



Full wwPDB X-ray Structure Validation Report ⓘ

May 18, 2020 – 09:05 pm BST

PDB ID : 2E1M
Title : Crystal Structure of L-Glutamate Oxidase from Streptomyces sp. X-119-6
Authors : Sasaki, C.; Kashima, A.; Sakaguchi, C.; Mizuno, H.; Arima, J.; Kusakabe, H.;
Tamura, T.; Sugio, S.; Inagaki, K.
Deposited on : 2006-10-26
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

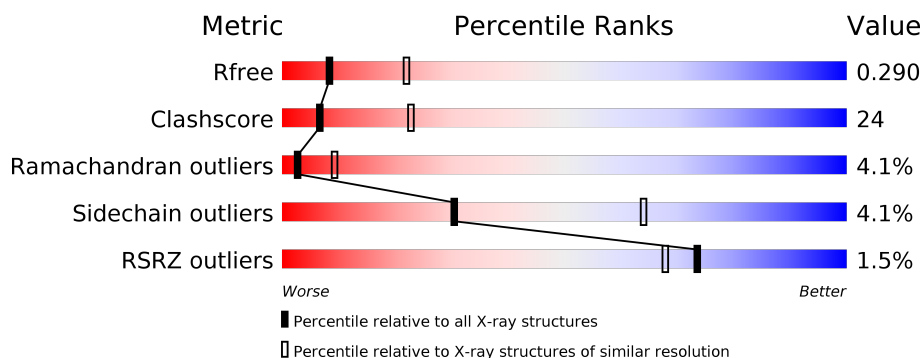
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	376	<div> <div>2%</div> <div> <div>50%</div> <div>39%</div> <div>5%</div> <div>5%</div> </div> </div>
2	B	130	<div> <div>39%</div> <div>28%</div> <div>31%</div> </div>
3	C	181	<div> <div>54%</div> <div>25%</div> <div>17%</div> </div>

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
4	PO4	A	903	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4807 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 L-glutamate oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	356	Total	C	N	O	S	0	0	0
			2818	1786	497	526	9			

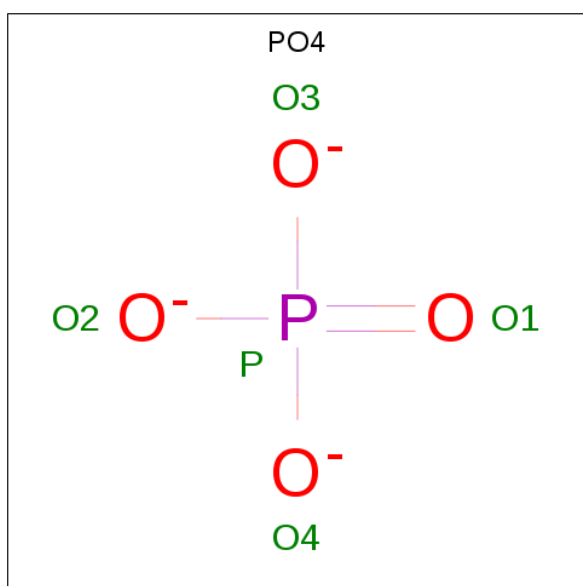
- Molecule 2 is a protein called L-glutamate oxidase.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	90	Total	C	N	O	0	0	0
			751	488	124	139			

- Molecule 3 is a protein called L-glutamate oxidase.

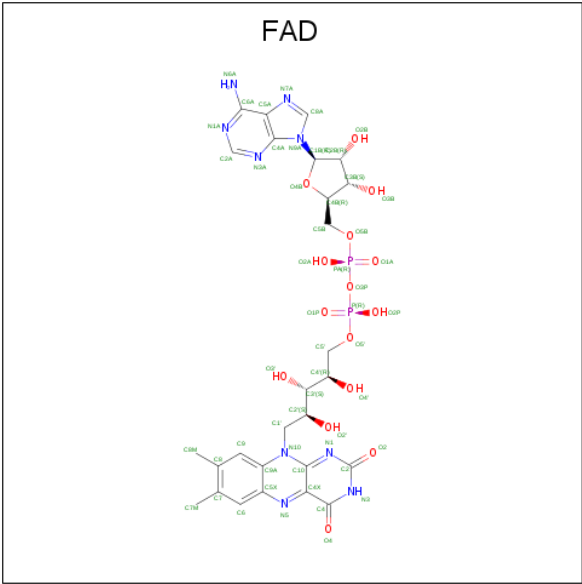
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	151	Total	C	N	O	S	0	0	0
			1170	740	205	222	3			

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



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

- Molecule 5 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).

