



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 11:05 AM UTC

PDB ID : 1E3W / pdb_00001e3w
Title : Rat brain 3-hydroxyacyl-CoA dehydrogenase binary complex with NADH and 3-keto butyrate
Authors : Powell, A.J.; Read, J.A.; Brady, R.L.
Deposited on : 2000-06-26
Resolution : 2.00 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

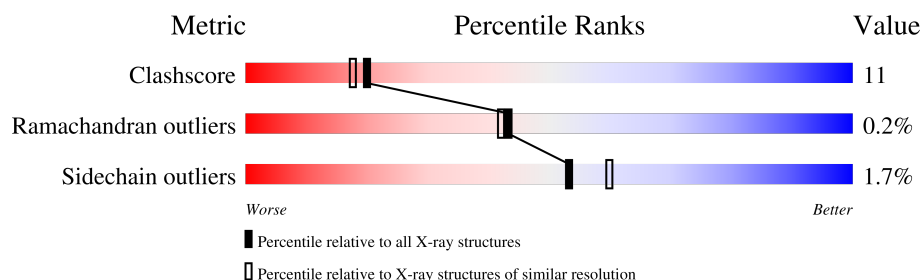
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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	261	62% 29% 6% .
2	B	261	67% 24% . 5%
2	C	261	73% 18% . 5%
2	D	261	68% 25% . . .

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
4	TRS	A	302	-	X	-	-
4	TRS	B	302	-	X	-	-
5	SO4	B	303	-	-	X	-

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 8558 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.

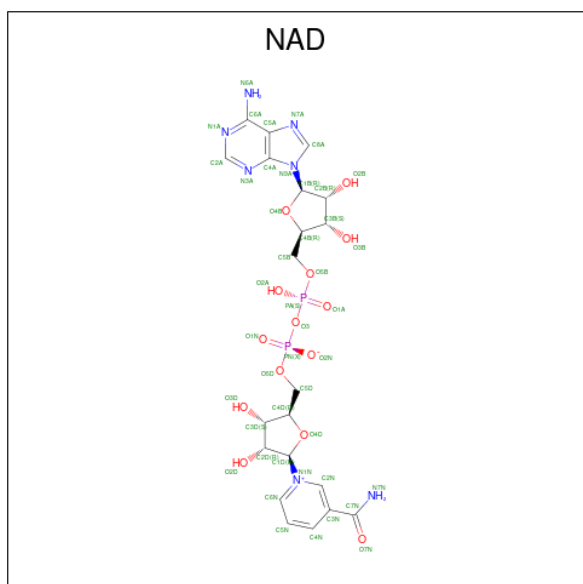
- Molecule 1 is a protein called SHORT CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	251	Total	C	N	O	S	27	8	0
			1868	1178	330	353	7			

- Molecule 2 is a protein called SHORT CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE.

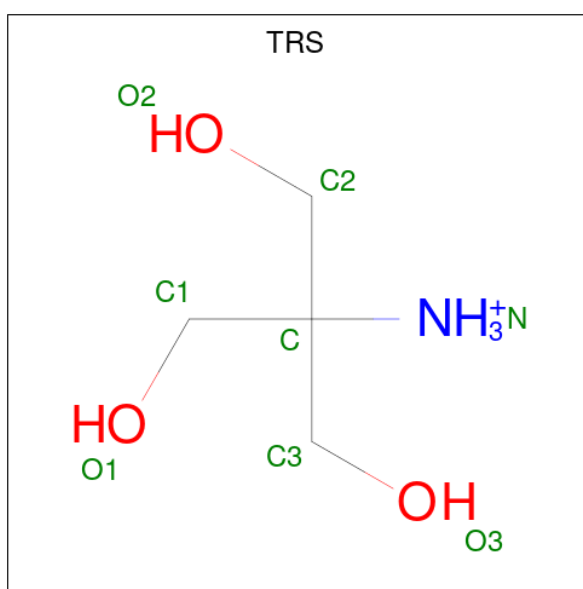
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	247	Total	C	N	O	S	4	11	0
			1852	1169	329	348	6			
2	C	248	Total	C	N	O	S	18	5	0
			1838	1161	326	344	7			
2	D	255	Total	C	N	O	S	23	2	0
			1879	1189	332	352	6			

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



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

- Molecule 4 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: C₄H₁₂NO₃).



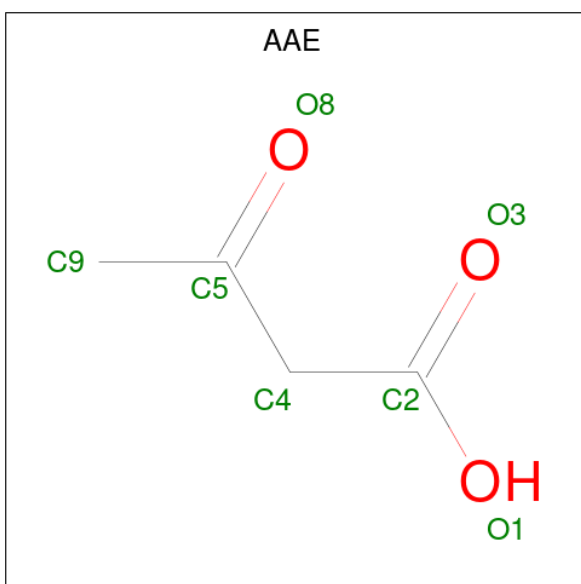
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			8	4	1	3		
4	B	1	Total	C	N	O	0	0
			8	4	1	3		
4	C	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 6 is ACETOACETIC ACID (CCD ID: AAE) (formula: C₄H₆O₃).



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

- Molecule 7 is water.

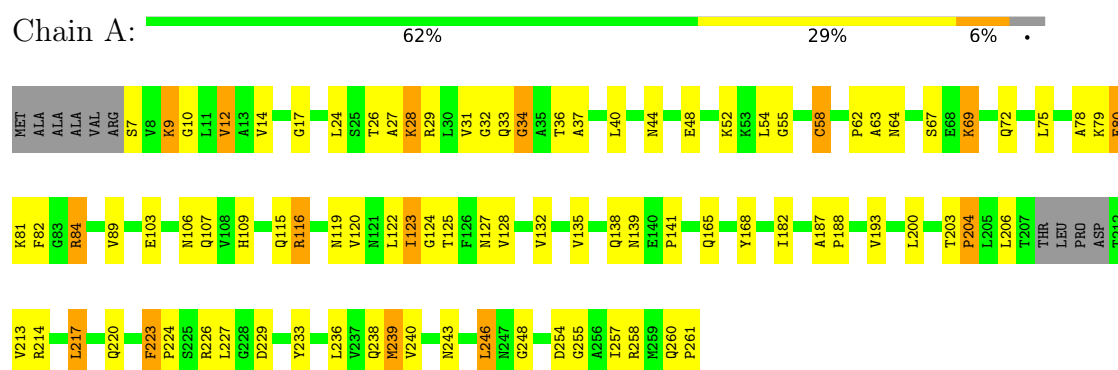
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	213	Total	O	0	0
			213	213		
7	B	226	Total	O	0	0
			226	226		
7	C	242	Total	O	0	0
			242	242		
7	D	208	Total	O	0	0
			208	208		

3 Residue-property plots

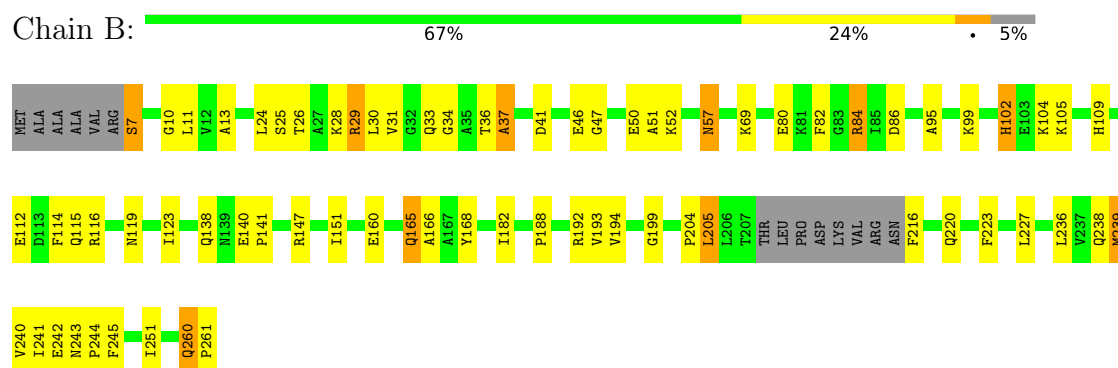
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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.

