



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2026 – 11:04 PM EDT

PDB ID : 1N63 / pdb_00001n63
Title : Crystal Structure of the Cu,Mo-CO Dehydrogenase (CODH); Carbon monoxide reduced state
Authors : Dobbek, H.; Gremer, L.; Kiefersauer, R.; Huber, R.; Meyer, O.
Deposited on : 2002-11-08
Resolution : 1.21 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) : 2.50

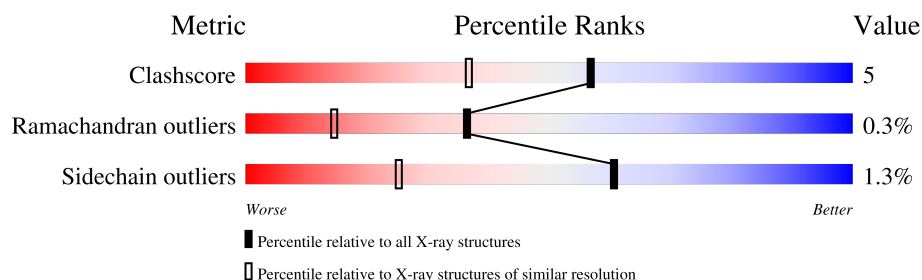
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.21 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	2061 (1.24-1.20)
Ramachandran outliers	187476	2009 (1.24-1.20)
Sidechain outliers	187428	2008 (1.24-1.20)

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	166	
1	D	166	
2	B	809	
2	E	809	
3	C	288	
3	F	288	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 22119 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 Carbon monoxide dehydrogenase small chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	160	Total	C	N	O	S	2	4	0
			1206	748	214	227	17			
1	D	158	Total	C	N	O	S	7	6	0
			1202	745	217	223	17			

- Molecule 2 is a protein called Carbon monoxide dehydrogenase large chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	805	Total	C	N	O	S	70	23	0
			6292	4003	1070	1170	49			
2	E	795	Total	C	N	O	S	71	15	0
			6187	3936	1052	1152	47			

- Molecule 3 is a protein called Carbon monoxide dehydrogenase medium chain.

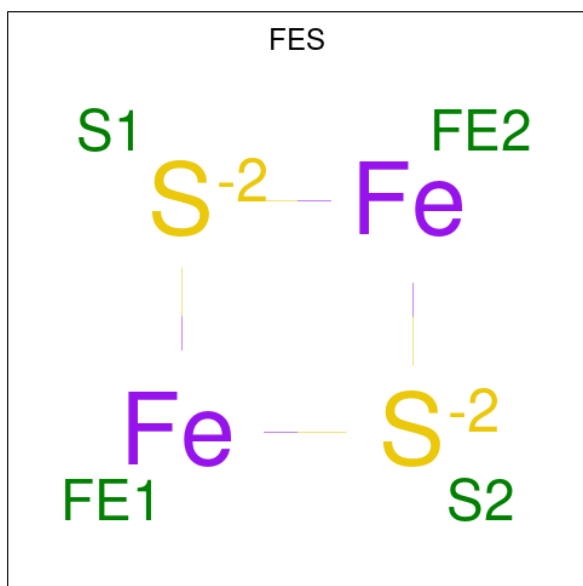
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	287	Total	C	N	O	S	38	9	0
			2143	1354	376	401	12			
3	F	286	Total	C	N	O	S	38	7	0
			2123	1341	370	399	13			

- Molecule 4 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 5 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



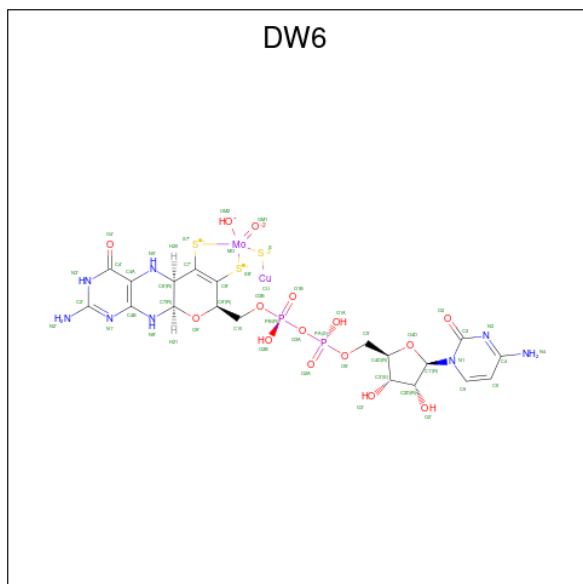
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	Fe	S	0	0
			4	2	2		
5	A	1	Total	Fe	S	0	0
			4	2	2		
5	D	1	Total	Fe	S	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 6 is CuSMo(=O)OH pterin (CCD ID: DW6) (formula: $C_{19}H_{25}CuMoN_8O_{15}P_2S_3$).



Mol	Chain	Residues	Atoms								ZeroOcc	AltConf
6	B	1	Total	C	Cu	Mo	N	O	P	S	0	0
			49	19	1	1	8	15	2	3		
6	E	1	Total	C	Cu	Mo	N	O	P	S	0	0
			49	19	1	1	8	15	2	3		

- Molecule 7 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



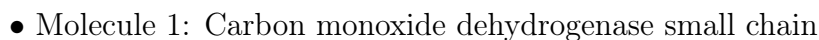
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
7	F	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 8 is water.

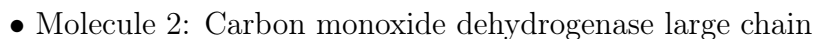
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	196	Total	O	0	0
			196	196		
8	B	864	Total	O	0	0
			864	864		
8	C	361	Total	O	0	1
			362	362		
8	D	196	Total	O	0	0
			196	196		
8	E	831	Total	O	0	0
			831	831		
8	F	292	Total	O	0	0
			292	292		

Note EDS was not executed.

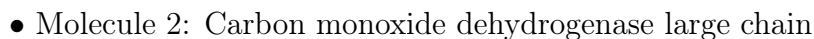
- Chain A: 87% 10% .

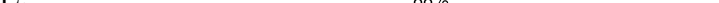


- Chain D:  87% 7% • 5%

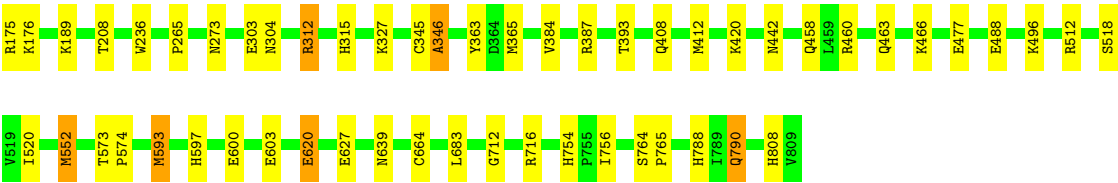


- Chain B: 87% 11% •

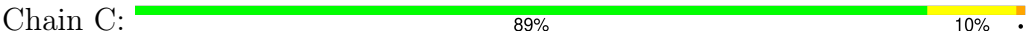


- Chain E:  88% 9% ..