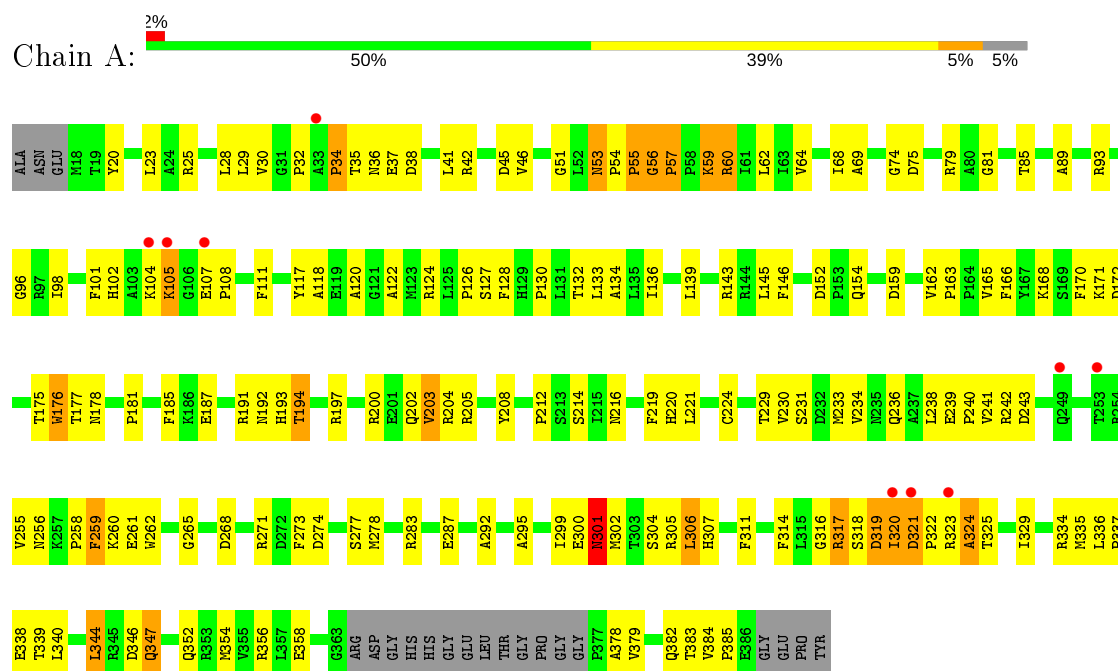


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	
			53	27	9	15	2	

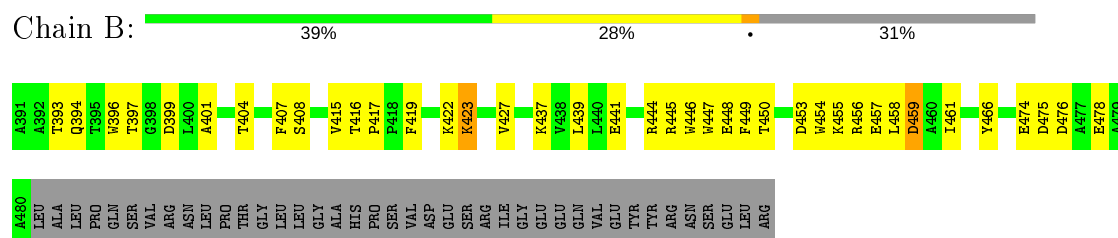
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

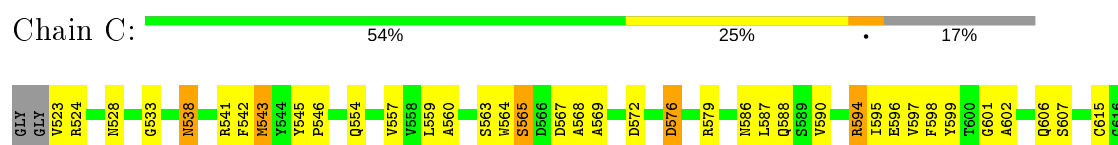
• Molecule 1: L-glutamate oxidase



• Molecule 2: L-glutamate oxidase



• Molecule 3: L-glutamate oxidase





4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	123.88 Å 123.88 Å 168.76 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.27 – 2.80 49.82 – 2.59	Depositor EDS
% Data completeness (in resolution range)	98.4 (45.27-2.80) 99.9 (49.82-2.59)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.63 (at 2.58 Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.248 , 0.308 0.230 , 0.290	Depositor DCC
R_{free} test set	1166 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å ²)	45.5	Xtriage
Anisotropy	0.388	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4807	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.12% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, FAD

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.38	0/2887	0.69	1/3918 (0.0%)
2	B	0.42	0/775	0.67	0/1057
3	C	0.41	0/1208	0.68	0/1655
All	All	0.39	0/4870	0.68	1/6630 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	277	SER	N-CA-C	-5.15	97.09	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2818	0	2770	167	0
2	B	751	0	714	41	0
3	C	1170	0	1079	52	0
4	A	15	0	0	4	0
5	A	53	0	31	7	0
All	All	4807	0	4594	221	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 24.

