	2.11	12 (40%)
3	NAD	B	502	-	46,48,48	1.14	4 (8%)	64,73,73	1.64	11 (17%)
4	SO4	B	506	-	4,4,4	0.43	0	6,6,6	0.13	0
4	SO4	B	507	-	4,4,4	0.44	0	6,6,6	0.04	0
7	PEG	D	508	-	6,6,6	0.48	0	5,5,5	0.22	0
4	SO4	D	505	-	4,4,4	0.42	0	6,6,6	0.11	0
4	SO4	B	504	-	4,4,4	0.42	0	6,6,6	0.10	0
2	7CY	D	501	-	21,21,21	1.58	5 (23%)	30,31,31	2.13	10 (33%)
3	NAD	D	502	-	46,48,48	1.14	6 (13%)	64,73,73	1.61	10 (15%)
4	SO4	D	503	-	4,4,4	0.45	0	6,6,6	0.10	0
6	GOL	A	507	-	5,5,5	0.32	0	5,5,5	0.25	0
4	SO4	A	503	-	4,4,4	0.42	0	6,6,6	0.07	0
4	SO4	A	504	-	4,4,4	0.45	0	6,6,6	0.10	0
6	GOL	C	504	-	5,5,5	0.31	0	5,5,5	0.20	0
3	NAD	C	502	-	46,48,48	1.19	5 (10%)	64,73,73	1.63	10 (15%)
2	7CY	A	501	-	21,21,21	1.62	5 (23%)	30,31,31	2.10	13 (43%)

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
7	PEG	D	506	-	-	2/4/4/4	-
7	PEG	D	507	-	-	3/4/4/4	-
7	PEG	D	508	-	-	1/4/4/4	-
2	7CY	B	501	-	-	5/6/22/22	0/3/3/3
2	7CY	C	501	-	-	3/6/22/22	0/3/3/3
2	7CY	D	501	-	-	5/6/22/22	0/3/3/3
6	GOL	C	504	-	-	2/4/4/4	-
3	NAD	B	502	-	-	5/30/62/62	0/5/5/5
3	NAD	D	502	-	-	6/30/62/62	0/5/5/5
3	NAD	A	502	-	-	5/30/62/62	0/5/5/5
5	P6G	B	508	-	-	7/16/16/16	-
6	GOL	A	507	-	-	0/4/4/4	-
3	NAD	C	502	-	-	5/30/62/62	0/5/5/5
5	P6G	A	506	-	-	7/16/16/16	-
2	7CY	A	501	-	-	3/6/22/22	0/3/3/3

All (44) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	7CY	C5-C4	4.58	1.47	1.39
3	A	502	NAD	C5A-C4A	4.48	1.47	1.39
2	C	501	7CY	C5-C4	4.42	1.47	1.39
2	A	501	7CY	C5-C4	4.41	1.47	1.39
3	B	502	NAD	C5A-C4A	4.35	1.46	1.39
2	D	501	7CY	C5-C4	4.35	1.46	1.39
3	C	502	NAD	C5A-C4A	4.32	1.46	1.39
3	D	502	NAD	C5A-C4A	4.14	1.46	1.39
2	C	501	7CY	C1'-N9	2.82	1.49	1.47
2	D	501	7CY	C5-C6	2.76	1.48	1.41
2	C	501	7CY	C5-C6	2.75	1.48	1.41
3	C	502	NAD	C5A-C6A	2.74	1.48	1.41
2	A	501	7CY	C5-C6	2.74	1.48	1.41
3	B	502	NAD	C5A-C6A	2.72	1.48	1.41
2	A	501	7CY	C4-N9	-2.72	1.32	1.37
2	B	501	7CY	C5-C6	2.67	1.48	1.41
3	D	502	NAD	C5A-C6A	2.66	1.48	1.41
3	A	502	NAD	C5A-N7A	-2.65	1.34	1.39
3	A	502	NAD	C5A-C6A	2.62	1.48	1.41
2	C	501	7CY	C8-N7	2.55	1.36	1.31
3	C	502	NAD	C8A-N7A	2.55	1.36	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	7CY	C8-N7	2.54	1.36	1.31
2	D	501	7CY	C4-N9	-2.52	1.32	1.37
2	B	501	7CY	C8-N7	2.49	1.36	1.31
3	B	502	NAD	C8A-N7A	2.48	1.36	1.31
3	A	502	NAD	O4D-C1D	2.46	1.44	1.40
3	A	502	NAD	C8A-N7A	2.45	1.36	1.31
2	B	501	7CY	C5-N7	-2.38	1.34	1.39
2	C	501	7CY	C4-N9	-2.38	1.32	1.37
2	D	501	7CY	C5-N7	-2.36	1.34	1.39
2	C	501	7CY	C5-N7	-2.35	1.34	1.39
2	D	501	7CY	C8-N7	2.35	1.36	1.31
3	A	502	NAD	PN-O3	2.32	1.62	1.59
3	B	502	NAD	C5A-N7A	-2.32	1.34	1.39
2	A	501	7CY	C5-N7	-2.32	1.34	1.39
2	B	501	7CY	C4-N9	-2.29	1.32	1.37
3	D	502	NAD	O4D-C1D	2.29	1.43	1.40
3	D	502	NAD	C5A-N7A	-2.28	1.34	1.39
3	C	502	NAD	C5A-N7A	-2.28	1.34	1.39
3	A	502	NAD	PA-O3	2.27	1.62	1.59
3	C	502	NAD	O4D-C1D	2.27	1.43	1.40
3	D	502	NAD	C8A-N7A	2.27	1.36	1.31
3	D	502	NAD	C4A-N9A	-2.05	1.33	1.37
2	B	501	7CY	C1'-N9	2.02	1.48	1.47

