



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 05:07 AM BST

PDB ID : 1H81
Title : STRUCTURE OF POLYAMINE OXIDASE IN THE REDUCED STATE
Authors : Binda, C.; Coda, A.; Angelini, R.; Federico, R.; Ascenzi, P.; Mattevi, A.
Deposited on : 2001-01-24
Resolution : 2.10 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

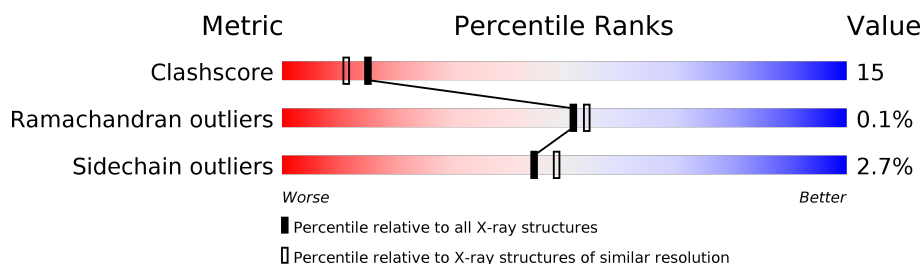
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	472	
1	B	472	
1	C	472	
2	D	2	
2	E	2	
3	F	5	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 12113 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 POLYAMINE OXIDASE.

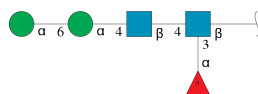
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	459	Total	C	N	O	S	55	0	0
			3684	2353	621	696	14			
1	B	462	Total	C	N	O	S	61	0	0
			3715	2374	627	700	14			
1	C	462	Total	C	N	O	S	50	0	0
			3715	2374	627	700	14			

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



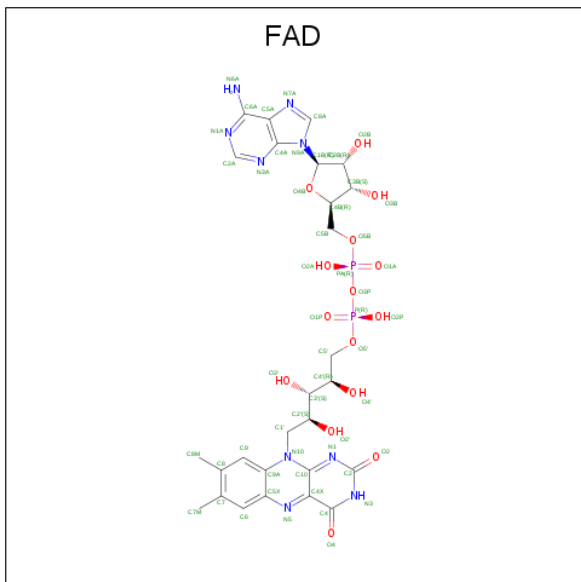
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-D-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	F	5	Total	C	N	O	0	0	0
			60	34	2	24			

- Molecule 4 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $\text{C}_{27}\text{H}_{33}\text{N}_9\text{O}_{15}\text{P}_2$).

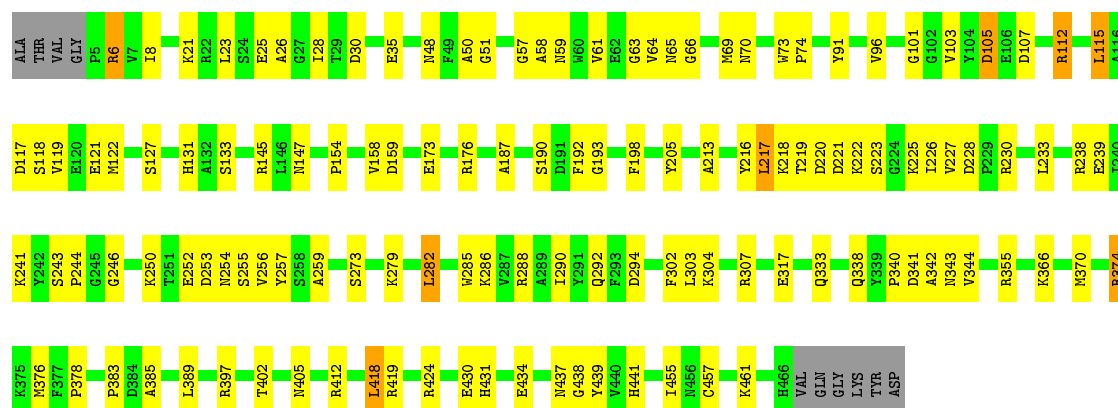


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 53	C 27	N 9	O 15	P 2	0	0
4	B	1	Total 53	C 27	N 9	O 15	P 2	0	0
4	C	1	Total 53	C 27	N 9	O 15	P 2	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	224	Total O 224 224	0	0
5	B	245	Total O 245 245	0	0
5	C	255	Total O 255 255	0	0

Chain C:  71% 26% . .



- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:  100%

HAG1
HAG2

- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  100%

HAG1
HAG2

- Molecule 3: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-D-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  40% 60%

HAG1
HAG2
HAI3
HAI4
FCA5

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	181.77Å 181.77Å 277.53Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.10	Depositor
% Data completeness (in resolution range)	99.1 (20.00-2.10)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT 5D	Depositor
R, R_{free}	0.191 , 0.235	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	12113	wwPDB-VP
Average B, all atoms (Å ²)	19.0	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: FCA, NAG, FAD, MAN

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	0.54	0/3775	1.30	16/5116 (0.3%)
1	B	0.53	0/3808	1.26	15/5160 (0.3%)
1	C	0.55	0/3808	1.29	21/5160 (0.4%)
All	All	0.54	0/11391	1.28	52/15436 (0.3%)

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	C	1	0

There are no bond length outliers.

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	355	ARG	NE-CZ-NH2	-12.67	113.97	120.30
1	A	117	ASP	CB-CG-OD1	-10.79	108.59	118.30
1	C	230	ARG	NE-CZ-NH1	-10.74	114.93	120.30
1	C	145	ARG	NE-CZ-NH2	-10.13	115.24	120.30
1	B	135	ARG	NE-CZ-NH1	-9.11	115.74	120.30
1	B	355	ARG	NE-CZ-NH2	-9.02	115.79	120.30
1	C	145	ARG	NE-CZ-NH1	8.78	124.69	120.30
1	C	112	ARG	NE-CZ-NH1	8.18	124.39	120.30
1	C	307	ARG	NE-CZ-NH1	-7.40	116.60	120.30
1	C	355	ARG	NE-CZ-NH2	-7.38	116.61	120.30
1	A	101	GLY	N-CA-C	7.15	130.99	113.10
1	B	22	ARG	NE-CZ-NH1	6.98	123.79	120.30
1	C	176	ARG	NE-CZ-NH2	-6.86	116.87	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	355	ARG	NE-CZ-NH1	6.84	123.72	120.30
1	A	61	VAL	N-CA-C	-6.79	92.66	111.00
1	B	252	GLU	N-CA-CB	-6.60	98.72	110.60
1	C	115	LEU	CB-CG-CD1	-6.59	99.79	111.00
1	C	6	ARG	NE-CZ-NH2	-6.26	117.17	120.30
1	B	351	ASP	N-CA-CB	-6.20	99.44	110.60
1	B	61	VAL	N-CA-C	-6.18	94.32	111.00
1	A	260	ASP	CB-CG-OD2	6.11	123.80	118.30
1	C	397	ARG	NE-CZ-NH2	-6.08	117.26	120.30
1	A	136	ASP	CB-CG-OD2	-6.07	112.84	118.30
1	C	105	ASP	CB-CG-OD1	6.06	123.75	118.30
1	A	326	ARG	NE-CZ-NH1	-6.04	117.28	120.30
1	A	351	ASP	N-CA-CB	-6.03	99.74	110.60
1	C	374	ARG	NE-CZ-NH2	-5.87	117.37	120.30
1	C	61	VAL	N-CA-C	-5.85	95.21	111.00
1	A	60	TRP	CB-CA-C	-5.82	98.77	110.40
1	A	374	ARG	NE-CZ-NH1	-5.79	117.41	120.30
1	B	307	ARG	NE-CZ-NH2	-5.72	117.44	120.30
1	B	43	ARG	NE-CZ-NH1	-5.67	117.47	120.30
1	C	273	SER	C-N-CA	-5.62	107.64	121.70
1	A	56	LEU	CB-CG-CD2	-5.62	101.45	111.00
1	A	176	ARG	NE-CZ-NH2	-5.57	117.52	120.30
1	A	414	GLU	CA-CB-CG	-5.54	101.22	113.40
1	C	340	PRO	C-N-CA	-5.52	107.90	121.70
1	C	282	LEU	CB-CG-CD1	5.49	120.34	111.00
1	B	396	ASP	CB-CG-OD2	-5.44	113.41	118.30
1	B	126	LEU	CB-CG-CD2	-5.40	101.81	111.00
1	B	201	ASP	CB-CG-OD2	-5.40	113.44	118.30
1	B	217	LEU	CB-CG-CD2	-5.38	101.86	111.00
1	C	307	ARG	NE-CZ-NH2	5.37	122.98	120.30
1	C	397	ARG	NE-CZ-NH1	5.26	122.93	120.30
1	B	6	ARG	NE-CZ-NH1	-5.24	117.68	120.30
1	C	288	ARG	NE-CZ-NH1	-5.20	117.70	120.30
1	A	381	ASP	N-CA-C	-5.20	96.97	111.00
1	C	341	ASP	CB-CA-C	5.15	120.69	110.40
1	B	101	GLY	N-CA-C	5.14	125.94	113.10
1	B	381	ASP	N-CA-C	-5.13	97.14	111.00
1	A	44	MET	N-CA-C	-5.04	97.38	111.00
1	C	418	LEU	CB-CA-C	-5.01	100.68	110.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	C	386	THR	CB

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	3684	0	3584	113	0
1	B	3715	0	3614	110	0
1	C	3715	0	3614	99	0
2	D	28	0	26	3	0
2	E	28	0	26	4	0
3	F	60	0	52	6	0
4	A	53	0	31	2	0
4	B	53	0	31	2	0
4	C	53	0	31	5	0
5	A	224	0	0	4	0
5	B	245	0	0	10	0
5	C	255	0	0	5	0
All	All	12113	0	11009	326	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 15.

