



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 16, 2024 – 03:17 PM EDT

PDB ID : 5DQR  
Title : The crystal structure of Arabidopsis 7-hydroxymethyl chlorophyll a reductase (HCAR)  
Authors : Wang, X.; Liu, L.  
Deposited on : 2015-09-15  
Resolution : 2.70 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](mailto: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>.

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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) : 1.13  
EDS : 2.37.1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.37.1

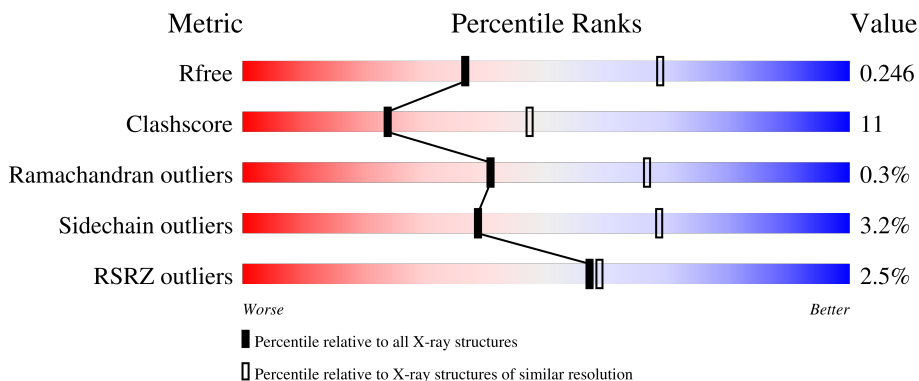
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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.



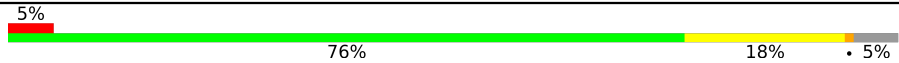
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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  $\geq 3$ , 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	437	 5% 73% 20% • 5%
1	B	437	 % 73% 19% • 6%
1	C	437	 % 76% 19% • •
1	D	437	 % 73% 19% • 6%
1	E	437	 73% 18% • 7%

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Mol	Chain	Length	Quality of chain
1	F	437	 <p>5% 76% 18% • 5%</p>

## 2 Entry composition [i](#)

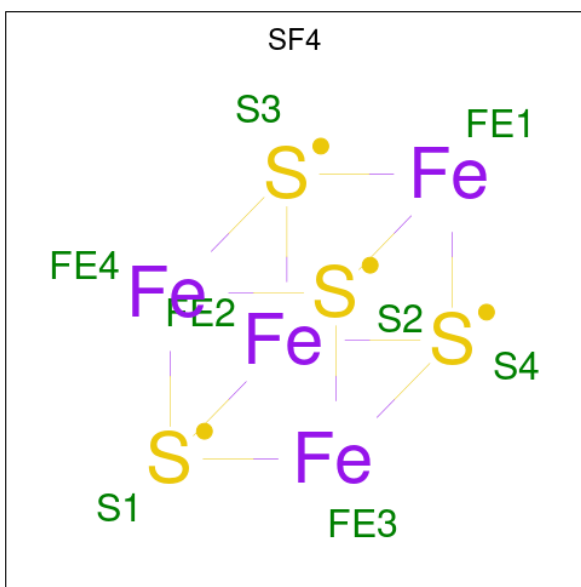
There are 4 unique types of molecules in this entry. The entry contains 20316 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 7-hydroxymethyl chlorophyll a reductase, chloroplastic.

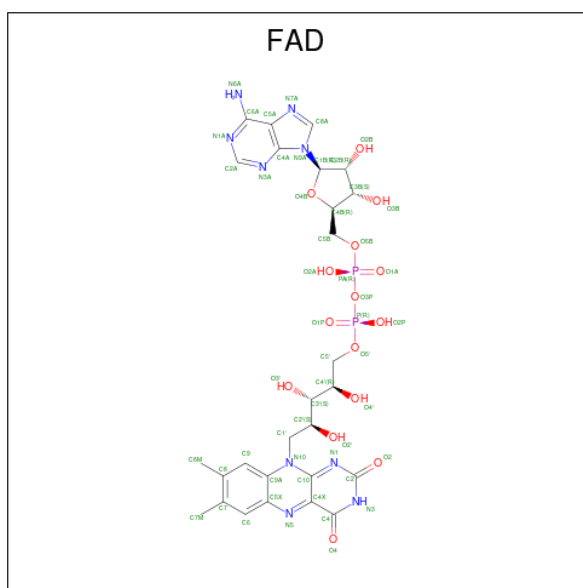
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	414	Total 3227	C 2050	N 558	O 599	S 20	0	1	0
1	B	411	Total 3197	C 2033	N 548	O 596	S 20	0	1	0
1	C	421	Total 3294	C 2089	N 567	O 618	S 20	0	1	0
1	D	411	Total 3198	C 2032	N 550	O 596	S 20	0	0	0
1	E	406	Total 3150	C 2002	N 542	O 586	S 20	0	0	0
1	F	413	Total 3214	C 2043	N 551	O 600	S 20	0	1	0

- Molecule 2 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe<sub>4</sub>S<sub>4</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Fe S 8 4 4	0	0
2	A	1	Total Fe S 8 4 4	0	0
2	B	1	Total Fe S 8 4 4	0	0
2	B	1	Total Fe S 8 4 4	0	0
2	C	1	Total Fe S 8 4 4	0	0
2	C	1	Total Fe S 8 4 4	0	0
2	D	1	Total Fe S 8 4 4	0	0
2	D	1	Total Fe S 8 4 4	0	0
2	E	1	Total Fe S 8 4 4	0	0
2	E	1	Total Fe S 8 4 4	0	0
2	F	1	Total Fe S 8 4 4	0	0
2	F	1	Total Fe S 8 4 4	0	0

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



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

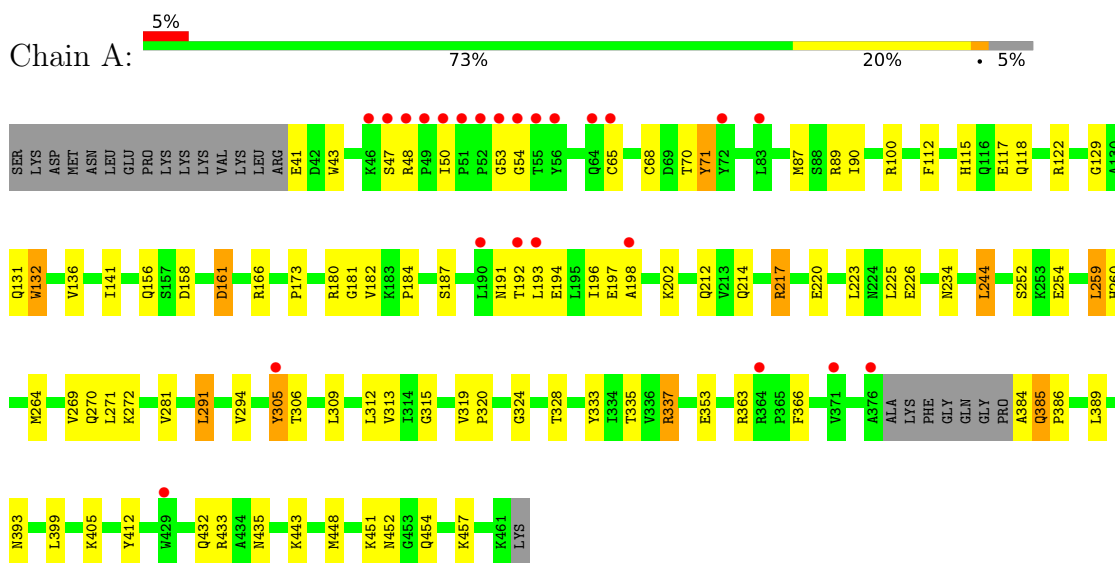
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	81	Total	O	0	0
			81	81		
4	B	118	Total	O	0	0
			118	118		
4	C	103	Total	O	0	0
			103	103		
4	D	151	Total	O	0	0
			151	151		
4	E	108	Total	O	0	0
			108	108		
4	F	61	Total	O	0	0
			61	61		

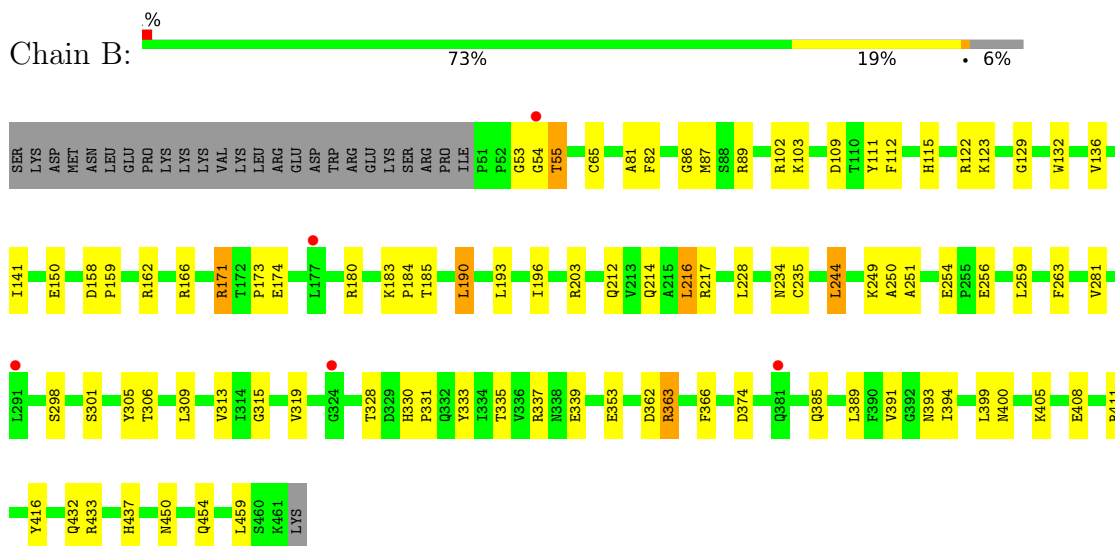
### 3 Residue-property plots [i](#)

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

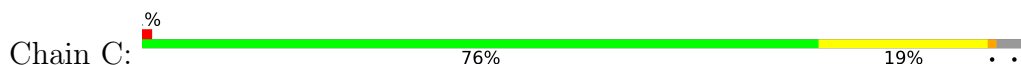
- Molecule 1: 7-hydroxymethyl chlorophyll a reductase, chloroplactic

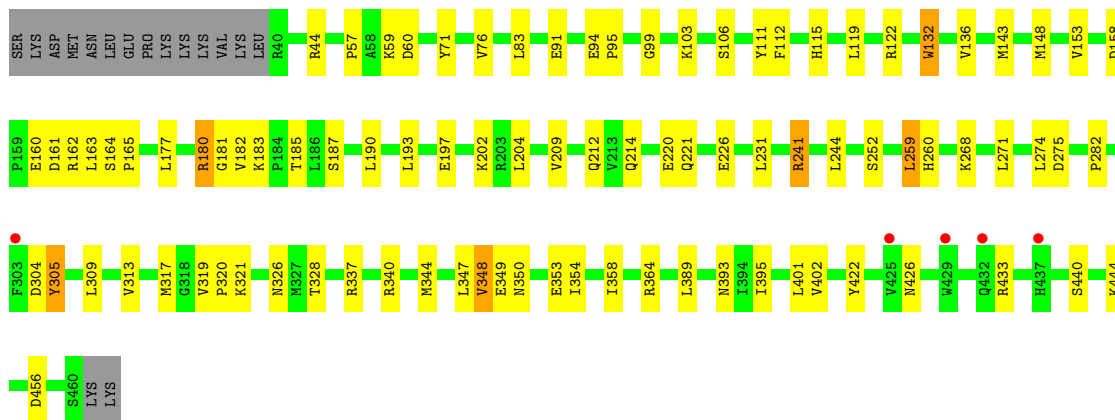


- Molecule 1: 7-hydroxymethyl chlorophyll a reductase, chloroplactic

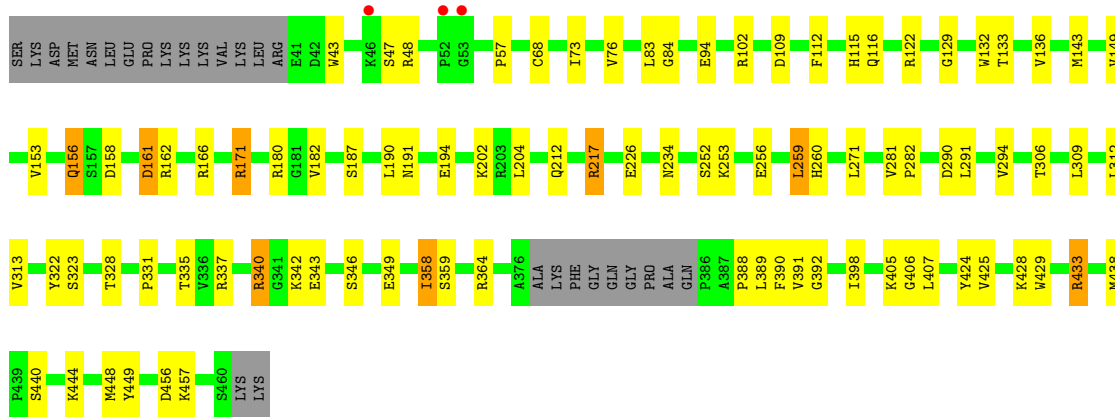
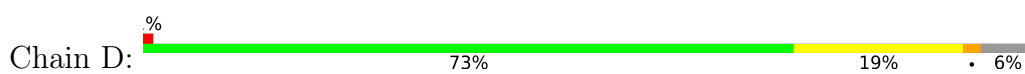