All (89) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	502	NAD	C5A-C4A-N3A	-5.75	118.81	126.72
3	B	502	NAD	C5A-C4A-N3A	-5.72	118.84	126.72
3	D	502	NAD	C5A-C4A-N3A	-5.71	118.85	126.72
3	A	502	NAD	C5A-C4A-N3A	-5.64	118.95	126.72
2	B	501	7CY	C5-C4-N3	-5.21	119.55	126.72
2	C	501	7CY	C5-C4-N3	-5.17	119.59	126.72
2	D	501	7CY	C5-C4-N3	-5.04	119.77	126.72
2	A	501	7CY	C5-C4-N3	-4.96	119.89	126.72
3	D	502	NAD	N3A-C4A-N9A	4.47	134.77	127.17
3	C	502	NAD	N3A-C4A-N9A	4.45	134.73	127.17
3	B	502	NAD	N3A-C4A-N9A	4.43	134.70	127.17
3	A	502	NAD	N3A-C4A-N9A	4.32	134.52	127.17
3	C	502	NAD	C2A-N3A-C4A	3.93	121.44	111.83
3	C	502	NAD	N3A-C2A-N1A	-3.92	122.64	128.58
2	B	501	7CY	N3-C4-N9	3.88	133.76	127.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	502	NAD	C2A-N3A-C4A	3.85	121.24	111.83
2	D	501	7CY	C4-C5-N7	-3.80	106.24	110.58
2	D	501	7CY	N3-C4-N9	3.79	133.61	127.17
3	D	502	NAD	C2A-N3A-C4A	3.78	121.07	111.83
2	A	501	7CY	N3-C2-N1	-3.77	122.88	128.58
3	B	502	NAD	N3A-C2A-N1A	-3.77	122.88	128.58
3	A	502	NAD	C2A-N3A-C4A	3.75	121.00	111.83
3	A	502	NAD	N3A-C2A-N1A	-3.73	122.93	128.58
2	C	501	7CY	N3-C4-N9	3.73	133.50	127.17
2	C	501	7CY	N3-C2-N1	-3.71	122.96	128.58
3	D	502	NAD	C4A-C5A-N7A	-3.70	106.35	110.58
2	C	501	7CY	C2-N3-C4	3.69	120.85	111.83
2	A	501	7CY	C2-N3-C4	3.68	120.82	111.83
2	B	501	7CY	N3-C2-N1	-3.68	123.02	128.58
3	D	502	NAD	N3A-C2A-N1A	-3.67	123.03	128.58
3	C	502	NAD	C4A-C5A-N7A	-3.66	106.40	110.58
2	D	501	7CY	N3-C2-N1	-3.65	123.05	128.58
2	B	501	7CY	C2-N3-C4	3.64	120.72	111.83
2	C	501	7CY	C4-C5-N7	-3.60	106.46	110.58
3	B	502	NAD	C4A-C5A-N7A	-3.60	106.46	110.58
2	A	501	7CY	N3-C4-N9	3.60	133.28	127.17
2	D	501	7CY	C2-N3-C4	3.59	120.60	111.83
2	A	501	7CY	C4-C5-N7	-3.54	106.54	110.58
2	B	501	7CY	C4-C5-N7	-3.53	106.54	110.58
3	A	502	NAD	C4A-C5A-N7A	-3.52	106.56	110.58
3	D	502	NAD	C4A-N9A-C8A	3.20	109.09	105.74
2	D	501	7CY	C4-N9-C8	3.17	109.07	105.74
3	C	502	NAD	C4A-N9A-C8A	3.11	109.01	105.74
3	B	502	NAD	C3N-C7N-N7N	3.01	121.45	117.74
3	D	502	NAD	C5A-N7A-C8A	2.91	108.02	103.45
3	B	502	NAD	C5A-N7A-C8A	2.91	108.02	103.45
3	C	502	NAD	C5A-N7A-C8A	2.91	108.02	103.45
3	B	502	NAD	C4A-N9A-C8A	2.90	108.78	105.74
2	A	501	7CY	C4-N9-C8	2.87	108.75	105.74
3	A	502	NAD	C3N-C7N-N7N	2.83	121.23	117.74
2	D	501	7CY	C5-N7-C8	2.76	107.78	103.45
3	A	502	NAD	C5A-N7A-C8A	2.74	107.76	103.45
3	C	502	NAD	N9A-C8A-N7A	-2.70	110.11	113.94
3	D	502	NAD	N9A-C8A-N7A	-2.67	110.14	113.94
2	B	501	7CY	C4-N9-C8	2.66	108.54	105.74
2	C	501	7CY	C4-N9-C8	2.66	108.53	105.74
2	C	501	7CY	C5-N7-C8	2.62	107.57	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	502	NAD	N9A-C8A-N7A	-2.58	110.27	113.94
3	A	502	NAD	C4A-N9A-C8A	2.57	108.44	105.74
2	A	501	7CY	C6-C5-N7	2.57	137.03	132.09
2	D	501	7CY	N9-C8-N7	-2.56	110.30	113.94
2	B	501	7CY	C5-N7-C8	2.55	107.46	103.45
2	D	501	7CY	C6-C5-N7	2.55	137.00	132.09
2	C	501	7CY	C6-C5-N7	2.53	136.97	132.09
3	D	502	NAD	C3N-C7N-N7N	2.46	120.76	117.74
2	C	501	7CY	N9-C8-N7	-2.39	110.54	113.94
2	B	501	7CY	C6-C5-N7	2.38	136.69	132.09
3	C	502	NAD	C6A-C5A-N7A	2.36	136.64	132.09
2	A	501	7CY	C5-N7-C8	2.36	107.16	103.45
3	A	502	NAD	N9A-C8A-N7A	-2.27	110.71	113.94
2	A	501	7CY	N9-C8-N7	-2.26	110.73	113.94
3	B	502	NAD	C6A-C5A-N7A	2.24	136.41	132.09
2	B	501	7CY	N9-C8-N7	-2.24	110.76	113.94
2	C	501	7CY	C3'-C2'-C1'	2.24	105.88	102.46
2	B	501	7CY	C2-N1-C6	2.23	122.40	118.73
3	C	502	NAD	C6N-N1N-C1D	2.22	124.09	119.73
3	B	502	NAD	C6N-N1N-C1D	2.19	124.03	119.73
3	D	502	NAD	C6A-C5A-N7A	2.18	136.29	132.09
2	A	501	7CY	C3'-C2'-C1'	2.15	105.75	102.46
2	D	501	7CY	C2-N1-C6	2.15	122.26	118.73
2	A	501	7CY	C2-N1-C6	2.14	122.24	118.73
3	A	502	NAD	C6A-C5A-N7A	2.09	136.12	132.09
2	A	501	7CY	C6'-C1'-N9	-2.07	110.78	113.40
3	A	502	NAD	C6N-N1N-C1D	2.07	123.78	119.73
2	C	501	7CY	C2-N1-C6	2.06	122.12	118.73
2	B	501	7CY	C6'-C1'-N9	-2.04	110.81	113.40
2	A	501	7CY	C4-N9-C1'	-2.03	122.20	126.01
3	A	502	NAD	C2A-N1A-C6A	2.02	122.05	118.73
2	C	501	7CY	C4-N9-C1'	-2.00	122.26	126.01

There are no chirality outliers.

All (59) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	501	7CY	C3'-C4'-C5'-O5'
2	B	501	7CY	C6'-C4'-C5'-O5'
2	D	501	7CY	C3'-C4'-C5'-O5'
2	D	501	7CY	C6'-C4'-C5'-O5'
3	A	502	NAD	O4D-C1D-N1N-C2N

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Mol	Chain	Res	Type	Atoms
3	A	502	NAD	O4D-C1D-N1N-C6N
3	A	502	NAD	C2D-C1D-N1N-C2N
3	A	502	NAD	C2D-C1D-N1N-C6N
3	B	502	NAD	O4D-C1D-N1N-C2N
3	B	502	NAD	O4D-C1D-N1N-C6N
3	B	502	NAD	C2D-C1D-N1N-C2N
3	B	502	NAD	C2D-C1D-N1N-C6N
3	C	502	NAD	O4D-C1D-N1N-C2N
3	C	502	NAD	O4D-C1D-N1N-C6N
3	C	502	NAD	C2D-C1D-N1N-C2N
3	C	502	NAD	C2D-C1D-N1N-C6N
3	D	502	NAD	O4D-C1D-N1N-C2N
3	D	502	NAD	O4D-C1D-N1N-C6N
3	D	502	NAD	C2D-C1D-N1N-C2N
3	D	502	NAD	C2D-C1D-N1N-C6N
6	C	504	GOL	O1-C1-C2-C3
5	B	508	P6G	O10-C11-C12-O13
7	D	507	PEG	O2-C3-C4-O4
5	B	508	P6G	O4-C5-C6-O7
6	C	504	GOL	O1-C1-C2-O2
5	B	508	P6G	O1-C2-C3-O4
5	A	506	P6G	O16-C17-C18-O19
7	D	506	PEG	O2-C3-C4-O4
5	A	506	P6G	O1-C2-C3-O4
7	D	507	PEG	O1-C1-C2-O2
5	A	506	P6G	O4-C5-C6-O7
7	D	508	PEG	O1-C1-C2-O2
3	D	502	NAD	O4B-C4B-C5B-O5B
5	A	506	P6G	O10-C11-C12-O13
5	A	506	P6G	C14-C15-O16-C17
5	B	508	P6G	C8-C9-O10-C11
2	A	501	7CY	C2'-C1'-N9-C4
2	A	501	7CY	C6'-C1'-N9-C4
2	B	501	7CY	C2'-C1'-N9-C4
2	C	501	7CY	C2'-C1'-N9-C4
2	D	501	7CY	C2'-C1'-N9-C4
2	D	501	7CY	C6'-C1'-N9-C4
5	B	508	P6G	C2-C3-O4-C5
2	C	501	7CY	C2'-C1'-N9-C8
7	D	507	PEG	C1-C2-O2-C3
3	B	502	NAD	O4B-C4B-C5B-O5B
3	D	502	NAD	C3B-C4B-C5B-O5B

Continued on next page...

