



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:05 PM UTC

PDB ID : 1NM5 / pdb_00001nm5
Title : R. rubrum transhydrogenase (dI.Q132N)2(dIII)1 asymmetric complex
Authors : Van Boxel, G.I.; Quirk, P.G.; Cotton, N.P.; White, S.A.; Jackson, J.B.
Deposited on : 2003-01-09
Resolution : 2.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

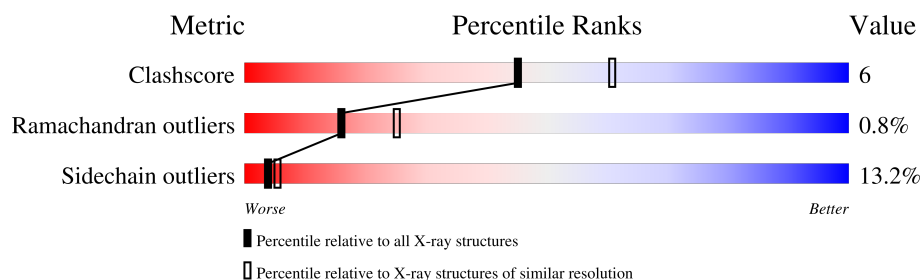
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	384	
1	B	384	
2	C	203	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6785 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 NAD(P) transhydrogenase subunit alpha part 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	360	Total	C	N	O	S	0	1	0
			2649	1674	458	500	17			
1	B	358	Total	C	N	O	S	0	1	0
			2634	1667	457	494	16			

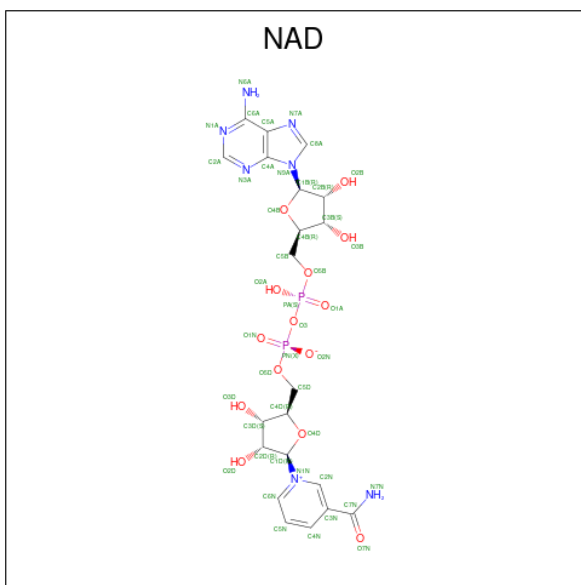
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	132	ASN	GLN	engineered mutation	UNP Q60164
B	132	ASN	GLN	engineered mutation	UNP Q60164

- Molecule 2 is a protein called NAD(P) transhydrogenase subunit beta.

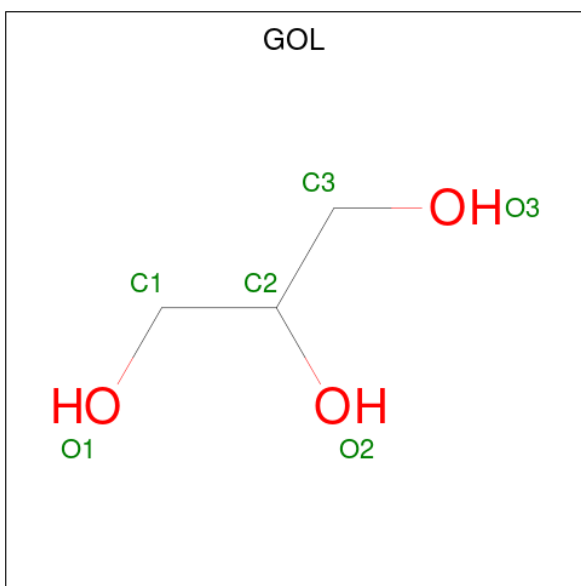
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	174	Total	C	N	O	S	0	0	0
			1310	830	217	252	11			

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 44	C 21	N 7	O 14	P 2	0	0
3	B	1	Total 27	C 10	N 5	O 10	P 2	0	0

