



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 09:20 AM EDT

PDB ID : 1ZXI / pdb_00001zxi
Title : Reconstituted CO dehydrogenase from Oligotropha carboxidovorans
Authors : Resch, M.; Dobbek, H.; Meyer, O.
Deposited on : 2005-06-08
Resolution : 1.70 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

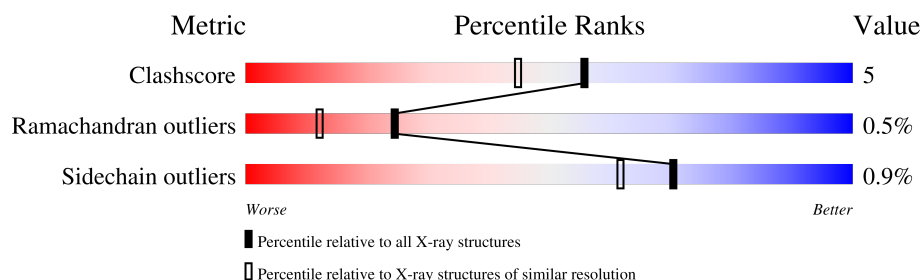
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)

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	87% 10% ..
1	D	166	87% 7% • 5%
2	B	809	85% 13% ..
2	E	809	83% 14% ..
3	C	288	90% 10%
3	F	288	89% 9% ..

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 21735 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	161	Total	C	N	O	S	2	0	0
			1204	746	215	228	15			
1	D	158	Total	C	N	O	S	5	0	0
			1175	727	212	221	15			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	804	Total	C	N	O	S	73	0	0
			6198	3934	1061	1162	41			
2	E	795	Total	C	N	O	S	61	0	0
			6130	3894	1049	1146	41			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	670	ILE	VAL	conflict	UNP P19919
E	670	ILE	VAL	conflict	UNP P19919

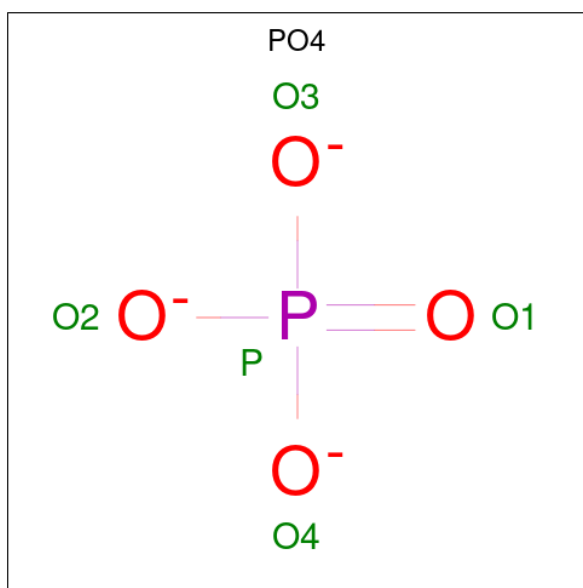
- Molecule 3 is a protein called Carbon monoxide dehydrogenase medium chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	287	Total	C	N	O	S	26	0	0
			2112	1333	372	396	11			
3	F	286	Total	C	N	O	S	26	0	0
			2103	1327	370	395	11			

There are 2 discrepancies between the modelled and reference sequences:

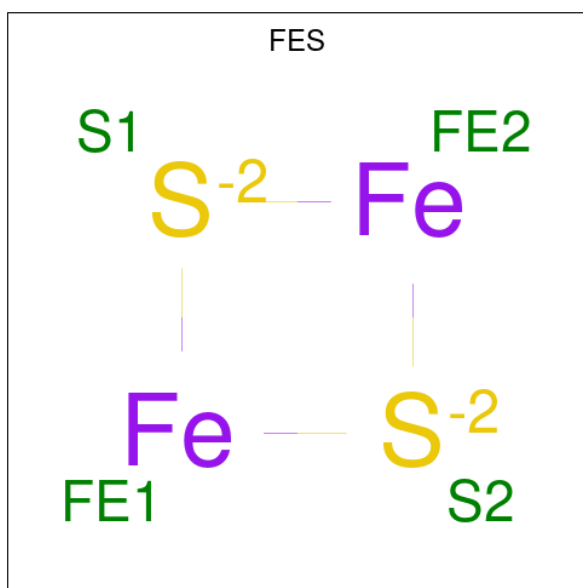
Chain	Residue	Modelled	Actual	Comment	Reference
C	211	SER	THR	conflict	UNP P19920
F	211	SER	THR	conflict	UNP P19920

- Molecule 4 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



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		

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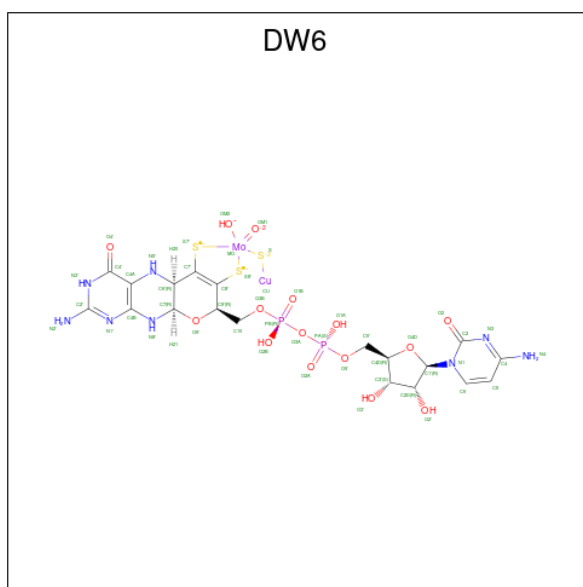
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	Fe	S	0	0
			4	2	2		
5	D	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 6 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

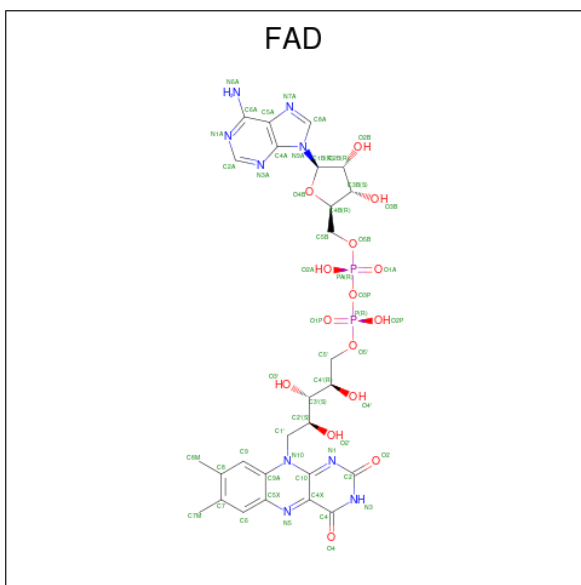
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Cu	0	0
			1	1		
6	E	1	Total	Cu	0	1
			1	1		

- Molecule 7 is CuSMo(=O)OH pterin (CCD ID: DW6) (formula: C₁₉H₂₅CuMoN₈O₁₅P₂S₃).