- Molecule 1: 7-hydroxymethyl chlorophyll a reductase, chloroplactic

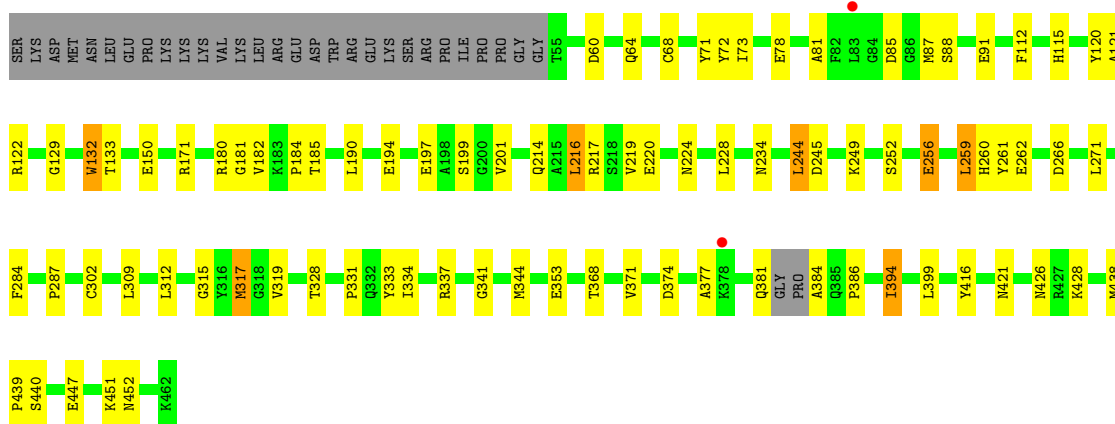




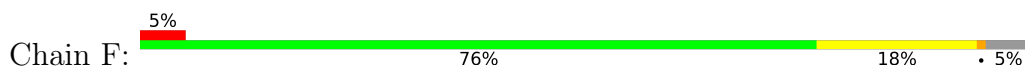
• Molecule 1: 7-hydroxymethyl chlorophyll a reductase, chloroplastic



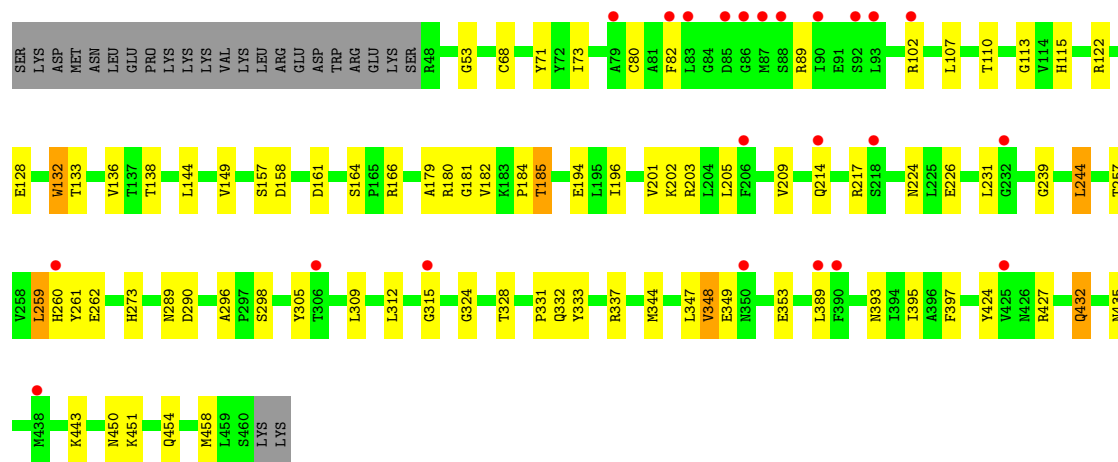
• Molecule 1: 7-hydroxymethyl chlorophyll a reductase, chloroplastic



• Molecule 1: 7-hydroxymethyl chlorophyll a reductase, chloroplastic







## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.11Å 89.11Å 273.31Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.61 – 2.70 44.61 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.7 (44.61-2.70) 97.8 (44.61-2.70)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.35 (at 2.69Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.202 , 0.246 0.203 , 0.246	Depositor DCC
$R_{free}$ test set	3321 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.6	Xtrriage
Anisotropy	0.061	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 25.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.010 for -h,-k,l 0.043 for h,-h-k,-l 0.058 for -k,-h,-l	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	20316	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.50% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 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: FAD, SF4

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	0.22	0/3300	0.45	3/4478 (0.1%)
1	B	0.22	0/3271	0.42	1/4437 (0.0%)
1	C	0.28	0/3370	0.55	4/4574 (0.1%)
1	D	0.21	0/3268	0.48	3/4436 (0.1%)
1	E	0.21	0/3216	0.45	3/4361 (0.1%)
1	F	0.26	0/3288	0.45	2/4464 (0.0%)
All	All	0.24	0/19713	0.47	16/26750 (0.1%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	348	VAL	CB-CA-C	-15.97	81.05	111.40
1	C	349	GLU	N-CA-CB	-10.82	91.12	110.60
1	C	348	VAL	N-CA-C	10.10	138.28	111.00
1	D	161	ASP	CB-CA-C	8.95	128.29	110.40
1	D	161	ASP	N-CA-C	-8.10	89.14	111.00
1	F	132	TRP	N-CA-C	7.19	130.42	111.00
1	E	132	TRP	N-CA-C	6.96	129.79	111.00
1	D	156	GLN	CB-CA-C	-6.63	97.14	110.40
1	A	132	TRP	N-CA-C	6.22	127.79	111.00
1	F	179	ALA	CB-CA-C	5.77	118.76	110.10
1	E	199	SER	CB-CA-C	5.58	120.70	110.10
1	C	132	TRP	N-CA-C	5.53	125.94	111.00
1	B	459	LEU	CB-CA-C	5.53	120.71	110.20
1	A	198	ALA	CB-CA-C	5.49	118.33	110.10
1	A	161	ASP	CB-CA-C	5.39	121.18	110.40
1	E	78	GLU	CB-CA-C	5.05	120.50	110.40

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	3227	0	3194	80	0
1	B	3197	0	3165	73	1
1	C	3294	0	3257	71	1
1	D	3198	0	3155	76	0
1	E	3150	0	3114	69	0
1	F	3214	0	3190	65	0
2	A	16	0	0	0	0
2	B	16	0	0	1	0
2	C	16	0	0	0	0
2	D	16	0	0	0	0
2	E	16	0	0	0	0
2	F	16	0	0	0	0
3	A	53	0	31	3	0
3	B	53	0	30	2	0
3	C	53	0	31	4	0
3	D	53	0	30	4	0
3	E	53	0	31	3	0
3	F	53	0	31	4	0
4	A	81	0	0	31	2
4	B	118	0	0	30	0
4	C	103	0	0	34	2
4	D	151	0	0	34	3
4	E	108	0	0	25	5
4	F	61	0	0	24	0
All	All	20316	0	19259	431	7

