



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:20 PM UTC

PDB ID : 7E2V / pdb_00007e2v
Title : Crystal structure of MaDA-3
Authors : Gao, L.; Du, X.; Fan, J.; Lei, X.
Deposited on : 2021-02-07
Resolution : 2.94 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

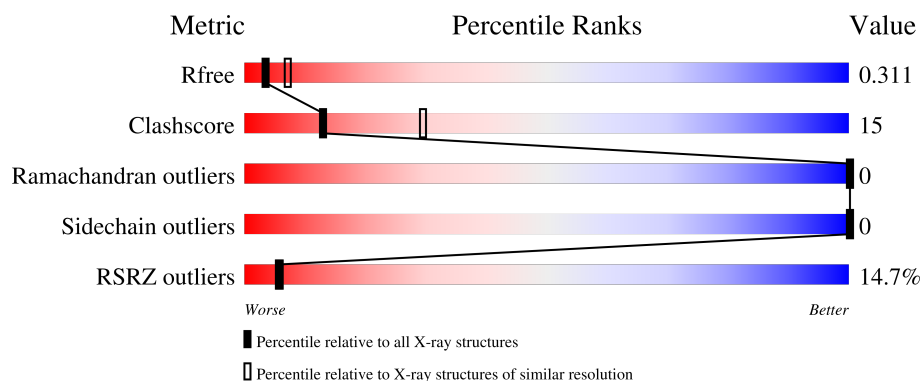
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.94 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}	180053	1159 (2.96-2.92)
Clashscore	190562	1184 (2.96-2.92)
Ramachandran outliers	187476	1131 (2.96-2.92)
Sidechain outliers	187428	1131 (2.96-2.92)
RSRZ outliers	180081	1159 (2.96-2.92)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	550	7% 67% 24% 9%
1	B	550	19% 57% 30% 13%

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 7885 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 MaDA-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	500	Total	C	N	O	S	0	0	0
			3974	2555	686	723	10			
1	B	477	Total	C	N	O	S	0	0	0
			3777	2440	641	686	10			

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



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

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).