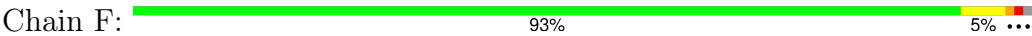




● Molecule 3: Carbon monoxide dehydrogenase medium chain



● Molecule 3: Carbon monoxide dehydrogenase medium chain



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	118.96Å 131.27Å 159.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	17.00 – 1.21	Depositor
% Data completeness (in resolution range)	(Not available) (17.00-1.21)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS, REFMAC	Depositor
R, R_{free}	0.149 , 0.185	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	22119	wwPDB-VP
Average B, all atoms (Å ²)	18.0	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: FES, PO4, DW6, FAD

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	0/1244	1.01	0/1681
1	D	1.02	2/1246 (0.2%)	1.08	3/1681 (0.2%)
2	B	1.10	12/6542 (0.2%)	1.07	15/8875 (0.2%)
2	E	1.18	17/6400 (0.3%)	1.08	16/8678 (0.2%)
3	C	1.03	6/2216 (0.3%)	1.05	3/3007 (0.1%)
3	F	1.22	6/2186 (0.3%)	1.01	6/2966 (0.2%)
All	All	1.12	43/19834 (0.2%)	1.06	43/26888 (0.2%)

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	2
1	D	0	1
2	B	0	18
2	E	0	19
3	C	0	9
3	F	0	5
All	All	0	54

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	303	GLU	CD-OE1	-33.40	0.61	1.25
2	E	303	GLU	CD-OE2	31.38	1.84	1.25
3	F	49	GLU	CD-OE2	31.03	1.84	1.25
2	B	139	ASP	CG-OD1	23.23	1.69	1.25
3	F	23	LYS	CD-CE	-22.45	0.85	1.52
2	B	741	LYS	CE-NZ	20.44	2.10	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	139	ASP	CG-OD2	-20.28	0.86	1.25
2	E	162	GLU	CD-OE1	17.91	1.59	1.25
2	E	37	LYS	CE-NZ	-16.97	0.98	1.49
2	E	189	LYS	CE-NZ	-12.22	1.12	1.49
3	C	287	LYS	CB-CG	11.93	1.88	1.52
2	B	809	VAL	CB-CG1	-11.48	1.14	1.52
2	B	63	ARG	CD-NE	-11.20	1.30	1.46
3	C	240	LYS	CE-NZ	-11.02	1.16	1.49
2	B	325	ASP	CG-OD1	10.81	1.45	1.25
2	E	167	LYS	CD-CE	10.77	1.84	1.52
3	F	49	GLU	CG-CD	-10.01	1.27	1.52
2	E	88	LYS	CE-NZ	9.80	1.78	1.49
2	E	15	ALA	CA-CB	9.79	1.84	1.52
2	B	664	CYS	N-CA	9.64	1.57	1.46
2	B	593	MET	SD-CE	-9.41	1.56	1.79
3	C	142	GLU	CG-CD	8.67	1.73	1.52
2	E	91	ASN	CG-ND2	-8.62	1.15	1.33
3	C	265	GLU	CD-OE1	-8.40	1.09	1.25
3	C	162	GLU	CD-OE2	8.38	1.41	1.25
2	B	664	CYS	CA-CB	8.37	1.73	1.53
2	E	639	ASN	CG-OD1	-8.26	1.07	1.23
1	D	16	GLU	CG-CD	8.01	1.72	1.52
1	D	3	LYS	CE-NZ	-7.74	1.26	1.49
2	E	171	ALA	CA-CB	-7.68	1.42	1.53
3	C	287	LYS	C-O	-7.55	1.08	1.23
2	B	167	LYS	CB-CG	7.29	1.74	1.52
2	E	496	LYS	CD-CE	6.61	1.72	1.52
2	E	664	CYS	CA-CB	6.24	1.65	1.53
2	E	365	MET	SD-CE	6.06	1.94	1.79
2	E	17	LYS	CA-CB	-5.86	1.43	1.53
2	E	593	MET	SD-CE	5.56	1.93	1.79
2	B	5	THR	CB-OG1	5.55	1.52	1.43
3	F	90	LYS	CE-NZ	-5.36	1.33	1.49
3	F	86	PHE	CD2-CE2	-5.33	1.22	1.38
2	E	664	CYS	N-CA	5.31	1.52	1.46
3	F	240	LYS	CB-CG	5.23	1.68	1.52
2	B	466	LYS	CE-NZ	-5.18	1.33	1.49

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	5	THR	N-CA-CB	17.96	142.03	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	639	ASN	OD1-CG-ND2	-16.78	105.82	122.60
2	E	91	ASN	OD1-CG-ND2	-15.09	107.51	122.60
2	B	139	ASP	CB-CG-OD2	12.31	146.71	118.40
2	E	15	ALA	N-CA-CB	11.61	127.81	110.40
2	E	303	GLU	CG-CD-OE2	-10.96	93.19	118.40
3	C	287	LYS	CA-C-O	10.92	139.37	120.80
3	F	49	GLU	CB-CG-CD	10.88	131.10	112.60
2	E	303	GLU	CG-CD-OE1	10.34	142.18	118.40
3	C	142	GLU	CB-CG-CD	-9.03	97.25	112.60
3	F	177	THR	OG1-CB-CG2	8.65	126.61	109.30
2	B	325	ASP	CA-CB-CG	8.32	120.92	112.60
2	B	139	ASP	CB-CG-OD1	-8.30	99.31	118.40
3	C	287	LYS	CA-CB-CG	-8.29	97.53	114.10
2	B	175	ARG	NE-CZ-NH1	-8.20	113.30	121.50
2	E	162	GLU	CG-CD-OE1	-8.06	99.86	118.40
2	E	16	GLU	CG-CD-OE1	-8.04	99.90	118.40
2	E	639	ASN	CB-CG-OD1	7.68	136.16	120.80
2	E	15	ALA	CB-CA-C	-7.55	99.18	110.50
2	E	91	ASN	CB-CG-ND2	7.45	127.58	116.40
2	B	809	VAL	CA-CB-CG1	7.07	122.42	110.40
2	E	496	LYS	CG-CD-CE	-7.06	95.07	111.30
2	E	189	LYS	CD-CE-NZ	6.84	133.78	111.90
2	B	664	CYS	N-CA-C	-6.68	98.51	109.40
1	D	135	ASN	CA-C-O	6.28	127.02	120.30
3	F	86	PHE	CD1-CG-CD2	-6.28	109.18	118.60
2	E	16	GLU	CB-CA-C	6.22	121.43	110.85
2	B	809	VAL	CG1-CB-CG2	6.19	124.42	110.80
3	F	177	THR	CA-CB-CG2	-6.14	100.06	110.50
2	B	175	ARG	NE-CZ-NH2	6.05	124.64	119.20
3	F	86	PHE	CB-CG-CD2	5.95	130.81	120.70
1	D	135	ASN	O-C-N	-5.80	116.54	123.27
2	B	347	ASP	N-CA-C	-5.73	103.03	108.19
2	B	325	ASP	CB-CG-OD1	-5.57	105.59	118.40
2	E	167	LYS	CG-CD-CE	-5.31	99.08	111.30
2	E	346[A]	ALA	CA-C-O	-5.20	114.55	120.58
2	E	346[B]	ALA	CA-C-O	-5.20	114.55	120.58
2	B	626	LYS	CD-CE-NZ	5.19	128.51	111.90
2	B	688	THR	OG1-CB-CG2	-5.18	98.94	109.30
3	F	45	LEU	CD1-CG-CD2	5.12	122.06	110.80
2	B	346[A]	ALA	CA-C-O	-5.06	114.92	120.69
2	B	346[B]	ALA	CA-C-O	-5.06	114.92	120.69
1	D	147	LYS	CG-CD-CE	5.03	122.87	111.30

There are no chirality outliers.