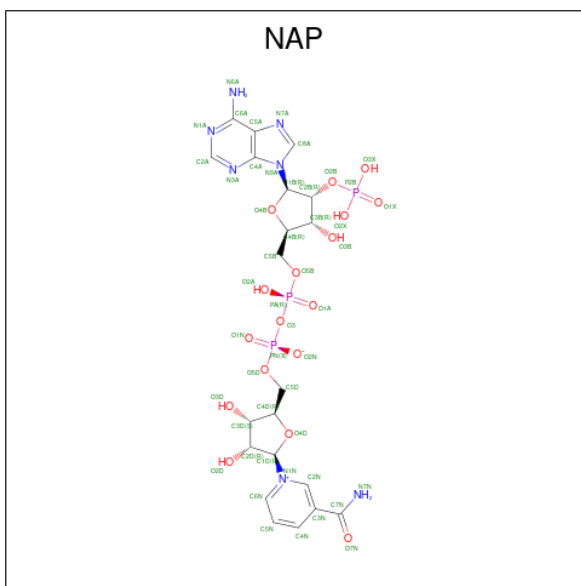
- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $\text{C}_3\text{H}_8\text{O}_3$).



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

- Molecule 5 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD

ID: NAP) (formula: $\text{C}_{21}\text{H}_{28}\text{N}_7\text{O}_{17}\text{P}_3$).



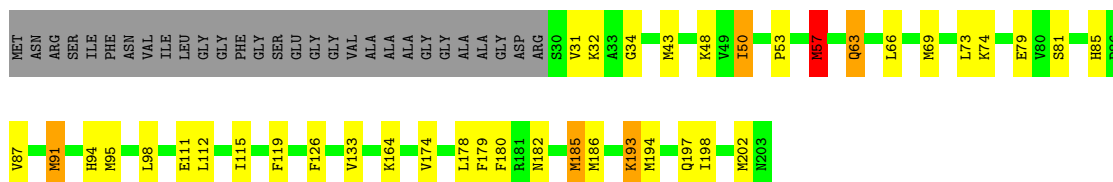
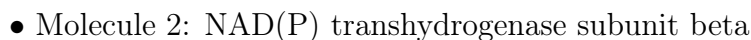
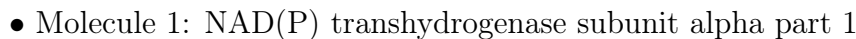
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	C	1	Total 48	C 21	N 7	O 17	P 3	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	28	Total O 28 28	0	0
6	B	31	Total O 31 31	0	0
6	C	8	Total O 8 8	0	0

Note EDS was not executed.

- Chain A: 73% 18% 6%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	71.94 Å 73.89 Å 205.26 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 2.40	Depositor
% Data completeness (in resolution range)	90.9 (100.00-2.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
Refinement program	REFMAC 5.1.25	Depositor
R, R_{free}	0.236 , 0.264	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6785	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAP, GOL, 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	0.87	5/2682 (0.2%)	0.92	0/3632
1	B	0.77	1/2669 (0.0%)	0.91	3/3619 (0.1%)
2	C	0.70	1/1333 (0.1%)	0.90	0/1803
All	All	0.80	7/6684 (0.1%)	0.91	3/9054 (0.0%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	184	GLY	C-O	15.08	1.44	1.23
1	A	184	GLY	CA-C	6.43	1.60	1.51
1	B	122	MET	SD-CE	-6.22	1.64	1.79
1	A	180	VAL	C-O	6.13	1.31	1.24
1	A	180	VAL	N-CA	5.60	1.53	1.46
1	A	239	MET	C-O	5.34	1.30	1.24
2	C	57	MET	SD-CE	-5.12	1.66	1.79

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	322	ASN	CA-C-N	5.59	123.76	120.24
1	B	322	ASN	C-N-CA	5.59	123.76	120.24
1	B	308	LYS	N-CA-C	5.16	116.64	108.96

