Full wwPDB X-ray Structure Validation Report (i)

Nov 5, 2023 – 09:39 AM EST

PDB ID	:	6BB0
Title	:	Lactate Dehydrogenase in complex with inhibitor (R)-3-((2-chlorophenyl)thio)-6-(3-((4-fluorophenyl)amino)phenyl)-4-hydroxy-6-(thiophen-3-yl)-5,6-dihydro-2H-pyran-2-one
Authors	:	Ultsch, M.; Eigenbrot, C.
Deposited on	:	2017-10-16
Resolution	:	1.95 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 (i) 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 (i)) were used in the production of this report:

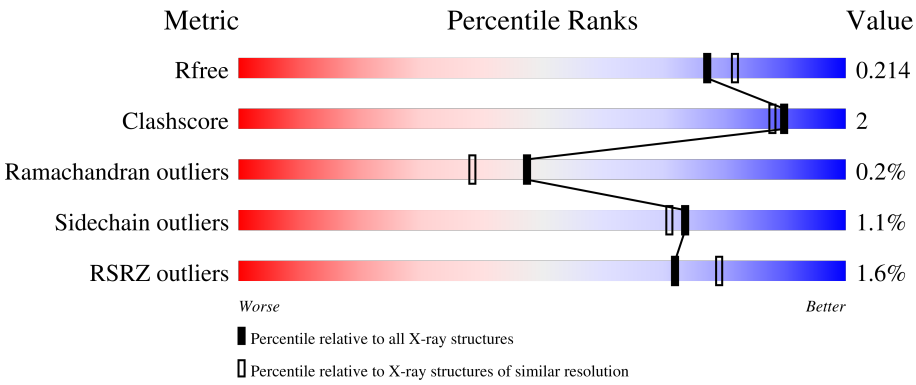
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	331	92% 5% •
1	B	331	2% 93% 5% •
1	C	331	3% 94% • •
1	D	331	% 92% 7% •

2 Entry composition (i)

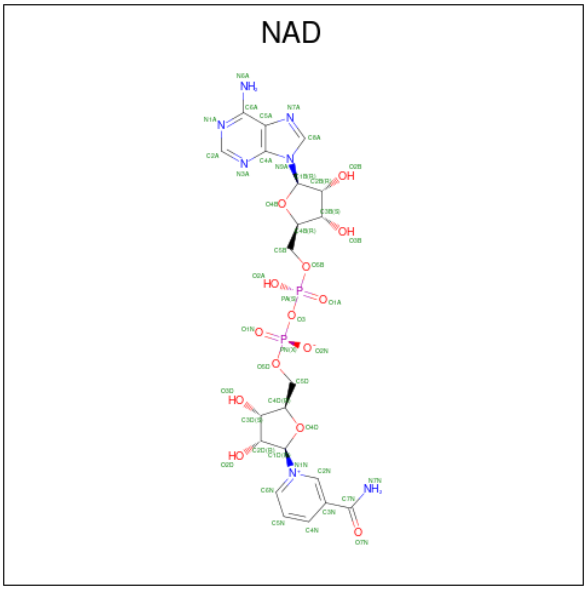
There are 7 unique types of molecules in this entry. The entry contains 11187 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called L-lactate dehydrogenase A chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	323	2519	1615	423	467	14	0	4	0
1	B	324	2527	1617	431	466	13	0	2	0
1	C	325	2528	1619	429	467	13	0	2	0
1	D	327	2558	1637	435	472	14	0	4	0

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



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

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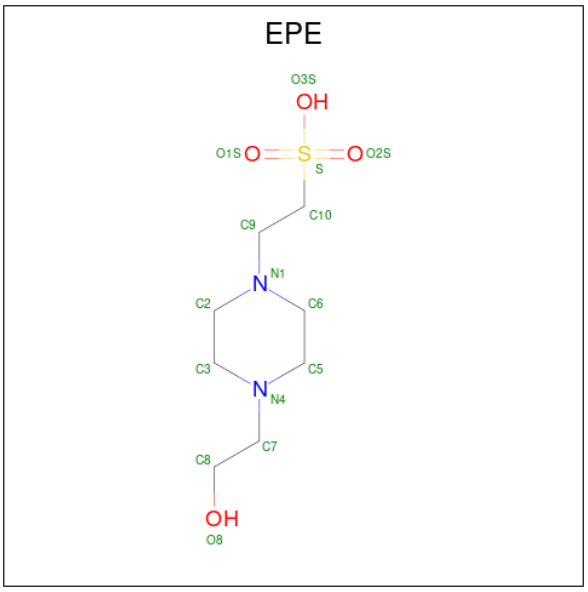
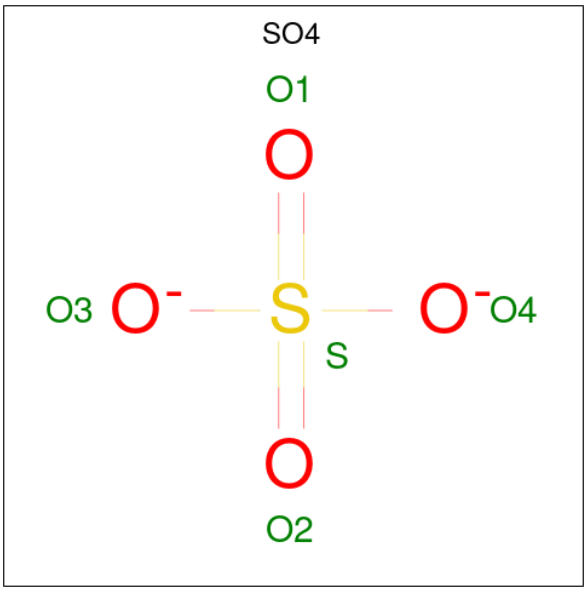
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	C	1	44	21	7	14	2	0	0
			Total	C	N	O	P		
2	D	1	44	21	7	14	2	0	0

- Molecule 3 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).



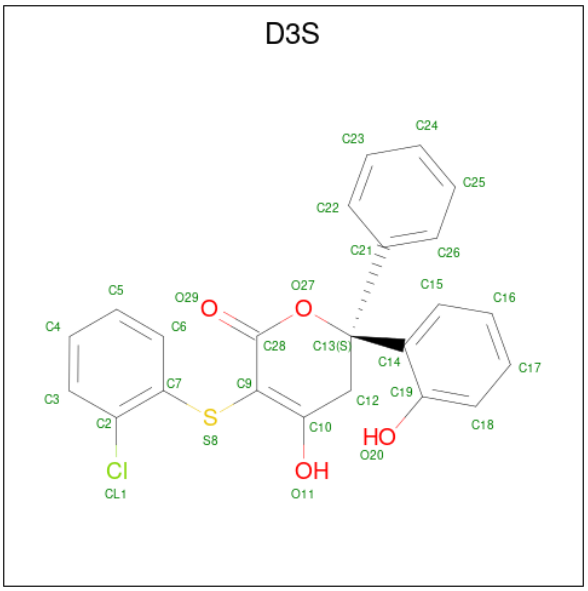
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	A	1	15	8	2	4	1	0	0
			Total	C	N	O	S		
3	B	1	15	8	2	4	1	0	0
			Total	C	N	O	S		
3	C	1	15	8	2	4	1	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



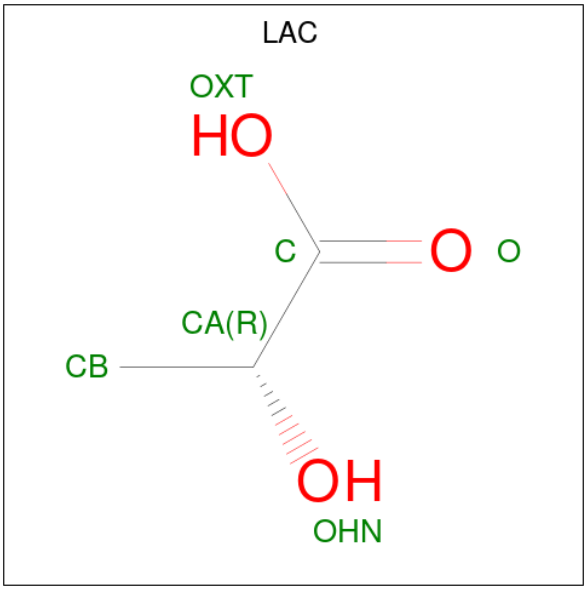
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	C	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0

- Molecule 5 is (6S)-3-[(2-chlorophenyl)sulfanyl]-4-hydroxy-6-(2-hydroxyphenyl)-6-phenyl-5,6 -dihydro-2H-pyran-2-one (three-letter code: D3S) (formula: $C_{23}H_{17}ClO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total 29	C 23	Cl 1	O 4	S 1	0	0
5	C	1	Total 29	C 23	Cl 1	O 4	S 1	0	0
5	D	1	Total 29	C 23	Cl 1	O 4	S 1	0	0

- Molecule 6 is LACTIC ACID (three-letter code: LAC) (formula: $C_3H_6O_3$).