All (54) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	31	GLU	Mainchain
1	A	82	ALA	Mainchain
2	B	134	GLU	Sidechain
2	B	162	GLU	Sidechain
2	B	185	GLU	Sidechain
2	B	19	GLN	Sidechain
2	B	27	ARG	Sidechain
2	B	303	GLU	Sidechain
2	B	312	ARG	Sidechain
2	B	346[A]	ALA	Mainchain
2	B	346[B]	ALA	Mainchain
2	B	363	TYR	Sidechain
2	B	387	ARG	Sidechain
2	B	471	LYS	Mainchain
2	B	53	ASP	Sidechain
2	B	549[A]	ASP	Sidechain
2	B	549[B]	ASP	Sidechain
2	B	689[A]	ARG	Sidechain
2	B	689[B]	ARG	Sidechain
2	B	88	LYS	Mainchain
3	C	10	ARG	Sidechain
3	C	221[A]	ASN	Sidechain
3	C	221[B]	ASN	Sidechain
3	C	286	ALA	Peptide
3	C	29	ARG	Sidechain
3	C	44	ARG	Sidechain,Mainchain
3	C	55[A]	ARG	Sidechain
3	C	55[B]	ARG	Sidechain
1	D	138	ARG	Sidechain
2	E	140	TYR	Sidechain
2	E	16	GLU	Sidechain
2	E	162	GLU	Sidechain
2	E	168	MET	Mainchain
2	E	175	ARG	Sidechain
2	E	27	ARG	Sidechain
2	E	312	ARG	Sidechain
2	E	346[A]	ALA	Mainchain
2	E	346[B]	ALA	Mainchain
2	E	363	TYR	Sidechain
2	E	387	ARG	Sidechain

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Mol	Chain	Res	Type	Group
2	E	412[A]	MET	Mainchain
2	E	412[B]	MET	Mainchain
2	E	512	ARG	Sidechain
2	E	53	ASP	Mainchain
2	E	600	GLU	Sidechain
2	E	620	GLU	Mainchain
2	E	627	GLU	Sidechain
2	E	808	HIS	Mainchain
3	F	45	LEU	Mainchain
3	F	49	GLU	Sidechain
3	F	69	ASP	Mainchain
3	F	85	ASP	Mainchain
3	F	86	PHE	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	1206	0	1184	18	0
1	D	1202	0	1190	12	0
2	B	6292	0	6169	70	1
2	E	6187	0	6051	41	1
3	C	2143	0	2198	20	0
3	F	2123	0	2168	23	0
4	A	5	0	0	1	0
5	A	8	0	0	0	0
5	D	8	0	0	0	0
6	B	49	0	0	1	0
6	E	49	0	0	0	0
7	C	53	0	31	2	0
7	F	53	0	31	3	0
8	A	196	0	0	1	1
8	B	864	0	0	18	1
8	C	362	0	0	2	0
8	D	196	0	0	2	0
8	E	831	0	0	12	1
8	F	292	0	0	4	0
All	All	22119	0	19022	175	3

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 5.