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

- Molecule 8 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



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

- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	190	Total O 190 190	0	0
9	B	804	Total O 804 804	0	0
9	C	342	Total O 342 342	0	0
9	D	189	Total O 189 189	0	0
9	E	749	Total O 749 749	0	0
9	F	312	Total O 312 312	0	0

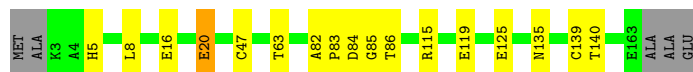
3 Residue-property plots

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: Carbon monoxide dehydrogenase small chain

Chain A: 



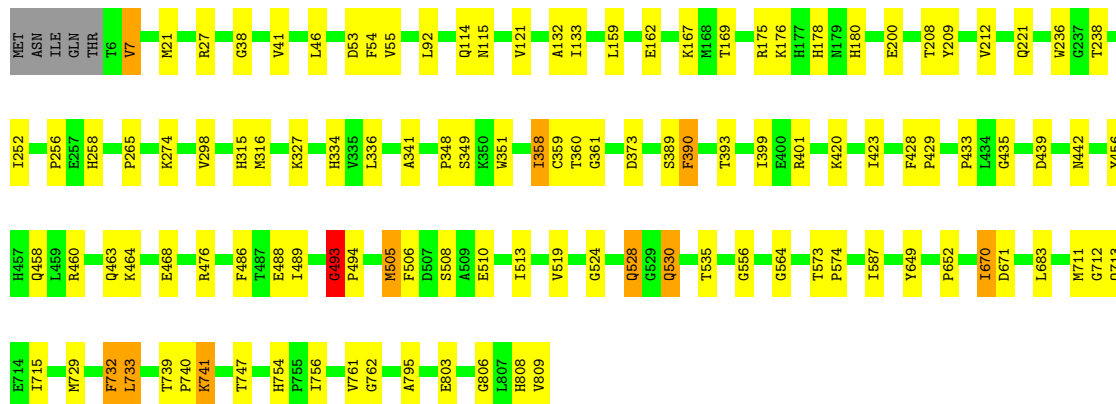
- Molecule 1: Carbon monoxide dehydrogenase small chain

Chain D: 



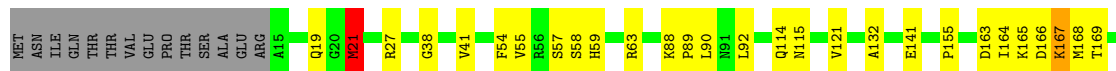
- Molecule 2: Carbon monoxide dehydrogenase large chain

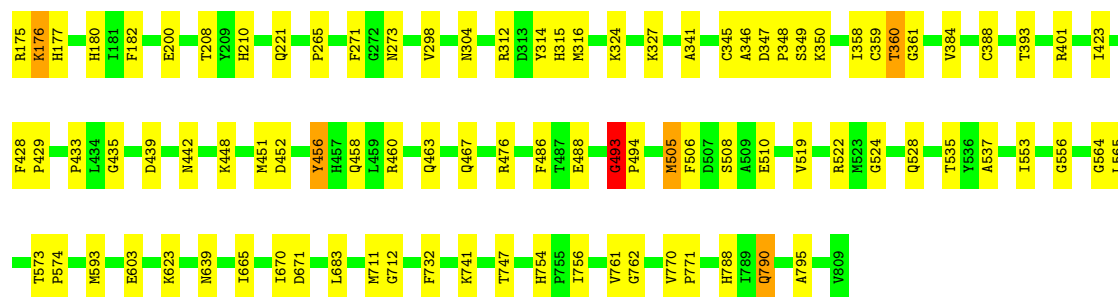
Chain B: 



- Molecule 2: Carbon monoxide dehydrogenase large chain

Chain E: 

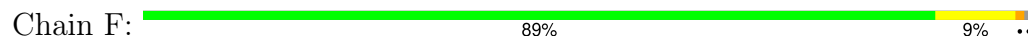




- Molecule 3: Carbon monoxide dehydrogenase medium chain



- 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	118.84Å 131.32Å 159.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.70	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-1.70)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.166 , 0.194	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	21735	wwPDB-VP
Average B, all atoms (Å ²)	18.0	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: PO4, FES, DW6, FAD, CU

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	0.65	0/1225	0.99	4/1656 (0.2%)
1	D	0.68	0/1195	1.01	5/1616 (0.3%)
2	B	0.59	0/6351	1.02	40/8617 (0.5%)
2	E	0.59	1/6282 (0.0%)	1.02	37/8522 (0.4%)
3	C	0.54	0/2149	1.01	14/2918 (0.5%)
3	F	0.58	0/2140	1.01	15/2907 (0.5%)
All	All	0.59	1/19342 (0.0%)	1.02	115/26236 (0.4%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	21	MET	SD-CE	-5.80	1.65	1.79