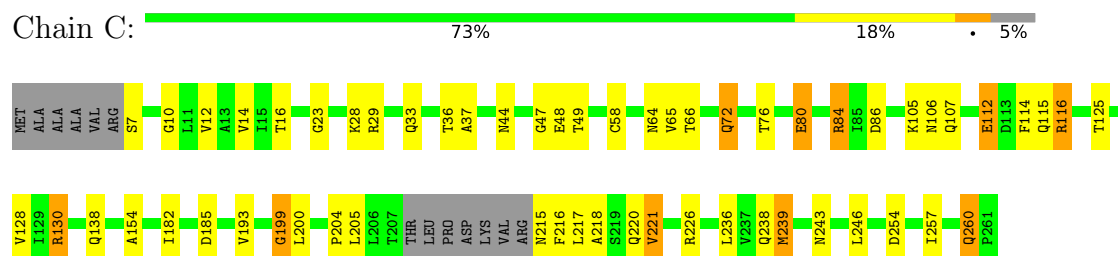
• Molecule 1: SHORT CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE



• Molecule 2: SHORT CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE



• Molecule 2: SHORT CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE



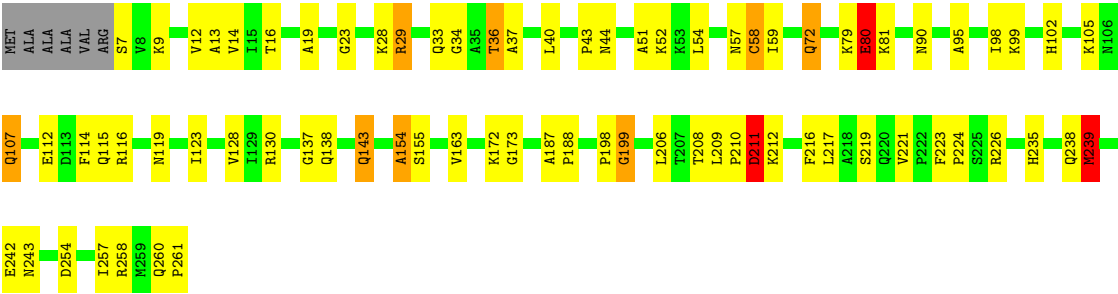
• Molecule 2: SHORT CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE

Chain D:

68%

25%

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4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	57.60Å 67.43Å 67.50Å 65.22° 73.27° 75.67°	Depositor
Resolution (Å)	40.00 – 2.00	Depositor
% Data completeness (in resolution range)	94.9 (40.00-2.00)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.189 , 0.226	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8558	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

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: SO4, TRS, NAD, AAE

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	1.75	37/1933 (1.9%)	2.16	54/2621 (2.1%)
2	B	1.62	21/1932 (1.1%)	1.94	49/2617 (1.9%)
2	C	1.43	7/1888 (0.4%)	1.93	40/2559 (1.6%)
2	D	1.66	27/1918 (1.4%)	2.00	44/2603 (1.7%)
All	All	1.62	92/7671 (1.2%)	2.01	187/10400 (1.8%)

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	A	0	3
2	B	0	2
2	C	0	3
2	D	0	2
All	All	0	10

All (92) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	239	MET	SD-CE	15.25	2.17	1.79
1	A	58	CYS	CB-SG	11.79	2.20	1.81
2	D	211	ASP	CB-CG	10.96	1.79	1.52
2	C	217	LEU	CA-CB	10.89	1.70	1.53
2	D	217	LEU	CB-CG	10.72	1.74	1.53
2	D	209	LEU	CB-CG	-10.38	1.32	1.53
2	D	59	ILE	C-O	9.90	1.34	1.23
2	D	14	VAL	C-O	9.71	1.34	1.24
2	B	30	LEU	C-O	9.28	1.34	1.24
1	A	128	VAL	C-O	9.23	1.35	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	58	CYS	C-O	8.82	1.33	1.24
1	A	78	ALA	C-O	8.72	1.34	1.24
2	D	143	GLN	CA-CB	-8.63	1.38	1.53
1	A	28	LYS	C-O	8.51	1.34	1.24
1	A	34	GLY	C-N	8.50	1.45	1.33
2	B	31	VAL	C-O	8.49	1.34	1.24
1	A	261	PRO	N-CD	8.30	1.59	1.47
1	A	217	LEU	CB-CG	8.18	1.69	1.53
2	B	29	ARG	C-O	8.01	1.33	1.24
2	B	26	THR	C-O	-7.86	1.15	1.24
2	B	51	ALA	C-O	-7.70	1.15	1.24
1	A	48[A]	GLU	C-O	7.55	1.33	1.24
1	A	48[B]	GLU	C-O	7.55	1.33	1.24
2	D	13	ALA	C-N	-7.42	1.24	1.33
1	A	135	VAL	C-O	7.42	1.32	1.24
1	A	124	GLY	C-O	7.33	1.32	1.23
2	D	57	ASN	C-O	7.17	1.33	1.24
1	A	79	LYS	CG-CD	-7.12	1.31	1.52
2	D	28	LYS	C-O	7.05	1.32	1.24
2	D	19	ALA	C-N	7.03	1.42	1.33
2	D	37	ALA	C-O	-7.03	1.16	1.24
1	A	62	PRO	C-N	6.94	1.42	1.33
1	A	24	LEU	C-O	6.89	1.32	1.24
2	C	66	THR	N-CA	6.85	1.55	1.46
2	C	154	ALA	CA-C	-6.79	1.50	1.53
2	D	198	PRO	C-O	6.79	1.31	1.23
1	A	31	VAL	C-O	6.78	1.32	1.24
1	A	168	TYR	C-N	6.72	1.43	1.34
1	A	123	ILE	C-O	-6.70	1.16	1.24
2	D	29	ARG	N-CA	6.67	1.54	1.46
2	D	235	HIS	CE1-NE2	6.65	1.39	1.32
2	D	261	PRO	N-CD	6.64	1.57	1.47
1	A	122	LEU	C-O	-6.60	1.16	1.23
1	A	127	ASN	C-O	6.56	1.31	1.24
2	D	114	PHE	N-CA	6.54	1.54	1.46
1	A	125	THR	C-O	-6.45	1.16	1.24
2	B	114	PHE	C-O	6.45	1.31	1.24
2	D	99	LYS	C-O	6.37	1.31	1.23
1	A	26	THR	C-O	-6.28	1.16	1.24
1	A	120	VAL	C-O	-6.23	1.17	1.24
2	C	64	ASN	C-N	5.99	1.40	1.34
1	A	246	LEU	C-O	5.98	1.31	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	13	ALA	C-O	5.96	1.31	1.24
2	D	23	GLY	CA-C	5.83	1.58	1.52
1	A	123	ILE	CA-C	5.82	1.60	1.52
2	C	28	LYS	N-CA	5.77	1.53	1.46
1	A	27	ALA	N-CA	5.77	1.53	1.46
2	B	109	HIS	CE1-NE2	5.73	1.38	1.32
1	A	17	GLY	C-N	-5.72	1.24	1.33
2	D	154	ALA	CA-C	-5.63	1.50	1.53
2	B	168	TYR	C-O	5.59	1.30	1.24
1	A	52	LYS	C-O	5.57	1.30	1.24
2	D	58	CYS	C-O	5.54	1.30	1.24
1	A	26	THR	CA-C	5.51	1.59	1.52
1	A	27	ALA	C-O	-5.49	1.17	1.24
2	D	163	VAL	N-CA	5.48	1.52	1.46
1	A	67	SER	C-O	5.43	1.30	1.24
2	D	239	MET	C-N	5.41	1.40	1.33
1	A	12	VAL	CA-C	5.36	1.59	1.52
1	A	233	TYR	C-N	5.36	1.41	1.33
2	D	59	ILE	C-N	-5.34	1.26	1.33
2	B	25	SER	N-CA	5.33	1.52	1.46
1	A	141	PRO	C-O	5.32	1.29	1.23
2	B	109	HIS	N-CA	5.31	1.52	1.46
2	B	240	VAL	C-N	5.29	1.40	1.33
2	B	28	LYS	C-O	-5.26	1.18	1.24
2	B	52	LYS	N-CA	5.24	1.52	1.46
2	B	251	ILE	C-O	5.24	1.29	1.24
1	A	132	VAL	C-O	5.23	1.30	1.24
2	D	29	ARG	CD-NE	5.20	1.53	1.46
2	D	226	ARG	C-O	5.19	1.29	1.23
2	D	154	ALA	C-N	5.19	1.39	1.33
1	A	109	HIS	CE1-NE2	5.17	1.37	1.32
2	B	119[A]	ASN	C-O	5.12	1.30	1.24
2	B	119[B]	ASN	C-O	5.12	1.30	1.24
1	A	69	LYS	CG-CD	5.11	1.67	1.52
2	B	24	LEU	C-N	5.10	1.40	1.34
2	B	13	ALA	N-CA	5.09	1.52	1.46
2	B	261	PRO	N-CD	5.06	1.54	1.47
2	B	160	GLU	C-N	5.03	1.37	1.33
2	C	37	ALA	C-O	-5.02	1.17	1.23
1	A	255	GLY	CA-C	5.01	1.58	1.51