All (221) 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:347:GLN:N	1:A:347:GLN:HE21	1.39	1.18
1:A:304:SER:HB2	3:C:565:SER:HB3	1.31	1.10
1:A:216:ASN:HB3	1:A:221:LEU:HD12	1.52	0.89
1:A:53:ASN:O	1:A:55:PRO:HD3	1.72	0.88
1:A:192:ASN:HB3	1:A:205:ARG:HB2	1.57	0.85
1:A:347:GLN:N	1:A:347:GLN:NE2	2.22	0.84
1:A:347:GLN:HE21	1:A:347:GLN:H	1.26	0.82
1:A:212:PRO:HB2	1:A:216:ASN:HD21	1.41	0.82
1:A:321:ASP:HB3	1:A:324:ALA:HB2	1.59	0.81
1:A:323:ARG:HH11	1:A:323:ARG:HB2	1.46	0.79
1:A:238:LEU:HB2	1:A:242:ARG:HH12	1.50	0.76
1:A:238:LEU:HB2	1:A:242:ARG:NH1	2.01	0.74
1:A:212:PRO:HB2	1:A:216:ASN:ND2	2.04	0.73
1:A:274:ASP:OD2	3:C:627:THR:HG23	1.89	0.72
1:A:321:ASP:CB	1:A:324:ALA:HB2	2.18	0.72
2:B:437:LYS:HG2	3:C:559:LEU:HD11	1.71	0.72
1:A:256:ASN:HB3	1:A:262:TRP:CD1	2.26	0.71
1:A:53:ASN:HB3	1:A:54:PRO:HD3	1.72	0.70
1:A:358:GLU:HG3	2:B:416:THR:HG23	1.73	0.69
1:A:347:GLN:H	1:A:347:GLN:NE2	1.89	0.67
5:A:801:FAD:H5'2	3:C:645:GLU:HB2	1.76	0.67
1:A:323:ARG:NH1	1:A:323:ARG:HB2	2.10	0.67
1:A:260:LYS:HE2	1:A:261:GLU:OE2	1.96	0.66
2:B:445:ARG:HG2	2:B:447:TRP:CZ2	2.29	0.66
1:A:30:VAL:HG22	1:A:170:PHE:CZ	2.31	0.66
1:A:221:LEU:HD21	1:A:292:ALA:HA	1.78	0.65
1:A:194:THR:OG1	1:A:205:ARG:HD2	1.97	0.65
3:C:634:VAL:HG11	3:C:663:ARG:NH2	2.11	0.65
1:A:352:GLN:NE2	1:A:383:THR:OG1	2.30	0.65
1:A:301:ASN:HD22	1:A:301:ASN:C	2.01	0.63
1:A:60:ARG:HH12	1:A:85:THR:CB	2.12	0.63
1:A:323:ARG:O	1:A:323:ARG:HG2	1.99	0.62
3:C:650:LYS:O	3:C:653:TRP:HB2	1.99	0.62
1:A:166:PHE:HE2	1:A:168:LYS:HG3	1.64	0.62
1:A:53:ASN:HB3	1:A:54:PRO:CD	2.30	0.62
1:A:120:ALA:HB1	3:C:606:GLN:HG2	1.81	0.61
1:A:354:MET:HA	1:A:383:THR:HG22	1.82	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:384:VAL:HG13	1:A:385:PRO:HD2	1.82	0.61
1:A:122:ALA:HA	5:A:801:FAD:C4X	2.30	0.61
1:A:166:PHE:CE2	1:A:168:LYS:HG3	2.36	0.61
1:A:229:THR:O	1:A:233:MET:HG3	2.01	0.61
1:A:134:ALA:HA	1:A:178:ASN:HD21	1.64	0.61
1:A:230:VAL:HG21	1:A:299:ILE:HB	1.82	0.60
3:C:533:GLY:HA2	3:C:545:TYR:CE1	2.36	0.60
1:A:46:VAL:O	1:A:51:GLY:HA2	2.02	0.60
1:A:242:ARG:HH21	1:A:317:ARG:HD2	1.66	0.60
1:A:192:ASN:HB3	1:A:205:ARG:CB	2.28	0.60
1:A:329:ILE:HG21	1:A:335:MET:HB2	1.84	0.60
1:A:356:ARG:HB3	1:A:382:GLN:HB3	1.84	0.60
1:A:283:ARG:O	1:A:287:GLU:HA	2.01	0.59
1:A:102:HIS:CE1	1:A:334:ARG:HD3	2.37	0.59
1:A:136:ILE:HG12	1:A:336:LEU:HD13	1.85	0.59
1:A:166:PHE:CD1	1:A:177:THR:HG22	2.37	0.59
1:A:136:ILE:CD1	1:A:329:ILE:HD11	2.32	0.58
1:A:300:GLU:O	1:A:302:MET:HG3	2.03	0.58
1:A:200:ARG:HD3	2:B:478:GLU:OE2	2.03	0.58
1:A:136:ILE:HD13	1:A:329:ILE:HD11	1.86	0.58
1:A:305:ARG:NE	3:C:564:TRP:CE3	2.72	0.58
1:A:122:ALA:HA	5:A:801:FAD:N5	2.18	0.57
1:A:316:GLY:O	1:A:317:ARG:C	2.42	0.57
1:A:154:GLN:HE21	1:A:154:GLN:HA	1.69	0.57
1:A:301:ASN:HB2	3:C:542:PHE:CE1	2.40	0.57
1:A:154:GLN:NE2	1:A:154:GLN:HA	2.20	0.57
1:A:36:ASN:O	1:A:171:LYS:HE2	2.04	0.57
1:A:53:ASN:CB	1:A:54:PRO:CD	2.83	0.56
1:A:133:LEU:HB3	1:A:165:VAL:HG22	1.88	0.56
2:B:408:SER:OG	3:C:615:CYS:HB2	2.05	0.56
2:B:474:GLU:CG	3:C:523:VAL:HA	2.35	0.55
1:A:301:ASN:H	3:C:542:PHE:HZ	1.54	0.55
1:A:203:VAL:HG23	1:A:204:ARG:O	2.07	0.55
1:A:111:PHE:HB3	2:B:441:GLU:CD	2.27	0.54
1:A:37:GLU:OE1	1:A:42:ARG:NH2	2.40	0.54
1:A:301:ASN:HB2	3:C:542:PHE:CZ	2.43	0.54
2:B:449:PHE:CZ	2:B:457:GLU:HG2	2.42	0.54
1:A:274:ASP:OD2	3:C:624:HIS:HA	2.07	0.54