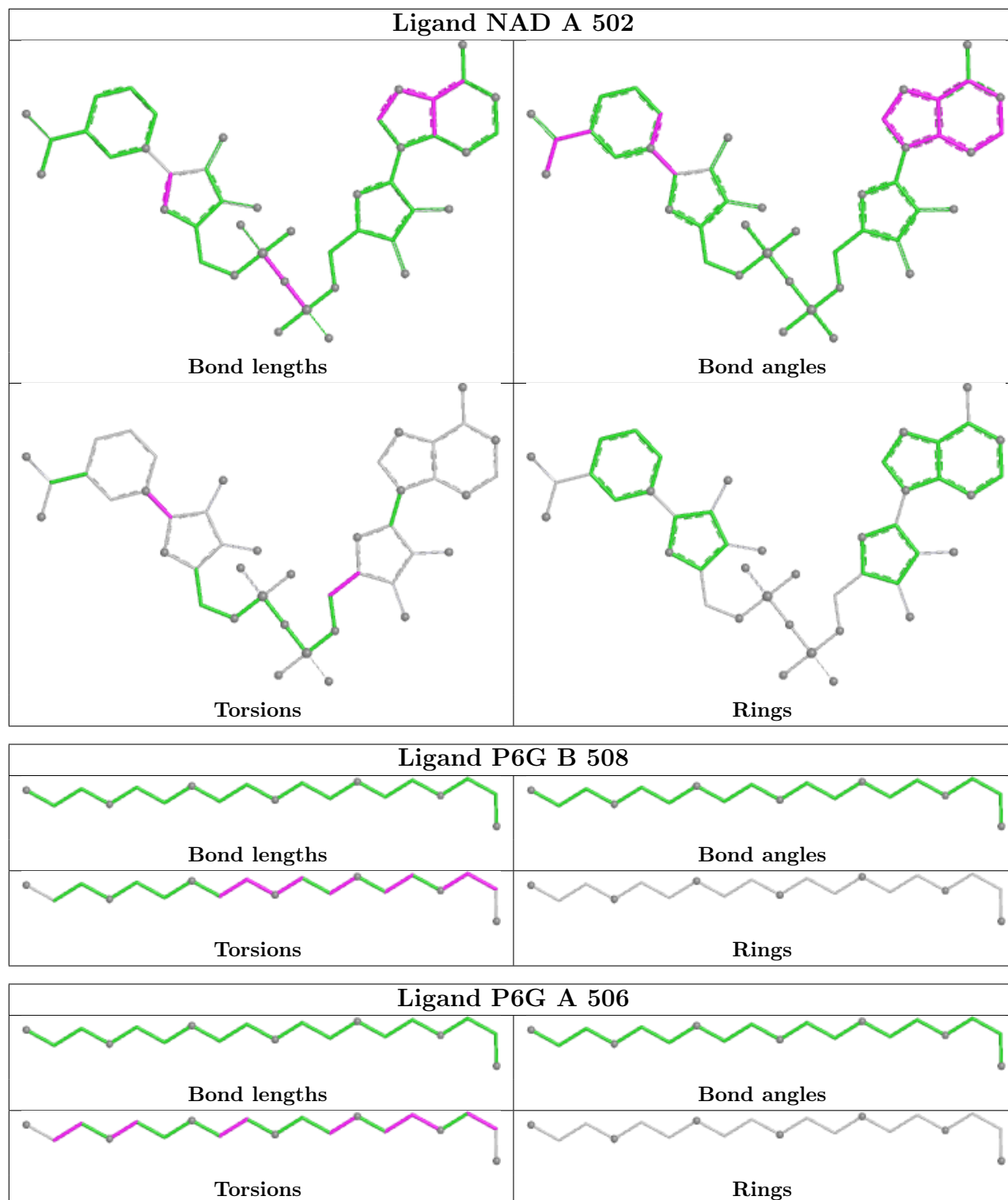
Continued from previous page...

Mol	Chain	Res	Type	Atoms
5	A	506	P6G	C9-C8-O7-C6
7	D	506	PEG	C4-C3-O2-C2
5	A	506	P6G	C6-C5-O4-C3
3	C	502	NAD	O4B-C4B-C5B-O5B
5	B	508	P6G	C12-C11-O10-C9
5	B	508	P6G	C9-C8-O7-C6
3	A	502	NAD	O4B-C4B-C5B-O5B
2	A	501	7CY	C6'-C1'-N9-C8
2	D	501	7CY	C6'-C1'-N9-C8
2	B	501	7CY	C6'-C1'-N9-C4
2	C	501	7CY	C6'-C1'-N9-C4
2	B	501	7CY	C2'-C1'-N9-C8

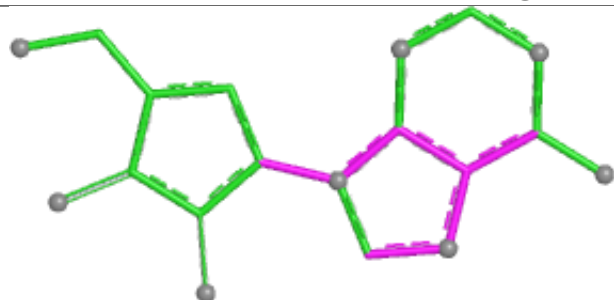
There are no ring outliers.

No monomer is involved in short contacts.

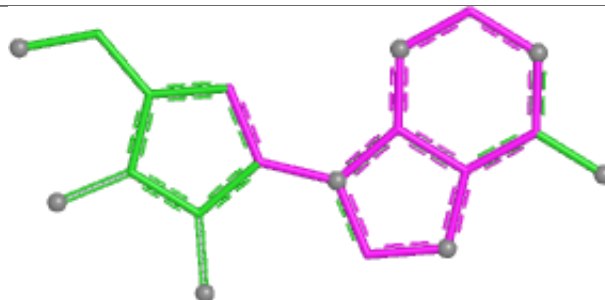
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