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

- Molecule 7 is water.

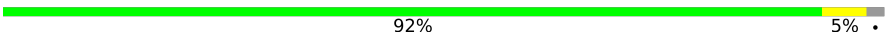
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	183	Total 183	O 183	0	0
7	B	186	Total 186	O 186	0	0
7	C	154	Total 154	O 154	0	0
7	D	198	Total 198	O 198	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

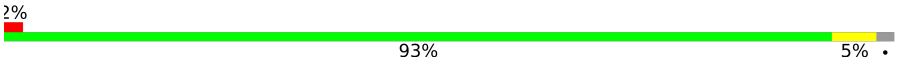
• Molecule 1: L-lactate dehydrogenase A chain

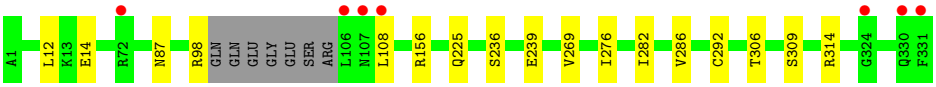
Chain A:



• Molecule 1: L-lactate dehydrogenase A chain

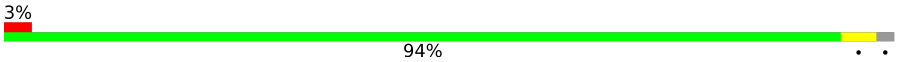
Chain B:

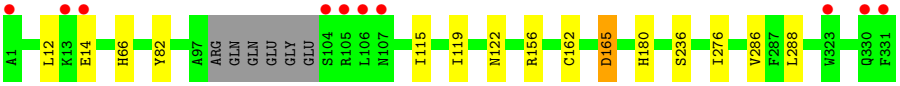




• Molecule 1: L-lactate dehydrogenase A chain

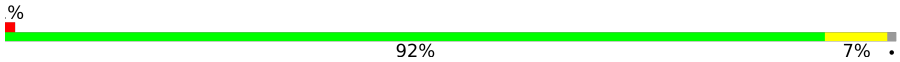
Chain C:





• Molecule 1: L-lactate dehydrogenase A chain

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	78.12Å 80.97Å 103.21Å 90.00° 98.33° 90.00°	Depositor
Resolution (Å)	38.65 – 1.95 38.65 – 1.95	Depositor EDS
% Data completeness (in resolution range)	97.9 (38.65-1.95) 97.9 (38.65-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$< I/\sigma(I) >$ [1]	2.07 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.166 , 0.215 0.174 , 0.214	Depositor DCC
R_{free} test set	1830 reflections (2.01%)	wwPDB-VP
Wilson B-factor (Å^2)	31.2	Xtriage
Anisotropy	0.028	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 38.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	11187	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 5.32% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: LAC, D3S, EPE, NAD, 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	0.49	0/2574	0.67	2/3481 (0.1%)
1	B	0.50	0/2573	0.68	1/3479 (0.0%)
1	C	0.49	0/2577	0.67	1/3484 (0.0%)
1	D	0.53	0/2610	0.69	1/3528 (0.0%)
All	All	0.50	0/10334	0.68	5/13972 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	156	ARG	NE-CZ-NH2	6.13	123.37	120.30
1	A	156	ARG	NE-CZ-NH1	5.71	123.16	120.30
1	B	156	ARG	NE-CZ-NH1	5.64	123.12	120.30
1	A	45	ASP	CB-CG-OD1	5.53	123.28	118.30
1	D	72	ARG	NE-CZ-NH2	5.47	123.04	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2519	0	2617	9	0
1	B	2527	0	2622	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2528	0	2628	7	0
1	D	2558	0	2660	14	0
2	A	44	0	25	0	0
2	B	44	0	25	1	0
2	C	44	0	25	0	0
2	D	44	0	25	0	0
3	A	15	0	17	0	0
3	B	15	0	17	0	0
3	C	15	0	17	0	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
4	C	5	0	0	0	0
4	D	5	0	0	0	0
5	A	29	0	0	1	0
5	C	29	0	0	0	0
5	D	29	0	0	0	0
6	B	6	0	0	0	0
7	A	183	0	0	2	0
7	B	186	0	0	3	0
7	C	154	0	0	0	0
7	D	198	0	0	1	0
All	All	11187	0	10678	37	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 2.

All (37) 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:D:203[A]:MET:CE	1:D:217:LEU:HD21	2.23	0.68
1:A:257:ASP:OD2	7:A:901:HOH:O	2.14	0.65
1:D:203[A]:MET:HE1	1:D:217:LEU:HD11	1.82	0.62
1:B:276:ILE:HD11	1:B:286:VAL:HG23	1.82	0.61
1:A:168:ARG:NH2	5:A:804:D3S:CL1	2.75	0.57
1:B:276:ILE:HD13	1:B:282:ILE:HD13	1.87	0.57
1:A:72:ARG:NH1	7:A:902:HOH:O	2.38	0.56
1:C:276:ILE:HD11	1:C:286:VAL:HG23	1.89	0.55
1:D:203[A]:MET:HE2	1:D:217:LEU:HD21	1.88	0.55
1:D:232:GLN:O	1:D:236:SER:OG	2.21	0.54
1:B:314:ARG:NH2	7:B:901:HOH:O	2.32	0.50
1:D:293[A]:ILE:HD12	1:D:301:ASP:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:293:ILE:HD12	1:A:301:ASP:HB2	1.94	0.50
1:B:236:SER:HA	1:B:239:GLU:HB2	1.94	0.49
1:B:98:ARG:HD3	2:B:801:NAD:O2N	2.14	0.47
1:B:87:ASN:ND2	7:B:907:HOH:O	2.48	0.47
1:D:115:ILE:HG22	1:D:119:ILE:HD12	1.96	0.47
1:A:141:ILE:HG13	1:A:322:LEU:HD22	1.97	0.46
1:C:115:ILE:HG22	1:C:119:ILE:HD12	1.98	0.46
1:D:200:TRP:CE3	1:D:203[B]:MET:SD	3.10	0.45
1:C:82:TYR:CG	1:C:122:ASN:HB3	2.52	0.44
1:C:276:ILE:HG12	1:C:288:LEU:HB2	2.00	0.44
1:A:82:TYR:CG	1:A:122:ASN:HB3	2.53	0.43
1:B:306:THR:HG21	7:B:1055:HOH:O	2.18	0.42
1:D:274:THR:O	1:D:287:PHE:HA	2.20	0.42
1:B:276:ILE:HD13	1:B:282:ILE:CD1	2.49	0.42
1:D:254[B]:SER:OG	7:D:901:HOH:O	2.22	0.41
1:A:266:LEU:O	1:C:180:HIS:HB2	2.20	0.41
1:C:162:CYS:HA	1:C:165:ASP:OD1	2.21	0.41
1:A:16:GLN:NE2	1:D:297:ASN:OD1	2.52	0.41
1:D:112:ASN:HB3	1:D:142:LEU:HD11	2.02	0.41
1:D:203[A]:MET:HG2	1:D:210:LEU:HD22	2.02	0.41
1:D:302:LEU:HD12	1:D:302:LEU:C	2.41	0.41
1:A:272:VAL:O	1:A:289:SER:HA	2.21	0.40
1:C:66:HIS:CE1	1:D:236:SER:HB3	2.56	0.40
1:B:269:VAL:HA	1:B:292:CYS:O	2.22	0.40
1:B:12:LEU:O	1:B:12:LEU:HD12	2.22	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	323/331 (98%)	318 (98%)	5 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	322/331 (97%)	316 (98%)	5 (2%)	1 (0%)	41	30
1	C	323/331 (98%)	315 (98%)	7 (2%)	1 (0%)	41	30
1	D	327/331 (99%)	321 (98%)	6 (2%)	0	100	100
All	All	1295/1324 (98%)	1270 (98%)	23 (2%)	2 (0%)	47	38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	14	GLU
1	B	14	GLU

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	284/287 (99%)	282 (99%)	2 (1%)	84	82
1	B	283/287 (99%)	280 (99%)	3 (1%)	73	71
1	C	284/287 (99%)	281 (99%)	3 (1%)	73	71
1	D	288/287 (100%)	284 (99%)	4 (1%)	67	62
All	All	1139/1148 (99%)	1127 (99%)	12 (1%)	73	71

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	165	ASP
1	A	236	SER
1	B	108	LEU
1	B	225	GLN
1	B	309	SER
1	C	12	LEU
1	C	165	ASP
1	C	236	SER
1	D	12	LEU

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Mol	Chain	Res	Type
1	D	16	GLN
1	D	165	ASP
1	D	275	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	16	GLN
1	B	87	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