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)
3:F:10:ARG:NH2	3:F:55:ARG:CZ	1.97	1.28
2:E:593:MET:HG2	2:E:603:GLU:OE1	1.19	1.27
3:F:10:ARG:HH21	3:F:55:ARG:NE	1.35	1.24
1:D:59:VAL:HG11	1:D:64:MET:HE1	1.22	1.13
3:F:10:ARG:HH21	3:F:55:ARG:CZ	1.58	1.11
3:F:10:ARG:NH2	3:F:55:ARG:NE	2.00	1.09
1:D:59:VAL:HG11	1:D:64:MET:CE	1.89	1.02
2:E:593:MET:CG	2:E:603:GLU:OE1	2.15	0.91
2:B:95[B]:MET:HE2	8:B:4413:HOH:O	1.70	0.89
3:F:10:ARG:HD2	3:F:55:ARG:HD3	1.53	0.87
2:B:528:GLN:H	2:B:530:GLN:HE22	1.22	0.84
1:A:68:GLN:HE21	3:C:55[A]:ARG:HH12	1.25	0.84
2:E:208:THR:H	2:E:790:GLN:HE22	1.23	0.84
1:D:11:ASN:HD21	1:D:76:THR:H	1.24	0.83
2:E:716:ARG:NE	8:E:5343:HOH:O	2.09	0.83
3:F:10:ARG:CZ	8:F:5072:HOH:O	2.28	0.82
2:B:808:HIS:O	2:B:809:VAL:HB	1.79	0.82
2:B:159:LEU:HD13	2:B:162:GLU:HG2	1.62	0.82
2:B:460:ARG:HH11	2:B:463:GLN:HE22	1.28	0.82
8:B:4101:HOH:O	3:C:1[A]:MET:HE1	1.79	0.82
1:D:3:LYS:N	8:D:5042:HOH:O	2.13	0.80
1:D:59:VAL:CG1	1:D:64:MET:HE1	2.10	0.78
3:F:10:ARG:HH22	3:F:55:ARG:CZ	1.97	0.77
1:A:59:VAL:HG11	1:A:64[A]:MET:CE	2.15	0.77
2:E:408:GLN:NE2	8:E:5704:HOH:O	2.17	0.77
1:D:59:VAL:CG1	1:D:64:MET:CE	2.64	0.75
1:A:59:VAL:HG11	1:A:64[A]:MET:HE3	1.69	0.75
2:B:713[A]:GLN:CD	2:B:731:PHE:CZ	2.65	0.74
3:F:10:ARG:CD	3:F:55:ARG:HD3	2.18	0.74
2:B:46:LEU:HD11	2:B:236[C]:TRP:CZ3	2.22	0.73
2:E:273:ASN:HD21	2:E:304:ASN:HD21	1.36	0.73
2:B:716:ARG:NE	8:B:4266:HOH:O	2.21	0.72
2:B:159:LEU:CD1	2:B:162:GLU:HG2	2.20	0.71
2:E:460:ARG:HH11	2:E:463:GLN:HE22	1.36	0.71
1:D:159:VAL:HB	1:D:160:PRO:HD3	1.74	0.69
2:E:477:GLU:OE2	8:E:5270:HOH:O	2.11	0.69
3:F:10:ARG:HH21	3:F:55:ARG:CD	2.06	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:46:LEU:HD11	2:E:236[B]:TRP:CZ3	2.28	0.68
2:B:528:GLN:H	2:B:530:GLN:NE2	1.91	0.67
2:B:803:GLU:OE1	2:B:808:HIS:HD2	1.77	0.67
2:E:593:MET:HG2	2:E:603:GLU:CD	2.16	0.67
6:B:810:DW6:OM1	6:B:810:DW6:MO	1.66	0.65
1:A:27:HIS:HD2	2:B:127:TYR:OH	1.80	0.65
3:C:53:ASP:OD2	3:C:55[A]:ARG:HD2	1.97	0.65
2:E:754:HIS:HD2	2:E:756:ILE:H	1.45	0.65
2:E:716:ARG:CZ	8:E:5343:HOH:O	2.45	0.63
2:E:593:MET:HE2	8:E:5100:HOH:O	1.97	0.63
3:C:10:ARG:CZ	3:C:55[B]:ARG:HD3	2.29	0.63
2:B:159:LEU:HD13	2:B:162:GLU:CG	2.28	0.63
2:B:530:GLN:HE21	2:B:530:GLN:H	1.47	0.62
2:B:248:VAL:HG22	8:B:4721:HOH:O	1.99	0.62
1:A:135:ASN:HD21	3:C:105:GLN:HE22	1.46	0.61
2:B:303:GLU:HG2	8:B:4311:HOH:O	2.00	0.61
2:E:458:GLN:HG3	8:E:5132:HOH:O	2.00	0.61
2:B:593:MET:CE	2:B:640:LEU:HD21	2.30	0.60
1:D:118[A]:GLN:NE2	8:D:4977:HOH:O	2.32	0.60
3:F:10:ARG:HD2	3:F:55:ARG:CD	2.31	0.58
2:B:300:ASP:HB2	2:B:303:GLU:OE1	2.03	0.58
2:B:53:ASP:CG	8:B:4714:HOH:O	2.46	0.58
1:A:5:HIS:HD2	4:A:3001:PO4:O1	1.87	0.58
3:C:118:ASN:HD22	7:C:3932:FAD:H4B	1.69	0.57
2:B:21[A]:MET:HE1	8:B:4456:HOH:O	2.05	0.56
2:B:442:ASN:C	2:B:442:ASN:HD22	2.12	0.56
2:B:350:LYS:HE3	8:B:4605:HOH:O	2.04	0.56
2:E:208:THR:H	2:E:790:GLN:NE2	2.01	0.56
2:B:670:VAL:O	2:B:808:HIS:HE1	1.89	0.56
1:A:135:ASN:ND2	3:C:105:GLN:HE22	2.04	0.55
2:B:754:HIS:HD2	2:B:756:ILE:H	1.53	0.55
1:A:5:HIS:HE1	1:A:16:GLU:OE2	1.89	0.55
2:B:716:ARG:CZ	8:B:4266:HOH:O	2.54	0.55
3:F:162:GLU:HB3	3:F:163:PRO:HD2	1.89	0.55
3:F:118:ASN:HD22	7:F:4931:FAD:H4B	1.72	0.55
1:A:68:GLN:HE21	3:C:55[A]:ARG:NH1	2.00	0.54
2:E:208:THR:OG1	2:E:315:HIS:HD2	1.90	0.54
2:B:21[A]:MET:CE	8:B:4456:HOH:O	2.55	0.54
2:B:718:ASP:HB3	2:B:724:LEU:HD11	1.90	0.54
2:E:593:MET:HE1	8:E:5566:HOH:O	2.08	0.53
1:A:59:VAL:HG11	1:A:64[A]:MET:HE1	1.87	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:327:LYS:HG2	2:B:420:LYS:HE3	1.90	0.53
1:A:59:VAL:CG1	1:A:64[A]:MET:HE3	2.37	0.53
2:E:442:ASN:HD22	2:E:442:ASN:C	2.16	0.53
2:E:754:HIS:CD2	2:E:756:ILE:H	2.26	0.53
1:D:96[A]:MET:HE3	2:E:26[A]:LYS:HZ3	1.73	0.52
2:B:334:HIS:HE1	2:B:373:ASP:OD2	1.92	0.52
2:E:466:LYS:HE3	8:E:5712:HOH:O	2.07	0.52
3:F:202:LEU:C	3:F:202:LEU:HD12	2.34	0.52
3:C:222:THR:HB	3:C:223:PRO:HD2	1.92	0.52
3:F:106[B]:ILE:HD13	7:F:4931:FAD:C7	2.40	0.51
2:E:88:LYS:CB	2:E:89:PRO:HD3	2.41	0.51
2:E:597:HIS:HD2	8:E:5552:HOH:O	1.94	0.50
2:B:683:LEU:HD23	2:B:683:LEU:C	2.36	0.50
2:B:754:HIS:CD2	2:B:756:ILE:H	2.28	0.50
2:B:172:HIS:HD2	8:B:4586:HOH:O	1.95	0.50
1:A:27:HIS:HE1	8:B:4061:HOH:O	1.94	0.50
2:B:8:GLU:HG3	2:B:8:GLU:O	2.10	0.50
2:B:489:ILE:HD11	2:B:655[A]:MET:HG3	1.92	0.50
2:E:520:ILE:CD1	2:E:552[A]:MET:HG2	2.42	0.49
2:B:53:ASP:HB3	2:B:133:ILE:HD11	1.93	0.49
2:E:327:LYS:HE2	2:E:420:LYS:NZ	2.26	0.49
2:E:788:HIS:HE2	2:E:790:GLN:NE2	2.10	0.49
2:B:593:MET:HG2	2:B:603:GLU:OE2	2.12	0.49
2:E:19[B]:GLN:NE2	8:E:5286:HOH:O	2.16	0.49
2:B:238:THR:HB	2:B:274:LYS:HD3	1.95	0.49
2:B:593:MET:HE2	2:B:640:LEU:HD21	1.95	0.49
2:E:683:LEU:C	2:E:683:LEU:HD23	2.38	0.49
3:C:106:ILE:HD13	7:C:3932:FAD:C7	2.43	0.48
1:D:96[A]:MET:HE3	2:E:26[A]:LYS:NZ	2.27	0.48
2:B:593:MET:HE1	2:B:640:LEU:HD21	1.95	0.48
2:B:153:MET:HA	2:B:177:HIS:CE1	2.48	0.48
2:B:530:GLN:NE2	2:B:530:GLN:H	2.11	0.48
3:C:10:ARG:NH1	3:C:55[B]:ARG:HD3	2.27	0.48
3:F:221:ASN:ND2	8:F:5098:HOH:O	2.45	0.48
2:B:144:PRO:HD2	8:B:4722:HOH:O	2.14	0.48
2:E:19[A]:GLN:HE21	2:E:25:ARG:HG3	1.78	0.48
2:B:713[B]:GLN:NE2	2:B:733[B]:LEU:HD23	2.30	0.47
2:B:121:VAL:HG11	2:B:132:ALA:HB3	1.95	0.47
2:B:716:ARG:HD2	8:B:4752:HOH:O	2.13	0.47
2:B:510:GLU:HG3	2:B:647[A]:VAL:HG12	1.97	0.47
3:F:276:ARG:NH1	8:F:5118:HOH:O	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:803:GLU:OE1	2:B:808:HIS:CD2	2.64	0.46
3:C:138:LEU:HD23	3:C:167:LEU:HA	1.97	0.46
2:B:168:MET:HA	2:B:168:MET:HE2	1.96	0.46
3:F:79:HIS:HD2	8:F:5160:HOH:O	1.99	0.46
1:A:27:HIS:CD2	2:B:127:TYR:OH	2.65	0.46
2:E:53:ASP:CG	2:E:54:PHE:H	2.24	0.45
2:B:208:THR:OG1	2:B:315:HIS:HD2	2.00	0.45
1:A:54:LEU:C	1:A:54:LEU:HD23	2.42	0.45
3:F:10:ARG:NH2	3:F:55:ARG:NH1	2.58	0.45
1:A:84:ASP:OD1	1:A:86:THR:HG23	2.17	0.45
1:D:59:VAL:CG1	1:D:64:MET:HE3	2.47	0.45
2:B:53:ASP:CG	2:B:54:PHE:H	2.25	0.44
2:B:460:ARG:NH1	2:B:463:GLN:HE22	2.06	0.44
3:C:242:ALA:HA	8:C:4201:HOH:O	2.17	0.44
3:F:49:GLU:OE2	3:F:49:GLU:CG	2.64	0.44
2:B:17:LYS:HG3	8:B:4482:HOH:O	2.17	0.44
2:B:458:GLN:HE21	2:B:458:GLN:H	1.66	0.43
2:B:315:HIS:HE1	8:B:4009:HOH:O	2.01	0.43
2:B:346[B]:ALA:O	2:B:347:ASP:CG	2.61	0.43
2:E:345:CYS:SG	2:E:384:VAL:HG23	2.58	0.43
2:B:428:PHE:HA	2:B:429:PRO:C	2.44	0.43
2:E:63:ARG:HB2	2:E:141:GLU:HB2	2.01	0.43
3:F:10:ARG:HH22	3:F:55:ARG:NH2	2.15	0.43
2:B:358:ILE:HD11	2:B:438:TYR:CE1	2.53	0.43
3:F:10:ARG:HD3	3:F:55:ARG:HH11	1.84	0.43
2:B:258:HIS:H	2:B:258:HIS:CD2	2.37	0.42
2:B:808:HIS:O	2:B:809:VAL:CB	2.57	0.42
1:A:96:MET:HA	1:A:96:MET:HE2	2.01	0.42
1:A:101:GLN:HB2	1:A:139:CYS:HB3	2.01	0.42
3:C:280:GLU:HG3	8:C:4283:HOH:O	2.18	0.42
2:B:176:LYS:HG2	2:B:180:HIS:ND1	2.34	0.42
1:A:87:LEU:HD12	8:B:4704:HOH:O	2.19	0.42
3:C:103:ASP:CG	3:C:106:ILE:HD12	2.45	0.42
2:E:121:VAL:HG11	2:E:132:ALA:HB3	2.02	0.42
2:B:258:HIS:CD2	2:E:518:SER:HB2	2.55	0.42
2:B:389:SER:HB2	2:B:392:VAL:HB	2.01	0.42
2:B:713[B]:GLN:HE21	2:B:733[B]:LEU:HD23	1.85	0.42
2:B:175:ARG:NH1	2:B:178:HIS:O	2.53	0.42
2:B:127:TYR:HA	3:C:2:ILE:HG21	2.03	0.41
3:C:10:ARG:CZ	3:C:55[A]:ARG:HD3	2.51	0.41
2:B:303:GLU:HG2	8:B:4394:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:466:LYS:CE	8:E:5712:HOH:O	2.68	0.41
2:B:203:SER:O	2:B:319:GLU:HA	2.21	0.41
2:E:764:SER:N	2:E:765:PRO:HD2	2.34	0.41
3:F:10:ARG:HD3	3:F:55:ARG:NH1	2.36	0.41
2:B:510:GLU:CG	2:B:647[A]:VAL:HG12	2.51	0.40
2:E:151:LYS:NZ	8:E:5468:HOH:O	2.54	0.40
2:E:52:GLY:HA2	2:E:121:VAL:O	2.19	0.40
2:B:713[A]:GLN:CG	2:B:731:PHE:CE1	3.04	0.40
3:C:202:LEU:C	3:C:202:LEU:HD12	2.47	0.40
2:E:573:THR:HB	2:E:574:PRO:HD3	2.04	0.40
8:A:4096:HOH:O	3:C:31:LEU:HD11	2.21	0.40
2:E:164:ILE:HG13	2:E:165:LYS:HG2	2.04	0.40
3:F:106[B]:ILE:HD13	7:F:4931:FAD:C8	2.52	0.40