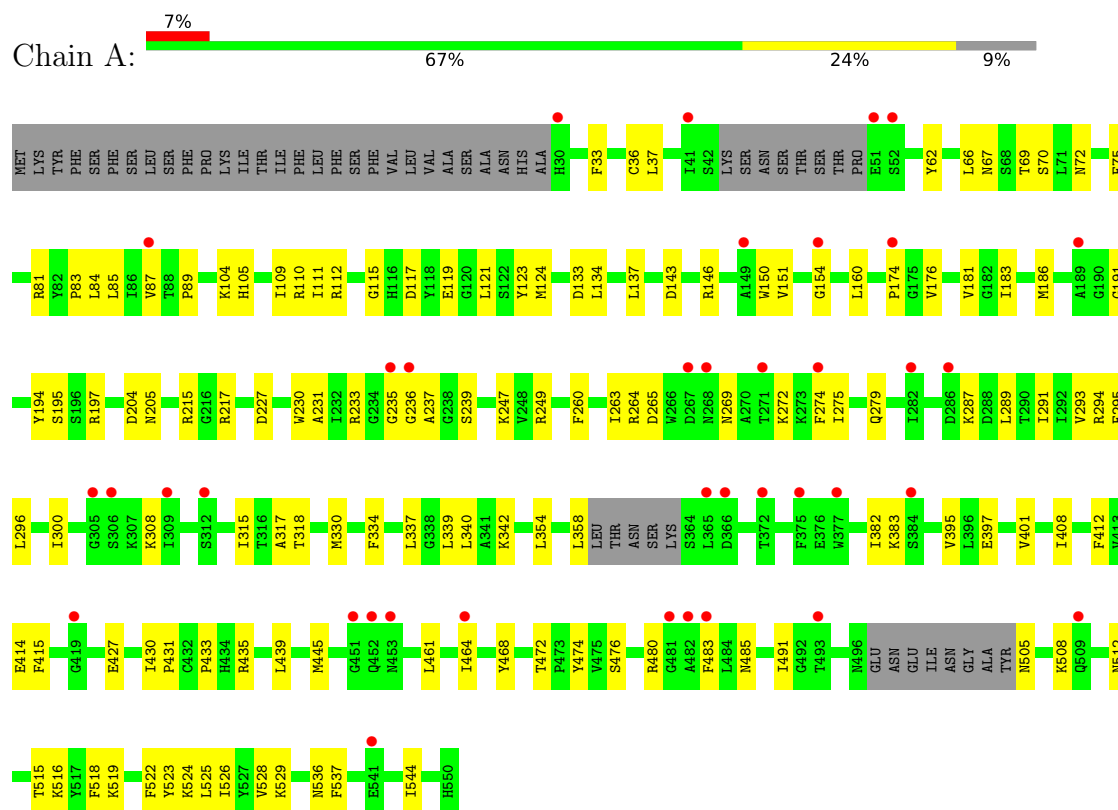


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

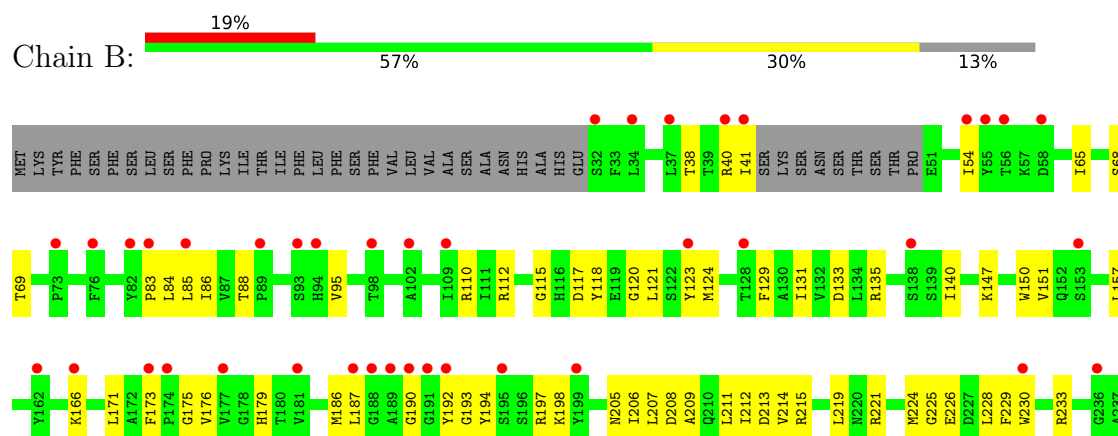
3 Residue-property plots

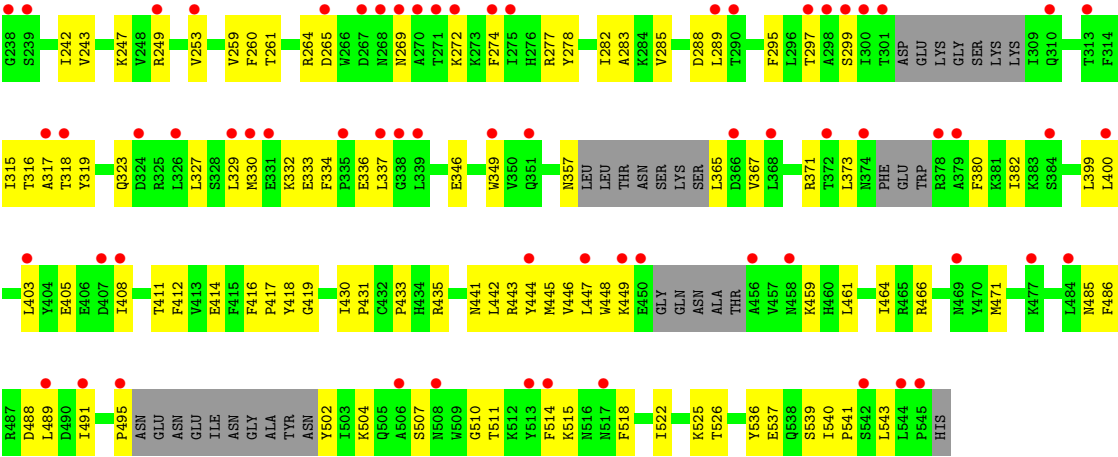
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: MaDA-3



• Molecule 1: MaDA-3





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	83.03Å 79.17Å 95.01Å 90.00° 98.23° 90.00°	Depositor
Resolution (Å)	43.59 – 2.94 43.59 – 2.94	Depositor EDS
% Data completeness (in resolution range)	99.3 (43.59-2.94) 99.2 (43.59-2.94)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.47 (at 2.95Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874, PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.267 , 0.308 0.268 , 0.311	Depositor DCC
R_{free} test set	1300 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	53.9	Xtriage
Anisotropy	0.220	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 44.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	7885	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.51% 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: FAD, NAG

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	0.21	0/4068	0.55	0/5513
1	B	0.20	0/3865	0.54	0/5239
All	All	0.20	0/7933	0.54	0/10752

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

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	3974	0	3935	102	1
1	B	3777	0	3741	131	0
2	A	53	0	30	3	0
2	B	53	0	29	3	0
3	A	28	0	26	0	0
All	All	7885	0	7761	234	1

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 15.

