Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 07:34 am BST

PDB ID	:	1TOX
Title	:	DIPHTHERIA TOXIN DIMER COMPLEXED WITH NAD
Authors	:	Bell, C.E.; Eisenberg, D.
Deposited on	:	1995-10-06
Resolution	:	2.30 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 following versions of software and data (see references ⓘ) were used in the production of this report:

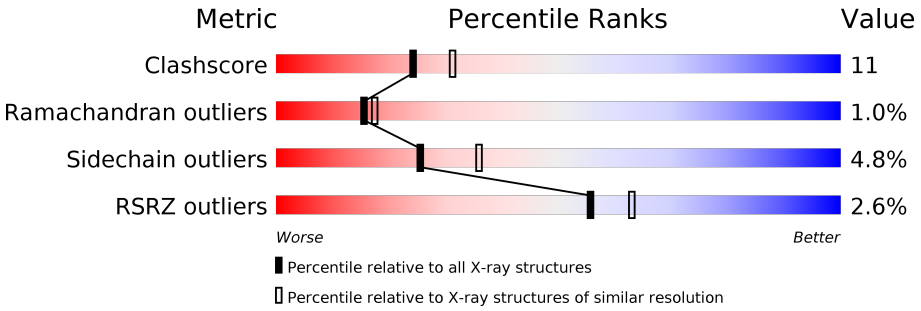
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 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))
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (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 on 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	535	2% 71% 24%
1	B	535	3% 71% 23%

2 Entry composition

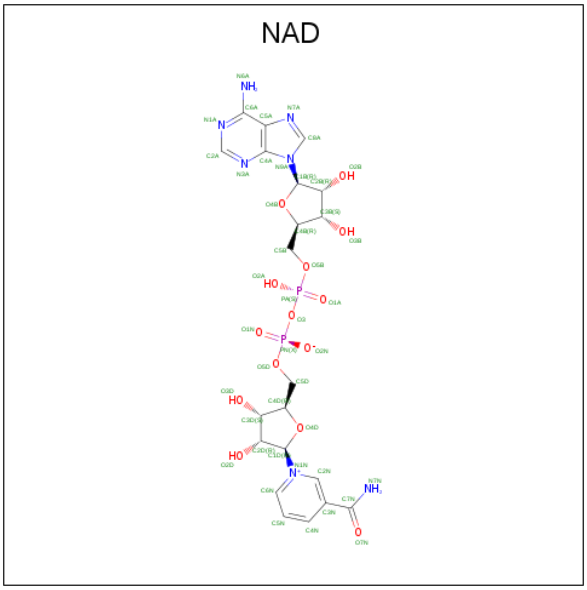
There are 3 unique types of molecules in this entry. The entry contains 8295 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 DIPHTHERIA TOXIN (DIMERIC).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	515	Total	C	N	O	S	0	0	0
			3960	2496	672	780	12			
1	B	513	Total	C	N	O	S	0	0	0
			3945	2487	670	776	12			

- 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
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 3 is water.

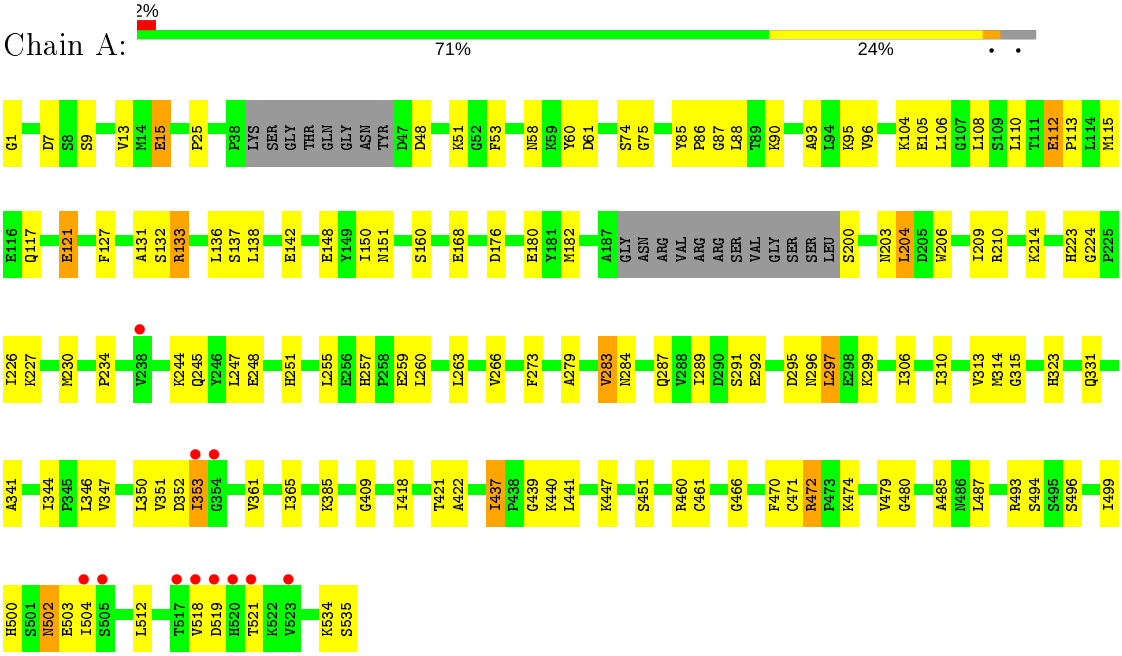
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	150	Total O 150 150	0	0
3	B	152	Total O 152 152	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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.