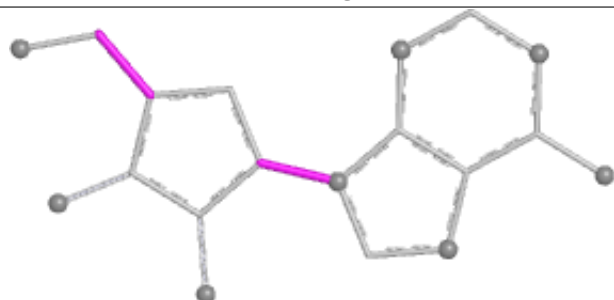
Ligand 7CY B 501



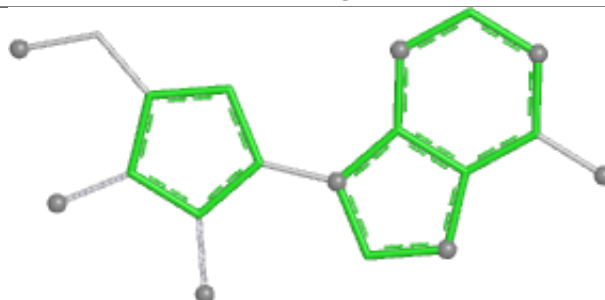
Bond lengths



Bond angles

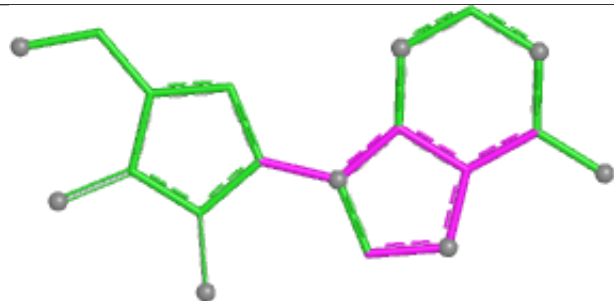


Torsions

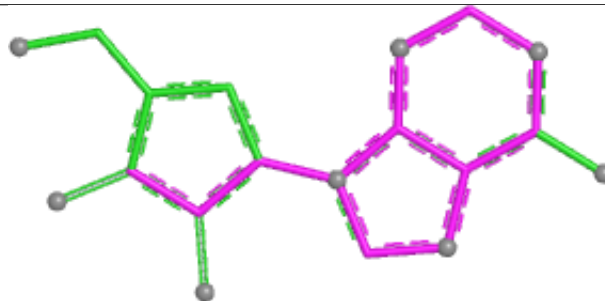


Rings

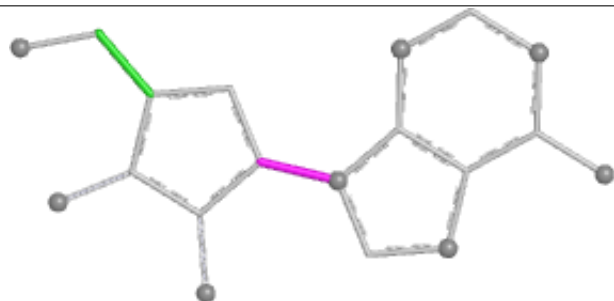
Ligand 7CY C 501



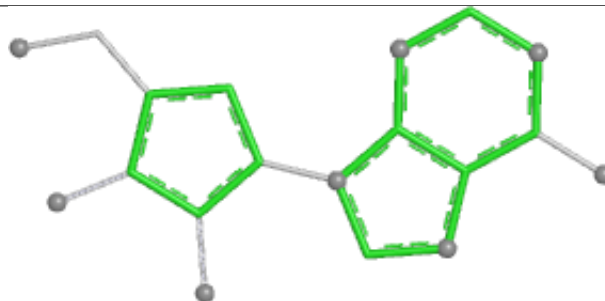
Bond lengths



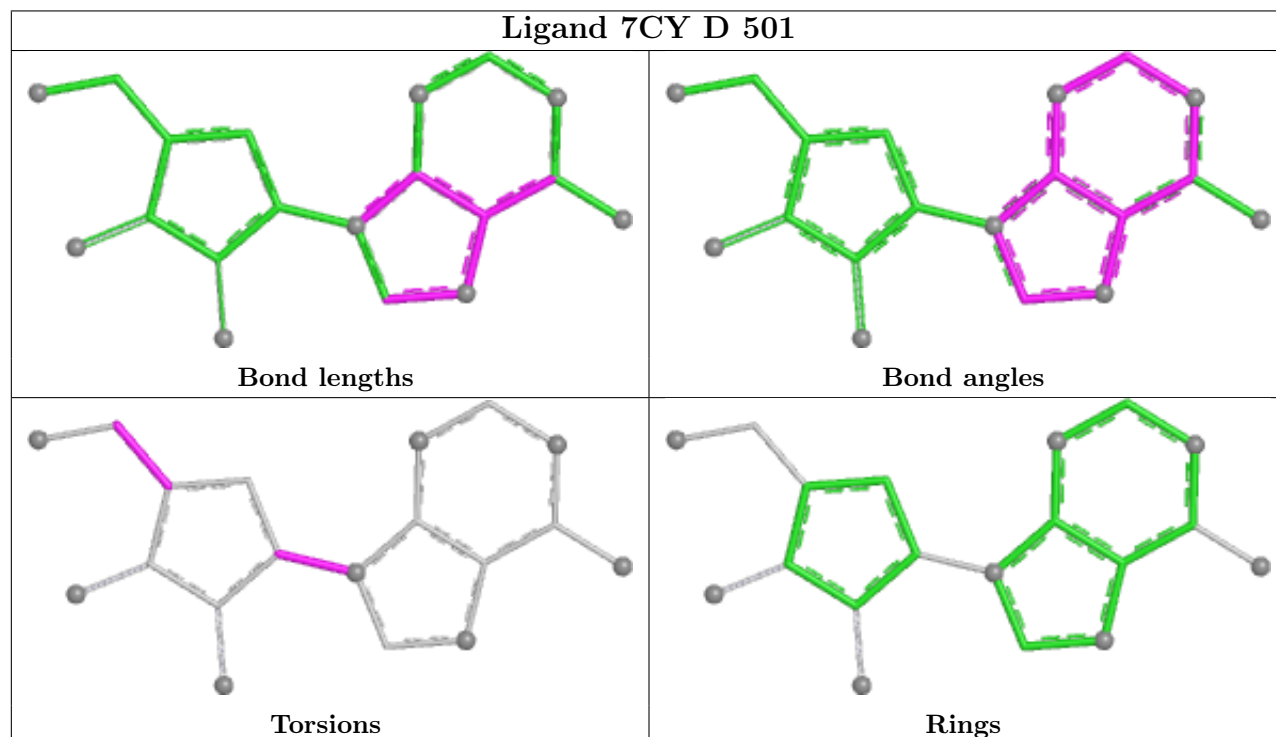
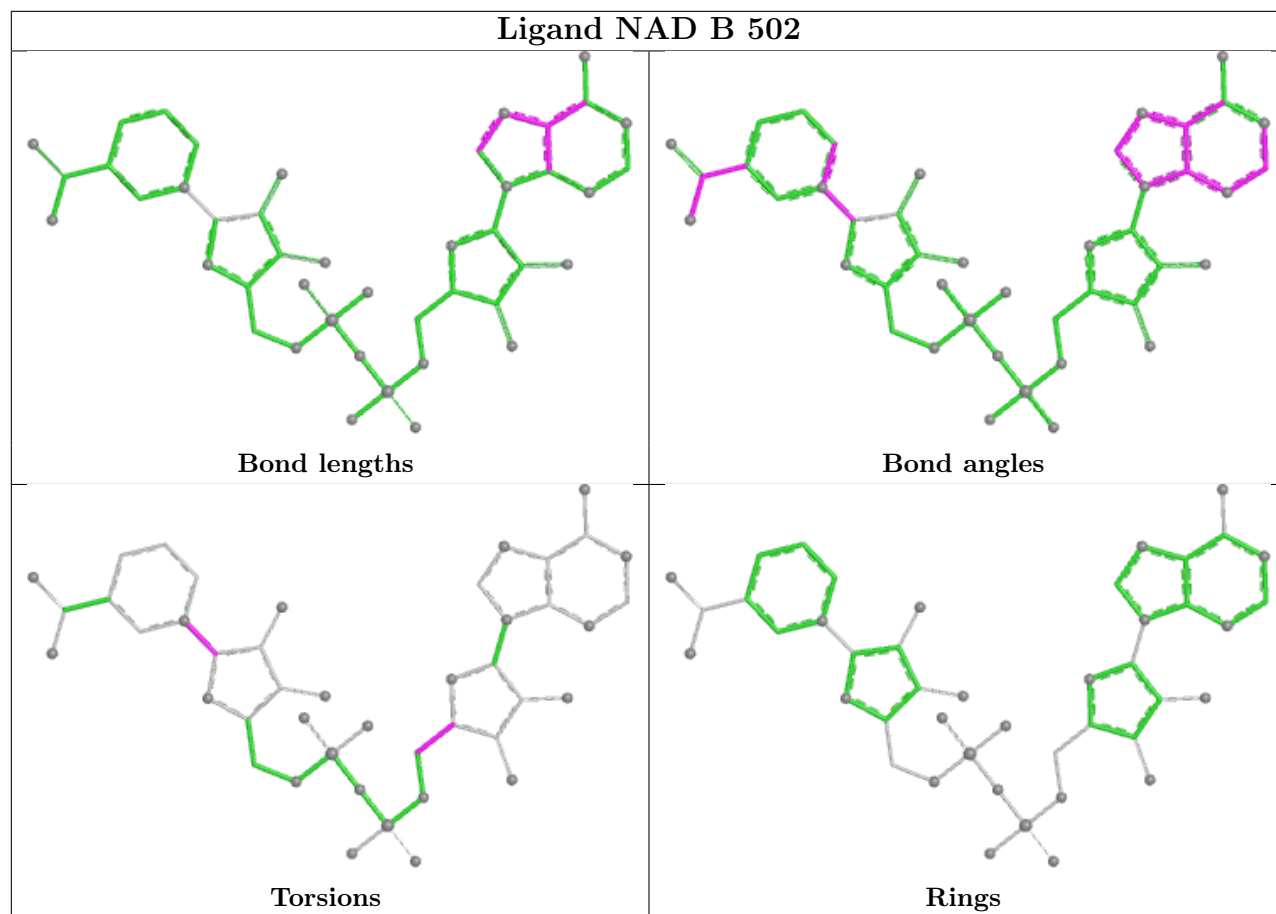
Bond angles