All (326) 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:69:MET:CE	1:B:73:TRP:HB3	1.81	1.11
1:A:373:LEU:HD23	1:A:376:MET:HE3	1.34	1.08
1:B:69:MET:HE2	1:B:74:PRO:HD3	1.35	1.03
1:A:69:MET:CE	1:A:73:TRP:HB3	1.90	1.02
1:B:69:MET:HE3	1:B:73:TRP:HB3	1.44	0.99
3:F:1:NAG:C4	3:F:2:NAG:C1	2.41	0.98
1:C:131:HIS:CD2	1:C:133:SER:H	1.83	0.97
1:B:411:ASN:ND2	1:B:414:GLU:H	1.66	0.93
1:B:69:MET:CE	1:B:74:PRO:HD3	2.01	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:394:TRP:HE1	1:B:152:ASN:ND2	1.70	0.89
1:A:372:VAL:HG12	1:A:376:MET:CE	2.03	0.89
1:A:69:MET:HE2	1:A:74:PRO:HD3	1.54	0.89
1:A:69:MET:HE3	1:A:73:TRP:HB3	1.54	0.87
2:E:1:NAG:C4	2:E:2:NAG:C1	2.54	0.86
1:A:372:VAL:HG12	1:A:376:MET:HE2	1.55	0.85
1:B:219:THR:HG22	1:B:226:ILE:HA	1.59	0.84
1:B:119:VAL:HA	1:B:122:MET:HE3	1.57	0.84
1:C:112:ARG:HD3	1:C:159:ASP:OD1	1.77	0.84
1:C:216:TYR:CE1	1:C:217:LEU:HD13	2.13	0.84
1:B:308:LYS:HE3	1:B:310:TRP:O	1.76	0.83
1:B:220:ASP:HB3	1:B:223:SER:OG	1.81	0.80
2:D:1:NAG:C4	2:D:2:NAG:C1	2.60	0.80
1:C:117:ASP:O	1:C:121:GLU:HG3	1.82	0.80
1:C:69:MET:HE3	1:C:70:ASN:H	1.47	0.78
1:C:216:TYR:CD1	1:C:217:LEU:HD13	2.18	0.78
1:A:366:LYS:HD2	1:A:385:ALA:HB3	1.66	0.76
3:F:1:NAG:H3	3:F:5:FCA:O2	1.84	0.76
1:B:131:HIS:CD2	1:B:133:SER:H	2.03	0.75
1:C:220:ASP:HB3	1:C:223:SER:OG	1.86	0.75
1:A:394:TRP:HE1	1:B:152:ASN:HD22	1.35	0.75
1:A:431:HIS:H	1:A:431:HIS:CD2	2.03	0.75
1:A:50:ALA:HB1	1:A:304:LYS:HD2	1.69	0.75
1:C:131:HIS:HD2	1:C:133:SER:H	1.35	0.74
1:A:69:MET:CE	1:A:74:PRO:HD3	2.16	0.74
3:F:1:NAG:O4	3:F:2:NAG:C2	2.35	0.74
1:A:117:ASP:O	1:A:121:GLU:HG3	1.88	0.73
1:B:411:ASN:HD22	1:B:414:GLU:H	1.37	0.72
1:C:69:MET:HE3	1:C:69:MET:HA	1.71	0.72
1:C:292:GLN:OE1	5:C:2137:HOH:O	2.07	0.72
1:A:23:LEU:HD13	1:A:451:ALA:HB1	1.71	0.71
1:B:131:HIS:HD2	1:B:133:SER:H	1.38	0.71
1:B:419:ARG:HG2	5:B:2227:HOH:O	1.90	0.71
1:B:419:ARG:HD3	5:B:2218:HOH:O	1.90	0.71
1:C:69:MET:HE3	1:C:70:ASN:N	2.06	0.70
1:A:220:ASP:HB3	1:A:223:SER:HB3	1.72	0.70
1:B:216:TYR:CD1	1:B:217:LEU:HD13	2.27	0.70
1:A:218:LYS:H	1:A:228:ASP:HB2	1.57	0.70
1:A:63:GLY:HA2	1:A:193:GLY:O	1.93	0.69
1:B:107:ASP:O	1:B:111:LYS:HG3	1.93	0.69
1:C:131:HIS:HD2	1:C:133:SER:OG	1.76	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:6:ARG:HH11	1:C:6:ARG:HG3	1.57	0.69
1:A:117:ASP:OD1	5:A:2050:HOH:O	2.11	0.68
1:B:185:PRO:HA	5:B:2054:HOH:O	1.94	0.68
1:C:69:MET:CE	1:C:70:ASN:N	2.58	0.67
1:A:273:SER:O	1:A:274:ASP:HB2	1.94	0.67
1:C:131:HIS:HD2	1:C:133:SER:CB	2.07	0.66
1:B:449:ASP:O	1:B:453:ILE:HG13	1.97	0.65
1:A:372:VAL:HG12	1:A:376:MET:HE1	1.79	0.65
1:A:158:VAL:HG13	1:A:159:ASP:N	2.13	0.64
3:F:1:NAG:H4	3:F:2:NAG:C1	2.28	0.64
1:B:412:ARG:HG3	5:B:2215:HOH:O	1.96	0.64
1:C:69:MET:CE	1:C:70:ASN:H	2.11	0.64
1:A:216:TYR:CD1	1:A:217:LEU:HD13	2.31	0.64
1:A:412:ARG:NH1	1:A:434:GLU:OE2	2.30	0.64
1:B:63:GLY:HA2	1:B:193:GLY:O	1.98	0.62
1:A:58:ALA:HA	4:A:579:FAD:C4X	2.30	0.62
3:F:1:NAG:O6	3:F:2:NAG:C1	2.48	0.61
1:A:220:ASP:CB	1:A:223:SER:HB3	2.29	0.61
1:A:220:ASP:CG	1:A:223:SER:HB3	2.21	0.61
3:F:1:NAG:C3	3:F:5:FCA:O2	2.48	0.61
1:A:130:LEU:HD22	1:A:136:ASP:HB2	1.82	0.60
1:C:131:HIS:CD2	1:C:133:SER:OG	2.53	0.60
1:C:220:ASP:OD2	1:C:222:LYS:N	2.34	0.60
1:C:419:ARG:NH2	1:C:434:GLU:HA	2.17	0.60
1:C:131:HIS:CD2	1:C:133:SER:CB	2.85	0.60
1:C:431:HIS:CD2	1:C:431:HIS:H	2.18	0.60
1:A:49:PHE:N	1:A:52:ILE:O	2.30	0.60
1:A:177:VAL:HG11	1:B:176:ARG:HD2	1.83	0.59
1:C:412:ARG:NH1	1:C:434:GLU:OE2	2.33	0.59
2:E:1:NAG:O4	2:E:2:NAG:C2	2.47	0.59
1:A:152:ASN:ND2	1:B:394:TRP:HE1	2.01	0.59
1:C:69:MET:HE2	1:C:70:ASN:O	2.03	0.58
1:A:218:LYS:N	1:A:228:ASP:HB2	2.18	0.58
1:C:219:THR:HG22	1:C:226:ILE:HA	1.85	0.58
1:B:69:MET:HE2	1:B:70:ASN:O	2.04	0.58
1:B:431:HIS:H	1:B:431:HIS:CD2	2.20	0.58
1:B:26:ALA:HB2	1:B:455:ILE:HD13	1.85	0.58
1:B:273:SER:O	1:B:274:ASP:HB2	2.03	0.57
1:C:69:MET:HE3	1:C:69:MET:CA	2.35	0.57
1:B:304:LYS:HG3	1:B:305:PHE:N	2.20	0.57
1:C:6:ARG:HA	1:C:30:ASP:O	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243:SER:HB2	1:B:244:PRO:CD	2.35	0.57
1:C:131:HIS:HD2	1:C:133:SER:N	2.03	0.57
1:A:243:SER:HB2	1:A:244:PRO:CD	2.34	0.56
1:A:342:ALA:O	1:A:343:ASN:HB2	2.04	0.56
1:A:50:ALA:CB	1:A:304:LYS:HD2	2.36	0.56
1:C:101:GLY:HA3	1:C:378:PRO:HG3	1.87	0.56
1:B:6:ARG:HA	1:B:30:ASP:O	2.06	0.56
1:C:218:LYS:H	1:C:228:ASP:HB2	1.71	0.56
1:B:216:TYR:CE1	1:B:217:LEU:HD13	2.41	0.56
1:A:219:THR:HG22	1:A:226:ILE:HA	1.89	0.55
1:B:23:LEU:HD13	1:B:451:ALA:HB1	1.88	0.55
1:B:58:ALA:HA	4:B:579:FAD:C4X	2.36	0.55
1:B:119:VAL:CA	1:B:122:MET:HE3	2.32	0.55
1:B:457:CYS:HA	1:B:462:MET:O	2.07	0.55
1:A:47:THR:O	1:A:53:ASN:HA	2.07	0.54
1:A:64:VAL:HG12	1:A:65:ASN:N	2.21	0.54
1:C:290:ILE:HA	1:C:418:LEU:HD21	1.89	0.54
1:B:454:LEU:C	1:B:454:LEU:HD12	2.28	0.54
1:C:219:THR:HA	1:C:225:LYS:O	2.07	0.54