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	2649	0	2785	30	0
1	B	2634	0	2771	33	0
2	C	1310	0	1303	19	0
3	A	44	0	26	1	0
3	B	27	0	12	1	0
4	B	6	0	8	0	0
5	C	48	0	25	0	0
6	A	28	0	0	0	0
6	B	31	0	0	0	0
6	C	8	0	0	0	0
All	All	6785	0	6930	80	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (80) 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:142:ASN:HD21	1:B:186:GLN:HE21	1.03	0.93
2:C:53:PRO:HB2	2:C:95:MET:HE2	1.64	0.79
1:B:142:ASN:ND2	1:B:186:GLN:HE21	1.82	0.72
1:A:329:ALA:HB3	1:B:158:ARG:HG3	1.72	0.70
1:A:207:THR:HA	1:A:210:GLN:HE21	1.56	0.69
1:B:142:ASN:HD21	1:B:186:GLN:NE2	1.85	0.68
2:C:63:GLN:HG2	2:C:98:LEU:HB3	1.76	0.68
2:C:50:ILE:HG22	2:C:81:SER:HB2	1.76	0.67
2:C:53:PRO:HB3	2:C:57:MET:HE3	1.78	0.66
1:B:284:MET:HE1	1:B:290:ILE:HD11	1.83	0.60
1:B:351:THR:O	1:B:351:THR:HG22	2.00	0.60
2:C:198:ILE:HG22	2:C:202:MET:HE3	1.83	0.59
2:C:50:ILE:HD11	2:C:119:PHE:CD1	2.37	0.59
1:B:10:ARG:NH1	1:B:76:ARG:O	2.37	0.57
1:A:156:PHE:CZ	1:A:259:ASP:HB3	2.40	0.57
2:C:95:MET:HE3	2:C:95:MET:HA	1.88	0.55
1:B:156:PHE:CZ	1:B:259:ASP:HB3	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:ILE:HG13	1:A:70:VAL:HG13	1.91	0.53
1:A:5:ILE:HD13	1:A:18:ILE:HD13	1.91	0.52
1:A:203:VAL:HG11	1:A:239:MET:HG3	1.91	0.52
2:C:69:MET:HE1	2:C:126:PHE:CE2	2.45	0.52
1:A:13:GLU:OE1	1:A:75:GLN:NE2	2.44	0.50
1:B:13:GLU:OE1	1:B:75:GLN:NE2	2.32	0.49
3:B:500:NAD:H3B	3:B:500:NAD:PA	2.51	0.49
1:A:177:VAL:HG13	1:A:177:VAL:O	2.13	0.49
1:A:122:MET:HE1	1:A:342:PHE:CE2	2.47	0.49
2:C:69:MET:HE1	2:C:126:PHE:CD2	2.48	0.49
1:B:87:VAL:HG23	1:B:112:LEU:HD23	1.93	0.48
1:B:1:MET:H3	1:B:1:MET:HE3	1.77	0.48
2:C:193:LYS:HD2	2:C:197:GLN:NE2	2.29	0.48
1:A:135:ASP:OD2	3:A:400:NAD:H4N	2.14	0.48
1:B:156:PHE:CG	1:B:260:ILE:HD11	2.48	0.48
1:A:278:GLU:O	1:A:281:VAL:HG22	2.14	0.48
1:A:87:VAL:HG13	1:A:112:LEU:HD23	1.95	0.47
2:C:85:HIS:CE1	2:C:87:VAL:HG22	2.49	0.47
1:A:178:PHE:HB3	1:A:275:LEU:HD13	1.97	0.47
2:C:91:MET:HE2	2:C:94:HIS:HA	1.96	0.47
1:B:4:ALA:HA	1:B:34:ILE:O	2.14	0.46
1:A:106:ARG:N	1:A:107:PRO:CD	2.78	0.46
1:B:284:MET:CE	1:B:290:ILE:HD11	2.46	0.46
1:B:180:VAL:O	1:B:180:VAL:HG12	2.15	0.46
1:A:158:ARG:HB3	1:B:330:ASP:OD2	2.15	0.46
1:A:202:ASP:CB	1:A:207:THR:HG21	2.47	0.45
2:C:112:LEU:C	2:C:112:LEU:HD23	2.41	0.45
1:B:88:ALA:HA	1:B:115:ARG:NE	2.32	0.45
1:B:337:LYS:HD2	1:B:341:ASN:ND2	2.32	0.44
1:B:2:LYS:HE3	1:B:34:ILE:HD11	1.99	0.44
1:A:180:VAL:HA	1:A:184:GLY:HA3	2.00	0.44
1:A:323:VAL:N	1:A:324:PRO:CD	2.80	0.44
1:A:5:ILE:CD1	1:A:18:ILE:HD13	2.48	0.44
1:B:73:LYS:HZ2	1:B:73:LYS:HB2	1.82	0.44
1:B:106:ARG:N	1:B:107:PRO:CD	2.80	0.44
1:B:97:MET:HE1	1:B:343:LEU:HD13	2.00	0.43
2:C:34:GLY:HA3	2:C:185:MET:SD	2.58	0.43
2:C:43:MET:HE1	2:C:69:MET:SD	2.58	0.43
2:C:57:MET:HE2	2:C:66:LEU:CD2	2.49	0.43
1:B:242:GLU:O	1:B:243:PHE:C	2.60	0.43
1:A:163:MET:HB2	1:A:170:VAL:HG13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:ASP:HB2	1:A:207:THR:HG21	2.01	0.43
1:B:350:ASP:O	1:B:351:THR:C	2.62	0.42
1:A:158:ARG:NH1	1:B:330:ASP:OD1	2.51	0.42
2:C:63:GLN:CG	2:C:98:LEU:HB3	2.46	0.42
1:B:270:LYS:HB3	1:B:271:PRO:HD2	2.01	0.42
1:A:321:THR:O	1:A:322:ASN:C	2.63	0.42
2:C:69:MET:O	2:C:73:LEU:HB2	2.19	0.42
1:A:103:LEU:HD13	1:A:124:LEU:HD11	2.02	0.42
1:A:296:GLU:OE1	1:A:321:THR:HA	2.20	0.42
1:A:344:THR:N	1:A:345:PRO:CD	2.83	0.42
1:B:93:GLY:HA2	1:B:116:LYS:O	2.20	0.41
1:B:293:LEU:HD23	1:B:293:LEU:HA	1.91	0.41
1:A:203:VAL:CG1	1:A:239:MET:HE2	2.50	0.41
1:A:165:THR:OG1	1:A:168:GLY:O	2.32	0.41
1:A:279:GLU:O	1:A:282:THR:HB	2.21	0.41
1:B:160:PHE:N	1:B:161:PRO:HD2	2.36	0.41
1:A:374:ILE:HG22	1:A:374:ILE:O	2.20	0.41
2:C:179:PHE:HA	2:C:186:MET:HE3	2.04	0.41
1:B:277:THR:O	1:B:281:VAL:HG13	2.21	0.40
1:B:58:ALA:HB3	1:B:64:ALA:HB2	2.04	0.40
1:B:73:LYS:CB	1:B:73:LYS:NZ	2.84	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	356/384 (93%)	341 (96%)	14 (4%)	1 (0%)	36	50
1	B	354/384 (92%)	337 (95%)	13 (4%)	4 (1%)	11	18
2	C	172/203 (85%)	165 (96%)	5 (3%)	2 (1%)	10	16
All	All	882/971 (91%)	843 (96%)	32 (4%)	7 (1%)	16	25

