



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 12, 2024 – 11:06 AM EST

PDB ID : 3P4Q  
Title : Crystal structure of Menaquinol:oxidoreductase in complex with oxaloacetate  
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Deposited on : 2010-10-06  
Resolution : 3.35 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:

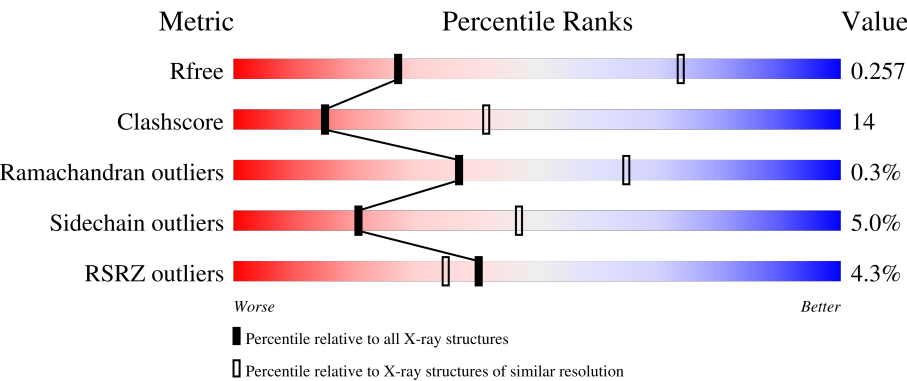
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.35 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 <sub>free</sub>	164625	1012 (3.40-3.32)
Clashscore	180529	1035 (3.40-3.32)
Ramachandran outliers	177936	1037 (3.40-3.32)
Sidechain outliers	177891	1037 (3.40-3.32)
RSRZ outliers	164620	1012 (3.40-3.32)

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	577	<div><div></div><div>77%22%.</div></div>
1	M	577	<div><div>14%</div><div>63%34%.</div></div>
2	B	243	<div><div></div><div>71%28%.</div></div>
2	N	243	<div><div>3%</div><div>72%27%.</div></div>

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Mol	Chain	Length	Quality of chain
3	C	130	
3	O	130	
4	D	119	
4	P	119	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
8	F3S	B	245	-	-	X	-
8	F3S	N	246	-	-	X	-
9	SF4	B	246	-	-	X	-
9	SF4	N	244	-	-	X	-

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 16804 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 Fumarate reductase flavoprotein subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	577	Total	C	N	O	S	0	0	0
			4449	2775	802	841	31			
1	M	577	Total	C	N	O	S	0	0	0
			4449	2775	802	841	31			

- Molecule 2 is a protein called Fumarate reductase iron-sulfur protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	243	Total	C	N	O	S	0	0	0
			1888	1189	323	357	19			
2	N	243	Total	C	N	O	S	0	0	0
			1888	1189	323	357	19			

- Molecule 3 is a protein called Fumarate reductase subunit C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	130	Total	C	N	O	S	0	0	0
			1058	720	166	169	3			
3	O	130	Total	C	N	O	S	0	0	0
			1058	720	166	169	3			

- Molecule 4 is a protein called Fumarate reductase subunit D.

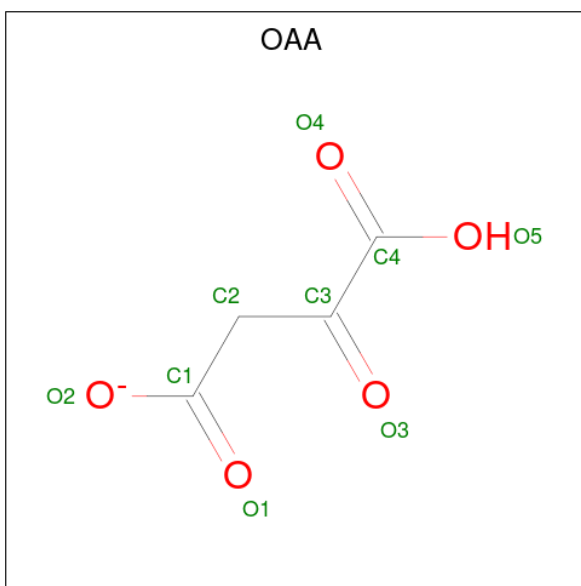
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	119	Total	C	N	O	S	0	0	0
			926	626	151	142	7			
4	P	119	Total	C	N	O	S	0	0	0
			926	626	151	142	7			

- Molecule 5 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C<sub>27</sub>H<sub>33</sub>N<sub>9</sub>O<sub>15</sub>P<sub>2</sub>).



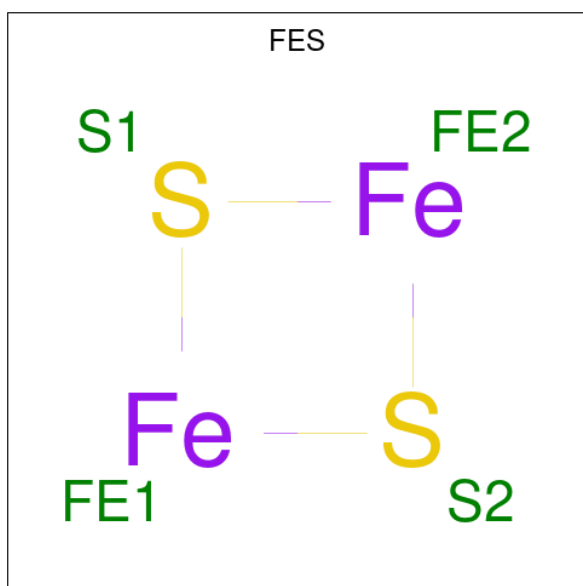
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total 53	C 27	N 9	O 15	P 2	0	0
5	M	1	Total 53	C 27	N 9	O 15	P 2	0	0

- Molecule 6 is OXALOACETATE ION (three-letter code: OAA) (formula:  $\text{C}_4\text{H}_3\text{O}_5$ ).



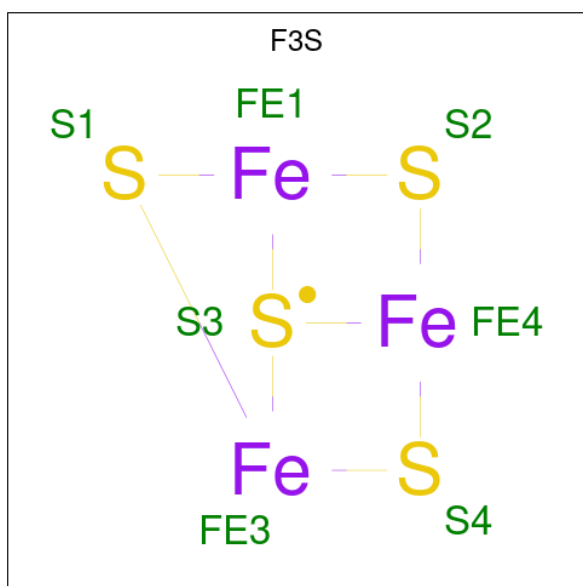
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total 9	C 4	O 5	0	0
6	M	1	Total 9	C 4	O 5	0	0

- Molecule 7 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula:  $\text{Fe}_2\text{S}_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	Fe	S	0	0
			4	2	2		
7	N	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 8 is FE3-S4 CLUSTER (three-letter code: F3S) (formula:  $\text{Fe}_3\text{S}_4$ ).



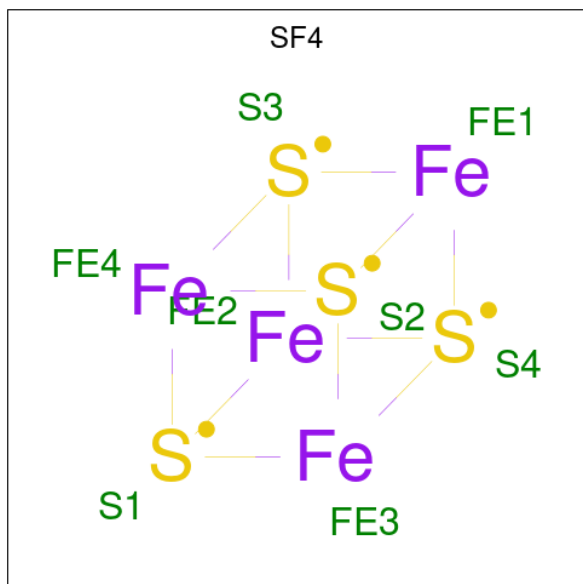
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	Fe	S	0	0
			7	3	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	N	1	Total	Fe	S	0	0
			7	3	4		

- Molecule 9 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe<sub>4</sub>S<sub>4</sub>).

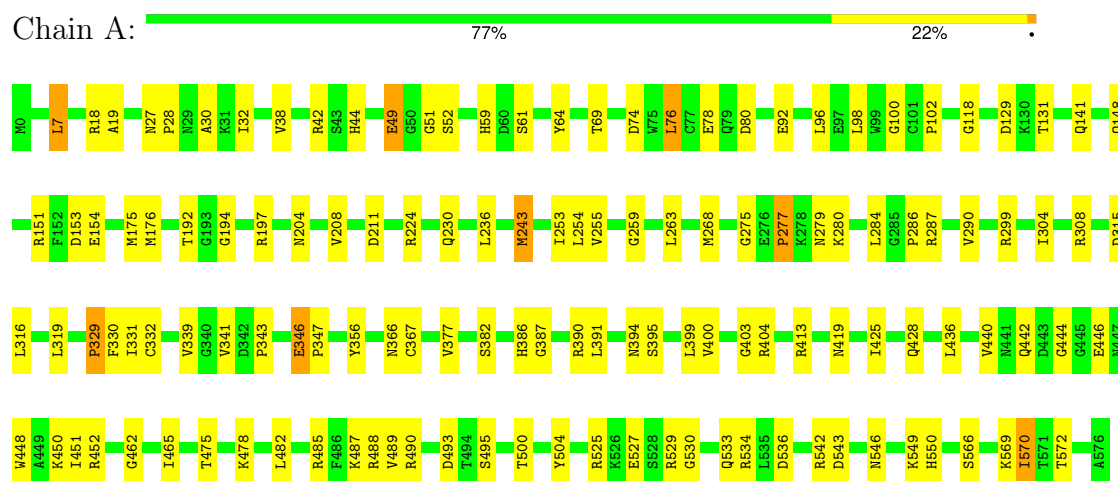


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	Fe	S	0	0
			8	4	4		
9	N	1	Total	Fe	S	0	0
			8	4	4		