15 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	SO4	D	803	-	4,4,4	0.43	0	6,6,6	0.41	0
3	EPE	B	802	-	15,15,15	1.62	1 (6%)	18,20,20	4.25	12 (66%)
5	D3S	C	804	-	31,32,32	0.98	0	34,46,46	1.18	3 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
2	NAD	B	801	-	42,48,48	2.53	13 (30%)	50,73,73	1.71	8 (16%)
6	LAC	B	804	-	5,5,5	0.91	0	4,6,6	0.65	0
4	SO4	A	803	-	4,4,4	0.34	0	6,6,6	0.13	0
4	SO4	B	803	-	4,4,4	0.59	0	6,6,6	0.30	0
5	D3S	D	802	-	31,32,32	0.98	1 (3%)	34,46,46	1.17	6 (17%)
3	EPE	A	802	-	15,15,15	1.82	1 (6%)	18,20,20	4.28	8 (44%)
2	NAD	A	801	-	42,48,48	2.52	12 (28%)	50,73,73	1.84	11 (22%)
3	EPE	C	802	-	15,15,15	1.51	1 (6%)	18,20,20	3.33	12 (66%)
5	D3S	A	804	-	31,32,32	1.20	1 (3%)	34,46,46	1.39	4 (11%)
2	NAD	D	801	-	42,48,48	2.49	13 (30%)	50,73,73	1.88	12 (24%)
2	NAD	C	801	-	42,48,48	2.71	13 (30%)	50,73,73	1.97	10 (20%)
4	SO4	C	803	-	4,4,4	0.42	0	6,6,6	0.73	0

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	EPE	B	802	-	-	6/9/19/19	0/1/1/1
5	D3S	C	804	-	-	1/16/34/34	0/4/4/4
2	NAD	B	801	-	-	3/26/62/62	0/5/5/5
6	LAC	B	804	-	-	4/4/4/4	-
5	D3S	D	802	-	-	1/16/34/34	0/4/4/4
3	EPE	A	802	-	-	6/9/19/19	0/1/1/1
2	NAD	A	801	-	-	5/26/62/62	0/5/5/5
3	EPE	C	802	-	-	6/9/19/19	0/1/1/1
5	D3S	A	804	-	-	2/16/34/34	0/4/4/4
2	NAD	D	801	-	-	3/26/62/62	0/5/5/5
2	NAD	C	801	-	-	2/26/62/62	0/5/5/5

All (56) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	802	EPE	C10-S	-6.56	1.68	1.77
2	C	801	NAD	C4N-C3N	6.40	1.50	1.39
2	C	801	NAD	C7N-N7N	6.26	1.44	1.33
2	A	801	NAD	C4N-C3N	6.11	1.49	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	801	NAD	C2N-C3N	6.10	1.48	1.39
2	A	801	NAD	C7N-N7N	5.93	1.44	1.33
2	D	801	NAD	C7N-N7N	5.81	1.44	1.33
2	B	801	NAD	C4N-C3N	5.76	1.49	1.39
2	A	801	NAD	C5N-C4N	5.72	1.51	1.38
2	D	801	NAD	C4N-C3N	5.67	1.49	1.39
2	D	801	NAD	C2N-C3N	5.63	1.47	1.39
3	B	802	EPE	C10-S	-5.60	1.69	1.77
2	D	801	NAD	C5N-C4N	5.60	1.50	1.38
2	B	801	NAD	C5N-C4N	5.51	1.50	1.38
2	C	801	NAD	C6N-C5N	5.42	1.50	1.38
2	B	801	NAD	C7N-N7N	5.42	1.43	1.33
2	A	801	NAD	C2N-C3N	5.28	1.47	1.39
2	C	801	NAD	C5N-C4N	5.18	1.49	1.38
2	D	801	NAD	C6N-C5N	5.17	1.50	1.38
2	B	801	NAD	C6N-C5N	5.13	1.50	1.38
3	C	802	EPE	C10-S	-5.12	1.70	1.77
2	B	801	NAD	C2N-C3N	5.04	1.46	1.39
2	A	801	NAD	C6N-C5N	4.67	1.49	1.38
2	C	801	NAD	C2N-N1N	4.63	1.40	1.35
2	B	801	NAD	C2B-C3B	-4.51	1.41	1.53
2	C	801	NAD	C2B-C3B	-4.42	1.41	1.53
2	D	801	NAD	C2B-C3B	-4.37	1.41	1.53
2	A	801	NAD	C2B-C3B	-4.28	1.41	1.53
5	A	804	D3S	C7-S8	3.77	1.82	1.77
2	A	801	NAD	C2N-N1N	3.68	1.39	1.35
2	D	801	NAD	O2D-C2D	-3.51	1.34	1.43
2	D	801	NAD	C2N-N1N	3.45	1.39	1.35
2	B	801	NAD	O2D-C2D	-3.45	1.34	1.43
2	C	801	NAD	O2D-C2D	-3.42	1.34	1.43
2	B	801	NAD	C2N-N1N	3.39	1.39	1.35
2	B	801	NAD	C6N-N1N	3.32	1.43	1.35
2	D	801	NAD	C6N-N1N	3.28	1.43	1.35
2	C	801	NAD	C6A-N6A	3.27	1.46	1.34
2	A	801	NAD	C6N-N1N	3.22	1.43	1.35
2	B	801	NAD	C5D-C4D	-3.18	1.41	1.51
2	B	801	NAD	C6A-N6A	3.14	1.45	1.34
2	D	801	NAD	C6A-N6A	2.97	1.44	1.34
2	A	801	NAD	C5D-C4D	-2.91	1.42	1.51
2	A	801	NAD	O2D-C2D	-2.88	1.36	1.43
2	A	801	NAD	C6A-N6A	2.88	1.44	1.34
2	C	801	NAD	C6N-N1N	2.85	1.42	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	801	NAD	C5D-C4D	-2.72	1.43	1.51
2	C	801	NAD	C2D-C3D	-2.57	1.46	1.53
2	B	801	NAD	C2B-C1B	-2.47	1.50	1.53
5	D	802	D3S	C7-S8	2.30	1.80	1.77
2	C	801	NAD	C2B-C1B	-2.27	1.50	1.53
2	D	801	NAD	C5D-C4D	-2.16	1.44	1.51
2	D	801	NAD	C2D-C1D	-2.09	1.50	1.53
2	D	801	NAD	C5B-C4B	-2.05	1.45	1.51
2	B	801	NAD	C2D-C3D	-2.02	1.47	1.53
2	A	801	NAD	C2D-C1D	-2.01	1.50	1.53