All (234) 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:294:ARG:HD2	1:A:296:LEU:HD23	1.64	0.79
1:B:380:PHE:HB3	1:B:447:LEU:HD23	1.65	0.79
1:B:526:THR:HG22	1:B:543:LEU:H	1.51	0.76
1:B:323:GLN:HB2	1:B:346:GLU:HG3	1.68	0.75
1:A:176:VAL:HG13	1:A:186:MET:HE3	1.68	0.75
1:B:433:PRO:HG3	1:B:515:LYS:H	1.53	0.74
1:B:112:ARG:HH11	1:B:123:TYR:HB3	1.52	0.73
1:A:191:GLY:N	1:A:485:ASN:OD1	2.24	0.70
1:B:173:PHE:HE1	1:B:205:ASN:HB2	1.58	0.69
1:A:264:ARG:HB3	1:A:272:LYS:HG2	1.75	0.68
1:B:68:SER:HG	1:B:135:ARG:HH12	1.38	0.68
1:A:293:VAL:HG22	1:A:415:PHE:HB2	1.75	0.68
1:A:433:PRO:HG3	1:A:519:LYS:H	1.57	0.68
1:B:211:LEU:HD13	1:B:243:VAL:HG22	1.74	0.68
1:B:253:VAL:HG11	1:B:349:TRP:HB2	1.75	0.68
1:A:150:TRP:CE2	1:A:247:LYS:HB2	2.29	0.67
1:B:150:TRP:CE2	1:B:247:LYS:HB2	2.30	0.67
1:B:219:LEU:HD13	1:B:224:MET:HB3	1.77	0.66
1:B:522:ILE:O	1:B:526:THR:HG23	1.95	0.66
1:B:65:ILE:O	1:B:135:ARG:NH1	2.30	0.65
1:A:134:LEU:HG	1:A:137:LEU:HD12	1.77	0.64
1:A:233:ARG:O	1:A:431:PRO:HD2	1.96	0.64
1:A:491:ILE:HG23	1:A:516:LYS:HD2	1.80	0.64
1:A:151:VAL:HG11	1:A:183:ILE:HG13	1.81	0.63
1:A:264:ARG:HD2	1:A:272:LYS:HE2	1.81	0.62
1:B:190:GLY:O	1:B:485:ASN:ND2	2.30	0.62
1:B:68:SER:OG	1:B:135:ARG:NH1	2.28	0.62
1:B:518:PHE:CZ	1:B:522:ILE:HD11	2.35	0.62
1:B:197:ARG:HD2	1:B:417:PRO:HB2	1.82	0.62
1:B:526:THR:CG2	1:B:543:LEU:H	2.13	0.62
1:B:380:PHE:CD2	1:B:382:ILE:HD11	2.37	0.60
1:B:213:ASP:OD1	1:B:214:VAL:N	2.34	0.60
1:B:264:ARG:CB	1:B:272:LYS:HD3	2.31	0.60
1:B:274:PHE:HZ	1:B:315:ILE:HG12	1.67	0.60
1:B:405:GLU:OE2	1:B:466:ARG:NH2	2.35	0.59
1:A:522:PHE:HA	1:A:525:LEU:HD12	1.84	0.59
1:B:176:VAL:HG22	1:B:186:MET:HE3	1.83	0.59
1:B:526:THR:HG21	1:B:543:LEU:HD12	1.85	0.58
1:A:67:ASN:OD1	1:A:81:ARG:NH1	2.36	0.58
1:A:291:ILE:HG12	1:A:317:ALA:HB2	1.84	0.58
1:B:207:LEU:HD21	1:B:249:ARG:HE	1.67	0.57
1:A:260:PHE:CE1	1:A:317:ALA:HB3	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:PRO:HB3	1:A:195:SER:HB2	1.86	0.57
1:A:151:VAL:HG21	1:A:160:LEU:HD22	1.87	0.57
1:A:269:ASN:HB2	1:A:272:LYS:HD2	1.87	0.56
1:A:382:ILE:HG12	1:A:445:MET:HG3	1.85	0.56
1:A:505:ASN:HB3	1:A:508:LYS:HB3	1.88	0.56
1:B:259:VAL:HG12	1:B:318:THR:HG22	1.88	0.56
1:A:461:LEU:O	1:A:464:ILE:HG22	2.05	0.56
1:B:179:HIS:HB3	1:B:357:ASN:ND2	2.19	0.56
1:B:213:ASP:OD2	1:B:215:ARG:NH1	2.39	0.56
1:B:118:TYR:OH	1:B:443:ARG:NH2	2.39	0.56
1:B:412:PHE:HB2	1:B:445:MET:HB3	1.87	0.56
1:B:118:TYR:CG	1:B:382:ILE:HD13	2.41	0.56
1:B:233:ARG:O	1:B:431:PRO:HD2	2.06	0.55
1:B:277:ARG:NH2	1:B:336:GLU:OE1	2.40	0.55
1:A:134:LEU:O	1:A:154:GLY:HA3	2.07	0.55
1:A:81:ARG:HB3	1:A:124:MET:HE3	1.88	0.55
1:A:197:ARG:NH1	1:A:289:LEU:O	2.40	0.55
1:A:340:LEU:HD13	1:A:342:LYS:HE2	1.89	0.54
1:B:264:ARG:HB2	1:B:272:LYS:HD3	1.89	0.54
1:A:265:ASP:N	1:A:272:LYS:HD3	2.22	0.54
1:A:69:THR:HB	1:A:115:GLY:HA3	1.90	0.54
1:B:68:SER:HG	1:B:135:ARG:NH1	2.04	0.54
1:B:365:LEU:O	1:B:367:VAL:N	2.35	0.53
1:A:36:CYS:SG	1:A:104:LYS:HE3	2.48	0.53
1:B:282:ILE:O	1:B:285:VAL:HG12	2.08	0.53
1:B:380:PHE:CD2	1:B:445:MET:HE1	2.44	0.53
1:B:380:PHE:CE2	1:B:382:ILE:HD11	2.44	0.53
1:B:537:GLU:OE2	1:B:537:GLU:N	2.40	0.52
1:B:219:LEU:HD13	1:B:224:MET:CB	2.39	0.52
1:A:269:ASN:CB	1:A:272:LYS:HD2	2.40	0.52
1:B:442:LEU:HD22	1:B:444:TYR:CZ	2.44	0.52
1:B:330:MET:HE1	1:B:337:LEU:HD22	1.91	0.52
2:B:601:FAD:H51A	2:B:601:FAD:H5'1	1.92	0.52
1:A:395:VAL:HG11	1:A:474:TYR:CD1	2.45	0.51
1:B:84:LEU:HD23	1:B:85:LEU:HB2	1.92	0.51