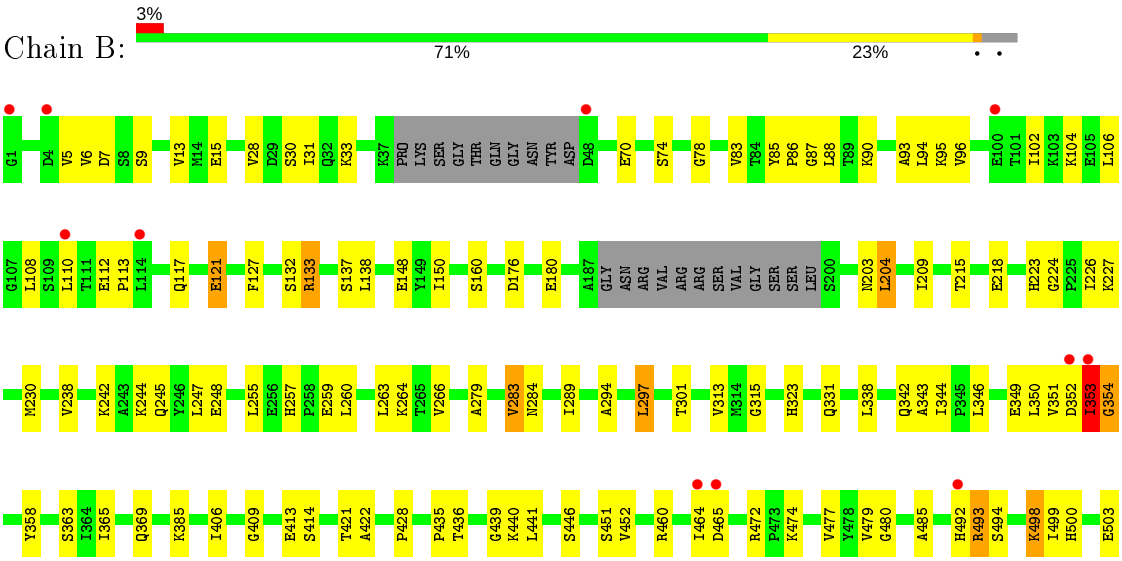
- Molecule 1: DIPHTHERIA TOXIN (DIMERIC)

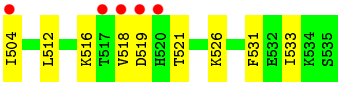
Chain A:



- Molecule 1: DIPHTHERIA TOXIN (DIMERIC)

Chain B:




I504
L512
K516
T517
V518
D519
H520
T521
K526
F531
E532
I533
K534
S535

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	105.00Å 89.50Å 130.10Å 90.00° 94.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.30 68.04 – 2.31	Depositor EDS
% Data completeness (in resolution range)	92.6 (10.00-2.30) 93.2 (68.04-2.31)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.15 (at 2.32Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.227 , 0.307 0.211 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	27.6	Xtriage
Anisotropy	0.127	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 59.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.54$, $< L^2 > = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	8295	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 49.44 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.4607e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAD

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	0/4039	0.76	4/5471 (0.1%)
1	B	0.59	0/4023	0.76	2/5448 (0.0%)
All	All	0.60	0/8062	0.76	6/10919 (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	B	0	1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	472	ARG	NE-CZ-NH2	-5.79	117.40	120.30
1	A	437	ILE	N-CA-C	-5.60	95.87	111.00
1	A	472	ARG	NE-CZ-NH1	5.51	123.06	120.30
1	A	466	GLY	N-CA-C	5.44	126.69	113.10
1	B	472	ARG	NE-CZ-NH2	-5.43	117.58	120.30
1	B	493	ARG	NE-CZ-NH2	-5.34	117.63	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	358	TYR	Sidechain

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	3960	0	3896	89	0
1	B	3945	0	3885	85	0
2	A	44	0	26	1	0
2	B	44	0	26	1	0
3	A	150	0	0	2	0
3	B	152	0	0	3	0
All	All	8295	0	7833	174	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 11.