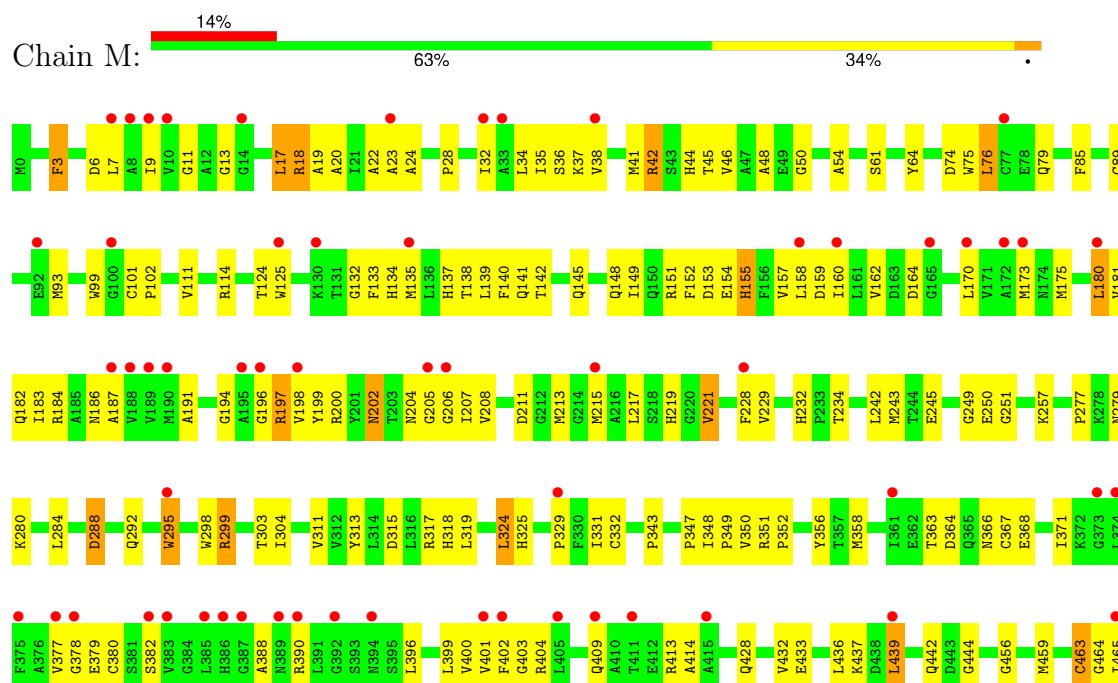
### 3 Residue-property plots

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 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.

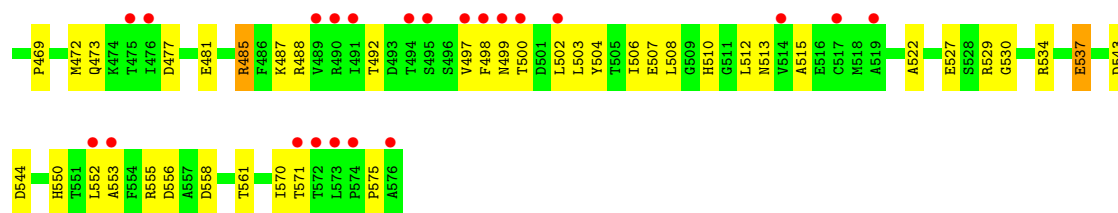
#### • Molecule 1: Fumarate reductase flavoprotein subunit



#### • Molecule 1: Fumarate reductase flavoprotein subunit

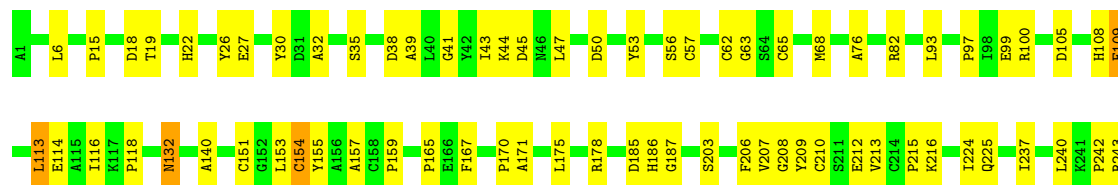






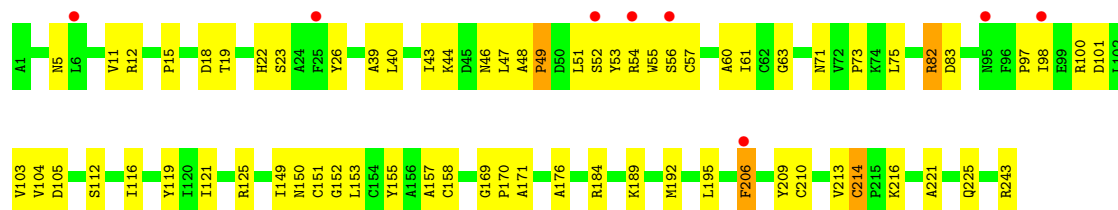
• Molecule 2: Fumarate reductase iron-sulfur protein

Chain B: 71% 28% .



• Molecule 2: Fumarate reductase iron-sulfur protein

Chain N: 3% 72% 27% .



• Molecule 3: Fumarate reductase subunit C

Chain C: 75% 23% .



• Molecule 3: Fumarate reductase subunit C

Chain O: 85% 14% .



• Molecule 4: Fumarate reductase subunit D

Chain D: 3% 76% 24% .

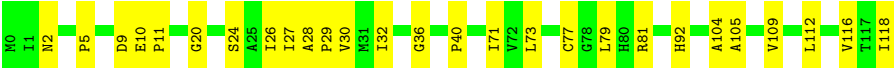


• Molecule 4: Fumarate reductase subunit D

Chain P: 

77%

23%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	96.64Å 137.96Å 272.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.57 – 3.35 47.57 – 3.35	Depositor EDS
% Data completeness (in resolution range)	89.2 (47.57-3.35) 88.9 (47.57-3.35)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.72 (at 3.33Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.220 , 0.261 0.219 , 0.257	Depositor DCC
$R_{free}$ test set	1036 reflections (1.94%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	66.7	Xtriage
Anisotropy	0.365	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 41.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.42$ , $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	16804	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.58% 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: F3S, SF4, FAD, FES, OAA

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	0.37	0/4541	0.52	0/6139
1	M	0.34	0/4541	0.56	0/6139
2	B	0.36	0/1931	0.53	0/2617
2	N	0.33	0/1931	0.51	0/2617
3	C	0.34	0/1094	0.49	0/1496
3	O	0.35	0/1094	0.45	0/1496
4	D	0.38	0/956	0.53	0/1303
4	P	0.34	0/956	0.48	0/1303
All	All	0.35	0/17044	0.52	0/23110

There are no bond length outliers.

There are no bond angle outliers.

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	4449	0	4335	101	0
1	M	4449	0	4333	180	0
2	B	1888	0	1840	63	0
2	N	1888	0	1838	64	0
3	C	1058	0	1108	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	O	1058	0	1108	16	0
4	D	926	0	971	19	0
4	P	926	0	971	17	0
5	A	53	0	31	10	0
5	M	53	0	31	20	0
6	A	9	0	2	0	0
6	M	9	0	2	2	0
7	B	4	0	0	0	0
7	N	4	0	0	1	0
8	B	7	0	0	2	0
8	N	7	0	0	3	0
9	B	8	0	0	7	0
9	N	8	0	0	2	0
All	All	16804	0	16570	451	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 14.