1:A:119:GLU:HB2	1:A:121:LEU:HD13	1.92	0.51
1:A:397:GLU:O	1:A:401:VAL:HG23	2.11	0.51
1:A:215:ARG:HD2	1:A:217:ARG:HH11	1.74	0.51
1:A:264:ARG:HB3	1:A:272:LYS:CG	2.41	0.51
1:A:529:LYS:HZ1	1:A:536:ASN:HA	1.76	0.51
1:B:208:ASP:OD1	1:B:209:ALA:N	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:523:TYR:O	1:A:526:ILE:HG12	2.11	0.51
1:A:194:TYR:HB3	1:A:318:THR:HB	1.93	0.50
1:B:133:ASP:CG	1:B:135:ARG:HG3	2.36	0.50
1:B:269:ASN:HB2	1:B:272:LYS:HZ3	1.75	0.50
1:B:536:TYR:H	1:B:539:SER:HB3	1.77	0.50
1:B:264:ARG:HB3	1:B:272:LYS:HD3	1.92	0.50
1:B:110:ARG:HD2	1:B:121:LEU:O	2.12	0.50
1:A:354:LEU:O	1:A:358:LEU:HG	2.12	0.50
1:B:147:LYS:HG2	1:B:171:LEU:HD21	1.93	0.50
1:B:212:ILE:HB	1:B:242:ILE:HG23	1.93	0.50
1:B:430:ILE:HD11	1:B:435:ARG:HH22	1.77	0.50
1:B:224:MET:CE	1:B:228:LEU:HD22	2.43	0.49
1:B:261:THR:HG22	1:B:316:THR:HG22	1.94	0.49
1:B:461:LEU:O	1:B:464:ILE:HG22	2.12	0.49
1:B:230:TRP:HA	1:B:233:ARG:HH21	1.77	0.49
1:A:275:ILE:HG13	1:A:295:PHE:HZ	1.76	0.49
1:B:86:ILE:HG12	1:B:131:ILE:HB	1.93	0.49
1:B:269:ASN:HB2	1:B:272:LYS:NZ	2.27	0.49
1:A:315:ILE:HG21	1:A:337:LEU:HD21	1.95	0.49
1:B:88:THR:HA	1:B:133:ASP:O	2.13	0.49
1:A:476:SER:O	1:A:480:ARG:HG3	2.12	0.49
1:B:187:LEU:HD22	1:B:206:ILE:HD11	1.94	0.49
1:A:72:ASN:HB3	1:A:75:PHE:CD2	2.48	0.48
1:B:411:THR:HG22	1:B:446:VAL:HG23	1.94	0.48
1:A:89:PRO:HD2	1:A:133:ASP:O	2.12	0.48
1:B:289:LEU:HB2	1:B:319:TYR:HD1	1.78	0.48
1:B:403:LEU:HD13	1:B:411:THR:OG1	2.13	0.48
1:A:36:CYS:HB2	1:A:105:HIS:HE1	1.78	0.48
1:A:150:TRP:CZ2	1:A:247:LYS:HB2	2.49	0.48
1:A:87:VAL:HG12	1:A:89:PRO:HD3	1.96	0.48
1:B:118:TYR:CD2	1:B:486:PHE:HA	2.48	0.48
1:B:140:ILE:HG12	1:B:151:VAL:HG23	1.95	0.48
1:A:430:ILE:HG12	1:A:435:ARG:NH2	2.29	0.47
1:B:329:LEU:HD12	1:B:332:LYS:HE2	1.96	0.47
1:B:260:PHE:CE2	1:B:317:ALA:HB3	2.50	0.47
1:A:525:LEU:O	1:A:528:VAL:HG22	2.14	0.47
1:B:285:VAL:HG23	1:B:333:GLU:CD	2.39	0.47
1:A:300:ILE:O	1:A:308:LYS:N	2.39	0.47
1:A:427:GLU:HG2	1:A:433:PRO:O	2.14	0.47
1:B:197:ARG:HE	1:B:419:GLY:H	1.62	0.47
1:A:529:LYS:HE3	1:A:544:ILE:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:522:PHE:O	1:A:525:LEU:HB2	2.14	0.47
1:B:190:GLY:C	1:B:485:ASN:HD21	2.21	0.47
1:B:274:PHE:O	1:B:278:TYR:N	2.35	0.47
1:B:488:ASP:O	1:B:491:ILE:HG12	2.14	0.47
1:A:117:ASP:HB2	2:A:601:FAD:H52A	1.97	0.46
1:A:143:ASP:CG	1:A:146:ARG:HD3	2.40	0.46
1:A:518:PHE:HB2	1:A:522:PHE:HB2	1.96	0.46
1:B:299:SER:H	1:B:408:ILE:HD11	1.79	0.46
1:B:120:GLY:O	1:B:124:MET:HG2	2.16	0.46
1:B:166:LYS:HA	1:B:166:LYS:HD2	1.67	0.46
1:A:433:PRO:HG3	1:A:519:LYS:N	2.28	0.46
1:B:83:PRO:HB3	1:B:129:PHE:CE2	2.51	0.46
1:B:511:THR:HA	1:B:514:PHE:O	2.16	0.46
1:B:197:ARG:NH1	1:B:289:LEU:O	2.49	0.46
1:A:62:TYR:OH	1:A:83:PRO:O	2.27	0.45
1:B:265:ASP:O	1:B:272:LYS:NZ	2.39	0.45
1:A:84:LEU:HD22	1:A:85:LEU:HD23	1.99	0.45
1:B:323:GLN:HG2	1:B:327:LEU:HD23	1.98	0.45
1:A:294:ARG:HG3	1:A:414:GLU:OE2	2.16	0.45
1:A:383:LYS:HE3	1:A:468:TYR:CG	2.51	0.45
1:A:512:ASN:O	1:A:516:LYS:HE3	2.16	0.45
1:B:121:LEU:HD23	1:B:536:TYR:CD2	2.52	0.45
1:A:112:ARG:HH11	1:A:123:TYR:HB3	1.81	0.45
1:B:68:SER:OG	1:B:135:ARG:NH2	2.50	0.45
1:B:274:PHE:CZ	1:B:315:ILE:HG12	2.49	0.45
1:B:118:TYR:CD2	1:B:382:ILE:HD13	2.51	0.45
1:B:157:LEU:HD21	1:B:175:GLY:HA3	1.99	0.45
1:B:433:PRO:HG3	1:B:514:PHE:HA	1.98	0.45
1:A:143:ASP:OD1	1:A:146:ARG:HD3	2.17	0.45
1:A:274:PHE:HE1	1:A:334:PHE:CD2	2.34	0.45
1:A:227:ASP:HB3	1:A:528:VAL:HG12	1.99	0.45