All (115) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	195	THR	N-CA-C	-10.92	99.46	111.36
3	F	195	THR	N-CA-C	-10.15	100.30	111.36
2	E	55	VAL	N-CA-C	-10.13	94.00	108.58
1	A	47	CYS	N-CA-C	9.66	123.03	111.82
2	B	55	VAL	N-CA-C	-9.61	94.75	108.58
1	D	47	CYS	N-CA-C	9.18	122.46	111.82
2	E	423	ILE	N-CA-C	-8.21	98.98	109.58
2	E	358	ILE	N-CA-C	-8.11	104.66	112.29
2	E	348	PRO	N-CA-C	-8.06	98.39	111.21
2	B	423	ILE	N-CA-C	-7.99	99.32	109.30
2	E	435	GLY	N-CA-C	7.98	124.18	114.69
2	B	435	GLY	N-CA-C	7.90	124.33	114.37
2	B	348	PRO	N-CA-C	-7.88	98.69	111.21
3	C	55	ARG	N-CA-C	7.72	120.59	111.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	38	GLY	N-CA-C	-7.70	102.68	112.54
2	B	358	ILE	N-CA-C	-7.70	105.06	111.91
1	D	140	THR	N-CA-C	7.68	122.75	113.23
3	C	223	PRO	N-CA-C	-7.28	101.03	111.22
3	F	223	PRO	N-CA-C	-7.24	101.09	111.22
2	B	535	THR	N-CA-C	7.10	119.09	111.36
2	E	54	PHE	N-CA-C	7.10	121.59	110.17
1	A	140	THR	N-CA-C	6.99	121.90	113.23
3	C	70	VAL	N-CA-C	-6.92	98.49	108.17
3	F	167	LEU	N-CA-C	-6.87	98.74	109.25
3	C	2	ILE	N-CA-C	6.87	115.46	107.77
2	E	535	THR	N-CA-C	6.87	118.84	111.36
2	E	556	GLY	N-CA-C	6.85	123.82	114.92
2	B	556	GLY	N-CA-C	6.82	122.80	114.69
1	D	20	GLU	N-CA-C	-6.68	101.65	109.93
2	B	341	ALA	N-CA-C	6.59	119.47	111.82
2	B	493	GLY	CA-C-N	-6.57	112.90	119.93
2	B	493	GLY	C-N-CA	-6.57	112.90	119.93
3	F	2	ILE	N-CA-C	6.55	115.11	107.77
2	E	38	GLY	N-CA-C	-6.47	102.61	112.51
2	E	341	ALA	N-CA-C	6.44	119.29	111.82
2	E	41	VAL	N-CA-C	6.42	117.10	110.36
2	E	493	GLY	CA-C-O	-6.40	112.36	121.52
3	F	194	ALA	N-CA-C	6.39	119.50	110.23
1	D	139	CYS	N-CA-C	6.38	121.31	112.45
2	B	54	PHE	N-CA-C	6.37	120.20	109.76
2	E	316	MET	N-CA-C	6.23	119.90	107.62
3	F	45	LEU	N-CA-C	-6.21	104.40	112.23
3	C	36	SER	N-CA-C	-6.20	105.61	113.43
3	F	36	SER	N-CA-C	-6.20	105.61	113.43
2	B	505	MET	N-CA-C	6.18	119.26	110.68
2	B	795	ALA	N-CA-C	6.14	117.64	111.07
3	F	102	ALA	N-CA-C	6.13	117.62	108.31
1	A	139	CYS	N-CA-C	6.11	120.95	112.45
3	C	45	LEU	N-CA-C	-6.10	105.33	112.89
2	B	7	VAL	N-CA-C	-6.03	104.86	110.53
2	E	493	GLY	CA-C-N	-6.03	112.30	119.84
2	E	493	GLY	C-N-CA	-6.03	112.30	119.84
2	B	316	MET	N-CA-C	6.01	118.64	107.99
2	B	762	GLY	N-CA-C	6.01	120.17	112.83
2	E	27	ARG	N-CA-C	6.01	118.97	109.96
2	E	747	THR	N-CA-C	-6.01	100.19	109.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	194	ALA	N-CA-C	5.99	118.91	110.23
2	E	741	LYS	N-CA-C	-5.95	101.67	110.48
2	E	508	SER	N-CA-C	5.95	117.82	108.96
2	B	519	VAL	N-CA-C	5.92	117.21	108.45
2	E	486	PHE	N-CA-C	5.90	118.66	109.52
2	B	508	SER	N-CA-C	5.88	117.72	108.96
2	B	336	LEU	N-CA-C	-5.86	99.17	108.73
2	B	349	SER	N-CA-C	5.86	119.53	112.38
2	E	795	ALA	N-CA-C	5.84	117.65	111.28
3	C	167	LEU	N-CA-C	-5.82	100.34	109.25
2	B	747	THR	N-CA-C	-5.81	100.49	109.14
2	B	493	GLY	CA-C-O	-5.80	113.23	121.52
2	E	456	TYR	N-CA-C	5.80	118.07	111.11
2	B	27	ARG	N-CA-C	5.79	118.65	109.96
2	E	177	HIS	N-CA-C	-5.79	99.90	108.99
3	F	70	VAL	N-CA-C	-5.79	100.06	108.17
2	E	359	CYS	N-CA-C	5.78	120.07	113.19
2	E	349	SER	N-CA-C	5.76	119.41	112.38
3	F	152	TYR	N-CA-C	5.76	120.03	112.89
2	E	361	GLY	N-CA-C	5.75	121.50	111.50
2	B	361	GLY	N-CA-C	5.73	121.47	111.50
3	F	102	ALA	CB-CA-C	-5.72	109.96	116.54
3	C	102	ALA	N-CA-C	5.69	116.96	108.31
2	E	519	VAL	N-CA-C	5.64	116.80	108.45
3	F	118	ASN	N-CA-C	5.64	117.88	111.11
2	B	456	TYR	N-CA-C	5.61	117.86	111.02
2	B	41	VAL	N-CA-C	5.55	116.19	110.36
2	B	741	LYS	N-CA-C	-5.54	101.44	110.20
3	C	102	ALA	CB-CA-C	-5.53	110.19	116.54
2	E	439	ASP	N-CA-C	5.52	118.14	111.40
3	F	222	THR	CB-CA-C	-5.52	102.81	110.37
2	B	732	PHE	N-CA-C	5.50	117.43	108.63
2	E	505	MET	N-CA-C	5.50	119.23	110.70
2	B	715	ILE	N-CA-C	-5.50	99.64	107.77
2	E	57	SER	N-CA-C	5.48	118.18	109.96
2	E	711	MET	N-CA-C	5.38	120.00	113.38
3	C	35	HIS	N-CA-C	5.38	119.55	113.15
2	B	351	TRP	CA-C-N	5.33	124.99	119.56
2	B	351	TRP	C-N-CA	5.33	124.99	119.56
2	B	649	TYR	N-CA-C	-5.29	99.89	108.52
2	E	360	THR	N-CA-C	-5.28	106.61	113.16
2	B	439	ASP	N-CA-C	5.27	118.17	111.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	271	ALA	N-CA-C	-5.27	105.54	111.28
2	E	528	GLN	N-CA-C	-5.25	104.32	111.56
2	B	486	PHE	N-CA-C	5.24	117.64	109.52
2	E	762	GLY	N-CA-C	5.23	119.21	112.83
2	B	711	MET	N-CA-C	5.21	119.79	113.38
3	F	35	HIS	N-CA-C	5.19	119.25	113.02
2	B	528	GLN	N-CA-C	-5.17	104.42	111.56
2	E	493	GLY	N-CA-C	5.14	122.83	112.34
1	A	20	GLU	N-CA-C	-5.13	102.76	110.24
2	B	652	PRO	N-CA-C	5.12	116.94	110.70
3	C	84	SER	N-CA-C	5.11	116.51	109.15
3	F	271	ALA	N-CA-C	-5.05	105.78	111.28
1	D	145	ILE	N-CA-C	-5.04	105.63	110.72
2	E	210	HIS	N-CA-C	5.02	117.01	110.43
2	E	732	PHE	N-CA-C	5.01	116.65	108.63
2	B	733	LEU	N-CA-C	-5.01	99.53	109.10
2	B	209	TYR	N-CA-C	-5.00	98.45	107.75

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1204	0	1178	12	0
1	D	1175	0	1157	5	0
2	B	6198	0	6072	65	0
2	E	6130	0	6007	69	0
3	C	2112	0	2170	11	0
3	F	2103	0	2157	15	0
4	A	5	0	0	0	0
5	A	8	0	0	0	0
5	D	8	0	0	0	0
6	B	1	0	0	0	0
6	E	1	0	0	0	0
7	B	49	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	E	49	0	0	0	0
8	C	53	0	31	1	0
8	F	53	0	31	0	0
9	A	190	0	0	2	0
9	B	804	0	0	6	0
9	C	342	0	0	0	0
9	D	189	0	0	1	0
9	E	749	0	0	6	0
9	F	312	0	0	2	0
All	All	21735	0	18803	174	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 5.

