



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:44 AM UTC

PDB ID : 1I3K / pdb_00001i3k
Title : MOLECULAR BASIS FOR SEVERE EPIMERASE-DEFICIENCY GALACTOSEMIA: X-RAY STRUCTURE OF THE HUMAN V94M-SUBSTITUTED UDP-GALACTOSE 4-EPIMERASE
Authors : Thoden, J.B.; Wohlers, T.M.; Fridovich-Keil, J.L.; Holden, H.M.
Deposited on : 2001-02-15
Resolution : 1.50 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

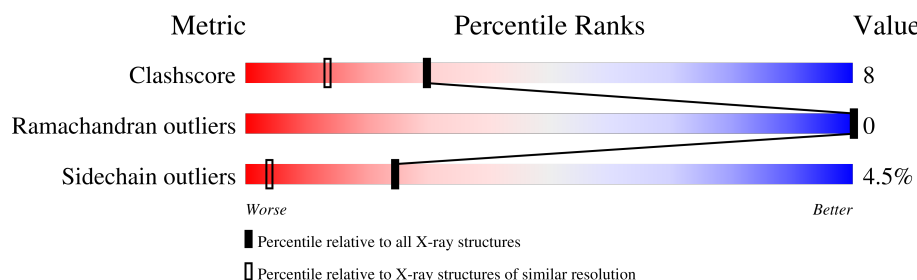
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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	4235 (1.50-1.50)
Ramachandran outliers	187476	4153 (1.50-1.50)
Sidechain outliers	187428	4150 (1.50-1.50)

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	348	
1	B	348	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	EDO	B	972	-	-	X	-

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 6568 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 UDP-GLUCOSE 4-EPIMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	347	Total	C	N	O	S	0	3	0
			2697	1706	467	508	16			
1	B	345	Total	C	N	O	S	0	12	0
			2716	1723	465	511	17			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	94	MET	VAL	engineered mutation	UNP Q14376
B	94	MET	VAL	engineered mutation	UNP Q14376

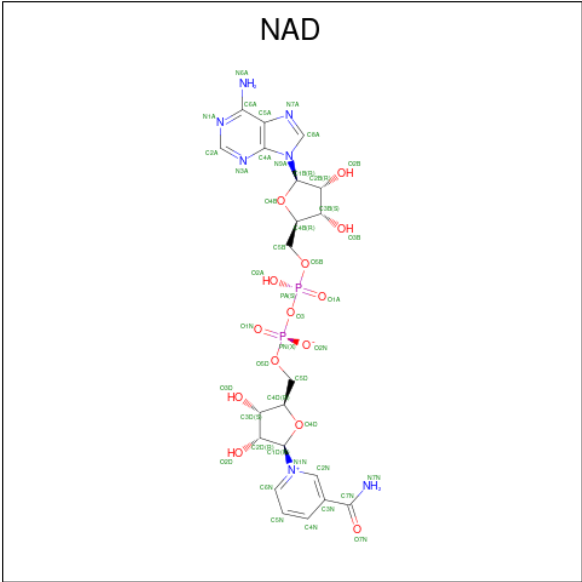
- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cl	0	0
			1	1		
2	B	3	Total	Cl	0	0
			3	3		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

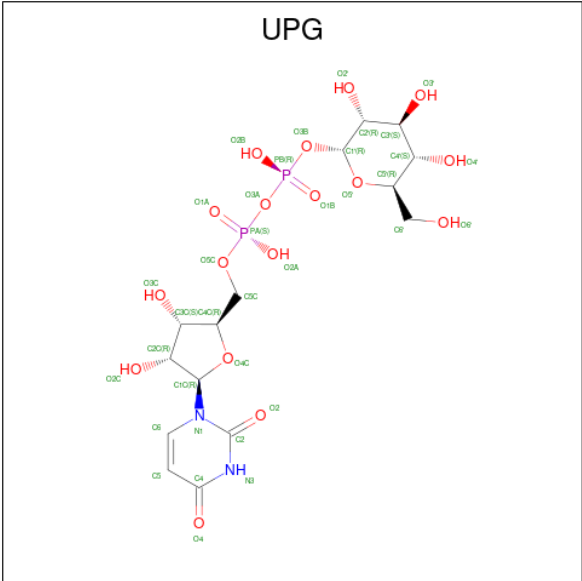
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).



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

- Molecule 5 is URIDINE-5'-DIPHOSPHATE-GLUCOSE (CCD ID: UPG) (formula: C₁₅H₂₄N₂O₁₇P₂).



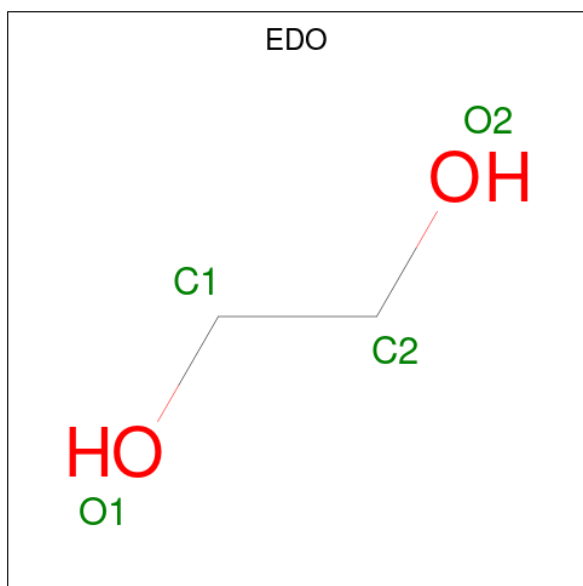
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	1
			37	15	2	18	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	P	0	0
			36	15	2	17	2		