All (451) 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:44:HIS:NE2	5:A:601:FAD:HM82	1.42	1.34
2:N:11:VAL:HA	2:N:23:SER:OG	1.20	1.24
1:M:37:LYS:HE3	5:M:601:FAD:C8A	1.75	1.17
2:N:54:ARG:HH21	2:N:103:VAL:HG12	1.06	1.15
1:A:44:HIS:NE2	5:A:601:FAD:C8M	2.17	1.06
1:M:37:LYS:CE	5:M:601:FAD:C8A	2.34	1.05
2:B:154:CYS:SG	9:B:246:SF4:FE3	1.51	1.00
1:M:37:LYS:HE2	5:M:601:FAD:N7A	1.77	1.00
1:M:48:ALA:HB3	1:M:132:GLY:HA3	1.43	0.96
2:N:11:VAL:CA	2:N:23:SER:OG	2.15	0.93
2:N:54:ARG:HH21	2:N:103:VAL:CG1	1.83	0.91
4:D:55:LEU:HG	4:D:59:GLN:HE21	1.36	0.91
1:M:197:ARG:HD2	1:M:197:ARG:C	1.88	0.91
2:N:11:VAL:HA	2:N:23:SER:HG	1.35	0.90
2:N:54:ARG:NH2	2:N:103:VAL:HG12	1.86	0.89
1:M:37:LYS:CE	5:M:601:FAD:N7A	2.36	0.87
2:B:154:CYS:HG	9:B:246:SF4:FE3	0.87	0.87
1:M:250:GLU:O	1:M:319:LEU:HD11	1.73	0.87
2:B:154:CYS:SG	9:B:246:SF4:S2	2.74	0.86
1:M:527:GLU:OE2	1:M:529:ARG:NH1	2.08	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:GLU:HA	1:A:129:ASP:O	1.76	0.85
3:O:31:THR:HG21	3:O:82:HIS:HB2	1.59	0.84
1:M:377:VAL:HG21	1:M:403:GLY:HA2	1.59	0.84
2:N:26:TYR:HB3	2:N:47:LEU:HD13	1.58	0.84
1:A:500:THR:HB	1:A:504:TYR:CE1	2.15	0.82
1:M:497:VAL:HG21	3:O:4:ARG:HB3	1.61	0.82
2:B:242:PRO:HB2	4:P:92:HIS:HB3	1.62	0.82
2:B:212:GLU:HG3	3:C:21:PHE:HE2	1.46	0.81
1:M:36:SER:HA	5:M:601:FAD:N3A	1.94	0.81
1:M:61:SER:HB3	1:M:64:TYR:HD1	1.43	0.80
1:M:197:ARG:HD2	1:M:197:ARG:O	1.82	0.80
2:N:18:ASP:CG	2:N:22:HIS:HE2	1.86	0.79
2:N:43:ILE:HD13	2:N:47:LEU:HD12	1.64	0.77
3:C:103:MET:HG2	3:C:104:GLY:H	1.50	0.77
1:M:199:TYR:CD2	1:M:459:MET:HB3	2.19	0.77
2:N:116:ILE:CG2	2:N:176:ALA:HB2	2.15	0.76
3:C:50:LYS:HZ2	4:D:117:THR:HG22	1.51	0.75
1:M:570:ILE:HG21	1:M:575:PRO:HD3	1.66	0.75
2:B:154:CYS:HB2	2:B:170:PRO:HG2	1.68	0.75
2:B:151:CYS:SG	9:B:246:SF4:FE1	1.80	0.74
1:M:215:MET:HB3	1:M:510:HIS:CE1	2.23	0.74
2:N:116:ILE:HG21	2:N:176:ALA:HB2	1.69	0.73
1:A:197:ARG:HB2	1:A:208:VAL:O	1.89	0.73
1:A:546:ASN:O	1:A:549:LYS:HE2	1.88	0.73
1:M:377:VAL:HG23	1:M:402:PHE:O	1.89	0.72
2:B:15:PRO:HB3	3:C:5:LYS:H	1.54	0.71
1:M:37:LYS:HE3	5:M:601:FAD:H8A	1.68	0.71
1:A:49:GLU:CA	1:A:129:ASP:O	2.38	0.70
1:M:251:GLY:HA2	1:M:277:PRO:HG2	1.72	0.70
1:M:556:ASP:HB2	1:M:558:ASP:OD1	1.91	0.70
2:B:57:CYS:HB3	2:B:62:CYS:HB3	1.73	0.70
1:M:194:GLY:O	1:M:208:VAL:HG12	1.91	0.70
3:C:33:VAL:HA	4:D:82:MET:HE2	1.74	0.70
2:N:51:LEU:HD23	2:N:52:SER:N	2.07	0.70
1:A:341:VAL:HG13	1:A:346:GLU:HB3	1.74	0.70
2:B:151:CYS:HG	9:B:246:SF4:FE1	1.07	0.70
2:N:210:CYS:SG	2:N:221:ALA:HB2	2.32	0.69
2:B:155:TYR:HE1	2:B:171:ALA:HB3	1.58	0.69
1:M:152:PHE:HB3	1:M:155:HIS:NE2	2.07	0.69
2:B:132:ASN:HD22	2:B:132:ASN:H	1.40	0.69
4:D:55:LEU:HG	4:D:59:GLN:NE2	2.07	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:18:ASP:OD2	2:B:22:HIS:CD2	2.46	0.69
2:N:214:CYS:SG	9:N:244:SF4:FE3	1.85	0.69
1:A:346:GLU:HG3	1:A:347:PRO:HD2	1.75	0.68
3:C:103:MET:HG2	3:C:104:GLY:N	2.08	0.68
1:A:570:ILE:HD13	1:A:570:ILE:H	1.58	0.68
1:M:24:ALA:HB2	1:M:32:ILE:HD11	1.76	0.68
1:M:245:GLU:HB2	6:M:802:OAA:O5	1.94	0.68
1:A:98:LEU:HD23	2:B:132:ASN:HD21	1.58	0.67
2:N:40:LEU:HB3	2:N:53:TYR:CE2	2.30	0.66
1:M:211:ASP:OD2	1:M:507:GLU:HG2	1.95	0.66
2:B:65:CYS:HB3	2:B:76:ALA:H	1.60	0.66
4:P:10:GLU:N	4:P:11:PRO:HD2	2.10	0.66
3:C:19:LEU:HB2	3:C:22:TYR:CD2	2.31	0.65
1:M:205:GLY:HA3	2:N:56:SER:O	1.95	0.65
2:B:206:PHE:HE2	3:C:89:LEU:HD22	1.62	0.65
2:B:18:ASP:OD2	2:B:22:HIS:NE2	2.29	0.65
1:A:275:GLY:O	1:A:277:PRO:HD3	1.97	0.65
3:O:33:VAL:HB	3:O:34:PRO:HD3	1.79	0.64
1:M:137:HIS:HD2	1:M:141:GLN:HE21	1.45	0.64
3:C:33:VAL:HA	4:D:82:MET:CE	2.28	0.64
1:M:299:ARG:HE	1:M:299:ARG:HA	1.63	0.64
1:M:197:ARG:O	1:M:197:ARG:CD	2.46	0.63
1:A:243:MET:HA	1:A:243:MET:HE2	1.79	0.63
1:M:292:GLN:HG2	1:M:465:ILE:HG21	1.80	0.63
1:M:472:MET:HE1	1:M:522:ALA:HB1	1.81	0.63
1:M:444:GLY:HA3	1:M:488:ARG:O	1.98	0.63
9:B:246:SF4:FE3	9:B:246:SF4:S2	1.90	0.63
4:P:79:LEU:HD12	4:P:104:ALA:HB2	1.80	0.62
2:N:54:ARG:HE	2:N:103:VAL:HG13	1.63	0.62
2:N:151:CYS:SG	2:N:153:LEU:HD12	2.40	0.62
1:M:215:MET:HB3	1:M:510:HIS:HE1	1.64	0.62
1:A:308:ARG:HH12	1:A:339:VAL:HA	1.64	0.62
2:N:51:LEU:HD23	2:N:52:SER:H	1.63	0.62
1:M:204:ASN:OD1	5:M:601:FAD:HM83	1.99	0.62
2:B:97:PRO:HG2	2:B:105:ASP:HB3	1.82	0.61
1:A:49:GLU:CB	1:A:129:ASP:O	2.49	0.61
2:B:212:GLU:HG3	3:C:21:PHE:CE2	2.33	0.61
2:N:192:MET:HA	2:N:195:LEU:HD22	1.82	0.61
4:P:105:ALA:O	4:P:109:VAL:HG23	2.01	0.61
2:N:60:ALA:HA	7:N:245:FES:S1	2.40	0.61
1:M:433:GLU:O	1:M:437:LYS:HB2	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:THR:HA	1:A:391:LEU:HD22	1.82	0.61
1:M:211:ASP:OD1	1:M:507:GLU:HA	2.00	0.61
1:M:304:ILE:HG21	1:M:313:TYR:CE1	2.35	0.60
1:M:28:PRO:O	1:M:148:GLN:HG2	2.01	0.60
1:M:37:LYS:HE2	5:M:601:FAD:C5A	2.30	0.60
1:A:44:HIS:CE1	5:A:601:FAD:HM82	2.31	0.60
1:M:37:LYS:HE2	5:M:601:FAD:C8A	2.16	0.60
1:M:217:LEU:HD23	1:M:555:ARG:N	2.17	0.60
1:M:18:ARG:NH1	1:M:404:ARG:HA	2.17	0.59
2:B:167:PHE:CD1	2:B:203:SER:HB2	2.37	0.59
2:N:71:ASN:HB3	3:O:18:LYS:HE2	1.85	0.59
1:M:137:HIS:HD2	1:M:141:GLN:NE2	2.01	0.59
1:A:386:HIS:ND1	1:A:390:ARG:HG3	2.17	0.59
1:M:35:ILE:HG13	1:M:155:HIS:HB2	1.84	0.59
1:A:462:GLY:HA3	1:A:475:THR:OG1	2.03	0.58
1:A:197:ARG:HG3	1:A:208:VAL:O	2.03	0.58
1:M:20:ALA:HB2	1:M:34:LEU:HD12	1.85	0.58
1:M:114:ARG:O	1:M:124:THR:HB	2.02	0.58
1:M:234:THR:HG22	1:M:350:VAL:HG11	1.85	0.58
1:A:390:ARG:HD2	1:A:395:SER:HB2	1.84	0.58
1:M:48:ALA:HB3	1:M:132:GLY:CA	2.26	0.58
1:M:50:GLY:HA3	5:M:601:FAD:O4	2.03	0.58
1:M:61:SER:HB3	1:M:64:TYR:CD1	2.33	0.58
1:A:263:LEU:O	1:A:268:MET:HB2	2.04	0.57
1:M:44:HIS:CE1	1:M:204:ASN:HA	2.40	0.57
1:M:298:TRP:HA	1:M:303:THR:HG23	1.85	0.57
2:N:97:PRO:HA	3:O:7:TYR:O	2.04	0.57
1:M:358:MET:HG2	1:M:390:ARG:HB2	1.87	0.57
1:M:180:LEU:H	1:M:180:LEU:HD22	1.69	0.57
1:M:158:LEU:HD13	1:M:436:LEU:HG	1.85	0.57
1:M:219:HIS:NE2	1:M:371:ILE:HG12	2.20	0.56
3:C:113:TRP:O	3:C:117:VAL:HG23	2.05	0.56
1:M:162:VAL:HG21	1:M:219:HIS:HE1	1.69	0.56
2:N:54:ARG:NH2	2:N:103:VAL:CG1	2.58	0.56
2:N:155:TYR:HE1	2:N:171:ALA:HB3	1.69	0.56
1:A:356:TYR:HE1	5:A:601:FAD:O3'	1.89	0.56
4:D:20:GLY:HA2	4:D:73:LEU:HB3	1.88	0.56
2:N:151:CYS:SG	2:N:152:GLY:N	2.78	0.56
2:B:170:PRO:HA	2:B:224:ILE:HD11	1.88	0.56
4:D:1:ILE:O	4:D:3:PRO:HD3	2.05	0.56
1:M:41:MET:HB2	1:M:137:HIS:CE1	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:225:GLN:HE21	3:O:93:ALA:HB2	1.71	0.56
2:B:108:HIS:CE1	2:B:165:PRO:O	2.60	0.55
1:A:51:GLY:HA2	1:A:131:THR:HG21	1.87	0.55
4:P:2:ASN:O	4:P:5:PRO:HD3	2.05	0.55
1:A:386:HIS:CE1	1:A:390:ARG:HG3	2.42	0.55
1:M:217:LEU:HD23	1:M:555:ARG:H	1.71	0.55
1:M:18:ARG:HH12	1:M:22:ALA:HB2	1.70	0.55
1:M:37:LYS:HD2	1:M:207:ILE:HB	1.88	0.55
1:M:245:GLU:CB	6:M:802:OAA:O5	2.55	0.55
2:N:51:LEU:HD22	2:N:53:TYR:CD2	2.42	0.55