3:C:563:SER:O	3:C:568:ALA:HB2	2.08	0.54
1:A:28:LEU:HD22	1:A:262:TRP:CZ2	2.42	0.54
1:A:197:ARG:HD3	3:C:590:VAL:HG22	1.90	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:283:ARG:HH22	4:A:903:PO4:P	2.30	0.53
1:A:133:LEU:HB3	1:A:165:VAL:CG2	2.39	0.53
1:A:346:ASP:C	1:A:347:GLN:HE21	2.06	0.53
2:B:450:THR:H	2:B:453:ASP:HB2	1.73	0.53
3:C:579:ARG:HH12	3:C:607:SER:HB2	1.73	0.52
1:A:241:VAL:HG22	1:A:273:PHE:CZ	2.45	0.52
1:A:208:TYR:CD1	1:A:212:PRO:HA	2.44	0.52
1:A:305:ARG:O	1:A:307:HIS:N	2.43	0.52
2:B:454:TRP:CZ2	3:C:594:ARG:HD3	2.45	0.52
1:A:25:ARG:HH11	1:A:30:VAL:CG1	2.22	0.52
1:A:93:ARG:NH2	1:A:96:GLY:O	2.42	0.52
2:B:475:ASP:OD2	2:B:476:ASP:N	2.43	0.52
1:A:111:PHE:HB3	2:B:441:GLU:OE2	2.11	0.51
1:A:32:PRO:C	1:A:34:PRO:HD2	2.30	0.51
1:A:162:VAL:HG12	1:A:163:PRO:O	2.09	0.51
1:A:165:VAL:HG23	1:A:178:ASN:HD22	1.74	0.51
1:A:25:ARG:HH11	1:A:30:VAL:HG12	1.75	0.51
1:A:68:ILE:HG23	1:A:69:ALA:N	2.25	0.51
1:A:28:LEU:O	1:A:29:LEU:HB2	2.10	0.51
2:B:454:TRP:O	2:B:458:LEU:HB2	2.11	0.51
1:A:55:PRO:O	1:A:56:GLY:O	2.29	0.51
1:A:152:ASP:HA	1:A:191:ARG:HD2	1.93	0.51
1:A:57:PRO:HG2	1:A:59:LYS:NZ	2.26	0.50
1:A:93:ARG:NH1	4:A:901:PO4:O3	2.44	0.50
2:B:474:GLU:OE2	3:C:524:ARG:N	2.35	0.50
1:A:278:MET:HG2	1:A:302:MET:HE3	1.93	0.50
1:A:42:ARG:O	1:A:45:ASP:HB3	2.11	0.50
1:A:268:ASP:HA	1:A:271:ARG:NH1	2.26	0.50
1:A:314:PHE:O	1:A:317:ARG:HB2	2.11	0.50
1:A:145:LEU:HD21	1:A:187:GLU:HB3	1.93	0.50
1:A:334:ARG:HD2	1:A:338:GLU:OE2	2.12	0.49
1:A:46:VAL:HG21	3:C:666:ILE:HD11	1.93	0.49
2:B:423:LYS:NZ	3:C:632:ASP:O	2.37	0.49
1:A:334:ARG:HG3	1:A:335:MET:N	2.28	0.49
1:A:265:GLY:O	1:A:268:ASP:HB2	2.13	0.49
1:A:378:ALA:HB3	2:B:399:ASP:HA	1.94	0.49
1:A:127:SER:HB3	1:A:325:THR:H	1.78	0.49
1:A:197:ARG:NH2	2:B:478:GLU:OE2	2.45	0.49
1:A:38:ASP:OD2	1:A:41:LEU:HG	2.13	0.48
3:C:646:HIS:HA	3:C:651:HIS:CD2	2.47	0.48
3:C:524:ARG:HH11	3:C:524:ARG:HG2	1.78	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:PHE:C	1:A:130:PRO:HD3	2.33	0.48
1:A:323:ARG:HH11	1:A:323:ARG:CB	2.20	0.48
1:A:320:ILE:O	1:A:322:PRO:HD3	2.14	0.48
1:A:302:MET:O	1:A:306:LEU:HD13	2.13	0.48
2:B:394:GLN:HG2	2:B:396:TRP:CH2	2.49	0.47
1:A:383:THR:HG1	2:B:396:TRP:HZ3	1.62	0.47
2:B:407:PHE:CD1	2:B:427:VAL:HG22	2.49	0.47
1:A:42:ARG:O	1:A:46:VAL:HG23	2.15	0.47
1:A:255:VAL:HG13	1:A:255:VAL:O	2.15	0.47
3:C:533:GLY:HA2	3:C:545:TYR:CD1	2.48	0.47
1:A:139:LEU:HD11	1:A:340:LEU:HD21	1.97	0.47
1:A:54:PRO:O	1:A:56:GLY:N	2.48	0.47
2:B:446:TRP:CE3	2:B:447:TRP:N	2.83	0.47
1:A:89:ALA:HB2	5:A:801:FAD:C2A	2.45	0.47
1:A:301:ASN:ND2	1:A:301:ASN:C	2.68	0.46
2:B:444:ARG:HA	3:C:554:GLN:O	2.15	0.46
3:C:538:ASN:OD1	3:C:586:ASN:HB3	2.16	0.46
1:A:139:LEU:HD22	1:A:339:THR:HG22	1.98	0.46
1:A:268:ASP:HA	1:A:271:ARG:HH12	1.81	0.46
1:A:384:VAL:CG1	1:A:385:PRO:HD2	2.45	0.46
1:A:166:PHE:CE2	1:A:168:LYS:HE2	2.51	0.46
1:A:268:ASP:OD1	1:A:271:ARG:NH1	2.45	0.46
1:A:319:ASP:O	1:A:321:ASP:N	2.48	0.46
1:A:334:ARG:O	1:A:337:PRO:HD2	2.16	0.46
1:A:175:THR:O	1:A:176:TRP:HB2	2.15	0.46
2:B:461:ILE:HD11	3:C:598:PHE:HE2	1.81	0.46
1:A:104:LYS:O	1:A:105:LYS:C	2.54	0.46
1:A:107:GLU:HB2	1:A:108:PRO:CD	2.46	0.46
1:A:126:PRO:HB3	1:A:128:PHE:CE2	2.51	0.46
1:A:132:THR:O	1:A:136:ILE:HG13	2.16	0.45
1:A:197:ARG:HH11	1:A:202:GLN:HB2	1.81	0.45
1:A:42:ARG:HD3	3:C:666:ILE:HD13	1.97	0.45