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		
6	B	1	Total	C	O	0	0
			4	2	2		
6	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	494	Total	O	0	0
			494	494		
7	B	483	Total	O	0	0
			483	483		

3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

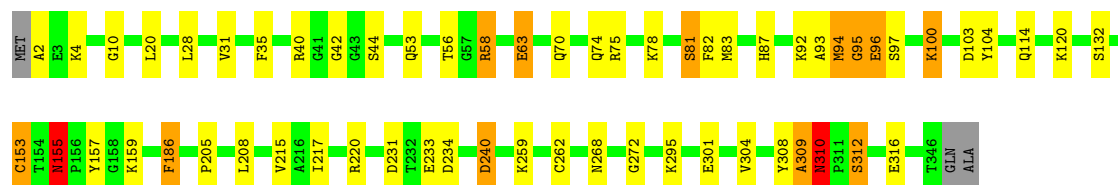
• Molecule 1: UDP-GLUCOSE 4-EPIMERASE

Chain A: 



• Molecule 1: UDP-GLUCOSE 4-EPIMERASE

Chain B: 



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	78.10Å 89.90Å 96.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.50	Depositor
% Data completeness (in resolution range)	99.1 (50.00-1.50)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	0.174 , 0.198	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6568	wwPDB-VP
Average B, all atoms (Å ²)	24.0	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: EDO, CL, MG, UPG, 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	0.93	0/2766	1.38	18/3740 (0.5%)
1	B	0.96	0/2825	1.40	20/3821 (0.5%)
All	All	0.95	0/5591	1.39	38/7561 (0.5%)

There are no bond length outliers.

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	94	MET	N-CA-C	-10.47	100.74	112.57
1	A	92	LYS	CA-C-N	-9.88	108.60	122.93
1	A	92	LYS	C-N-CA	-9.88	108.60	122.93
1	A	208	LEU	N-CA-C	8.75	121.69	111.02
1	B	94	MET	N-CA-C	-8.13	99.28	111.81
1	B	92	LYS	CA-C-N	-7.93	110.83	122.65
1	B	92	LYS	C-N-CA	-7.93	110.83	122.65
1	A	186	PHE	CA-CB-CG	-7.44	106.36	113.80
1	B	95	GLY	CA-C-N	7.24	130.57	120.29
1	B	95	GLY	C-N-CA	7.24	130.57	120.29
1	B	208	LEU	N-CA-C	7.06	118.67	110.97
1	B	92	LYS	N-CA-CB	6.79	120.82	110.70
1	B	96	GLU	N-CA-C	6.74	118.70	111.36
1	B	240	ASP	CA-CB-CG	6.68	119.28	112.60
1	A	175	ASP	CA-CB-CG	6.37	118.97	112.60
1	B	309	ALA	N-CA-C	6.28	120.15	110.42
1	A	240	ASP	CA-CB-CG	6.16	118.76	112.60
1	B	312	SER	N-CA-C	6.08	117.58	111.07
1	B	87	HIS	N-CA-C	6.02	119.24	107.57
1	A	272	GLY	N-CA-C	-5.85	107.25	115.32
1	A	30	VAL	N-CA-C	-5.83	99.14	107.77
1	B	155	ASN	N-CA-C	5.82	119.59	109.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	186	PHE	CA-CB-CG	-5.55	108.25	113.80
1	A	154	THR	CA-C-N	-5.49	116.05	123.96
1	A	154	THR	C-N-CA	-5.49	116.05	123.96
1	A	310	ASN	N-CA-C	-5.43	97.77	109.01
1	A	151	GLY	N-CA-C	-5.42	105.77	112.33
1	B	205	PRO	N-CA-CB	5.40	108.12	103.31
1	B	316	GLU	N-CA-C	5.33	116.90	111.14
1	B	262	CYS	N-CA-C	5.31	119.38	113.01
1	B	234	ASP	CA-CB-CG	5.28	117.88	112.60
1	A	312	SER	N-CA-C	5.25	117.00	111.28
1	A	87	HIS	N-CA-C	5.25	117.75	107.57
1	A	92	LYS	N-CA-CB	5.25	118.79	110.87
1	B	268	ASN	CB-CA-C	-5.22	99.84	109.46
1	A	122	HIS	CA-CB-CG	-5.20	108.60	113.80
1	A	309	ALA	N-CA-C	5.20	118.13	110.59
1	B	310	ASN	N-CA-C	-5.09	99.52	108.69

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	2697	0	2648	45	0
1	B	2716	0	2677	47	0
2	A	1	0	0	0	0
2	B	3	0	0	0	0
3	A	1	0	0	0	0
4	A	44	0	26	3	0
4	B	44	0	26	1	0
5	A	37	0	6	1	0
5	B	36	0	22	2	0
6	A	4	0	6	0	0
6	B	8	0	12	4	0
7	A	494	0	0	11	0
7	B	483	0	0	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6568	0	5423	94	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 8.