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	243	PHE
1	B	350	ASP
1	B	351	THR
2	C	182	ASN
1	A	179	GLY
1	B	352	LYS
2	C	31	VAL

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	281/296 (95%)	240 (85%)	41 (15%)	3	4
1	B	280/296 (95%)	247 (88%)	33 (12%)	5	7
2	C	138/154 (90%)	120 (87%)	18 (13%)	4	5
All	All	699/746 (94%)	607 (87%)	92 (13%)	4	5

All (92) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	7	LYS
1	A	24	LYS
1	A	34	ILE
1	A	48	ASP
1	A	50	LEU
1	A	56	THR
1	A	60	THR
1	A	65	LEU
1	A	70	VAL
1	A	76	ARG
1	A	81	GLU
1	A	91	LYS
1	A	92	GLU

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Mol	Chain	Res	Type
1	A	95	VAL
1	A	96	LEU
1	A	103	LEU
1	A	106	ARG
1	A	114	LYS
1	A	130	ARG
1	A	132	ASN
1	A	164	MET
1	A	170	VAL
1	A	176	LEU
1	A	207	THR
1	A	217	LYS
1	A	221	VAL
1	A	238	GLU
1	A	242[A]	GLU
1	A	244	ARG
1	A	251	VAL
1	A	256	VAL
1	A	257	LYS
1	A	278	GLU
1	A	279	GLU
1	A	296	GLU
1	A	327	VAL
1	A	349	LYS
1	A	353	THR
1	A	362	THR
1	A	370	ARG
1	B	1	MET
1	B	35	VAL
1	B	50	LEU
1	B	56	THR
1	B	59	SER
1	B	73	LYS
1	B	74	VAL
1	B	89	LEU
1	B	92	GLU
1	B	100	LEU
1	B	108	VAL
1	B	115	ARG
1	B	129	SER
1	B	137	LEU
1	B	176	LEU