1:A:239:GLU:N	1:A:240:PRO:HD2	2.32	0.45
3:C:597:VAL:HG23	3:C:598:PHE:N	2.31	0.45
1:A:242:ARG:NH2	1:A:319:ASP:OD2	2.49	0.45
1:A:166:PHE:HE2	1:A:168:LYS:HE2	1.82	0.45
1:A:20:TYR:CZ	1:A:271:ARG:HG3	2.51	0.45
1:A:35:THR:O	1:A:36:ASN:HB2	2.17	0.45
2:B:393:THR:OG1	2:B:394:GLN:N	2.49	0.45
1:A:107:GLU:HB2	1:A:108:PRO:HD2	1.99	0.45
1:A:219:PHE:O	1:A:220:HIS:HB2	2.17	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:422:LYS:HD3	2:B:422:LYS:HA	1.79	0.45
1:A:307:HIS:HA	4:A:903:PO4:O4	2.17	0.45
1:A:379:VAL:O	2:B:397:THR:HA	2.16	0.44
2:B:458:LEU:HD23	2:B:466:TYR:HA	2.00	0.44
1:A:378:ALA:HB3	2:B:399:ASP:O	2.16	0.44
1:A:101:PHE:O	1:A:117:TYR:HB2	2.17	0.44
1:A:62:LEU:O	2:B:401:ALA:HA	2.17	0.44
1:A:242:ARG:NH2	1:A:317:ARG:HD2	2.30	0.44
1:A:64:VAL:O	2:B:404:THR:OG1	2.29	0.44
1:A:231:SER:O	1:A:234:VAL:N	2.49	0.44
3:C:569:ALA:O	3:C:572:ASP:HB2	2.18	0.44
1:A:274:ASP:CG	3:C:627:THR:HG23	2.38	0.44
1:A:230:VAL:O	1:A:234:VAL:HG23	2.18	0.44
1:A:197:ARG:HD2	1:A:202:GLN:OE1	2.18	0.43
1:A:240:PRO:O	1:A:243:ASP:HB2	2.18	0.43
2:B:394:GLN:HB3	2:B:396:TRP:CZ3	2.53	0.43
1:A:314:PHE:O	1:A:317:ARG:CB	2.66	0.43
1:A:321:ASP:HB2	1:A:324:ALA:HB2	1.99	0.43
5:A:801:FAD:H5'2	3:C:645:GLU:CB	2.45	0.43
2:B:454:TRP:CH2	3:C:594:ARG:HD3	2.54	0.43
1:A:283:ARG:NH2	4:A:903:PO4:O2	2.51	0.43
1:A:317:ARG:HE	1:A:317:ARG:HB3	1.69	0.43
1:A:197:ARG:HG3	1:A:202:GLN:HB2	2.01	0.43
1:A:96:GLY:C	1:A:98:ILE:H	2.22	0.43
3:C:563:SER:HB2	3:C:567:ASP:CB	2.49	0.43
3:C:588:GLN:NE2	3:C:596:GLU:HB3	2.34	0.43
1:A:59:LYS:NZ	3:C:671:ALA:O	2.36	0.43
1:A:258:PRO:O	1:A:259:PHE:C	2.56	0.43
1:A:242:ARG:HE	1:A:317:ARG:HH11	1.66	0.43
5:A:801:FAD:HM83	3:C:617:GLU:HG3	2.01	0.43
2:B:461:ILE:HD11	3:C:598:PHE:CE2	2.53	0.43
1:A:23:LEU:HD11	3:C:627:THR:HA	2.01	0.43
1:A:118:ALA:HB1	2:B:439:LEU:HD22	2.01	0.42
1:A:74:GLY:O	1:A:344:LEU:HD21	2.19	0.42
1:A:75:ASP:HA	1:A:344:LEU:HD21	2.02	0.42
3:C:543:MET:HG2	3:C:560:ALA:O	2.19	0.42
1:A:295:ALA:O	1:A:299:ILE:HG12	2.20	0.41
2:B:416:THR:HA	2:B:417:PRO:C	2.37	0.41
2:B:455:LYS:O	2:B:459:ASP:HB2	2.20	0.41
3:C:599:TYR:CE2	3:C:601:GLY:HA2	2.55	0.41
1:A:79:ARG:HH11	1:A:79:ARG:HG3	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:546:PRO:HG3	3:C:557:VAL:O	2.20	0.41
3:C:671:ALA:HA	3:C:672:PRO:HD3	1.90	0.41
1:A:133:LEU:HA	1:A:133:LEU:HD23	1.72	0.41
2:B:456:ARG:HG2	2:B:457:GLU:N	2.35	0.41
3:C:543:MET:CE	3:C:587:LEU:HD12	2.50	0.41
1:A:205:ARG:HG2	1:A:205:ARG:HH11	1.85	0.41
1:A:124:ARG:HD3	1:A:146:PHE:CE2	2.55	0.41
1:A:205:ARG:NH1	1:A:205:ARG:HG2	2.36	0.41
5:A:801:FAD:HM83	3:C:617:GLU:CG	2.51	0.41
2:B:415:VAL:HG11	2:B:419:PHE:CE2	2.56	0.41
3:C:543:MET:HE2	3:C:587:LEU:HD12	2.03	0.41
1:A:163:PRO:HD3	1:A:185:PHE:CG	2.56	0.41
1:A:38:ASP:HB3	1:A:41:LEU:HD12	2.03	0.41
3:C:588:GLN:HG3	3:C:595:ILE:HD11	2.03	0.40
2:B:441:GLU:OE2	3:C:602:ALA:HB3	2.21	0.40
2:B:448:GLU:O	3:C:528:ASN:ND2	2.54	0.40
1:A:143:ARG:NH1	1:A:162:VAL:HG11	2.36	0.40
1:A:68:ILE:CG2	1:A:69:ALA:N	2.85	0.40
2:B:474:GLU:OE2	3:C:523:VAL:HA	2.21	0.40
3:C:634:VAL:HG11	3:C:663:ARG:CZ	2.51	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	352/376 (94%)	297 (84%)	35 (10%)	20 (6%)	1 5
2	B	88/130 (68%)	80 (91%)	8 (9%)	0	100 100
3	C	149/181 (82%)	129 (87%)	16 (11%)	4 (3%)	5 17
All	All	589/687 (86%)	506 (86%)	59 (10%)	24 (4%)	3 9