All (3) 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:5:THR:CG2	2:B:254:GLY:O[4_477]	1.75	0.45
2:E:458:GLN:OE1	8:B:4741:HOH:O[4_577]	2.01	0.19
8:A:4083:HOH:O	8:E:5155:HOH:O[4_477]	2.12	0.08

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	162/166 (98%)	159 (98%)	3 (2%)	0	100	100
1	D	162/166 (98%)	159 (98%)	3 (2%)	0	100	100
2	B	826/809 (102%)	798 (97%)	24 (3%)	4 (0%)	24	6
2	E	807/809 (100%)	781 (97%)	23 (3%)	3 (0%)	30	10

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	293/288 (102%)	289 (99%)	4 (1%)	0	100	100
3	F	289/288 (100%)	285 (99%)	4 (1%)	0	100	100
All	All	2539/2526 (100%)	2471 (97%)	61 (2%)	7 (0%)	36	14

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	312	ARG
2	E	312	ARG
2	B	265	PRO
2	B	712	GLY
2	E	265	PRO
2	E	712	GLY
2	B	761	VAL

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	132/131 (101%)	132 (100%)	0	100	100
1	D	132/131 (101%)	129 (98%)	3 (2%)	44	9
2	B	671/653 (103%)	658 (98%)	13 (2%)	50	13
2	E	654/653 (100%)	646 (99%)	8 (1%)	63	28
3	C	220/212 (104%)	216 (98%)	4 (2%)	51	16
3	F	216/212 (102%)	213 (99%)	3 (1%)	59	24
All	All	2025/1992 (102%)	1994 (98%)	31 (2%)	61	21

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	21[A]	MET
2	B	21[B]	MET
2	B	91	ASN

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Mol	Chain	Res	Type
2	B	159	LEU
2	B	251[A]	LEU
2	B	251[B]	LEU
2	B	313	ASP
2	B	345[A]	CYS
2	B	345[B]	CYS
2	B	393	THR
2	B	458	GLN
2	B	488	GLU
2	B	530	GLN
3	C	26	GLU
3	C	45	LEU
3	C	87[A]	LEU
3	C	87[B]	LEU
1	D	147	LYS
1	D	155[A]	LYS
1	D	155[B]	LYS
2	E	65	LYS
2	E	176	LYS
2	E	393	THR
2	E	488	GLU
2	E	552[A]	MET
2	E	552[B]	MET
2	E	620	GLU
2	E	790	GLN
3	F	45	LEU
3	F	221	ASN
3	F	240	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	HIS
1	A	27	HIS
1	A	33	GLN
1	A	68	GLN
1	A	135	ASN
2	B	19	GLN
2	B	59	HIS
2	B	115	ASN
2	B	172	HIS
2	B	258	HIS

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Mol	Chain	Res	Type
2	B	315	HIS
2	B	334	HIS
2	B	442	ASN
2	B	458	GLN
2	B	463	GLN
2	B	530	GLN
2	B	597	HIS
2	B	634	ASN
2	B	639	ASN
2	B	754	HIS
2	B	808	HIS
3	C	118	ASN
3	C	130	GLN
1	D	5	HIS
1	D	11	ASN
2	E	103	GLN
2	E	115	ASN
2	E	273	ASN
2	E	315	HIS
2	E	334	HIS
2	E	442	ASN
2	E	457	HIS
2	E	463	GLN
2	E	592	GLN
2	E	597	HIS
2	E	639	ASN
2	E	713	GLN
2	E	754	HIS
2	E	790	GLN
2	E	804	GLN
3	F	118	ASN
3	F	154	GLN
3	F	221	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

9 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
7	FAD	C	3932	-	58,58,58	1.50	9 (15%)	85,89,89	1.50	13 (15%)
5	FES	D	4908	1	0,4,4	-	-	-		
5	FES	D	4907	1	0,4,4	-	-	-		
5	FES	A	3908	1	0,4,4	-	-	-		
6	DW6	E	810	8,2	46,54,54	1.88	11 (23%)	54,87,87	1.63	10 (18%)
5	FES	A	3907	1	0,4,4	-	-	-		
7	FAD	F	4931	-	58,58,58	1.26	6 (10%)	85,89,89	1.32	11 (12%)
6	DW6	B	810	8,2	46,54,54	1.98	12 (26%)	54,87,87	1.46	7 (12%)
4	PO4	A	3001	-	4,4,4	2.04	2 (50%)	6,6,6	1.30	1 (16%)