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (431) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:LEU:HG	4:A:613:HOH:O	1.34	1.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:117:GLU:HB3	4:A:610:HOH:O	1.33	1.25
1:C:143:MET:SD	4:C:702:HOH:O	2.00	1.19
1:F:315:GLY:O	1:F:333:TYR:HB3	1.37	1.18
1:F:157:SER:C	4:F:601:HOH:O	1.82	1.18
1:A:90:ILE:CB	4:A:602:HOH:O	1.87	1.18
1:F:158:ASP:N	4:F:601:HOH:O	1.81	1.13
1:C:95:PRO:C	4:C:601:HOH:O	1.84	1.12
1:A:100[B]:ARG:NH1	4:A:601:HOH:O	1.82	1.12
1:D:391:VAL:N	4:D:602:HOH:O	1.83	1.11
1:C:364:ARG:NH1	4:C:603:HOH:O	1.82	1.09
1:A:182:VAL:N	4:A:603:HOH:O	1.85	1.07
1:A:315:GLY:O	1:A:333:TYR:HB3	1.52	1.07
1:C:433:ARG:NH2	4:C:607:HOH:O	1.88	1.06
1:B:249:LYS:HB2	4:B:607:HOH:O	1.59	1.03
1:A:41:GLU:N	4:A:604:HOH:O	1.91	1.02
1:B:432:GLN:CB	4:B:604:HOH:O	2.08	1.01
1:F:349:GLU:N	4:F:603:HOH:O	1.92	1.01
1:D:405:LYS:HD3	4:D:733:HOH:O	1.59	1.00
1:D:158:ASP:O	1:D:161:ASP:O	1.79	0.99
2:B:501:SF4:S1	4:B:678:HOH:O	2.20	0.98
1:F:435:ASN:OD1	4:F:602:HOH:O	1.82	0.98
1:B:250:ALA:N	4:B:607:HOH:O	1.97	0.97
1:A:433:ARG:NH2	4:A:605:HOH:O	1.96	0.97
1:C:94:GLU:O	4:C:601:HOH:O	1.80	0.97
1:C:321:LYS:O	4:C:602:HOH:O	1.81	0.97
1:B:254:GLU:OE1	4:B:601:HOH:O	1.84	0.95
1:A:90:ILE:CG1	4:A:602:HOH:O	2.10	0.95
1:E:266:ASP:OD2	4:E:601:HOH:O	1.82	0.95
1:A:90:ILE:HB	4:A:602:HOH:O	1.54	0.94
1:C:91:GLU:OE2	4:C:605:HOH:O	1.86	0.94
1:C:103:LYS:O	4:C:604:HOH:O	1.84	0.93
1:A:90:ILE:N	4:A:602:HOH:O	1.83	0.92
1:B:408:GLU:OE2	4:B:602:HOH:O	1.87	0.92
1:D:226:GLU:OE1	4:D:604:HOH:O	1.89	0.90
1:E:262:GLU:OE2	4:E:602:HOH:O	1.88	0.90
1:C:220:GLU:OE2	4:C:606:HOH:O	1.87	0.90
1:A:217:ARG:NH2	4:A:608:HOH:O	2.03	0.90
1:D:457:LYS:NZ	4:D:610:HOH:O	2.05	0.90
1:B:432:GLN:HB3	4:B:604:HOH:O	1.69	0.89
1:B:393:ASN:O	4:B:605:HOH:O	1.90	0.89
1:F:132:TRP:O	1:F:328:THR:HA	1.71	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:323:SER:O	1:E:368:THR:HG21	1.72	0.89
1:D:162:ARG:NH2	4:D:607:HOH:O	2.02	0.89
1:B:432:GLN:N	4:B:604:HOH:O	1.90	0.89
1:F:315:GLY:O	1:F:333:TYR:CB	2.20	0.89
1:E:60:ASP:HA	4:E:613:HOH:O	1.72	0.88
1:A:181:GLY:HA2	4:A:603:HOH:O	1.74	0.87
1:D:116:GLN:OE1	4:D:605:HOH:O	1.92	0.86
1:A:90:ILE:HG13	4:A:602:HOH:O	1.69	0.86
1:C:433:ARG:CZ	4:C:607:HOH:O	2.22	0.86
1:C:60:ASP:O	4:C:610:HOH:O	1.94	0.85
1:C:275:ASP:OD1	4:C:609:HOH:O	1.94	0.85
1:F:443:LYS:NZ	4:F:606:HOH:O	2.00	0.84
1:D:166:ARG:NH1	4:D:603:HOH:O	1.87	0.84
1:A:87:MET:O	4:A:602:HOH:O	1.96	0.83
1:B:339:GLU:OE1	4:B:606:HOH:O	1.96	0.82
1:A:220:GLU:O	4:A:606:HOH:O	1.96	0.82
1:F:166:ARG:HB2	4:F:601:HOH:O	1.81	0.81
1:A:315:GLY:O	1:A:333:TYR:CB	2.27	0.81
1:F:432:GLN:OE1	4:F:605:HOH:O	1.99	0.81
1:A:53:GLY:O	4:A:607:HOH:O	2.00	0.80
1:D:392:GLY:N	4:D:602:HOH:O	2.09	0.80
1:E:447:GLU:OE1	4:E:603:HOH:O	1.98	0.80
1:C:132:TRP:O	1:C:328:THR:HA	1.81	0.80
1:D:191:ASN:HB2	4:D:632:HOH:O	1.82	0.79
1:B:362:ASP:OD1	4:B:608:HOH:O	1.98	0.79
1:D:343:GLU:OE2	4:D:606:HOH:O	2.00	0.79
1:E:60:ASP:CA	4:E:613:HOH:O	2.28	0.79
1:C:364:ARG:CZ	4:C:603:HOH:O	2.20	0.78
1:C:95:PRO:CA	4:C:601:HOH:O	2.24	0.78
1:E:214:GLN:OE1	4:E:604:HOH:O	2.00	0.78
1:D:456:ASP:OD1	4:D:608:HOH:O	2.02	0.78
1:D:166:ARG:NH2	4:D:603:HOH:O	2.11	0.77
1:A:131:GLN:HB2	4:A:603:HOH:O	1.84	0.77
1:F:348:VAL:C	4:F:603:HOH:O	2.18	0.77
1:C:221:GLN:NE2	4:C:612:HOH:O	2.09	0.77
1:F:324:GLY:CA	4:F:612:HOH:O	2.33	0.77
1:A:158:ASP:O	1:A:161:ASP:O	2.02	0.76
1:E:64:GLN:NE2	4:E:608:HOH:O	2.10	0.76
1:F:166:ARG:CB	4:F:601:HOH:O	2.33	0.76
1:B:123:LYS:O	4:B:611:HOH:O	2.03	0.76
1:F:349:GLU:OE1	4:F:607:HOH:O	2.03	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:374:ASP:OD1	4:E:605:HOH:O	2.04	0.76
1:D:156:GLN:OE1	4:D:603:HOH:O	2.04	0.76
1:E:194:GLU:OE1	4:E:607:HOH:O	2.04	0.76
1:C:456:ASP:O	4:C:611:HOH:O	2.04	0.75
1:E:381:GLN:O	4:E:606:HOH:O	2.03	0.75
1:D:449:TYR:O	4:D:609:HOH:O	2.04	0.75
1:F:450:ASN:ND2	4:F:611:HOH:O	2.19	0.74
1:F:324:GLY:N	4:F:612:HOH:O	2.20	0.74
1:B:89:ARG:NH2	4:B:619:HOH:O	2.20	0.74
1:C:321:LYS:C	4:C:602:HOH:O	2.22	0.74
1:E:262:GLU:CD	4:E:602:HOH:O	2.24	0.73
1:D:94:GLU:OE1	4:D:611:HOH:O	2.05	0.73
1:E:416:TYR:OH	4:E:605:HOH:O	2.02	0.73
1:D:156:GLN:O	1:D:166:ARG:N	2.20	0.73
1:A:193:LEU:N	4:A:613:HOH:O	2.21	0.72
1:B:263:PHE:O	4:B:613:HOH:O	2.08	0.72
1:D:342:LYS:NZ	4:D:601:HOH:O	1.80	0.71
1:A:191:ASN:O	1:A:192:THR:OG1	2.07	0.70
1:E:132:TRP:O	1:E:328:THR:HA	1.91	0.70
1:A:191:ASN:C	4:A:613:HOH:O	2.30	0.69
1:B:411:ARG:NH2	4:B:610:HOH:O	2.03	0.69
1:A:264:MET:SD	4:A:678:HOH:O	2.50	0.69
1:F:451:LYS:O	4:F:609:HOH:O	2.09	0.69
1:D:171:ARG:CG	4:D:615:HOH:O	2.41	0.69
1:B:249:LYS:C	4:B:607:HOH:O	2.30	0.68
1:A:217:ARG:NH1	1:A:309:LEU:O	2.27	0.68
1:B:132:TRP:O	1:B:328:THR:HA	1.94	0.68
1:A:132:TRP:O	1:A:328:THR:HA	1.94	0.68
1:D:256:GLU:CG	4:D:613:HOH:O	2.41	0.68
1:B:433:ARG:NH2	4:B:617:HOH:O	2.17	0.68
1:B:103:LYS:O	4:B:615:HOH:O	2.12	0.67
1:A:112:PHE:O	1:A:337:ARG:NH2	2.26	0.67
1:C:182:VAL:HG13	3:C:503:FAD:HM82	1.76	0.67
1:E:122:ARG:NH1	1:E:353:GLU:OE2	2.28	0.67
1:D:84:GLY:O	1:D:433:ARG:NH2	2.28	0.67
1:D:112:PHE:O	1:D:337:ARG:NH2	2.28	0.66
1:A:117:GLU:OE1	4:A:610:HOH:O	2.14	0.66
1:E:261:TYR:O	4:E:609:HOH:O	2.12	0.66
1:D:291:LEU:O	1:D:294:VAL:HG22	1.95	0.66
1:C:158:ASP:O	1:C:161:ASP:O	2.14	0.65
1:A:315:GLY:O	1:A:333:TYR:N	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:339:GLU:CD	4:B:606:HOH:O	2.33	0.64
1:D:217:ARG:NH2	4:D:628:HOH:O	2.31	0.64
1:F:182:VAL:HG13	3:F:503:FAD:HM82	1.79	0.64
1:A:131:GLN:OE1	4:A:603:HOH:O	2.15	0.64
1:A:254:GLU:HA	1:E:256:GLU:HG3	1.80	0.64
1:D:256:GLU:OE2	4:D:613:HOH:O	2.15	0.64
1:B:249:LYS:CB	4:B:607:HOH:O	2.29	0.63
1:B:184:PRO:HG2	1:B:244:LEU:HD11	1.79	0.63
1:D:166:ARG:CZ	4:D:603:HOH:O	2.29	0.63
1:C:252:SER:HB2	1:C:271:LEU:HD22	1.80	0.63
1:D:390:PHE:C	4:D:602:HOH:O	2.23	0.63
1:B:159:PRO:HD3	1:B:166:ARG:HE	1.63	0.62
1:F:389:LEU:O	1:F:393:ASN:ND2	2.32	0.62
1:E:262:GLU:OE1	4:E:602:HOH:O	2.16	0.62
1:A:223:LEU:HB3	1:A:225:LEU:HD13	1.80	0.62
1:E:384:ALA:N	4:E:606:HOH:O	2.32	0.61
1:A:389:LEU:O	1:A:393:ASN:ND2	2.33	0.61
1:D:217:ARG:O	4:D:614:HOH:O	2.16	0.61
1:F:180:ARG:HG2	1:F:180:ARG:HH11	1.65	0.61
1:C:95:PRO:O	4:C:601:HOH:O	2.06	0.61
1:A:43:TRP:O	1:A:47:SER:OG	2.17	0.61
1:B:249:LYS:CA	4:B:607:HOH:O	2.47	0.61
3:D:503:FAD:H6	4:D:715:HOH:O	2.00	0.61
1:A:315:GLY:O	1:A:333:TYR:CA	2.48	0.61
1:D:43:TRP:O	1:D:47:SER:OG	2.18	0.60
1:F:80:CYS:O	1:F:89:ARG:NH2	2.29	0.60
1:D:122:ARG:HB3	1:D:331:PRO:HA	1.83	0.60
1:A:305:TYR:OH	4:A:611:HOH:O	2.15	0.60
1:B:112:PHE:O	1:B:337:ARG:NH2	2.34	0.60
1:F:184:PRO:HG2	1:F:244:LEU:HD11	1.82	0.60
1:D:202:LYS:HE3	1:D:226:GLU:HG3	1.83	0.59
1:A:448:MET:O	1:A:451:LYS:NZ	2.36	0.59
1:B:86:GLY:HA3	1:B:437:HIS:HD2	1.67	0.59
1:D:132:TRP:O	1:D:328:THR:HA	2.01	0.59
1:B:162:ARG:NH2	1:B:256:GLU:O	2.35	0.59
1:C:241:ARG:NH2	4:C:618:HOH:O	2.28	0.59
1:D:440:SER:OG	1:D:444:LYS:NZ	2.35	0.59
1:E:219:VAL:HG12	1:E:219:VAL:O	2.01	0.59
1:D:171:ARG:HG3	4:D:615:HOH:O	2.03	0.58
1:E:184:PRO:HG2	1:E:244:LEU:HD11	1.85	0.58
1:A:115:HIS:HA	1:A:337:ARG:HA	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:156:GLN:O	1:D:166:ARG:HB3	2.04	0.58
1:A:184:PRO:HG2	1:A:244:LEU:HD11	1.84	0.58
1:B:393:ASN:ND2	4:B:627:HOH:O	2.37	0.57
1:D:256:GLU:HG2	4:D:613:HOH:O	2.03	0.57
1:B:234:ASN:HD22	1:B:306:THR:HA	1.69	0.57
1:C:440:SER:OG	1:C:444:LYS:NZ	2.36	0.57
1:B:400:ASN:O	1:B:405:LYS:NZ	2.35	0.56
1:B:54:GLY:O	1:B:55:THR:HB	2.06	0.56
1:C:401:LEU:HD12	1:C:402:VAL:HG13	1.87	0.56
1:C:389:LEU:O	1:C:393:ASN:ND2	2.37	0.56
1:A:182:VAL:HG13	3:A:503:FAD:HM82	1.87	0.56
1:C:143:MET:HE1	1:C:344:MET:HG2	1.88	0.56
1:D:340:ARG:NH1	4:D:633:HOH:O	2.39	0.56
1:E:72:TYR:OH	1:E:197:GLU:OE2	2.19	0.56
1:E:182:VAL:HG13	3:E:503:FAD:HM82	1.87	0.56
1:E:394:ILE:HD12	1:F:395:ILE:HD13	1.88	0.56
1:E:319:VAL:HG23	1:E:333:TYR:HB2	1.88	0.56
1:B:115:HIS:HA	1:B:337:ARG:HA	1.89	0.55
1:A:202:LYS:HE3	1:A:226:GLU:HG3	1.88	0.55
1:B:129:GLY:HA3	1:B:180:ARG:HE	1.71	0.55
1:D:252:SER:HB2	1:D:271:LEU:HD22	1.89	0.55
1:B:389:LEU:O	1:B:391:VAL:N	2.36	0.55
1:B:450:ASN:O	1:B:450:ASN:ND2	2.39	0.55
1:E:194:GLU:HB2	4:E:632:HOH:O	2.06	0.54
1:C:304:ASP:OD2	4:C:615:HOH:O	2.18	0.54
1:A:313:VAL:HB	1:A:335:THR:HB	1.90	0.54
1:B:122:ARG:HG3	1:B:353:GLU:HB3	1.90	0.54
1:C:112:PHE:O	1:C:337:ARG:NH2	2.40	0.54
1:A:252:SER:HB2	1:A:271:LEU:HD22	1.89	0.54
1:B:158:ASP:O	4:B:618:HOH:O	2.19	0.54
1:B:335:THR:OG1	4:B:603:HOH:O	1.90	0.54
1:F:324:GLY:HA2	4:F:612:HOH:O	2.02	0.54
1:F:202:LYS:HE3	1:F:226:GLU:HG3	1.88	0.54
1:A:264:MET:HE2	1:A:270:GLN:HB3	1.90	0.53
1:C:148:MET:O	4:C:614:HOH:O	2.17	0.53
1:C:99:GLY:N	4:C:601:HOH:O	2.30	0.53
1:C:305:TYR:OH	4:C:613:HOH:O	2.17	0.53
1:E:129:GLY:HA3	1:E:180:ARG:HE	1.73	0.53
1:D:171:ARG:NH1	4:D:615:HOH:O	2.20	0.53
1:F:261:TYR:N	4:F:616:HOH:O	2.31	0.53
1:A:156:GLN:OE1	1:A:166:ARG:NH2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:111:TYR:OH	1:B:363:ARG:NH1	2.42	0.53
1:A:324:GLY:O	1:B:454:GLN:NE2	2.41	0.53
1:C:122:ARG:NE	1:C:353:GLU:OE1	2.42	0.52
1:F:231:LEU:HB2	1:F:344:MET:HE1	1.91	0.52
1:F:166:ARG:HB3	4:F:601:HOH:O	2.04	0.52
1:A:141:ILE:HG23	1:A:173:PRO:HB3	1.91	0.52
1:D:182:VAL:HG13	3:D:503:FAD:HM82	1.92	0.52
1:D:217:ARG:NH1	1:D:309:LEU:O	2.42	0.52
1:E:214:GLN:HA	1:E:309:LEU:HD12	1.92	0.52
1:A:405:LYS:HD2	4:A:620:HOH:O	2.08	0.51
1:D:449:TYR:HB3	4:D:609:HOH:O	2.10	0.51
1:E:217:ARG:HG3	1:E:309:LEU:HB3	1.91	0.51
1:E:426:ASN:OD1	4:E:610:HOH:O	2.19	0.51
1:A:181:GLY:CA	4:A:603:HOH:O	2.38	0.51
1:F:347:LEU:HD12	4:F:661:HOH:O	2.11	0.51
1:A:129:GLY:HA3	1:A:180:ARG:HE	1.76	0.51
1:C:103:LYS:HE3	1:C:106:SER:HB2	1.93	0.51
1:B:141:ILE:HG23	1:B:173:PRO:HB3	1.93	0.51
1:F:315:GLY:O	1:F:333:TYR:CA	2.59	0.51
1:F:180:ARG:HG2	1:F:180:ARG:NH1	2.25	0.50
1:B:313:VAL:HG21	1:B:337:ARG:HH11	1.76	0.50
1:F:450:ASN:CG	4:F:611:HOH:O	2.49	0.50
1:E:122:ARG:HB3	1:E:331:PRO:HA	1.92	0.50
1:C:202:LYS:HE3	1:C:226:GLU:HG3	1.92	0.50
1:B:103:LYS:NZ	4:B:612:HOH:O	2.04	0.50
1:C:143:MET:CE	4:C:702:HOH:O	2.46	0.50
1:A:384:ALA:N	4:A:627:HOH:O	2.45	0.50
1:D:115:HIS:HA	1:D:337:ARG:HA	1.94	0.50
1:D:102:ARG:HB3	1:D:109:ASP:HB3	1.92	0.50
1:E:122:ARG:HB2	1:E:133:THR:HG21	1.93	0.50
1:C:95:PRO:HA	4:C:601:HOH:O	1.99	0.50
1:C:111:TYR:O	4:C:616:HOH:O	2.19	0.49
1:E:219:VAL:O	1:E:219:VAL:CG1	2.60	0.49
1:E:428:LYS:NZ	4:E:621:HOH:O	2.42	0.49
1:F:181:GLY:O	3:F:503:FAD:H8A	2.12	0.49
1:A:50:ILE:HD13	1:A:68:CYS:HB3	1.95	0.49
1:E:150:GLU:HG3	1:E:201:VAL:HG13	1.94	0.49
1:C:158:ASP:HB3	1:C:161:ASP:O	2.13	0.49
1:C:187:SER:O	1:C:212:GLN:NE2	2.46	0.49
1:D:129:GLY:HA3	1:D:180:ARG:HE	1.77	0.49
1:B:184:PRO:O	1:B:185:THR:HG23	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:424:TYR:CE2	4:F:608:HOH:O	2.55	0.49
1:D:390:PHE:N	4:D:602:HOH:O	2.46	0.49
1:C:59:LYS:HB2	4:C:628:HOH:O	2.13	0.48
1:C:268:LYS:HG2	1:C:282:PRO:HA	1.95	0.48
1:A:363:ARG:HB2	1:A:412:TYR:HB2	1.94	0.48
1:D:158:ASP:HB3	1:D:161:ASP:O	2.13	0.48
1:B:408:GLU:CD	4:B:602:HOH:O	2.46	0.48
1:E:451:LYS:HE3	4:E:640:HOH:O	2.13	0.48
1:B:374:ASP:OD1	1:B:416:TYR:OH	2.29	0.48
1:B:103:LYS:CE	4:B:612:HOH:O	2.57	0.48
1:C:162:ARG:HG3	1:C:163:LEU:HD13	1.95	0.48
1:F:196:ILE:HG23	1:F:201:VAL:HB	1.95	0.48
1:F:122:ARG:HG3	1:F:133:THR:HG21	1.96	0.47
1:E:190:LEU:HD11	1:E:216:LEU:HG	1.96	0.47
1:A:71:TYR:CE2	1:A:194:GLU:HG2	2.49	0.47
1:C:328:THR:OG1	4:C:617:HOH:O	2.20	0.47
1:F:115:HIS:HA	1:F:337:ARG:HA	1.95	0.47
1:A:136:VAL:HG11	3:A:503:FAD:H4B	1.97	0.47
1:B:333:TYR:OH	4:B:603:HOH:O	2.15	0.47
1:D:388:PRO:O	4:D:602:HOH:O	2.20	0.47
1:E:302:CYS:O	1:E:421:ASN:ND2	2.39	0.47
1:D:57:PRO:HG2	1:D:76:VAL:HG21	1.96	0.47
1:E:245:ASP:OD1	1:E:249:LYS:NZ	2.48	0.47
1:D:156:GLN:O	1:D:166:ARG:CA	2.62	0.47
1:F:214:GLN:HA	1:F:309:LEU:HD12	1.97	0.47
1:A:315:GLY:C	1:A:333:TYR:HB3	2.30	0.46
1:F:424:TYR:HE2	4:F:608:HOH:O	1.95	0.46
1:C:57:PRO:HG2	1:C:76:VAL:HG21	1.96	0.46
1:D:194:GLU:HB2	4:D:637:HOH:O	2.13	0.46
1:E:181:GLY:O	3:E:503:FAD:H8A	2.15	0.46
1:B:183:LYS:O	1:B:185:THR:N	2.48	0.46
1:B:122:ARG:HB3	1:B:331:PRO:HA	1.98	0.46
1:E:120:TYR:CD1	1:E:319:VAL:HG22	2.51	0.46
1:E:71:TYR:OH	1:E:197:GLU:OE1	2.21	0.46
1:F:149:VAL:HA	1:F:203:ARG:HB3	1.98	0.46
1:F:257:THR:HG23	1:F:273:HIS:ND1	2.30	0.46
1:C:153:VAL:HG23	1:C:204:LEU:HD11	1.98	0.46
1:F:262:GLU:HA	4:F:621:HOH:O	2.15	0.46
1:A:291:LEU:HD12	1:A:294:VAL:HG11	1.98	0.45
1:F:203:ARG:NE	4:F:624:HOH:O	2.49	0.45
1:E:132:TRP:O	1:E:328:THR:CA	2.62	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:259:LEU:O	1:E:260:HIS:CD2	2.69	0.45
1:B:122:ARG:NH2	4:B:632:HOH:O	2.48	0.45
1:B:190:LEU:HD11	1:B:216:LEU:HG	1.99	0.45
1:C:231:LEU:HB2	1:C:344:MET:HE1	1.98	0.45
1:E:171:ARG:NH1	4:E:630:HOH:O	2.49	0.45
1:A:193:LEU:HA	1:A:196:ILE:HD12	1.98	0.45
1:C:275:ASP:CG	4:C:609:HOH:O	2.49	0.45
1:C:119:LEU:HD13	1:C:354:ILE:HG23	1.99	0.45
1:E:60:ASP:CB	4:E:613:HOH:O	2.61	0.45
1:E:216:LEU:O	1:E:220:GLU:N	2.50	0.45
1:F:107:LEU:HA	1:F:110:THR:HG22	1.98	0.45
1:D:398:ILE:HD11	1:E:399:LEU:HD12	1.99	0.45
1:A:192:THR:O	1:A:196:ILE:HG13	2.17	0.45
1:B:171:ARG:HB2	4:B:640:HOH:O	2.16	0.45
1:C:214:GLN:HA	1:C:309:LEU:HD12	1.99	0.45
1:F:185:THR:HG22	1:F:244:LEU:HD12	1.97	0.45
1:E:234:ASN:HD22	1:E:315:GLY:HA3	1.82	0.45
1:F:289:ASN:HA	1:F:290:ASP:HA	1.70	0.45
1:F:454:GLN:OE1	1:F:454:GLN:N	2.48	0.45
1:A:117:GLU:CB	4:A:610:HOH:O	2.17	0.45
1:C:44:ARG:NH2	1:C:197:GLU:OE2	2.41	0.45
1:D:68:CYS:SG	1:D:73:ILE:HG13	2.57	0.45
1:E:115:HIS:HA	1:E:337:ARG:HA	1.99	0.45
1:B:54:GLY:O	1:B:55:THR:CB	2.65	0.45
1:C:422:TYR:O	1:C:426:ASN:ND2	2.34	0.45
1:C:340:ARG:O	1:C:344:MET:HG3	2.16	0.44
1:C:364:ARG:HD2	4:C:603:HOH:O	2.17	0.44
1:D:122:ARG:HB2	1:D:133:THR:HG21	1.98	0.44
1:B:174:GLU:OE1	1:B:174:GLU:N	2.49	0.44
1:E:112:PHE:O	1:E:337:ARG:NH2	2.50	0.44
1:B:217:ARG:HG3	1:B:309:LEU:HB3	1.99	0.44
1:D:102:ARG:NH2	4:D:612:HOH:O	2.09	0.44
1:D:323:SER:C	1:E:368:THR:HG21	2.36	0.44
1:A:122:ARG:NH2	1:A:353:GLU:OE1	2.49	0.44
1:D:259:LEU:O	1:D:260:HIS:CD2	2.70	0.44
1:E:371:VAL:HG12	1:E:416:TYR:HD1	1.82	0.44
1:A:260:HIS:O	1:A:272:LYS:N	2.46	0.44
1:C:313:VAL:HG21	1:C:337:ARG:HH11	1.82	0.44
1:E:377:ALA:HA	4:E:652:HOH:O	2.17	0.44
1:A:191:ASN:CA	4:A:613:HOH:O	2.66	0.44
1:E:68:CYS:SG	1:E:73:ILE:HG13	2.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:136:VAL:HG11	3:D:503:FAD:H4B	1.98	0.44
1:A:259:LEU:HD22	1:A:260:HIS:CE1	2.53	0.43
1:B:81:ALA:HB1	1:B:87:MET:HG2	2.00	0.43
1:D:187:SER:O	1:D:212:GLN:NE2	2.50	0.43
1:F:71:TYR:CE2	1:F:194:GLU:HG3	2.53	0.43
1:C:115:HIS:HA	1:C:337:ARG:HA	2.00	0.43
1:E:81:ALA:HB1	1:E:87:MET:HG2	1.99	0.43
1:F:217:ARG:HG3	1:F:309:LEU:HB3	2.00	0.43
1:F:427:ARG:NH2	1:F:458:MET:O	2.51	0.43
1:C:136:VAL:HG11	3:C:503:FAD:H4B	2.00	0.43
1:E:252:SER:HB2	1:E:271:LEU:HD22	1.99	0.43
1:E:452:ASN:OD1	4:E:611:HOH:O	2.21	0.43
1:F:138:THR:HG22	1:F:348:VAL:HG11	2.00	0.43
1:F:158:ASP:CA	4:F:601:HOH:O	2.51	0.43
1:D:444:LYS:O	1:D:448:MET:HG3	2.18	0.43
1:F:102:ARG:NE	1:F:113:GLY:HA2	2.34	0.43
1:F:202:LYS:NZ	1:F:224:ASN:O	2.43	0.43
1:C:181:GLY:O	3:C:503:FAD:H8A	2.19	0.43
1:F:144:LEU:HD23	1:F:149:VAL:HG23	2.00	0.43
1:A:234:ASN:HD22	1:A:306:THR:HA	1.84	0.43
1:E:121:ALA:HB3	1:E:334:ILE:HD12	1.99	0.43
1:F:133:THR:OG1	1:F:332:GLN:OE1	2.27	0.43
1:A:118:GLN:NE2	1:A:333:TYR:OH	2.50	0.43
1:D:425:VAL:O	1:D:429:TRP:HB2	2.19	0.43
1:A:181:GLY:O	3:A:503:FAD:H8A	2.18	0.43
1:C:158:ASP:OD1	1:C:160:GLU:HG2	2.19	0.43
3:C:503:FAD:H9	3:C:503:FAD:H1'1	1.85	0.43
1:A:71:TYR:OH	1:A:197:GLU:OE1	2.27	0.43
1:B:102:ARG:HB3	1:B:109:ASP:HB3	2.01	0.43
1:A:269:VAL:HB	1:A:281:VAL:HG13	2.01	0.42
1:D:234:ASN:HD22	1:D:306:THR:HA	1.84	0.42
1:D:313:VAL:HB	1:D:335:THR:HB	2.01	0.42
1:E:438:MET:HA	1:E:439:PRO:HD3	1.90	0.42
1:A:214:GLN:OE1	4:A:614:HOH:O	2.21	0.42
1:C:143:MET:HG2	1:C:148:MET:HE2	2.01	0.42
1:D:290:ASP:O	4:D:616:HOH:O	2.21	0.42
1:D:390:PHE:HE2	1:E:284:PHE:HB3	1.84	0.42
1:E:85:ASP:O	1:E:88:SER:OG	2.24	0.42
1:D:390:PHE:CE2	1:E:284:PHE:HB3	2.54	0.42
1:F:161:ASP:OD2	1:F:164:SER:OG	2.30	0.42
1:C:164:SER:HA	1:C:165:PRO:HD3	1.81	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:177:LEU:O	1:C:180:ARG:HD3	2.20	0.42
1:C:259:LEU:HD22	1:C:260:HIS:CD2	2.55	0.42
1:C:259:LEU:HG	1:C:274:LEU:HD23	2.01	0.42
1:E:287:PRO:HA	1:E:386:PRO:HG3	2.02	0.42
1:A:435:ASN:O	1:A:443:LYS:NZ	2.47	0.42
1:D:156:GLN:O	1:D:166:ARG:CB	2.66	0.42
1:D:346:SER:HA	1:D:349:GLU:HG3	2.02	0.42
1:B:315:GLY:O	1:B:333:TYR:N	2.49	0.42
1:F:122:ARG:HB2	1:F:331:PRO:HA	2.00	0.42
1:A:65:CYS:HB2	1:A:212:GLN:HG2	2.02	0.42
1:B:193:LEU:HA	1:B:196:ILE:HD12	2.01	0.42
3:E:503:FAD:H9	3:E:503:FAD:H1'1	1.88	0.42
1:F:259:LEU:O	1:F:260:HIS:CD2	2.73	0.42
1:B:214:GLN:HA	1:B:309:LEU:HD12	2.02	0.41
1:B:235:CYS:HA	3:B:503:FAD:N5	2.35	0.41
1:D:424:TYR:CE2	1:D:428:LYS:HD2	2.54	0.41
1:E:224:ASN:HB3	4:E:658:HOH:O	2.19	0.41
1:A:187:SER:O	1:A:212:GLN:NE2	2.54	0.41
1:B:86:GLY:HA3	1:B:437:HIS:CD2	2.50	0.41
1:B:251:ALA:O	1:B:281:VAL:HG21	2.20	0.41
1:E:91:GLU:OE2	1:E:440:SER:HB3	2.20	0.41
1:A:70:THR:HB	1:A:194:GLU:HG3	2.01	0.41
1:D:143:MET:HB3	1:D:149:VAL:HG22	2.02	0.41
3:F:503:FAD:H9	3:F:503:FAD:H1'1	1.85	0.41
1:B:150:GLU:HG3	1:B:203:ARG:HB2	2.02	0.41
1:C:160:GLU:HA	4:C:662:HOH:O	2.20	0.41
1:F:315:GLY:O	1:F:333:TYR:N	2.53	0.41
1:C:326:ASN:HB2	4:C:617:HOH:O	2.20	0.41
1:F:136:VAL:HG11	3:F:503:FAD:H4B	2.02	0.41
1:B:394:ILE:HD13	1:C:395:ILE:HD13	2.01	0.41
1:F:122:ARG:O	1:F:353:GLU:N	2.52	0.41
1:A:193:LEU:CG	4:A:613:HOH:O	2.21	0.41
1:A:319:VAL:HA	1:A:320:PRO:HD3	1.97	0.41
1:B:136:VAL:HG11	3:B:503:FAD:H4B	2.03	0.41
1:F:82:PHE:CZ	1:F:298:SER:HB2	2.56	0.41
1:A:193:LEU:CB	4:A:613:HOH:O	2.64	0.41
1:B:184:PRO:O	1:B:244:LEU:HG	2.20	0.41
1:B:366:PHE:CE1	1:B:399:LEU:HD12	2.55	0.41
1:D:281:VAL:HA	1:D:282:PRO:HD3	1.90	0.41
1:D:358:ILE:O	1:D:406:GLY:HA3	2.21	0.41
3:D:503:FAD:H9	3:D:503:FAD:H1'1	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:394:ILE:H	1:E:394:ILE:HG12	1.59	0.41
1:A:366:PHE:HE1	1:A:399:LEU:HG	1.84	0.41
1:B:301:SER:O	1:B:437:HIS:HE1	2.04	0.41
1:C:59:LYS:CB	4:C:628:HOH:O	2.68	0.41
1:F:239:GLY:HA2	1:F:296:ALA:HB2	2.03	0.41
1:A:385:GLN:HA	1:A:386:PRO:HD3	1.85	0.40
1:B:132:TRP:CZ3	1:B:330:HIS:HB3	2.56	0.40
1:F:68:CYS:SG	1:F:73:ILE:HG13	2.61	0.40
1:A:452:ASN:HB2	1:A:454:GLN:NE2	2.36	0.40
1:B:65:CYS:HB2	1:B:212:GLN:HG2	2.03	0.40
1:E:317:MET:HB3	4:E:612:HOH:O	2.21	0.40
1:B:53:GLY:HA2	1:B:54:GLY:HA3	1.61	0.40
1:C:190:LEU:HG	1:C:193:LEU:HD11	2.04	0.40
1:D:359:SER:HB2	1:D:407:LEU:HB2	2.04	0.40
1:E:341:GLY:HA2	1:E:344:MET:HE3	2.03	0.40
1:B:82:PHE:CZ	1:B:298:SER:HB2	2.57	0.40
1:C:221:GLN:HB2	4:C:612:HOH:O	2.21	0.40
1:D:153:VAL:HG23	1:D:204:LEU:HD11	2.04	0.40
1:C:319:VAL:HA	1:C:320:PRO:HD3	1.95	0.40
1:D:322:TYR:CE1	1:D:331:PRO:HG2	2.56	0.40