All (174) 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:E:537:ALA:HB2	2:E:553:ILE:HD11	1.49	0.92
2:B:528:GLN:H	2:B:530:GLN:HE22	1.20	0.86
1:D:11:ASN:HD21	1:D:76:THR:H	1.23	0.86
2:E:460:ARG:HH11	2:E:463:GLN:HE22	1.25	0.84
2:E:670:ILE:HD12	2:E:671:ASP:N	1.94	0.83
2:E:208:THR:H	2:E:790:GLN:HE22	1.25	0.82
2:B:476:ARG:O	2:B:670:ILE:HD12	1.80	0.82
2:E:476:ARG:NH2	2:E:670:ILE:HD11	1.96	0.80
2:B:458:GLN:HE21	2:B:458:GLN:HA	1.47	0.80
2:E:155:PRO:HA	2:E:169:THR:HB	1.65	0.79
2:E:21:MET:HE2	9:E:4465:HOH:O	1.84	0.78
1:A:82:ALA:HB3	1:A:86:THR:HG22	1.65	0.78
2:E:670:ILE:HD12	2:E:670:ILE:C	2.10	0.77
2:E:537:ALA:HB2	2:E:553:ILE:CD1	2.15	0.77
1:D:3:LYS:N	9:D:4009:HOH:O	2.17	0.76
2:B:92:LEU:HD21	2:B:252:ILE:CG2	2.16	0.76
2:B:530:GLN:HE21	2:B:530:GLN:H	1.34	0.75
3:F:240:LYS:HG2	3:F:241:PRO:HD3	1.71	0.72
2:E:458:GLN:HG3	9:E:4134:HOH:O	1.89	0.71
2:B:528:GLN:H	2:B:530:GLN:NE2	1.88	0.71
2:E:593:MET:HG2	2:E:603:GLU:OE2	1.90	0.71
2:E:273:ASN:HD21	2:E:304:ASN:HD21	1.37	0.71
2:E:754:HIS:HD2	2:E:756:ILE:H	1.39	0.71
2:B:92:LEU:HD21	2:B:252:ILE:HG23	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:176:LYS:HB3	2:E:180:HIS:ND1	2.08	0.68
2:B:458:GLN:HA	2:B:458:GLN:NE2	2.08	0.68
2:E:168:MET:HG2	2:E:175:ARG:O	1.95	0.67
2:B:460:ARG:HH11	2:B:463:GLN:HE22	1.39	0.67
2:B:803:GLU:OE1	2:B:808:HIS:HD2	1.78	0.66
3:F:43:THR:OG1	3:F:45:LEU:HG	1.96	0.66
3:F:121:PRO:HD2	9:F:5179:HOH:O	1.95	0.65
2:E:476:ARG:HH21	2:E:670:ILE:HD11	1.61	0.64
2:E:90:LEU:O	2:E:92:LEU:HD13	1.97	0.63
2:B:53:ASP:HB3	2:B:133:ILE:HD11	1.80	0.63
2:E:88:LYS:HB2	2:E:89:PRO:HD3	1.81	0.62
2:B:212:VAL:HB	9:B:4369:HOH:O	2.01	0.60
2:B:530:GLN:H	2:B:530:GLN:NE2	1.99	0.59
2:B:670:ILE:O	2:B:808:HIS:HE1	1.86	0.59
2:B:754:HIS:HD2	2:B:756:ILE:H	1.51	0.58
7:B:3911:DW6:OM1	7:B:3911:DW6:MO	1.73	0.58
3:C:240:LYS:HB3	3:C:241:PRO:HD3	1.85	0.58
2:B:493:GLY:HA2	2:B:505:MET:O	2.04	0.58
2:E:754:HIS:CD2	2:E:756:ILE:H	2.21	0.58
2:B:358:ILE:HD12	2:B:489:ILE:HB	1.85	0.57
2:B:458:GLN:HG2	9:B:4217:HOH:O	2.05	0.57
1:A:125:GLU:OE2	2:B:741:LYS:HD3	2.05	0.57
1:A:20:GLU:HG3	9:A:4028:HOH:O	2.05	0.56
3:F:221:ASN:HD22	3:F:221:ASN:N	2.02	0.56
9:A:4006:HOH:O	2:B:741:LYS:HD2	2.06	0.56
2:E:670:ILE:C	2:E:670:ILE:CD1	2.79	0.56
2:B:573:THR:HB	2:B:574:PRO:HD3	1.88	0.56
1:A:135:ASN:HD21	3:C:105:GLN:HE22	1.53	0.55
2:E:476:ARG:NH2	2:E:670:ILE:CD1	2.68	0.55
3:C:275:LEU:HD23	3:C:275:LEU:C	2.30	0.55
2:E:788:HIS:HE2	2:E:790:GLN:NE2	2.05	0.55
2:E:200:GLU:HB3	2:E:324:LYS:HE3	1.87	0.55
2:B:238:THR:HB	2:B:274:LYS:HD3	1.90	0.55
3:F:221:ASN:ND2	9:F:5097:HOH:O	2.39	0.55
3:F:221:ASN:HD22	3:F:221:ASN:H	1.55	0.54
3:F:197:ALA:HB3	3:F:217:THR:HB	1.89	0.54
1:A:135:ASN:ND2	3:C:105:GLN:HE22	2.05	0.54
2:B:683:LEU:HD23	2:B:683:LEU:C	2.32	0.54
2:E:350:LYS:HE3	9:E:4572:HOH:O	2.08	0.54
2:B:114:GLN:O	2:B:115:ASN:HB2	2.09	0.53
2:B:713:GLN:HG3	2:B:732:PHE:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:164:ILE:HG13	2:E:165:LYS:HG2	1.91	0.53
3:F:239:ASP:CG	3:F:241:PRO:HD2	2.33	0.53
2:B:334:HIS:HE1	2:B:373:ASP:OD2	1.90	0.53
3:C:197:ALA:HB3	3:C:217:THR:HB	1.90	0.53
2:E:21:MET:HE1	2:E:756:ILE:HD12	1.91	0.52
2:B:754:HIS:CD2	2:B:756:ILE:H	2.27	0.52
2:E:493:GLY:HA2	2:E:505:MET:O	2.08	0.52
2:E:476:ARG:CZ	2:E:670:ILE:HD11	2.39	0.52
2:B:803:GLU:OE1	2:B:808:HIS:CD2	2.62	0.52
2:E:442:ASN:HD22	2:E:442:ASN:C	2.17	0.52
2:E:770:VAL:HB	2:E:771:PRO:HD3	1.92	0.51
2:B:442:ASN:C	2:B:442:ASN:HD22	2.18	0.51
2:B:208:THR:OG1	2:B:315:HIS:HD2	1.94	0.51
2:B:159:LEU:HD21	2:B:162:GLU:HG2	1.94	0.50
2:B:493:GLY:O	2:B:494:PRO:C	2.51	0.50
2:B:713:GLN:NE2	2:B:733:LEU:HD23	2.27	0.50
1:A:84:ASP:OD1	1:A:86:THR:HG22	2.11	0.50
2:E:524:GLY:HA3	2:E:564:GLY:HA3	1.93	0.49
2:B:21:MET:HE1	2:B:756:ILE:HD12	1.93	0.49
2:E:208:THR:OG1	2:E:315:HIS:HD2	1.96	0.49