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
7	FAD	C	3932	-	-	2/34/50/50	0/6/6/6
6	DW6	E	810	8,2	-	1/22/82/82	0/6/6/6
5	FES	D	4907	1	-	-	0/1/1/1
5	FES	A	3908	1	-	-	0/1/1/1
5	FES	D	4908	1	-	-	0/1/1/1
5	FES	A	3907	1	-	-	0/1/1/1
7	FAD	F	4931	-	-	2/34/50/50	0/6/6/6
6	DW6	B	810	8,2	-	1/22/82/82	0/6/6/6

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	810	DW6	C7-C6'	-7.47	1.47	1.53
7	C	3932	FAD	C4X-N5	5.86	1.43	1.30
6	E	810	DW6	C10-C9'	-5.27	1.44	1.51
6	E	810	DW6	PA-O3A	4.26	1.64	1.59
7	C	3932	FAD	C5'-C4'	3.99	1.57	1.51
6	B	810	DW6	MO-S8'	3.93	2.45	2.39
6	B	810	DW6	C4B-N8'	3.62	1.39	1.35
6	B	810	DW6	C6-C5	-3.54	1.26	1.35
6	E	810	DW6	MO-S8'	3.53	2.44	2.39
7	F	4931	FAD	C4X-N5	3.47	1.38	1.30
4	A	3001	PO4	P-O4	-3.29	1.45	1.54
7	F	4931	FAD	O4-C4	3.17	1.29	1.23
7	C	3932	FAD	C10-N1	3.00	1.39	1.33
7	C	3932	FAD	O4B-C4B	-2.84	1.38	1.45
6	E	810	DW6	C4A-C4B	2.81	1.43	1.38
7	F	4931	FAD	C5'-C4'	2.76	1.55	1.51
7	C	3932	FAD	P-O3P	2.75	1.62	1.59
7	C	3932	FAD	C5A-C4A	2.57	1.43	1.39
6	B	810	DW6	C6'-N5'	2.54	1.49	1.46
6	B	810	DW6	O9'-C9'	2.46	1.48	1.43
6	B	810	DW6	C4A-C4'	-2.40	1.34	1.41
7	C	3932	FAD	C1'-C2'	-2.40	1.49	1.52
6	B	810	DW6	C10-C9'	2.40	1.55	1.51
4	A	3001	PO4	P-O1	2.35	1.56	1.50
6	E	810	DW6	C2D-C1'	2.35	1.60	1.53
6	B	810	DW6	PA-O3A	2.31	1.62	1.59
7	F	4931	FAD	C2A-N3A	2.31	1.38	1.33
6	E	810	DW6	C6-C5	2.28	1.40	1.35
6	E	810	DW6	C4A-C4'	-2.26	1.35	1.41
6	B	810	DW6	C4'-N3'	2.24	1.43	1.38
7	F	4931	FAD	C3B-C4B	-2.20	1.47	1.53
6	E	810	DW6	OM1-MO	2.19	1.74	1.69
6	E	810	DW6	C1'-N1	-2.16	1.41	1.47
6	E	810	DW6	C4B-N8'	2.12	1.37	1.35
7	C	3932	FAD	C2A-N1A	2.08	1.37	1.33
7	F	4931	FAD	C5B-C4B	2.05	1.57	1.51
7	C	3932	FAD	C4X-C10	-2.04	1.38	1.44
6	B	810	DW6	C2'-N3'	2.04	1.42	1.37
6	B	810	DW6	C2'-N1'	-2.04	1.28	1.33
6	E	810	DW6	O2-C2	2.00	1.27	1.23

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	C	3932	FAD	N3A-C2A-N1A	-4.62	121.58	128.58
7	F	4931	FAD	C4X-C10-N10	4.25	122.56	116.48
6	B	810	DW6	C7-C6'-N5'	4.22	112.02	107.87
7	C	3932	FAD	C2A-N1A-C6A	3.90	125.13	118.73
6	E	810	DW6	C5-C4-N3	-3.82	114.88	121.32
6	E	810	DW6	C8'-C7'-S7'	3.67	122.23	120.15
6	E	810	DW6	C2'-N1'-C4B	3.64	119.79	113.36
7	C	3932	FAD	C5A-C4A-N3A	-3.43	122.00	126.72
6	E	810	DW6	O9'-C7-C6'	3.33	111.19	108.96
6	E	810	DW6	C4-N3-C2	3.29	125.44	120.26
7	C	3932	FAD	C4X-C10-N10	3.26	121.15	116.48
6	B	810	DW6	O4'-C4'-N3'	-3.12	114.24	120.11
7	C	3932	FAD	O4'-C4'-C5'	-3.03	103.30	109.99
7	C	3932	FAD	C5X-C9A-N10	3.00	120.68	117.97
7	F	4931	FAD	C4-N3-C2	-2.98	120.35	125.64
7	C	3932	FAD	C9A-C5X-N5	-2.93	119.35	122.45
6	B	810	DW6	C8'-C7'-S7'	2.89	121.79	120.15
7	F	4931	FAD	C9-C8-C7	-2.88	115.47	119.69
7	F	4931	FAD	C9A-C9-C8	2.86	124.98	119.22
6	B	810	DW6	C7'-C8'-S8'	-2.81	118.56	120.15
7	C	3932	FAD	C4A-C5A-N7A	-2.73	107.46	110.58
4	A	3001	PO4	O3-P-O1	-2.71	101.37	110.95
7	F	4931	FAD	C4X-C4-N3	2.63	119.96	113.25
6	B	810	DW6	C2'-N3'-C4'	-2.63	120.34	125.11
6	E	810	DW6	O3'-C3'-C2D	-2.60	103.48	111.82
7	F	4931	FAD	C5X-C9A-N10	2.59	120.31	117.97
6	B	810	DW6	O9'-C9'-C8'	2.59	112.75	109.09
7	C	3932	FAD	C4-C4X-N5	2.55	121.73	118.21
6	E	810	DW6	N4-C4-N3	2.55	122.47	117.91
6	E	810	DW6	N3'-C2'-N1'	-2.55	118.66	123.32
7	F	4931	FAD	C10-C4X-N5	-2.53	119.64	124.81
7	C	3932	FAD	C6A-C5A-C4A	2.44	120.51	117.18
7	F	4931	FAD	C10-N1-C2	2.43	122.10	116.85
7	F	4931	FAD	C4-C4X-N5	2.30	121.38	118.21
7	C	3932	FAD	C4X-C4-N3	2.28	119.05	113.25
6	E	810	DW6	O4D-C1'-C2D	-2.27	101.77	106.62
6	E	810	DW6	C6-C5-C4	2.22	121.17	117.53
7	F	4931	FAD	C4X-C10-N1	-2.17	119.28	124.59
7	C	3932	FAD	C5'-C4'-C3'	2.15	116.27	112.22
6	B	810	DW6	O3'-C3'-C2D	-2.10	105.07	111.82
7	C	3932	FAD	C6-C5X-C9A	2.07	121.90	119.05
7	F	4931	FAD	O4'-C4'-C5'	-2.04	105.48	109.99

There are no chirality outliers.