All (174) 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:B:460:ARG:HG3	1:B:474:LYS:HE2	1.38	1.02
1:A:500:HIS:H	1:A:503:GLU:HG3	1.32	0.93
1:A:214:LYS:HE2	3:A:685:HOH:O	1.73	0.87
1:B:409:GLY:HA2	1:B:498:LYS:HE2	1.59	0.85
1:A:74:SER:HB2	1:A:297:LEU:HD13	1.60	0.84
1:B:279:ALA:O	1:B:283:VAL:HG13	1.86	0.76
1:A:279:ALA:O	1:A:283:VAL:HG13	1.85	0.75
1:A:460:ARG:HB3	1:A:474:LYS:HE2	1.69	0.74
1:A:112:GLU:HG2	1:A:117:GLN:HG3	1.70	0.73
1:B:104:LYS:HA	1:B:110:LEU:HD11	1.68	0.73
1:A:112:GLU:HG2	1:A:117:GLN:CG	2.20	0.71
1:B:257:HIS:CE1	1:B:259:GLU:HG3	2.25	0.70
1:A:296:ASN:HB3	1:A:299:LYS:HB2	1.74	0.68
1:B:263:LEU:H	1:B:331:GLN:HE22	1.41	0.68
1:A:226:ILE:HG22	1:A:230:MET:HE2	1.75	0.68
1:A:283:VAL:O	1:A:287:GLN:HG3	1.93	0.68
1:B:226:ILE:HG22	1:B:230:MET:HE3	1.76	0.68
1:B:344:ILE:HB	1:B:352:ASP:HB3	1.76	0.68
1:A:289:ILE:O	1:A:350:LEU:HD22	1.94	0.67
1:A:176:ASP:O	1:A:180:GLU:HG3	1.95	0.66
1:A:439:GLY:O	1:A:494:SER:HB2	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:13:VAL:HG12	1:B:88:LEU:HD12	1.77	0.65
1:B:498:LYS:HE3	1:B:498:LYS:H	1.61	0.65
1:B:349:GLU:O	1:B:349:GLU:HG2	1.96	0.65
1:A:58:ASN:HB3	1:A:61:ASP:HB2	1.77	0.65
1:A:93:ALA:HA	1:A:137:SER:HB3	1.80	0.62
1:A:344:ILE:HB	1:A:352:ASP:HB3	1.81	0.61
1:A:226:ILE:O	1:A:230:MET:HG3	2.00	0.61
1:B:5:VAL:HG23	1:B:6:VAL:HG23	1.83	0.61
1:A:283:VAL:HB	1:A:347:VAL:HG21	1.81	0.60
1:B:226:ILE:HG22	1:B:230:MET:CE	2.31	0.59
1:A:223:HIS:HD2	1:A:226:ILE:HG13	1.68	0.59
1:A:263:LEU:H	1:A:331:GLN:HE22	1.51	0.59
1:B:414:SER:CB	1:B:493:ARG:HH22	2.16	0.59
1:A:247:LEU:HD12	1:A:283:VAL:HG12	1.86	0.58
1:A:257:HIS:CE1	1:A:259:GLU:HG3	2.39	0.58
1:A:460:ARG:NH1	1:A:474:LYS:HA	2.17	0.58
1:A:226:ILE:HG22	1:A:230:MET:CE	2.34	0.57
1:B:148:GLU:OE2	2:B:536:NAD:H6N	2.05	0.57
1:B:83:VAL:HA	1:B:160:SER:O	2.04	0.57
1:B:516:LYS:HA	3:B:623:HOH:O	2.05	0.56
1:B:365:ILE:O	1:B:369:GLN:HG3	2.06	0.55
1:B:226:ILE:O	1:B:230:MET:HG3	2.06	0.55
1:A:260:LEU:HA	1:A:331:GLN:NE2	2.22	0.54
1:A:350:LEU:H	1:A:350:LEU:HD23	1.72	0.54
1:A:244:LYS:HB3	1:A:244:LYS:NZ	2.22	0.54
1:A:247:LEU:CD1	1:A:283:VAL:HG12	2.38	0.53
1:B:435:PRO:HB2	1:B:504:ILE:HD11	1.90	0.53
1:A:441:LEU:CD2	1:A:504:ILE:HD11	2.39	0.53
1:A:1:GLY:O	1:A:105:GLU:HB3	2.09	0.53
1:A:315:GLY:HA3	1:A:323:HIS:CD2	2.44	0.52
1:B:112:GLU:HB2	1:B:117:GLN:NE2	2.23	0.52
1:A:148:GLU:OE1	2:A:536:NAD:H6N	2.09	0.52
1:A:223:HIS:O	1:A:227:LYS:HG3	2.09	0.52
1:B:460:ARG:HG3	1:B:474:LYS:CE	2.27	0.52
1:A:234:PRO:HD2	1:A:346:LEU:HD21	1.92	0.52
1:A:409:GLY:HA2	1:A:496:SER:O	2.10	0.52
1:B:132:SER:HB2	1:B:133:ARG:CZ	2.40	0.52
1:B:247:LEU:HD12	1:B:283:VAL:HG12	1.92	0.51
1:A:121:GLU:H	1:A:121:GLU:CD	2.12	0.51
1:B:257:HIS:HE1	1:B:259:GLU:HG3	1.72	0.51
1:A:112:GLU:HG3	1:A:113:PRO:N	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:86:PRO:O	1:B:133:ARG:NH2	2.43	0.51
1:B:138:LEU:HD12	1:B:150:ILE:HD11	1.92	0.51
1:B:204:LEU:HG	1:B:209:ILE:HD11	1.93	0.51
1:B:422:ALA:HB3	1:B:480:GLY:HA2	1.93	0.51
1:A:53:PHE:HB3	1:A:151:ASN:HB2	1.92	0.51
1:A:499:ILE:HG23	1:A:503:GLU:HB2	1.93	0.51
1:A:461:CYS:HA	1:A:471:CYS:HA	1.92	0.50
1:A:132:SER:HB2	1:A:133:ARG:NH2	2.26	0.50
1:A:104:LYS:HA	1:A:110:LEU:HD11	1.93	0.50
1:A:422:ALA:HB3	1:A:480:GLY:HA2	1.93	0.50
1:A:86:PRO:O	1:A:133:ARG:NH2	2.43	0.50
1:B:132:SER:HB2	1:B:133:ARG:NH2	2.27	0.49
1:A:133:ARG:HD3	3:A:572:HOH:O	2.12	0.49
1:A:13:VAL:HG13	1:A:131:ALA:HB2	1.94	0.49
1:A:85:TYR:CE1	1:A:133:ARG:HD2	2.47	0.49
1:B:176:ASP:O	1:B:180:GLU:HG3	2.12	0.49
1:B:498:LYS:HE3	1:B:498:LYS:N	2.26	0.49
1:B:260:LEU:HA	1:B:331:GLN:NE2	2.26	0.49
1:A:112:GLU:HG3	1:A:113:PRO:HD2	1.95	0.49
1:A:90:LYS:HG2	1:A:127:PHE:O	2.11	0.49
1:B:436:THR:HG23	1:B:441:LEU:O	2.13	0.49
1:B:247:LEU:HD11	1:B:343:ALA:HB2	1.95	0.48
1:B:5:VAL:HG11	1:B:102:ILE:HA	1.95	0.48
1:A:15:GLU:HA	1:A:87:GLY:O	2.14	0.48
1:A:273:PHE:CD1	1:A:273:PHE:N	2.80	0.48
1:B:74:SER:HB2	1:B:297:LEU:HD13	1.94	0.48