1:C:253:ASP:O	1:C:254:ASN:HB2	2.08	0.54
1:B:119:VAL:HA	1:B:122:MET:CE	2.33	0.54
1:C:58:ALA:HA	4:C:579:FAD:C4X	2.38	0.54
1:B:223:SER:HB2	1:B:225:LYS:HG3	1.89	0.53
1:B:306:PRO:HG3	1:B:383:PRO:HB2	1.90	0.53
1:C:158:VAL:HG12	5:C:2073:HOH:O	2.06	0.53
1:A:216:TYR:CE1	1:A:217:LEU:HD13	2.43	0.53
1:B:69:MET:HE1	1:B:73:TRP:HB3	1.84	0.53
1:C:105:ASP:OD1	1:C:107:ASP:HB2	2.09	0.53
1:C:131:HIS:CD2	1:C:133:SER:N	2.65	0.52
1:A:156:THR:O	1:A:160:MET:HG3	2.09	0.52
1:B:131:HIS:HD2	1:B:133:SER:OG	1.93	0.52
1:C:35:GLU:HB3	1:C:233:LEU:HD23	1.90	0.52
1:A:143:MET:SD	1:A:147:ASN:ND2	2.83	0.52
1:B:98:LYS:HG3	1:B:102:GLY:O	2.10	0.52
1:C:21:LYS:HB2	1:C:216:TYR:CE2	2.45	0.52
1:C:112:ARG:NH2	1:C:115:LEU:HD11	2.24	0.52
1:C:246:GLY:HA2	1:C:424:ARG:HD3	1.92	0.51
1:C:376:MET:C	1:C:378:PRO:HD3	2.30	0.51
1:A:253:ASP:O	1:A:254:ASN:HB2	2.11	0.51
1:B:99:GLU:HA	1:B:321:TYR:CE1	2.46	0.51
1:C:57:GLY:HA2	4:C:579:FAD:C7M	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:GLU:O	1:A:333:GLN:HA	2.10	0.51
2:D:1:NAG:H4	2:D:2:NAG:C1	2.39	0.51
1:A:69:MET:HE2	1:A:70:ASN:O	2.10	0.51
1:B:219:THR:HG22	1:B:226:ILE:CA	2.37	0.51
1:B:342:ALA:O	1:B:343:ASN:HB2	2.11	0.51
1:C:119:VAL:HG13	1:C:147:ASN:HB2	1.93	0.51
1:C:73:TRP:HB3	1:C:74:PRO:HD3	1.93	0.51
1:B:419:ARG:CG	5:B:2227:HOH:O	2.55	0.50
1:A:81:LYS:O	1:A:203:ARG:NH2	2.45	0.50
1:C:216:TYR:CE1	1:C:217:LEU:CD1	2.91	0.50
1:C:218:LYS:N	1:C:228:ASP:HB2	2.27	0.50
1:C:57:GLY:HA2	4:C:579:FAD:HM72	1.93	0.50
1:A:176:ARG:HD2	1:B:177:VAL:HG21	1.93	0.50
1:C:239:GLU:OE2	1:C:279:LYS:HD3	2.12	0.50
1:A:373:LEU:CD2	1:A:376:MET:HE3	2.24	0.49
1:B:306:PRO:CG	1:B:383:PRO:HB2	2.42	0.49
1:A:152:ASN:HD22	1:B:394:TRP:HE1	1.59	0.49
1:B:451:ALA:O	1:B:455:ILE:HG13	2.12	0.49
1:C:243:SER:HB2	1:C:244:PRO:CD	2.42	0.49
2:E:1:NAG:H4	2:E:2:NAG:C1	2.39	0.49
1:A:120:GLU:OE1	1:A:166:LYS:NZ	2.40	0.49
1:A:415:TYR:O	1:A:418:LEU:HB2	2.13	0.49
1:B:218:LYS:N	1:B:228:ASP:HB2	2.28	0.49
1:A:187:ALA:O	1:A:191:ASP:N	2.35	0.49
1:A:304:LYS:NZ	1:A:342:ALA:O	2.46	0.49
1:B:243:SER:HB2	1:B:244:PRO:HD2	1.94	0.49
1:B:247:VAL:HG11	1:B:262:VAL:HB	1.95	0.49
1:B:69:MET:HE3	1:B:73:TRP:CB	2.29	0.49
1:C:69:MET:HE3	5:C:2101:HOH:O	2.13	0.49
1:A:243:SER:CB	1:A:244:PRO:CD	2.91	0.49
1:B:143:MET:SD	1:B:147:ASN:ND2	2.86	0.49
1:C:119:VAL:HA	1:C:122:MET:CE	2.43	0.49
2:E:1:NAG:O6	2:E:2:NAG:C1	2.60	0.49
1:A:430:GLU:HG2	4:A:579:FAD:O3'	2.13	0.48
1:C:63:GLY:HA2	1:C:193:GLY:O	2.14	0.48
1:A:414:GLU:O	1:A:414:GLU:HG2	2.14	0.48
1:C:96:VAL:O	1:C:103:VAL:HA	2.13	0.48
1:C:112:ARG:NH2	1:C:115:LEU:CD1	2.76	0.48
1:A:8:ILE:HG13	1:A:259:ALA:HB2	1.95	0.48
1:C:304:LYS:NZ	1:C:342:ALA:O	2.32	0.48
1:A:21:LYS:HB2	1:A:216:TYR:CE2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:PRO:HG3	1:A:324:SER:HA	1.96	0.48
1:B:69:MET:CE	1:B:74:PRO:CD	2.84	0.48
1:C:173:GLU:OE1	1:C:294:ASP:OD2	2.32	0.48
1:A:69:MET:CE	1:A:74:PRO:CD	2.90	0.48
1:A:243:SER:HB2	1:A:244:PRO:HD2	1.95	0.48
1:B:69:MET:HE2	1:B:74:PRO:CD	2.24	0.48
1:C:218:LYS:O	1:C:227:VAL:N	2.40	0.48
1:A:450:SER:HA	1:A:453:ILE:HD12	1.96	0.48
1:C:64:VAL:O	1:C:65:ASN:HB2	2.13	0.48
1:C:69:MET:HE2	1:C:70:ASN:N	2.29	0.48
1:B:454:LEU:HD12	1:B:454:LEU:O	2.14	0.47
1:B:21:LYS:HB2	1:B:216:TYR:CE2	2.49	0.47
1:B:83:ARG:NH2	1:B:337:LYS:O	2.48	0.47
1:C:402:THR:CB	4:C:579:FAD:HM83	2.44	0.47
1:C:131:HIS:CD2	1:C:133:SER:HB3	2.50	0.47
1:C:69:MET:CE	1:C:73:TRP:HB3	2.44	0.47
1:A:431:HIS:CD2	5:A:2208:HOH:O	2.66	0.47
1:B:430:GLU:O	1:B:437:ASN:HA	2.14	0.47
1:A:95:ASN:HB3	1:A:319:PHE:HB3	1.96	0.47
1:C:366:LYS:HD2	1:C:385:ALA:HB3	1.97	0.47
1:B:241:LYS:HA	1:B:279:LYS:O	2.15	0.47
1:B:411:ASN:ND2	1:B:414:GLU:N	2.50	0.47
1:B:360:GLN:NE2	5:B:2189:HOH:O	2.48	0.47
1:A:70:ASN:O	1:A:74:PRO:HD3	2.15	0.47
1:A:238:ARG:NH1	1:A:252:GLU:OE2	2.47	0.46
1:A:305:PHE:HB3	1:A:306:PRO:HD2	1.96	0.46
1:C:26:ALA:HB2	1:C:455:ILE:HD13	1.96	0.46
1:C:438:GLY:O	4:C:579:FAD:H1'2	2.15	0.46
1:A:35:GLU:HB3	1:A:233:LEU:HD23	1.96	0.46
1:A:21:LYS:O	1:A:25:GLU:HG3	2.15	0.46
1:C:255:SER:HB2	1:C:257:TYR:CE1	2.50	0.46
1:A:305:PHE:HB3	1:A:306:PRO:CD	2.45	0.46
1:A:350:THR:HA	1:A:354:SER:OG	2.15	0.46
1:B:145:ARG:O	1:B:149:HIS:N	2.47	0.46
1:B:53:ASN:HB3	5:B:2099:HOH:O	2.15	0.46
1:C:187:ALA:HA	1:C:190:SER:OG	2.14	0.46
1:A:158:VAL:CG1	1:A:159:ASP:N	2.77	0.46
1:C:374:ARG:HD2	5:C:2194:HOH:O	2.15	0.46
1:B:218:LYS:H	1:B:228:ASP:HB2	1.79	0.46
2:D:1:NAG:O6	2:D:2:NAG:C1	2.63	0.46
1:A:291:TYR:CG	1:B:146:LEU:HA	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:285:TRP:CZ3	1:C:286:LYS:HE2	2.51	0.46
1:B:131:HIS:CD2	1:B:133:SER:OG	2.69	0.45
1:B:131:HIS:HD2	1:B:133:SER:CB	2.29	0.45
1:B:317:GLU:O	1:B:333:GLN:HA	2.15	0.45
1:A:99:GLU:HA	1:A:321:TYR:CE1	2.51	0.45
1:A:49:PHE:O	1:A:50:ALA:HB3	2.16	0.45