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Mol	Chain	Res	Type
1	B	210	GLN
1	B	221	VAL
1	B	243	PHE
1	B	246	LYS
1	B	247	GLN
1	B	252	LEU
1	B	281	VAL
1	B	289	VAL
1	B	305	GLU
1	B	327	VAL
1	B	337	LYS
1	B	339	LEU
1	B	349[A]	LYS
1	B	353	THR
1	B	354	LEU
1	B	362	THR
1	B	366	THR
1	B	368	VAL
2	C	32	LYS
2	C	48	LYS
2	C	50	ILE
2	C	57	MET
2	C	63	GLN
2	C	74	LYS
2	C	79	GLU
2	C	91	MET
2	C	111	GLU
2	C	115	ILE
2	C	133	VAL
2	C	164	LYS
2	C	174	VAL
2	C	178	LEU
2	C	180	PHE
2	C	185	MET
2	C	193	LYS
2	C	194	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	142	ASN
1	A	186	GLN

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Mol	Chain	Res	Type
1	A	210	GLN
1	A	300	ASN
1	A	322	ASN
1	A	338	ASN
1	B	99	HIS
1	B	105	ASN
1	B	132	ASN
1	B	142	ASN
1	B	341	ASN
1	B	346	HIS
2	C	61	GLN
2	C	120	GLN
2	C	183	ASN
2	C	197	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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
5	NAP	C	300	-	50,52,52	1.58	6 (12%)	71,80,80	1.51	8 (11%)
4	GOL	B	501	-	5,5,5	0.50	0	5,5,5	0.62	0
3	NAD	B	500	-	28,29,48	1.36	4 (14%)	43,45,73	1.89	8 (18%)
3	NAD	A	400	-	46,48,48	1.70	5 (10%)	64,73,73	1.62	10 (15%)

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
5	NAP	C	300	-	-	9/35/67/67	0/5/5/5
4	GOL	B	501	-	-	2/4/4/4	-
3	NAD	B	500	-	-	9/16/32/62	0/3/3/5
3	NAD	A	400	-	-	3/30/62/62	0/5/5/5

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	400	NAD	O7N-C7N	9.33	1.41	1.24
5	C	300	NAP	O7N-C7N	8.46	1.39	1.24
3	B	500	NAD	PA-O3	4.13	1.64	1.59
3	A	400	NAD	C2A-N3A	3.01	1.39	1.33
5	C	300	NAP	C2A-N1A	2.84	1.39	1.33
3	B	500	NAD	C2A-N1A	2.73	1.38	1.33
3	B	500	NAD	C2A-N3A	2.64	1.38	1.33
3	B	500	NAD	C8A-N7A	2.54	1.36	1.31
3	A	400	NAD	C2A-N1A	2.43	1.38	1.33
5	C	300	NAP	C8A-N7A	2.39	1.36	1.31
3	A	400	NAD	C2N-N1N	2.27	1.37	1.35
5	C	300	NAP	C2N-N1N	2.24	1.37	1.35
5	C	300	NAP	C2A-N3A	2.19	1.37	1.33
5	C	300	NAP	C5A-N7A	-2.15	1.35	1.39
3	A	400	NAD	C8A-N7A	2.11	1.35	1.31

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	500	NAD	N3A-C2A-N1A	-6.39	118.92	128.58
3	A	400	NAD	N3A-C2A-N1A	-5.57	120.15	128.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	300	NAP	N3A-C2A-N1A	-5.35	120.49	128.58
5	C	300	NAP	C5A-C4A-N3A	-4.49	120.54	126.72
3	A	400	NAD	C5A-C4A-N3A	-4.37	120.70	126.72
3	A	400	NAD	N9A-C8A-N7A	-4.30	107.84	113.94
3	B	500	NAD	C5A-C4A-N3A	-4.25	120.86	126.72
5	C	300	NAP	N9A-C8A-N7A	-4.18	108.00	113.94
5	C	300	NAP	C5A-N7A-C8A	3.75	109.35	103.45
3	B	500	NAD	N9A-C8A-N7A	-3.74	108.63	113.94
3	B	500	NAD	C2A-N3A-C4A	3.68	120.83	111.83
3	A	400	NAD	C5A-N7A-C8A	3.54	109.02	103.45
3	A	400	NAD	C3N-C7N-N7N	3.53	122.08	117.74
3	A	400	NAD	C2A-N3A-C4A	3.50	120.38	111.83
5	C	300	NAP	C2A-N3A-C4A	3.36	120.03	111.83
3	B	500	NAD	C5A-N7A-C8A	3.32	108.66	103.45
5	C	300	NAP	O2A-PA-O3	2.81	114.88	107.27
3	A	400	NAD	N3A-C4A-N9A	2.78	131.90	127.17
5	C	300	NAP	C4A-C5A-N7A	-2.77	107.41	110.58
5	C	300	NAP	N3A-C4A-N9A	2.71	131.77	127.17
3	B	500	NAD	N3A-C4A-N9A	2.66	131.69	127.17
3	A	400	NAD	C4A-C5A-N7A	-2.66	107.55	110.58
3	B	500	NAD	O5D-PN-O3	2.63	113.47	104.64
3	A	400	NAD	C4A-N9A-C8A	2.34	108.19	105.74
3	B	500	NAD	C4A-C5A-N7A	-2.22	108.04	110.58
3	A	400	NAD	O7N-C7N-N7N	-2.07	119.62	122.62