1:A:340:LEU:HD13	1:A:342:LYS:HB2	1.98	0.45
1:A:505:ASN:HD22	1:A:508:LYS:HB2	1.82	0.45
1:A:412:PHE:HB2	1:A:445:MET:HB3	2.00	0.44
1:B:504:LYS:O	1:B:507:SER:OG	2.26	0.44
1:B:175:GLY:O	1:B:193:GLY:HA3	2.18	0.44
1:B:221:ARG:HH21	1:B:226:GLU:CD	2.25	0.44
1:A:66:LEU:O	1:A:70:SER:OG	2.28	0.44
1:B:205:ASN:HB3	1:B:249:ARG:HB3	2.00	0.44
1:B:221:ARG:HA	1:B:224:MET:SD	2.57	0.44
1:B:295:PHE:CG	1:B:400:LEU:HD11	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:194:TYR:HB3	1:B:318:THR:OG1	2.17	0.44
1:B:297:THR:HG23	1:B:403:LEU:HB3	1.99	0.44
1:B:433:PRO:HG3	1:B:515:LYS:N	2.26	0.44
1:A:230:TRP:CE3	1:A:524:LYS:HE2	2.52	0.44
1:A:265:ASP:H	1:A:272:LYS:HD3	1.82	0.44
1:A:279:GLN:O	1:A:439:LEU:HD23	2.18	0.44
1:A:110:ARG:HA	1:A:110:ARG:HD3	1.77	0.44
1:B:418:TYR:CE1	1:B:441:ASN:HB2	2.53	0.43
1:A:433:PRO:HG3	1:A:518:PHE:HA	2.00	0.43
1:B:399:LEU:HB2	1:B:471:MET:HE3	2.00	0.43
1:A:236:GLY:O	1:A:239:SER:OG	2.28	0.43
1:A:526:ILE:HG22	1:A:544:ILE:HG23	2.00	0.43
1:A:205:ASN:HB3	1:A:249:ARG:HB3	2.01	0.43
1:A:483:PHE:CE2	1:A:485:ASN:HB2	2.53	0.43
1:B:283:ALA:O	1:B:419:GLY:HA3	2.18	0.43
1:A:275:ILE:O	1:A:279:GLN:HG3	2.18	0.43
1:A:263:ILE:O	1:A:264:ARG:NH1	2.51	0.43
1:A:529:LYS:NZ	1:A:536:ASN:HA	2.33	0.43
1:B:459:LYS:HD2	1:B:459:LYS:HA	1.80	0.43
1:B:510:GLY:HA3	1:B:518:PHE:CD1	2.54	0.43
1:A:176:VAL:HB	2:A:601:FAD:C4	2.49	0.43
1:A:515:THR:HA	1:A:518:PHE:O	2.18	0.43
1:B:416:PHE:CE2	1:B:443:ARG:HD2	2.53	0.43
1:B:208:ASP:HB3	1:B:247:LYS:HB3	2.00	0.43
1:B:525:LYS:HE2	1:B:540:ILE:O	2.19	0.43
1:B:150:TRP:CZ2	1:B:247:LYS:HB2	2.53	0.42
1:B:121:LEU:HD11	1:B:489:LEU:HD21	2.02	0.42
1:B:371:ARG:HG2	1:B:373:LEU:H	1.83	0.42
1:B:502:TYR:CZ	1:B:541:PRO:HB3	2.54	0.42
1:B:38:THR:HG22	1:B:54:ILE:HD13	2.02	0.42
1:B:121:LEU:HD23	1:B:536:TYR:HD2	1.83	0.42
1:B:112:ARG:NH1	1:B:123:TYR:HB3	2.28	0.42
1:B:176:VAL:H	1:B:186:MET:CE	2.32	0.42
1:B:176:VAL:H	1:B:186:MET:HE3	1.83	0.42
1:A:33:PHE:CZ	1:A:37:LEU:HD11	2.55	0.42
1:A:109:ILE:HD12	1:A:537:PHE:CE2	2.55	0.42
1:B:69:THR:O	1:B:115:GLY:HA3	2.19	0.42
1:B:224:MET:HG3	1:B:225:GLY:O	2.20	0.42
1:A:491:ILE:O	1:A:516:LYS:NZ	2.38	0.42
1:B:414:GLU:HB2	1:B:443:ARG:HB2	2.02	0.42
1:A:472:THR:OG1	1:A:480:ARG:NH2	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:GLY:O	1:A:237:ALA:N	2.53	0.41
1:B:323:GLN:N	1:B:346:GLU:OE2	2.36	0.41
1:A:408:ILE:HD12	1:A:408:ILE:H	1.85	0.41
1:B:198:LYS:NZ	1:B:288:ASP:OD1	2.37	0.41
1:B:448:TRP:HD1	1:B:449:LYS:O	2.03	0.41
1:A:269:ASN:HD22	1:A:269:ASN:HA	1.66	0.41
1:A:330:MET:HG3	1:A:339:LEU:HD23	2.03	0.41
1:A:508:LYS:HD2	1:A:508:LYS:C	2.46	0.41
1:B:380:PHE:HD2	1:B:445:MET:HE1	1.84	0.41
1:B:40:ARG:O	1:B:41:ILE:HD13	2.21	0.41
1:A:204:ASP:OD1	1:A:435:ARG:NH2	2.54	0.41
1:A:231:ALA:HB2	1:A:528:VAL:HG21	2.02	0.41
1:B:95:VAL:CG1	1:B:212:ILE:HG13	2.51	0.41
1:A:176:VAL:HG21	1:A:181:VAL:HG21	2.03	0.41
1:A:289:LEU:HD21	1:A:330:MET:HE1	2.03	0.41
1:B:382:ILE:HG13	1:B:445:MET:SD	2.61	0.41
1:A:33:PHE:CE2	1:A:37:LEU:HD11	2.55	0.40
1:A:75:PHE:HB3	1:A:124:MET:CE	2.50	0.40
1:B:117:ASP:HB2	2:B:601:FAD:O1A	2.21	0.40
1:A:111:ILE:O	2:A:601:FAD:H2B	2.21	0.40
1:B:224:MET:HE2	1:B:229:PHE:N	2.36	0.40
1:B:495:PRO:HD2	1:B:502:TYR:CE1	2.56	0.40
1:B:295:PHE:HB3	1:B:400:LEU:HD11	2.03	0.40
1:B:330:MET:HE3	1:B:334:PHE:HD1	1.86	0.40
1:B:192:TYR:O	2:B:601:FAD:N3	2.55	0.40
1:A:197:ARG:O	1:A:287:LYS:HB2	2.20	0.40
1:A:340:LEU:CD1	1:A:342:LYS:HB2	2.51	0.40
1:B:540:ILE:HA	1:B:541:PRO:HD3	1.97	0.40