1:B:158:VAL:HG12	5:B:2072:HOH:O	2.16	0.45
1:B:246:GLY:HA2	1:B:424:ARG:HD3	1.99	0.45
1:A:217:LEU:HD12	1:A:217:LEU:HA	1.65	0.45
1:A:292:GLN:OE1	5:A:2129:HOH:O	2.20	0.45
1:B:50:ALA:HB1	1:B:304:LYS:HD3	1.98	0.45
1:C:220:ASP:N	1:C:225:LYS:O	2.46	0.45
1:C:431:HIS:CD2	5:C:2231:HOH:O	2.69	0.45
1:C:430:GLU:O	1:C:437:ASN:HA	2.16	0.45
1:A:376:MET:C	1:A:378:PRO:HD3	2.36	0.45
1:C:250:LYS:HG2	1:C:256:VAL:HG22	1.97	0.45
1:C:8:ILE:HG13	1:C:259:ALA:HB2	1.99	0.45
1:A:300:LYS:HB3	1:A:346:LEU:HD11	1.98	0.45
1:B:141:LEU:HD22	1:B:176:ARG:HB3	1.97	0.45
1:B:307:ARG:HG2	1:B:383:PRO:HG3	1.99	0.45
1:B:411:ASN:HD21	1:B:414:GLU:H	1.58	0.44
1:B:411:ASN:HD21	1:B:414:GLU:HG3	1.82	0.44
1:A:303:LEU:O	1:A:344:VAL:HA	2.18	0.44
1:A:300:LYS:O	1:A:391:PRO:CD	2.65	0.44
1:A:256:VAL:HG12	1:A:257:TYR:N	2.32	0.44
1:A:69:MET:HE1	1:A:73:TRP:HB3	1.93	0.44
1:C:303:LEU:O	1:C:344:VAL:HA	2.18	0.44
1:C:198:PHE:CE2	1:C:338:GLN:HG2	2.52	0.44
1:C:342:ALA:O	1:C:343:ASN:HB2	2.18	0.44
1:C:439:TYR:HB3	1:C:441:HIS:CE1	2.53	0.44
1:A:73:TRP:N	1:A:74:PRO:CD	2.80	0.44
1:A:69:MET:HE2	1:A:74:PRO:CD	2.35	0.44
1:C:238:ARG:HD3	1:C:252:GLU:OE2	2.18	0.44
1:A:394:TRP:NE1	1:B:152:ASN:ND2	2.52	0.43
1:C:457:CYS:O	1:C:461:LYS:HA	2.19	0.43
1:A:452:GLU:HA	1:A:455:ILE:HD12	1.99	0.43
1:B:52:ILE:HG13	1:B:54:VAL:HG13	2.00	0.43
1:A:426:TYR:CE1	1:A:454:LEU:HD13	2.53	0.43
1:C:302:PHE:HB2	1:C:389:LEU:HB3	2.01	0.43
1:A:309:PHE:CD2	1:A:383:PRO:HD2	2.54	0.43
1:B:366:LYS:HD2	1:B:385:ALA:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:VAL:HB	1:A:252:GLU:HB2	2.01	0.43
1:A:73:TRP:HB3	1:A:74:PRO:HD3	1.99	0.43
1:B:293:PHE:CZ	1:B:406:TRP:HA	2.54	0.43
1:B:47:THR:O	1:B:53:ASN:HA	2.19	0.43
1:A:294:ASP:O	1:A:404:SER:HA	2.19	0.42
1:B:133:SER:O	1:B:411:ASN:HB2	2.19	0.42
1:C:243:SER:CB	1:C:244:PRO:CD	2.97	0.42
1:B:154:PRO:HB3	1:B:159:ASP:HB3	2.00	0.42
1:B:40:ILE:HD13	1:B:40:ILE:HG21	1.73	0.42
1:A:100:ASP:OD1	1:A:375:LYS:HE2	2.19	0.42
1:A:373:LEU:HA	1:A:376:MET:CE	2.49	0.42
1:A:370:MET:HG3	1:A:384:ASP:OD2	2.19	0.42
1:A:246:GLY:HA2	1:A:424:ARG:HD3	2.01	0.42
1:A:306:PRO:HG2	1:A:383:PRO:HB2	2.01	0.42
1:C:219:THR:CA	1:C:225:LYS:O	2.67	0.42
1:A:414:GLU:HG3	1:A:417:GLN:OE1	2.20	0.42
1:A:52:ILE:HG21	1:A:52:ILE:HD13	1.77	0.42
1:A:457:CYS:O	1:A:461:LYS:HA	2.20	0.42
1:C:118:SER:O	1:C:122:MET:HE2	2.20	0.42
1:A:302:PHE:HB2	1:A:389:LEU:HB3	2.02	0.42
1:A:64:VAL:CG1	1:A:65:ASN:N	2.82	0.42
1:A:180:LEU:HD12	1:A:184:VAL:HB	2.02	0.42
1:B:134:GLY:HA2	1:B:181:GLN:OE1	2.20	0.42
1:B:243:SER:O	1:B:424:ARG:HD2	2.20	0.42
1:C:294:ASP:HB2	1:C:405:ASN:O	2.19	0.42
1:B:243:SER:CB	1:B:244:PRO:CD	2.95	0.41
1:C:91:TYR:N	1:C:91:TYR:CD1	2.87	0.41
1:B:420:ALA:HA	1:B:421:PRO:HD3	1.90	0.41
1:C:48:ASN:HD21	1:C:51:GLY:HA2	1.85	0.41
1:C:69:MET:CE	1:C:69:MET:CA	2.97	0.41
1:A:302:PHE:O	1:A:388:ILE:HA	2.19	0.41
1:C:241:LYS:HA	1:C:279:LYS:O	2.20	0.41
1:A:220:ASP:OD1	1:A:223:SER:HB3	2.20	0.41
1:A:91:TYR:CG	1:A:315:GLY:HA3	2.55	0.41
1:B:319:PHE:CZ	1:B:332:TRP:HB3	2.55	0.41
1:C:370:MET:HE1	1:C:383:PRO:O	2.21	0.41
1:A:430:GLU:O	1:A:437:ASN:HA	2.20	0.41
1:A:400:LYS:HB3	1:B:151:PRO:HG3	2.01	0.41
1:B:158:VAL:CG1	5:B:2072:HOH:O	2.68	0.41
1:B:332:TRP:CZ3	1:B:347:VAL:HB	2.56	0.41
1:B:303:LEU:O	1:B:344:VAL:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:430:GLU:OE1	1:B:438:GLY:N	2.51	0.41
1:A:271:LEU:HD23	1:A:271:LEU:HA	1.83	0.41
1:A:370:MET:CE	1:A:384:ASP:HA	2.51	0.41
1:B:75:ILE:HA	1:B:79:THR:HB	2.02	0.41
1:B:302:PHE:HB2	1:B:389:LEU:HB3	2.03	0.41
1:C:66:GLY:HA3	1:C:192:PHE:C	2.41	0.41
1:C:6:ARG:HG3	1:C:6:ARG:NH1	2.29	0.41
1:B:148:GLU:O	1:B:149:HIS:HB2	2.21	0.41
1:B:312:GLU:OE2	5:B:2148:HOH:O	2.22	0.41
1:C:21:LYS:O	1:C:25:GLU:HG3	2.20	0.41
1:C:23:LEU:HB3	1:C:28:ILE:HB	2.01	0.41
1:A:235:LYS:HA	1:A:235:LYS:HD3	1.74	0.41
1:B:216:TYR:CD1	1:B:217:LEU:CD1	3.00	0.41
1:B:8:ILE:O	1:B:262:VAL:HA	2.21	0.41
1:B:411:ASN:C	1:B:411:ASN:HD22	2.24	0.41
1:C:213:ALA:O	1:C:217:LEU:HB2	2.21	0.41
1:A:273:SER:O	1:A:274:ASP:CB	2.57	0.40
1:A:69:MET:HE3	1:A:73:TRP:CB	2.37	0.40
1:A:360:GLN:NE2	5:A:2173:HOH:O	2.54	0.40
1:B:220:ASP:CB	1:B:223:SER:OG	2.61	0.40
1:B:228:ASP:OD1	1:B:229:PRO:HD2	2.22	0.40
1:C:119:VAL:HA	1:C:122:MET:HE2	2.03	0.40
1:B:26:ALA:CB	1:B:455:ILE:HD13	2.50	0.40
1:B:57:GLY:HA2	4:B:579:FAD:C7M	2.51	0.40
1:C:154:PRO:HB3	1:C:159:ASP:HB3	2.03	0.40
1:C:50:ALA:HB1	1:C:304:LYS:HD3	2.03	0.40
1:C:317:GLU:O	1:C:333:GLN:HA	2.22	0.40
1:A:91:TYR:N	1:A:91:TYR:CD1	2.89	0.40
1:B:381:ASP:O	1:B:383:PRO:HD3	2.21	0.40
1:B:370:MET:HG3	1:B:384:ASP:OD2	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	457/472 (97%)	437 (96%)	19 (4%)	1 (0%)	47	49
1	B	460/472 (98%)	444 (96%)	16 (4%)	0	100	100
1	C	460/472 (98%)	442 (96%)	18 (4%)	0	100	100
All	All	1377/1416 (97%)	1323 (96%)	53 (4%)	1 (0%)	51	54