All (86) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	802	EPE	O1S-S-C10	-11.67	92.87	106.92
3	A	802	EPE	O1S-S-C10	-11.54	93.01	106.92
3	A	802	EPE	O2S-S-C10	-8.52	96.66	106.92
3	B	802	EPE	O2S-S-C10	-7.60	97.76	106.92
2	C	801	NAD	C2N-N1N-C1D	7.51	135.87	119.14
2	A	801	NAD	C2N-N1N-C1D	6.56	133.74	119.14
3	B	802	EPE	O3S-S-C10	-6.55	95.17	105.77
3	C	802	EPE	O2S-S-C10	-6.43	99.18	106.92
3	A	802	EPE	O3S-S-C10	-6.20	95.74	105.77
2	B	801	NAD	C2N-N1N-C1D	6.13	132.79	119.14
2	D	801	NAD	C2N-N1N-C1D	5.92	132.31	119.14
2	C	801	NAD	C5N-C4N-C3N	-5.53	113.80	120.34
2	A	801	NAD	C5N-C4N-C3N	-5.32	114.05	120.34
2	D	801	NAD	C5N-C4N-C3N	-5.26	114.12	120.34
3	A	802	EPE	C6-N1-C2	4.98	120.04	108.83
2	B	801	NAD	C5N-C4N-C3N	-4.81	114.65	120.34
3	C	802	EPE	C6-N1-C2	4.78	119.58	108.83
5	A	804	D3S	O27-C28-O29	4.66	123.50	117.58
2	B	801	NAD	N3A-C2A-N1A	-4.65	121.41	128.68
3	C	802	EPE	C5-N4-C3	4.63	119.25	108.83
2	C	801	NAD	C6N-N1N-C2N	-4.62	117.76	121.97
2	C	801	NAD	N3A-C2A-N1A	-4.56	121.56	128.68
3	C	802	EPE	O3S-S-O2S	4.49	122.24	111.27
3	A	802	EPE	O3S-S-O1S	4.41	122.06	111.27
3	B	802	EPE	C5-C6-N1	-4.20	102.02	110.64
3	C	802	EPE	O3S-S-C10	-4.19	98.99	105.77
2	A	801	NAD	N3A-C2A-N1A	-4.19	122.13	128.68
2	D	801	NAD	N3A-C2A-N1A	-4.17	122.15	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	802	EPE	C2-C3-N4	3.74	118.32	110.64
3	C	802	EPE	C5-C6-N1	3.73	118.31	110.64
2	A	801	NAD	O4B-C1B-C2B	-3.71	101.51	106.93
2	D	801	NAD	C3N-C2N-N1N	3.60	123.95	120.43
3	B	802	EPE	C6-C5-N4	-3.59	103.28	110.64
5	C	804	D3S	O27-C28-O29	3.45	121.96	117.58
3	A	802	EPE	C3-C2-N1	3.37	117.56	110.64
3	C	802	EPE	C8-C7-N4	-3.32	101.46	113.40
3	C	802	EPE	O3S-S-O1S	-3.25	103.33	111.27
3	C	802	EPE	C3-C2-N1	3.25	117.31	110.64
2	D	801	NAD	PN-O3-PA	-3.15	122.01	132.83
2	D	801	NAD	C3N-C7N-N7N	3.07	121.44	117.75
5	D	802	D3S	O27-C13-C21	3.07	113.64	106.98
5	A	804	D3S	C15-C14-C13	3.03	122.62	120.53
3	B	802	EPE	C3-C2-N1	3.02	116.84	110.64
3	A	802	EPE	C6-C5-N4	-2.98	104.52	110.64
2	D	801	NAD	C6N-N1N-C2N	-2.96	119.27	121.97
2	A	801	NAD	C6N-N1N-C2N	-2.94	119.30	121.97
2	D	801	NAD	C4A-C5A-N7A	-2.91	106.37	109.40
3	B	802	EPE	O3S-S-O1S	2.81	118.14	111.27
2	B	801	NAD	PN-O3-PA	-2.77	123.32	132.83
5	A	804	D3S	O27-C13-C21	2.75	112.94	106.98
2	D	801	NAD	O7N-C7N-N7N	-2.74	118.68	122.58
5	D	802	D3S	C7-S8-C9	2.71	106.25	102.81
3	B	802	EPE	C2-C3-N4	2.69	116.16	110.64
5	D	802	D3S	O27-C28-O29	2.65	120.95	117.58
2	B	801	NAD	C3N-C2N-N1N	2.65	123.02	120.43
3	A	802	EPE	O3S-S-O2S	2.64	117.74	111.27
3	C	802	EPE	C6-C5-N4	2.62	116.01	110.64
5	A	804	D3S	C7-C2-CL1	2.59	124.23	119.69
2	C	801	NAD	PN-O3-PA	-2.57	124.00	132.83
3	B	802	EPE	C6-N1-C2	2.56	114.59	108.83
5	C	804	D3S	C7-S8-C9	2.54	106.04	102.81
3	B	802	EPE	O3S-S-O2S	2.53	117.45	111.27
2	C	801	NAD	C3N-C2N-N1N	2.50	122.88	120.43
5	D	802	D3S	C15-C14-C19	2.48	119.42	117.10
5	C	804	D3S	C7-C2-CL1	2.46	124.01	119.69
2	D	801	NAD	O5D-C5D-C4D	2.44	117.40	108.99
2	A	801	NAD	O5B-C5B-C4B	2.43	117.35	108.99
2	C	801	NAD	O7N-C7N-N7N	-2.43	119.13	122.58
2	A	801	NAD	C3N-C2N-N1N	2.35	122.72	120.43
3	B	802	EPE	O2S-S-O1S	2.30	121.91	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	801	NAD	O4B-C1B-C2B	-2.29	103.58	106.93
2	B	801	NAD	O5D-C5D-C4D	2.25	116.72	108.99
3	C	802	EPE	O2S-S-O1S	2.23	121.68	113.95
2	C	801	NAD	O4B-C1B-C2B	-2.23	103.66	106.93
5	D	802	D3S	C21-C13-C14	2.19	114.02	109.66
2	C	801	NAD	C4A-C5A-N7A	-2.19	107.11	109.40
2	A	801	NAD	O5D-C5D-C4D	2.19	116.54	108.99
2	A	801	NAD	C4A-C5A-N7A	-2.16	107.15	109.40
5	D	802	D3S	C15-C14-C13	2.11	121.99	120.53
2	D	801	NAD	C6N-C5N-C4N	2.11	122.51	119.44
2	A	801	NAD	PN-O3-PA	-2.09	125.67	132.83
2	A	801	NAD	O7N-C7N-N7N	-2.08	119.62	122.58
3	B	802	EPE	C5-N4-C3	2.07	113.49	108.83
2	C	801	NAD	C6N-C5N-C4N	2.03	122.39	119.44
2	B	801	NAD	C6N-N1N-C2N	-2.02	120.13	121.97
2	B	801	NAD	O7N-C7N-N7N	-2.00	119.73	122.58

There are no chirality outliers.

All (39) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	NAD	O4D-C1D-N1N-C2N
2	A	801	NAD	O4D-C1D-N1N-C6N
2	B	801	NAD	O4D-C1D-N1N-C2N
2	B	801	NAD	O4D-C1D-N1N-C6N
2	C	801	NAD	O4D-C1D-N1N-C6N
2	D	801	NAD	O4D-C1D-N1N-C2N
2	D	801	NAD	O4D-C1D-N1N-C6N
3	A	802	EPE	C10-C9-N1-C6
3	A	802	EPE	C9-C10-S-O1S
3	A	802	EPE	C9-C10-S-O3S
3	B	802	EPE	C10-C9-N1-C6
3	B	802	EPE	C9-C10-S-O1S
6	B	804	LAC	OXT-C-CA-OHN
3	B	802	EPE	N4-C7-C8-O8
3	A	802	EPE	N4-C7-C8-O8
3	C	802	EPE	C9-C10-S-O3S
6	B	804	LAC	O-C-CA-CB
6	B	804	LAC	OXT-C-CA-CB
3	B	802	EPE	C9-C10-S-O3S
6	B	804	LAC	O-C-CA-OHN
3	B	802	EPE	C10-C9-N1-C2

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Mol	Chain	Res	Type	Atoms
3	C	802	EPE	C10-C9-N1-C2
3	C	802	EPE	C10-C9-N1-C6
3	C	802	EPE	C8-C7-N4-C5
2	A	801	NAD	C5D-O5D-PN-O3
3	A	802	EPE	C9-C10-S-O2S
3	B	802	EPE	C9-C10-S-O2S
3	C	802	EPE	C9-C10-S-O1S
3	C	802	EPE	C9-C10-S-O2S
5	A	804	D3S	C21-C13-C14-C15
5	D	802	D3S	C21-C13-C14-C15
3	A	802	EPE	C10-C9-N1-C2
5	C	804	D3S	C21-C13-C14-C15
5	A	804	D3S	O27-C13-C14-C15
2	C	801	NAD	O4B-C4B-C5B-O5B
2	A	801	NAD	O4B-C4B-C5B-O5B
2	B	801	NAD	O4B-C4B-C5B-O5B
2	A	801	NAD	C5D-O5D-PN-O1N
2	D	801	NAD	O4B-C4B-C5B-O5B

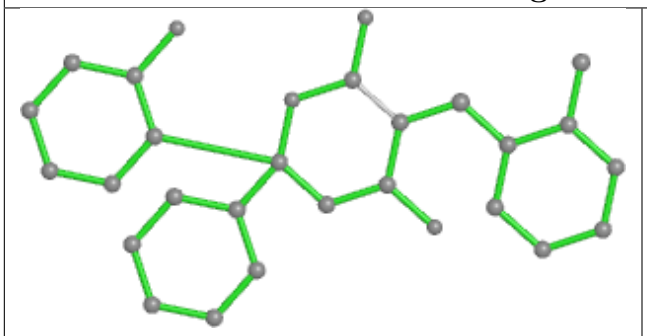
There are no ring outliers.

2 monomers are involved in 2 short contacts:

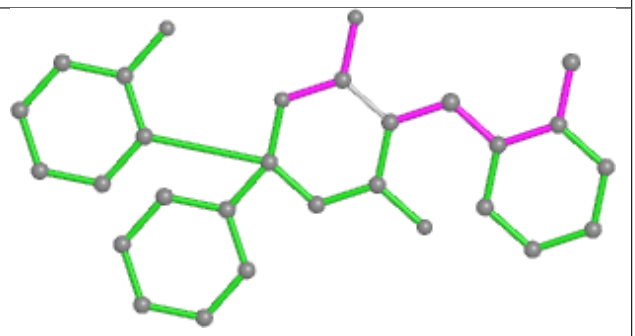
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	801	NAD	1	0
5	A	804	D3S	1	0

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 then 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 D3S C 804