1:A:61:SER:HB3	1:A:64:TYR:CD2	2.42	0.54
2:B:35:SER:O	2:B:38:ASP:HB2	2.08	0.54
3:C:87:PHE:HE2	4:D:25:ALA:HB1	1.72	0.54
1:M:23:ALA:HB1	1:M:32:ILE:HG21	1.89	0.54
1:M:41:MET:HG2	1:M:42:ARG:HE	1.71	0.54
1:A:243:MET:HA	1:A:243:MET:CE	2.37	0.54
3:C:87:PHE:CE1	3:C:112:LEU:HB3	2.43	0.54
1:M:50:GLY:CA	5:M:601:FAD:O4	2.56	0.54
2:N:98:ILE:HB	3:O:7:TYR:HB3	1.90	0.54
1:M:199:TYR:CE2	1:M:459:MET:HB3	2.43	0.54
3:C:33:VAL:HB	3:C:34:PRO:HD3	1.90	0.53
1:M:54:ALA:HB3	1:M:125:TRP:NE1	2.24	0.53
1:M:221:VAL:HG22	1:M:371:ILE:HD13	1.90	0.53
3:C:130:TRP:HB2	4:D:53:ARG:HH21	1.74	0.53
1:M:36:SER:HA	5:M:601:FAD:C2A	2.39	0.53
2:N:63:GLY:O	2:N:151:CYS:HA	2.09	0.53
2:N:73:PRO:HG2	2:N:213:VAL:HG11	1.91	0.53
1:A:192:THR:HA	5:A:601:FAD:O4B	2.09	0.53
1:A:446:GLU:HB2	1:A:488:ARG:O	2.09	0.53
1:M:331:ILE:HD12	1:M:331:ILE:H	1.73	0.53
1:A:204:ASN:N	1:A:204:ASN:HD22	2.05	0.53
2:B:154:CYS:SG	9:B:246:SF4:S4	3.06	0.53
1:M:152:PHE:HB3	1:M:155:HIS:CD2	2.44	0.53
3:O:90:ALA:N	3:O:91:PRO:HD2	2.24	0.52
2:B:185:ASP:OD1	2:B:187:GLY:N	2.31	0.52
2:B:159:PRO:HG3	3:C:22:TYR:CE1	2.45	0.52
3:C:27:LEU:HD13	3:C:81:LEU:HD21	1.92	0.52
2:B:39:ALA:O	2:B:43:ILE:HG12	2.10	0.52
1:M:151:ARG:NH1	1:M:153:ASP:OD1	2.35	0.52
2:N:44:LYS:HA	2:N:48:ALA:O	2.10	0.52
1:A:129:ASP:OD2	1:A:329:PRO:HD2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:37:LYS:HG3	1:M:38:VAL:H	1.75	0.52
1:A:18:ARG:HG2	1:A:400:VAL:HA	1.91	0.52
1:M:288:ASP:O	1:M:292:GLN:HG3	2.10	0.52
1:A:18:ARG:NH1	1:A:92:GLU:OE2	2.42	0.51
1:A:118:GLY:HA2	1:A:279:ASN:HD21	1.75	0.51
2:B:185:ASP:OD1	2:B:185:ASP:C	2.49	0.51
1:A:332:CYS:HA	1:A:343:PRO:HG3	1.91	0.51
4:D:27:ILE:O	4:D:27:ILE:HG22	2.10	0.51
1:A:446:GLU:HB2	1:A:489:VAL:HA	1.93	0.51
1:M:199:TYR:CE1	1:M:229:VAL:HG11	2.46	0.51
1:M:101:CYS:HB2	1:M:138:THR:HG21	1.93	0.50
1:A:80:ASP:OD2	1:A:569:LYS:HG2	2.12	0.50
2:B:65:CYS:CB	2:B:76:ALA:H	2.25	0.50
1:M:45:THR:HG23	5:M:601:FAD:H5'1	1.92	0.50
1:A:425:ILE:O	1:A:428:GLN:HB2	2.11	0.50
1:M:7:LEU:HB2	1:M:32:ILE:HG22	1.92	0.50
1:M:377:VAL:CG2	1:M:402:PHE:O	2.59	0.50
1:M:378:GLY:HA2	1:M:399:LEU:HD23	1.93	0.50
2:N:43:ILE:CD1	2:N:47:LEU:HD12	2.37	0.50
1:A:243:MET:HE2	1:A:331:ILE:HD12	1.93	0.50
1:M:46:VAL:CG2	1:M:133:PHE:HD1	2.25	0.50
1:M:553:ALA:HB1	1:M:561:THR:HG21	1.94	0.50
1:M:304:ILE:N	1:M:304:ILE:HD12	2.27	0.50
2:B:57:CYS:HB3	2:B:62:CYS:CB	2.40	0.50
1:A:448:TRP:CH2	1:A:504:TYR:HB3	2.46	0.50
1:M:35:ILE:HG12	5:M:601:FAD:H2A	1.93	0.50
1:A:525:ARG:NH1	1:A:527:GLU:OE2	2.44	0.49
1:M:481:GLU:HG2	1:M:485:ARG:HD3	1.93	0.49
2:N:54:ARG:NH2	2:N:104:VAL:O	2.45	0.49
1:A:27:ASN:OD1	1:A:30:ALA:N	2.43	0.49
3:C:19:LEU:HB2	3:C:22:TYR:HD2	1.77	0.49
1:M:213:MET:CE	1:M:380:CYS:HA	2.42	0.49
1:M:311:VAL:HG12	1:M:351:ARG:HB3	1.93	0.49
1:M:481:GLU:O	1:M:485:ARG:HD3	2.12	0.49
1:A:197:ARG:CB	1:A:208:VAL:O	2.60	0.49
2:B:185:ASP:OD1	2:B:186:HIS:N	2.46	0.49
1:M:211:ASP:O	1:M:510:HIS:ND1	2.43	0.49
4:P:112:LEU:O	4:P:116:VAL:HG22	2.12	0.49
1:A:230:GLN:HB3	1:A:356:TYR:HB3	1.95	0.49
1:M:553:ALA:HB1	1:M:561:THR:CG2	2.42	0.49
1:A:98:LEU:CD2	2:B:132:ASN:HD21	2.25	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:ILE:HG13	1:A:315:ASP:HB3	1.94	0.49
1:M:199:TYR:HE2	1:M:459:MET:O	1.96	0.49
2:N:19:THR:HA	3:O:5:LYS:NZ	2.28	0.49
1:A:395:SER:HB3	5:A:601:FAD:N1	2.27	0.49
1:A:504:TYR:CE1	2:B:44:LYS:HE2	2.48	0.49
2:N:82:ARG:HD2	2:N:83:ASP:OD1	2.13	0.49
1:A:504:TYR:CD1	2:B:44:LYS:HE2	2.48	0.49
1:M:469:PRO:HG3	1:M:534:ARG:HH21	1.78	0.49
1:M:537:GLU:H	1:M:537:GLU:CD	2.16	0.49
3:C:85:THR:O	3:C:89:LEU:HG	2.13	0.48
3:O:39:SER:OG	4:P:71:ILE:O	2.31	0.48
4:D:48:ALA:O	4:D:53:ARG:HD3	2.14	0.48
1:A:49:GLU:HB3	1:A:129:ASP:O	2.12	0.48
2:N:18:ASP:OD2	2:N:22:HIS:NE2	2.41	0.48
2:B:206:PHE:CD1	2:B:225:GLN:HG3	2.48	0.48
1:M:197:ARG:O	1:M:197:ARG:CG	2.61	0.48
1:M:459:MET:O	1:M:463:CYS:O	2.32	0.48
1:M:37:LYS:O	1:M:154:GLU:HA	2.13	0.48
1:M:11:GLY:HA3	1:M:191:ALA:O	2.14	0.48
4:P:36:GLY:O	4:P:40:PRO:HG3	2.14	0.48
2:B:65:CYS:HB3	2:B:76:ALA:HB3	1.95	0.48
1:M:299:ARG:HE	1:M:299:ARG:CA	2.27	0.48
2:B:113:LEU:HD23	2:B:175:LEU:HD23	1.96	0.48
2:N:18:ASP:CG	2:N:22:HIS:NE2	2.62	0.48
1:A:550:HIS:HB2	1:A:566:SER:OG	2.14	0.47
4:D:68:PHE:CE1	4:D:72:VAL:HG21	2.50	0.47
1:M:37:LYS:O	1:M:175:MET:SD	2.72	0.47
1:M:363:THR:HB	1:M:367:CYS:HA	1.95	0.47
1:A:304:ILE:HD12	1:A:304:ILE:H	1.79	0.47
4:D:79:LEU:HD12	4:D:104:ALA:HB2	1.96	0.47
1:M:157:VAL:H	5:M:601:FAD:H62A	1.62	0.47
1:M:279:ASN:O	1:M:280:LYS:HB2	2.14	0.47
2:B:132:ASN:HD22	2:B:132:ASN:N	2.11	0.47
1:M:377:VAL:HG22	1:M:378:GLY:N	2.29	0.47
2:N:26:TYR:HB3	2:N:47:LEU:CD1	2.37	0.47
1:A:197:ARG:CG	1:A:208:VAL:O	2.62	0.47
2:N:158:CYS:CA	8:N:246:F3S:S4	3.03	0.47
1:A:7:LEU:CD2	1:A:32:ILE:HG12	2.45	0.47
1:A:391:LEU:O	1:A:394:ASN:HB2	2.14	0.47
1:M:313:TYR:HD2	1:M:347:PRO:HG2	1.78	0.47
1:A:452:ARG:NH2	2:B:45:ASP:OD2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:130:TRP:OXT	4:D:53:ARG:NE	2.48	0.47
1:M:500:THR:HB	1:M:504:TYR:CE1	2.49	0.47
2:N:158:CYS:HA	8:N:246:F3S:S4	2.55	0.47
1:A:176:MET:CG	3:C:4:ARG:HH11	2.27	0.47
1:M:196:GLY:HA3	1:M:204:ASN:HD22	1.79	0.47
1:A:436:LEU:O	1:A:440:VAL:HG23	2.14	0.47
1:M:18:ARG:HH12	1:M:404:ARG:HA	1.81	0.46
2:N:214:CYS:HG	9:N:244:SF4:FE3	1.32	0.46
2:B:63:GLY:O	2:B:151:CYS:HA	2.16	0.46
4:D:112:LEU:O	4:D:116:VAL:HG22	2.15	0.46
2:B:175:LEU:HD12	2:B:175:LEU:HA	1.60	0.46
1:A:96:LEU:HD11	1:A:400:VAL:HG11	1.97	0.46
1:M:17:LEU:C	1:M:17:LEU:HD22	2.35	0.46
1:M:158:LEU:HD21	1:M:506:ILE:HD13	1.96	0.46
1:M:503:LEU:HA	1:M:506:ILE:HD12	1.97	0.46
1:A:286:PRO:O	1:A:290:VAL:HG23	2.16	0.46
1:A:451:ILE:HG23	1:A:482:LEU:HD22	1.97	0.46
1:M:79:GLN:HB2	1:M:571:THR:HG23	1.97	0.46
3:O:76:LEU:HD13	4:P:32:ILE:HB	1.97	0.46
2:B:207:VAL:HG23	8:B:245:F3S:S2	2.55	0.46
1:M:473:GLN:NE2	1:M:477:ASP:OD1	2.48	0.46
1:M:217:LEU:HD12	1:M:221:VAL:O	2.15	0.46
1:M:311:VAL:HG21	1:M:349:PRO:HB3	1.98	0.46
3:C:111:SER:O	3:C:115:VAL:HG23	2.16	0.46
1:M:17:LEU:HA	1:M:34:LEU:HD11	1.97	0.46
1:A:194:GLY:O	1:A:208:VAL:HG13	2.16	0.46
1:M:162:VAL:CG2	1:M:219:HIS:HE1	2.29	0.46
1:M:388:ALA:HB1	1:M:530:GLY:HA3	1.97	0.46
1:M:506:ILE:O	1:M:510:HIS:HD2	1.99	0.46
2:B:210:CYS:O	2:B:213:VAL:HG22	2.16	0.46
1:M:85:PHE:HD1	1:M:402:PHE:CE2	2.33	0.46
1:A:534:ARG:HH21	1:A:536:ASP:CG	2.20	0.45
1:A:527:GLU:OE2	1:A:529:ARG:NH1	2.49	0.45
1:M:37:LYS:HG2	5:M:601:FAD:O2B	2.16	0.45
1:M:366:ASN:HB3	1:M:409:GLN:HG3	1.98	0.45
4:P:77:CYS:O	4:P:81:ARG:HG3	2.16	0.45
1:A:76:LEU:O	1:A:387:GLY:HA2	2.15	0.45
1:A:450:LYS:HA	1:A:450:LYS:HD3	1.75	0.45
2:B:154:CYS:HB2	2:B:170:PRO:CG	2.42	0.45
2:B:50:ASP:O	2:B:100:ARG:NH2	2.49	0.45
3:C:90:ALA:N	3:C:91:PRO:CD	2.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:32:ALA:O	2:B:82:ARG:NH1	2.49	0.45