1:B:30:SER:HA	1:B:33:LYS:HE3	1.95	0.48
1:B:518:VAL:HG22	1:B:519:ASP:H	1.79	0.48
1:B:351:VAL:HG13	1:B:351:VAL:O	2.13	0.48
1:A:263:LEU:HA	1:A:266:VAL:HG22	1.95	0.48
1:B:352:ASP:OD2	1:B:353:ILE:HG13	2.13	0.48
1:B:7:ASP:HB2	1:B:95:LYS:HG2	1.95	0.48
1:A:112:GLU:HG3	1:A:113:PRO:CD	2.43	0.47
1:B:441:LEU:HB2	1:B:499:ILE:HD11	1.95	0.47
1:B:215:THR:O	1:B:218:GLU:HB3	2.15	0.47
1:B:344:ILE:HD13	1:B:352:ASP:HA	1.96	0.47
1:B:439:GLY:O	1:B:494:SER:HB2	2.15	0.46
1:B:113:PRO:O	1:B:117:GLN:HG3	2.16	0.46
1:B:121:GLU:H	1:B:121:GLU:CD	2.19	0.46
1:B:263:LEU:H	1:B:331:GLN:NE2	2.10	0.46
1:B:289:ILE:CG2	1:B:294:ALA:HB2	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:518:VAL:HG22	1:A:519:ASP:H	1.81	0.46
1:B:238:VAL:HG12	1:B:346:LEU:HB3	1.98	0.46
1:B:106:LEU:HB2	1:B:108:LEU:HG	1.98	0.46
1:B:413:GLU:OE2	1:B:492:HIS:CD2	2.68	0.45
1:A:418:ILE:HB	1:A:487:LEU:HB3	1.97	0.45
1:A:470:PHE:HE2	1:A:472:ARG:CZ	2.29	0.45
1:A:85:TYR:CD1	1:A:133:ARG:HD2	2.51	0.45
1:B:30:SER:O	1:B:33:LYS:HB2	2.16	0.45
1:A:112:GLU:HG2	1:A:117:GLN:HG2	1.96	0.45
1:A:341:ALA:HA	1:A:352:ASP:HB2	1.98	0.45
1:B:15:GLU:HA	1:B:87:GLY:O	2.16	0.45
1:B:255:LEU:O	1:B:264:LYS:HD3	2.17	0.45
1:B:257:HIS:CE1	1:B:259:GLU:CG	2.96	0.44
1:B:223:HIS:HD2	1:B:226:ILE:HG13	1.80	0.44
1:B:452:VAL:CG2	1:B:477:VAL:HG13	2.48	0.44
1:A:112:GLU:O	1:A:117:GLN:NE2	2.50	0.44
1:B:93:ALA:HA	1:B:137:SER:HB3	1.99	0.44
1:B:85:TYR:CE1	1:B:133:ARG:HD2	2.53	0.44
1:A:7:ASP:HB2	1:A:95:LYS:HG2	1.99	0.44
1:A:451:SER:O	1:A:485:ALA:HA	2.18	0.44
1:B:301:THR:HA	1:B:363:SER:OG	2.18	0.44
1:B:435:PRO:HG3	1:B:531:PHE:CE2	2.53	0.43
1:B:406:ILE:O	1:B:533:ILE:HA	2.19	0.43
1:B:451:SER:O	1:B:485:ALA:HA	2.17	0.43
1:A:292:GLU:O	1:A:299:LYS:HE3	2.19	0.43
1:A:441:LEU:HD22	1:A:504:ILE:HD11	1.99	0.43
1:B:138:LEU:HD12	1:B:150:ILE:CD1	2.47	0.43
1:A:138:LEU:HD12	1:A:150:ILE:HD11	2.01	0.43
1:B:440:LYS:O	1:B:493:ARG:HG2	2.18	0.43
1:A:74:SER:CB	1:A:297:LEU:HD13	2.41	0.43
1:B:526:LYS:NZ	3:B:688:HOH:O	2.36	0.43
1:A:257:HIS:CE1	1:A:259:GLU:CG	3.02	0.43
1:B:500:HIS:O	1:B:503:GLU:HB3	2.19	0.43
1:A:534:LYS:O	1:A:535:SER:HB2	2.20	0.42
1:B:242:LYS:O	1:B:242:LYS:HD3	2.19	0.42
1:A:244:LYS:O	1:A:248:GLU:HG3	2.19	0.42
1:B:247:LEU:CD1	1:B:283:VAL:HG12	2.49	0.42
1:A:115:MET:SD	1:A:136:LEU:HD12	2.60	0.42
1:A:306:ILE:HG21	1:A:306:ILE:HD13	1.86	0.42
1:A:351:VAL:HB	1:A:353:ILE:HG13	2.01	0.42
1:A:204:LEU:HG	1:A:209:ILE:HD11	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:519:ASP:C	1:B:521:THR:H	2.23	0.42
1:A:25:PRO:HB3	1:A:168:GLU:OE1	2.19	0.41
1:A:48:ASP:HA	1:A:51:LYS:HG2	2.00	0.41
1:A:519:ASP:C	1:A:521:THR:H	2.23	0.41
1:B:421:THR:HA	1:B:479:VAL:HB	2.02	0.41
1:A:500:HIS:N	1:A:503:GLU:HG3	2.14	0.41
1:B:315:GLY:HA3	1:B:323:HIS:CD2	2.55	0.41
1:B:428:PRO:HA	1:B:477:VAL:O	2.20	0.41
1:B:90:LYS:HG2	1:B:127:PHE:O	2.20	0.41
1:A:361:VAL:O	1:A:365:ILE:HG13	2.20	0.41
1:A:437:ILE:HD13	1:A:503:GLU:HB3	2.02	0.41
1:B:223:HIS:O	1:B:227:LYS:HG3	2.19	0.41
1:A:206:TRP:O	1:A:210:ARG:HG3	2.21	0.41
1:B:28:VAL:HG23	3:B:559:HOH:O	2.21	0.41
1:A:108:LEU:O	1:A:110:LEU:HD12	2.21	0.41
1:A:132:SER:HB2	1:A:133:ARG:CZ	2.51	0.41
1:A:421:THR:HA	1:A:479:VAL:HB	2.03	0.41
1:B:352:ASP:O	1:B:354:GLY:N	2.54	0.41
1:A:251:HIS:CE1	1:A:255:LEU:HD22	2.55	0.41
1:A:310:ILE:HD13	1:A:314:MET:HE3	2.03	0.41
1:A:60:TYR:CD1	1:A:182:MET:HA	2.56	0.40
1:B:94:LEU:HD13	1:B:102:ILE:HD13	2.02	0.40
1:B:28:VAL:O	1:B:31:ILE:HG22	2.21	0.40
1:A:440:LYS:NZ	1:A:503:GLU:OE2	2.48	0.40
1:B:452:VAL:HG21	1:B:477:VAL:HG13	2.03	0.40
1:A:106:LEU:HB2	1:A:108:LEU:HG	2.03	0.40
1:A:437:ILE:CD1	1:A:503:GLU:HB3	2.52	0.40
1:B:244:LYS:O	1:B:248:GLU:HG3	2.21	0.40
1:B:263:LEU:HA	1:B:266:VAL:HG22	2.04	0.40
1:B:338:LEU:O	1:B:342:GLN:HG2	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	509/535 (95%)	482 (95%)	23 (4%)	4 (1%)	19 23
1	B	507/535 (95%)	486 (96%)	15 (3%)	6 (1%)	13 14
All	All	1016/1070 (95%)	968 (95%)	38 (4%)	10 (1%)	15 17