Bond lengths



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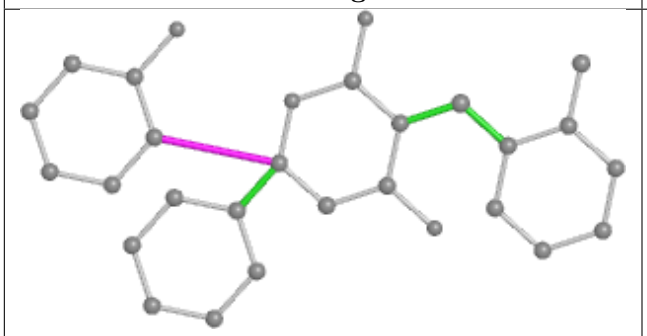
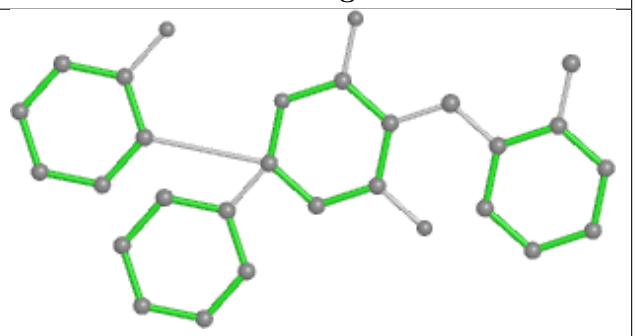
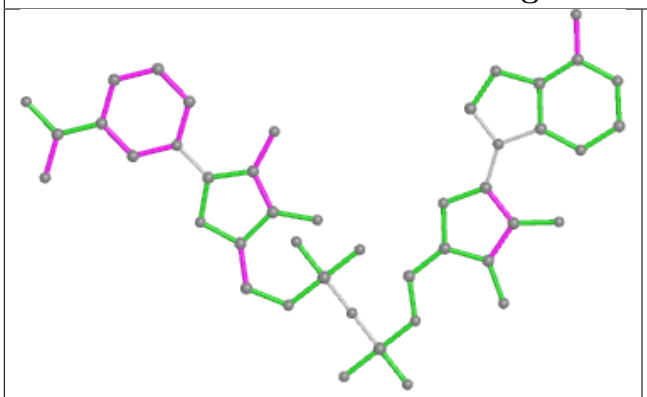