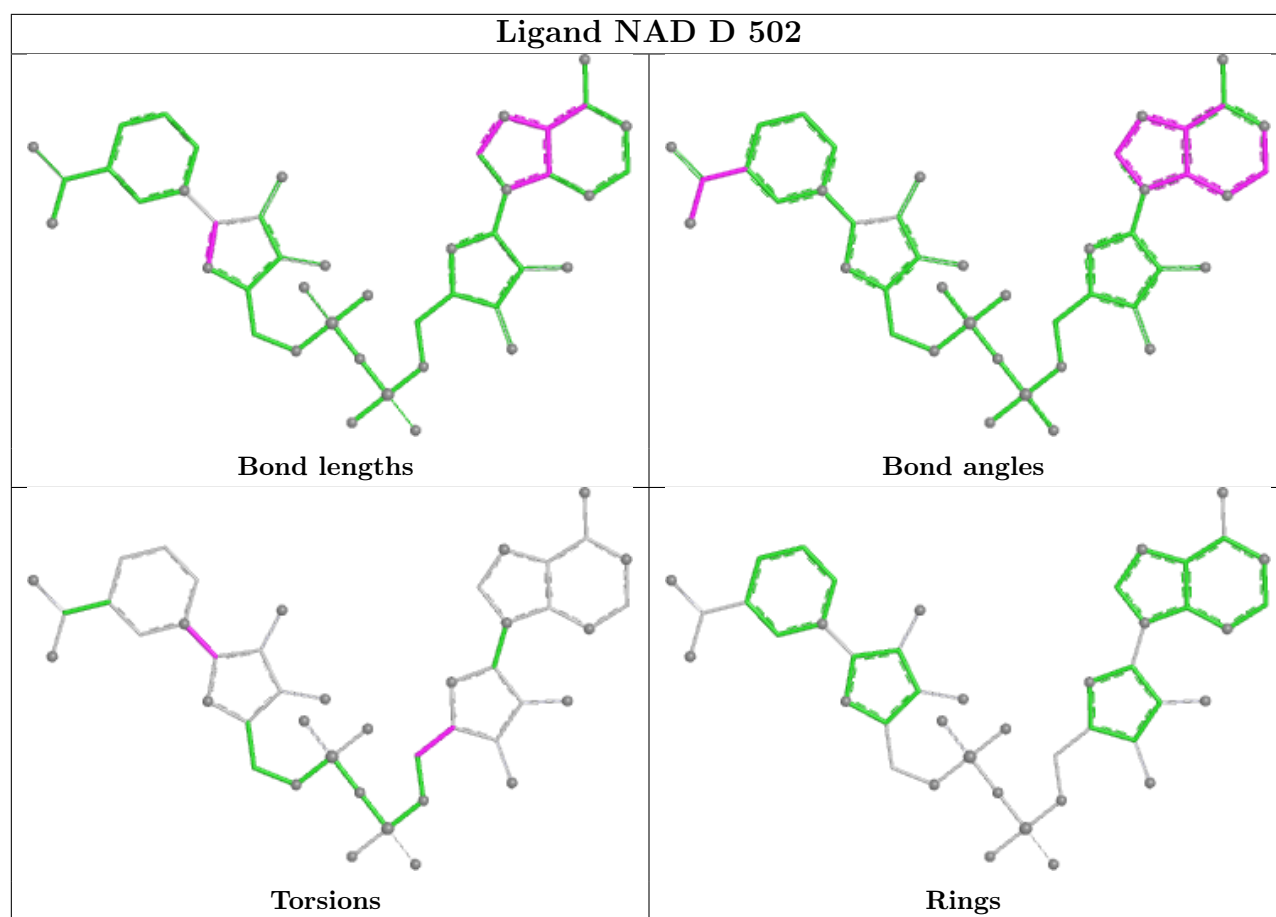


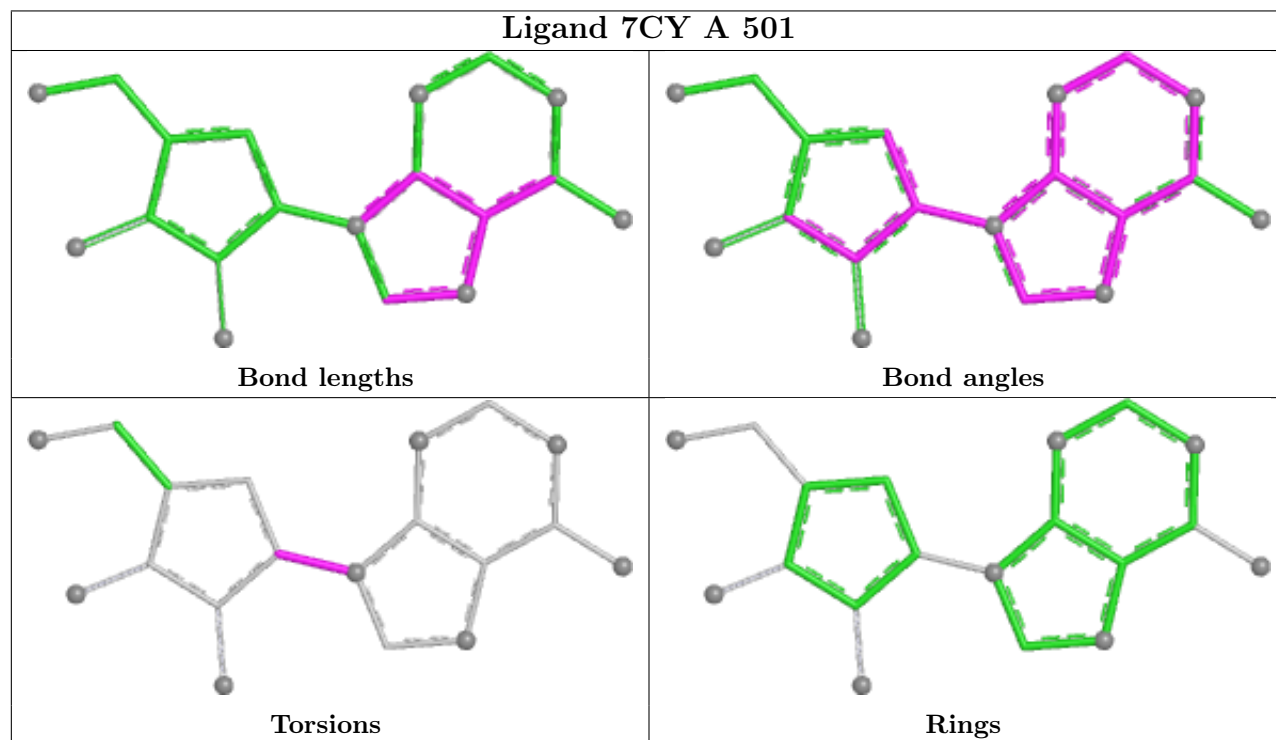
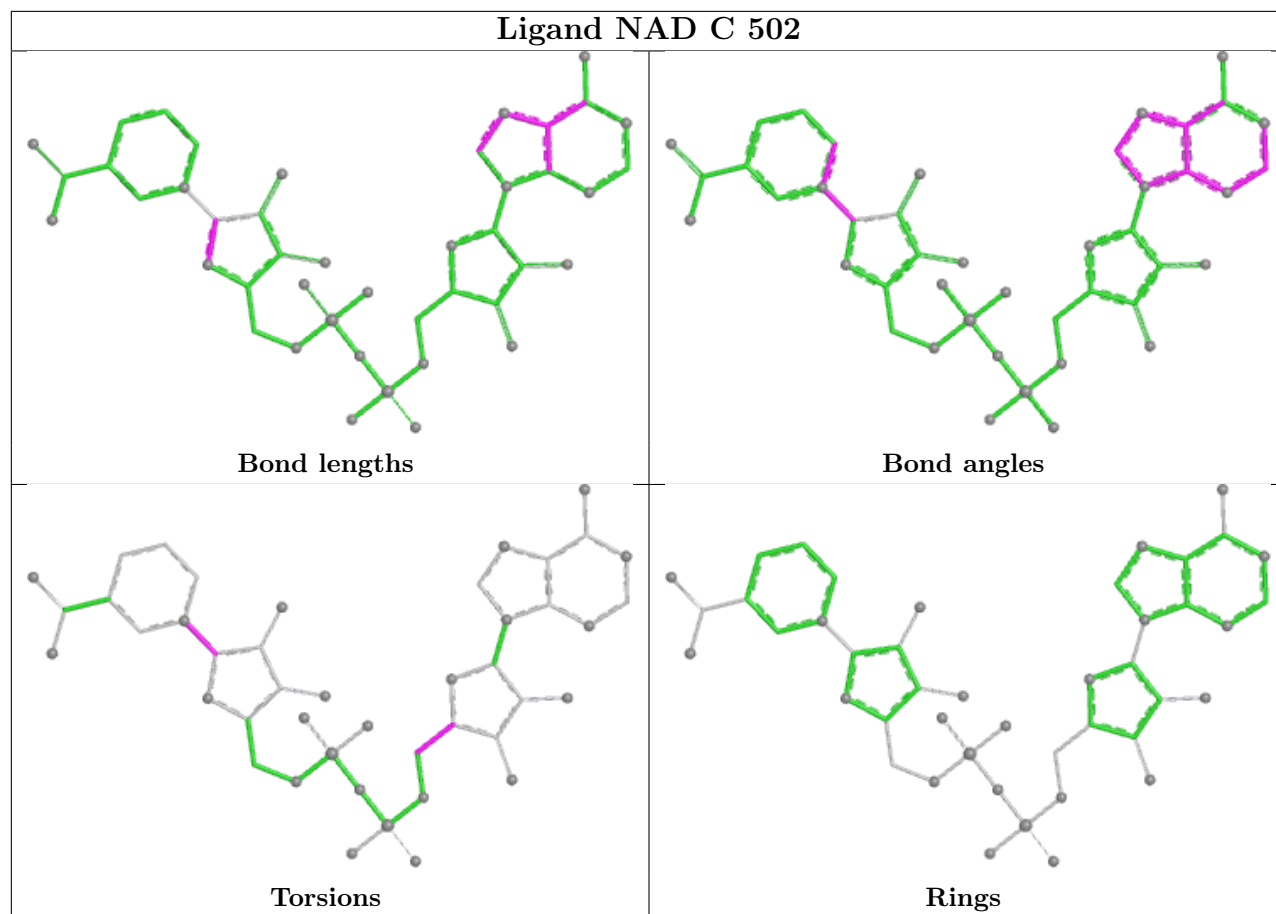
Torsions