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	353	ILE
1	A	502	ASN
1	A	224	GLY
1	B	350	LEU
1	B	224	GLY
1	B	465	ASP
1	B	354	GLY
1	B	78	GLY
1	A	75	GLY
1	B	353	ILE

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	436/452 (96%)	412 (94%)	24 (6%)	21 30
1	B	434/452 (96%)	416 (96%)	18 (4%)	30 43
All	All	870/904 (96%)	828 (95%)	42 (5%)	25 36

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	SER
1	A	15	GLU
1	A	88	LEU

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Mol	Chain	Res	Type
1	A	96	VAL
1	A	112	GLU
1	A	121	GLU
1	A	133	ARG
1	A	142	GLU
1	A	160	SER
1	A	200	SER
1	A	203	ASN
1	A	204	LEU
1	A	245	GLN
1	A	283	VAL
1	A	284	ASN
1	A	291	SER
1	A	295	ASP
1	A	297	LEU
1	A	313	VAL
1	A	385	LYS
1	A	447	LYS
1	A	493	ARG
1	A	502	ASN
1	A	512	LEU
1	B	9	SER
1	B	70	GLU
1	B	96	VAL
1	B	121	GLU
1	B	133	ARG
1	B	203	ASN
1	B	204	LEU
1	B	245	GLN
1	B	283	VAL
1	B	284	ASN
1	B	297	LEU
1	B	313	VAL
1	B	353	ILE
1	B	385	LYS
1	B	446	SER
1	B	464	ILE
1	B	498	LYS
1	B	512	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	203	ASN
1	A	223	HIS
1	A	228	ASN
1	A	284	ASN
1	A	331	GLN
1	A	369	GLN
1	A	387	GLN
1	A	524	ASN
1	B	36	GLN
1	B	184	GLN
1	B	203	ASN
1	B	223	HIS
1	B	228	ASN
1	B	277	ASN
1	B	284	ASN
1	B	331	GLN
1	B	369	GLN
1	B	387	GLN
1	B	492	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAD	B	536	-	42,48,48	1.21	3 (7%)	50,73,73	1.73	14 (28%)
2	NAD	A	536	-	42,48,48	1.39	4 (9%)	50,73,73	1.75	15 (30%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAD	B	536	-	-	11/26/62/62	0/5/5/5
2	NAD	A	536	-	-	3/26/62/62	0/5/5/5

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	536	NAD	C2N-N1N	4.99	1.41	1.35
2	B	536	NAD	C2N-N1N	4.55	1.40	1.35
2	A	536	NAD	C6N-N1N	3.35	1.43	1.35
2	A	536	NAD	C2D-C1D	-2.68	1.49	1.53
2	B	536	NAD	C6N-N1N	2.62	1.41	1.35
2	B	536	NAD	O4D-C1D	2.05	1.43	1.41
2	A	536	NAD	O4D-C1D	2.03	1.43	1.41

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	536	NAD	N3A-C2A-N1A	-4.56	121.56	128.68
2	B	536	NAD	C6N-N1N-C2N	-4.16	118.19	121.97
2	A	536	NAD	N3A-C2A-N1A	-4.11	122.25	128.68
2	A	536	NAD	O7N-C7N-C3N	-3.96	114.89	119.63
2	B	536	NAD	C4A-C5A-N7A	3.91	113.47	109.40
2	A	536	NAD	C5D-C4D-C3D	-3.59	101.71	115.18
2	B	536	NAD	O7N-C7N-C3N	-3.52	115.42	119.63
2	A	536	NAD	C4A-C5A-N7A	3.15	112.68	109.40
2	A	536	NAD	N6A-C6A-N1A	3.11	125.03	118.57
2	A	536	NAD	O5B-C5B-C4B	-2.92	98.96	108.99
2	A	536	NAD	C3N-C7N-N7N	2.72	121.02	117.75
2	A	536	NAD	PN-O3-PA	2.64	141.87	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	536	NAD	C3D-C2D-C1D	2.57	104.85	100.98
2	A	536	NAD	C2N-C3N-C4N	2.54	121.14	118.26
2	A	536	NAD	C6N-N1N-C2N	-2.54	119.66	121.97
2	B	536	NAD	O4B-C1B-C2B	-2.35	103.49	106.93
2	A	536	NAD	O4D-C1D-C2D	2.34	110.34	106.93
2	A	536	NAD	C1B-N9A-C4A	2.33	130.73	126.64
2	B	536	NAD	N6A-C6A-N1A	2.31	123.37	118.57
2	B	536	NAD	C3N-C7N-N7N	2.31	120.52	117.75
2	B	536	NAD	O3B-C3B-C2B	-2.25	104.53	111.82
2	A	536	NAD	O3D-C3D-C2D	2.25	119.11	111.82
2	B	536	NAD	C2A-N1A-C6A	2.21	122.53	118.75
2	B	536	NAD	O3D-C3D-C2D	2.16	118.81	111.82
2	B	536	NAD	C5D-C4D-C3D	-2.13	107.22	115.18
2	B	536	NAD	C5A-C6A-N1A	-2.12	115.54	120.35
2	B	536	NAD	O5D-C5D-C4D	2.11	116.26	108.99
2	A	536	NAD	C5A-C6A-N1A	-2.01	115.80	120.35
2	A	536	NAD	C3N-C2N-N1N	-2.01	118.47	120.43

There are no chirality outliers.