All (6) torsion outliers are listed below:

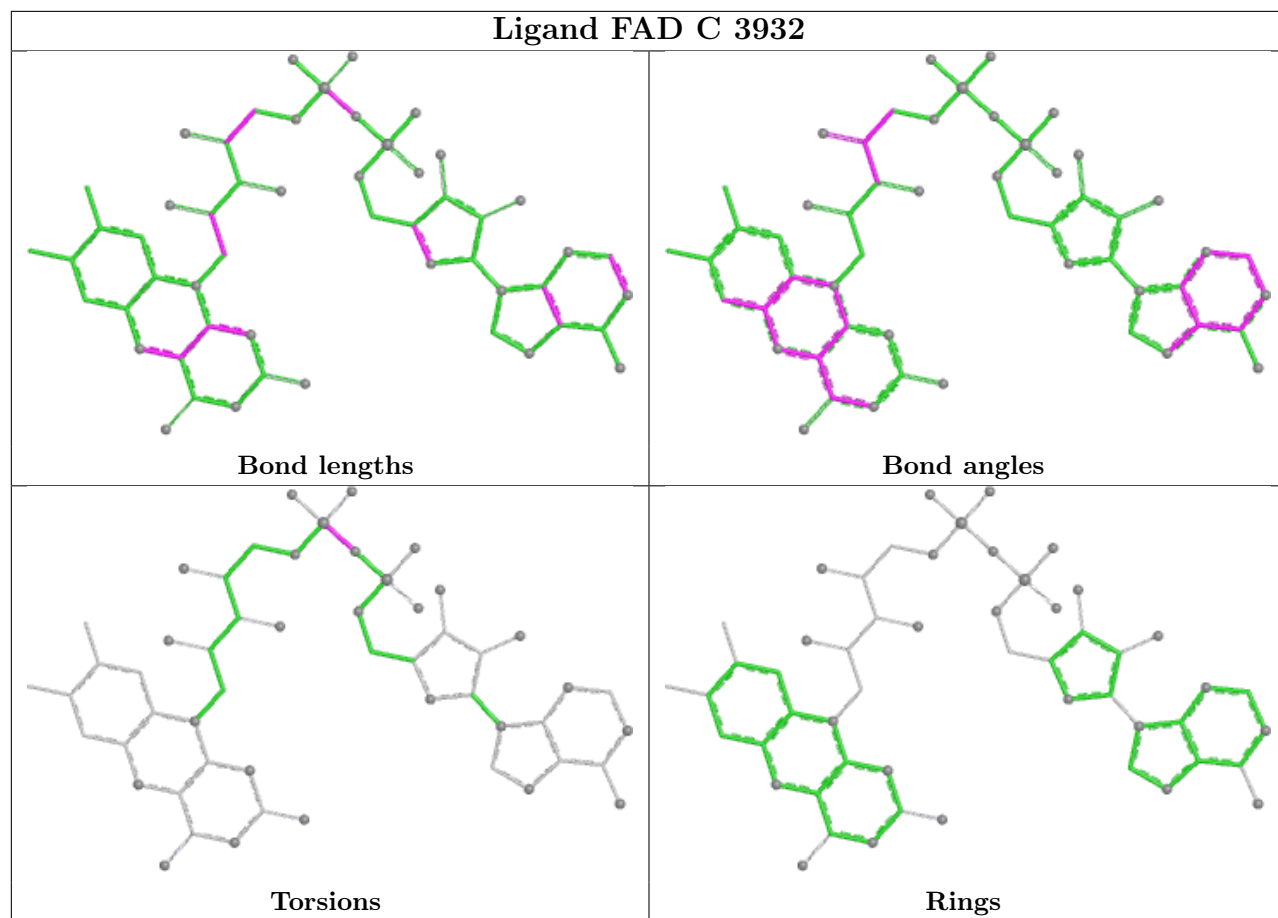
Mol	Chain	Res	Type	Atoms
6	B	810	DW6	C10-O3B-PB-O1B
6	E	810	DW6	C10-O3B-PB-O1B
7	C	3932	FAD	PA-O3P-P-O1P
7	C	3932	FAD	PA-O3P-P-O2P
7	F	4931	FAD	PA-O3P-P-O1P
7	F	4931	FAD	PA-O3P-P-O2P

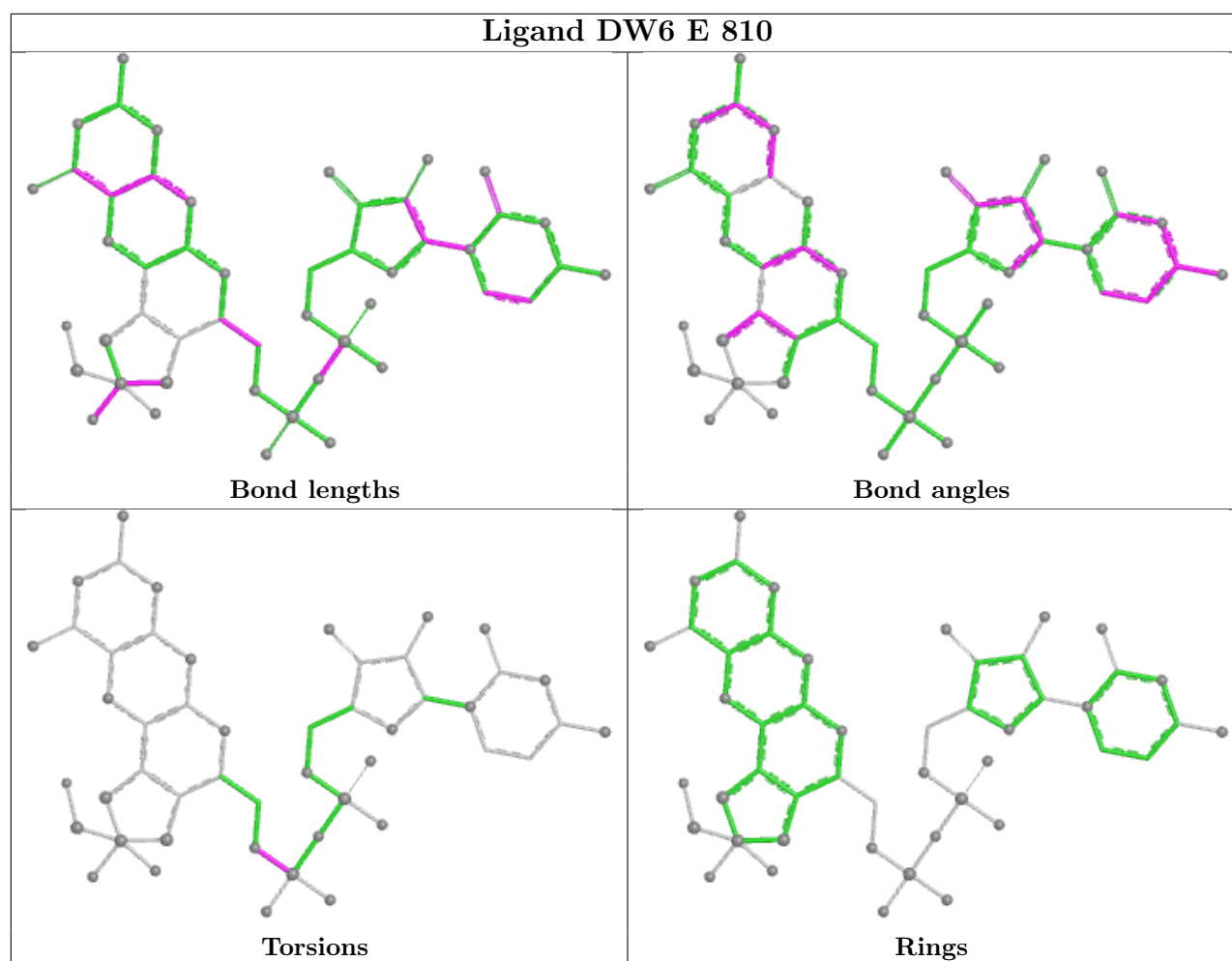
There are no ring outliers.