All (94) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:MET:HB3	1:A:96:GLU:HG3	1.44	0.97
1:B:58:ARG:HG3	1:B:58:ARG:HH11	1.38	0.89
1:B:94:MET:HB2	1:B:96:GLU:HG3	1.61	0.82
1:A:94:MET:HB3	1:A:96:GLU:CG	2.09	0.81
1:B:63:GLU:HG3	7:B:3032:HOH:O	1.83	0.78
1:B:42:GLY:HA2	7:B:1882:HOH:O	1.85	0.77
1:A:94:MET:HB2	7:A:2066:HOH:O	1.88	0.73
1:B:58:ARG:HG3	1:B:58:ARG:NH1	2.06	0.70
1:A:97:SER:HA	1:A:104:TYR:CE1	2.27	0.70
1:A:100:LYS:HE2	1:A:103:ASP:OD1	1.93	0.69
1:A:259:LYS:HD3	7:A:1620:HOH:O	1.94	0.67
1:B:100:LYS:HD3	1:B:103:ASP:HB2	1.77	0.66
1:B:83[B]:MET:HE1	1:B:259:LYS:HE2	1.77	0.66
1:A:155:ASN:OD1	1:A:157:TYR:HB3	1.96	0.65
1:A:61:GLU:HG2	7:A:1586:HOH:O	1.95	0.65
1:A:153:CYS:HB3	7:A:2072:HOH:O	1.97	0.64
1:A:312:SER:HA	1:A:315:GLN:CG	2.26	0.64
1:B:155:ASN:OD1	1:B:157:TYR:HB3	1.98	0.64
1:A:3:GLU:O	1:A:83:MET:HE2	1.97	0.64
1:B:100:LYS:HD2	1:B:104:TYR:CE1	2.33	0.64
1:B:70:GLN:HG2	7:B:2011:HOH:O	1.98	0.63
1:B:310:ASN:HD22	1:B:310:ASN:C	2.07	0.63
1:A:290:LYS:NZ	7:A:3037:HOH:O	2.32	0.62
1:A:58:ARG:NH1	7:A:1843:HOH:O	2.31	0.61
1:A:54:GLU:HG3	7:A:1850:HOH:O	2.01	0.60
1:B:78:LYS:HD2	6:B:972:EDO:O2	2.00	0.60
1:B:94:MET:HB2	1:B:96:GLU:CG	2.32	0.58
1:A:217:ILE:HG13	1:A:217:ILE:O	2.03	0.57
1:A:188:PRO:HD2	4:A:400:NAD:O7N	2.05	0.57
1:B:310:ASN:HD22	1:B:312:SER:H	1.53	0.57
1:A:290:LYS:HE3	7:A:3009:HOH:O	2.04	0.56
1:A:113:ILE:HG12	1:A:167:MET:HE1	1.88	0.56
1:B:310:ASN:ND2	1:B:312:SER:H	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:MET:HE3	7:A:1862:HOH:O	2.05	0.55
1:B:100:LYS:HD2	1:B:104:TYR:HE1	1.71	0.55
1:B:295:LYS:NZ	7:B:1953:HOH:O	2.40	0.54
1:A:93:ALA:C	1:A:95:GLY:H	2.15	0.53
1:B:74:GLN:HB3	6:B:972:EDO:H12	1.90	0.53
1:B:155:ASN:HD22	1:B:155:ASN:H	1.56	0.53
1:B:132:SER:OG	5:B:901:UPG:O4'	2.27	0.52
1:A:311:PRO:O	1:A:315:GLN:HG2	2.09	0.52
1:A:139:PRO:HB3	1:A:144:LEU:HD21	1.92	0.51
1:A:10:GLY:HA3	1:A:31:VAL:HG13	1.92	0.50
4:B:900:NAD:H4N	5:B:901:UPG:H4'	1.94	0.50
1:B:56:THR:O	1:B:58:ARG:NH1	2.44	0.50
1:B:97:SER:HA	1:B:104:TYR:CE1	2.46	0.50
1:B:70:GLN:HG3	7:B:1346:HOH:O	2.12	0.49
1:B:114:GLN:HB3	7:B:2011:HOH:O	2.13	0.48
1:B:53:GLN:HG3	1:B:58:ARG:O	2.13	0.48
1:B:83[B]:MET:CE	1:B:259:LYS:HE2	2.43	0.48
1:B:240:ASP:HB2	1:B:308:TYR:HA	1.96	0.47
1:B:100:LYS:HE2	1:B:103:ASP:OD1	2.13	0.47
1:B:2:ALA:HB3	1:B:81[B]:SER:HB3	1.97	0.47
1:A:310:ASN:OD1	1:A:312:SER:OG	2.33	0.46
1:B:155:ASN:HD22	1:B:155:ASN:N	2.12	0.46
1:A:167:MET:HE3	1:A:167:MET:HB3	1.76	0.46
1:A:94:MET:HB3	1:A:96:GLU:OE2	2.15	0.46
1:A:186:PHE:O	5:A:401[A]:UPG:H6'1	2.15	0.46
1:A:240:ASP:HB2	1:A:308:TYR:HA	1.98	0.46
1:A:315:GLN:HA	1:A:320:TRP:O	2.16	0.45
1:A:257:LYS:NZ	7:A:3053:HOH:O	2.50	0.45
1:B:2:ALA:N	1:B:82:PHE:O	2.50	0.45
1:A:173:GLN:HA	1:A:173:GLN:OE1	2.17	0.45
1:B:186:PHE:CE2	1:B:309:ALA:HB2	2.52	0.45
1:B:10:GLY:HA3	1:B:31:VAL:HG13	1.99	0.44
1:B:153:CYS:HB3	7:B:1318:HOH:O	2.17	0.44
1:A:328:ARG:HA	1:A:328:ARG:HD2	1.81	0.44
1:A:132:SER:HB2	4:A:400:NAD:H5N	1.99	0.44
1:B:93:ALA:C	1:B:95:GLY:H	2.26	0.44
1:B:74:GLN:CB	6:B:972:EDO:H12	2.49	0.43
1:A:94:MET:O	1:A:94:MET:HG3	2.18	0.43
1:B:155:ASN:H	1:B:155:ASN:ND2	2.16	0.43
1:B:215:VAL:HG22	1:B:220:ARG:HB2	2.01	0.43
1:A:169:ARG:HD3	7:A:1507:HOH:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:SER:HA	1:A:315:GLN:HG2	2.00	0.42
1:B:75:ARG:HD2	7:B:1737:HOH:O	2.18	0.42
1:A:169:ARG:HD3	1:A:169:ARG:HH11	1.68	0.42
1:A:142:LEU:HA	1:A:143:PRO:C	2.45	0.41
1:B:120[B]:LYS:NZ	7:B:1749:HOH:O	2.30	0.41
1:A:252:ILE:HD12	1:A:252:ILE:N	2.35	0.41
1:B:20:LEU:C	1:B:20:LEU:HD23	2.46	0.41
1:B:74:GLN:HB3	6:B:972:EDO:C1	2.51	0.41
1:A:94:MET:CB	1:A:96:GLU:HG3	2.32	0.41
1:A:294:TYR:CD2	1:A:294:TYR:C	2.99	0.41
1:A:53:GLN:HG3	1:A:58:ARG:O	2.20	0.40
1:A:315:GLN:HG2	1:A:315:GLN:H	1.69	0.40
1:B:35:PHE:CE2	1:B:40:ARG:HG3	2.55	0.40
1:A:204:ILE:HG12	1:A:220:ARG:NH1	2.36	0.40
1:B:2:ALA:N	1:B:82:PHE:C	2.79	0.40
1:B:4:LYS:NZ	1:B:28:LEU:HD13	2.37	0.40
1:A:168:ILE:HG21	1:A:182:LEU:HD21	2.03	0.40
1:B:272:GLY:HA2	1:B:309:ALA:O	2.21	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	348/348 (100%)	340 (98%)	8 (2%)	0	100	100
1	B	356/348 (102%)	349 (98%)	7 (2%)	0	100	100
All	All	704/696 (101%)	689 (98%)	15 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	283/282 (100%)	272 (96%)	11 (4%)	28	5
1	B	292/282 (104%)	274 (94%)	18 (6%)	16	1
All	All	575/564 (102%)	546 (95%)	29 (5%)	24	3