Rings







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	493/498 (98%)	-0.60	1 (0%) 91 90	26, 54, 90, 156	1 (0%)
1	B	494/498 (99%)	-0.65	1 (0%) 91 90	26, 51, 86, 162	2 (0%)
1	C	495/498 (99%)	-0.62	1 (0%) 91 90	25, 52, 106, 154	2 (0%)
1	D	495/498 (99%)	-0.65	1 (0%) 91 90	25, 51, 95, 146	3 (0%)
All	All	1977/1992 (99%)	-0.63	4 (0%) 91 90	25, 52, 95, 162	8 (0%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	1	TYR	3.2
1	C	128	ILE	2.7
1	A	2	LYS	2.1
1	B	2	LYS	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](#)

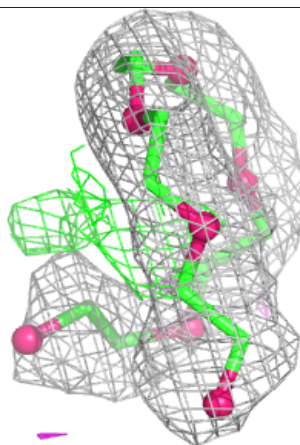
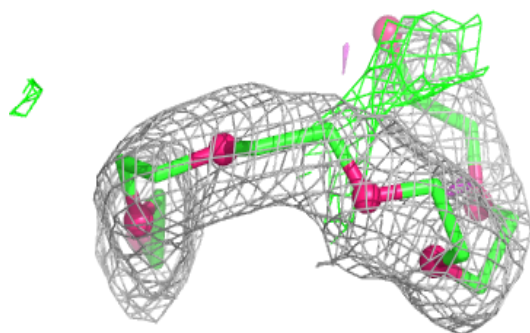
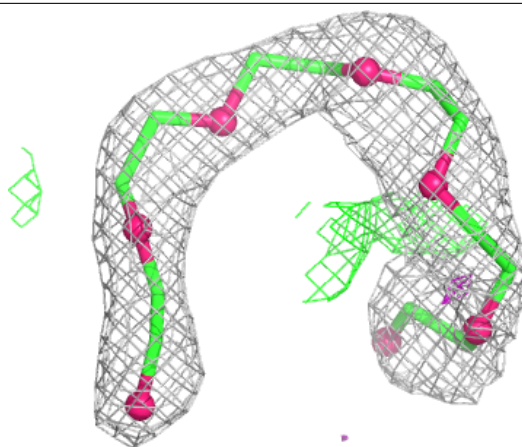
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists 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
4	SO4	B	506	5/5	0.65	0.12	57,59,60,63	5
4	SO4	B	505	5/5	0.73	0.10	63,63,67,67	5
4	SO4	A	505	5/5	0.73	0.10	62,63,65,68	5
4	SO4	B	507	5/5	0.75	0.11	58,59,61,64	5
6	GOL	C	504	6/6	0.75	0.13	78,79,81,81	0
4	SO4	B	504	5/5	0.76	0.15	50,53,56,56	5
4	SO4	D	504	5/5	0.78	0.11	59,62,64,65	5
6	GOL	A	507	6/6	0.79	0.15	76,82,85,85	0
4	SO4	A	504	5/5	0.79	0.09	49,53,55,56	5
7	PEG	D	506	7/7	0.79	0.16	67,71,75,76	0
4	SO4	D	505	5/5	0.80	0.09	54,56,57,57	5
7	PEG	D	508	7/7	0.83	0.10	65,73,78,80	0
5	P6G	A	506	19/19	0.87	0.12	76,83,92,93	0
7	PEG	D	507	7/7	0.88	0.15	65,68,71,73	0
5	P6G	B	508	19/19	0.88	0.10	67,83,88,89	0
4	SO4	A	503	5/5	0.89	0.10	86,86,88,91	0
4	SO4	D	503	5/5	0.90	0.12	79,81,85,91	0
4	SO4	C	503	5/5	0.92	0.07	81,84,85,92	0
4	SO4	B	503	5/5	0.93	0.15	34,35,36,37	5
2	7CY	B	501	19/19	0.97	0.06	42,46,49,50	0
2	7CY	C	501	19/19	0.97	0.05	40,43,50,52	0
2	7CY	A	501	19/19	0.97	0.07	43,47,53,57	0
3	NAD	D	502	44/44	0.98	0.05	35,38,41,42	0
2	7CY	D	501	19/19	0.98	0.06	39,41,53,55	0
3	NAD	A	502	44/44	0.98	0.05	36,40,43,43	0
3	NAD	B	502	44/44	0.98	0.05	34,37,42,44	0
3	NAD	C	502	44/44	0.98	0.05	35,39,43,45	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.