All (7) 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)
1:B:53:GLY:O	1:C:350:ASN:CB[1_565]	1.68	0.52
4:D:622:HOH:O	4:E:705:HOH:O[3_555]	1.87	0.33
4:A:681:HOH:O	4:D:749:HOH:O[1_655]	1.95	0.25
4:A:621:HOH:O	4:E:666:HOH:O[1_655]	2.00	0.20
4:D:720:HOH:O	4:E:700:HOH:O[3_555]	2.03	0.17
4:C:689:HOH:O	4:E:689:HOH:O[3_545]	2.13	0.07
4:C:689:HOH:O	4:E:619:HOH:O[3_545]	2.16	0.04

## 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	411/437 (94%)	391 (95%)	17 (4%)	3 (1%)	22	46
1	B	410/437 (94%)	394 (96%)	14 (3%)	2 (0%)	29	54
1	C	420/437 (96%)	403 (96%)	17 (4%)	0	100	100
1	D	407/437 (93%)	393 (97%)	13 (3%)	1 (0%)	47	73
1	E	402/437 (92%)	387 (96%)	15 (4%)	0	100	100
1	F	412/437 (94%)	392 (95%)	19 (5%)	1 (0%)	47	73
All	All	2462/2622 (94%)	2360 (96%)	95 (4%)	7 (0%)	41	66

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	53	GLY
1	B	385	GLN
1	A	48	ARG
1	A	385	GLN
1	B	55	THR
1	D	48	ARG
1	A	54	GLY

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	348/378 (92%)	337 (97%)	11 (3%)	39	68
1	B	345/378 (91%)	336 (97%)	9 (3%)	46	75
1	C	358/378 (95%)	344 (96%)	14 (4%)	32	61
1	D	345/378 (91%)	332 (96%)	13 (4%)	33	62
1	E	338/378 (89%)	329 (97%)	9 (3%)	44	74
1	F	349/378 (92%)	338 (97%)	11 (3%)	39	68
All	All	2083/2268 (92%)	2016 (97%)	67 (3%)	39	68