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	SER
1	A	61	GLU
1	A	92	LYS
1	A	94	MET
1	A	100	LYS
1	A	169	ARG
1	A	233	GLU
1	A	259	LYS
1	A	295	LYS
1	A	312	SER
1	A	315	GLN
1	B	44	SER
1	B	58	ARG
1	B	63	GLU
1	B	81[A]	SER
1	B	81[B]	SER
1	B	100	LYS
1	B	153	CYS
1	B	155	ASN
1	B	159	LYS
1	B	217[A]	ILE
1	B	217[B]	ILE
1	B	231[A]	ASP
1	B	231[B]	ASP
1	B	233[A]	GLU
1	B	233[B]	GLU
1	B	301	GLU

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Mol	Chain	Res	Type
1	B	304	VAL
1	B	310	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	GLN
1	A	138	ASN
1	A	206	ASN
1	A	339	GLN
1	B	36	HIS
1	B	114	GLN
1	B	138	ASN
1	B	206	ASN
1	B	310	ASN
1	B	339	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](#)

Of 13 ligands modelled in this entry, 5 are monoatomic - leaving 8 for Mogul analysis.

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	NAD	A	400	-	46,48,48	1.24	7 (15%)	64,73,73	1.63	4 (6%)
6	EDO	B	972	-	3,3,3	0.30	0	2,2,2	0.30	0
4	NAD	B	900	-	46,48,48	1.28	6 (13%)	64,73,73	1.54	6 (9%)
5	UPG	B	901	-	37,38,38	0.91	1 (2%)	55,58,58	1.02	4 (7%)
5	UPG	A	401[A]	-	37,38,38	1.66	2 (5%)	55,58,58	1.36	6 (10%)
6	EDO	A	971	-	3,3,3	0.36	0	2,2,2	0.28	0
5	UPG	A	401[B]	-	37,38,38	1.66	2 (5%)	55,58,58	1.36	6 (10%)
6	EDO	B	970	-	3,3,3	0.31	0	2,2,2	0.47	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
4	NAD	A	400	-	-	8/30/62/62	0/5/5/5
6	EDO	B	972	-	-	1/1/1/1	-
4	NAD	B	900	-	-	6/30/62/62	0/5/5/5
5	UPG	B	901	-	-	2/23/59/59	0/3/3/3
5	UPG	A	401[A]	-	-	2/23/59/59	0/3/3/3
6	EDO	A	971	-	-	1/1/1/1	-
5	UPG	A	401[B]	-	-	4/23/59/59	0/3/3/3
6	EDO	B	970	-	-	1/1/1/1	-

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	401[A]	UPG	PB-O3B	6.56	1.79	1.59
5	A	401[B]	UPG	PB-O3B	6.56	1.79	1.59
5	A	401[A]	UPG	PB-O3A	-6.23	1.52	1.59
5	A	401[B]	UPG	PB-O3A	-6.23	1.52	1.59
4	B	900	NAD	C4N-C3N	4.00	1.45	1.39
4	A	400	NAD	C2N-N1N	3.56	1.38	1.35
5	B	901	UPG	PA-O3A	3.50	1.63	1.59
4	B	900	NAD	C2N-N1N	2.96	1.38	1.35
4	A	400	NAD	PN-O3	2.91	1.62	1.59
4	A	400	NAD	C4N-C3N	2.52	1.43	1.39
4	B	900	NAD	C6N-N1N	2.50	1.41	1.35
4	B	900	NAD	PN-O3	2.35	1.62	1.59
4	A	400	NAD	PA-O3	-2.28	1.57	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	400	NAD	C2A-N1A	2.26	1.38	1.33
4	B	900	NAD	C3N-C7N	2.19	1.53	1.50
4	B	900	NAD	PA-O2A	-2.16	1.45	1.55
4	A	400	NAD	C6N-N1N	2.14	1.40	1.35
4	A	400	NAD	PA-O2A	-2.03	1.45	1.55