All (14) torsion outliers are listed below:

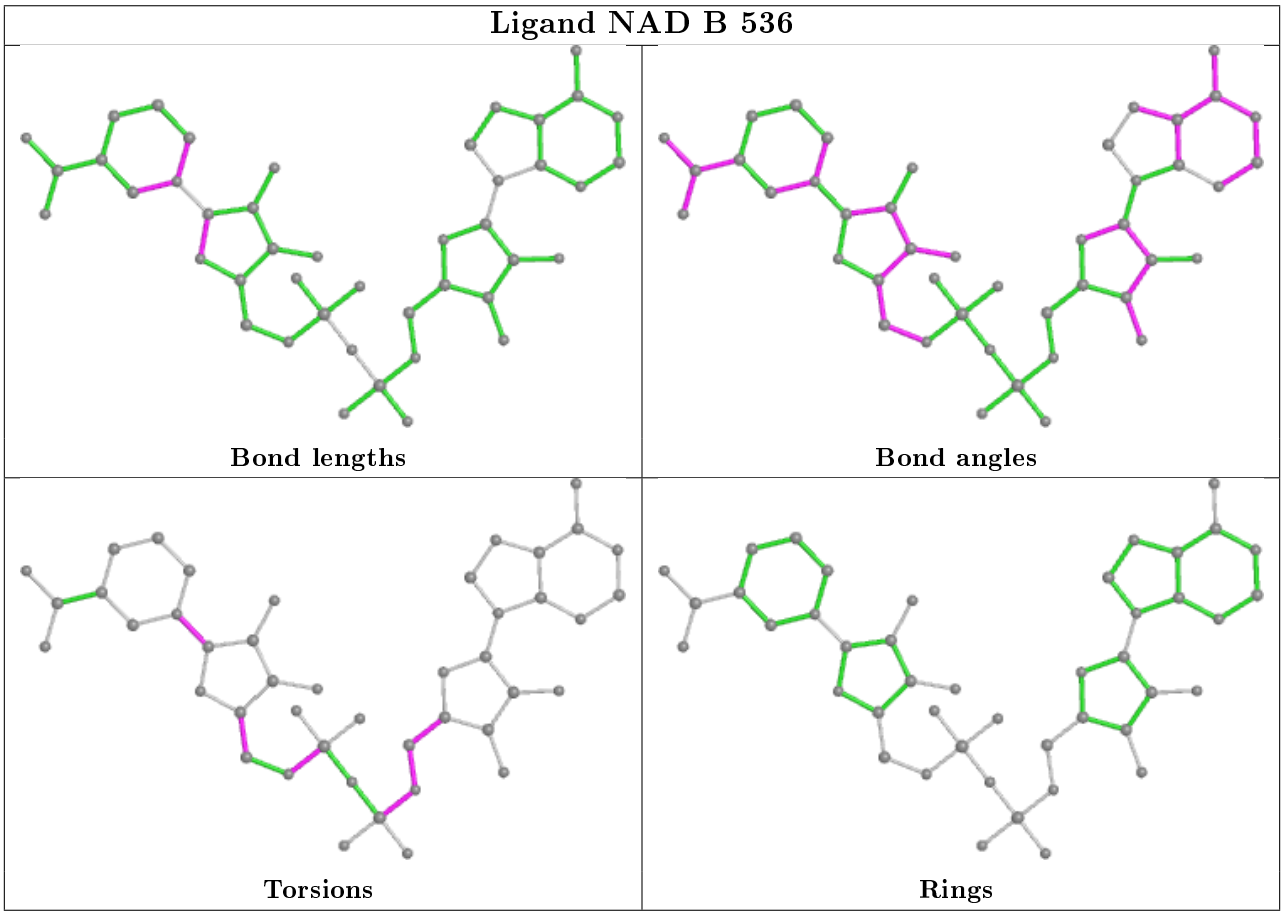
Mol	Chain	Res	Type	Atoms
2	B	536	NAD	C5B-O5B-PA-O1A
2	B	536	NAD	O4B-C4B-C5B-O5B
2	B	536	NAD	C3B-C4B-C5B-O5B
2	B	536	NAD	C5D-O5D-PN-O3
2	B	536	NAD	C5D-O5D-PN-O1N
2	B	536	NAD	O4D-C1D-N1N-C6N
2	B	536	NAD	C2D-C1D-N1N-C2N
2	A	536	NAD	O4B-C4B-C5B-O5B
2	A	536	NAD	C3B-C4B-C5B-O5B
2	B	536	NAD	O4D-C4D-C5D-O5D
2	A	536	NAD	PN-O3-PA-O1A
2	B	536	NAD	C5D-O5D-PN-O2N
2	B	536	NAD	C4B-C5B-O5B-PA
2	B	536	NAD	C3D-C4D-C5D-O5D

There are no ring outliers.