All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	TYR
1	A	89	ARG
1	A	217	ARG
1	A	244	LEU
1	A	259	LEU
1	A	291	LEU
1	A	305	TYR
1	A	312	LEU
1	A	337	ARG
1	A	432	GLN
1	A	457	LYS
1	B	171	ARG
1	B	190	LEU
1	B	216	LEU
1	B	228	LEU
1	B	244	LEU
1	B	259	LEU
1	B	305	TYR
1	B	319	VAL
1	B	363	ARG
1	C	71	TYR
1	C	83	LEU
1	C	180	ARG
1	C	183	LYS
1	C	185	THR
1	C	209	VAL
1	C	241	ARG
1	C	244	LEU
1	C	259	LEU
1	C	305	TYR
1	C	317	MET
1	C	347	LEU
1	C	348	VAL
1	C	358	ILE
1	D	83	LEU
1	D	171	ARG
1	D	190	LEU
1	D	217	ARG
1	D	253	LYS
1	D	259	LEU
1	D	312	LEU
1	D	340	ARG

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Mol	Chain	Res	Type
1	D	358	ILE
1	D	364	ARG
1	D	389	LEU
1	D	433	ARG
1	D	438	MET
1	E	185	THR
1	E	216	LEU
1	E	228	LEU
1	E	244	LEU
1	E	256	GLU
1	E	259	LEU
1	E	312	LEU
1	E	317	MET
1	E	394	ILE
1	F	128	GLU
1	F	185	THR
1	F	205	LEU
1	F	209	VAL
1	F	244	LEU
1	F	259	LEU
1	F	305	TYR
1	F	312	LEU
1	F	348	VAL
1	F	397	PHE
1	F	432	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	118	GLN
1	A	260	HIS
1	B	437	HIS
1	D	116	GLN
1	E	260	HIS
1	F	432	GLN
1	F	435	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

18 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
2	SF4	A	501	1	0,12,12	-	-	-		
2	SF4	D	501	1	0,12,12	-	-	-		
2	SF4	D	502	1	0,12,12	-	-	-		
2	SF4	A	502	1	0,12,12	-	-	-		
2	SF4	B	502	1	0,12,12	-	-	-		
3	FAD	E	503	-	53,58,58	2.03	16 (30%)	68,89,89	1.34	9 (13%)
2	SF4	F	502	1	0,12,12	-	-	-		
2	SF4	B	501	1	0,12,12	-	-	-		
2	SF4	C	501	1	0,12,12	-	-	-		
2	SF4	F	501	1	0,12,12	-	-	-		
3	FAD	B	503	-	53,58,58	2.03	16 (30%)	68,89,89	1.37	11 (16%)
3	FAD	F	503	-	53,58,58	2.03	16 (30%)	68,89,89	1.40	11 (16%)
2	SF4	C	502	1	0,12,12	-	-	-		
3	FAD	D	503	-	53,58,58	2.03	16 (30%)	68,89,89	1.38	11 (16%)
2	SF4	E	501	1	0,12,12	-	-	-		
2	SF4	E	502	1	0,12,12	-	-	-		
3	FAD	A	503	-	53,58,58	2.03	16 (30%)	68,89,89	1.37	11 (16%)
3	FAD	C	503	-	53,58,58	2.02	16 (30%)	68,89,89	1.39	10 (14%)

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	SF4	A	501	1	-	-	0/6/5/5
2	SF4	D	501	1	-	-	0/6/5/5
2	SF4	D	502	1	-	-	0/6/5/5
3	FAD	C	503	-	-	4/30/50/50	0/6/6/6
2	SF4	A	502	1	-	-	0/6/5/5
2	SF4	B	502	1	-	-	0/6/5/5
2	SF4	E	502	1	-	-	0/6/5/5
2	SF4	F	502	1	-	-	0/6/5/5
2	SF4	B	501	1	-	-	0/6/5/5
2	SF4	C	501	1	-	-	0/6/5/5
3	FAD	F	503	-	-	2/30/50/50	0/6/6/6
2	SF4	F	501	1	-	-	0/6/5/5
2	SF4	C	502	1	-	-	0/6/5/5
3	FAD	D	503	-	-	7/30/50/50	0/6/6/6
2	SF4	E	501	1	-	-	0/6/5/5
3	FAD	A	503	-	-	1/30/50/50	0/6/6/6
3	FAD	B	503	-	-	3/30/50/50	0/6/6/6
3	FAD	E	503	-	-	2/30/50/50	0/6/6/6

All (96) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	503	FAD	C5X-N5	5.86	1.50	1.39
3	D	503	FAD	C5X-N5	5.83	1.50	1.39
3	E	503	FAD	C2B-C1B	-5.79	1.45	1.53
3	D	503	FAD	C2B-C1B	-5.79	1.45	1.53
3	C	503	FAD	C5X-N5	5.78	1.50	1.39
3	B	503	FAD	C5X-N5	5.77	1.50	1.39
3	A	503	FAD	C2B-C1B	-5.77	1.45	1.53
3	A	503	FAD	C5X-N5	5.75	1.50	1.39
3	F	503	FAD	C2B-C1B	-5.73	1.45	1.53
3	B	503	FAD	C2B-C1B	-5.70	1.45	1.53
3	E	503	FAD	C5X-N5	5.69	1.50	1.39
3	C	503	FAD	C2B-C1B	-5.69	1.45	1.53
3	F	503	FAD	C2-N1	4.63	1.47	1.36
3	E	503	FAD	C2-N1	4.62	1.47	1.36
3	B	503	FAD	C2-N1	4.62	1.47	1.36
3	A	503	FAD	C2-N1	4.60	1.47	1.36
3	C	503	FAD	C2-N1	4.60	1.47	1.36
3	D	503	FAD	C2-N1	4.52	1.47	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	503	FAD	O4B-C1B	4.08	1.46	1.41
3	B	503	FAD	O4B-C1B	4.08	1.46	1.41
3	D	503	FAD	O4B-C1B	3.98	1.46	1.41
3	C	503	FAD	O4B-C1B	3.96	1.46	1.41
3	A	503	FAD	O4B-C1B	3.95	1.46	1.41
3	F	503	FAD	O4B-C1B	3.88	1.46	1.41
3	E	503	FAD	C2B-C3B	-3.87	1.42	1.53
3	D	503	FAD	C2B-C3B	-3.85	1.42	1.53
3	A	503	FAD	C2B-C3B	-3.84	1.42	1.53
3	C	503	FAD	C2B-C3B	-3.81	1.42	1.53
3	F	503	FAD	C2B-C3B	-3.79	1.43	1.53
3	B	503	FAD	C2B-C3B	-3.73	1.43	1.53
3	C	503	FAD	C2A-N3A	3.23	1.37	1.32
3	B	503	FAD	C2A-N3A	3.21	1.37	1.32
3	F	503	FAD	C2A-N3A	3.20	1.37	1.32
3	A	503	FAD	C2A-N3A	3.17	1.37	1.32
3	E	503	FAD	C2A-N3A	3.16	1.37	1.32
3	D	503	FAD	C2A-N3A	3.11	1.37	1.32
3	D	503	FAD	C6A-N6A	3.04	1.45	1.34
3	B	503	FAD	C6A-N6A	3.03	1.45	1.34
3	C	503	FAD	C6A-N6A	3.02	1.45	1.34
3	E	503	FAD	C6A-N6A	3.00	1.45	1.34
3	F	503	FAD	C6A-N6A	2.99	1.45	1.34
3	A	503	FAD	C6A-N6A	2.98	1.44	1.34
3	D	503	FAD	C3B-C4B	-2.81	1.45	1.53
3	C	503	FAD	C3B-C4B	-2.78	1.45	1.53
3	F	503	FAD	C3B-C4B	-2.76	1.45	1.53
3	E	503	FAD	C3B-C4B	-2.74	1.46	1.53
3	A	503	FAD	C3B-C4B	-2.74	1.46	1.53
3	B	503	FAD	C3B-C4B	-2.72	1.46	1.53
3	B	503	FAD	O3'-C3'	-2.65	1.36	1.43
3	D	503	FAD	O3'-C3'	-2.62	1.36	1.43
3	E	503	FAD	O4'-C4'	-2.61	1.37	1.43
3	B	503	FAD	O4'-C4'	-2.61	1.37	1.43
3	A	503	FAD	O3'-C3'	-2.58	1.36	1.43
3	F	503	FAD	O3'-C3'	-2.57	1.36	1.43
3	A	503	FAD	O4'-C4'	-2.57	1.37	1.43
3	D	503	FAD	O4'-C4'	-2.56	1.37	1.43
3	C	503	FAD	O3'-C3'	-2.55	1.37	1.43
3	E	503	FAD	O3'-C3'	-2.55	1.37	1.43
3	C	503	FAD	O4'-C4'	-2.52	1.38	1.43
3	B	503	FAD	C10-N10	2.50	1.42	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	503	FAD	O4'-C4'	-2.49	1.38	1.43
3	A	503	FAD	C10-N10	2.49	1.42	1.37
3	C	503	FAD	C10-N10	2.49	1.42	1.37
3	F	503	FAD	C1'-C2'	-2.46	1.49	1.52
3	E	503	FAD	C10-N10	2.46	1.42	1.37
3	F	503	FAD	C10-N10	2.42	1.42	1.37
3	B	503	FAD	C1'-C2'	-2.41	1.49	1.52
3	D	503	FAD	C1'-C2'	-2.40	1.49	1.52
3	A	503	FAD	C4X-C10	2.40	1.51	1.44
3	E	503	FAD	C1'-C2'	-2.39	1.49	1.52
3	B	503	FAD	C4X-C10	2.38	1.51	1.44
3	D	503	FAD	C4X-C10	2.37	1.51	1.44
3	E	503	FAD	C4X-C10	2.36	1.51	1.44
3	C	503	FAD	C4X-C10	2.36	1.51	1.44
3	C	503	FAD	C1'-C2'	-2.34	1.49	1.52
3	F	503	FAD	C4X-C10	2.33	1.51	1.44
3	D	503	FAD	C4'-C3'	-2.32	1.49	1.53
3	D	503	FAD	O2'-C2'	-2.31	1.38	1.43
3	A	503	FAD	C1'-C2'	-2.30	1.49	1.52
3	F	503	FAD	O2'-C2'	-2.30	1.38	1.43
3	B	503	FAD	O2'-C2'	-2.29	1.38	1.43
3	C	503	FAD	O2'-C2'	-2.27	1.38	1.43
3	D	503	FAD	C10-N10	2.25	1.42	1.37
3	E	503	FAD	O2'-C2'	-2.25	1.38	1.43
3	D	503	FAD	C4X-N5	2.25	1.35	1.30
3	A	503	FAD	O2'-C2'	-2.24	1.38	1.43
3	E	503	FAD	C4'-C3'	-2.22	1.49	1.53
3	F	503	FAD	C4X-N5	2.19	1.35	1.30
3	A	503	FAD	C4X-N5	2.17	1.35	1.30
3	C	503	FAD	C4X-N5	2.16	1.34	1.30
3	F	503	FAD	C4'-C3'	-2.15	1.49	1.53
3	B	503	FAD	C4'-C3'	-2.15	1.49	1.53
3	B	503	FAD	C4X-N5	2.13	1.34	1.30
3	A	503	FAD	C4'-C3'	-2.12	1.49	1.53
3	E	503	FAD	C4X-N5	2.07	1.34	1.30
3	C	503	FAD	C4'-C3'	-2.01	1.49	1.53

All (63) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	503	FAD	N3A-C2A-N1A	-5.51	120.07	128.68
3	B	503	FAD	N3A-C2A-N1A	-5.43	120.19	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	503	FAD	N3A-C2A-N1A	-5.42	120.21	128.68
3	F	503	FAD	N3A-C2A-N1A	-5.40	120.23	128.68
3	E	503	FAD	N3A-C2A-N1A	-5.40	120.24	128.68
3	C	503	FAD	N3A-C2A-N1A	-5.32	120.37	128.68
3	F	503	FAD	C3B-C2B-C1B	3.69	106.54	100.98
3	C	503	FAD	C3B-C2B-C1B	3.66	106.49	100.98
3	B	503	FAD	C3B-C2B-C1B	3.62	106.42	100.98
3	D	503	FAD	P-O3P-PA	-3.25	121.68	132.83
3	A	503	FAD	C3B-C2B-C1B	3.21	105.81	100.98
3	A	503	FAD	P-O3P-PA	-3.05	122.36	132.83
3	C	503	FAD	P-O3P-PA	-3.05	122.37	132.83
3	D	503	FAD	C3B-C2B-C1B	2.99	105.48	100.98
3	B	503	FAD	P-O3P-PA	-2.98	122.59	132.83
3	E	503	FAD	C3B-C2B-C1B	2.90	105.35	100.98
3	F	503	FAD	P-O3P-PA	-2.86	123.00	132.83
3	E	503	FAD	P-O3P-PA	-2.82	123.14	132.83
3	F	503	FAD	C4X-C4-N3	2.80	120.30	113.19
3	F	503	FAD	C4-N3-C2	-2.77	120.53	125.64
3	C	503	FAD	C4-N3-C2	-2.76	120.54	125.64
3	C	503	FAD	C4X-C4-N3	2.74	120.14	113.19
3	A	503	FAD	C4-N3-C2	-2.73	120.60	125.64
3	B	503	FAD	C4-N3-C2	-2.73	120.60	125.64
3	E	503	FAD	C4-N3-C2	-2.70	120.66	125.64
3	B	503	FAD	C4X-C4-N3	2.65	119.91	113.19
3	A	503	FAD	C4X-C4-N3	2.64	119.91	113.19
3	D	503	FAD	C4X-C4-N3	2.64	119.90	113.19
3	D	503	FAD	C4-N3-C2	-2.64	120.77	125.64
3	E	503	FAD	C4X-C4-N3	2.62	119.84	113.19
3	E	503	FAD	O4-C4-C4X	-2.61	119.68	126.60
3	B	503	FAD	O4-C4-C4X	-2.53	119.88	126.60
3	D	503	FAD	O4-C4-C4X	-2.53	119.89	126.60
3	C	503	FAD	C2B-C3B-C4B	2.52	107.54	102.64
3	F	503	FAD	O4-C4-C4X	-2.51	119.93	126.60
3	C	503	FAD	O4-C4-C4X	-2.50	119.98	126.60
3	F	503	FAD	C2B-C3B-C4B	2.45	107.40	102.64
3	A	503	FAD	O4-C4-C4X	-2.43	120.14	126.60
3	D	503	FAD	C4-C4X-N5	2.42	121.68	118.23
3	F	503	FAD	C4-C4X-N5	2.41	121.67	118.23
3	B	503	FAD	C2B-C3B-C4B	2.41	107.33	102.64
3	C	503	FAD	C4-C4X-N5	2.31	121.53	118.23
3	E	503	FAD	C4A-C5A-N7A	-2.30	107.00	109.40
3	A	503	FAD	C4-C4X-N5	2.30	121.51	118.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	503	FAD	C2B-C3B-C4B	2.25	107.02	102.64
3	D	503	FAD	C4A-C5A-N7A	-2.22	107.08	109.40
3	F	503	FAD	C4'-C3'-C2'	-2.21	108.77	113.36
3	F	503	FAD	C4A-C5A-N7A	-2.21	107.10	109.40
3	C	503	FAD	C4A-C5A-N7A	-2.20	107.11	109.40
3	A	503	FAD	C4'-C3'-C2'	-2.16	108.87	113.36
3	A	503	FAD	C10-C4X-N5	-2.15	120.29	124.86
3	B	503	FAD	C4A-C5A-N7A	-2.15	107.16	109.40
3	D	503	FAD	C2B-C3B-C4B	2.14	106.80	102.64
3	D	503	FAD	C10-C4X-N5	-2.11	120.37	124.86
3	A	503	FAD	C4A-C5A-N7A	-2.11	107.20	109.40
3	E	503	FAD	C2B-C3B-C4B	2.10	106.72	102.64
3	B	503	FAD	C4-C4X-N5	2.09	121.21	118.23
3	C	503	FAD	C10-C4X-N5	-2.08	120.44	124.86
3	F	503	FAD	C10-C4X-N5	-2.07	120.45	124.86
3	D	503	FAD	C5'-C4'-C3'	-2.06	108.22	112.20
3	B	503	FAD	C10-C4X-N5	-2.05	120.50	124.86
3	B	503	FAD	C4'-C3'-C2'	-2.02	109.16	113.36
3	E	503	FAD	C10-C4X-N5	-2.00	120.60	124.86