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	400	NAD	C5N-C4N-C3N	-8.40	112.11	120.36
4	A	400	NAD	C5N-C6N-N1N	-5.74	112.55	120.38
4	B	900	NAD	C5N-C4N-C3N	-5.50	114.95	120.36
4	B	900	NAD	C5N-C6N-N1N	-5.40	113.02	120.38
5	A	401[A]	UPG	O5'-C1'-O3B	-5.25	104.50	111.36
5	A	401[B]	UPG	O5'-C1'-O3B	-5.25	104.50	111.36
4	A	400	NAD	C6N-C5N-C4N	4.69	126.21	119.45
4	B	900	NAD	C6N-N1N-C2N	4.56	125.75	121.88
4	B	900	NAD	C6N-C5N-C4N	4.16	125.45	119.45
5	A	401[A]	UPG	O3B-C1'-C2'	-3.74	101.53	108.38
5	A	401[B]	UPG	O3B-C1'-C2'	-3.74	101.53	108.38
5	A	401[A]	UPG	O5'-C1'-C2'	-2.99	104.23	110.37
5	A	401[B]	UPG	O5'-C1'-C2'	-2.99	104.23	110.37
4	A	400	NAD	C2N-C3N-C4N	2.89	121.62	118.26
5	B	901	UPG	O3B-C1'-C2'	2.82	113.55	108.38
5	B	901	UPG	PB-O3B-C1'	-2.69	110.26	121.21
4	B	900	NAD	C3N-C7N-N7N	2.68	121.04	117.74
5	B	901	UPG	C4'-C3'-C2'	-2.59	106.29	110.83
5	A	401[A]	UPG	C1'-C2'-C3'	2.47	115.21	110.01
5	A	401[B]	UPG	C1'-C2'-C3'	2.47	115.21	110.01
4	B	900	NAD	N6A-C6A-N1A	2.40	123.72	118.38
5	A	401[A]	UPG	O2A-PA-O3A	2.26	113.39	107.27
5	A	401[B]	UPG	O2A-PA-O3A	2.26	113.39	107.27
5	B	901	UPG	O5'-C1'-O3B	2.13	114.14	111.36
5	A	401[A]	UPG	O3B-PB-O1B	-2.06	103.21	109.81
5	A	401[B]	UPG	O3B-PB-O1B	-2.06	103.21	109.81

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	400	NAD	C5B-O5B-PA-O2A
4	A	400	NAD	C5D-O5D-PN-O2N

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Mol	Chain	Res	Type	Atoms
4	A	400	NAD	O4D-C1D-N1N-C2N
4	B	900	NAD	O4D-C1D-N1N-C2N
5	A	401[A]	UPG	C1'-O3B-PB-O3A
5	A	401[B]	UPG	C1'-O3B-PB-O3A
5	A	401[B]	UPG	C4'-C5'-C6'-O6'
5	A	401[B]	UPG	O5'-C5'-C6'-O6'
6	A	971	EDO	O1-C1-C2-O2
6	B	972	EDO	O1-C1-C2-O2
5	B	901	UPG	PA-O3A-PB-O1B
6	B	970	EDO	O1-C1-C2-O2
4	A	400	NAD	C5D-O5D-PN-O3
4	B	900	NAD	C5D-O5D-PN-O3
4	B	900	NAD	C2D-C1D-N1N-C6N
4	A	400	NAD	O4D-C1D-N1N-C6N
4	B	900	NAD	O4D-C1D-N1N-C6N
5	A	401[A]	UPG	PA-O3A-PB-O1B
5	A	401[B]	UPG	PA-O3A-PB-O1B
4	A	400	NAD	PA-O3-PN-O1N
4	A	400	NAD	PA-O3-PN-O2N
4	B	900	NAD	PA-O3-PN-O1N
4	B	900	NAD	PA-O3-PN-O2N
4	A	400	NAD	O4B-C4B-C5B-O5B
5	B	901	UPG	PA-O3A-PB-O2B