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	400	NAD	C5D-O5D-PN-O2N
3	B	500	NAD	C5B-O5B-PA-O1A
3	B	500	NAD	C5B-O5B-PA-O2A
3	B	500	NAD	C5B-O5B-PA-O3
5	C	300	NAP	PA-O3-PN-O5D
5	C	300	NAP	O4D-C1D-N1N-C2N
5	C	300	NAP	O4D-C1D-N1N-C6N
3	B	500	NAD	O4B-C4B-C5B-O5B
5	C	300	NAP	C1B-C2B-O2B-P2B
3	B	500	NAD	C3B-C4B-C5B-O5B
4	B	501	GOL	C1-C2-C3-O3
4	B	501	GOL	O2-C2-C3-O3
5	C	300	NAP	C3B-C2B-O2B-P2B

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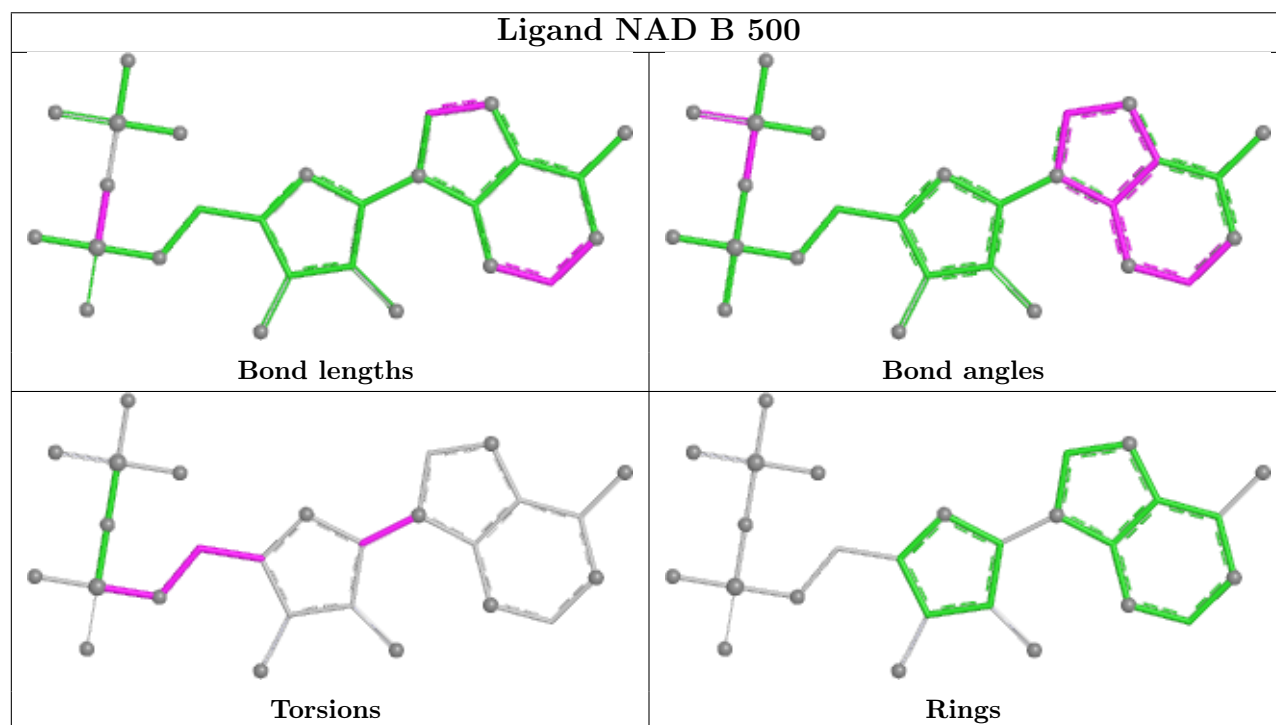
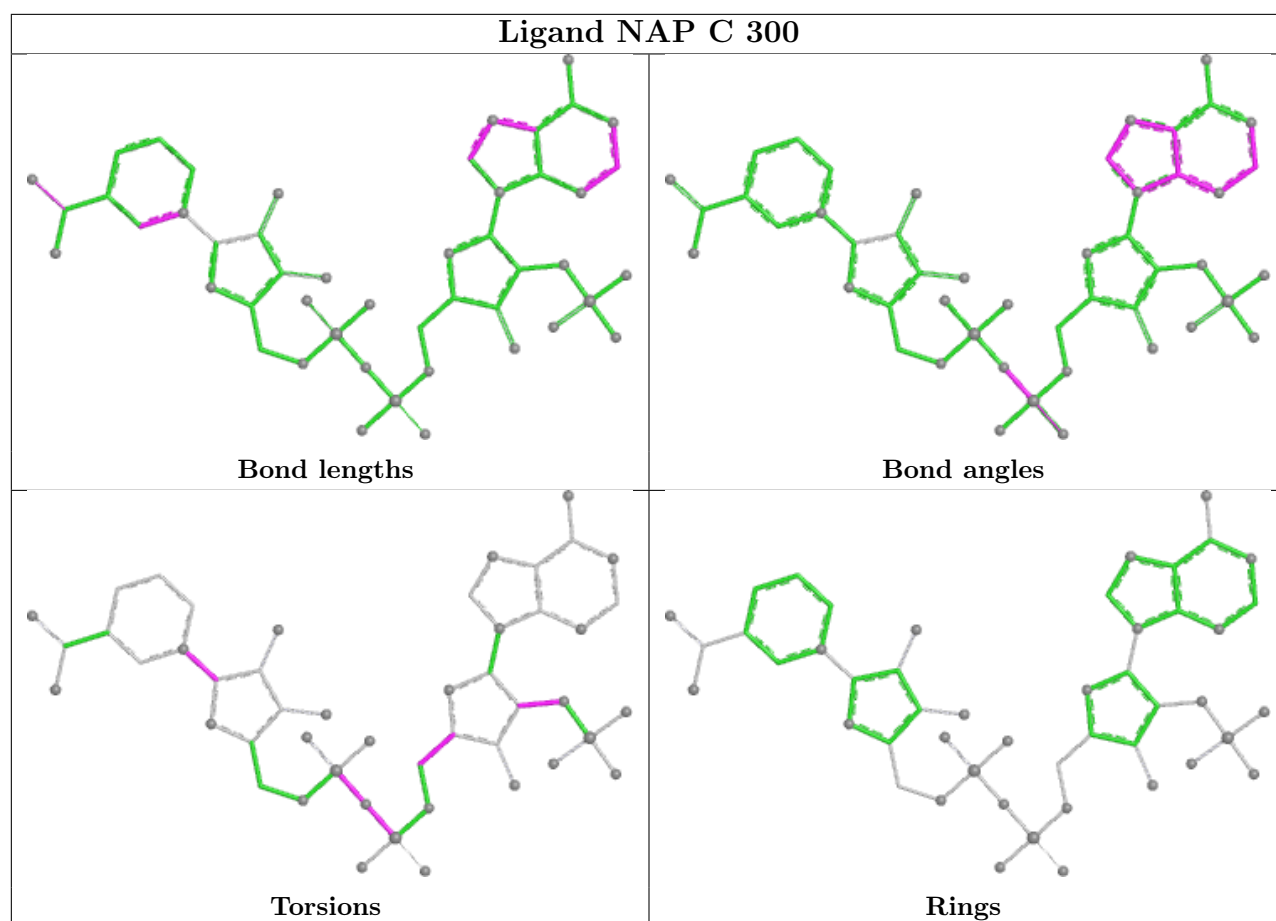
Mol	Chain	Res	Type	Atoms
3	B	500	NAD	C4B-C5B-O5B-PA
3	B	500	NAD	C2B-C1B-N9A-C8A
3	A	400	NAD	C5D-O5D-PN-O3
3	A	400	NAD	C5D-O5D-PN-O1N
3	B	500	NAD	C2B-C1B-N9A-C4A
5	C	300	NAP	C2D-C1D-N1N-C6N
3	B	500	NAD	O4B-C1B-N9A-C8A
5	C	300	NAP	PN-O3-PA-O1A
5	C	300	NAP	O4B-C4B-C5B-O5B
5	C	300	NAP	PN-O3-PA-O2A