All (187) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	84	ARG	CD-NE-CZ	35.86	174.60	124.40
1	A	84	ARG	NE-CZ-NH2	15.00	132.70	119.20
2	C	220	GLN	CB-CG-CD	-14.27	88.34	112.60
2	C	84[A]	ARG	CD-NE-CZ	13.26	142.96	124.40
2	C	84[B]	ARG	CD-NE-CZ	13.26	142.96	124.40
2	D	116	ARG	CD-NE-CZ	13.23	142.92	124.40
1	A	26	THR	O-C-N	12.17	134.61	122.07
1	A	44	ASN	CA-CB-CG	-10.21	102.39	112.60
2	D	211	ASP	CA-CB-CG	-10.20	102.40	112.60
2	B	80	GLU	CB-CG-CD	9.82	129.30	112.60
2	C	217	LEU	CB-CA-C	-9.56	94.60	110.85
2	B	239	MET	CG-SD-CE	-9.49	80.03	100.90
2	C	215	ASN	CA-CB-CG	9.48	122.08	112.60
1	A	213	VAL	N-CA-C	-9.38	101.72	110.82
2	D	216	PHE	CA-CB-CG	-9.13	104.67	113.80
2	D	211	ASP	CB-CG-OD1	-9.07	97.54	118.40
1	A	217	LEU	CA-C-O	8.94	130.91	121.07
1	A	12	VAL	O-C-N	8.85	133.46	123.10
2	D	57	ASN	OD1-CG-ND2	8.73	131.33	122.60
2	B	147	ARG	NE-CZ-NH2	8.60	126.94	119.20
2	D	44	ASN	CB-CA-C	8.43	125.18	112.03
2	B	7	SER	CA-C-O	8.36	135.01	120.80
1	A	75	LEU	O-C-N	8.24	131.55	122.15
2	B	34	GLY	CA-C-O	8.10	128.00	119.01
1	A	81	LYS	CA-CB-CG	8.09	130.28	114.10
2	D	44	ASN	O-C-N	8.04	132.03	122.46
2	D	90	ASN	OD1-CG-ND2	-7.99	114.61	122.60
2	C	204	PRO	O-C-N	-7.93	111.03	122.37
2	B	138	GLN	OE1-CD-NE2	-7.77	114.83	122.60
2	C	217	LEU	N-CA-C	7.70	119.75	111.36
2	B	50	GLU	CA-C-O	-7.68	112.27	120.42
1	A	64	ASN	OD1-CG-ND2	7.58	130.19	122.60
2	B	223	PHE	CA-CB-CG	-7.49	106.31	113.80
2	D	9	LYS	CB-CG-CD	-7.43	94.22	111.30
1	A	138	GLN	OE1-CD-NE2	-7.34	115.26	122.60
2	C	216	PHE	CA-C-N	7.33	130.71	120.29
2	C	216	PHE	C-N-CA	7.33	130.71	120.29
1	A	123	ILE	O-C-N	7.30	129.35	121.83
1	A	217	LEU	CA-C-N	7.30	130.38	120.38
1	A	217	LEU	C-N-CA	7.30	130.38	120.38
2	D	112	GLU	CG-CD-OE1	7.28	135.14	118.40
2	D	130	ARG	NE-CZ-NH2	-7.26	112.67	119.20
1	A	84	ARG	NE-CZ-NH1	-7.25	114.25	121.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	33	GLN	OE1-CD-NE2	7.25	129.85	122.60
2	D	44	ASN	CA-C-O	-7.22	114.07	122.37
2	C	80	GLU	CA-C-O	-7.16	113.33	120.70
2	D	90	ASN	CB-CG-ND2	7.09	127.03	116.40
1	A	213	VAL	CA-CB-CG1	7.07	122.42	110.40
2	C	200	LEU	CA-C-O	-7.05	112.56	120.32
2	B	11	LEU	O-C-N	7.04	131.17	122.86
1	A	116	ARG	CD-NE-CZ	-6.92	114.71	124.40
2	C	10	GLY	CA-C-O	-6.90	112.09	119.27
2	D	206	LEU	N-CA-C	6.89	120.78	112.38
2	B	192	ARG	NE-CZ-NH1	6.86	128.36	121.50
2	D	211	ASP	CB-CG-OD2	6.86	134.18	118.40
1	A	72	GLN	CG-CD-NE2	6.79	126.58	116.40
2	C	221	VAL	N-CA-C	6.70	114.40	108.63
2	B	260	GLN	CG-CD-NE2	6.70	126.45	116.40
2	D	57	ASN	CB-CG-ND2	-6.66	106.41	116.40
2	B	102	HIS	CA-C-O	-6.65	113.11	120.70
2	C	125	THR	O-C-N	-6.58	115.14	122.12
2	B	57	ASN	OD1-CG-ND2	6.52	129.12	122.60
2	C	185	ASP	CA-CB-CG	6.47	119.07	112.60
1	A	139	ASN	OD1-CG-ND2	-6.47	116.13	122.60
2	C	112	GLU	CB-CG-CD	6.44	123.55	112.60
1	A	229	ASP	CA-CB-CG	6.41	119.01	112.60
2	C	36	THR	CA-CB-OG1	6.41	119.21	109.60
1	A	26	THR	CA-C-N	-6.38	112.14	120.44
1	A	26	THR	C-N-CA	-6.38	112.14	120.44
2	B	84[A]	ARG	NE-CZ-NH2	6.38	124.94	119.20
2	B	84[B]	ARG	NE-CZ-NH2	6.38	124.94	119.20
1	A	165	GLN	OE1-CD-NE2	-6.36	116.24	122.60
1	A	63	ALA	N-CA-CB	6.34	121.30	110.77
2	D	40	LEU	CB-CA-C	6.29	120.50	110.19
1	A	127	ASN	OD1-CG-ND2	6.28	128.88	122.60
2	B	119[A]	ASN	CA-C-O	-6.26	113.78	120.42
2	B	119[B]	ASN	CA-C-O	-6.26	113.78	120.42
2	B	227	LEU	CA-C-N	6.25	126.28	120.34
2	B	227	LEU	C-N-CA	6.25	126.28	120.34
2	D	19	ALA	CA-C-O	6.25	127.11	119.11
2	B	205	LEU	CB-CA-C	6.24	122.57	110.46
2	B	260	GLN	OE1-CD-NE2	-6.22	116.38	122.60
2	B	245	PHE	CA-C-O	-6.14	112.02	119.32
2	B	52	LYS	O-C-N	-6.12	115.47	122.09
2	B	245	PHE	O-C-N	6.10	129.62	122.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	199	GLY	CA-C-O	-6.09	109.97	120.57
2	B	165	GLN	O-C-N	-6.06	115.06	122.34
2	C	243	ASN	CA-CB-CG	-6.06	106.54	112.60
2	D	217	LEU	CB-CG-CD2	6.04	128.80	110.70
2	D	243	ASN	CA-CB-CG	-6.02	106.58	112.60
2	C	23	GLY	O-C-N	6.01	128.02	122.19
2	B	11	LEU	CA-C-N	-6.00	115.32	123.12
2	B	11	LEU	C-N-CA	-6.00	115.32	123.12
1	A	243	ASN	CA-CB-CG	-5.99	106.61	112.60
2	D	81	LYS	N-CA-CB	5.98	118.64	109.91
1	A	116	ARG	NE-CZ-NH1	-5.96	115.54	121.50
2	D	98	ILE	O-C-N	5.90	129.11	123.03
1	A	14	VAL	CA-C-O	-5.88	114.27	120.57
1	A	123	ILE	CA-C-O	-5.88	114.62	120.85
1	A	258	ARG	CA-C-N	-5.88	113.10	121.50
1	A	258	ARG	C-N-CA	-5.88	113.10	121.50
1	A	107	GLN	CG-CD-NE2	-5.84	107.63	116.40
2	D	34	GLY	N-CA-C	5.82	123.47	115.27
2	C	130	ARG	O-C-N	5.80	129.40	122.27
2	D	219	SER	CA-C-O	-5.79	113.56	120.10
2	D	155	SER	O-C-N	5.79	128.62	123.41
2	D	173	GLY	CA-C-O	5.76	126.62	120.40
1	A	106	ASN	CA-CB-CG	-5.76	106.84	112.60
2	D	43	PRO	O-C-N	-5.74	115.34	122.23
2	C	72	GLN	CA-C-O	-5.73	114.47	120.55
1	A	248	GLY	CA-C-O	-5.69	112.18	119.58
1	A	33[A]	GLN	OE1-CD-NE2	5.68	128.28	122.60
1	A	33[B]	GLN	OE1-CD-NE2	5.68	128.28	122.60
2	B	147	ARG	NE-CZ-NH1	-5.65	115.85	121.50
2	B	205	LEU	O-C-N	-5.65	115.76	122.20
2	C	44	ASN	CA-CB-CG	5.64	118.25	112.60
1	A	72	GLN	CG-CD-OE1	-5.62	109.56	120.80
2	D	212	LYS	N-CA-C	-5.60	106.42	113.20
2	B	240	VAL	CA-C-N	-5.57	112.83	120.46
2	B	240	VAL	C-N-CA	-5.57	112.83	120.46
2	B	243	ASN	CA-CB-CG	-5.56	107.04	112.60
1	A	12	VAL	CA-C-O	-5.55	114.59	120.53
2	D	115	GLN	OE1-CD-NE2	-5.55	117.05	122.60
2	B	41	ASP	O-C-N	5.52	129.05	123.26
2	B	205	LEU	N-CA-CB	-5.49	101.46	110.14
2	C	64	ASN	CA-CB-CG	-5.49	107.11	112.60
1	A	119	ASN	CA-C-O	-5.49	115.05	120.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	44	ASN	CB-CG-ND2	-5.48	108.18	116.40
1	A	89	VAL	O-C-N	-5.47	117.40	123.20
2	D	23	GLY	O-C-N	5.44	127.47	122.19
1	A	55	GLY	O-C-N	-5.43	116.95	122.98
2	D	13	ALA	CA-C-N	5.42	130.16	123.12
2	D	13	ALA	C-N-CA	5.42	130.16	123.12
2	C	221	VAL	N-CA-CB	-5.40	104.45	110.23
2	B	260	GLN	CB-CG-CD	5.39	121.77	112.60
2	C	14	VAL	CA-C-O	-5.38	114.78	120.48
1	A	227	LEU	CA-C-N	5.34	125.42	120.34
1	A	227	LEU	C-N-CA	5.34	125.42	120.34
2	C	48	GLU	CB-CG-CD	-5.33	103.55	112.60
1	A	226	ARG	NE-CZ-NH2	5.32	123.99	119.20
2	C	65	VAL	O-C-N	5.30	129.52	122.31
1	A	168	TYR	CA-C-O	5.29	126.38	120.82
2	C	205	LEU	O-C-N	-5.28	116.04	122.22
1	A	62	PRO	CA-C-O	5.28	127.05	121.03
2	B	116[A]	ARG	NE-CZ-NH2	-5.28	114.45	119.20
2	B	116[B]	ARG	NE-CZ-NH2	-5.28	114.45	119.20
2	C	204	PRO	CA-C-N	5.26	127.85	120.28
2	C	204	PRO	C-N-CA	5.26	127.85	120.28
2	D	242	GLU	CA-C-O	-5.26	114.40	120.24
2	B	11	LEU	CA-C-O	-5.26	115.83	121.56
2	D	154	ALA	CA-C-O	5.25	120.99	117.94
1	A	239[A]	MET	CB-CG-SD	5.25	128.45	112.70
1	A	239[B]	MET	CB-CG-SD	5.25	128.45	112.70
2	C	65	VAL	CA-C-N	-5.25	112.88	122.38
2	C	65	VAL	C-N-CA	-5.25	112.88	122.38
2	B	260	GLN	N-CA-C	-5.22	104.12	110.13
1	A	31	VAL	CA-CB-CG1	5.20	119.24	110.40
1	A	32	GLY	N-CA-C	-5.19	106.42	113.37
2	C	116	ARG	NE-CZ-NH1	-5.17	116.33	121.50
2	B	47	GLY	CA-C-N	-5.17	112.95	120.29
2	B	47	GLY	C-N-CA	-5.17	112.95	120.29
2	D	33	GLN	CA-C-O	5.17	125.61	119.56
1	A	223	PHE	CA-CB-CG	-5.16	108.64	113.80
2	D	80	GLU	O-C-N	5.15	127.65	122.09
2	B	37	ALA	CA-C-O	5.15	126.78	120.60
2	B	29	ARG	O-C-N	-5.14	116.29	122.15
2	B	80	GLU	CA-C-O	-5.13	115.11	120.55
2	D	173	GLY	O-C-N	-5.13	116.80	122.24
2	C	260[A]	GLN	OE1-CD-NE2	-5.13	117.47	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	260[B]	GLN	OE1-CD-NE2	-5.13	117.47	122.60
2	D	258	ARG	N-CA-C	-5.13	100.09	108.76
2	B	241	ILE	O-C-N	5.12	126.84	121.87
2	C	37	ALA	CA-C-N	-5.12	116.47	123.12
2	C	37	ALA	C-N-CA	-5.12	116.47	123.12
2	D	36	THR	CA-CB-OG1	5.11	117.26	109.60
1	A	75	LEU	CA-C-O	-5.10	115.01	120.42
1	A	240	VAL	O-C-N	5.09	127.07	121.83
2	B	51	ALA	CA-C-N	-5.08	113.53	120.44
2	B	51	ALA	C-N-CA	-5.08	113.53	120.44
1	A	127	ASN	N-CA-C	-5.08	105.75	111.28
2	D	112	GLU	OE1-CD-OE2	-5.08	110.72	122.90
2	D	137	GLY	CA-C-O	-5.07	112.42	119.01
2	B	46	GLU	O-C-N	-5.04	115.92	122.37
2	B	7	SER	N-CA-C	5.04	125.11	111.00
2	C	76	THR	CA-C-O	-5.04	115.08	120.42
2	D	155	SER	CA-C-O	-5.01	115.50	121.06
2	C	47	GLY	O-C-N	5.01	127.09	122.13