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	101	GLY

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	394/404 (98%)	381 (97%)	13 (3%)	38	40
1	B	397/404 (98%)	384 (97%)	13 (3%)	38	40
1	C	397/404 (98%)	391 (98%)	6 (2%)	65	71
All	All	1188/1212 (98%)	1156 (97%)	32 (3%)	44	48

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	LEU
1	A	28	ILE
1	A	52	ILE
1	A	59	ASN
1	A	136	ASP
1	A	168	ASP
1	A	186	LEU
1	A	190	SER
1	A	205	TYR

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Mol	Chain	Res	Type
1	A	215	GLN
1	A	217	LEU
1	A	282	LEU
1	A	386	THR
1	B	23	LEU
1	B	59	ASN
1	B	105	ASP
1	B	115	LEU
1	B	154	PRO
1	B	157	PRO
1	B	158	VAL
1	B	168	ASP
1	B	205	TYR
1	B	217	LEU
1	B	411	ASN
1	B	430	GLU
1	B	454	LEU
1	C	59	ASN
1	C	127	SER
1	C	205	TYR
1	C	217	LEU
1	C	221	ASP
1	C	282	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	152	ASN
1	A	292	GLN
1	A	360	GLN
1	A	431	HIS
1	B	131	HIS
1	B	152	ASN
1	B	360	GLN
1	B	411	ASN
1	B	431	HIS
1	B	466	HIS
1	C	48	ASN
1	C	131	HIS
1	C	152	ASN
1	C	360	GLN
1	C	431	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 ⓘ

9 monosaccharides 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	NAG	D	1	1,2	14,14,15	0.89	0	17,19,21	1.83	6 (35%)
2	NAG	D	2	2	14,14,15	0.91	1 (7%)	17,19,21	1.38	3 (17%)
2	NAG	E	1	1,2	14,14,15	1.11	2 (14%)	17,19,21	2.00	5 (29%)
2	NAG	E	2	2	14,14,15	0.95	1 (7%)	17,19,21	1.92	4 (23%)
3	NAG	F	1	1,3	14,14,15	1.08	1 (7%)	17,19,21	1.99	4 (23%)
3	NAG	F	2	3	14,14,15	1.17	2 (14%)	17,19,21	1.94	4 (23%)
3	MAN	F	3	3	11,11,12	0.67	0	15,15,17	3.27	4 (26%)
3	MAN	F	4	3	11,11,12	0.55	0	15,15,17	1.14	2 (13%)
3	FCA	F	5	3	10,10,11	1.31	1 (10%)	14,14,16	1.87	4 (28%)

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	NAG	D	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	NAG	E	1	1,2	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	E	2	2	-	2/6/23/26	0/1/1/1
3	NAG	F	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	F	2	3	-	2/6/23/26	0/1/1/1
3	MAN	F	3	3	-	0/2/19/22	0/1/1/1
3	MAN	F	4	3	-	2/2/19/22	0/1/1/1
3	FCA	F	5	3	-	-	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	2	NAG	O5-C1	-3.36	1.38	1.43
3	F	5	FCA	C2-C3	-3.06	1.48	1.52
2	E	2	NAG	O5-C1	-2.63	1.39	1.43
2	E	1	NAG	O5-C1	-2.44	1.39	1.43
2	D	2	NAG	O5-C1	-2.36	1.39	1.43
2	E	1	NAG	C1-C2	-2.32	1.48	1.52
3	F	1	NAG	C1-C2	-2.26	1.49	1.52
3	F	2	NAG	C1-C2	-2.16	1.49	1.52

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	3	MAN	O2-C2-C3	11.62	133.41	110.14
3	F	1	NAG	C1-C2-N2	-4.70	102.45	110.49
3	F	2	NAG	O5-C5-C6	-4.62	99.96	107.20
2	E	2	NAG	O5-C5-C6	-4.48	100.18	107.20
2	E	1	NAG	C2-N2-C7	-4.07	117.11	122.90
3	F	1	NAG	C1-O5-C5	3.82	117.37	112.19
2	E	1	NAG	C1-O5-C5	3.73	117.25	112.19
3	F	5	FCA	C3-C4-C5	-3.67	104.06	109.77
2	E	2	NAG	C2-N2-C7	-3.63	117.73	122.90
2	E	1	NAG	O5-C5-C6	-3.50	101.72	107.20
3	F	5	FCA	C1-C2-C3	3.37	113.81	109.67
2	D	2	NAG	C1-C2-N2	-3.34	104.78	110.49
2	D	1	NAG	O5-C5-C6	-3.28	102.07	107.20
3	F	2	NAG	O5-C1-C2	-3.17	106.29	111.29
2	D	1	NAG	C1-O5-C5	3.11	116.41	112.19
2	D	1	NAG	C1-C2-N2	-3.09	105.21	110.49
2	E	2	NAG	C1-O5-C5	3.08	116.36	112.19
3	F	1	NAG	C8-C7-N2	-3.04	110.95	116.10
2	D	1	NAG	C8-C7-N2	-2.98	111.05	116.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	4	MAN	O2-C2-C3	2.76	115.67	110.14
3	F	4	MAN	C2-C3-C4	-2.73	106.18	110.89
2	E	1	NAG	O3-C3-C2	2.57	114.79	109.47
3	F	3	MAN	O5-C5-C6	2.52	111.16	107.20
2	E	2	NAG	C1-C2-N2	-2.49	106.24	110.49
3	F	5	FCA	C2-C3-C4	-2.43	106.69	110.89
2	E	1	NAG	C1-C2-N2	-2.40	106.38	110.49
2	D	1	NAG	C6-C5-C4	2.36	118.54	113.00
3	F	3	MAN	O3-C3-C2	2.36	114.50	109.99
3	F	1	NAG	C4-C3-C2	2.35	114.46	111.02
2	D	1	NAG	O3-C3-C4	2.21	115.45	110.35
3	F	5	FCA	C1-O5-C5	2.20	117.77	112.78
3	F	2	NAG	C3-C4-C5	2.17	114.11	110.24
3	F	3	MAN	O5-C1-C2	2.14	114.07	110.77
3	F	2	NAG	O3-C3-C2	-2.12	105.08	109.47
2	D	2	NAG	C2-N2-C7	-2.11	119.89	122.90
2	D	2	NAG	C8-C7-N2	-2.08	112.58	116.10

There are no chirality outliers.

All (14) torsion outliers are listed below:

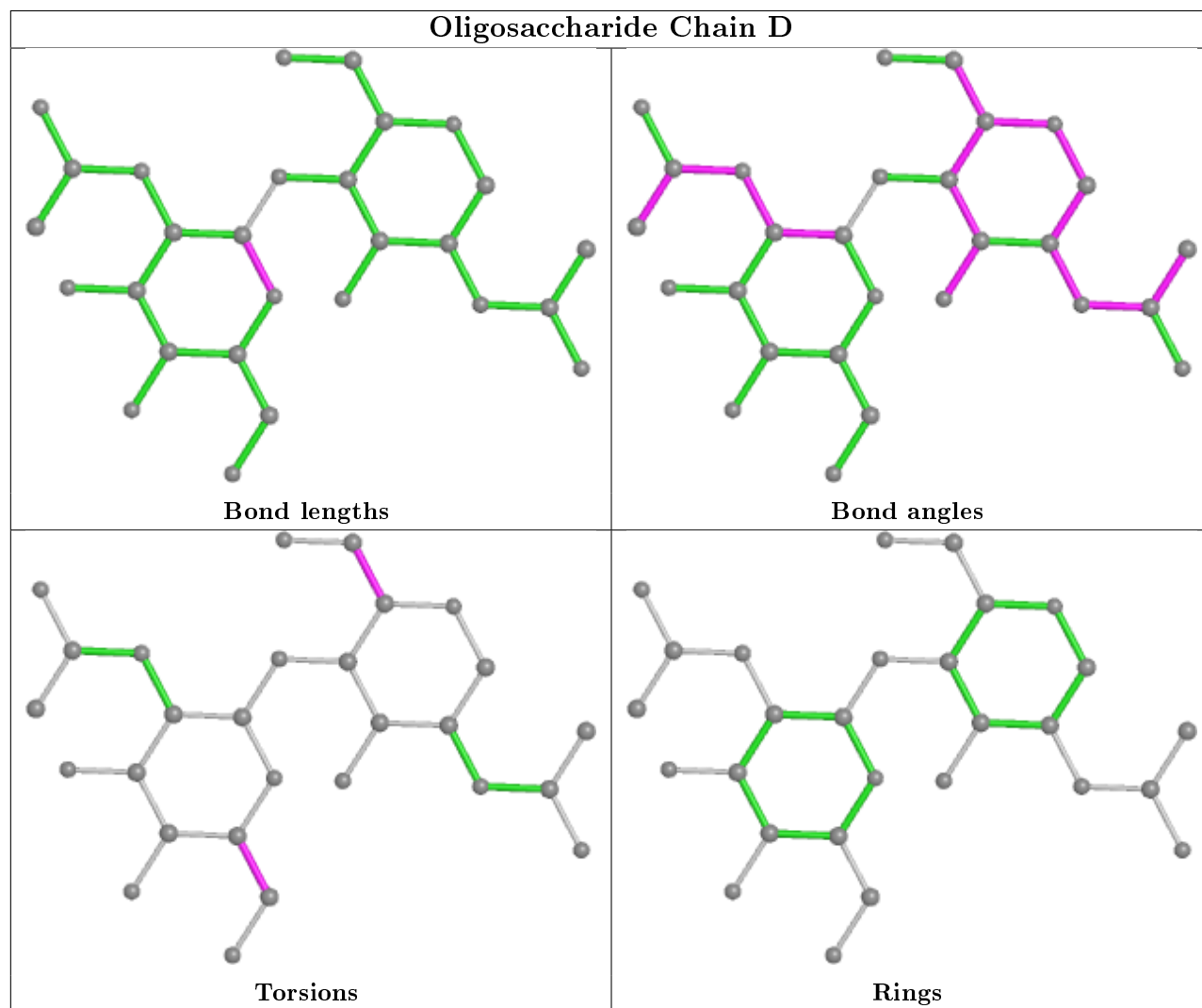
Mol	Chain	Res	Type	Atoms
3	F	1	NAG	C4-C5-C6-O6
2	D	1	NAG	C4-C5-C6-O6
2	E	2	NAG	C4-C5-C6-O6
3	F	2	NAG	C4-C5-C6-O6
2	D	2	NAG	C4-C5-C6-O6
2	E	1	NAG	C4-C5-C6-O6
2	D	1	NAG	O5-C5-C6-O6
3	F	1	NAG	O5-C5-C6-O6
2	E	2	NAG	O5-C5-C6-O6
2	D	2	NAG	O5-C5-C6-O6
2	E	1	NAG	O5-C5-C6-O6
3	F	4	MAN	O5-C5-C6-O6
3	F	2	NAG	O5-C5-C6-O6
3	F	4	MAN	C4-C5-C6-O6

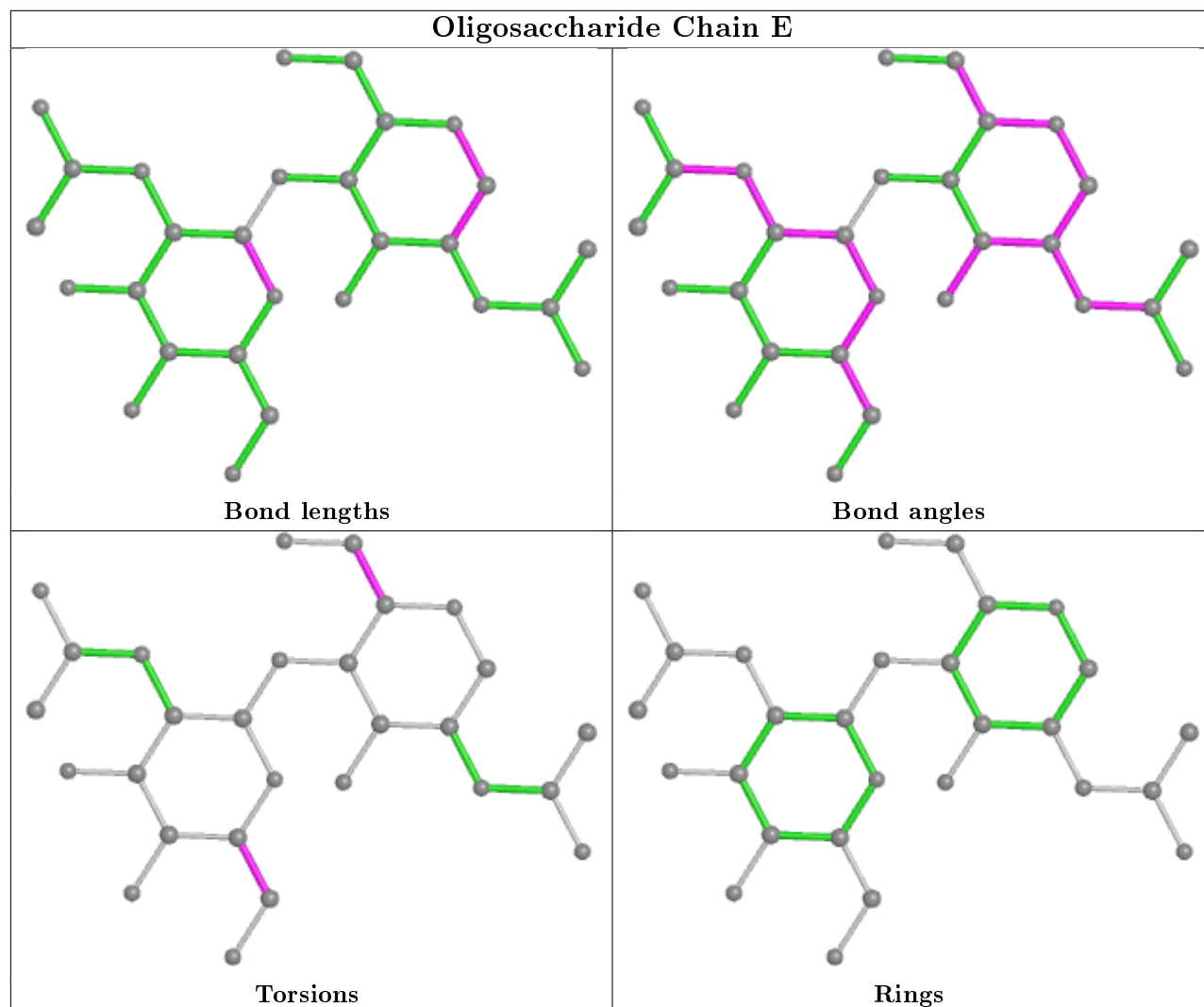
There are no ring outliers.

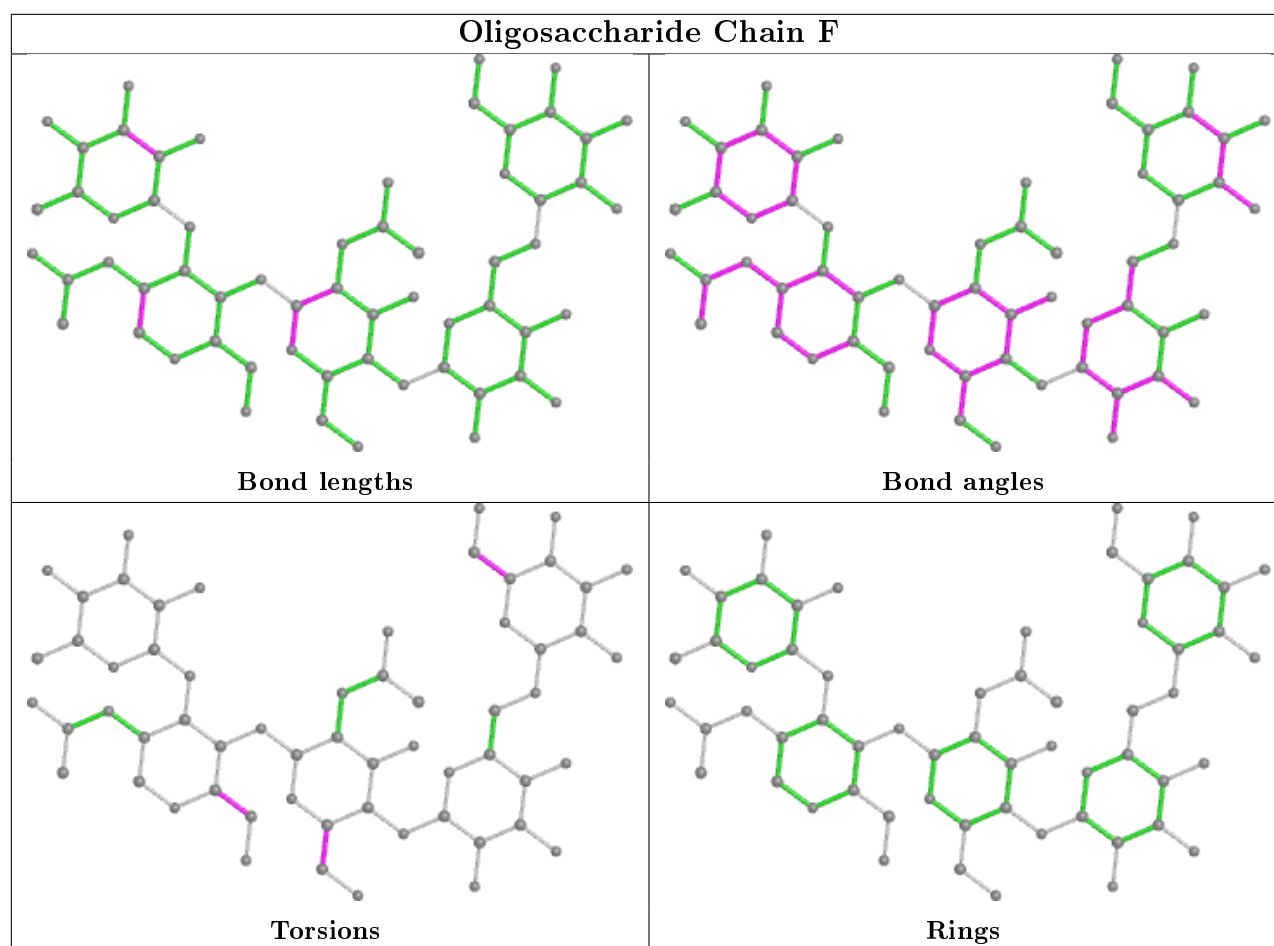
7 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	1	NAG	6	0
2	D	1	NAG	3	0
2	E	2	NAG	4	0
3	F	5	FCA	2	0
3	F	2	NAG	4	0
2	D	2	NAG	3	0
2	E	1	NAG	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.