All (1) 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:A:146:ARG:NH2	1:A:536:ASN:O[2_655]	2.17	0.03

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	492/550 (90%)	467 (95%)	25 (5%)	0	100	100
1	B	463/550 (84%)	438 (95%)	25 (5%)	0	100	100
All	All	955/1100 (87%)	905 (95%)	50 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	425/480 (88%)	425 (100%)	0	100	100
1	B	404/480 (84%)	404 (100%)	0	100	100
All	All	829/960 (86%)	829 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	169	GLN
1	A	210	GLN
1	A	370	ASN
1	A	434	HIS
1	A	438	ASN
1	A	505	ASN

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Mol	Chain	Res	Type
1	A	512	ASN
1	B	136	ASN
1	B	169	GLN
1	B	170	ASN
1	B	441	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
3	NAG	A	602	1	14,14,15	0.69	0	17,19,21	0.66	0
3	NAG	A	603	1	14,14,15	0.25	0	17,19,21	0.76	1 (5%)
2	FAD	B	601	1	58,58,58	0.28	0	85,89,89	0.35	0
2	FAD	A	601	1	58,58,58	0.39	0	85,89,89	0.39	0

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
3	NAG	A	602	1	-	3/6/23/26	0/1/1/1
3	NAG	A	603	1	-	4/6/23/26	0/1/1/1
2	FAD	B	601	1	-	9/34/50/50	0/6/6/6
2	FAD	A	601	1	-	2/34/50/50	0/6/6/6

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	603	NAG	C1-O5-C5	2.10	114.99	112.19

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	FAD	C2'-C3'-C4'-O4'
2	B	601	FAD	O3'-C3'-C4'-O4'
2	B	601	FAD	O3'-C3'-C4'-C5'
2	B	601	FAD	C3'-C4'-C5'-O5'
2	B	601	FAD	O4'-C4'-C5'-O5'
2	B	601	FAD	C5'-O5'-P-O1P
2	B	601	FAD	C5'-O5'-P-O2P
2	B	601	FAD	C5'-O5'-P-O3P
3	A	602	NAG	O5-C5-C6-O6
3	A	602	NAG	C4-C5-C6-O6
2	B	601	FAD	C2'-C3'-C4'-C5'
3	A	603	NAG	O5-C5-C6-O6
3	A	603	NAG	C4-C5-C6-O6
3	A	603	NAG	C1-C2-N2-C7
2	A	601	FAD	PA-O3P-P-O2P
3	A	602	NAG	C3-C2-N2-C7
3	A	603	NAG	C3-C2-N2-C7
2	A	601	FAD	PA-O3P-P-O1P

There are no ring outliers.

2 monomers are involved in 6 short contacts:

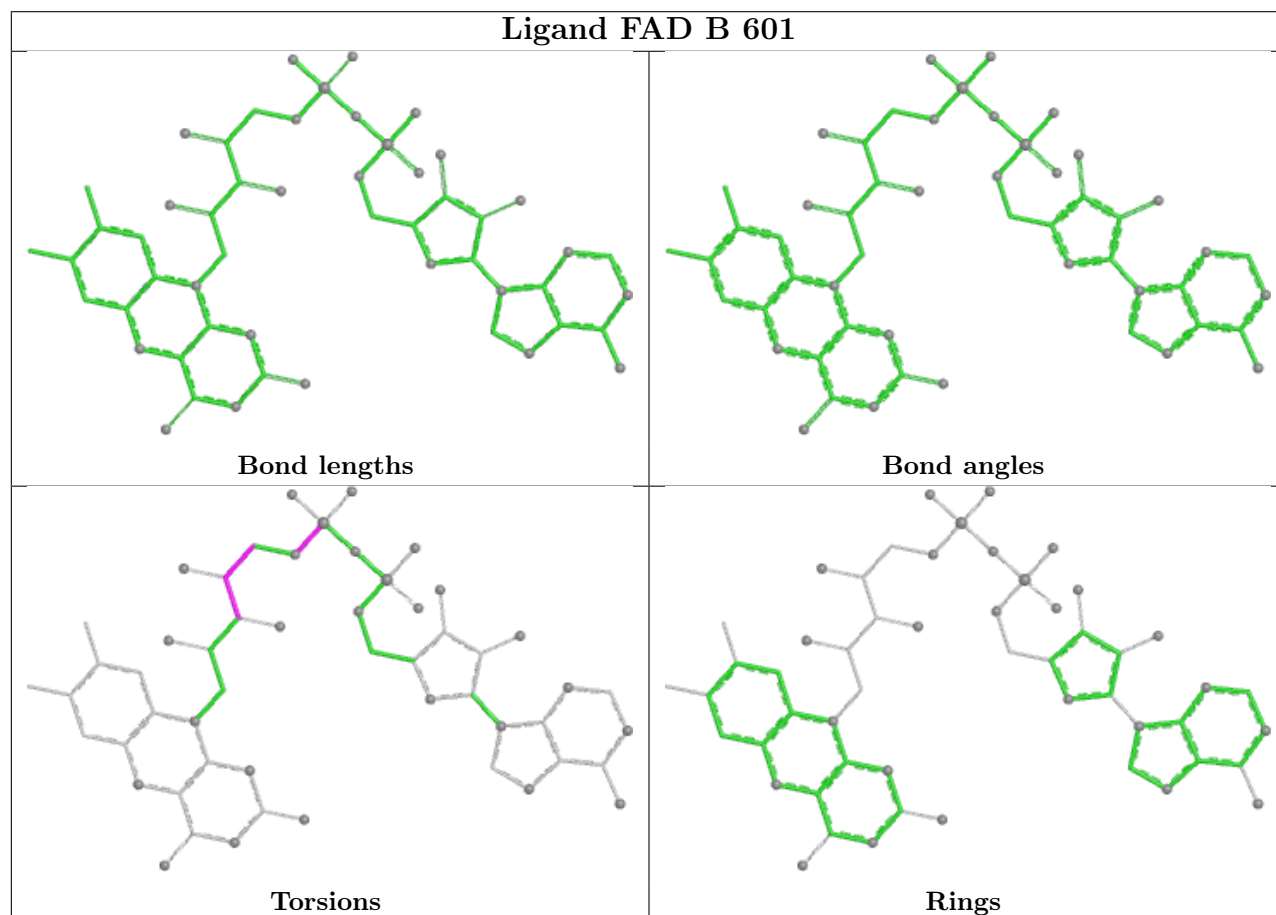
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	FAD	3	0

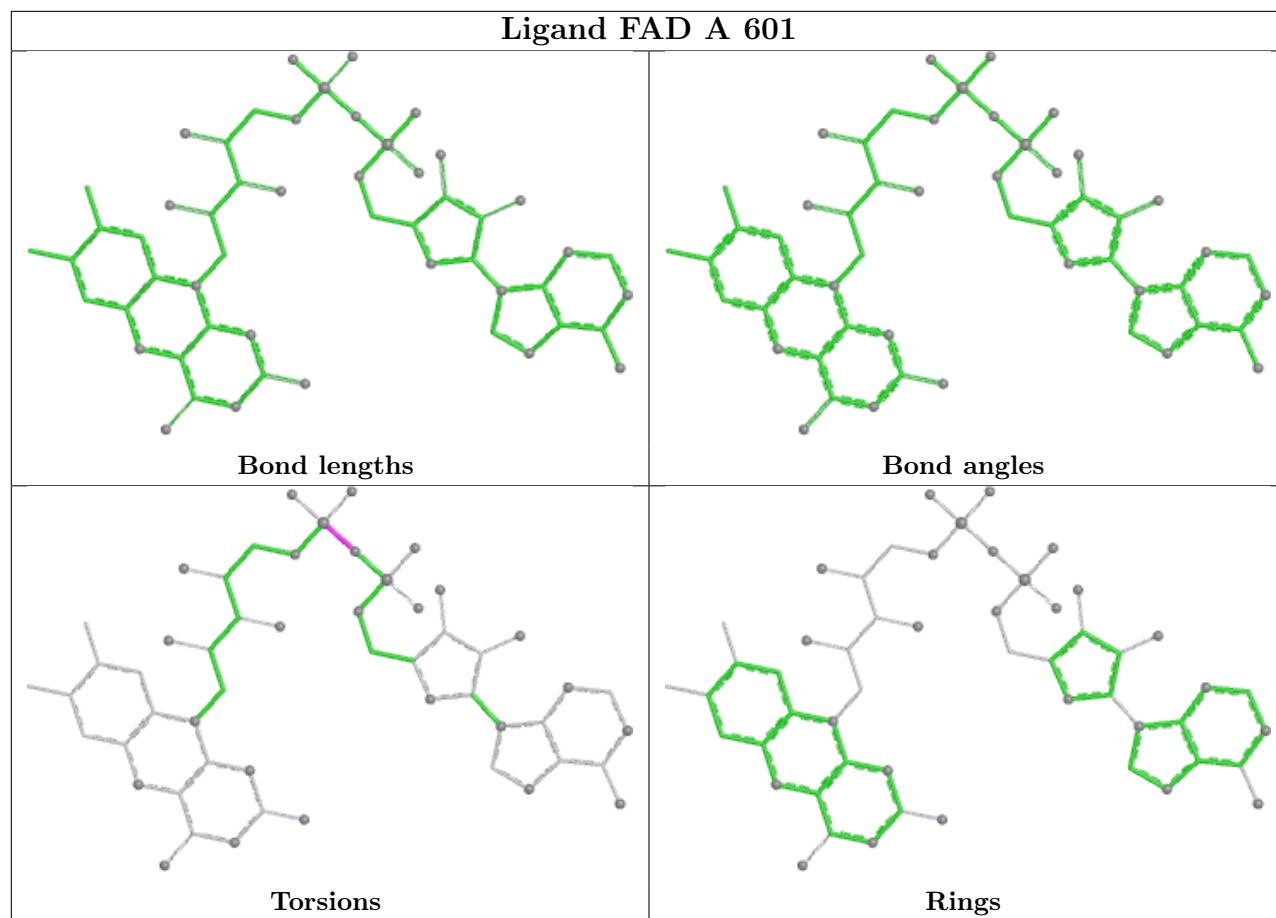
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	FAD	3	0