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	214	ARG	Sidechain
1	A	34	GLY	Mainchain
1	A	80	GLU	Mainchain
2	B	199	GLY	Mainchain
2	B	95	ALA	Mainchain
2	C	130	ARG	Sidechain
2	C	199	GLY	Mainchain
2	C	80	GLU	Mainchain
2	D	199	GLY	Mainchain
2	D	211	ASP	Sidechain

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	1868	0	1931	52	0
2	B	1852	0	1922	58	1
2	C	1838	0	1901	52	0
2	D	1879	0	1943	45	1
3	A	44	0	26	0	0
3	B	44	0	26	0	0
3	C	44	0	26	1	0
3	D	44	0	26	1	0
4	A	8	0	12	0	0
4	B	8	0	12	0	0
4	C	8	0	12	0	0
5	A	10	0	0	0	0
5	B	5	0	0	2	0
5	C	5	0	0	0	0
5	D	5	0	0	0	0
6	D	7	0	5	2	0
7	A	213	0	0	9	0
7	B	226	0	0	7	0
7	C	242	0	0	8	0
7	D	208	0	0	6	0
All	All	8558	0	7842	175	1

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 (175) 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)
2:B:239:MET:CE	2:B:239:MET:SD	2.17	1.33
1:A:58:CYS:SG	1:A:58:CYS:CB	2.20	1.30
2:B:236:LEU:HD12	2:D:239:MET:HE2	1.09	1.04
1:A:239[A]:MET:CG	2:C:239[A]:MET:HG3	1.85	1.04
2:B:239:MET:HB2	2:D:239:MET:HE3	1.05	1.02
2:B:239:MET:CB	2:D:239:MET:HE3	1.92	0.99
2:B:236:LEU:HD12	2:D:239:MET:CE	1.94	0.97
2:B:239:MET:HB2	2:D:239:MET:CE	1.98	0.92
2:D:29:ARG:HE	2:D:238[B]:GLN:HE21	1.16	0.92
2:C:29:ARG:HE	2:C:238[B]:GLN:HE21	1.16	0.92
2:C:29:ARG:HH21	2:C:238[B]:GLN:HE22	1.12	0.91
2:B:29:ARG:HE	2:B:238[B]:GLN:HE21	1.17	0.91
1:A:29:ARG:HH21	1:A:238[B]:GLN:HE22	1.18	0.87
2:B:29:ARG:HH21	2:B:238[B]:GLN:HE22	1.20	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:236:LEU:CD1	2:D:239:MET:HE2	2.02	0.87
1:A:29:ARG:HE	1:A:238[B]:GLN:HE21	1.21	0.84
1:A:239[A]:MET:HG2	2:C:239[A]:MET:HG3	1.57	0.83
2:B:239:MET:CE	2:B:239:MET:CG	2.58	0.82
2:D:29:ARG:HE	2:D:238[B]:GLN:NE2	1.81	0.77
2:B:239:MET:CE	2:B:239:MET:HG3	2.14	0.77
1:A:239[A]:MET:HG3	2:C:239[A]:MET:HG3	1.64	0.77
2:B:238[A]:GLN:NE2	7:B:401:HOH:O	2.12	0.76
2:C:29:ARG:HE	2:C:238[B]:GLN:NE2	1.84	0.75
2:D:36:THR:HG23	7:D:2143:HOH:O	1.85	0.74
2:D:29:ARG:HH21	2:D:238[B]:GLN:HE22	1.37	0.73
2:B:29:ARG:HE	2:B:238[B]:GLN:NE2	1.85	0.72
2:C:29:ARG:HH21	2:C:238[B]:GLN:NE2	1.88	0.71
2:B:36[B]:THR:HG21	2:B:82:PHE:CE2	2.25	0.71
1:A:29:ARG:HH21	1:A:238[B]:GLN:NE2	1.88	0.70
2:B:36[B]:THR:HG21	2:B:82:PHE:CZ	2.27	0.69
2:D:260:GLN:HG2	7:D:2064:HOH:O	1.91	0.69
1:A:29:ARG:HE	1:A:238[B]:GLN:NE2	1.92	0.68
2:D:102:HIS:HD2	2:D:105:LYS:H	1.42	0.67
7:B:563:HOH:O	2:D:239:MET:SD	2.52	0.66
2:B:36[B]:THR:HG21	2:B:82:PHE:CE1	2.31	0.66
2:C:49:THR:HG23	7:C:551:HOH:O	1.95	0.66
2:B:36[B]:THR:HG22	2:B:37:ALA:N	2.10	0.65
2:B:104:LYS:HE2	2:B:105:LYS:HZ1	1.60	0.65
2:D:95:ALA:HB3	2:D:208:THR:HG21	1.78	0.65
2:B:29:ARG:HH21	2:B:238[B]:GLN:NE2	1.94	0.65
1:A:239[A]:MET:HB2	2:C:239[A]:MET:HG3	1.79	0.64
1:A:116:ARG:NH1	7:A:401:HOH:O	2.30	0.64
2:D:72:GLN:HG3	7:D:2002:HOH:O	1.98	0.63
2:D:7:SER:HA	7:D:2016:HOH:O	1.98	0.63
2:D:51:ALA:HA	2:D:58:CYS:SG	2.39	0.62
1:A:115[B]:GLN:NE2	2:B:123:ILE:HD13	2.14	0.62
2:C:115[A]:GLN:CD	2:D:123[A]:ILE:HD13	2.26	0.61
1:A:36[A]:THR:HG23	7:A:454:HOH:O	2.01	0.60
2:B:36[B]:THR:HG21	2:B:82:PHE:CD2	2.35	0.60
2:B:7:SER:HA	7:B:401:HOH:O	2.01	0.60
2:B:36[B]:THR:CG2	2:B:82:PHE:CE2	2.84	0.60
2:C:12:VAL:HG23	2:C:84[A]:ARG:NH1	2.18	0.59
2:B:239:MET:HE3	2:D:239:MET:HB2	1.84	0.59
2:B:36[B]:THR:CG2	2:B:82:PHE:CZ	2.86	0.59
6:D:302[L]:AAE:O3	6:D:302[L]:AAE:H92	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:112:GLU:HA	2:C:115[B]:GLN:HE21	1.69	0.57
2:C:236:LEU:CD1	2:C:239[B]:MET:HE3	2.34	0.57
2:C:115[A]:GLN:NE2	2:D:123[A]:ILE:CD1	2.68	0.56
2:D:102:HIS:CD2	2:D:105:LYS:H	2.22	0.56
1:A:239[A]:MET:HG2	2:C:239[A]:MET:CG	2.31	0.56
2:B:36[B]:THR:HG23	2:B:57:ASN:O	2.04	0.56
1:A:260[B]:GLN:HG2	7:A:500:HOH:O	2.05	0.56
1:A:123:ILE:HD13	2:B:115[B]:GLN:OE1	2.06	0.55
1:A:239[A]:MET:CG	2:C:239[A]:MET:CG	2.73	0.55
2:C:116:ARG:NH1	7:C:401:HOH:O	2.40	0.55
2:C:12:VAL:HG23	2:C:84[A]:ARG:HH11	1.72	0.55
2:C:218:ALA:HB1	2:C:226:ARG:HA	1.88	0.54
1:A:103:GLU:OE2	2:B:188:PRO:HB2	2.08	0.54
1:A:123:ILE:HD13	2:B:115[B]:GLN:CD	2.32	0.54
2:C:221:VAL:HG21	7:C:485:HOH:O	2.06	0.54
2:C:106:ASN:HB2	7:C:479:HOH:O	2.08	0.53
2:B:69:LYS:NZ	5:B:303:SO4:O3	2.31	0.53
2:B:84[B]:ARG:HD3	7:B:454:HOH:O	2.08	0.53
2:C:84[A]:ARG:CZ	2:C:86:ASP:OD2	2.57	0.52
2:C:239[B]:MET:HE1	2:C:246:LEU:HD21	1.91	0.52
2:D:254:ASP:HB2	2:D:257:ILE:HG22	1.90	0.52
2:B:10:GLY:O	2:B:84[A]:ARG:NH1	2.43	0.52
1:A:239[A]:MET:SD	1:A:246:LEU:CD2	2.97	0.52
2:B:239:MET:HE3	2:D:239:MET:CA	2.39	0.51
2:D:107:GLN:HG2	7:D:2026:HOH:O	2.09	0.51
1:A:36[B]:THR:HG21	1:A:82:PHE:CD1	2.45	0.51
2:B:239:MET:HE3	2:D:239:MET:HA	1.92	0.51
2:B:102:HIS:NE2	2:B:104:LYS:HD3	2.26	0.51