2:E:573:THR:HB	2:E:574:PRO:HD3	1.94	0.49
2:B:713:GLN:OE1	9:B:4369:HOH:O	2.19	0.49
2:B:46:LEU:HD11	2:B:236:TRP:CZ3	2.48	0.49
1:A:5:HIS:NE2	1:A:16:GLU:HG3	2.27	0.48
2:B:493:GLY:CA	2:B:505:MET:O	2.62	0.48
2:B:464:LYS:O	2:B:468:GLU:HG3	2.14	0.47
2:E:114:GLN:O	2:E:115:ASN:HB2	2.13	0.47
2:E:683:LEU:C	2:E:683:LEU:HD23	2.39	0.47
1:A:115:ARG:O	1:A:119:GLU:HG3	2.13	0.47
2:E:493:GLY:O	2:E:494:PRO:C	2.54	0.47
2:E:553:ILE:HD12	2:E:553:ILE:N	2.28	0.47
2:E:476:ARG:HH21	2:E:670:ILE:CD1	2.26	0.47
2:E:463:GLN:O	2:E:467:GLN:HG3	2.15	0.47
3:C:103:ASP:HB2	3:C:104:PRO:CD	2.45	0.47
2:E:19:GLN:NE2	9:E:4402:HOH:O	2.48	0.47
3:F:214:ILE:HD13	3:F:275:LEU:HD11	1.97	0.46
2:B:200:GLU:HG3	9:B:4461:HOH:O	2.15	0.46
3:F:138:LEU:HD23	3:F:167:LEU:HA	1.96	0.46
2:E:208:THR:H	2:E:790:GLN:NE2	2.03	0.46
2:E:451:MET:HE3	2:E:456:TYR:CD2	2.51	0.46
2:E:665:ILE:HD12	2:E:665:ILE:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:8:TYR:OH	3:F:10:ARG:HD3	2.16	0.46
2:B:176:LYS:HG2	2:B:180:HIS:ND1	2.30	0.46
2:B:327:LYS:HG2	2:B:420:LYS:HE3	1.97	0.46
2:E:63:ARG:HH11	2:E:63:ARG:HG2	1.80	0.46
2:E:121:VAL:HG11	2:E:132:ALA:HB3	1.98	0.46
2:B:428:PHE:HA	2:B:429:PRO:C	2.41	0.46
3:F:240:LYS:CG	3:F:241:PRO:HD3	2.42	0.46
3:C:115:ASN:OD1	3:C:125:MET:HB2	2.15	0.46
3:F:239:ASP:OD1	3:F:241:PRO:HD2	2.16	0.45
2:B:493:GLY:HA2	2:B:505:MET:HB2	1.98	0.45
3:C:118:ASN:HD22	8:C:4932:FAD:H4B	1.82	0.45
2:B:221:GLN:HB3	2:B:298:VAL:HA	1.99	0.45
2:B:809:VAL:OXT	2:B:809:VAL:HG23	2.17	0.45
3:C:204:MET:HG3	3:C:286:ALA:HB1	1.97	0.45
2:E:345:CYS:SG	2:E:384:VAL:HG23	2.57	0.45
2:B:713:GLN:HB3	9:B:4369:HOH:O	2.16	0.45
3:C:204:MET:HG3	3:C:286:ALA:CB	2.47	0.45
3:C:138:LEU:HD23	3:C:167:LEU:HA	1.98	0.45
2:E:384:VAL:HG13	2:E:388:CYS:SG	2.57	0.45
2:B:670:ILE:HD13	2:B:671:ASP:N	2.31	0.44
2:B:159:LEU:CD2	2:B:162:GLU:HG2	2.48	0.44
2:B:175:ARG:NH2	2:B:178:HIS:O	2.51	0.44
2:B:524:GLY:HA3	2:B:564:GLY:HA3	2.00	0.44
2:E:166:ASP:O	2:E:168:MET:N	2.51	0.44
2:B:121:VAL:HG11	2:B:132:ALA:HB3	1.98	0.44
2:B:389:SER:O	2:B:390:PHE:HB2	2.18	0.44
1:A:83:PRO:C	1:A:85:GLY:H	2.26	0.43
2:E:360:THR:HG21	2:E:433:PRO:HG2	2.00	0.43
2:E:522:ARG:NH1	9:E:4339:HOH:O	2.43	0.43
2:B:360:THR:HG21	2:B:433:PRO:HG2	2.00	0.43
2:E:505:MET:HA	2:E:565:LEU:HG	2.00	0.43
2:E:537:ALA:CB	2:E:553:ILE:HD11	2.35	0.43
2:E:200:GLU:OE1	2:E:324:LYS:HG2	2.18	0.43
2:B:513:ILE:HD11	2:B:587:ILE:HG21	2.01	0.43
1:D:101:GLN:HB2	1:D:139:CYS:HB3	1.99	0.43
2:E:163:ASP:OD2	2:E:164:ILE:HG23	2.18	0.43
1:A:8:LEU:N	1:A:8:LEU:HD23	2.34	0.42
2:B:713:GLN:HE21	2:B:733:LEU:HD23	1.84	0.42
2:E:182:PHE:CD1	2:E:182:PHE:C	2.98	0.42
2:E:347:ASP:HB2	9:E:4020:HOH:O	2.18	0.42
2:E:448:LYS:HE3	2:E:452:ASP:OD2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:739:THR:HA	2:B:740:PRO:HD3	1.92	0.42
2:E:63:ARG:HD2	2:E:141:GLU:OE1	2.20	0.42
2:E:623:LYS:HA	2:E:623:LYS:HD3	1.88	0.42
2:B:510:GLU:OE2	2:E:510:GLU:OE2	2.37	0.42
1:A:84:ASP:OD1	1:A:84:ASP:C	2.62	0.42
2:B:729:MET:HE3	2:B:729:MET:HB3	1.74	0.42
2:E:428:PHE:HA	2:E:429:PRO:C	2.45	0.42
2:B:806:GLY:O	2:B:809:VAL:HG22	2.19	0.41
1:D:159:VAL:HB	1:D:160:PRO:HD3	2.02	0.41
2:B:358:ILE:CD1	2:B:489:ILE:HB	2.49	0.41
2:E:176:LYS:H	2:E:176:LYS:HG3	1.48	0.41
2:E:346:ALA:O	2:E:347:ASP:CG	2.63	0.41
1:D:44:THR:O	1:D:45:SER:HB2	2.20	0.41
2:E:221:GLN:HB3	2:E:298:VAL:HA	2.03	0.41
2:E:58:SER:OG	2:E:59:HIS:HD2	2.03	0.41
2:E:166:ASP:O	2:E:167:LYS:C	2.63	0.41
2:B:315:HIS:HE1	9:B:4008:HOH:O	2.04	0.41
2:B:359:CYS:O	2:B:399:ILE:HB	2.21	0.41
2:E:168:MET:HE3	2:E:175:ARG:HB2	2.02	0.41
3:F:35:HIS:HD2	3:F:106:ILE:HG12	1.85	0.41
1:A:63:THR:HG22	1:A:63:THR:O	2.21	0.41
2:B:506:PHE:CD1	2:B:506:PHE:C	2.99	0.41
2:E:506:PHE:CD1	2:E:506:PHE:C	2.99	0.41
2:B:256:PRO:HB2	2:B:258:HIS:CD2	2.57	0.40
2:B:167:LYS:C	2:B:169:THR:H	2.29	0.40
3:F:65:GLU:HB2	3:F:86:PHE:HZ	1.87	0.40