1:M:257:LYS:HA	1:M:304:ILE:HD11	1.98	0.45
1:M:232:HIS:O	1:M:352:PRO:HA	2.16	0.45
4:P:9:ASP:OD1	4:P:9:ASP:N	2.50	0.45
1:A:330:PHE:HE1	2:B:216:LYS:HZ2	1.62	0.45
1:M:99:TRP:CD1	1:M:142:THR:HG21	2.52	0.45
1:M:436:LEU:HA	1:M:439:LEU:HB2	1.99	0.45
2:N:112:SER:O	2:N:116:ILE:HG12	2.17	0.45
1:A:44:HIS:NE2	5:A:601:FAD:HM81	2.21	0.45
1:M:213:MET:HE3	1:M:380:CYS:HA	1.99	0.45
3:O:7:TYR:CD1	3:O:7:TYR:C	2.90	0.45
2:B:153:LEU:HD12	2:B:215:PRO:HD3	1.98	0.44
2:B:6:LEU:HB2	2:B:30:TYR:CE2	2.51	0.44
1:M:159:ASP:OD2	1:M:160:ILE:N	2.50	0.44
2:N:75:LEU:HG	2:N:153:LEU:HD11	1.98	0.44
1:A:211:ASP:CB	5:A:601:FAD:H61A	2.30	0.44
1:M:219:HIS:CD2	1:M:219:HIS:C	2.90	0.44
1:M:298:TRP:HA	1:M:303:THR:CG2	2.47	0.44
4:P:28:ALA:N	4:P:29:PRO:HD2	2.32	0.44
1:M:508:LEU:O	1:M:512:LEU:HG	2.17	0.44
1:A:478:LYS:HA	1:A:478:LYS:HD2	1.86	0.44
1:M:356:TYR:CZ	1:M:379:GLU:HG3	2.52	0.44
1:A:28:PRO:HA	1:A:148:GLN:HE21	1.83	0.44
1:A:255:VAL:HB	1:A:259:GLY:HA2	2.00	0.44
1:A:570:ILE:HD13	1:A:570:ILE:N	2.30	0.44
2:N:15:PRO:HD3	2:N:100:ARG:HG2	1.99	0.44
1:M:498:PHE:O	2:N:100:ARG:NH2	2.50	0.44
1:M:206:GLY:N	2:N:55:TRP:CZ3	2.86	0.43
1:A:377:VAL:HG21	1:A:403:GLY:HA2	2.00	0.43
1:A:543:ASP:OD2	1:A:546:ASN:ND2	2.51	0.43
2:B:157:ALA:HB1	2:B:209:TYR:CD2	2.53	0.43
1:M:79:GLN:NE2	1:M:571:THR:H	2.15	0.43
1:A:366:ASN:O	1:A:367:CYS:HB2	2.18	0.43
1:M:46:VAL:HG23	1:M:133:PHE:HD1	1.82	0.43
2:B:68:MET:HG2	2:B:93:LEU:HA	1.99	0.43
2:B:132:ASN:H	2:B:132:ASN:ND2	2.13	0.43
1:M:492:THR:CG2	2:N:49:PRO:HG2	2.49	0.43
1:A:399:LEU:HD11	5:A:601:FAD:H4'	2.00	0.43
1:M:315:ASP:OD1	1:M:317:ARG:HG2	2.19	0.43
1:M:428:GLN:O	1:M:432:VAL:HG23	2.17	0.43
4:P:10:GLU:N	4:P:11:PRO:CD	2.80	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:356:TYR:CE2	1:A:390:ARG:HD3	2.54	0.43
1:M:200:ARG:HB2	1:M:456:GLY:HA3	2.01	0.43
1:M:295:TRP:CD1	1:M:295:TRP:C	2.91	0.43
1:M:364:ASP:OD1	1:M:368:GLU:N	2.52	0.43
2:N:12:ARG:NE	2:N:101:ASP:OD2	2.48	0.43
1:A:154:GLU:O	1:A:175:MET:HB2	2.18	0.43
1:A:230:GLN:NE2	1:A:287:ARG:NH1	2.67	0.43
4:D:30:VAL:O	4:D:33:LEU:HB3	2.18	0.43
1:M:186:ASN:CB	1:M:414:ALA:HA	2.49	0.43
1:M:228:PHE:CZ	1:M:388:ALA:HA	2.53	0.43
4:P:26:ILE:HB	4:P:27:ILE:HD12	2.01	0.43
3:C:87:PHE:CE2	4:D:25:ALA:HB1	2.54	0.43
1:M:42:ARG:NH2	2:N:150:ASN:O	2.52	0.43
1:M:75:TRP:CD1	1:M:575:PRO:HA	2.54	0.43
1:M:292:GLN:HG2	1:M:465:ILE:CG2	2.46	0.43
1:M:7:LEU:CD2	1:M:187:ALA:HB3	2.49	0.43
2:N:157:ALA:HB1	2:N:209:TYR:CD2	2.54	0.43
1:M:442:GLN:NE2	1:M:487:LYS:HD3	2.34	0.42
1:M:324:LEU:HG	1:M:325:HIS:CE1	2.54	0.42
1:A:236:LEU:HD21	1:A:243:MET:SD	2.59	0.42
2:N:149:ILE:HG23	2:N:216:LYS:HG3	1.99	0.42
3:O:65:ASN:O	3:O:69:VAL:HG23	2.19	0.42
1:A:204:ASN:N	1:A:204:ASN:ND2	2.67	0.42
1:A:493:ASP:OD1	1:A:495:SER:OG	2.32	0.42
1:M:32:ILE:HG13	1:M:149:ILE:HA	2.01	0.42
1:A:279:ASN:O	1:A:280:LYS:HB2	2.20	0.42
1:M:242:LEU:HD22	5:M:601:FAD:H6	2.02	0.42
1:M:249:GLY:HA2	1:M:284:LEU:HD11	2.01	0.42
2:N:149:ILE:CG2	2:N:216:LYS:HG3	2.50	0.42
1:M:135:MET:HE1	1:M:396:LEU:HB3	2.01	0.42
1:M:196:GLY:HA3	1:M:204:ASN:ND2	2.34	0.42
1:A:529:ARG:HB2	1:A:542:ARG:HG3	2.02	0.42
1:M:9:ILE:HG21	1:M:19:ALA:HB3	2.00	0.42
2:N:46:ASN:HD22	2:N:46:ASN:N	2.17	0.42
1:A:18:ARG:HH12	1:A:404:ARG:HH11	1.68	0.42
1:A:100:GLY:O	1:A:102:PRO:HD3	2.18	0.42
1:A:224:ARG:NH2	1:A:382:SER:O	2.53	0.42
1:A:254:LEU:HD12	1:A:263:LEU:HD11	2.02	0.42
3:C:31:THR:O	3:C:34:PRO:HD2	2.20	0.42
1:M:17:LEU:HD11	1:M:139:LEU:CB	2.49	0.42
1:M:76:LEU:O	1:M:550:HIS:NE2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:464:GLY:O	1:M:465:ILE:C	2.58	0.42
1:M:537:GLU:CD	1:M:537:GLU:N	2.73	0.42
1:M:17:LEU:HD21	1:M:139:LEU:HB3	2.02	0.42
1:A:92:GLU:OE1	1:A:404:ARG:HD2	2.20	0.41
1:A:151:ARG:NH1	1:A:153:ASP:OD2	2.54	0.41
1:A:316:LEU:O	1:A:319:LEU:HB2	2.20	0.41
1:M:492:THR:HG23	2:N:49:PRO:HG2	2.01	0.41
1:M:513:ASN:HB3	1:M:555:ARG:HD2	2.02	0.41
2:N:51:LEU:HD22	2:N:53:TYR:HD2	1.82	0.41
2:B:57:CYS:HB3	2:B:62:CYS:SG	2.58	0.41
3:C:94:ALA:HB1	3:C:96:ILE:HD11	2.02	0.41
1:M:428:GLN:O	1:M:432:VAL:N	2.54	0.41
1:A:19:ALA:HA	1:A:403:GLY:O	2.20	0.41
1:A:49:GLU:H	1:A:49:GLU:HG2	1.75	0.41
1:A:442:GLN:NE2	1:A:487:LYS:C	2.74	0.41
1:M:332:CYS:SG	1:M:343:PRO:HG3	2.61	0.41
2:B:240:LEU:O	2:B:242:PRO:HD3	2.20	0.41
1:M:102:PRO:HG2	1:M:134:HIS:CD2	2.56	0.41
2:N:206:PHE:HA	8:N:246:F3S:S1	2.60	0.41
1:A:59:HIS:CD2	1:A:59:HIS:H	2.37	0.41
2:B:109:PHE:C	2:B:109:PHE:CD2	2.93	0.41
2:B:208:GLY:N	8:B:245:F3S:S1	2.90	0.41
1:M:3:PHE:HB3	1:M:183:ILE:HG23	2.02	0.41
1:M:37:LYS:N	5:M:601:FAD:N3A	2.69	0.41
1:M:183:ILE:HG22	1:M:184:ARG:N	2.35	0.41
1:A:141:GLN:HB3	2:B:118:PRO:O	2.21	0.41
3:C:87:PHE:O	3:C:91:PRO:HD3	2.20	0.41
1:M:76:LEU:HD22	1:M:76:LEU:HA	1.91	0.41
1:M:85:PHE:HB2	1:M:402:PHE:HE2	1.86	0.41
1:M:499:ASN:HA	2:N:100:ARG:HH22	1.85	0.41
2:B:15:PRO:HG3	2:B:99:GLU:O	2.21	0.41
1:M:13:GLY:HA3	5:M:601:FAD:O1P	2.20	0.41
1:M:79:GLN:OE1	1:M:570:ILE:HG23	2.21	0.41
1:A:151:ARG:NH2	2:B:114:GLU:OE2	2.54	0.41
1:M:145:GLN:HE21	2:N:119:TYR:HB2	1.85	0.41
1:M:181:VAL:HG12	1:M:182:GLN:N	2.36	0.41
1:M:198:VAL:HG11	1:M:515:ALA:HB2	2.03	0.41
5:M:601:FAD:H9	5:M:601:FAD:H1'1	1.81	0.41
2:N:39:ALA:O	2:N:43:ILE:HG12	2.21	0.41
4:P:20:GLY:HA2	4:P:73:LEU:HB3	2.03	0.41
4:P:24:SER:O	4:P:28:ALA:HB3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:41:GLY:HA2	2:B:53:TYR:OH	2.21	0.41
2:N:57:CYS:SG	2:N:61:ILE:HG22	2.61	0.41
2:N:97:PRO:HG2	2:N:105:ASP:HB3	2.02	0.41
1:A:530:GLY:O	1:A:533:GLN:NE2	2.53	0.40
2:B:26:TYR:HD2	2:B:47:LEU:HD12	1.85	0.40
1:M:400:VAL:HG23	1:M:401:VAL:HG23	2.02	0.40
1:A:78:GLU:OE1	1:A:569:LYS:HB3	2.21	0.40
5:A:601:FAD:H9	5:A:601:FAD:H1'1	1.88	0.40
4:D:28:ALA:O	4:D:32:ILE:HG13	2.21	0.40
1:M:42:ARG:HA	1:M:42:ARG:HD3	1.72	0.40
1:M:324:LEU:HG	1:M:325:HIS:ND1	2.37	0.40
2:N:155:TYR:CE2	2:N:169:GLY:HA3	2.56	0.40
1:A:176:MET:HG2	3:C:4:ARG:HH11	1.85	0.40
2:B:140:ALA:HB1	3:C:97:ILE:HD12	2.04	0.40
2:B:206:PHE:CE1	2:B:225:GLN:HG3	2.57	0.40
1:M:202:ASN:HD22	1:M:202:ASN:N	2.18	0.40
3:O:90:ALA:N	3:O:91:PRO:CD	2.84	0.40
3:C:63:LEU:HB2	4:D:40:PRO:HB3	2.03	0.40
3:C:70:ILE:O	3:C:74:ILE:HG13	2.22	0.40
2:N:19:THR:HA	3:O:5:LYS:HZ3	1.86	0.40
3:O:120:THR:HG23	4:P:30:VAL:HB	2.04	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	575/577 (100%)	551 (96%)	21 (4%)	3 (0%)	25 53
1	M	575/577 (100%)	541 (94%)	33 (6%)	1 (0%)	44 71
2	B	241/243 (99%)	231 (96%)	9 (4%)	1 (0%)	30 59
2	N	241/243 (99%)	228 (95%)	11 (5%)	2 (1%)	16 44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	128/130 (98%)	122 (95%)	6 (5%)	0	100	100
3	O	128/130 (98%)	123 (96%)	5 (4%)	0	100	100
4	D	117/119 (98%)	109 (93%)	8 (7%)	0	100	100
4	P	117/119 (98%)	115 (98%)	2 (2%)	0	100	100
All	All	2122/2138 (99%)	2020 (95%)	95 (4%)	7 (0%)	37	65