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	503	FAD	N10-C1'-C2'-O2'
3	D	503	FAD	C3'-C4'-C5'-O5'
3	D	503	FAD	O4'-C4'-C5'-O5'
3	D	503	FAD	C5'-O5'-P-O1P
3	D	503	FAD	C5'-O5'-P-O2P
3	D	503	FAD	C5'-O5'-P-O3P
3	C	503	FAD	C5B-O5B-PA-O3P
3	B	503	FAD	N10-C1'-C2'-O2'
3	C	503	FAD	N10-C1'-C2'-O2'
3	B	503	FAD	O4B-C4B-C5B-O5B
3	C	503	FAD	PA-O3P-P-O1P
3	B	503	FAD	C5B-O5B-PA-O3P
3	C	503	FAD	O4B-C4B-C5B-O5B
3	D	503	FAD	O4B-C4B-C5B-O5B
3	E	503	FAD	O4B-C4B-C5B-O5B
3	F	503	FAD	O4B-C4B-C5B-O5B
3	E	503	FAD	PA-O3P-P-O1P
3	A	503	FAD	O4B-C4B-C5B-O5B

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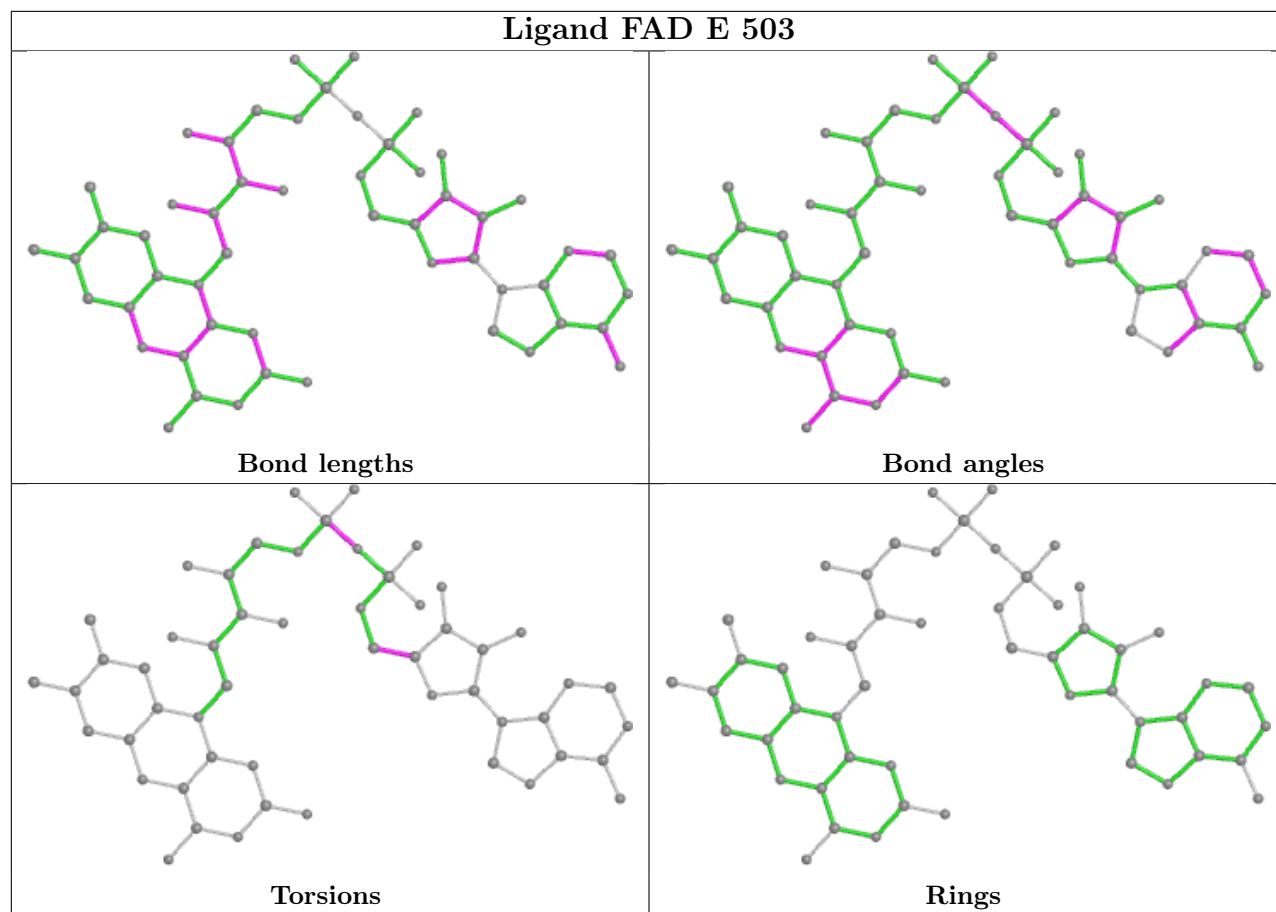
Mol	Chain	Res	Type	Atoms
3	F	503	FAD	N10-C1'-C2'-O2'

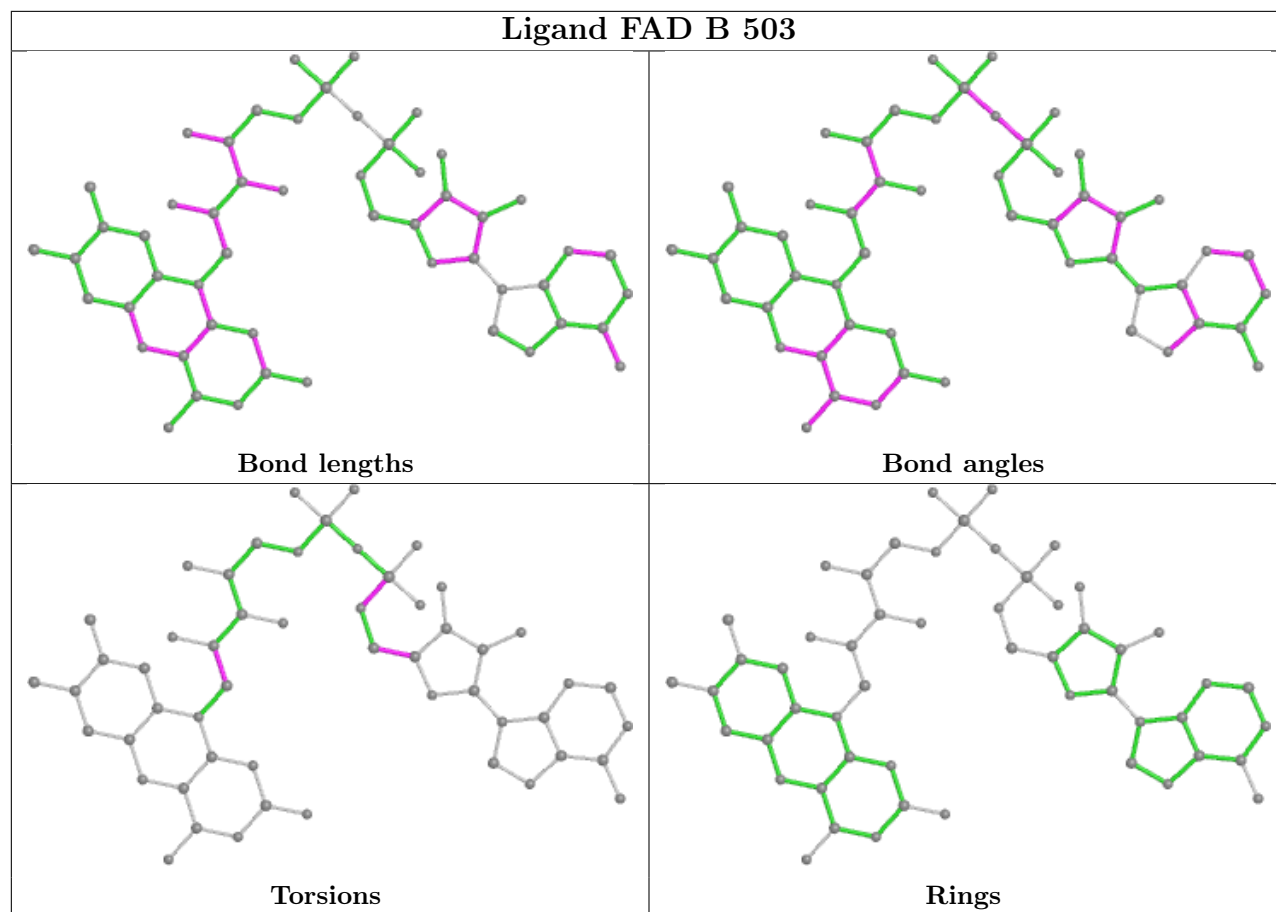
There are no ring outliers.

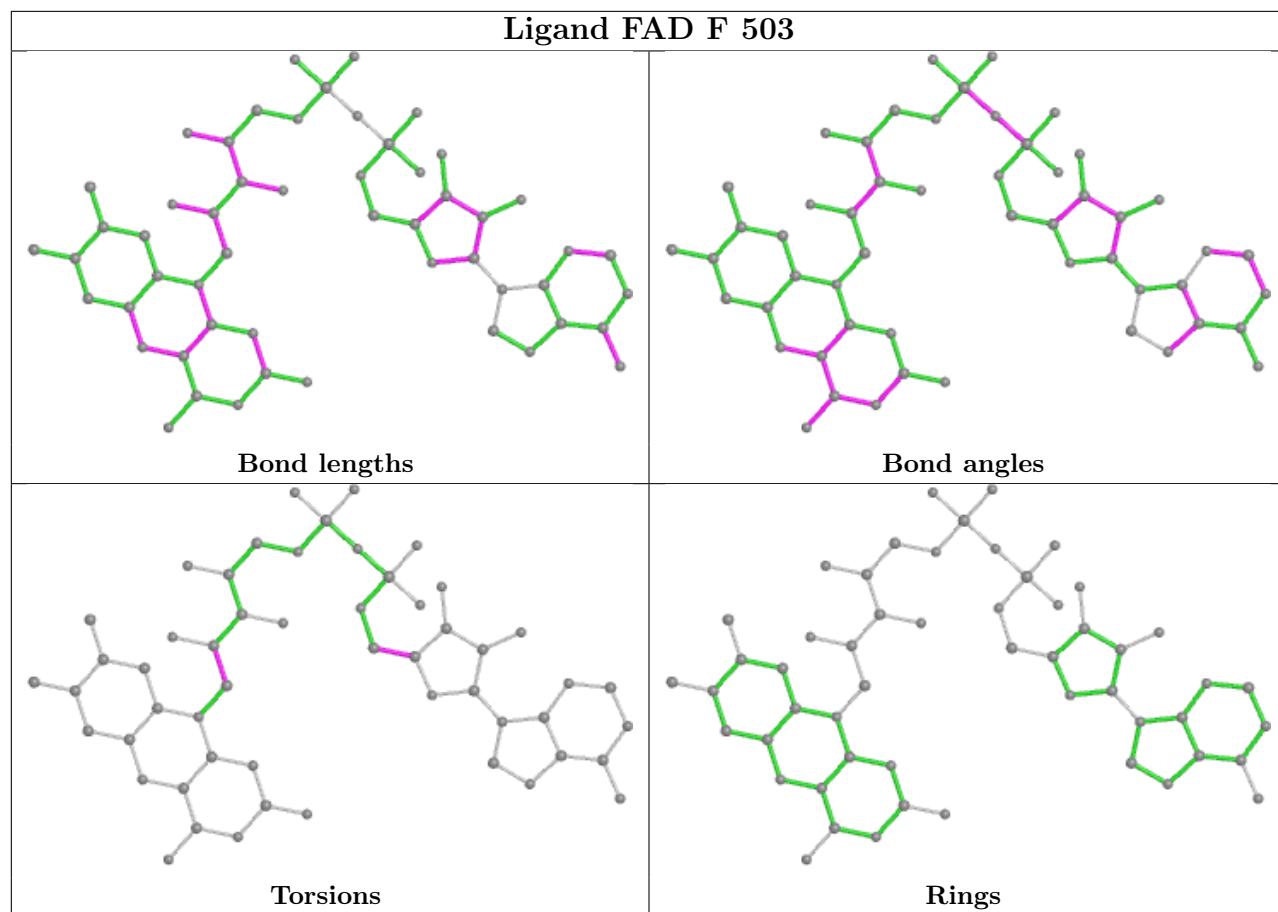
7 monomers are involved in 21 short contacts:

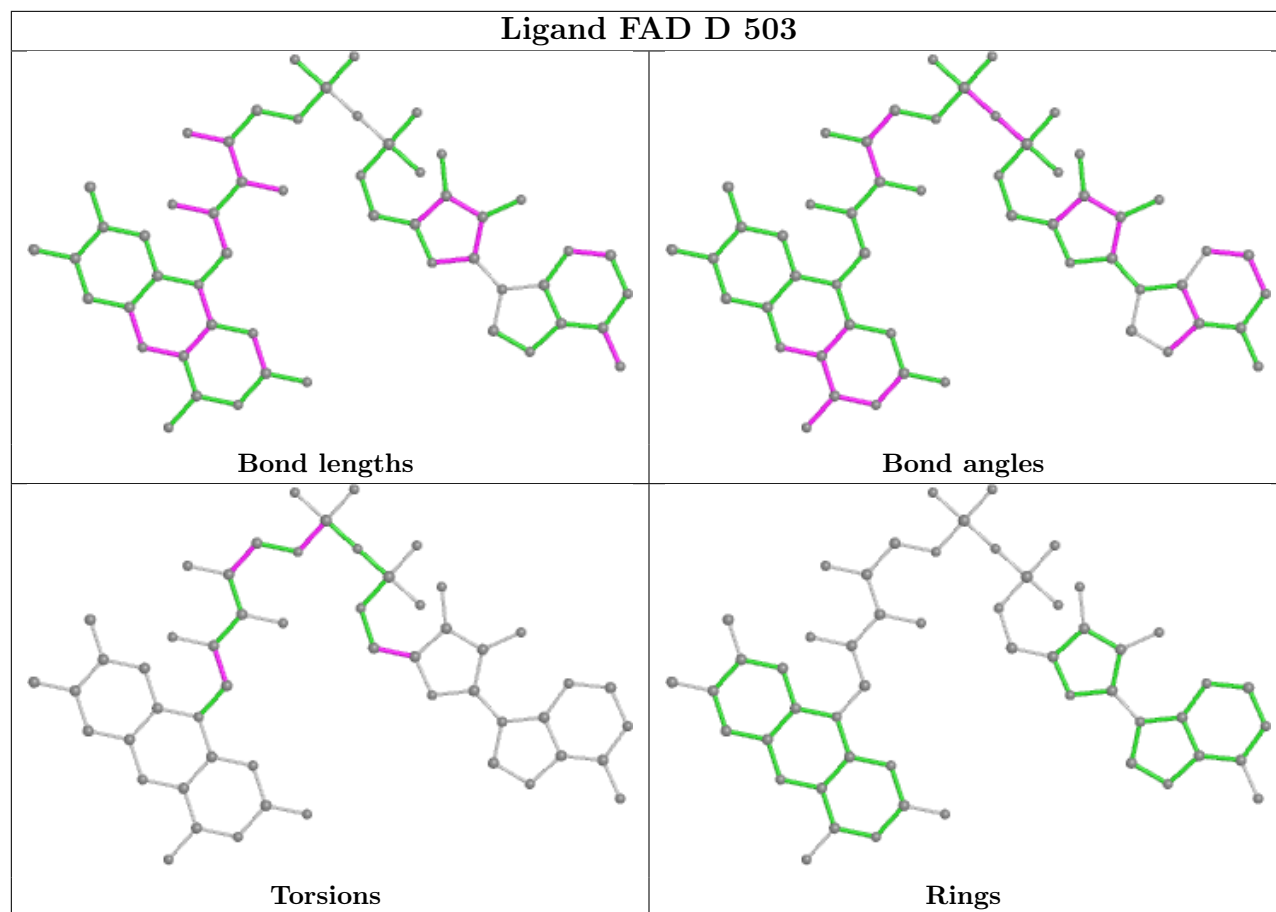
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	503	FAD	3	0
2	B	501	SF4	1	0
3	B	503	FAD	2	0
3	F	503	FAD	4	0
3	D	503	FAD	4	0
3	A	503	FAD	3	0
3	C	503	FAD	4	0

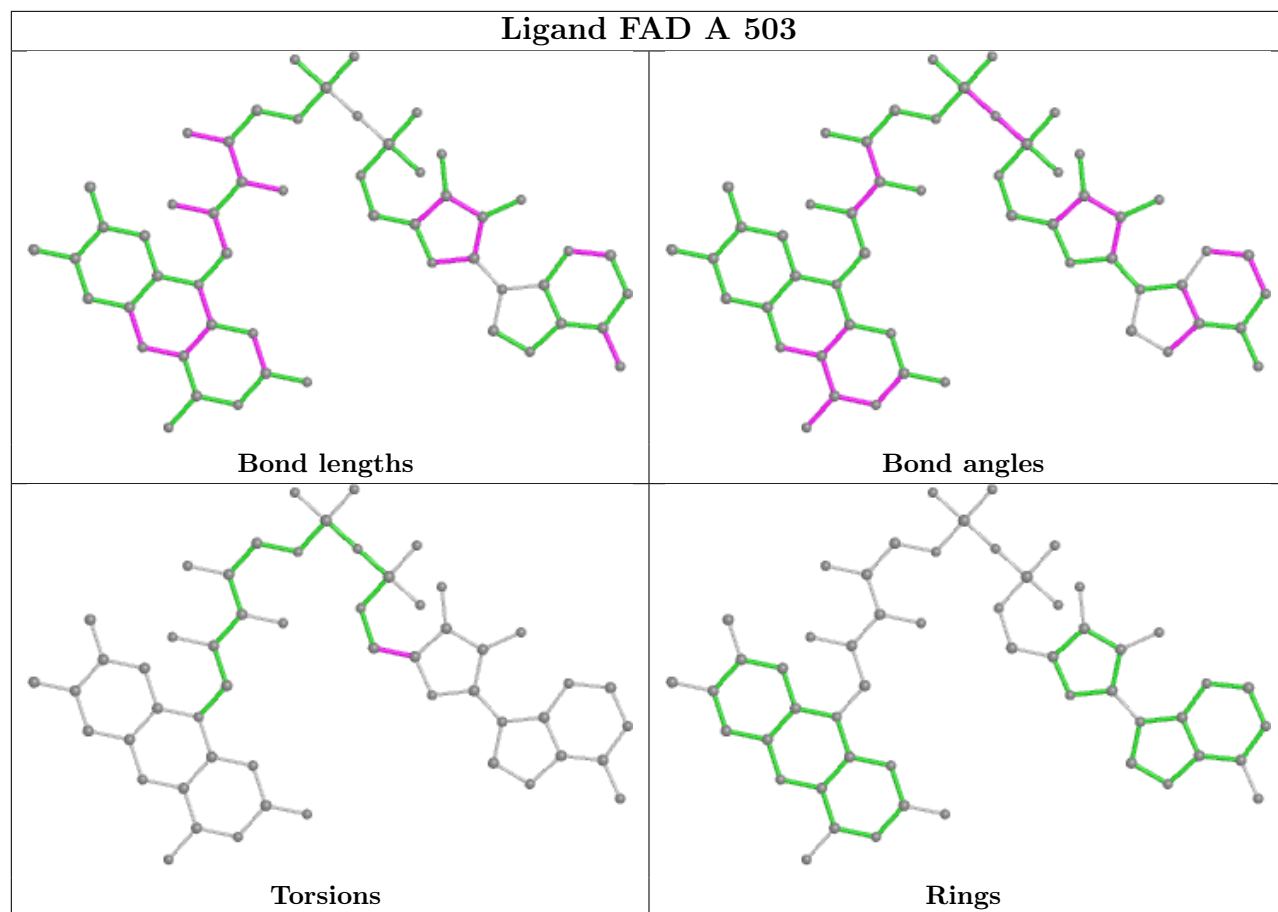
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

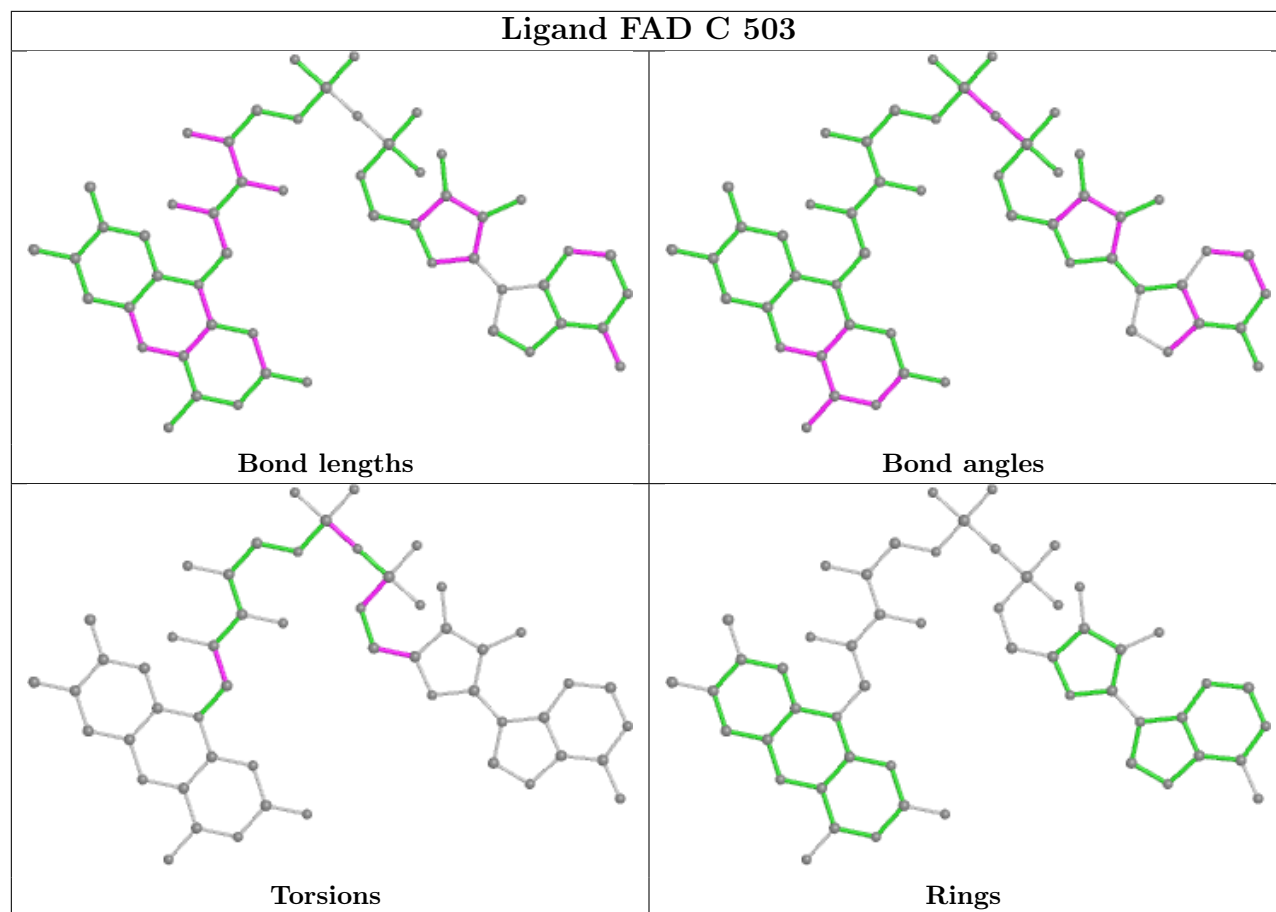












## 5.7 Other polymers [i](#)

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	414/437 (94%)	0.26	24 (5%) 23 22	8, 18, 37, 68	24 (5%)
1	B	411/437 (94%)	0.03	5 (1%) 79 80	3, 11, 34, 53	21 (5%)
1	C	421/437 (96%)	0.07	5 (1%) 79 80	5, 15, 35, 53	16 (3%)
1	D	411/437 (94%)	-0.07	3 (0%) 87 89	1, 7, 29, 44	20 (4%)
1	E	406/437 (92%)	-0.01	2 (0%) 91 92	3, 13, 38, 56	12 (2%)
1	F	413/437 (94%)	0.38	23 (5%) 24 23	12, 26, 44, 59	13 (3%)
All	All	2476/2622 (94%)	0.11	62 (2%) 57 59	1, 15, 39, 68	106 (4%)

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	52	PRO	8.4
1	A	54	GLY	5.4
1	B	291	LEU	4.5
1	A	83	LEU	4.1
1	A	193	LEU	4.0
1	A	53	GLY	3.8
1	D	52	PRO	3.8
1	F	83	LEU	3.6
1	A	198	ALA	3.6
1	A	49	PRO	3.4
1	A	51	PRO	3.3
1	A	376	ALA	3.3
1	A	48	ARG	3.2
1	F	315	GLY	3.2
1	F	218	SER	3.0
1	A	56	TYR	3.0
1	F	93	LEU	3.0
1	A	72	TYR	3.0
1	C	303	PHE	2.9

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	C	429	TRP	2.8
1	C	425	VAL	2.8
1	A	371	VAL	2.8
1	E	378	LYS	2.8
1	C	432	GLN	2.8
1	F	92	SER	2.7
1	F	390	PHE	2.6
1	F	102	ARG	2.6
1	F	306	THR	2.6
1	A	305	TYR	2.5
1	A	55	THR	2.5
1	A	190	LEU	2.5
1	F	82	PHE	2.4
1	F	87	MET	2.4
1	B	324	GLY	2.4
1	F	90	ILE	2.4
1	F	88	SER	2.4
1	B	54	GLY	2.4
1	F	425	VAL	2.4
1	A	50	ILE	2.3
1	F	206	PHE	2.3
1	B	381	GLN	2.3
1	A	47	SER	2.3
1	A	192	THR	2.3
1	A	65	CYS	2.3
1	A	429	TRP	2.2
1	F	79	ALA	2.2
1	F	86	GLY	2.2
1	F	232	GLY	2.2
1	F	438	MET	2.2
1	F	214	GLN	2.1
1	F	389	LEU	2.1
1	A	364	ARG	2.1
1	D	46	LYS	2.1
1	C	437	HIS	2.1
1	F	350	ASN	2.1
1	B	177	LEU	2.1
1	F	260	HIS	2.1
1	A	46	LYS	2.1
1	A	64	GLN	2.0
1	E	83	LEU	2.0
1	D	53	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	F	85	ASP	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