There are no symmetry-related clashes.

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	159/166 (96%)	156 (98%)	3 (2%)	0	100	100
1	D	156/166 (94%)	153 (98%)	3 (2%)	0	100	100
2	B	802/809 (99%)	775 (97%)	22 (3%)	5 (1%)	21	9
2	E	793/809 (98%)	761 (96%)	25 (3%)	7 (1%)	14	4
3	C	285/288 (99%)	280 (98%)	5 (2%)	0	100	100
3	F	284/288 (99%)	280 (99%)	4 (1%)	0	100	100
All	All	2479/2526 (98%)	2405 (97%)	62 (2%)	12 (0%)	24	12

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	176	LYS
2	E	167	LYS
2	B	493	GLY
2	B	712	GLY
2	E	493	GLY
2	E	712	GLY
2	B	265	PRO
2	E	265	PRO
2	B	390	PHE
2	E	312	ARG
2	E	761	VAL
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	129/131 (98%)	129 (100%)	0	100	100
1	D	126/131 (96%)	126 (100%)	0	100	100
2	B	648/653 (99%)	642 (99%)	6 (1%)	70	62
2	E	640/653 (98%)	632 (99%)	8 (1%)	61	48
3	C	211/212 (100%)	209 (99%)	2 (1%)	70	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F	210/212 (99%)	209 (100%)	1 (0%)	81	76
All	All	1964/1992 (99%)	1947 (99%)	17 (1%)	70	62

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	7	VAL
2	B	393	THR
2	B	401	ARG
2	B	488	GLU
2	B	530	GLN
2	B	670	ILE
3	C	106	ILE
3	C	287	LYS
2	E	21	MET
2	E	314	TYR
2	E	327	LYS
2	E	393	THR
2	E	401	ARG
2	E	488	GLU
2	E	639	ASN
2	E	790	GLN
3	F	221	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	HIS
1	A	32	GLN
1	A	34	ASN
1	A	135	ASN
2	B	115	ASN
2	B	172	HIS
2	B	258	HIS
2	B	273	ASN
2	B	304	ASN
2	B	315	HIS
2	B	334	HIS
2	B	442	ASN
2	B	458	GLN
2	B	463	GLN

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Mol	Chain	Res	Type
2	B	530	GLN
2	B	592	GLN
2	B	639	ASN
2	B	713	GLN
2	B	754	HIS
2	B	808	HIS
3	C	118	ASN
3	C	130	GLN
3	C	221	ASN
1	D	5	HIS
1	D	11	ASN
1	D	32	GLN
1	D	118	GLN
2	E	19	GLN
2	E	59	HIS
2	E	91	ASN
2	E	115	ASN
2	E	273	ASN
2	E	315	HIS
2	E	334	HIS
2	E	442	ASN
2	E	463	GLN
2	E	713	GLN
2	E	754	HIS
2	E	790	GLN
2	E	804	GLN
3	F	78	GLN
3	F	123	ASN
3	F	130	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](#)

Of 11 ligands modelled in this entry, 2 are monoatomic - leaving 9 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	FES	D	3907	1	0,4,4	-	-	-		
4	PO4	A	3001	-	4,4,4	1.25	0	6,6,6	0.48	0
8	FAD	F	4931	-	58,58,58	2.07	18 (31%)	85,89,89	1.01	4 (4%)
7	DW6	B	3911	6,2	46,54,54	2.59	19 (41%)	54,87,87	2.13	14 (25%)
5	FES	D	3908	1	0,4,4	-	-	-		
5	FES	A	3908	1	0,4,4	-	-	-		
8	FAD	C	4932	-	58,58,58	2.21	23 (39%)	85,89,89	1.09	8 (9%)
5	FES	A	3907	1	0,4,4	-	-	-		

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	FES	D	3907	1	-	-	0/1/1/1
8	FAD	F	4931	-	-	2/34/50/50	0/6/6/6
7	DW6	B	3911	6,2	-	2/22/82/82	0/6/6/6
5	FES	D	3908	1	-	-	0/1/1/1
5	FES	A	3908	1	-	-	0/1/1/1
8	FAD	C	4932	-	-	5/34/50/50	0/6/6/6
5	FES	A	3907	1	-	-	0/1/1/1

All (60) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	C	4932	FAD	P-O3P	-8.54	1.50	1.59
8	F	4931	FAD	P-O3P	-8.27	1.50	1.59
7	B	3911	DW6	C6'-N5'	7.74	1.55	1.46
7	B	3911	DW6	C7-C6'	-7.19	1.47	1.53
7	B	3911	DW6	C4B-N8'	6.09	1.41	1.35
7	B	3911	DW6	MO-S8'	5.61	2.47	2.39
8	C	4932	FAD	PA-O3P	5.44	1.65	1.59
7	B	3911	DW6	C4B-N1'	4.02	1.42	1.36
8	F	4931	FAD	PA-O2A	-3.90	1.37	1.55
8	C	4932	FAD	PA-O2A	-3.88	1.37	1.55
8	F	4931	FAD	PA-O3P	3.65	1.63	1.59
8	F	4931	FAD	C4X-N5	3.27	1.37	1.30
8	C	4932	FAD	O5'-C5'	3.18	1.56	1.44
8	C	4932	FAD	C8-C7	3.18	1.48	1.40
8	C	4932	FAD	C4X-N5	3.14	1.37	1.30
8	F	4931	FAD	C5A-C6A	3.13	1.49	1.41
8	C	4932	FAD	C5A-C6A	3.09	1.49	1.41
8	F	4931	FAD	C9A-N10	3.06	1.46	1.41
8	F	4931	FAD	C8-C7	3.04	1.48	1.40
7	B	3911	DW6	C6-N1	3.01	1.45	1.38
8	F	4931	FAD	C4A-N3A	2.99	1.40	1.34
8	C	4932	FAD	P-O2P	-2.90	1.41	1.55
8	C	4932	FAD	C9-C9A	2.88	1.44	1.39
7	B	3911	DW6	PA-O3A	2.86	1.62	1.59
8	F	4931	FAD	C9A-C5X	2.86	1.45	1.41
8	F	4931	FAD	P-O2P	-2.83	1.42	1.55
7	B	3911	DW6	C2D-C1'	2.78	1.62	1.53
8	F	4931	FAD	O5'-C5'	2.77	1.55	1.44
7	B	3911	DW6	C4A-N5'	2.76	1.44	1.37
8	C	4932	FAD	C9A-C5X	2.71	1.45	1.41
8	C	4932	FAD	C2A-N1A	2.70	1.38	1.33
8	C	4932	FAD	C4'-C3'	2.70	1.58	1.53
8	F	4931	FAD	C1'-C2'	2.67	1.56	1.52
8	C	4932	FAD	C4A-N3A	2.61	1.39	1.34
8	F	4931	FAD	C5B-C4B	2.59	1.59	1.51
7	B	3911	DW6	C1'-N1	2.53	1.54	1.47
8	C	4932	FAD	C5A-C4A	2.52	1.43	1.39
8	F	4931	FAD	C5A-C4A	2.47	1.43	1.39
8	C	4932	FAD	C10-N1	2.44	1.38	1.33
8	C	4932	FAD	O4B-C4B	2.43	1.50	1.45
7	B	3911	DW6	MO-S7'	2.40	2.42	2.39
8	F	4931	FAD	C6-C5X	2.39	1.43	1.40
7	B	3911	DW6	O9'-C9'	2.38	1.48	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	C	4932	FAD	C5B-C4B	2.32	1.58	1.51
7	B	3911	DW6	O3'-C3'	2.31	1.48	1.43
7	B	3911	DW6	O4D-C4D	2.29	1.50	1.45
7	B	3911	DW6	C5'-C4D	2.28	1.58	1.51
7	B	3911	DW6	C5-C4	2.27	1.48	1.42
8	C	4932	FAD	C6-C5X	2.26	1.43	1.40
8	C	4932	FAD	O2-C2	-2.26	1.19	1.24
8	C	4932	FAD	C9A-N10	2.23	1.45	1.41
7	B	3911	DW6	C4'-N3'	2.20	1.43	1.38
8	C	4932	FAD	O4B-C1B	2.18	1.47	1.42
7	B	3911	DW6	C4-N3	2.17	1.38	1.34
8	F	4931	FAD	O4B-C1B	2.14	1.46	1.42
8	F	4931	FAD	C4'-C3'	2.13	1.57	1.53
7	B	3911	DW6	C7-N8'	2.11	1.48	1.45
8	C	4932	FAD	P-O5'	-2.06	1.51	1.59
8	C	4932	FAD	C1'-C2'	2.06	1.55	1.52
8	F	4931	FAD	C2A-N1A	2.04	1.37	1.33