1:A:10:GLY:O	1:A:84:ARG:NH1	2.34	0.51
2:B:104:LYS:HE2	2:B:105:LYS:NZ	2.26	0.51
2:C:7:SER:HB2	7:C:408:HOH:O	2.11	0.51
1:A:7:SER:HA	7:A:407:HOH:O	2.09	0.51
1:A:12:VAL:HG23	1:A:84:ARG:HH11	1.75	0.51
1:A:239[B]:MET:HG3	2:C:239[B]:MET:HB2	1.92	0.51
3:D:301:NAD:O7N	6:D:302[L]:AAE:H91	2.11	0.50
2:C:236:LEU:HD12	2:C:239[B]:MET:HE3	1.93	0.50
1:A:239[A]:MET:HG3	2:C:239[A]:MET:CG	2.37	0.50
2:D:79:LYS:HZ2	2:D:138:GLN:CD	2.19	0.50
1:A:115[B]:GLN:CD	2:B:123:ILE:HD13	2.37	0.49
1:A:187:ALA:HB3	1:A:188:PRO:HD3	1.95	0.49
1:A:12:VAL:HG22	1:A:36[A]:THR:OG1	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:105:LYS:HB3	2:C:107:GLN:HG3	1.94	0.49
1:A:223:PHE:CD1	1:A:224:PRO:HA	2.48	0.48
2:C:254:ASP:HB2	2:C:257:ILE:HG22	1.93	0.48
2:D:119:ASN:OD1	2:D:123[A]:ILE:HD12	2.14	0.48
1:A:36[B]:THR:HG21	1:A:82:PHE:CE1	2.48	0.48
1:A:236:LEU:CD1	1:A:239[A]:MET:HE3	2.43	0.48
1:A:206:LEU:HD11	7:A:445:HOH:O	2.14	0.48
1:A:239[A]:MET:HE1	1:A:246:LEU:HD21	1.94	0.48
2:B:36[B]:THR:HG21	2:B:82:PHE:CG	2.48	0.48
1:A:239[B]:MET:HG2	2:C:239[B]:MET:HG2	1.95	0.47
2:C:114:PHE:CE1	2:D:123[B]:ILE:HD13	2.49	0.47
1:A:182:ILE:HG22	1:A:193:VAL:HG21	1.97	0.47
2:C:236:LEU:HD11	2:C:239[B]:MET:HE3	1.97	0.47
2:C:138:GLN:NE2	7:C:402:HOH:O	2.46	0.47
2:B:36[B]:THR:HG21	2:B:82:PHE:CD1	2.51	0.46
2:B:140:GLU:CD	2:B:141:PRO:HD2	2.40	0.46
2:B:236:LEU:CD1	2:D:239:MET:CE	2.78	0.46
1:A:254:ASP:HB2	1:A:257:ILE:HG22	1.98	0.46
2:C:29:ARG:NH2	2:C:238[B]:GLN:HE22	1.96	0.46
2:D:29:ARG:NE	2:D:238[B]:GLN:NE2	2.59	0.45
2:B:36[B]:THR:CG2	2:B:37:ALA:N	2.78	0.45
2:C:72:GLN:HE21	2:C:72:GLN:HA	1.81	0.45
2:C:115[A]:GLN:NE2	2:D:123[A]:ILE:HD13	2.31	0.45
2:C:115[A]:GLN:HE22	2:D:123[A]:ILE:CD1	2.28	0.45
2:D:7:SER:N	7:D:2001:HOH:O	2.48	0.45
1:A:238[A]:GLN:NE2	7:A:407:HOH:O	2.49	0.45
2:C:115[A]:GLN:OE1	2:D:123[A]:ILE:HD13	2.16	0.44
2:B:84[A]:ARG:NH1	2:B:86:ASP:OD2	2.51	0.44
2:B:239:MET:HE3	2:D:239:MET:CB	2.48	0.44
2:D:223:PHE:HA	2:D:224:PRO:C	2.42	0.44
2:D:12:VAL:HG22	2:D:36:THR:OG1	2.17	0.44
1:A:29:ARG:NH2	1:A:238[B]:GLN:NE2	2.63	0.44
1:A:116:ARG:HH11	1:A:116:ARG:HD3	1.46	0.44
2:C:260[B]:GLN:HG2	7:C:500:HOH:O	2.18	0.44
2:B:151:ILE:HA	2:B:194:VAL:O	2.18	0.43
2:C:112:GLU:H	2:C:112:GLU:CD	2.26	0.43
1:A:200:LEU:HD13	1:A:217:LEU:HB3	2.01	0.43
2:D:154:ALA:HA	2:D:172:LYS:HD2	2.00	0.43
2:C:221:VAL:HG22	2:C:257:ILE:HD12	2.01	0.43
1:A:223:PHE:HA	1:A:224:PRO:C	2.43	0.43
2:D:221:VAL:HG22	2:D:257:ILE:HD12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:ALA:O	1:A:58:CYS:HA	2.19	0.43
2:C:16:THR:HG21	2:C:128:VAL:HG21	2.01	0.42
2:C:199:GLY:O	3:C:301:NAD:H4N	2.19	0.42
1:A:217:LEU:O	1:A:220:GLN:HB2	2.18	0.42
1:A:123:ILE:CD1	2:B:115[B]:GLN:NE2	2.82	0.42
2:C:29:ARG:NH2	2:C:238[B]:GLN:NE2	2.62	0.42
1:A:69:LYS:HG3	7:A:408:HOH:O	2.19	0.42
2:B:182:ILE:HG22	2:B:193:VAL:HG21	2.01	0.42
2:D:16:THR:HG21	2:D:128:VAL:HG21	2.01	0.42
2:D:187:ALA:N	2:D:188:PRO:CD	2.83	0.42
1:A:29:ARG:HD2	7:A:471:HOH:O	2.20	0.42
2:B:99[A]:LYS:NZ	7:B:405:HOH:O	2.53	0.42
2:C:29:ARG:NE	2:C:238[B]:GLN:NE2	2.59	0.41
2:B:239:MET:HG3	2:D:239:MET:HB2	2.03	0.41
2:C:29:ARG:HD2	7:C:501:HOH:O	2.20	0.41
1:A:203:THR:O	1:A:204:PRO:C	2.62	0.41
2:D:80:GLU:HA	2:D:80:GLU:OE2	2.20	0.41
2:C:182:ILE:HG22	2:C:193:VAL:HG21	2.03	0.41
2:B:29:ARG:NE	2:B:238[B]:GLN:NE2	2.62	0.41
2:B:220:GLN:NE2	2:B:260:GLN:NE2	2.69	0.41
1:A:28:LYS:HG2	1:A:54:LEU:HD21	2.03	0.41
2:B:69:LYS:NZ	7:B:406:HOH:O	2.54	0.41
1:A:9:LYS:HE2	7:A:587:HOH:O	2.21	0.41
2:C:239[B]:MET:SD	2:C:246:LEU:CD2	3.09	0.41
2:B:165:GLN:O	2:B:166:ALA:C	2.63	0.40
2:B:33[B]:GLN:HE22	2:B:238[B]:GLN:CD	2.29	0.40
2:B:165:GLN:HG2	7:B:428:HOH:O	2.21	0.40
1:A:40:LEU:HD23	1:A:40:LEU:C	2.46	0.40
2:B:69:LYS:NZ	5:B:303:SO4:S	2.94	0.40
2:D:54:LEU:HB2	2:D:58:CYS:SG	2.61	0.40
2:B:242:GLU:O	2:B:244:PRO:HD3	2.21	0.40
2:C:114:PHE:CD1	2:D:123[B]:ILE:HD13	2.57	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:112[B]:GLU:OE2	2:D:52:LYS:NZ[1_645]	2.18	0.02

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	255/261 (98%)	249 (98%)	6 (2%)	0	100	100
2	B	254/261 (97%)	248 (98%)	6 (2%)	0	100	100
2	C	249/261 (95%)	241 (97%)	8 (3%)	0	100	100
2	D	255/261 (98%)	245 (96%)	8 (3%)	2 (1%)	16	11
All	All	1013/1044 (97%)	983 (97%)	28 (3%)	2 (0%)	43	42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	211	ASP
2	D	210	PRO

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	201/200 (100%)	198 (98%)	3 (2%)	57	64
2	B	200/200 (100%)	197 (98%)	3 (2%)	57	64
2	C	195/200 (98%)	193 (99%)	2 (1%)	68	75
2	D	199/200 (100%)	193 (97%)	6 (3%)	36	38
All	All	795/800 (99%)	781 (98%)	14 (2%)	53	58