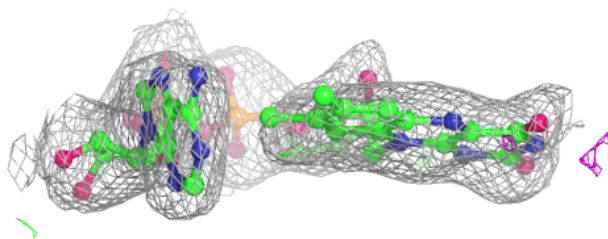
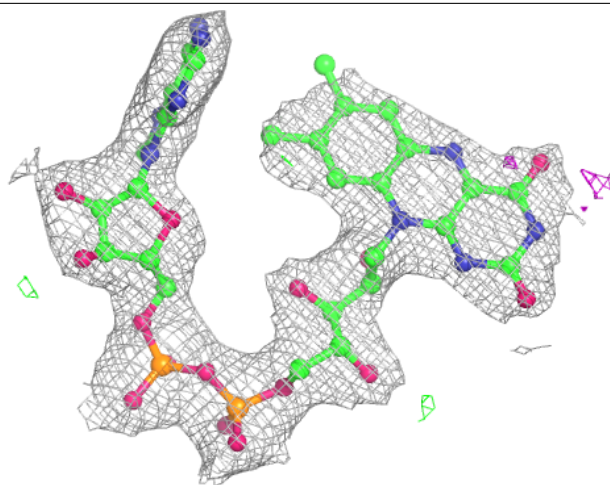
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	SF4	D	501	8/8	0.89	0.14	2,9,13,13	0
2	SF4	C	501	8/8	0.92	0.13	4,9,10,12	0
2	SF4	A	502	8/8	0.93	0.10	5,12,18,19	0
2	SF4	B	502	8/8	0.93	0.14	1,2,7,8	0
2	SF4	F	502	8/8	0.93	0.11	6,13,21,23	0
2	SF4	E	501	8/8	0.94	0.13	8,12,18,23	0
2	SF4	E	502	8/8	0.94	0.11	4,6,9,10	0
2	SF4	C	502	8/8	0.94	0.10	3,5,10,15	0
3	FAD	A	503	53/53	0.94	0.18	6,11,13,15	0
3	FAD	B	503	53/53	0.94	0.19	3,5,9,11	0
2	SF4	F	501	8/8	0.95	0.12	20,22,34,35	0
3	FAD	C	503	53/53	0.95	0.18	3,6,9,10	0
3	FAD	D	503	53/53	0.95	0.18	1,1,2,3	0
3	FAD	F	503	53/53	0.95	0.17	8,12,17,20	0
2	SF4	D	502	8/8	0.96	0.11	1,2,4,5	0
3	FAD	E	503	53/53	0.96	0.17	1,4,6,12	0
2	SF4	B	501	8/8	0.96	0.14	4,12,14,20	0
2	SF4	A	501	8/8	0.97	0.07	13,19,24,28	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

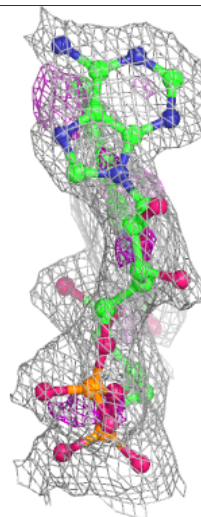
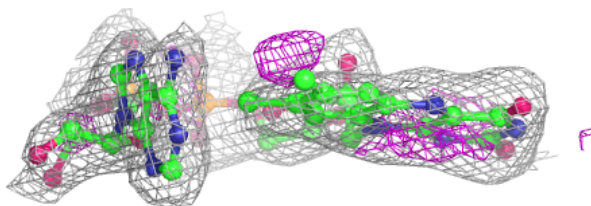
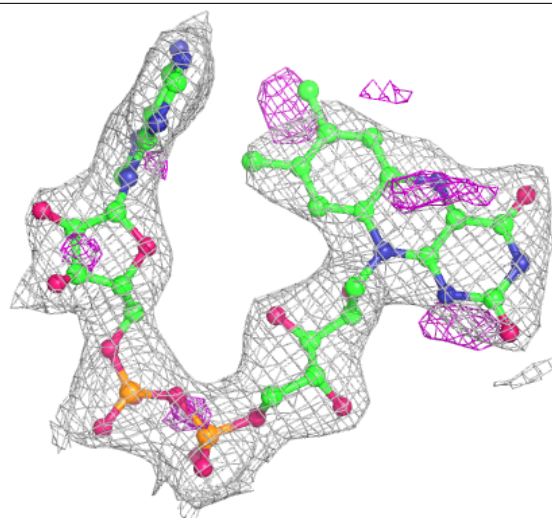
**Electron density around FAD A 503:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



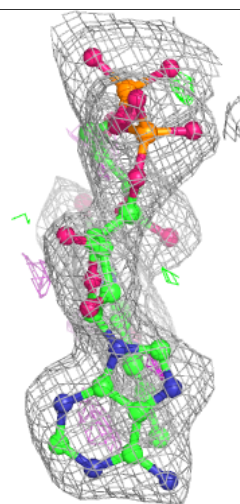
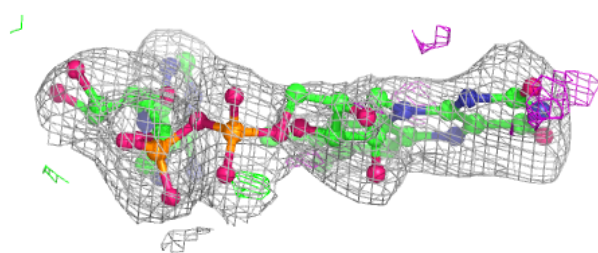
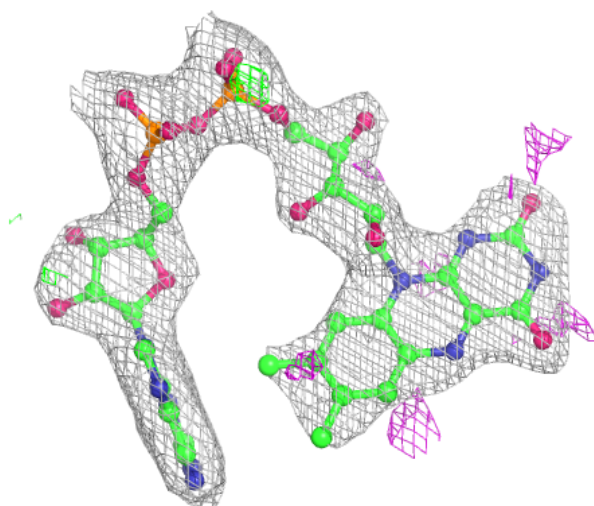
**Electron density around FAD B 503:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



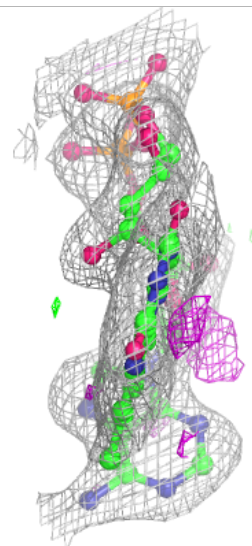
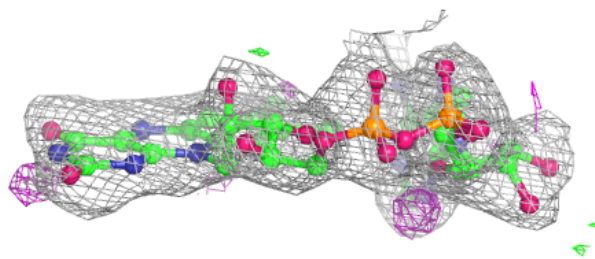
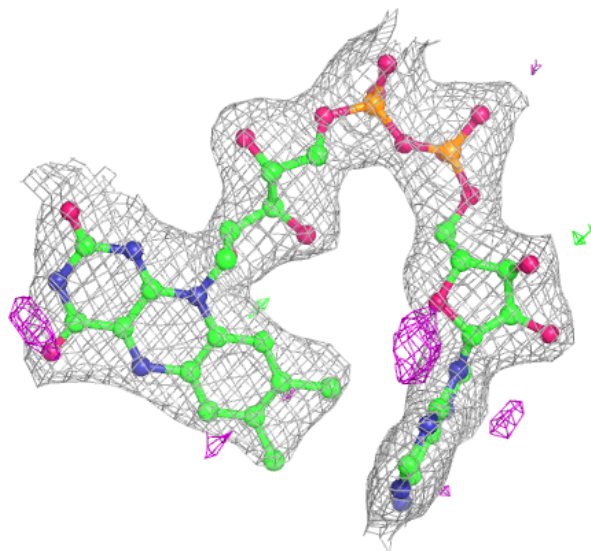
**Electron density around FAD C 503:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



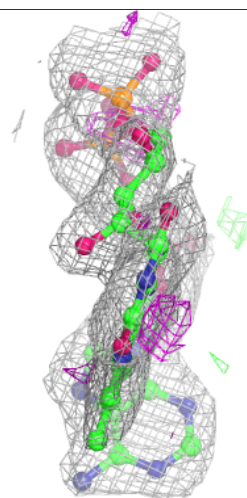
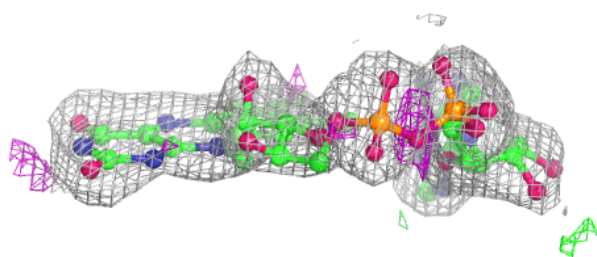
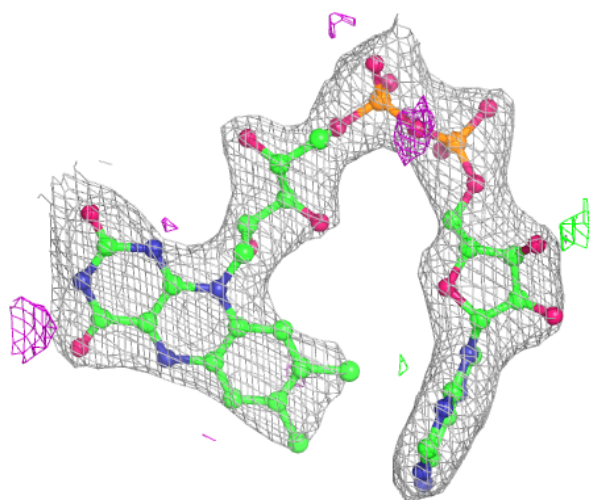
**Electron density around FAD D 503:**

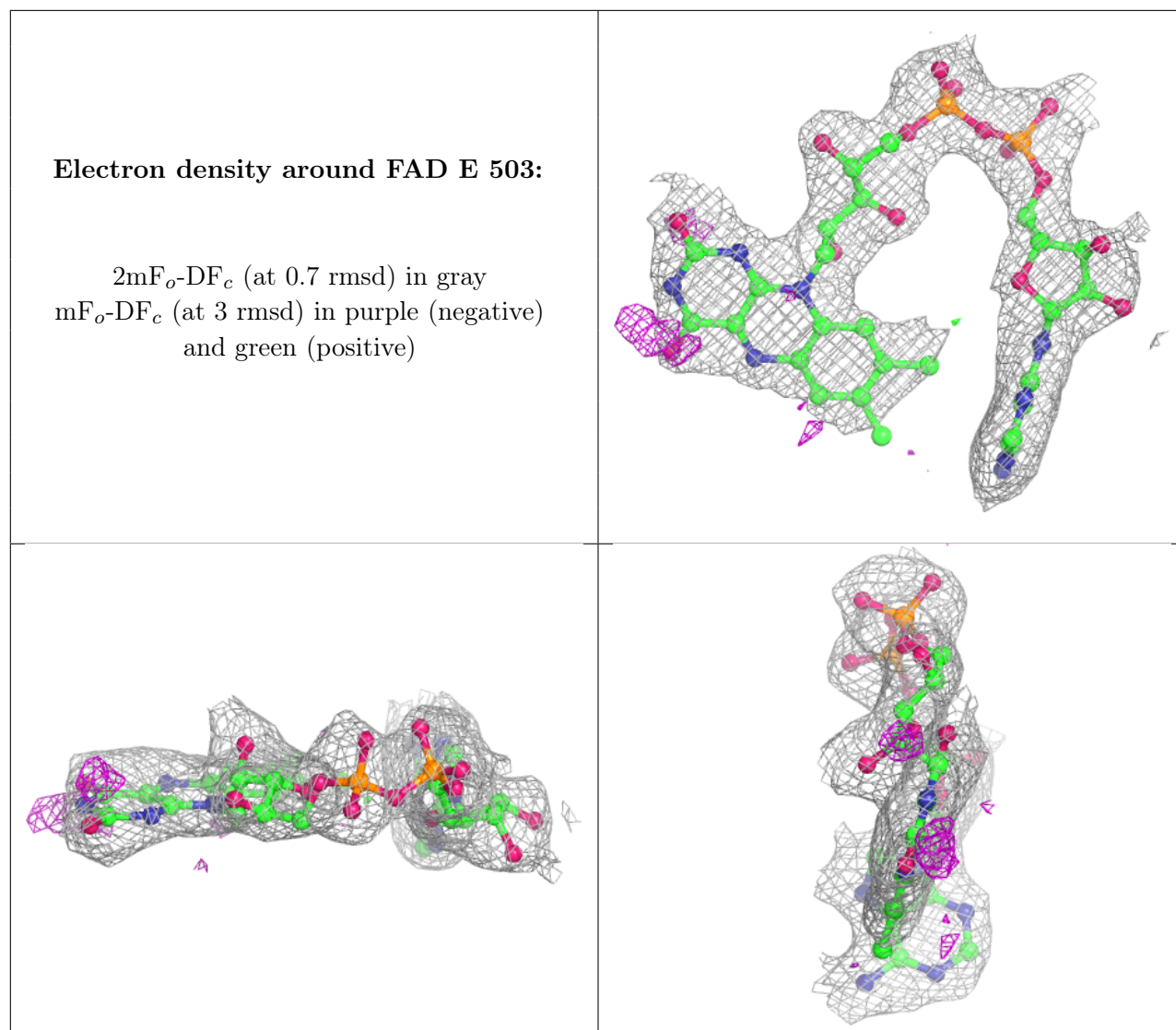
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around FAD F 503:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.