5.6 Ligand geometry [i](#)

3 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	FAD	C	579	-	51,58,58	1.30	5 (9%)	60,89,89	2.21	12 (20%)
4	FAD	A	579	-	51,58,58	1.08	3 (5%)	60,89,89	2.52	15 (25%)
4	FAD	B	579	-	51,58,58	1.01	3 (5%)	60,89,89	2.07	13 (21%)

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	FAD	C	579	-	-	2/30/50/50	0/6/6/6
4	FAD	A	579	-	-	2/30/50/50	0/6/6/6
4	FAD	B	579	-	-	3/30/50/50	0/6/6/6

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	579	FAD	C4X-C10	4.84	1.43	1.38
4	A	579	FAD	C4-N3	4.15	1.40	1.33
4	B	579	FAD	C4-N3	3.35	1.38	1.33
4	C	579	FAD	C4-N3	3.33	1.38	1.33
4	B	579	FAD	C4X-C10	3.22	1.42	1.38
4	A	579	FAD	C4X-C10	3.17	1.42	1.38
4	C	579	FAD	C10-N1	2.78	1.36	1.33
4	B	579	FAD	C2-N1	-2.74	1.32	1.38
4	C	579	FAD	C4X-N5	2.69	1.37	1.33
4	C	579	FAD	C2-N1	-2.67	1.32	1.38
4	A	579	FAD	C2-N1	-2.62	1.33	1.38

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	579	FAD	C4-N3-C2	10.13	123.70	115.14
4	A	579	FAD	C4-N3-C2	9.99	123.58	115.14
4	B	579	FAD	C4-N3-C2	9.22	122.93	115.14
4	A	579	FAD	C1'-N10-C9A	8.05	124.63	118.29
4	A	579	FAD	C4X-C4-N3	-6.71	114.26	123.43
4	C	579	FAD	C4-C4X-C10	-5.98	115.99	119.95
4	A	579	FAD	C10-C4X-N5	-5.54	117.43	121.26
4	C	579	FAD	C4X-C10-N10	-4.76	115.42	120.30
4	B	579	FAD	C4X-C4-N3	-4.60	117.14	123.43
4	C	579	FAD	C4X-C4-N3	-4.15	117.75	123.43
4	B	579	FAD	C1'-N10-C9A	4.09	121.51	118.29
4	C	579	FAD	C5'-C4'-C3'	-4.03	104.43	112.20
4	B	579	FAD	C4-C4X-C10	-3.99	117.31	119.95
4	B	579	FAD	C10-C4X-N5	-3.56	118.80	121.26
4	C	579	FAD	C4-C4X-N5	3.42	122.51	118.60
4	A	579	FAD	C9A-N10-C10	-3.42	117.44	121.91
4	C	579	FAD	O4B-C1B-C2B	-3.39	101.97	106.93
4	A	579	FAD	C4X-C10-N10	-3.39	116.82	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	579	FAD	C9A-C5X-N5	-3.29	117.21	122.36
4	A	579	FAD	C5'-C4'-C3'	-3.26	105.91	112.20
4	B	579	FAD	C4-C4X-N5	3.18	122.23	118.60
4	C	579	FAD	C1'-N10-C9A	3.09	120.72	118.29
4	C	579	FAD	O2A-PA-O1A	2.96	126.86	112.24
4	A	579	FAD	O4'-C4'-C3'	2.90	116.14	109.10
4	A	579	FAD	C6-C5X-C9A	2.82	122.75	119.05
4	B	579	FAD	O4B-C1B-C2B	-2.78	102.86	106.93
4	A	579	FAD	C4-C4X-C10	-2.78	118.11	119.95
4	B	579	FAD	C9A-N10-C10	-2.76	118.29	121.91
4	B	579	FAD	C5'-C4'-C3'	-2.53	107.33	112.20
4	A	579	FAD	O2A-PA-O1A	2.47	124.46	112.24
4	B	579	FAD	O3'-C3'-C4'	-2.38	103.05	108.81
4	A	579	FAD	C8M-C8-C9	-2.36	114.71	120.34
4	A	579	FAD	O2P-P-O1P	2.35	123.87	112.24
4	C	579	FAD	C4A-C5A-N7A	2.32	111.82	109.40
4	C	579	FAD	O2P-P-O1P	2.20	123.13	112.24
4	B	579	FAD	C4X-C10-N10	-2.20	118.05	120.30
4	A	579	FAD	C5A-C6A-N6A	2.18	123.66	120.35
4	B	579	FAD	O2A-PA-O1A	2.15	122.87	112.24
4	B	579	FAD	C4X-N5-C5X	-2.13	114.64	116.77
4	C	579	FAD	C2B-C3B-C4B	2.05	106.63	102.64

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	579	FAD	C5B-O5B-PA-O1A
4	B	579	FAD	O3'-C3'-C4'-C5'
4	A	579	FAD	PA-O3P-P-O5'
4	C	579	FAD	O4B-C4B-C5B-O5B
4	A	579	FAD	O4B-C4B-C5B-O5B
4	B	579	FAD	O4B-C4B-C5B-O5B
4	C	579	FAD	O3'-C3'-C4'-C5'

There are no ring outliers.

3 monomers are involved in 9 short contacts:

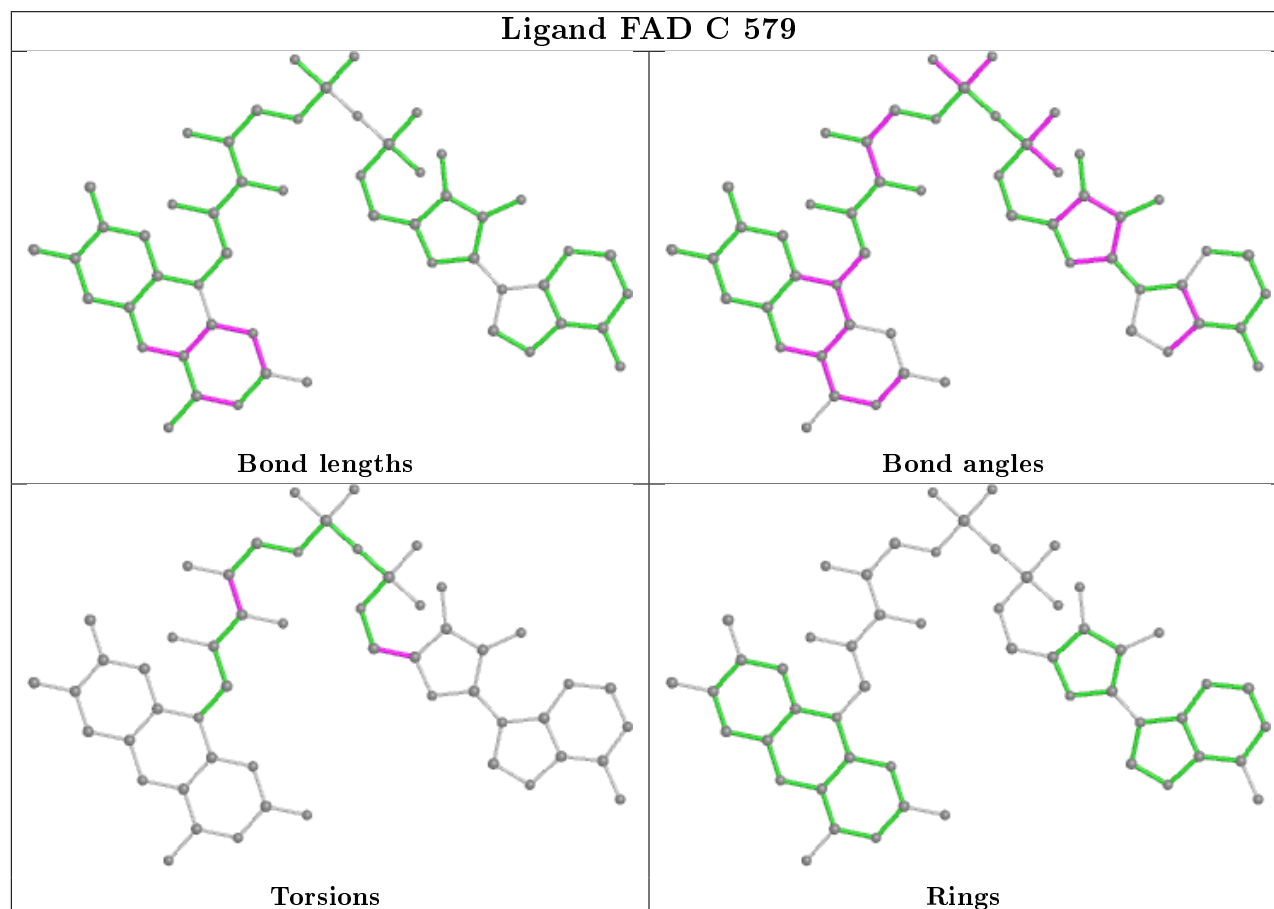
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	579	FAD	5	0
4	A	579	FAD	2	0