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	3911	DW6	C7-C6'-N5'	7.70	115.43	107.87
7	B	3911	DW6	C8'-C7'-S7'	6.98	124.11	120.15
7	B	3911	DW6	C7'-C8'-S8'	-4.73	117.47	120.15
7	B	3911	DW6	C4-N3-C2	3.78	126.22	120.26
7	B	3911	DW6	N1-C2-N3	-3.51	112.72	118.80
7	B	3911	DW6	O9'-C7-C6'	3.12	111.05	108.96
8	C	4932	FAD	O4B-C1B-N9A	-3.05	102.23	108.09
7	B	3911	DW6	C6-N1-C2	2.97	125.47	120.46
8	F	4931	FAD	O4B-C1B-N9A	-2.62	103.05	108.09
7	B	3911	DW6	C5-C6-N1	-2.58	117.65	121.84
7	B	3911	DW6	O2'-C2D-C3'	2.55	119.98	111.82
8	C	4932	FAD	O5B-PA-O1A	-2.41	99.38	108.94
8	C	4932	FAD	C5X-C9A-N10	-2.34	115.85	117.97
8	C	4932	FAD	O3'-C3'-C2'	-2.31	103.69	108.93
7	B	3911	DW6	O9'-C9'-C8'	-2.30	105.85	109.09
7	B	3911	DW6	O2-C2-N3	2.29	125.93	122.33
8	F	4931	FAD	C2A-N1A-C6A	2.28	122.48	118.73
7	B	3911	DW6	O1A-PA-O3A	-2.25	101.20	107.27
8	F	4931	FAD	C5'-C4'-C3'	-2.24	108.00	112.22
8	C	4932	FAD	C2A-N1A-C6A	2.23	122.39	118.73
8	C	4932	FAD	C4-N3-C2	-2.18	121.77	125.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	F	4931	FAD	O5B-PA-O1A	-2.11	100.58	108.94
8	C	4932	FAD	C5'-C4'-C3'	-2.06	108.33	112.22
7	B	3911	DW6	O2B-PB-O1B	2.04	121.96	112.44
8	C	4932	FAD	C10-N1-C2	2.03	121.23	116.85
7	B	3911	DW6	C2D-C1'-N1	-2.00	107.68	113.25

There are no chirality outliers.

All (9) torsion outliers are listed below:

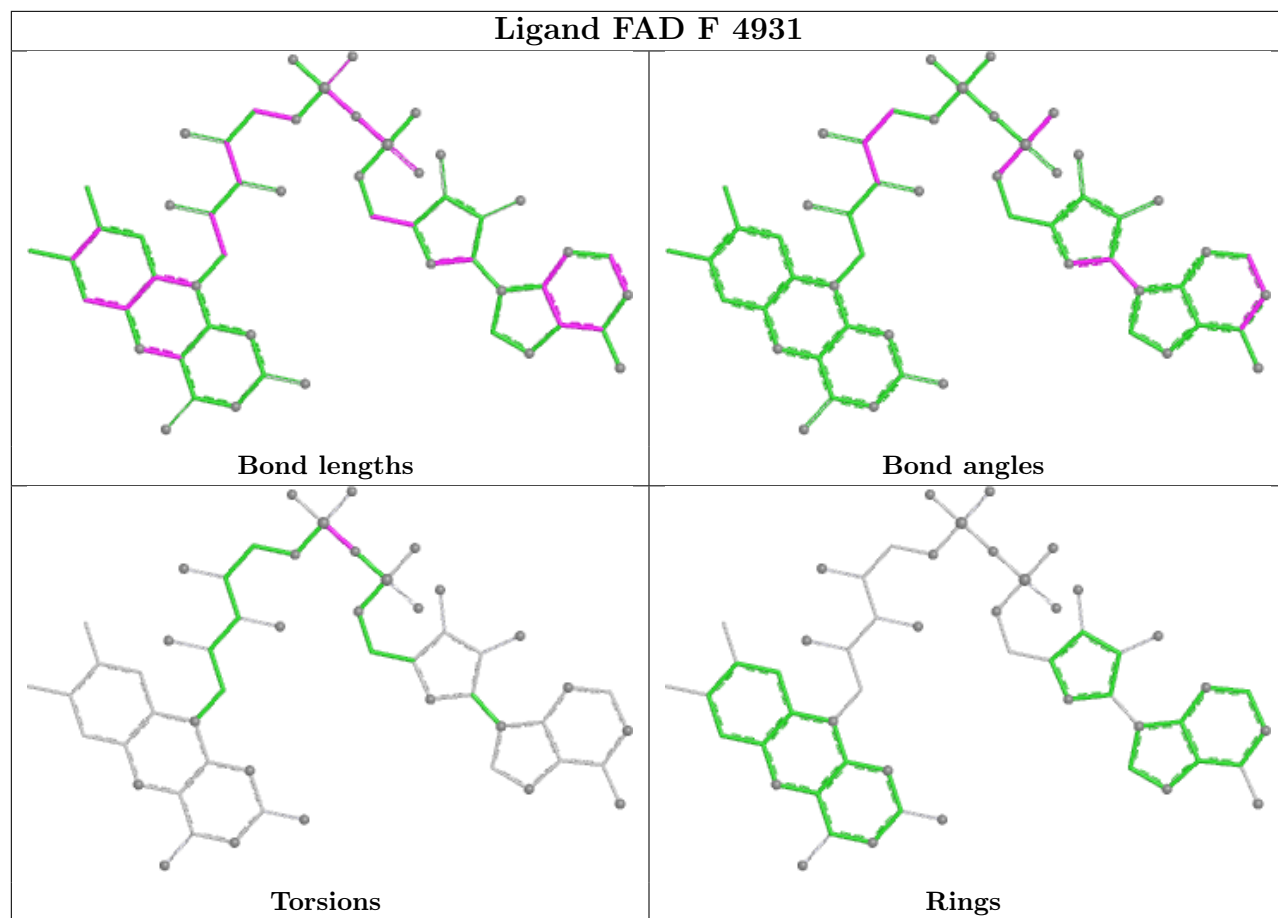
Mol	Chain	Res	Type	Atoms
7	B	3911	DW6	C10-O3B-PB-O1B
7	B	3911	DW6	C10-O3B-PB-O3A
8	C	4932	FAD	C5B-O5B-PA-O1A
8	F	4931	FAD	PA-O3P-P-O2P
8	C	4932	FAD	PA-O3P-P-O2P
8	C	4932	FAD	C3B-C4B-C5B-O5B
8	C	4932	FAD	PA-O3P-P-O1P
8	C	4932	FAD	O4B-C4B-C5B-O5B
8	F	4931	FAD	PA-O3P-P-O1P