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	LYS
1	A	80	GLU
1	A	204	PRO
2	B	204	PRO
2	B	205	LEU
2	B	216	PHE
2	C	239[A]	MET
2	C	239[B]	MET
2	D	72	GLN
2	D	80	GLU
2	D	107	GLN
2	D	143	GLN
2	D	211	ASP
2	D	239	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	106	ASN
1	A	143	GLN
2	B	220	GLN
2	B	260	GLN
2	C	72	GLN
2	C	106	ASN
2	C	119	ASN
2	C	138	GLN
2	D	44	ASN
2	D	102	HIS
2	D	115	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry

13 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	SO4	B	303	-	4,4,4	1.69	1 (25%)	6,6,6	0.91	0
4	TRS	B	302	-	7,7,7	1.86	3 (42%)	9,9,9	3.14	3 (33%)
5	SO4	A	303	-	4,4,4	1.35	1 (25%)	6,6,6	1.54	2 (33%)
5	SO4	C	302	-	4,4,4	0.86	0	6,6,6	0.60	0
3	NAD	C	301	-	46,48,48	1.46	8 (17%)	64,73,73	1.98	13 (20%)
4	TRS	A	302	-	7,7,7	2.48	4 (57%)	9,9,9	4.21	6 (66%)
4	TRS	C	303	-	7,7,7	0.91	0	9,9,9	1.19	2 (22%)
3	NAD	D	301	-	46,48,48	1.44	7 (15%)	64,73,73	2.50	16 (25%)
3	NAD	B	301	-	46,48,48	1.63	8 (17%)	64,73,73	2.19	15 (23%)
6	AAE	D	302[L]	-	6,6,6	1.59	2 (33%)	7,7,7	1.33	1 (14%)
5	SO4	D	303	-	4,4,4	0.78	0	6,6,6	1.00	0
3	NAD	A	301	-	46,48,48	1.43	6 (13%)	64,73,73	2.34	17 (26%)
5	SO4	A	304	-	4,4,4	0.60	0	6,6,6	0.38	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	TRS	B	302	-	-	4/9/9/9	-
3	NAD	C	301	-	-	9/30/62/62	0/5/5/5
4	TRS	A	302	-	-	4/9/9/9	-
4	TRS	C	303	-	-	2/9/9/9	-
3	NAD	D	301	-	-	7/30/62/62	0/5/5/5
3	NAD	B	301	-	-	7/30/62/62	0/5/5/5
6	AAE	D	302[L]	-	-	3/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAD	A	301	-	-	8/30/62/62	0/5/5/5

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	301	NAD	C4N-C3N	5.10	1.47	1.39
4	A	302	TRS	C1-C	5.03	1.66	1.53
3	A	301	NAD	C6N-N1N	4.34	1.45	1.35
3	D	301	NAD	C6N-N1N	4.32	1.45	1.35
3	B	301	NAD	C6N-N1N	4.31	1.45	1.35
3	C	301	NAD	C4N-C3N	4.14	1.45	1.39
3	C	301	NAD	C2A-N1A	3.79	1.40	1.33
3	A	301	NAD	C7N-N7N	3.76	1.39	1.33
3	A	301	NAD	C4N-C3N	3.72	1.45	1.39
3	D	301	NAD	C4N-C3N	3.39	1.44	1.39
3	D	301	NAD	PA-O3	3.32	1.63	1.59
3	C	301	NAD	C6N-N1N	3.11	1.42	1.35
5	B	303	SO4	O2-S	3.03	1.62	1.44
3	B	301	NAD	O4D-C1D	2.95	1.44	1.40
3	B	301	NAD	C2A-N1A	2.79	1.38	1.33
3	A	301	NAD	C2A-N1A	2.76	1.38	1.33
4	B	302	TRS	C-N	2.71	1.58	1.49
4	B	302	TRS	O1-C1	2.71	1.50	1.42
4	B	302	TRS	C3-C	-2.66	1.46	1.53
3	A	301	NAD	O7N-C7N	-2.66	1.19	1.24
3	B	301	NAD	C3N-C7N	2.61	1.54	1.50
3	D	301	NAD	C8A-N9A	2.58	1.41	1.37
6	D	302[L]	AAE	O1-C2	-2.42	1.22	1.30
3	B	301	NAD	C3B-C4B	2.38	1.59	1.53
3	C	301	NAD	O4D-C1D	2.33	1.43	1.40
3	C	301	NAD	C3N-C7N	2.29	1.54	1.50
3	B	301	NAD	C2N-C3N	-2.25	1.35	1.39
3	D	301	NAD	C7N-N7N	2.24	1.37	1.33
3	D	301	NAD	PN-O3	-2.22	1.57	1.59
6	D	302[L]	AAE	C4-C2	2.18	1.54	1.51
3	C	301	NAD	PA-O3	2.18	1.61	1.59
3	B	301	NAD	C2N-N1N	-2.17	1.32	1.35
5	A	303	SO4	O2-S	2.16	1.57	1.44
4	A	302	TRS	O3-C3	2.10	1.49	1.42
3	A	301	NAD	PN-O3	-2.09	1.57	1.59
4	A	302	TRS	O1-C1	2.06	1.48	1.42
4	A	302	TRS	C-N	-2.03	1.42	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	301	NAD	O4B-C1B	2.03	1.46	1.42
3	D	301	NAD	PN-O5D	2.03	1.67	1.59
3	C	301	NAD	C7N-N7N	2.00	1.36	1.33

All (75) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	301	NAD	C5N-C4N-C3N	-8.98	111.54	120.36
3	C	301	NAD	C5N-C4N-C3N	-8.92	111.60	120.36
3	D	301	NAD	C5N-C4N-C3N	-8.91	111.61	120.36
4	A	302	TRS	C1-C-N	-7.68	88.58	108.17
3	A	301	NAD	C5N-C6N-N1N	-7.28	110.45	120.38
3	A	301	NAD	C5N-C4N-C3N	-7.04	113.45	120.36
4	B	302	TRS	O2-C2-C	-6.74	92.10	110.88
3	A	301	NAD	C6N-C5N-C4N	6.56	128.90	119.45
4	A	302	TRS	O1-C1-C	-6.54	92.66	110.88
3	D	301	NAD	C6N-C5N-C4N	6.18	128.36	119.45
3	B	301	NAD	C6N-C5N-C4N	6.18	128.35	119.45
3	D	301	NAD	C2N-C3N-C4N	6.05	125.30	118.26
3	D	301	NAD	C5N-C6N-N1N	-6.03	112.16	120.38
3	A	301	NAD	O7N-C7N-C3N	5.50	126.32	119.60
3	D	301	NAD	C6N-N1N-C2N	5.31	126.40	121.88
3	B	301	NAD	C5N-C6N-N1N	-5.16	113.35	120.38
3	C	301	NAD	C2N-C3N-C4N	5.03	124.11	118.26
3	A	301	NAD	C4D-O4D-C1D	-5.01	105.33	109.92
3	C	301	NAD	C6N-C5N-C4N	4.84	126.42	119.45
4	A	302	TRS	C3-C-N	4.79	120.39	108.17
3	A	301	NAD	C6N-N1N-C2N	4.71	125.88	121.88
3	D	301	NAD	C4N-C3N-C7N	-4.64	108.44	121.06
4	A	302	TRS	C2-C-N	4.60	119.89	108.17
3	D	301	NAD	C4D-O4D-C1D	-4.35	105.94	109.92
3	D	301	NAD	C6N-N1N-C1D	-4.33	111.23	119.73
4	B	302	TRS	C2-C-N	-4.31	97.17	108.17
3	D	301	NAD	C3N-C7N-N7N	-4.26	112.49	117.74
3	B	301	NAD	O7N-C7N-C3N	4.23	124.77	119.60
3	A	301	NAD	C6N-N1N-C1D	-4.11	111.65	119.73
3	C	301	NAD	C4N-C3N-C7N	-3.87	110.52	121.06
3	D	301	NAD	O7N-C7N-C3N	3.84	124.29	119.60
4	B	302	TRS	C3-C-C2	3.66	120.39	110.66
3	C	301	NAD	C4D-O4D-C1D	-3.59	106.64	109.92
3	B	301	NAD	C6N-N1N-C1D	-3.58	112.71	119.73
3	B	301	NAD	C4N-C3N-C7N	-3.57	111.34	121.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	301	NAD	C5A-N7A-C8A	3.49	108.94	103.45
3	B	301	NAD	C2N-C3N-C4N	3.42	122.24	118.26
3	D	301	NAD	N9A-C8A-N7A	-3.40	109.12	113.94
3	B	301	NAD	C4D-O4D-C1D	-3.35	106.86	109.92
3	B	301	NAD	C3N-C7N-N7N	-3.33	113.64	117.74
3	C	301	NAD	C4B-O4B-C1B	-3.14	102.52	109.47
3	A	301	NAD	O7N-C7N-N7N	-2.97	118.32	122.62
3	A	301	NAD	C2N-C3N-C4N	2.95	121.69	118.26
3	C	301	NAD	N9A-C8A-N7A	-2.95	109.75	113.94
3	A	301	NAD	C4N-C3N-C7N	-2.94	113.04	121.06
3	C	301	NAD	C5N-C6N-N1N	-2.92	116.39	120.38
3	C	301	NAD	C5A-N7A-C8A	2.85	107.92	103.45
3	D	301	NAD	O2N-PN-O3	2.82	114.91	107.27
3	B	301	NAD	O3D-C3D-C4D	-2.73	103.25	111.08
3	C	301	NAD	N3A-C2A-N1A	-2.73	124.46	128.58
3	A	301	NAD	O3D-C3D-C4D	-2.57	103.69	111.08
3	B	301	NAD	O3-PN-O1N	-2.56	103.01	110.70
3	D	301	NAD	O3D-C3D-C4D	-2.51	103.88	111.08
4	A	302	TRS	O2-C2-C	-2.48	103.97	110.88
3	B	301	NAD	C2N-N1N-C1D	2.46	124.56	119.13
3	A	301	NAD	O3-PN-O1N	-2.42	103.43	110.70
3	B	301	NAD	C5A-N7A-C8A	2.41	107.24	103.45
3	B	301	NAD	C2N-C3N-C7N	2.36	126.28	119.46
4	C	303	TRS	C3-C-C1	2.36	116.94	110.66
3	D	301	NAD	C2N-C3N-C7N	2.36	126.26	119.46
3	C	301	NAD	O4B-C4B-C3B	2.34	109.79	105.15
6	D	302[L]	AAE	C5-C4-C2	-2.34	107.03	112.35
3	A	301	NAD	C5A-N7A-C8A	2.29	107.05	103.45
3	A	301	NAD	O2N-PN-O3	2.20	113.21	107.27
3	D	301	NAD	O3-PA-O1A	-2.20	104.10	110.70
5	A	303	SO4	O4-S-O2	-2.19	98.10	109.56
4	A	302	TRS	C3-C-C1	-2.18	104.84	110.66
3	C	301	NAD	O3-PN-O1N	-2.13	104.29	110.70
5	A	303	SO4	O3-S-O2	2.13	120.69	109.56
4	C	303	TRS	C2-C-C1	-2.11	105.05	110.66
3	A	301	NAD	N9A-C8A-N7A	-2.03	111.06	113.94
3	C	301	NAD	C2N-C3N-C7N	2.03	125.31	119.46
3	B	301	NAD	O4B-C4B-C3B	2.03	109.17	105.15
3	A	301	NAD	C2N-C3N-C7N	2.01	125.27	119.46
3	A	301	NAD	C3N-C7N-N7N	-2.00	115.27	117.74