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	56	SER
1	A	329	PRO
1	A	444	GLY
2	N	170	PRO
1	A	277	PRO
1	M	329	PRO
2	N	49	PRO

### 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	460/460 (100%)	442 (96%)	18 (4%)	27	54
1	M	460/460 (100%)	424 (92%)	36 (8%)	10	33
2	B	205/205 (100%)	195 (95%)	10 (5%)	21	48
2	N	205/205 (100%)	196 (96%)	9 (4%)	24	51
3	C	111/111 (100%)	107 (96%)	4 (4%)	30	56
3	O	111/111 (100%)	107 (96%)	4 (4%)	30	56
4	D	97/97 (100%)	92 (95%)	5 (5%)	19	46
4	P	97/97 (100%)	96 (99%)	1 (1%)	73	84
All	All	1746/1746 (100%)	1659 (95%)	87 (5%)	20	47

All (87) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	A	38	VAL
1	A	42	ARG
1	A	49	GLU
1	A	52	SER
1	A	74	ASP
1	A	76	LEU
1	A	243	MET
1	A	284	LEU
1	A	299	ARG
1	A	346	GLU
1	A	413	ARG
1	A	419	ASN
1	A	465	ILE
1	A	485	ARG
1	A	490	ARG
1	A	570	ILE
1	A	572	THR
2	B	19	THR
2	B	27	GLU
2	B	109	PHE
2	B	113	LEU
2	B	116	ILE
2	B	132	ASN
2	B	154	CYS
2	B	178	ARG
2	B	237	ILE
2	B	243	ARG
3	C	12	THR
3	C	21	PHE
3	C	27	LEU
3	C	84	LYS
4	D	9	ASP
4	D	47	ASP
4	D	62	ILE
4	D	113	ILE
4	D	118	ILE
1	M	3	PHE
1	M	6	ASP
1	M	17	LEU
1	M	18	ARG
1	M	42	ARG
1	M	74	ASP

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Mol	Chain	Res	Type
1	M	76	LEU
1	M	89	CYS
1	M	93	MET
1	M	111	VAL
1	M	140	PHE
1	M	155	HIS
1	M	164	ASP
1	M	170	LEU
1	M	173	MET
1	M	180	LEU
1	M	197	ARG
1	M	202	ASN
1	M	221	VAL
1	M	243	MET
1	M	288	ASP
1	M	295	TRP
1	M	299	ARG
1	M	318	HIS
1	M	324	LEU
1	M	348	ILE
1	M	382	SER
1	M	413	ARG
1	M	439	LEU
1	M	463	CYS
1	M	485	ARG
1	M	502	LEU
1	M	537	GLU
1	M	543	ASP
1	M	544	ASP
1	M	552	LEU
2	N	5	ASN
2	N	82	ARG
2	N	121	ILE
2	N	125	ARG
2	N	184	ARG
2	N	189	LYS
2	N	206	PHE
2	N	214	CYS
2	N	243	ARG
3	O	19	LEU
3	O	39	SER
3	O	53	PRO

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Mol	Chain	Res	Type
3	O	54	GLU
4	P	118	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	HIS
1	A	141	GLN
1	A	182	GLN
1	A	279	ASN
1	A	292	GLN
1	A	442	GLN
2	B	108	HIS
2	B	123	ASN
2	B	132	ASN
2	B	150	ASN
2	B	194	GLN
3	C	72	ASN
4	D	59	GLN
4	D	92	HIS
1	M	44	HIS
1	M	134	HIS
1	M	137	HIS
1	M	145	GLN
1	M	219	HIS
1	M	292	GLN
1	M	442	GLN
1	M	473	GLN
2	N	5	ASN
2	N	46	ASN
2	N	95	ASN
2	N	150	ASN
2	N	225	GLN
3	O	95	ASN

### 5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

10 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	FES	N	245	2	0,4,4	-	-	-		
8	F3S	B	245	2	0,9,9	-	-	-		
9	SF4	N	244	2	0,12,12	-	-	-		
5	FAD	A	601	-	54,58,58	1.03	4 (7%)	71,89,89	1.56	15 (21%)
8	F3S	N	246	2	0,9,9	-	-	-		
5	FAD	M	601	-	54,58,58	2.12	7 (12%)	71,89,89	1.79	13 (18%)
6	OAA	M	802	-	8,8,8	2.27	4 (50%)	8,10,10	1.42	1 (12%)
9	SF4	B	246	2	0,12,12	-	-	-		
6	OAA	A	702	-	8,8,8	2.25	3 (37%)	8,10,10	1.29	0
7	FES	B	244	2	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
7	FES	N	245	2	-	-	0/1/1/1
8	F3S	B	245	2	-	-	0/3/3/3
9	SF4	N	244	2	-	-	0/6/5/5
5	FAD	A	601	-	-	4/30/50/50	0/6/6/6

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	F3S	N	246	2	-	-	0/3/3/3
5	FAD	M	601	-	-	20/30/50/50	0/6/6/6
6	OAA	M	802	-	-	1/8/8/8	-
9	SF4	B	246	2	-	-	0/6/5/5
6	OAA	A	702	-	-	4/8/8/8	-
7	FES	B	244	2	-	-	0/1/1/1

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	M	601	FAD	O4B-C1B	8.80	1.52	1.40
5	M	601	FAD	C4A-N3A	6.74	1.44	1.35
5	M	601	FAD	C2A-N3A	-5.52	1.23	1.32
5	M	601	FAD	C2A-N1A	5.04	1.42	1.33
6	A	702	OAA	O3-C3	3.98	1.31	1.23
6	M	802	OAA	O3-C3	3.96	1.31	1.23
6	A	702	OAA	O4-C4	3.68	1.31	1.22
6	M	802	OAA	O4-C4	3.55	1.31	1.22
5	M	601	FAD	P-O3P	3.13	1.62	1.59
6	A	702	OAA	O1-C1	3.03	1.32	1.22
6	M	802	OAA	O1-C1	2.84	1.31	1.22
5	M	601	FAD	C4X-N5	2.81	1.36	1.30
5	A	601	FAD	C4X-N5	2.61	1.36	1.30
5	M	601	FAD	PA-O3P	2.61	1.62	1.59
5	A	601	FAD	C10-N10	2.49	1.42	1.37
5	A	601	FAD	O2B-C2B	-2.43	1.36	1.43
5	A	601	FAD	O3B-C3B	-2.30	1.37	1.43
6	M	802	OAA	C3-C4	-2.19	1.50	1.53

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	M	601	FAD	N3A-C2A-N1A	-6.58	119.74	128.67
5	A	601	FAD	N3A-C2A-N1A	-6.03	120.48	128.67
5	M	601	FAD	C4B-O4B-C1B	-5.88	104.54	109.92
5	M	601	FAD	C1B-N9A-C4A	-4.38	118.94	126.64
5	M	601	FAD	O4B-C1B-N9A	3.86	113.87	108.75
5	A	601	FAD	O4B-C1B-N9A	3.41	113.26	108.75
5	M	601	FAD	C4A-C5A-N7A	3.28	112.80	109.34
5	A	601	FAD	C1B-N9A-C4A	-3.19	121.04	126.64
5	A	601	FAD	C4-N3-C2	-3.05	120.23	125.64
5	M	601	FAD	C4X-C4-N3	2.90	120.63	113.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	M	601	FAD	C4-C4X-N5	2.83	122.11	118.21
5	M	601	FAD	C4-N3-C2	-2.83	120.62	125.64
5	A	601	FAD	C5X-N5-C4X	2.82	122.65	118.09
5	A	601	FAD	C4X-C4-N3	2.82	120.44	113.25
5	M	601	FAD	O4B-C4B-C5B	-2.71	100.67	109.33
6	M	802	OAA	O4-C4-C3	-2.65	118.52	121.81
5	A	601	FAD	O2B-C2B-C3B	-2.64	103.34	111.82
5	M	601	FAD	C9A-C5X-N5	-2.48	119.82	122.45
5	A	601	FAD	C4X-C10-N1	-2.44	118.60	124.59
5	A	601	FAD	C4A-C5A-N7A	-2.35	106.86	109.34
5	A	601	FAD	O4-C4-C4X	-2.33	120.38	126.53
5	A	601	FAD	C9A-C5X-N5	-2.30	120.01	122.45
5	M	601	FAD	O4-C4-C4X	-2.27	120.53	126.53
5	A	601	FAD	C10-C4X-N5	-2.26	120.19	124.81
5	A	601	FAD	C10-N1-C2	2.24	121.70	116.85
5	A	601	FAD	C4-C4X-N5	2.17	121.20	118.21
5	M	601	FAD	C10-C4X-N5	-2.15	120.42	124.81
5	M	601	FAD	C5X-N5-C4X	2.10	121.49	118.09
5	A	601	FAD	O3P-P-O1P	-2.10	104.39	110.70