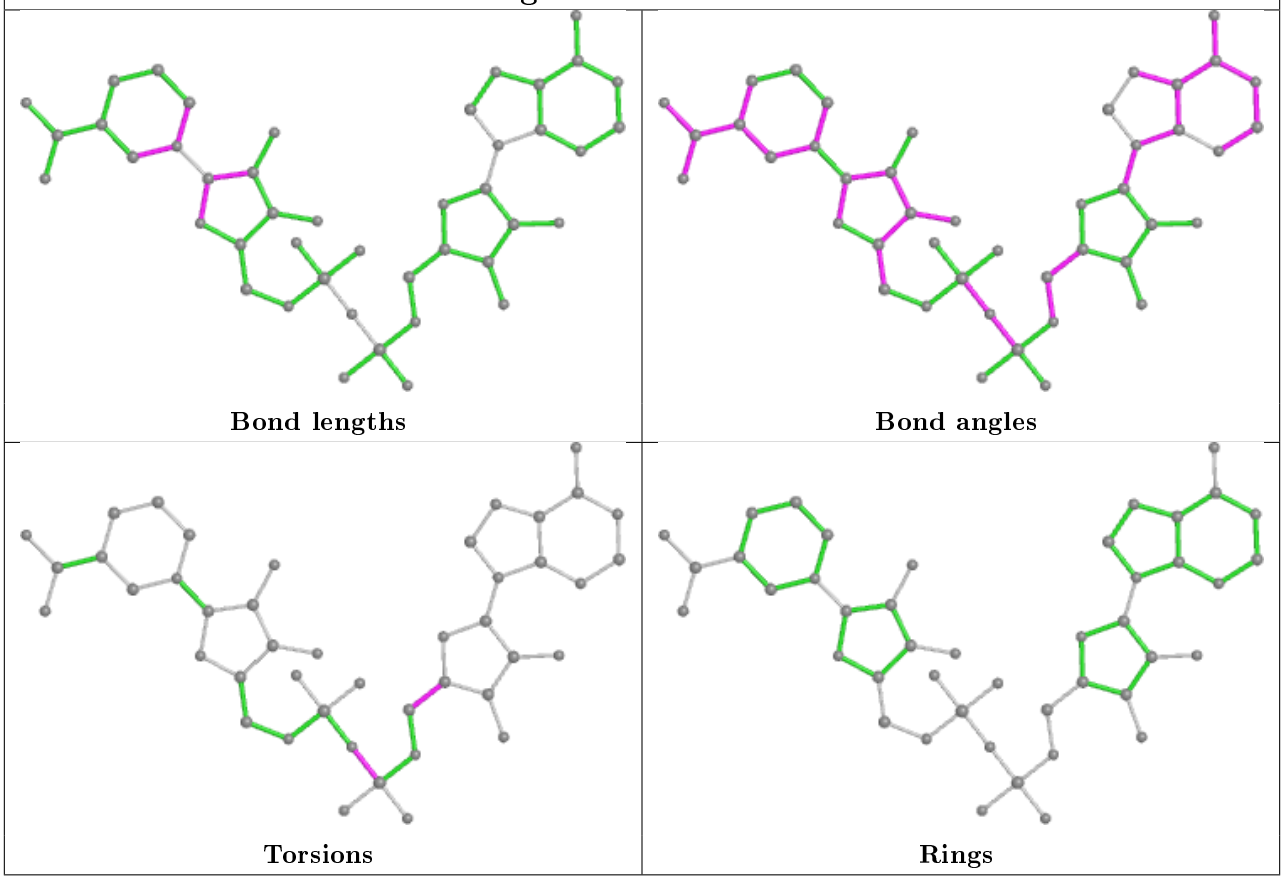
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	536	NAD	1	0
2	A	536	NAD	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 NAD A 536



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	515/535 (96%)	-0.05	11 (2%)	63	70	10, 21, 56, 90	0
1	B	513/535 (95%)	0.05	16 (3%)	49	56	10, 24, 56, 96	0
All	All	1028/1070 (96%)	-0.00	27 (2%)	56	63	10, 22, 56, 96	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	518	VAL	7.3
1	B	518	VAL	7.2
1	A	520	HIS	6.1
1	B	464	ILE	5.8
1	A	504	ILE	5.5
1	B	520	HIS	5.4
1	B	353	ILE	4.6
1	A	521	THR	4.2
1	A	519	ASP	4.1
1	B	352	ASP	3.6
1	B	517	THR	3.3
1	B	110	LEU	3.3
1	B	519	ASP	3.0
1	B	465	ASP	3.0
1	A	353	ILE	2.9
1	A	517	THR	2.7
1	B	504	ILE	2.7
1	A	523	VAL	2.7
1	B	100	GLU	2.6
1	B	4	ASP	2.6
1	B	48	ASP	2.5
1	B	1	GLY	2.4
1	A	505	SER	2.4
1	A	238	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	492	HIS	2.2
1	B	114	LEU	2.2
1	A	354	GLY	2.1

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 carbohydrates in this entry.