Torsions

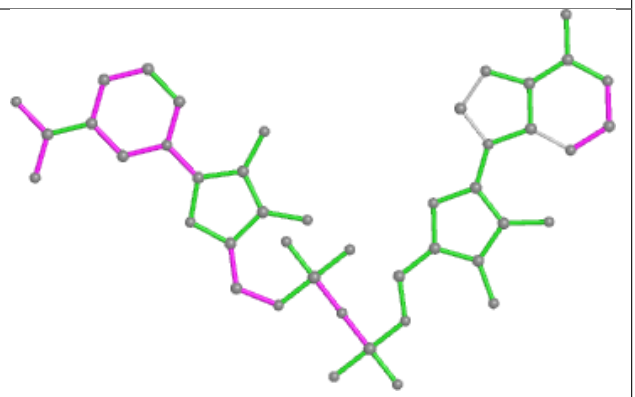


Rings

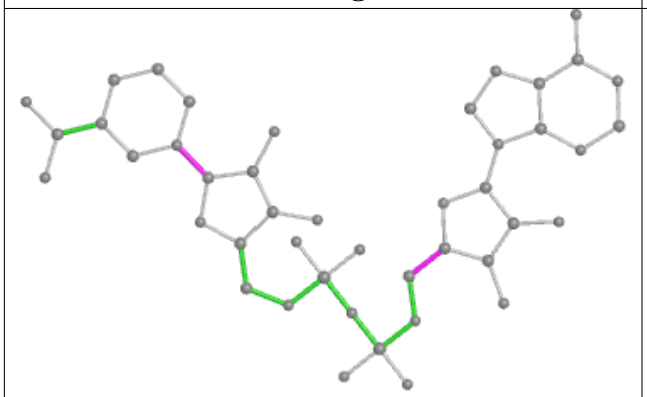
Ligand NAD B 801



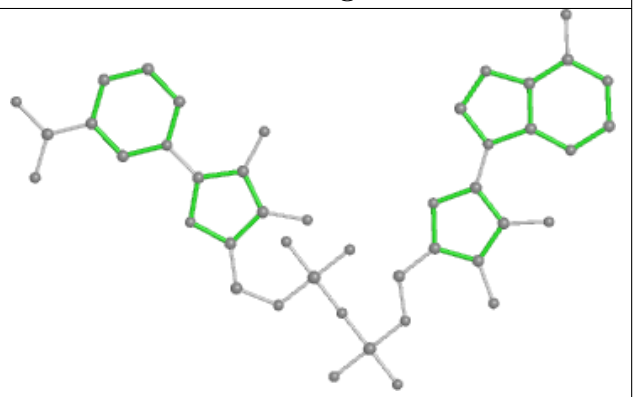
Bond lengths



Bond angles

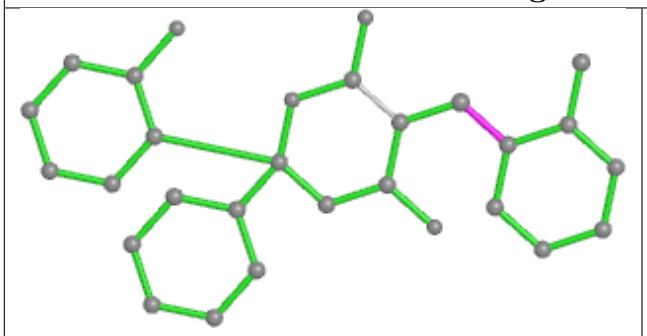


Torsions

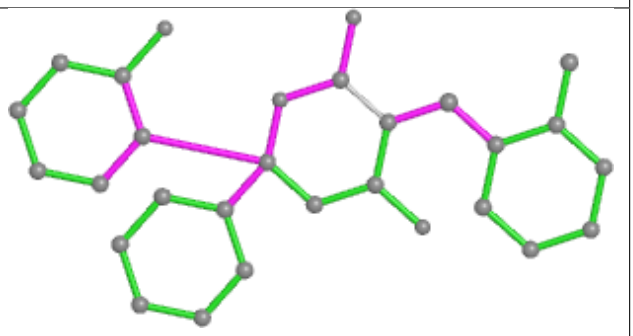


Rings

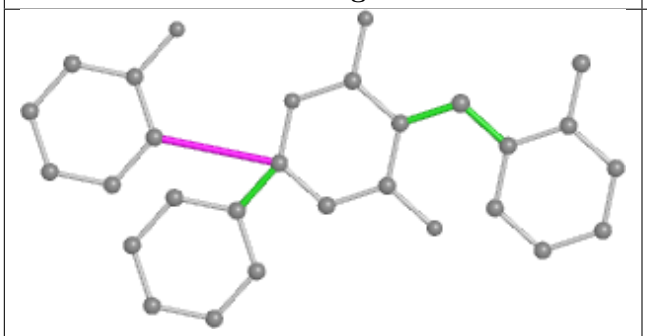
Ligand D3S D 802



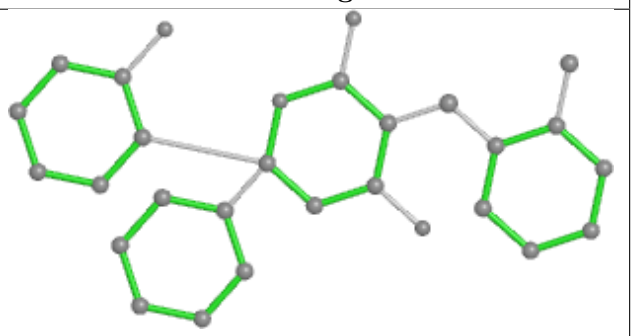
Bond lengths



Bond angles

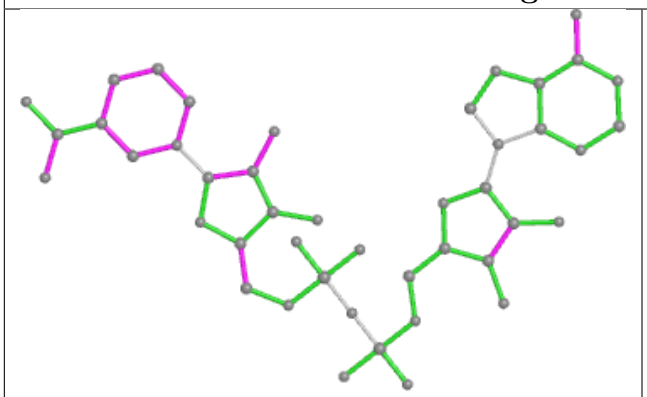


Torsions

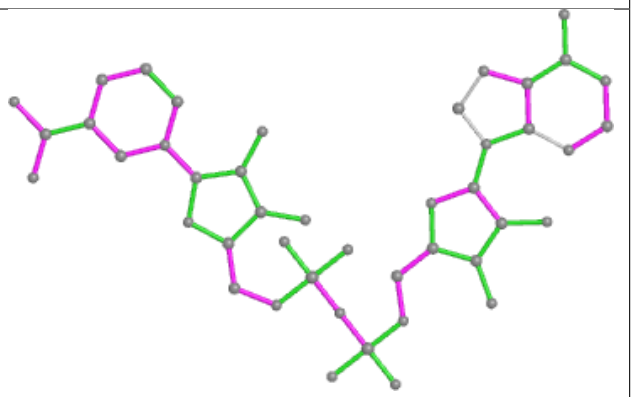


Rings

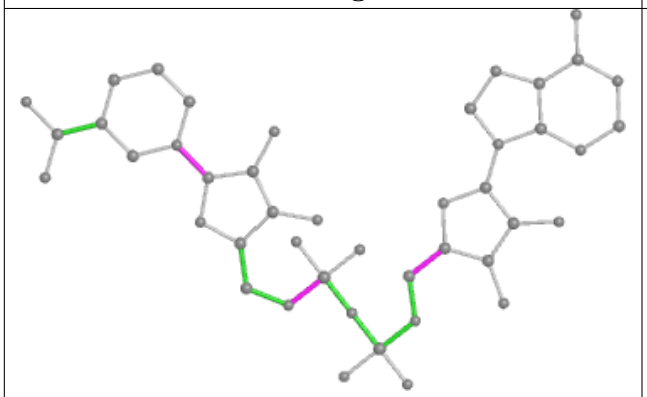
Ligand NAD A 801



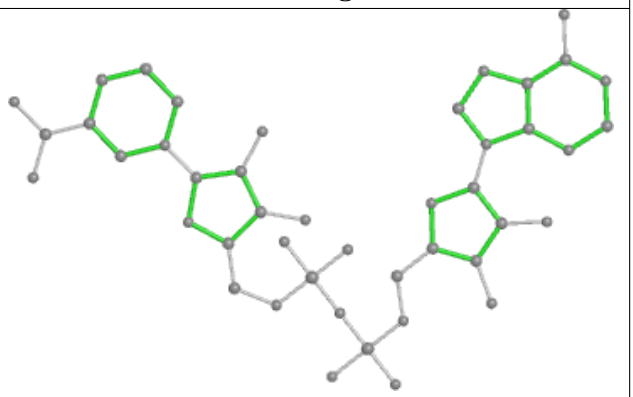
Bond lengths



Bond angles

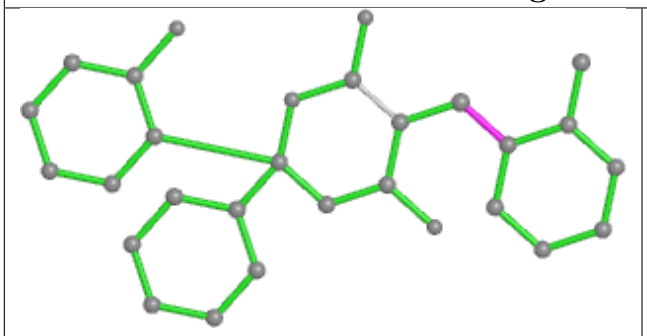


Torsions



Rings

Ligand D3S A 804



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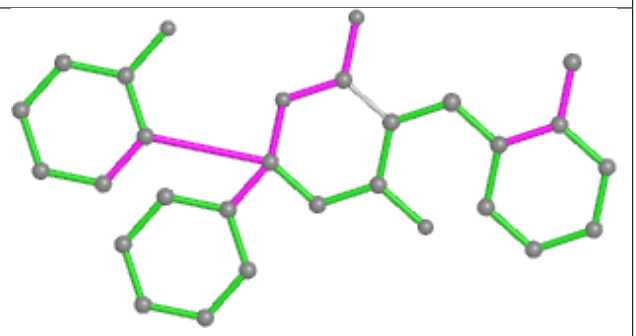
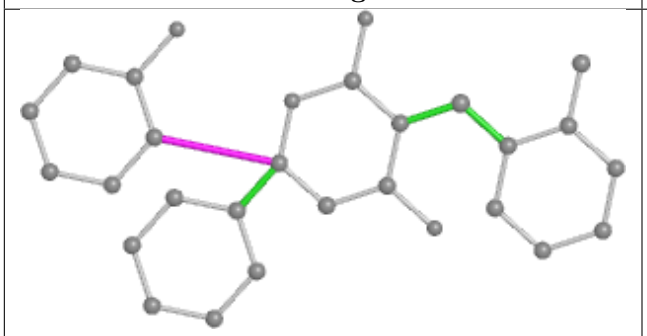
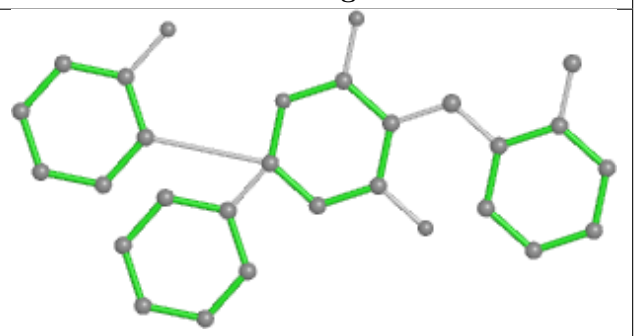