There are no chirality outliers.

All (44) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	301	NAD	PN-O3-PA-O5B
3	A	301	NAD	C5D-O5D-PN-O3
3	A	301	NAD	C5D-O5D-PN-O1N
3	A	301	NAD	C5D-O5D-PN-O2N
3	A	301	NAD	O4D-C1D-N1N-C2N
3	B	301	NAD	PN-O3-PA-O5B
3	B	301	NAD	C5D-O5D-PN-O3
3	B	301	NAD	C5D-O5D-PN-O1N
3	C	301	NAD	PN-O3-PA-O5B
3	C	301	NAD	C5D-O5D-PN-O3
3	C	301	NAD	C5D-O5D-PN-O1N
3	C	301	NAD	C5D-O5D-PN-O2N
3	C	301	NAD	O4D-C1D-N1N-C2N
3	D	301	NAD	C5D-O5D-PN-O3
3	D	301	NAD	C5D-O5D-PN-O1N
3	D	301	NAD	C5D-O5D-PN-O2N
4	A	302	TRS	N-C-C2-O2
4	B	302	TRS	N-C-C1-O1
4	B	302	TRS	N-C-C3-O3
6	D	302[L]	AAE	C2-C4-C5-O8
6	D	302[L]	AAE	C2-C4-C5-C9
4	B	302	TRS	C1-C-C3-O3
4	A	302	TRS	N-C-C3-O3
3	D	301	NAD	PN-O3-PA-O5B
6	D	302[L]	AAE	O1-C2-C4-C5
3	A	301	NAD	PA-O3-PN-O2N
3	D	301	NAD	PA-O3-PN-O2N
3	B	301	NAD	C5D-O5D-PN-O2N
3	B	301	NAD	PA-O3-PN-O1N
3	B	301	NAD	PA-O3-PN-O2N
3	C	301	NAD	PA-O3-PN-O1N
3	C	301	NAD	PA-O3-PN-O2N
4	A	302	TRS	C1-C-C2-O2
4	C	303	TRS	N-C-C3-O3
3	A	301	NAD	O4D-C1D-N1N-C6N
3	B	301	NAD	O4D-C1D-N1N-C2N
3	D	301	NAD	PA-O3-PN-O1N
4	A	302	TRS	C3-C-C2-O2
4	B	302	TRS	C2-C-C3-O3
4	C	303	TRS	C1-C-C3-O3
3	D	301	NAD	O4B-C4B-C5B-O5B
3	A	301	NAD	PA-O3-PN-O1N

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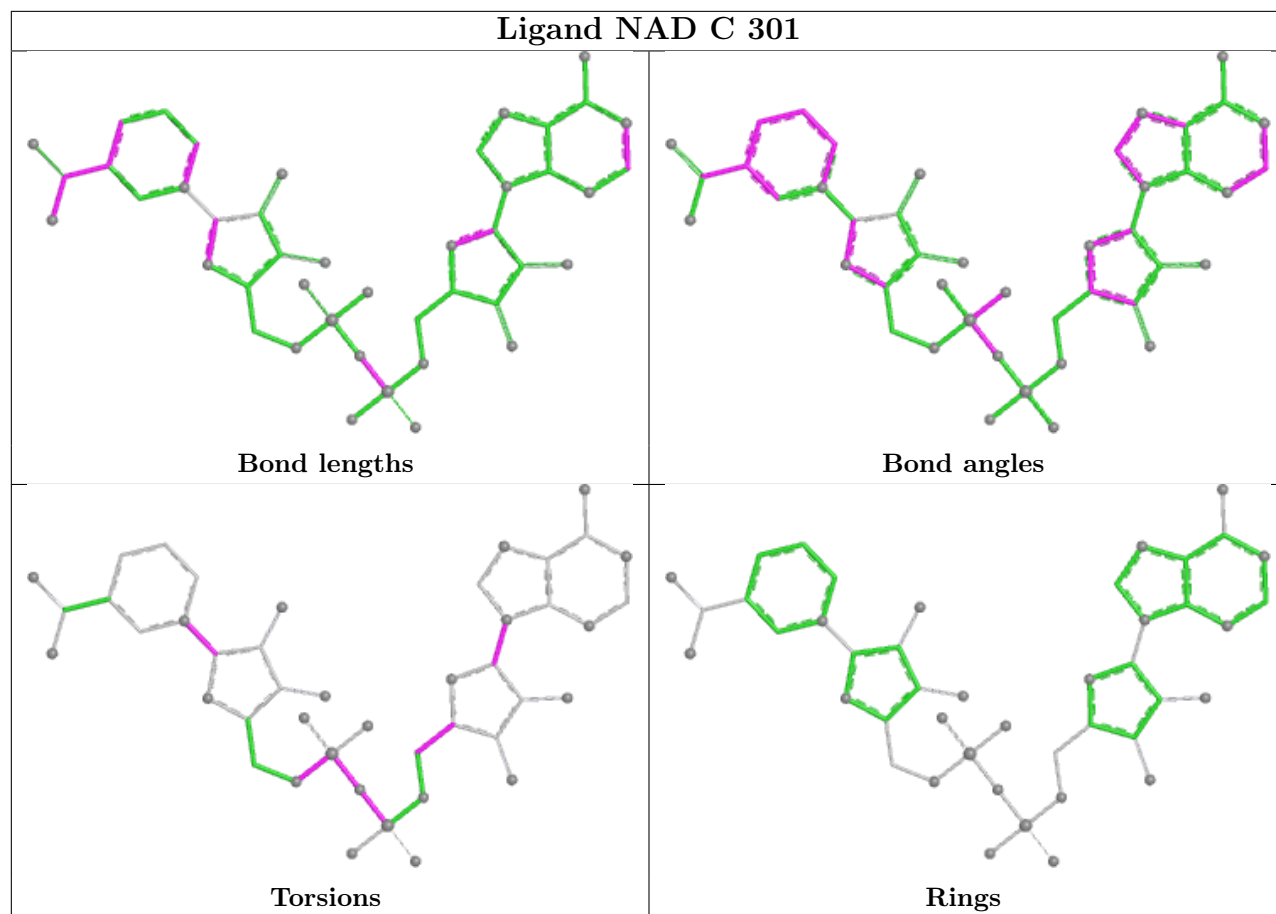
Mol	Chain	Res	Type	Atoms
3	C	301	NAD	C2B-C1B-N9A-C8A
3	C	301	NAD	O4B-C4B-C5B-O5B