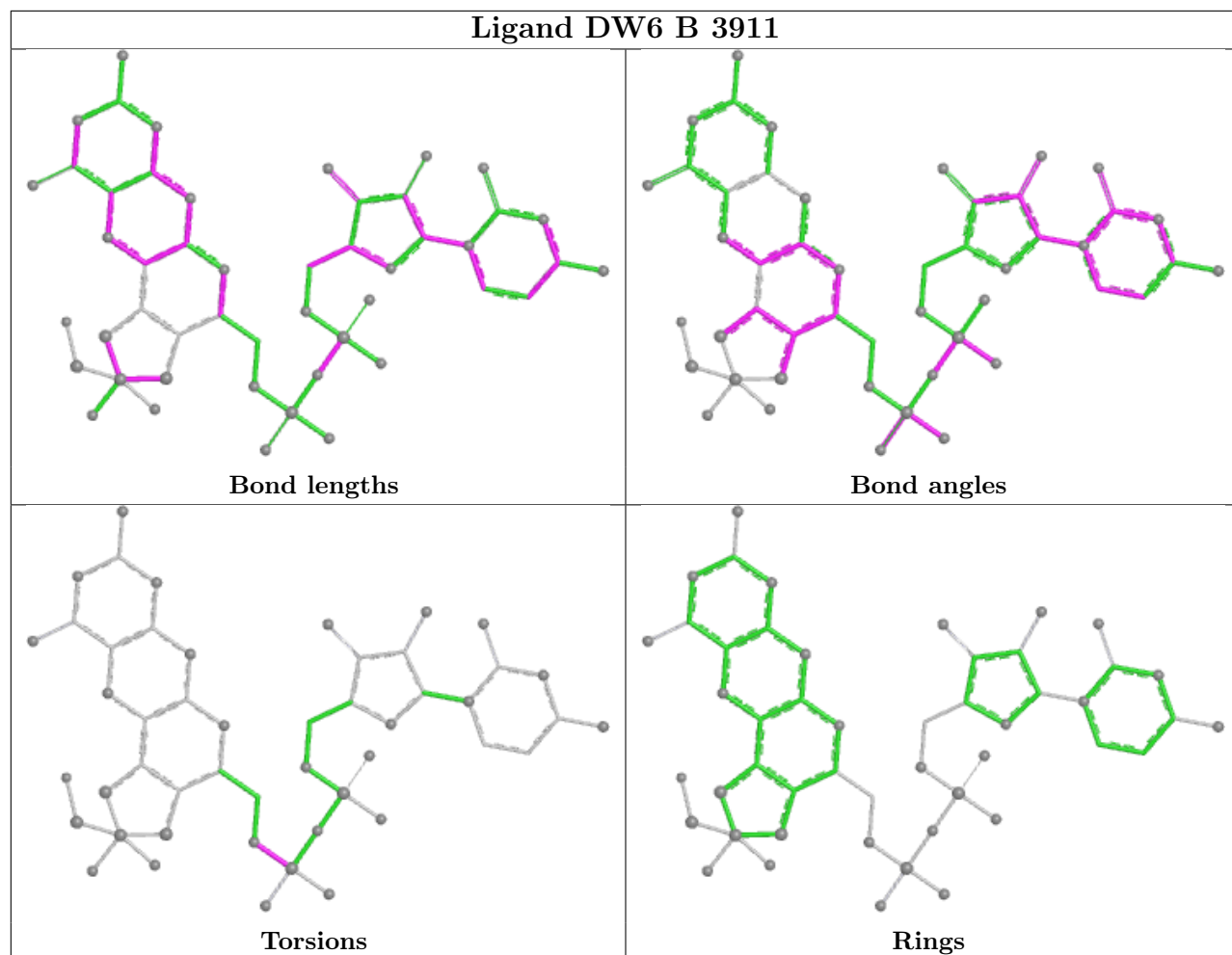
There are no ring outliers.

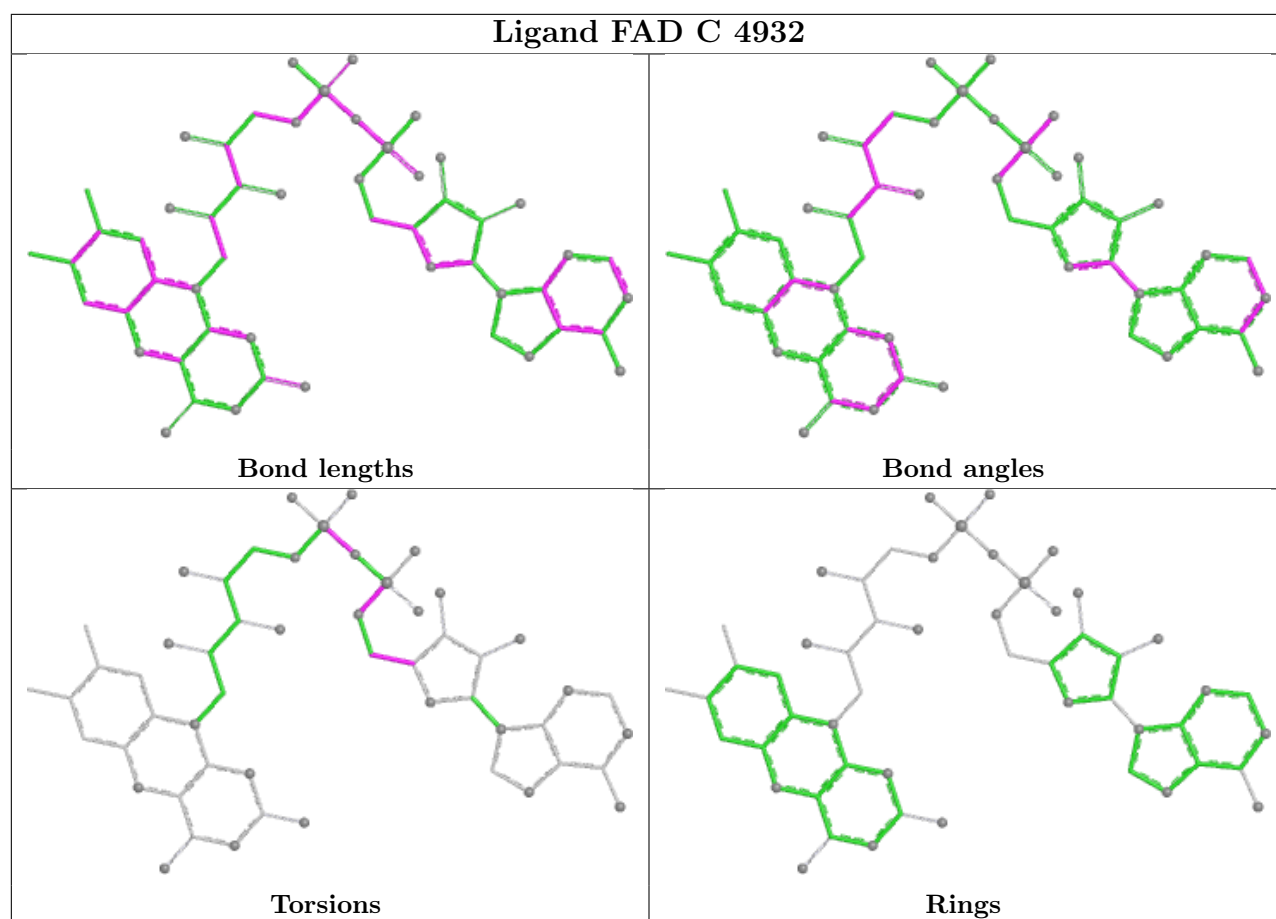
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	3911	DW6	1	0
8	C	4932	FAD	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.