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	53	ASN
1	A	172	ASP
1	A	259	PHE
1	A	306	LEU
1	A	320	ILE
1	A	56	GLY
1	A	301	ASN
1	A	319	ASP
1	A	34	PRO
1	A	214	SER
1	A	317	ARG
3	C	541	ARG
3	C	576	ASP
3	C	645	GLU
1	A	55	PRO
1	A	57	PRO
1	A	105	LYS
1	A	176	TRP
1	A	318	SER
1	A	324	ALA
1	A	344	LEU
3	C	565	SER
1	A	81	GLY
1	A	181	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	298/311 (96%)	286 (96%)	12 (4%)	31	65
2	B	76/111 (68%)	74 (97%)	2 (3%)	46	79
3	C	116/132 (88%)	110 (95%)	6 (5%)	23	55
All	All	490/554 (88%)	470 (96%)	20 (4%)	30	64

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	LYS
1	A	60	ARG
1	A	159	ASP
1	A	193	HIS
1	A	194	THR
1	A	203	VAL
1	A	224	CYS
1	A	236	GLN
1	A	301	ASN
1	A	311	PHE
1	A	321	ASP
1	A	347	GLN
2	B	423	LYS
2	B	459	ASP
3	C	538	ASN
3	C	543	MET
3	C	576	ASP
3	C	594	ARG
3	C	627	THR
3	C	629	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	GLN
1	A	50	ASN
1	A	154	GLN
1	A	158	GLN
1	A	178	ASN
1	A	216	ASN
1	A	236	GLN
1	A	301	ASN
1	A	347	GLN
1	A	352	GLN
1	A	382	GLN
2	B	471	GLN
3	C	586	ASN
3	C	630	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	PO4	A	901	-	4,4,4	2.39	3 (75%)	6,6,6	0.49	0
4	PO4	A	903	-	4,4,4	2.37	3 (75%)	6,6,6	0.49	0
4	PO4	A	902	-	4,4,4	2.22	3 (75%)	6,6,6	0.52	0
5	FAD	A	801	-	51,58,58	3.00	21 (41%)	60,89,89	1.86	13 (21%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	FAD	A	801	-	-	2/30/50/50	0/6/6/6