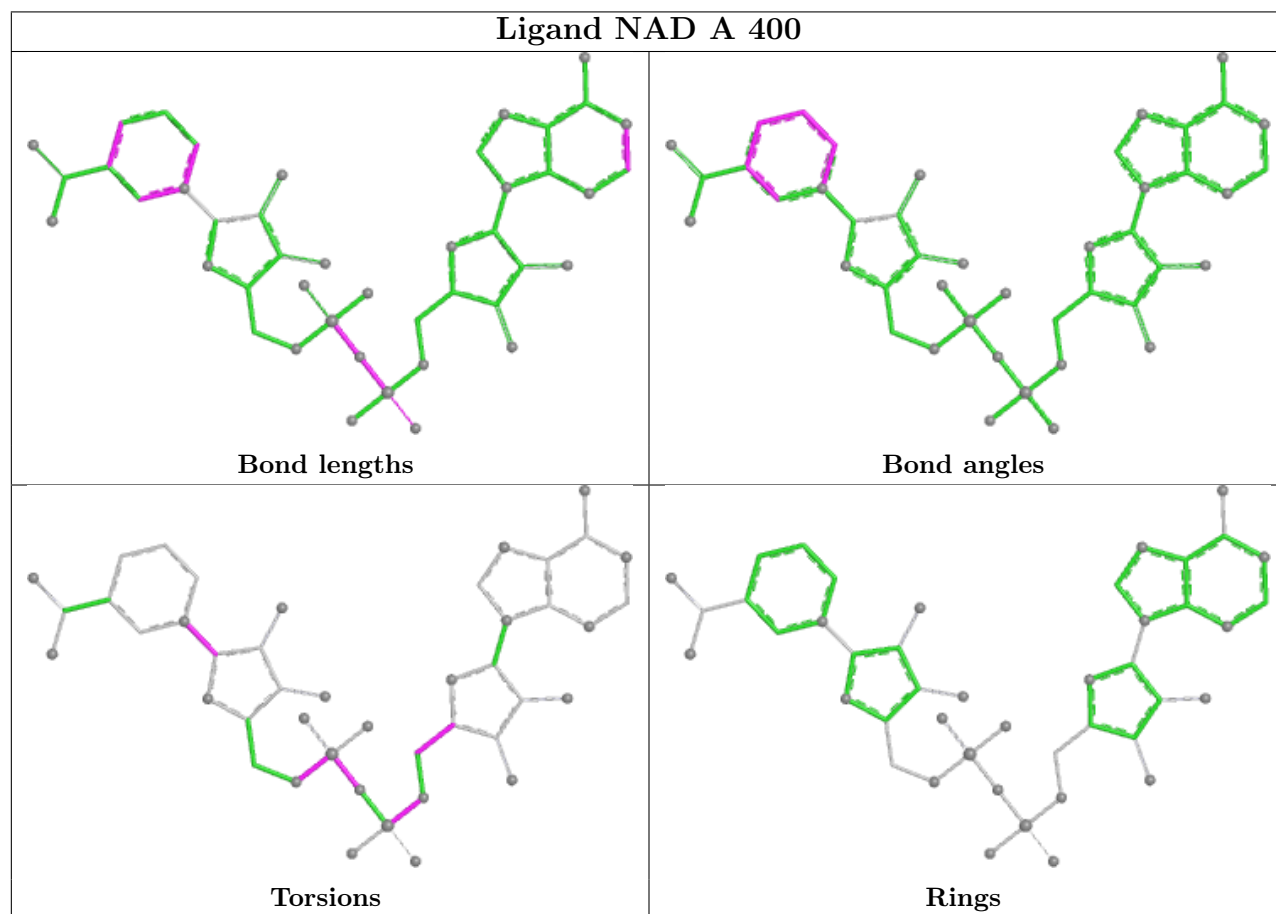
There are no ring outliers.

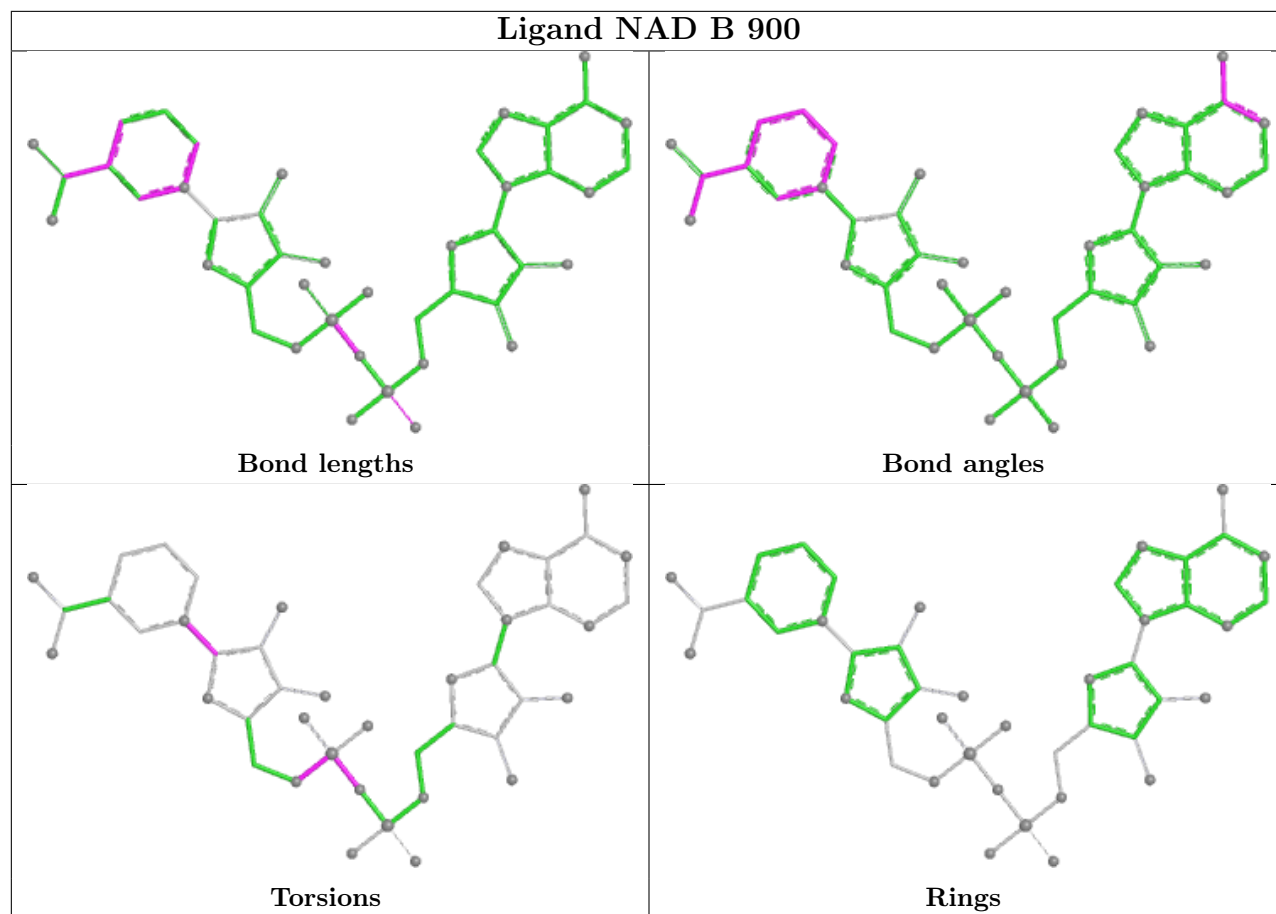
5 monomers are involved in 10 short contacts:

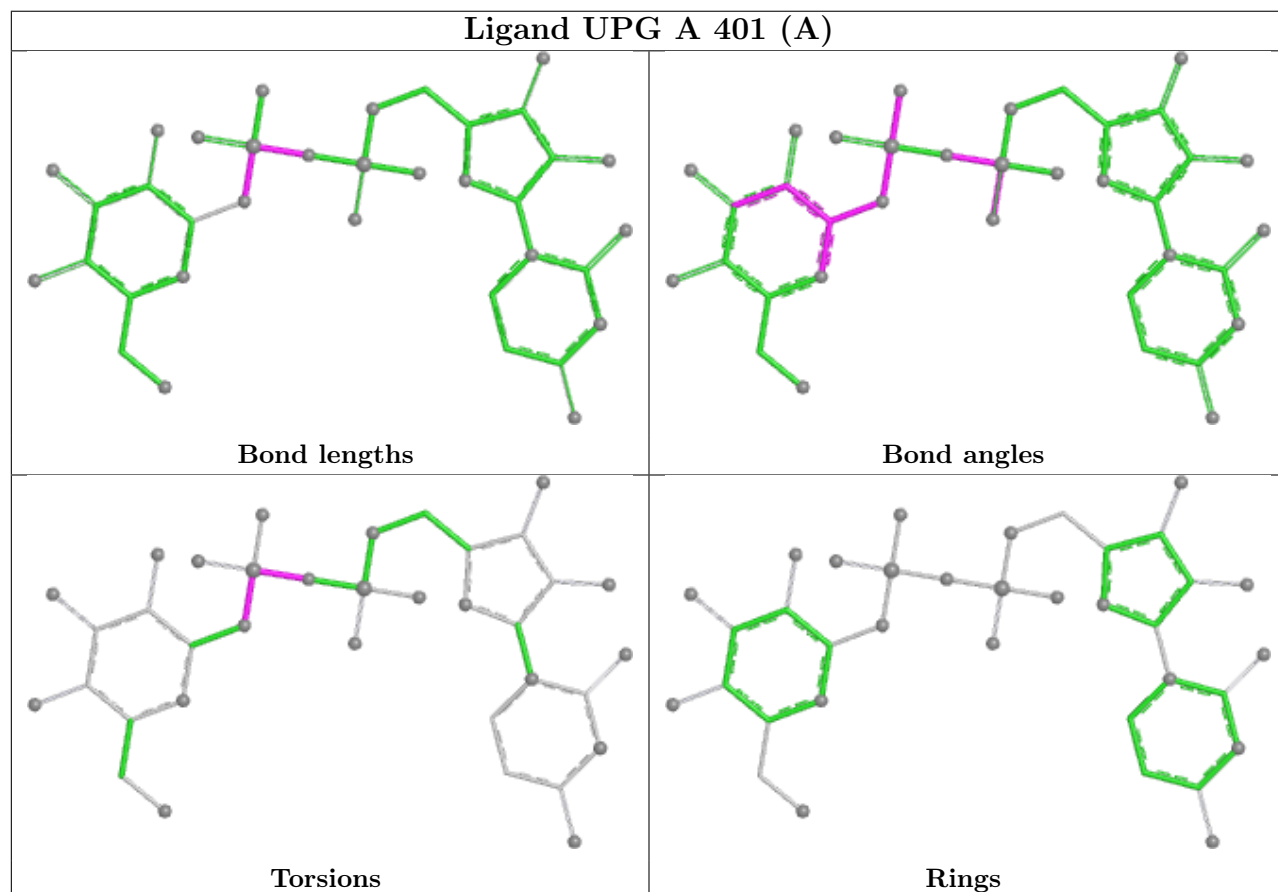
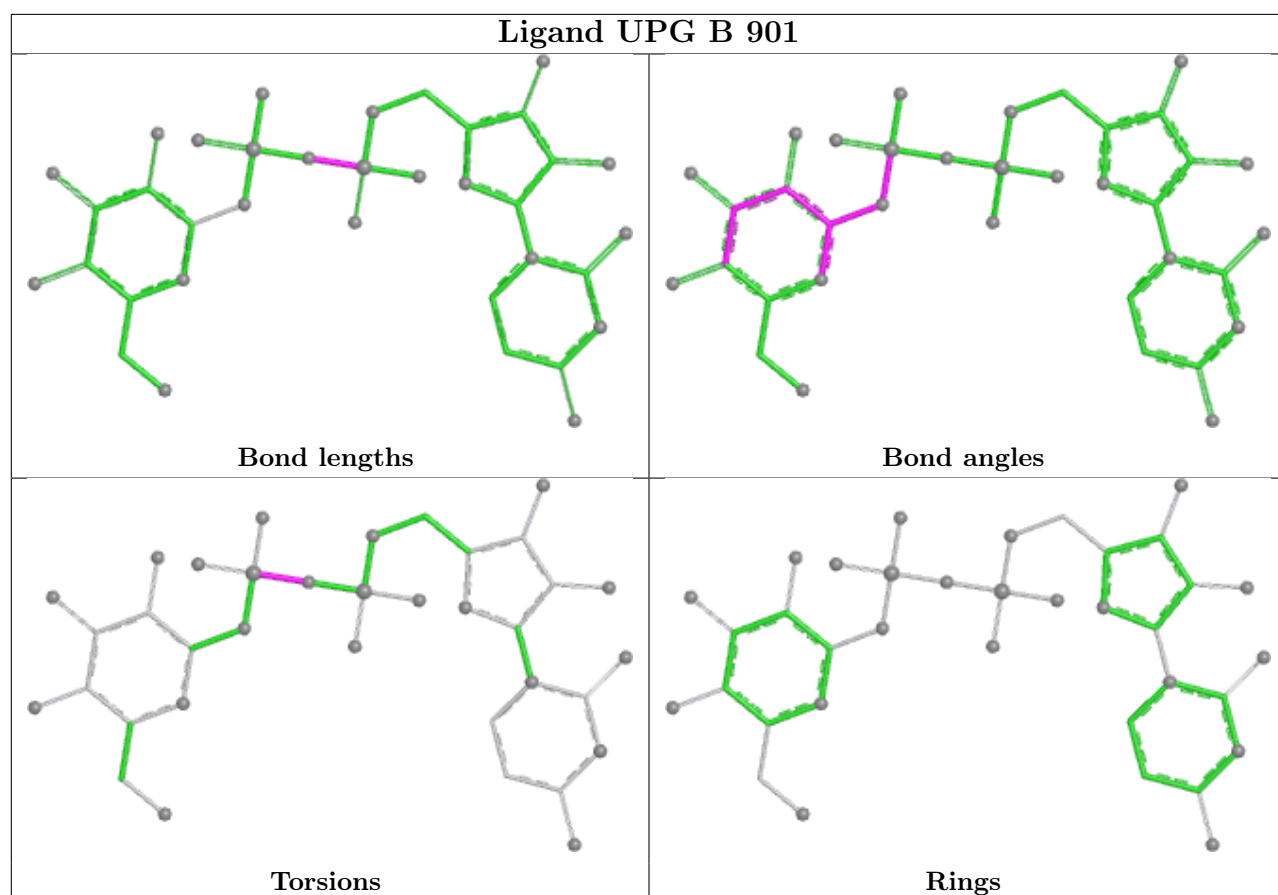
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	400	NAD	3	0
6	B	972	EDO	4	0
4	B	900	NAD	1	0
5	B	901	UPG	2	0
5	A	401[A]	UPG	1	0