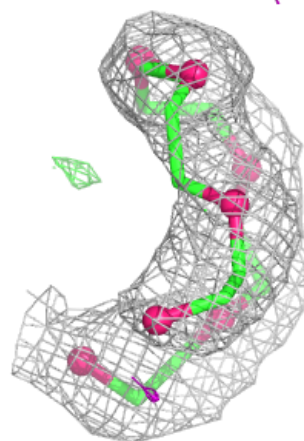
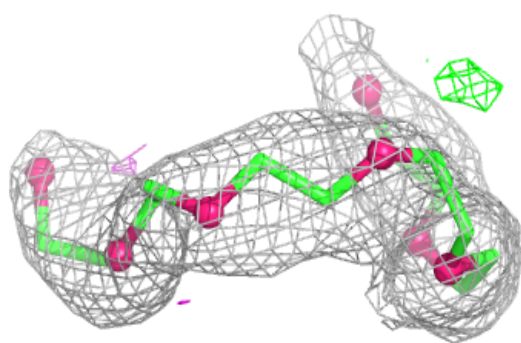
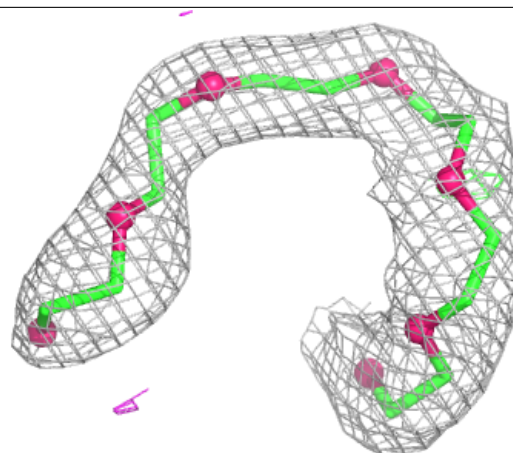
Electron density around P6G A 506:

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



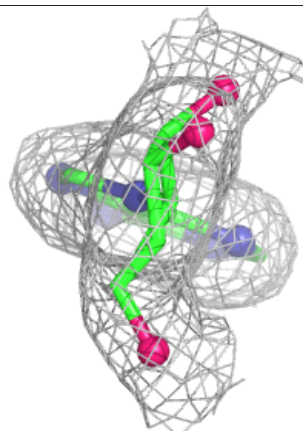
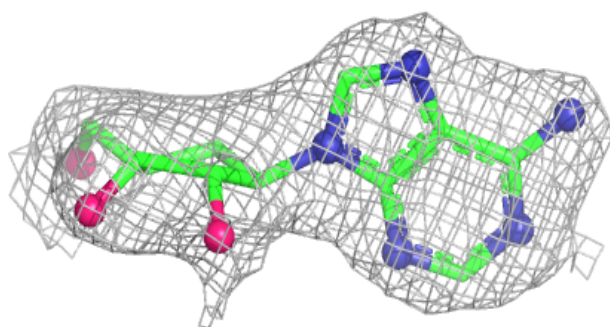
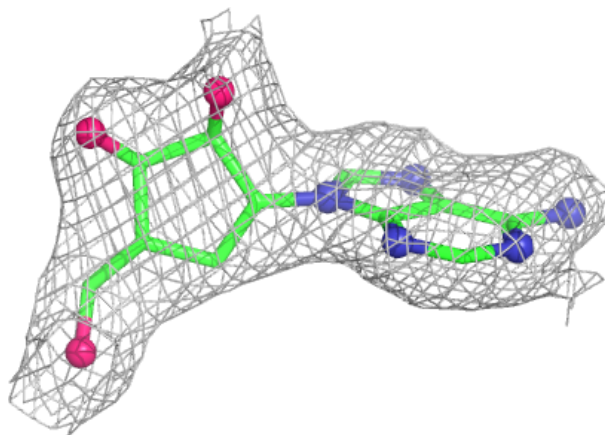
Electron density around P6G B 508:

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

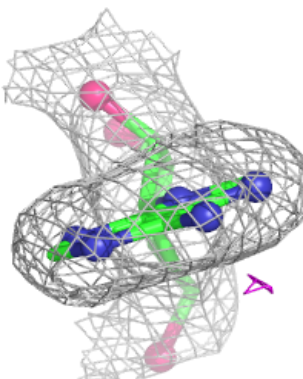
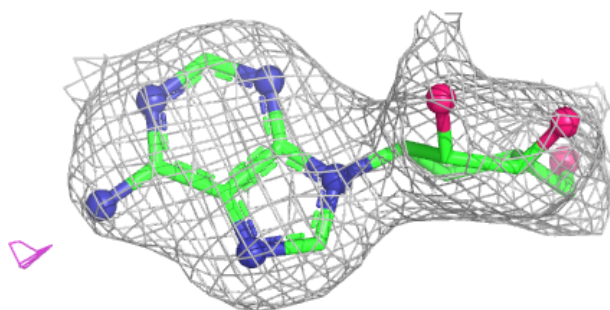
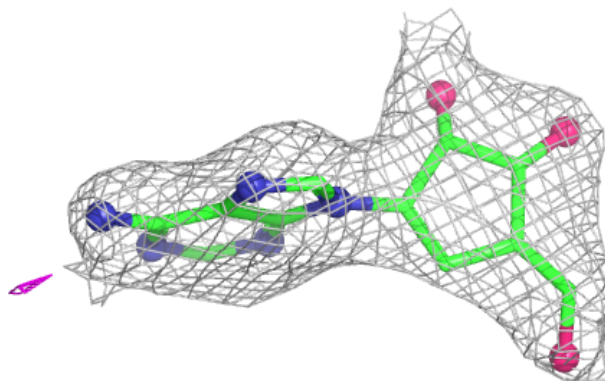


Electron density around 7CY B 501:

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

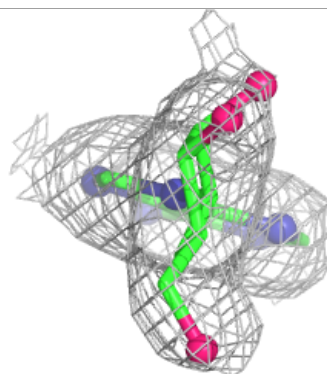
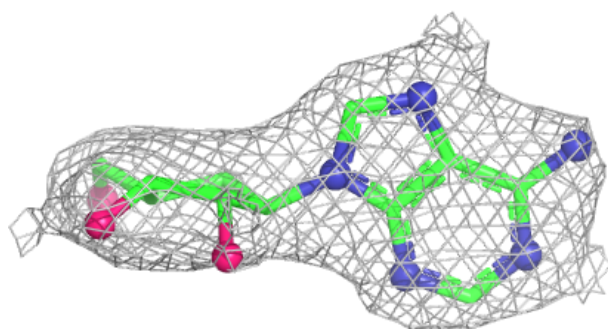
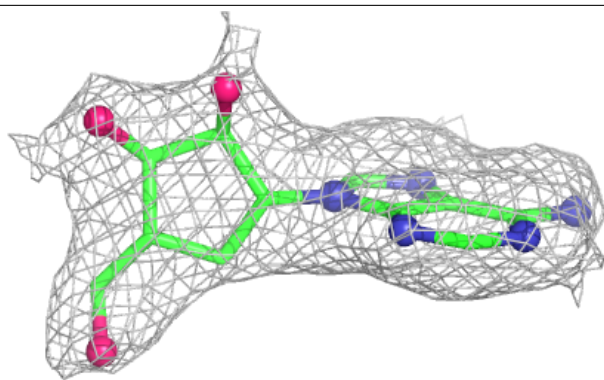
**Electron density around 7CY C 501:**