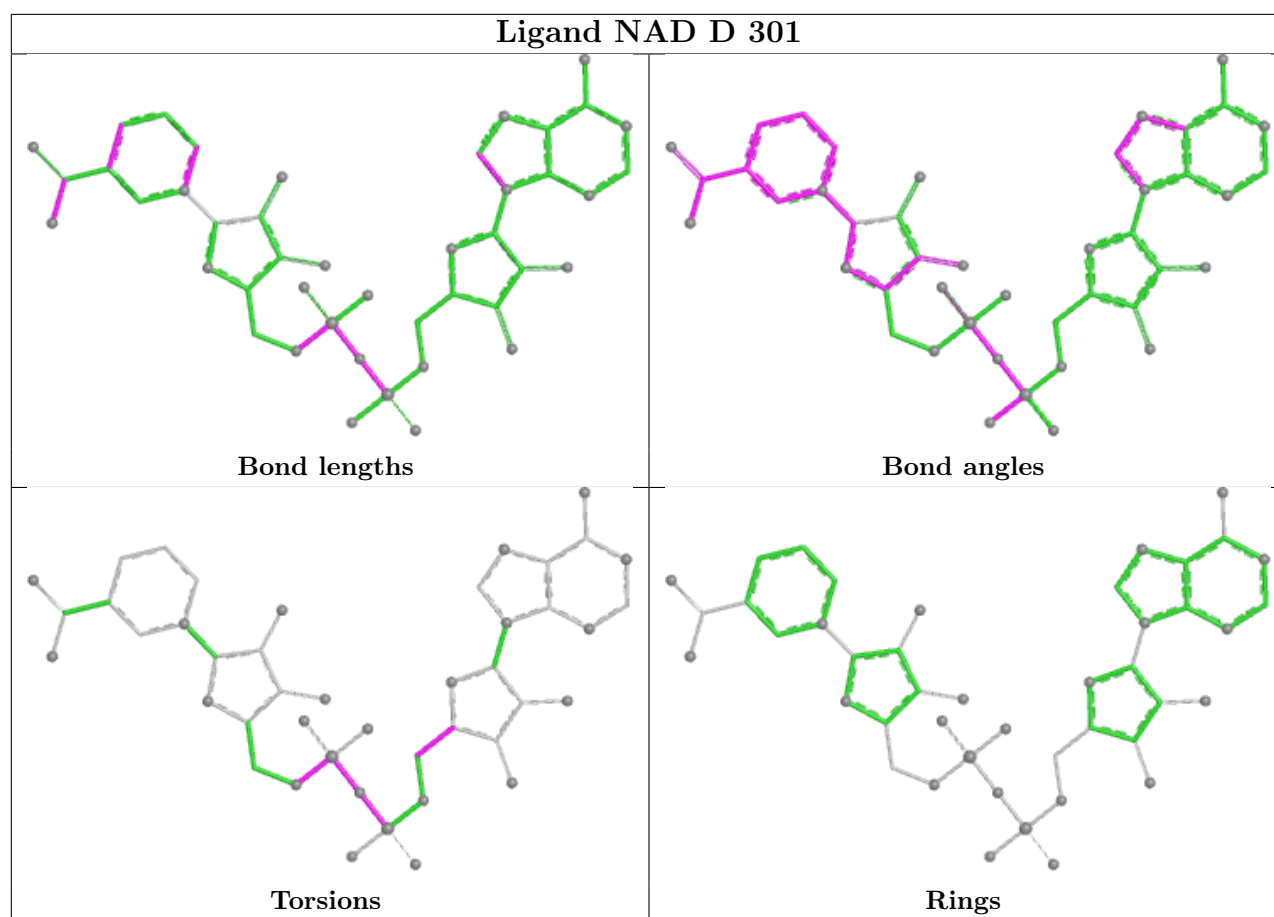
There are no ring outliers.

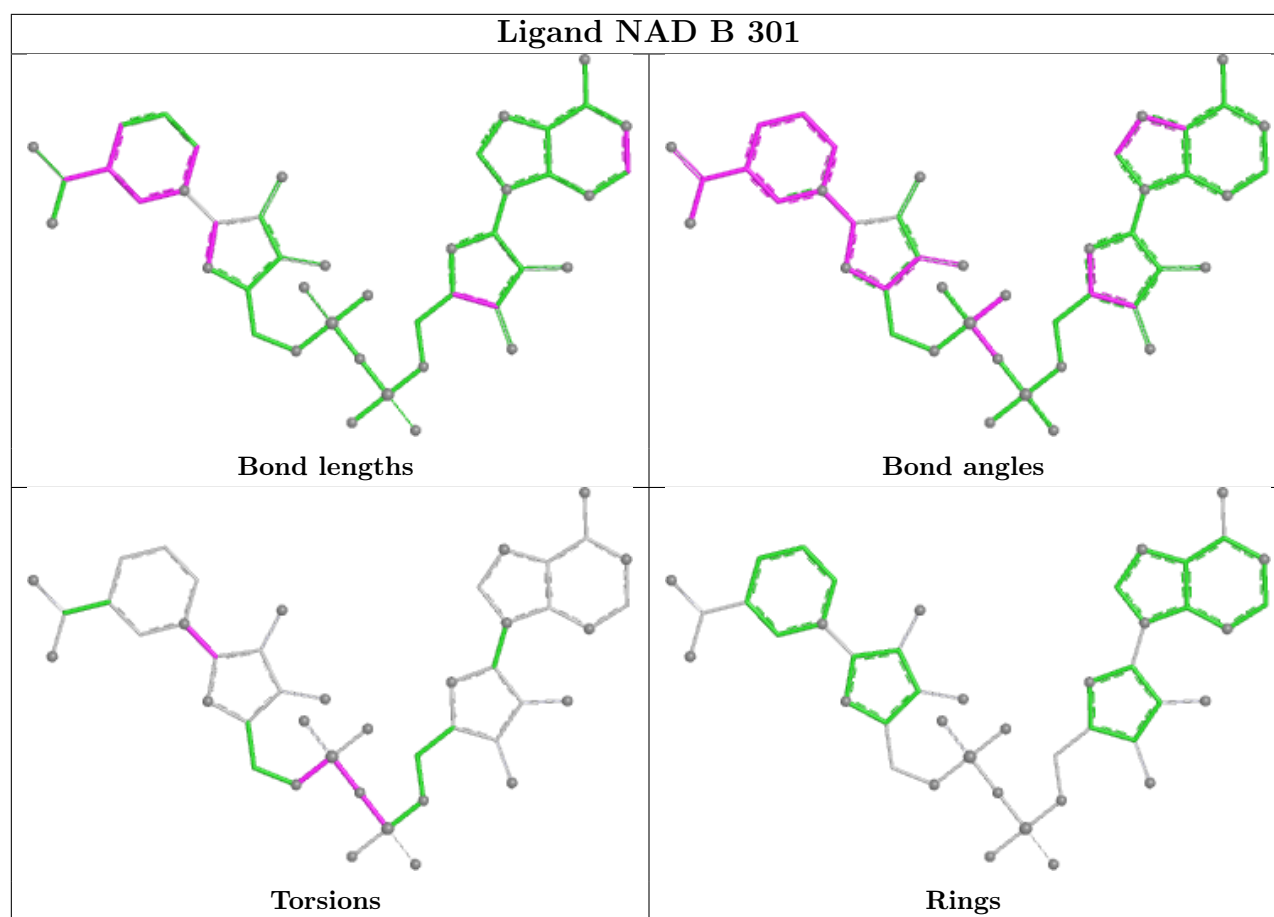
4 monomers are involved in 5 short contacts:

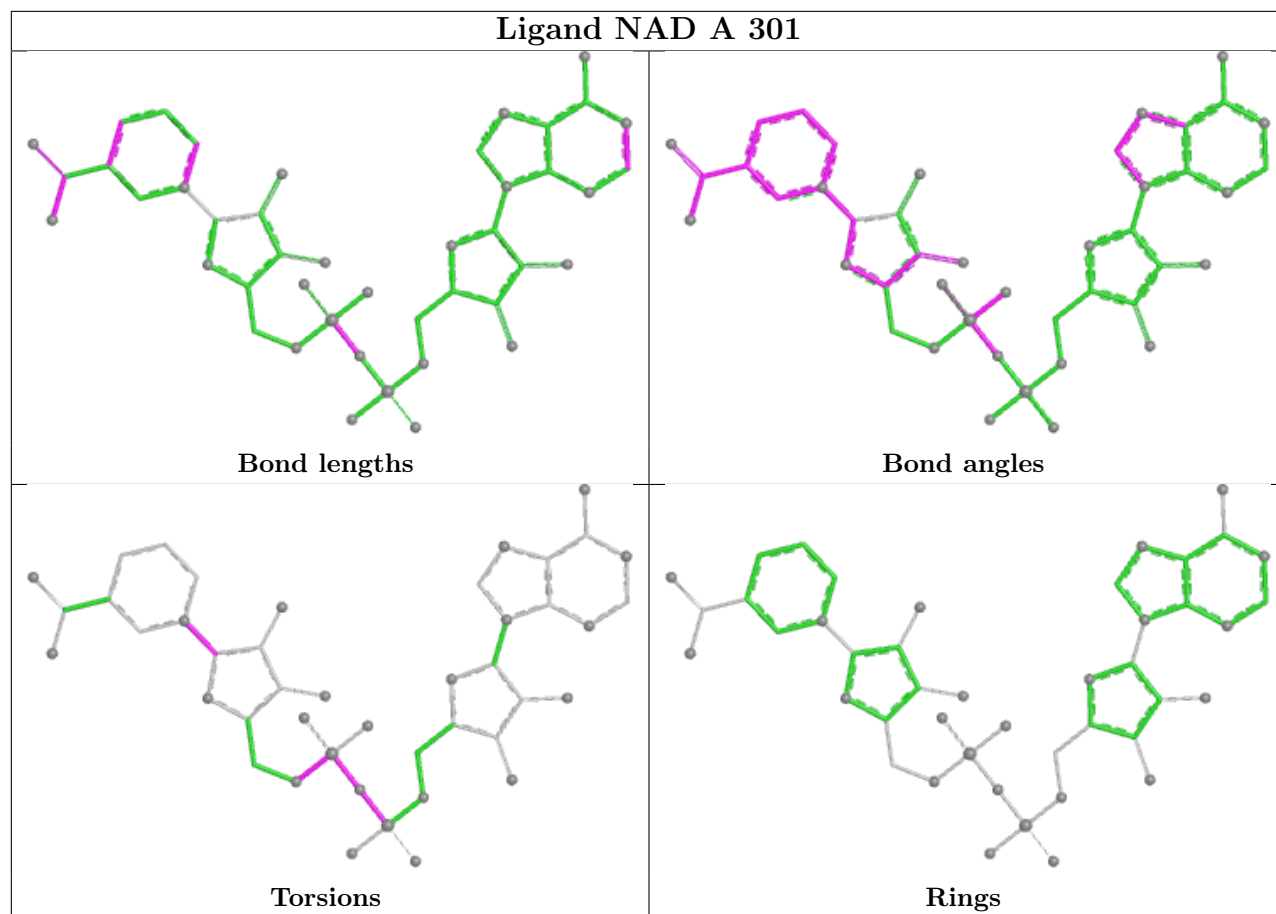
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	303	SO4	2	0
3	C	301	NAD	1	0
3	D	301	NAD	1	0
6	D	302[L]	AAE	2	0

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.