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	601	FAD	N10-C1'-C2'-O2'
5	A	601	FAD	C5'-O5'-P-O2P
5	M	601	FAD	C5B-O5B-PA-O2A
5	M	601	FAD	C5B-O5B-PA-O3P
5	M	601	FAD	P-O3P-PA-O5B
5	M	601	FAD	N10-C1'-C2'-O2'
5	M	601	FAD	N10-C1'-C2'-C3'
5	M	601	FAD	C1'-C2'-C3'-O3'
5	M	601	FAD	C1'-C2'-C3'-C4'
5	M	601	FAD	O2'-C2'-C3'-O3'
5	M	601	FAD	O2'-C2'-C3'-C4'
5	M	601	FAD	C2'-C3'-C4'-O4'
5	M	601	FAD	C2'-C3'-C4'-C5'
5	M	601	FAD	O3'-C3'-C4'-O4'
5	M	601	FAD	O3'-C3'-C4'-C5'
5	M	601	FAD	C5'-O5'-P-O2P
6	A	702	OAA	C2-C3-C4-O5
5	M	601	FAD	O4B-C4B-C5B-O5B

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Mol	Chain	Res	Type	Atoms
5	M	601	FAD	C3B-C4B-C5B-O5B
5	A	601	FAD	PA-O3P-P-O5'
6	A	702	OAA	C1-C2-C3-O3
6	A	702	OAA	O3-C3-C4-O4
6	A	702	OAA	C2-C3-C4-O4
5	M	601	FAD	C5'-O5'-P-O1P
5	M	601	FAD	C5'-O5'-P-O3P
5	M	601	FAD	PA-O3P-P-O1P
6	M	802	OAA	O1-C1-C2-C3
5	M	601	FAD	PA-O3P-P-O2P
5	A	601	FAD	PA-O3P-P-O2P

There are no ring outliers.

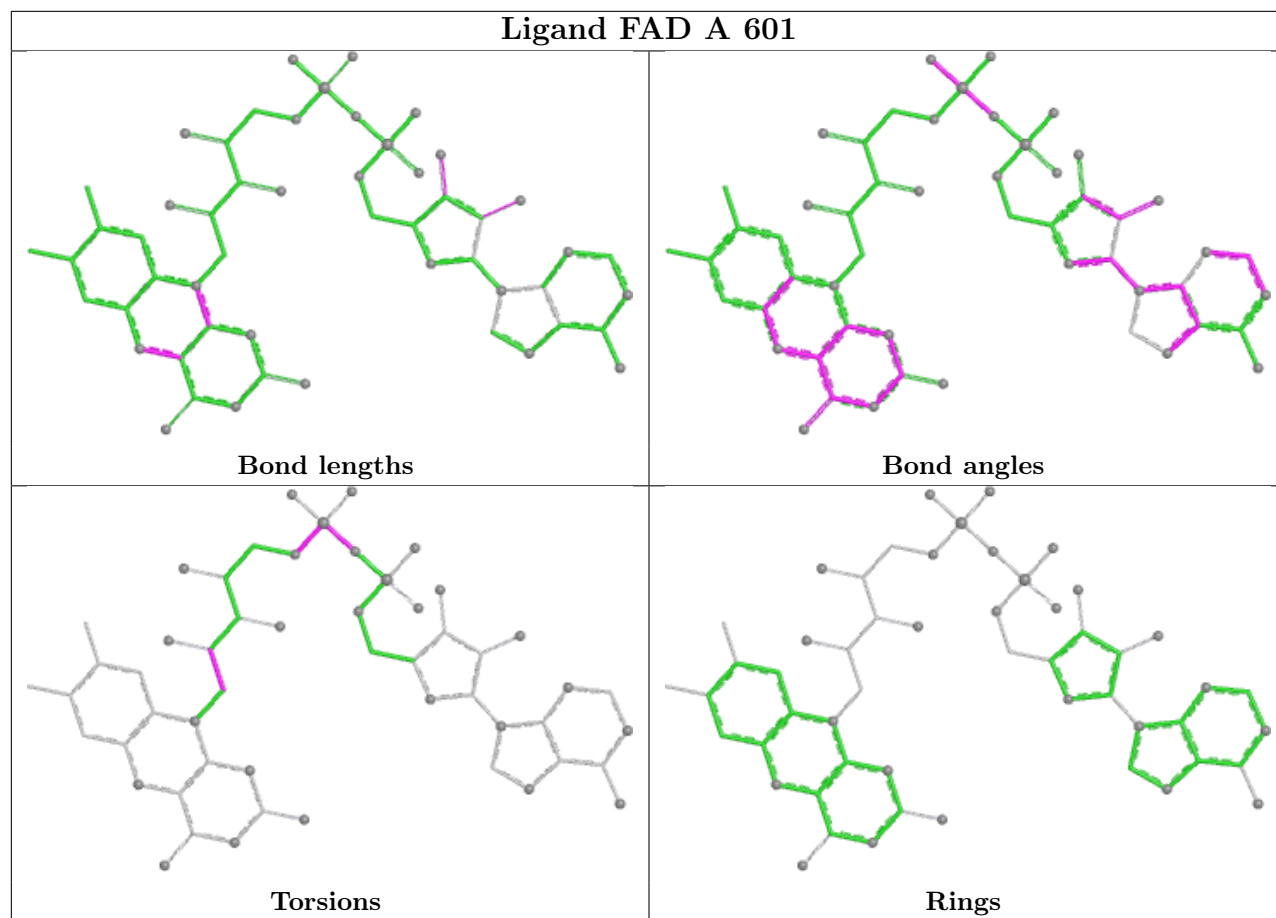
8 monomers are involved in 47 short contacts:

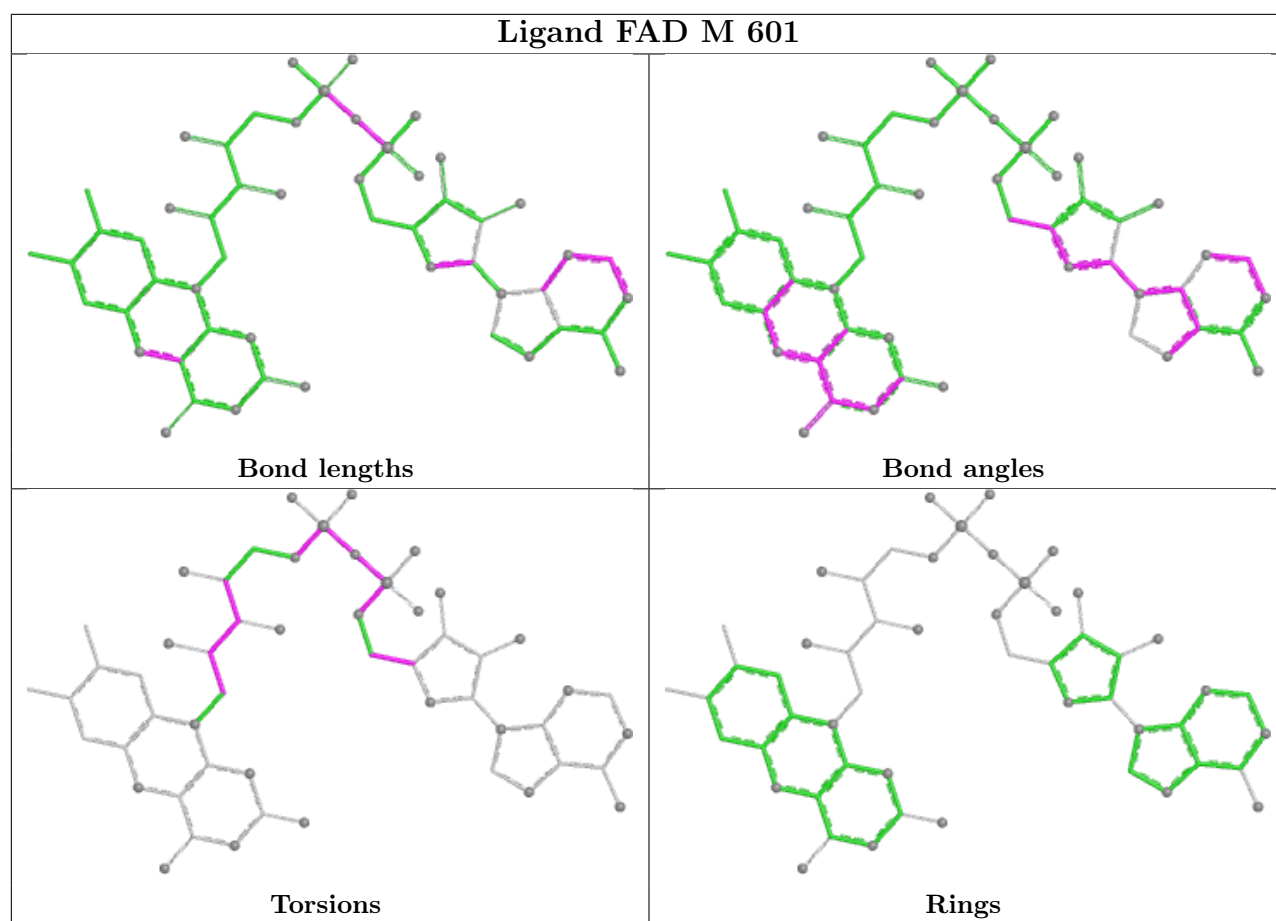
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	N	245	FES	1	0
8	B	245	F3S	2	0
9	N	244	SF4	2	0
5	A	601	FAD	10	0
8	N	246	F3S	3	0
5	M	601	FAD	20	0
6	M	802	OAA	2	0
9	B	246	SF4	7	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## Ligand FAD A 601





## 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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	577/577 (100%)	-0.69	0 <span>100</span> <span>100</span>	29, 46, 91, 117	0
1	M	577/577 (100%)	0.92	80 (13%) <span>7</span> <span>10</span>	88, 155, 184, 215	0
2	B	243/243 (100%)	-0.70	0 <span>100</span> <span>100</span>	29, 51, 75, 133	0
2	N	243/243 (100%)	0.50	8 (3%) <span>49</span> <span>42</span>	76, 129, 206, 230	0
3	C	130/130 (100%)	-0.59	0 <span>100</span> <span>100</span>	53, 69, 98, 108	0
3	O	130/130 (100%)	-0.13	0 <span>100</span> <span>100</span>	60, 93, 153, 194	0
4	D	119/119 (100%)	-0.41	3 (2%) <span>58</span> <span>49</span>	49, 65, 91, 108	0
4	P	119/119 (100%)	-0.29	0 <span>100</span> <span>100</span>	57, 81, 139, 168	0
All	All	2138/2138 (100%)	-0.04	91 (4%) <span>40</span> <span>35</span>	29, 80, 179, 230	0