6.4 Ligands (i)

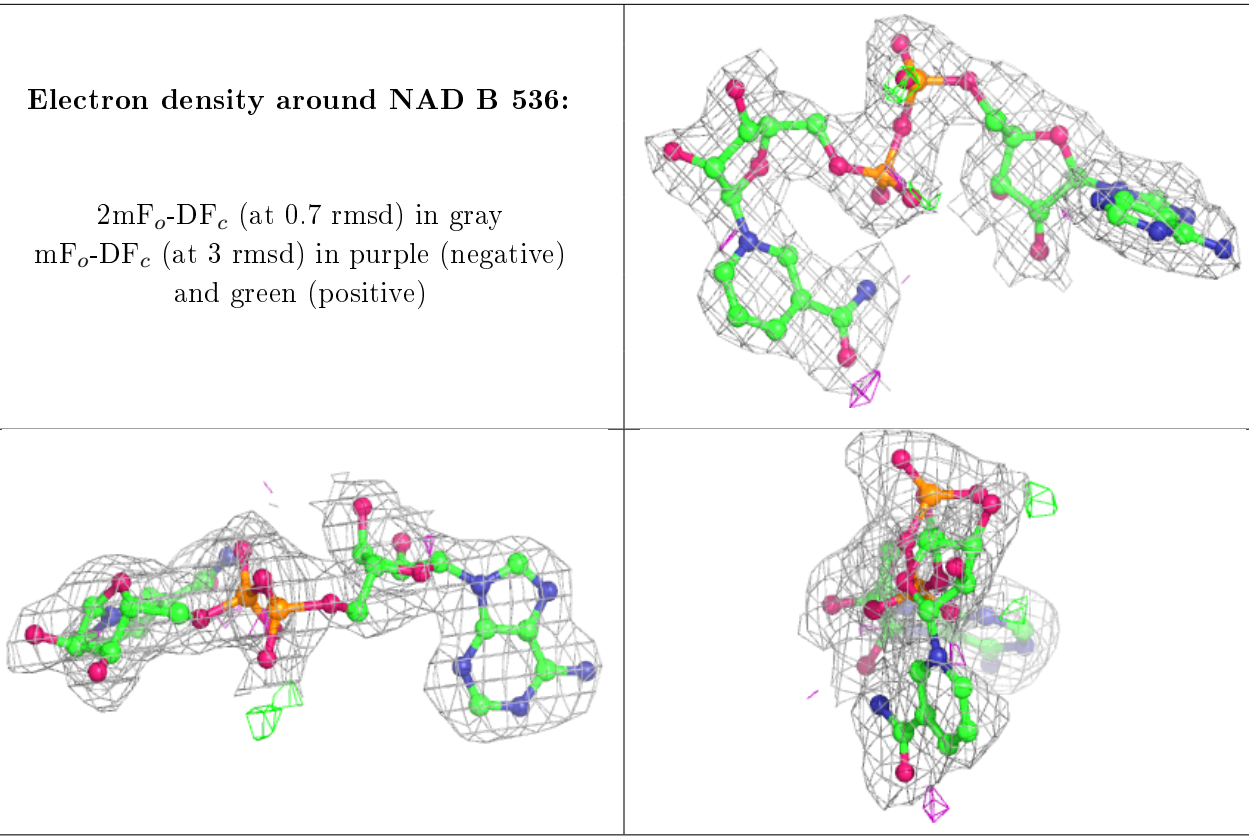
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	NAD	B	536	44/44	0.94	0.13	14,32,47,52	0
2	NAD	A	536	44/44	0.96	0.11	12,24,40,44	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.

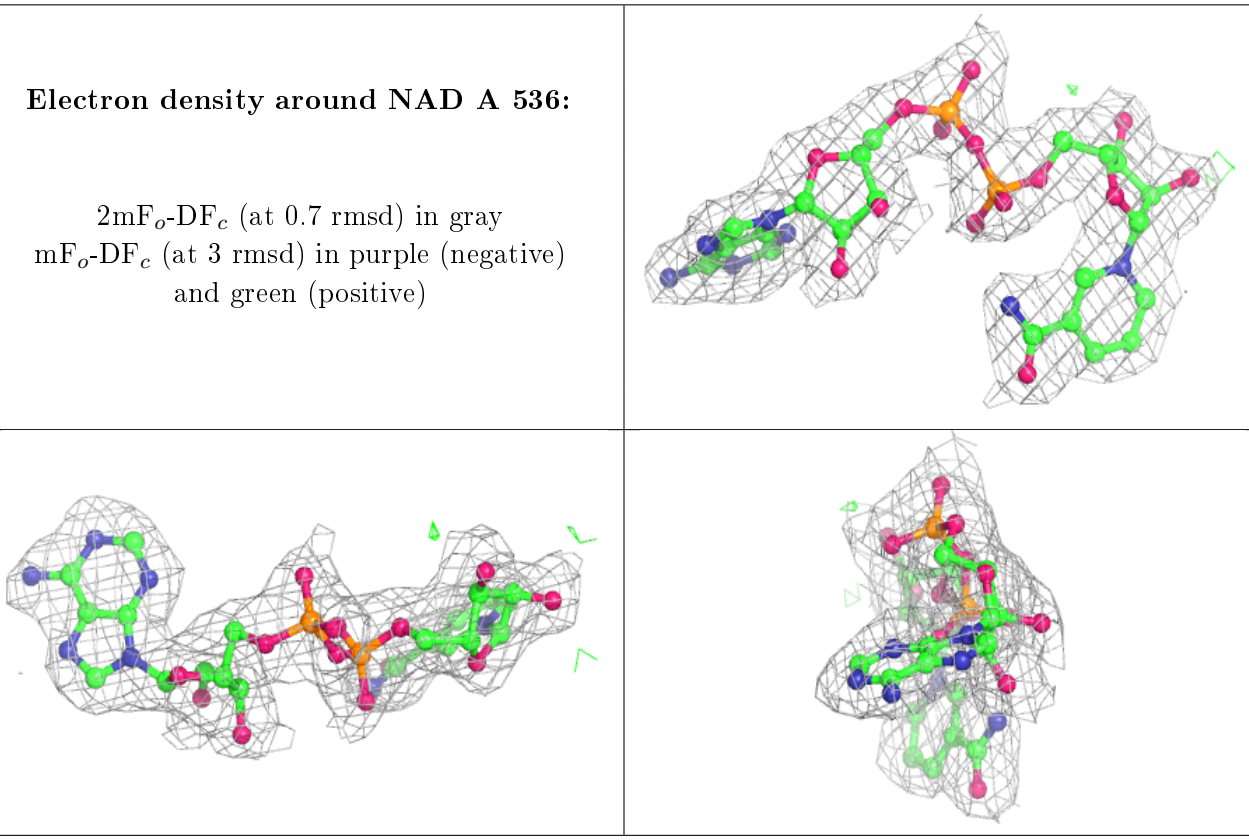
Electron density around NAD B 536:

$2mF_o$-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 536:

$2mF_o$-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.