Bond angles

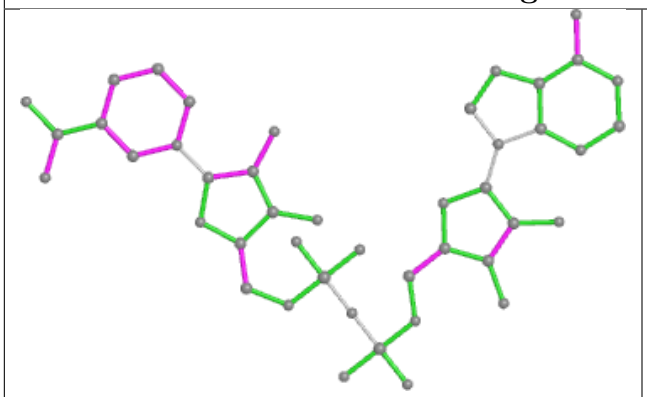


Torsions

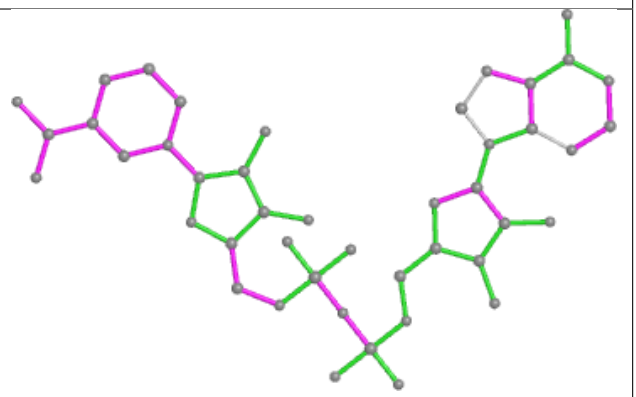


Rings

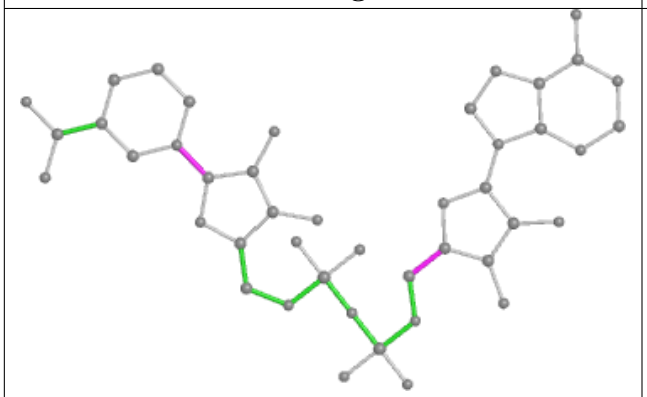
Ligand NAD D 801



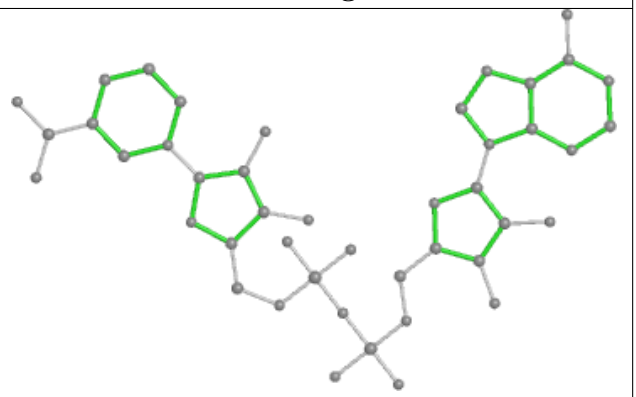
Bond lengths



Bond angles

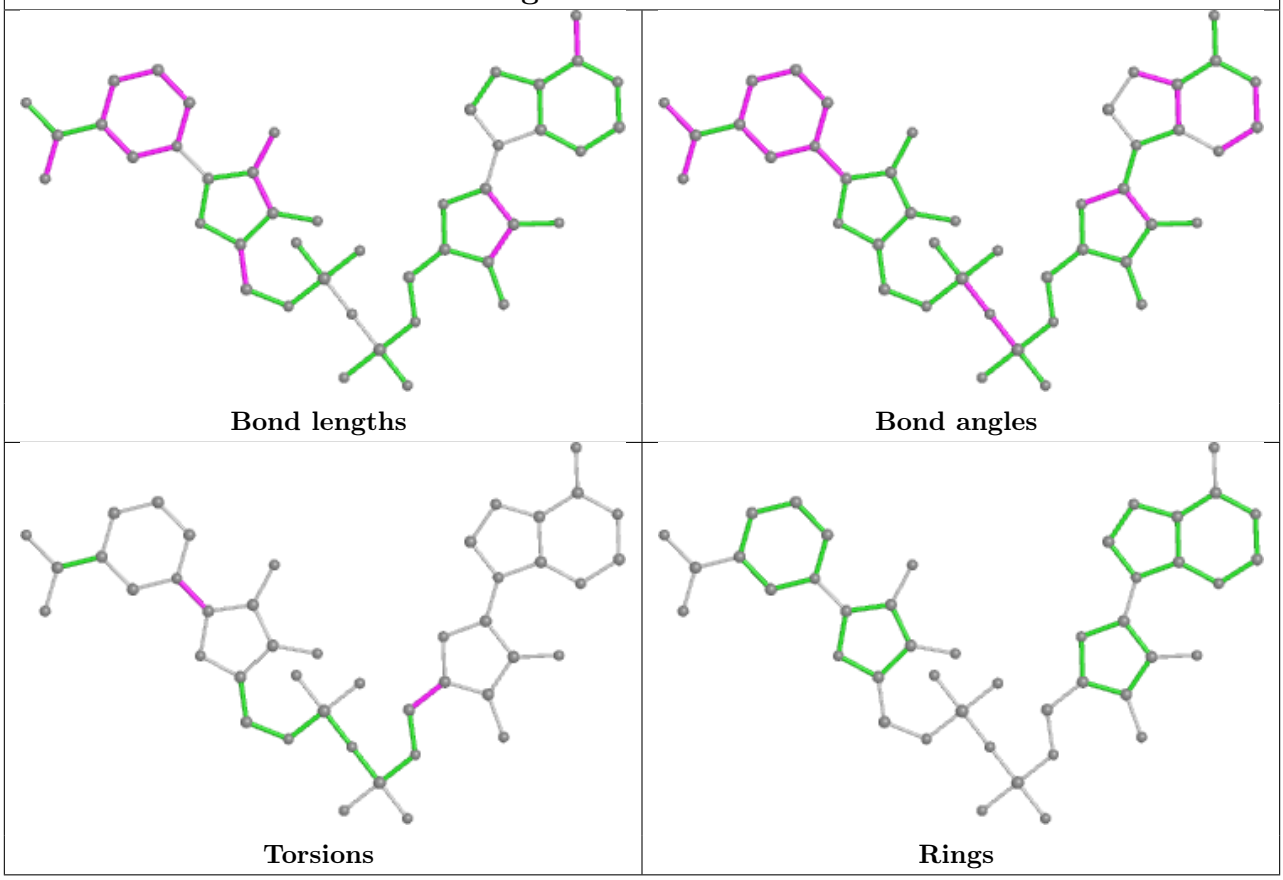


Torsions



Rings

Ligand NAD C 801



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	323/331 (97%)	-0.27	1 (0%)	94	96	21, 32, 63, 109	0
1	B	324/331 (97%)	-0.17	7 (2%)	62	70	22, 32, 68, 120	0
1	C	325/331 (98%)	-0.02	10 (3%)	49	58	20, 34, 72, 129	0
1	D	327/331 (98%)	-0.26	3 (0%)	84	89	19, 28, 65, 116	1 (0%)
All	All	1299/1324 (98%)	-0.18	21 (1%)	72	79	19, 32, 69, 129	1 (0%)

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	1	ALA	4.4
1	C	1	ALA	4.0
1	C	107	ASN	4.0
1	B	330	GLN	3.8
1	C	104	SER	3.5
1	C	14	GLU	3.4
1	C	330	GLN	3.4
1	B	331	PHE	3.4
1	B	107	ASN	3.2
1	C	106	LEU	3.2
1	B	324	GLY	3.1
1	B	106	LEU	3.1
1	C	331	PHE	3.1
1	C	323	TRP	3.0
1	C	13	LYS	2.9
1	D	97	ALA	2.5
1	C	105	ARG	2.5
1	D	15	GLU	2.4
1	B	72[A]	ARG	2.3
1	B	108	LEU	2.1
1	A	107	ASN	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 monosaccharides in this entry.

6.4 Ligands (i)

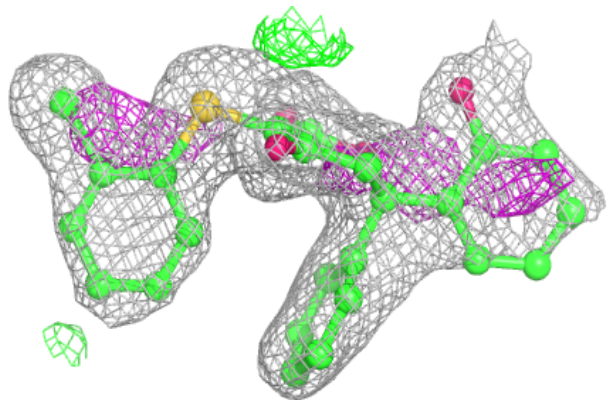
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

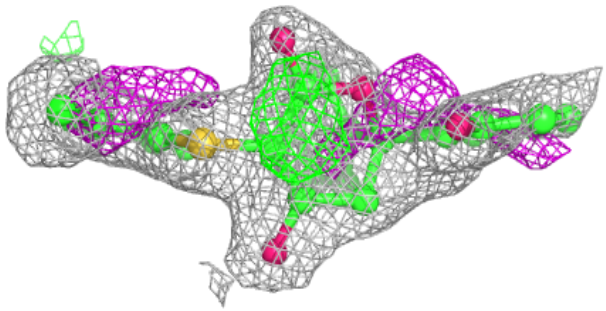
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	EPE	C	802	15/15	0.85	0.20	50,76,142,145	0
5	D3S	C	804	29/29	0.89	0.21	34,48,62,72	0
5	D3S	A	804	29/29	0.90	0.25	35,50,63,64	0
3	EPE	A	802	15/15	0.91	0.17	41,57,81,83	15
3	EPE	B	802	15/15	0.92	0.19	49,87,143,151	0
5	D3S	D	802	29/29	0.94	0.14	31,38,51,57	0
2	NAD	C	801	44/44	0.95	0.09	25,39,49,55	44
4	SO4	C	803	5/5	0.96	0.09	25,35,43,55	0
4	SO4	B	803	5/5	0.96	0.09	33,41,64,68	0
6	LAC	B	804	6/6	0.96	0.09	34,50,52,57	0
2	NAD	B	801	44/44	0.97	0.07	24,32,37,39	0
2	NAD	A	801	44/44	0.97	0.07	21,33,40,49	0
2	NAD	D	801	44/44	0.97	0.07	20,29,34,38	0
4	SO4	A	803	5/5	0.98	0.08	34,36,49,57	0
4	SO4	D	803	5/5	0.98	0.06	25,36,41,48	0

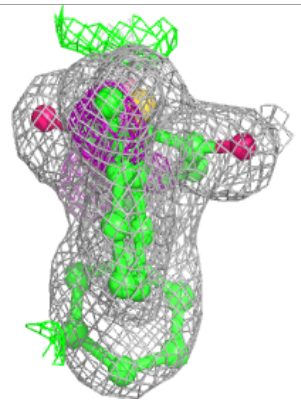
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around D3S C 804:

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

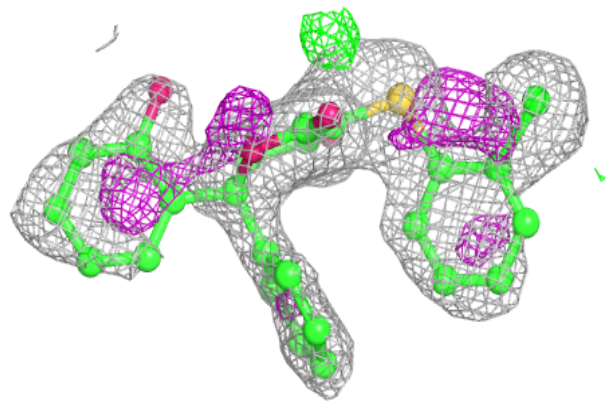


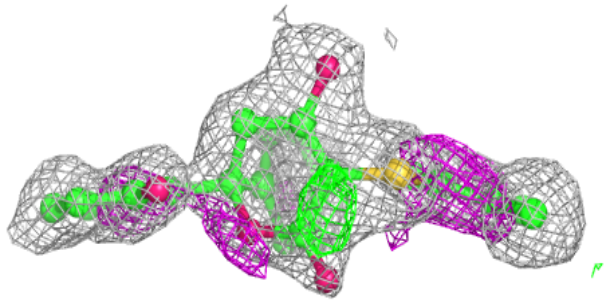


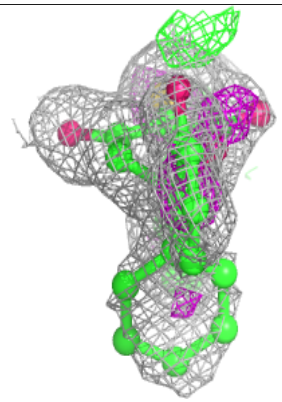


Electron density around D3S A 804:

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

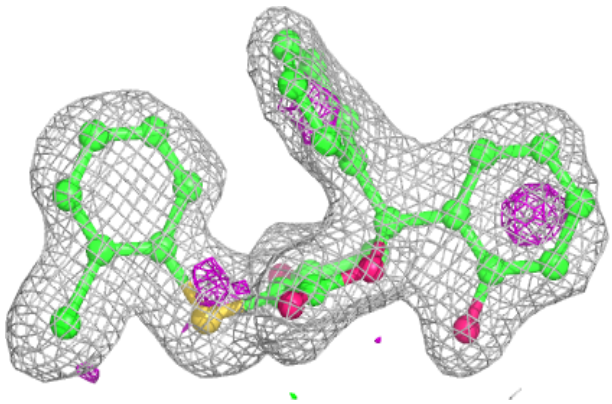


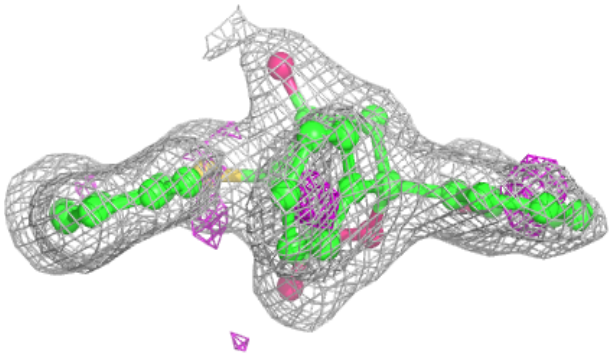


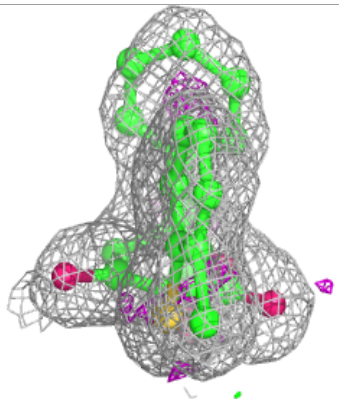


Electron density around D3S D 802:

$2mF_o$-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 801:

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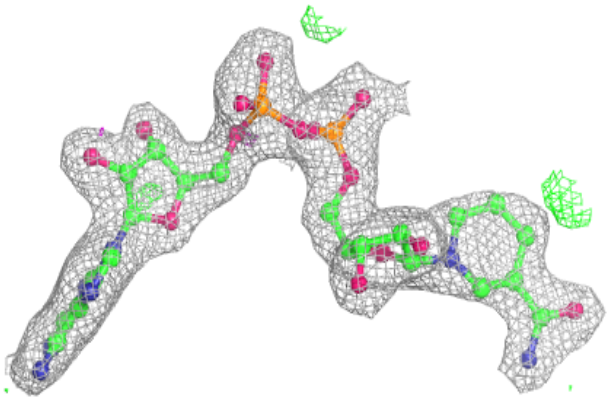
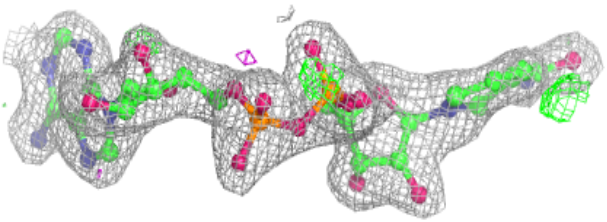
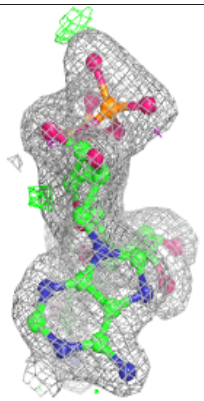
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

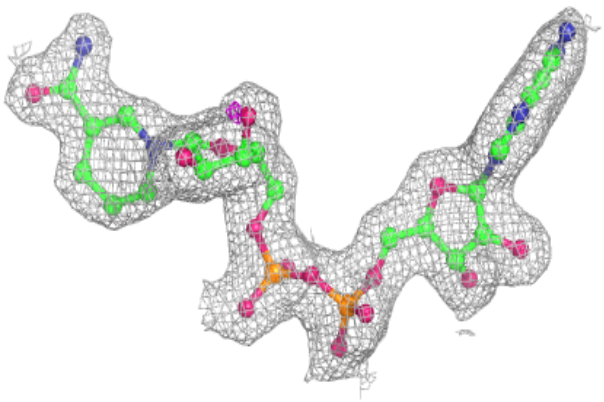


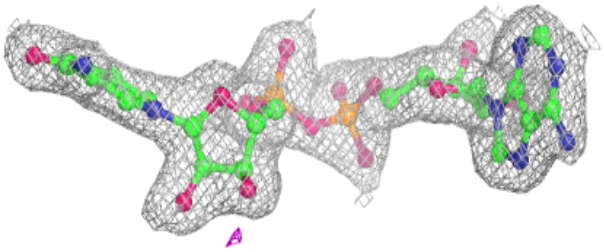


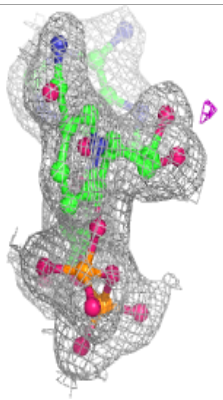


Electron density around NAD B 801:

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

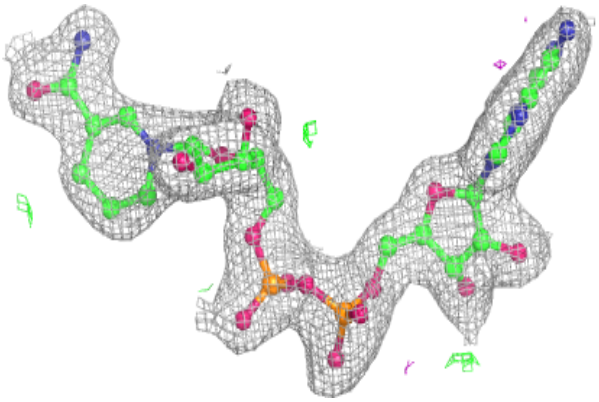


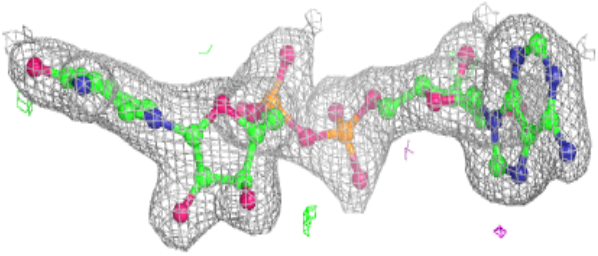


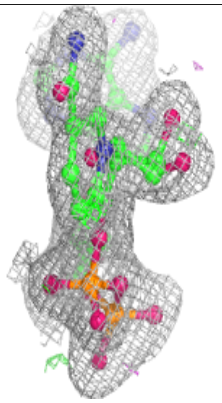


Electron density around NAD A 801:

$2mF_o$-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 D 801:

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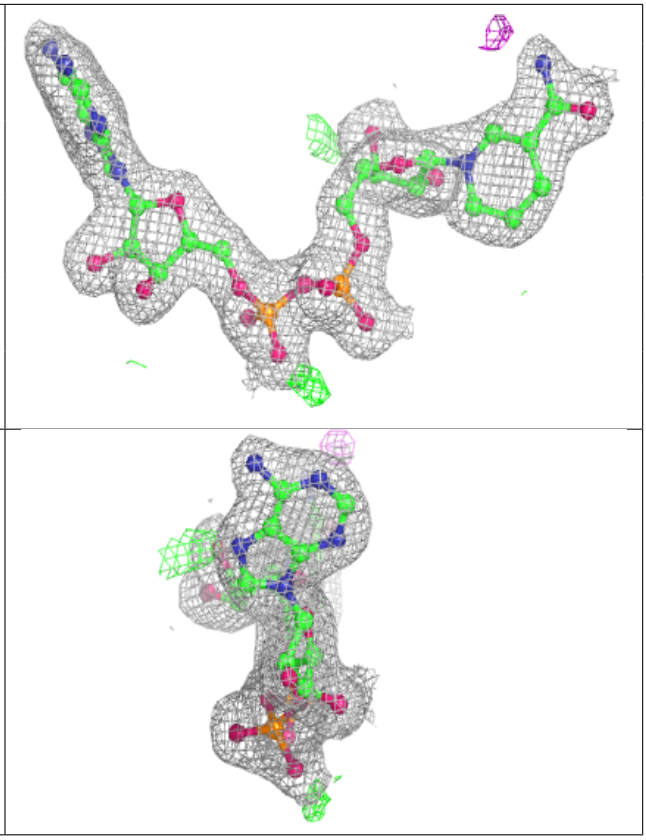
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.