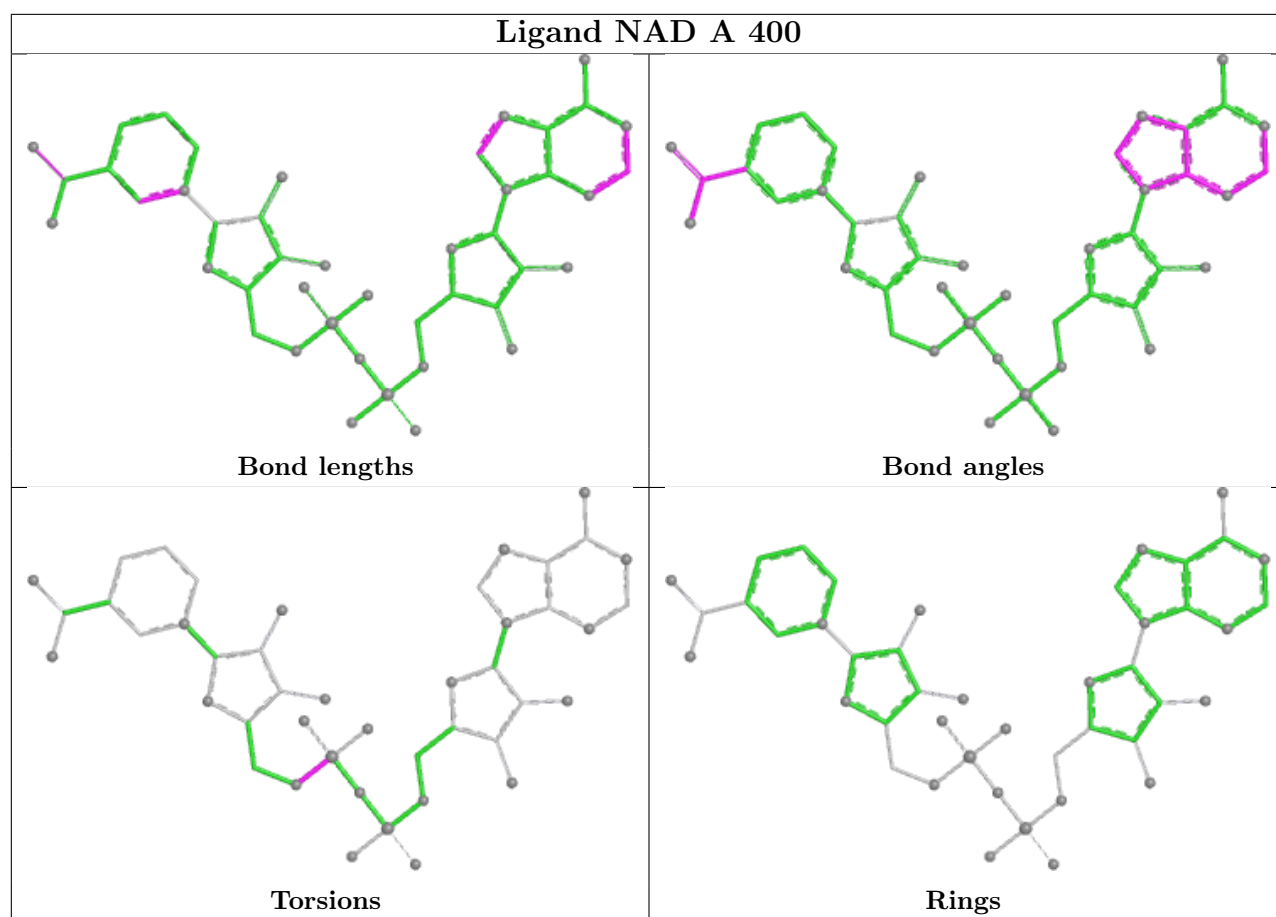
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	500	NAD	1	0
3	A	400	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 than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.