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	801	FAD	C4X-C10	11.75	1.50	1.38
5	A	801	FAD	C9A-N10	7.10	1.48	1.38
5	A	801	FAD	O4B-C1B	5.41	1.48	1.41
5	A	801	FAD	C10-N1	4.90	1.39	1.33

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	801	FAD	C4-N3	4.52	1.40	1.33
5	A	801	FAD	C4-C4X	4.38	1.48	1.41
5	A	801	FAD	C8-C7	3.86	1.50	1.40
5	A	801	FAD	PA-O2A	-3.75	1.37	1.55
5	A	801	FAD	O5'-C5'	3.58	1.58	1.44
5	A	801	FAD	C4X-N5	3.57	1.38	1.33
5	A	801	FAD	C4A-N3A	3.48	1.40	1.35
5	A	801	FAD	C5X-N5	3.15	1.40	1.35
5	A	801	FAD	C1'-N10	3.05	1.51	1.48
5	A	801	FAD	C2-N3	3.02	1.44	1.38
5	A	801	FAD	C2A-N3A	3.01	1.37	1.32
5	A	801	FAD	P-O2P	-2.94	1.41	1.55
5	A	801	FAD	C2B-C1B	-2.94	1.49	1.53
5	A	801	FAD	C2A-N1A	2.71	1.38	1.33
4	A	903	PO4	P-O4	-2.68	1.46	1.54
4	A	901	PO4	P-O3	-2.66	1.46	1.54
4	A	902	PO4	P-O2	-2.60	1.46	1.54
4	A	901	PO4	P-O2	-2.58	1.46	1.54
4	A	903	PO4	P-O2	-2.56	1.46	1.54
5	A	801	FAD	C9A-C5X	2.55	1.47	1.42
4	A	901	PO4	P-O4	-2.54	1.47	1.54
4	A	903	PO4	P-O3	-2.52	1.47	1.54
5	A	801	FAD	P-O5'	-2.28	1.50	1.59
4	A	902	PO4	P-O4	-2.27	1.47	1.54
4	A	902	PO4	P-O3	-2.23	1.47	1.54
5	A	801	FAD	C2-N1	-2.17	1.33	1.38

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	801	FAD	C4-N3-C2	8.42	122.25	115.14
5	A	801	FAD	C4X-C4-N3	-4.63	117.10	123.43
5	A	801	FAD	C4-C4X-C10	-4.44	117.01	119.95
5	A	801	FAD	C5'-C4'-C3'	-2.97	106.47	112.20
5	A	801	FAD	C2A-N1A-C6A	2.67	123.32	118.75
5	A	801	FAD	C5A-C6A-N6A	2.61	124.32	120.35
5	A	801	FAD	C5A-C6A-N1A	-2.38	114.96	120.35
5	A	801	FAD	C4-C4X-N5	2.24	121.15	118.60
5	A	801	FAD	O4'-C4'-C3'	2.22	114.50	109.10
5	A	801	FAD	O5'-P-O1P	-2.10	100.85	109.07
5	A	801	FAD	N3A-C2A-N1A	-2.05	125.47	128.68
5	A	801	FAD	C1'-N10-C10	2.04	120.24	118.41

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	801	FAD	C4X-N5-C5X	2.04	118.81	116.77

There are no chirality outliers.

All (2) torsion outliers are listed below:

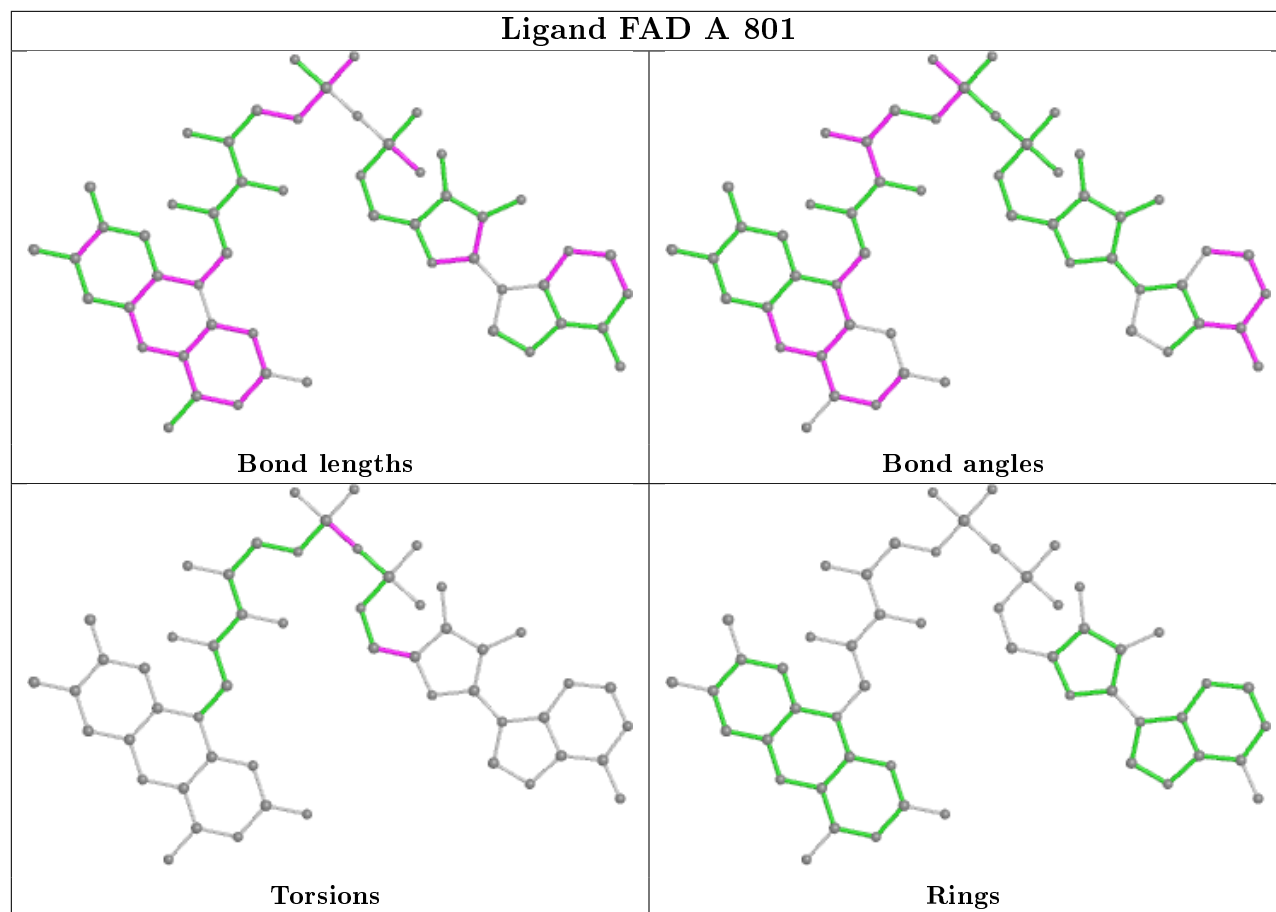
Mol	Chain	Res	Type	Atoms
5	A	801	FAD	PA-O3P-P-O5'
5	A	801	FAD	O4B-C4B-C5B-O5B

There are no ring outliers.