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

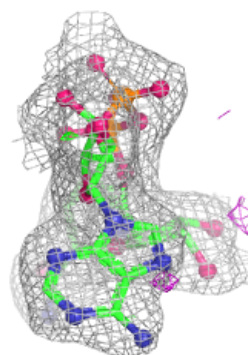
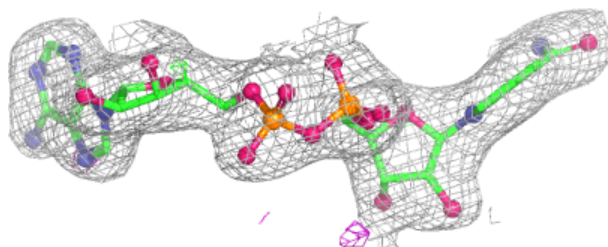
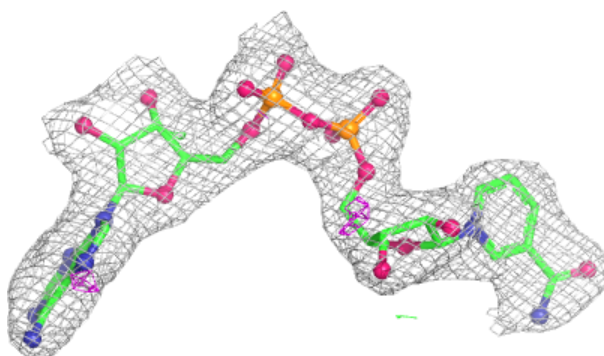


Electron density around 7CY A 501:

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

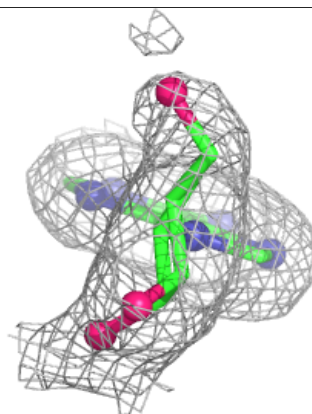
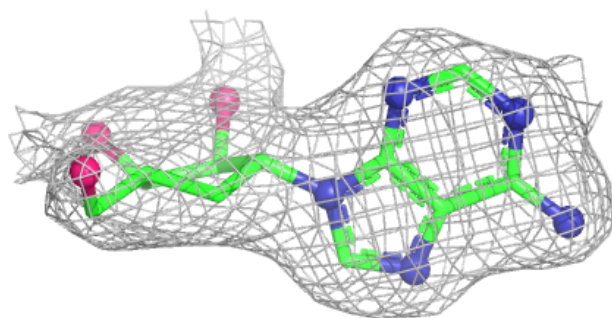
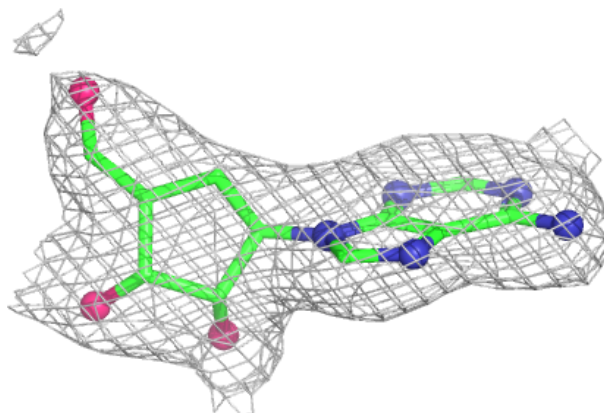
**Electron density around NAD D 502:**

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

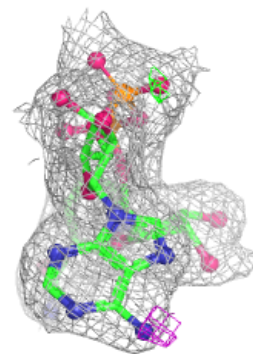
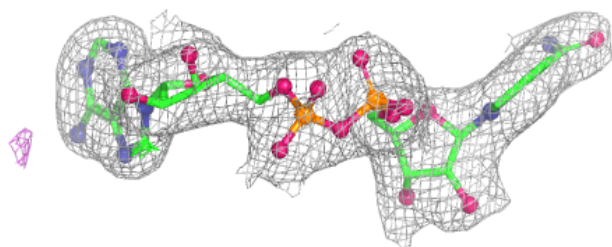
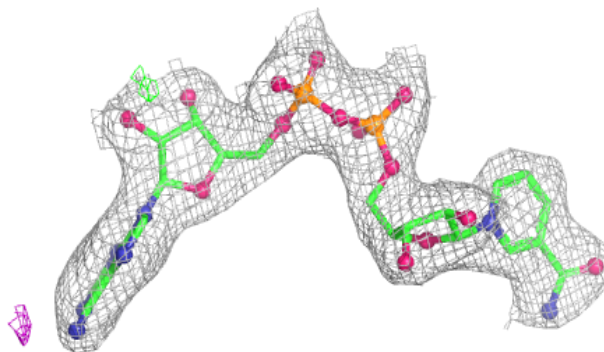


Electron density around 7CY D 501:

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and green (positive)

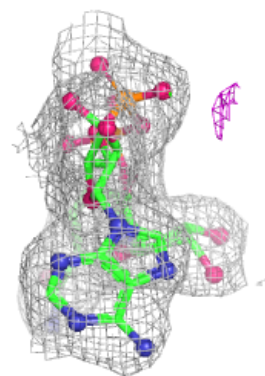
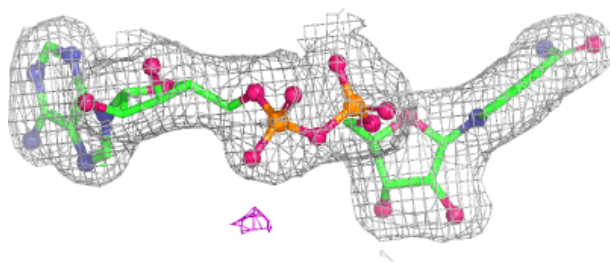
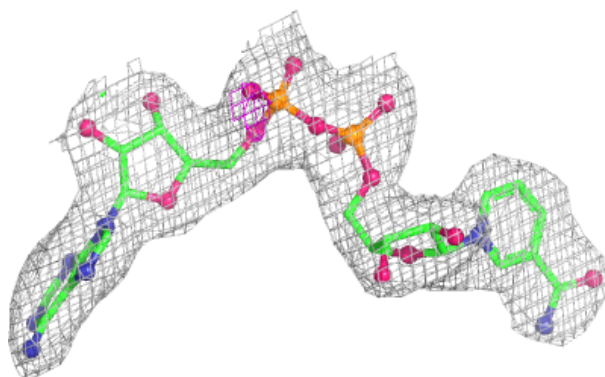
**Electron density around NAD A 502:**

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

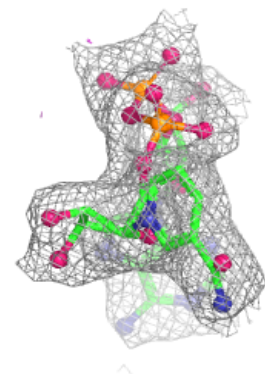
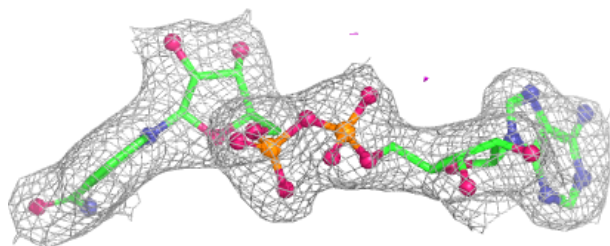
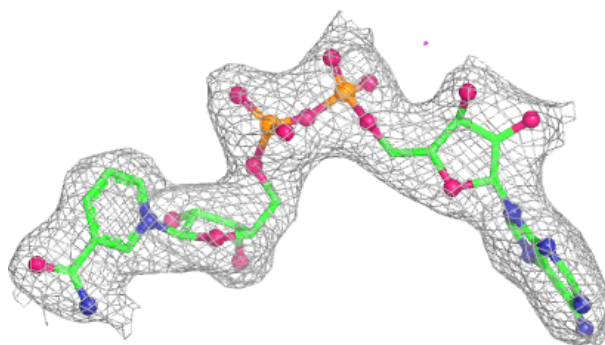


Electron density around NAD B 502:

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

**Electron density around NAD C 502:**

$2mF_o-DF_c$ (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.