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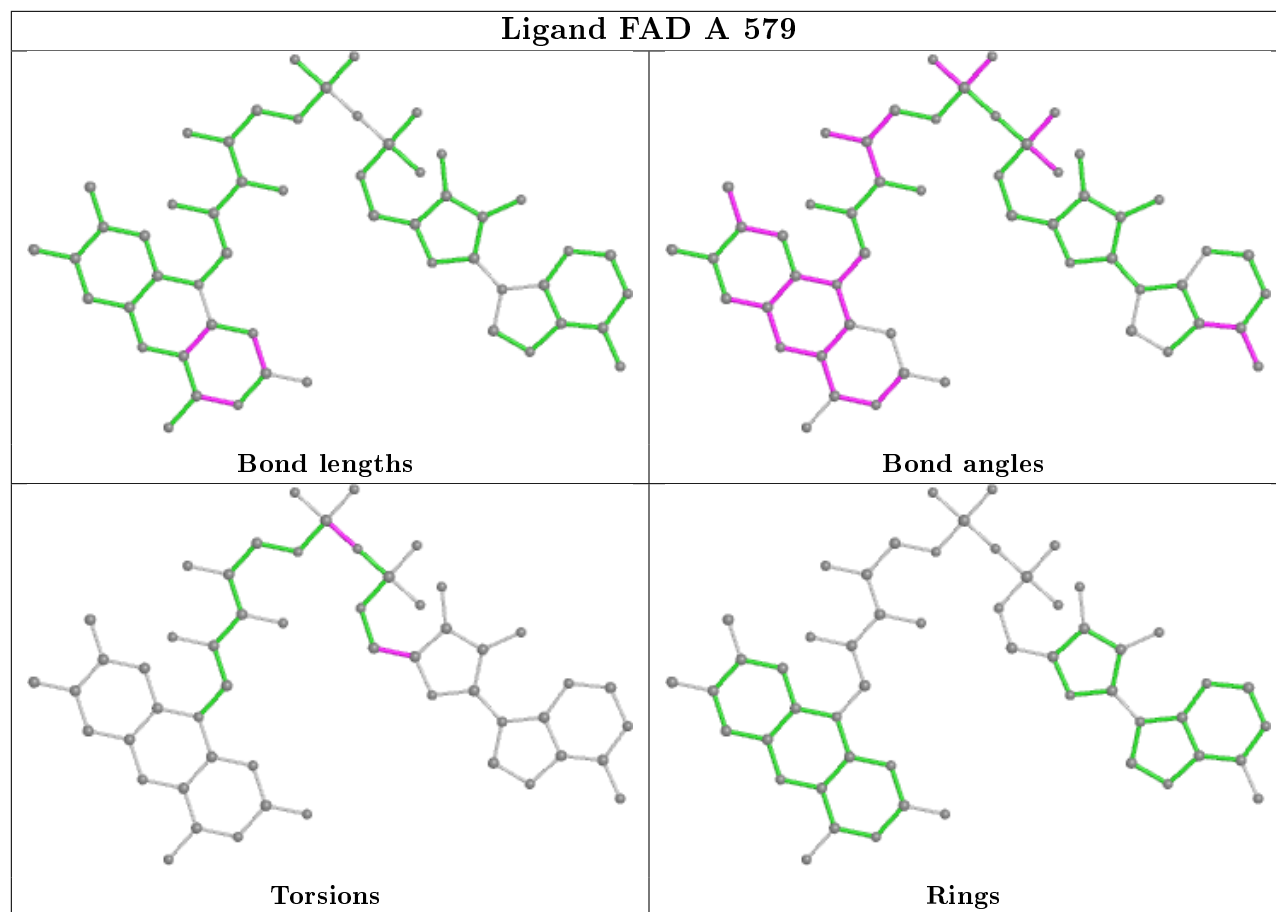
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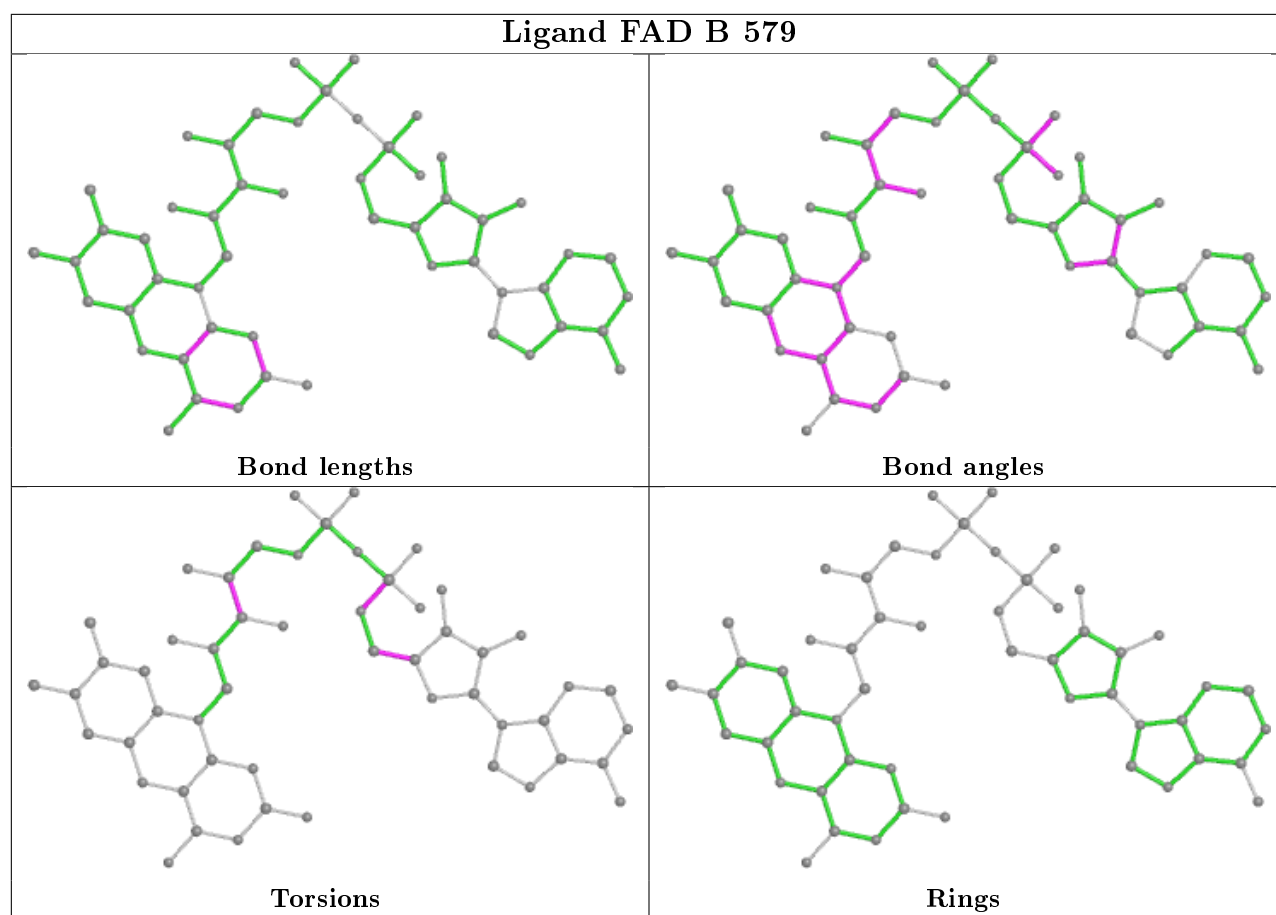
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	579	FAD	2	0

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.



Ligand FAD A 579





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.