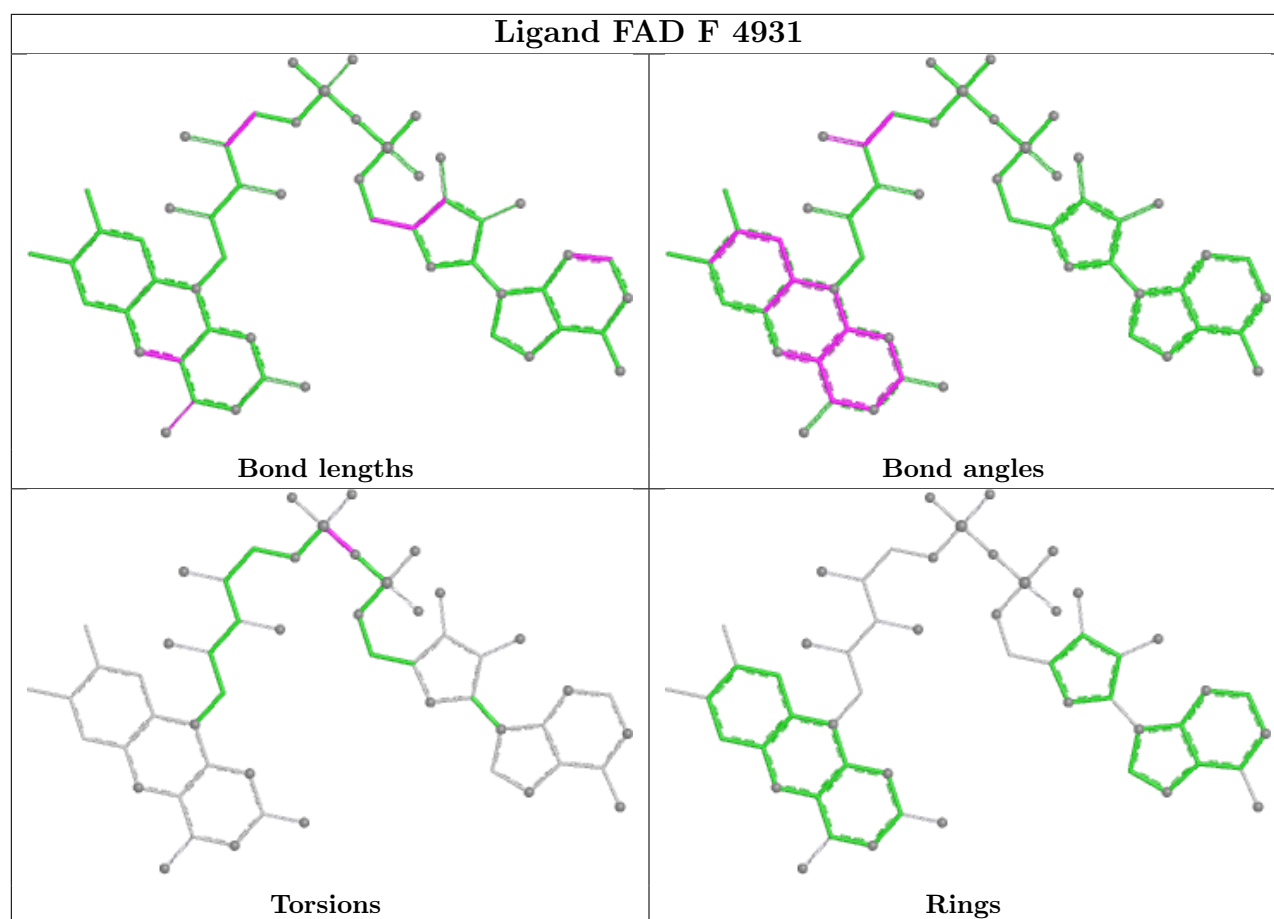
4 monomers are involved in 7 short contacts:

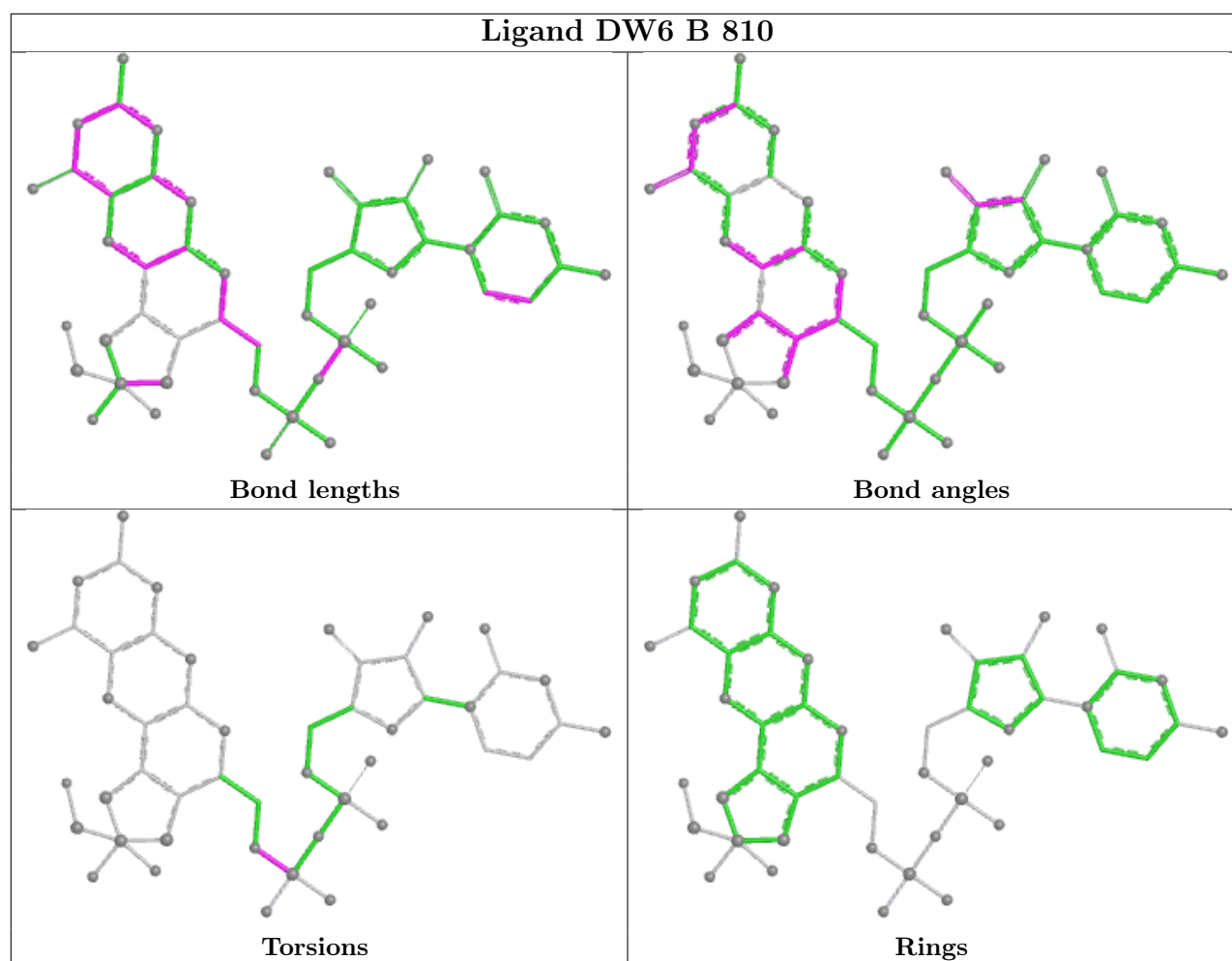
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	3932	FAD	2	0
7	F	4931	FAD	3	0
6	B	810	DW6	1	0
4	A	3001	PO4	1	0

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.