3 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	901	PO4	1	0
4	A	903	PO4	3	0
5	A	801	FAD	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.



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, 95th 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 ²)	Q<0.9
1	A	356/376 (94%)	-0.08	9 (2%) 57 47	16, 36, 59, 77	0
2	B	90/130 (69%)	-0.07	0 100 100	10, 29, 57, 59	0
3	C	151/181 (83%)	-0.21	0 100 100	8, 26, 50, 58	0
All	All	597/687 (86%)	-0.11	9 (1%) 73 68	8, 32, 57, 77	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	323	ARG	3.1
1	A	320	ILE	2.7
1	A	107	GLU	2.6
1	A	104	LYS	2.6
1	A	253	THR	2.6
1	A	249	GLN	2.3
1	A	105	LYS	2.3
1	A	33	ALA	2.2
1	A	321	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](#)

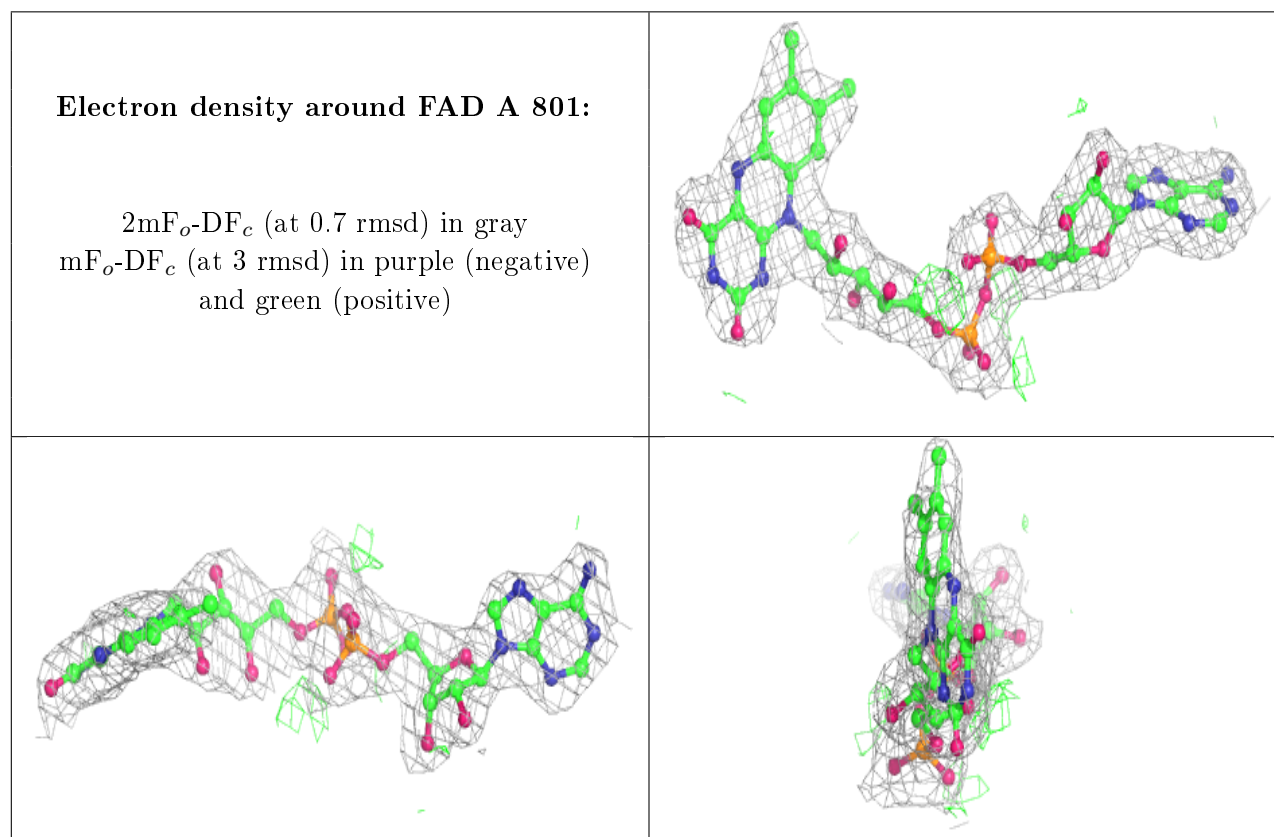
There are no carbohydrates in this entry.

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, 95th 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 ²)	Q<0.9
4	PO4	A	902	5/5	0.79	0.22	61,62,63,63	0
4	PO4	A	903	5/5	0.94	0.16	67,67,68,68	0
4	PO4	A	901	5/5	0.96	0.17	56,56,57,58	0
5	FAD	A	801	53/53	0.96	0.19	8,20,30,32	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.