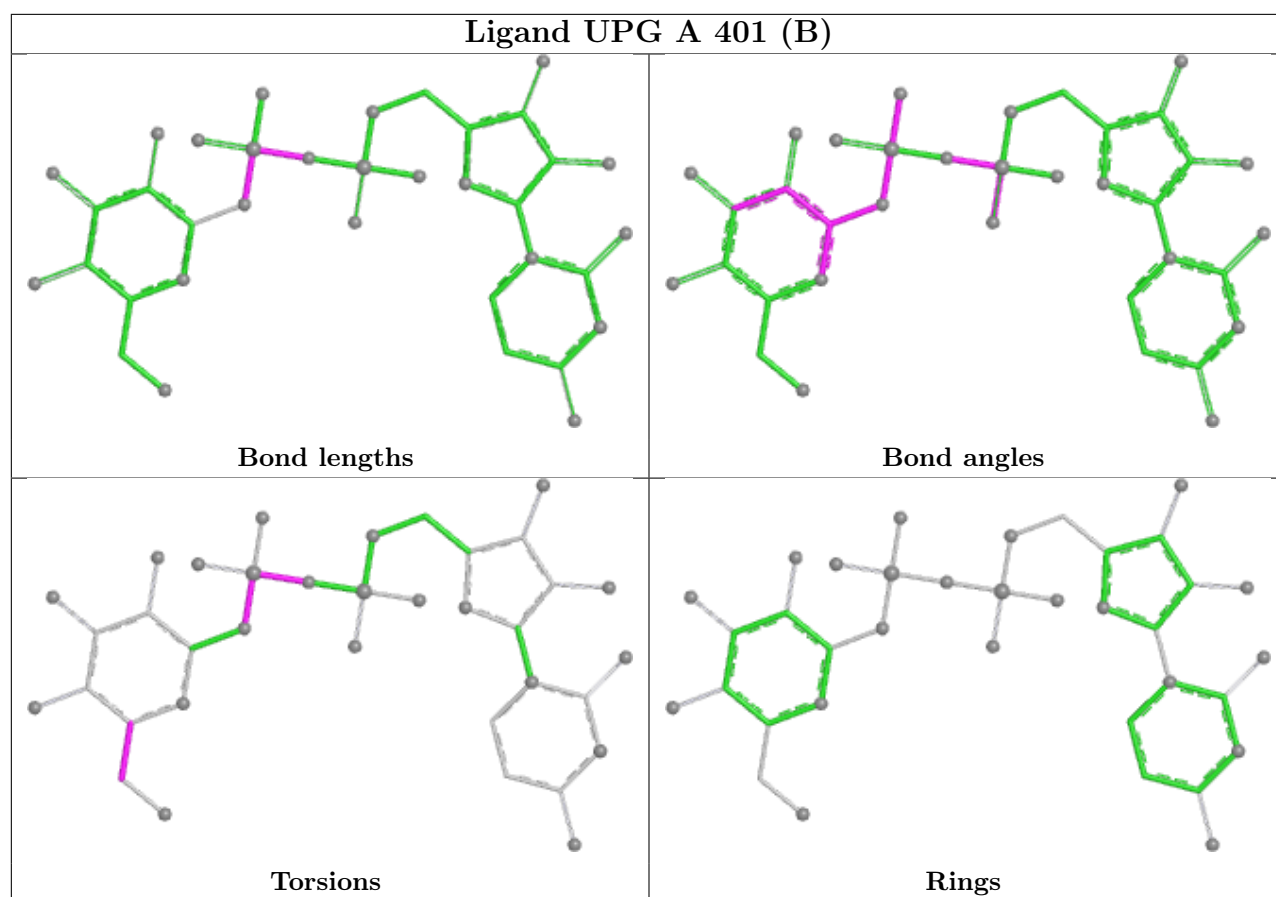
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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