All (91) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	188	VAL	6.9
1	M	189	VAL	5.9
1	M	387	GLY	5.3
1	M	394	ASN	5.0
2	N	52	SER	4.9
1	M	386	HIS	4.9
1	M	8	ALA	4.5
1	M	385	LEU	4.3
1	M	517	CYS	4.1
1	M	498	PHE	4.0
1	M	502	LEU	4.0
1	M	465	ILE	4.0
1	M	405	LEU	4.0
1	M	14	GLY	3.8
1	M	295	TRP	3.8
1	M	170	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	M	499	ASN	3.5
1	M	378	GLY	3.4
1	M	377	VAL	3.4
1	M	411	THR	3.3
1	M	33	ALA	3.2
1	M	160	ILE	3.2
1	M	196	GLY	3.1
1	M	573	LEU	3.0
1	M	489	VAL	3.0
1	M	491	ILE	3.0
4	D	118	ILE	3.0
1	M	409	GLN	2.9
1	M	514	VAL	2.9
1	M	10	VAL	2.8
1	M	402	PHE	2.8
1	M	195	ALA	2.8
1	M	439	LEU	2.7
1	M	165	GLY	2.7
1	M	215	MET	2.7
1	M	476	ILE	2.7
1	M	373	GLY	2.7
1	M	572	THR	2.7
1	M	574	PRO	2.6
1	M	77	CYS	2.6
1	M	576	ALA	2.6
1	M	475	THR	2.6
1	M	198	VAL	2.6
1	M	375	PHE	2.6
1	M	228	PHE	2.6
1	M	23	ALA	2.6
1	M	125	TRP	2.5
1	M	7	LEU	2.5
1	M	180	LEU	2.5
1	M	497	VAL	2.5
1	M	571	THR	2.4
1	M	495	SER	2.4
1	M	9	ILE	2.4
1	M	383	VAL	2.4
1	M	374	LEU	2.4
1	M	206	GLY	2.4
1	M	158	LEU	2.4
1	M	389	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
1	M	100	GLY	2.4
1	M	415	ALA	2.4
2	N	95	ASN	2.3
1	M	401	VAL	2.3
1	M	361	ILE	2.3
1	M	552	LEU	2.3
2	N	98	ILE	2.3
1	M	392	GLY	2.3
2	N	206	PHE	2.2
1	M	187	ALA	2.2
1	M	382	SER	2.2
4	D	117	THR	2.2
1	M	390	ARG	2.2
1	M	172	ALA	2.2
1	M	519	ALA	2.2
1	M	32	ILE	2.2
1	M	205	GLY	2.1
1	M	490	ARG	2.1
1	M	329	PRO	2.1
1	M	38	VAL	2.1
2	N	56	SER	2.1
1	M	500	THR	2.1
2	N	25	PHE	2.1
1	M	92	GLU	2.1
1	M	173	MET	2.1
1	M	553	ALA	2.1
1	M	190	MET	2.1
2	N	6	LEU	2.1
1	M	494	THR	2.1
1	M	135	MET	2.1
4	D	1	ILE	2.0
1	M	130	LYS	2.0
2	N	54	ARG	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.3 Carbohydrates ⓘ

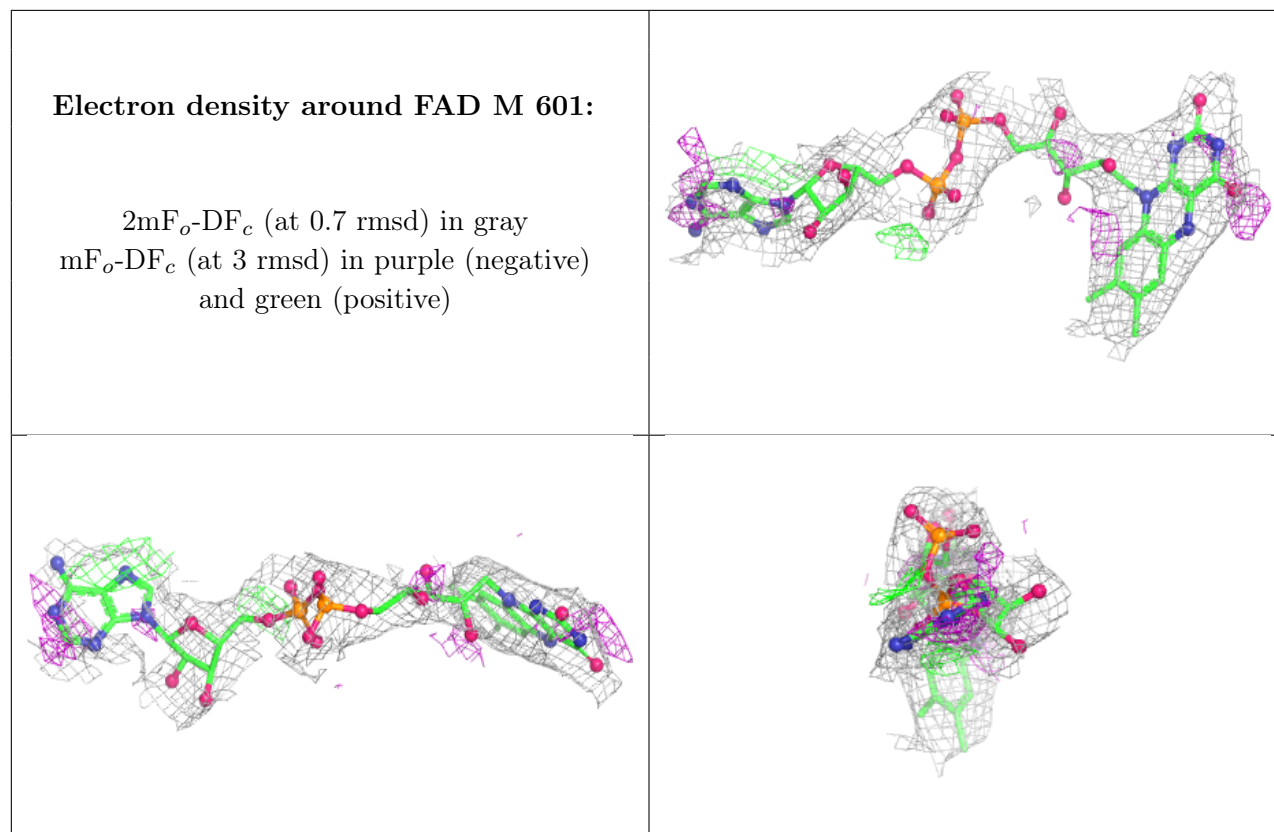
There are no monosaccharides in this entry.

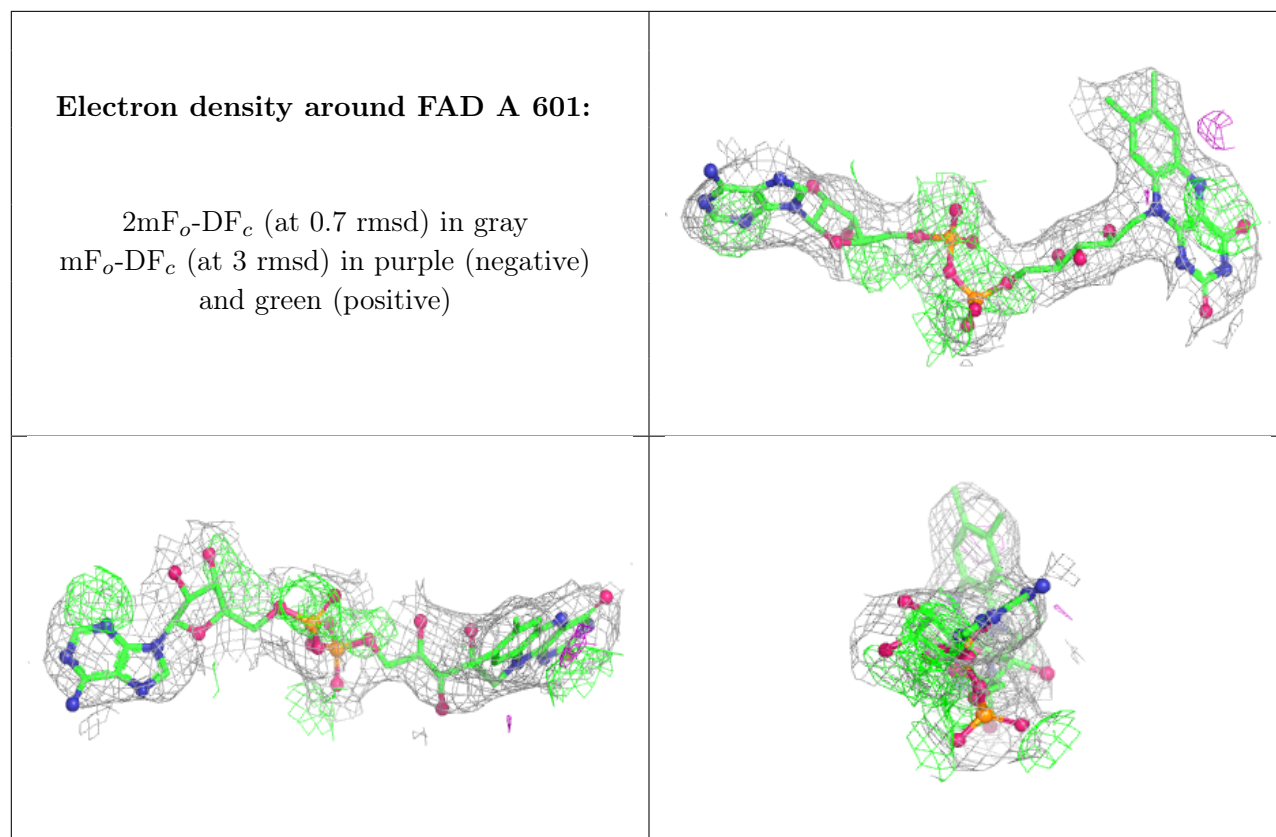
## 6.4 Ligands ⓘ

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
6	OAA	M	802	9/9	0.56	0.19	114,114,115,115	0
6	OAA	A	702	9/9	0.82	0.20	45,48,49,50	0
5	FAD	M	601	53/53	0.82	0.14	95,109,125,126	0
5	FAD	A	601	53/53	0.94	0.11	43,47,57,61	0
8	F3S	N	246	7/7	0.97	0.06	75,75,76,76	0
9	SF4	N	244	8/8	0.97	0.06	82,82,83,83	0
7	FES	N	245	4/4	0.98	0.05	88,88,89,90	0
9	SF4	B	246	8/8	0.99	0.06	63,65,66,66	0
8	F3S	B	245	7/7	0.99	0.04	45,47,47,47	0
7	FES	B	244	4/4	1.00	0.02	32,34,34,35	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.





## 6.5 Other polymers [i](#)

There are no such residues in this entry.