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, 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	500/550 (90%)	0.91	38 (7%)	20 17	32, 41, 64, 108	0
1	B	477/550 (86%)	1.42	106 (22%)	2 2	40, 60, 84, 118	0
All	All	977/1100 (88%)	1.16	144 (14%)	6 6	32, 49, 78, 118	0

All (144) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	253	VAL	5.2
1	B	372	THR	4.6
1	A	268	ASN	4.4
1	B	190	GLY	4.3
1	B	290	THR	4.2
1	B	274	PHE	4.2
1	A	375	PHE	3.8
1	B	477	LYS	3.7
1	B	54	ILE	3.6
1	B	236	GLY	3.5
1	B	351	GLN	3.5
1	A	174	PRO	3.5
1	A	271	THR	3.5
1	B	514	PHE	3.4
1	B	298	ALA	3.3
1	B	318	THR	3.2
1	B	76	PHE	3.2
1	B	495	PRO	3.1
1	B	153	SER	3.1
1	A	451	GLY	3.1
1	A	267	ASP	3.1
1	B	58	ASP	3.1
1	A	419	GLY	3.0
1	A	541	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	310	GLN	3.0
1	B	326	LEU	3.0
1	B	166	LYS	3.0
1	B	484	LEU	3.0
1	A	286	ASP	2.9
1	B	272	LYS	2.9
1	A	189	ALA	2.9
1	A	41	ILE	2.9
1	A	236	GLY	2.9
1	B	545	PRO	2.9
1	B	265	ASP	2.9
1	B	188	GLY	2.8
1	A	309	ILE	2.8
1	B	447	LEU	2.8
1	B	366	ASP	2.8
1	B	195	SER	2.8
1	B	400	LEU	2.8
1	A	365	LEU	2.7
1	B	191	GLY	2.7
1	B	93	SER	2.7
1	B	489	LEU	2.7
1	B	469	ASN	2.7
1	B	83	PRO	2.7
1	B	289	LEU	2.7
1	B	128	THR	2.6
1	B	270	ALA	2.6
1	B	271	THR	2.6
1	B	32	SER	2.5
1	B	162	TYR	2.5
1	B	337	LEU	2.5
1	A	274	PHE	2.5
1	A	366	ASP	2.5
1	A	52	SER	2.5
1	A	384	SER	2.5
1	B	239	SER	2.5
1	B	299	SER	2.5
1	B	55	TYR	2.5
1	B	173	PHE	2.5
1	B	102	ALA	2.5
1	B	456	ALA	2.5
1	B	329	LEU	2.4
1	B	275	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	300	ILE	2.4
1	B	82	TYR	2.4
1	B	189	ALA	2.4
1	B	449	LYS	2.4
1	B	297	THR	2.4
1	B	313	THR	2.4
1	B	34	LEU	2.4
1	A	464	ILE	2.4
1	B	177	VAL	2.4
1	B	301	THR	2.4
1	B	37	LEU	2.4
1	B	73	PRO	2.4
1	B	109	ILE	2.4
1	B	40	ARG	2.4
1	B	379	ALA	2.4
1	B	506	ALA	2.4
1	B	544	LEU	2.4
1	B	268	ASN	2.4
1	B	238	GLY	2.4
1	A	306	SER	2.3
1	A	453	ASN	2.3
1	B	317	ALA	2.3
1	B	331	GLU	2.3
1	A	312	SER	2.3
1	B	408	ILE	2.3
1	B	444	TYR	2.3
1	B	513	TYR	2.3
1	A	377	TRP	2.3
1	B	384	SER	2.3
1	B	89	PRO	2.3
1	A	305	GLY	2.3
1	B	269	ASN	2.3
1	A	51	GLU	2.3
1	B	450	GLU	2.3
1	B	339	LEU	2.3
1	A	30	HIS	2.3
1	B	94	HIS	2.3
1	B	138	SER	2.3
1	B	368	LEU	2.2
1	B	249	ARG	2.2
1	B	378	ARG	2.2
1	A	149	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	517	ASN	2.2
1	B	324	ASP	2.2
1	A	372	THR	2.2
1	B	335	PRO	2.2
1	B	123	TYR	2.2
1	B	458	ASN	2.2
1	B	403	LEU	2.2
1	A	482	ALA	2.2
1	B	174	PRO	2.2
1	A	452	GLN	2.1
1	B	508	ASN	2.1
1	B	267	ASP	2.1
1	B	187	LEU	2.1
1	B	542	SER	2.1
1	A	509	GLN	2.1
1	A	154	GLY	2.1
1	A	235	GLY	2.1
1	B	85	LEU	2.1
1	B	230	TRP	2.1
1	B	41	ILE	2.1
1	A	87	VAL	2.1
1	B	349	TRP	2.1
1	B	192	TYR	2.1
1	A	481	GLY	2.1
1	A	483	PHE	2.1
1	B	199	TYR	2.1
1	B	330	MET	2.0
1	B	407	ASP	2.0
1	B	491	ILE	2.0
1	B	374	ASN	2.0
1	B	338	GLY	2.0
1	A	282	ILE	2.0
1	A	493	THR	2.0
1	B	56	THR	2.0
1	B	98	THR	2.0
1	B	181	VAL	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 [i](#)

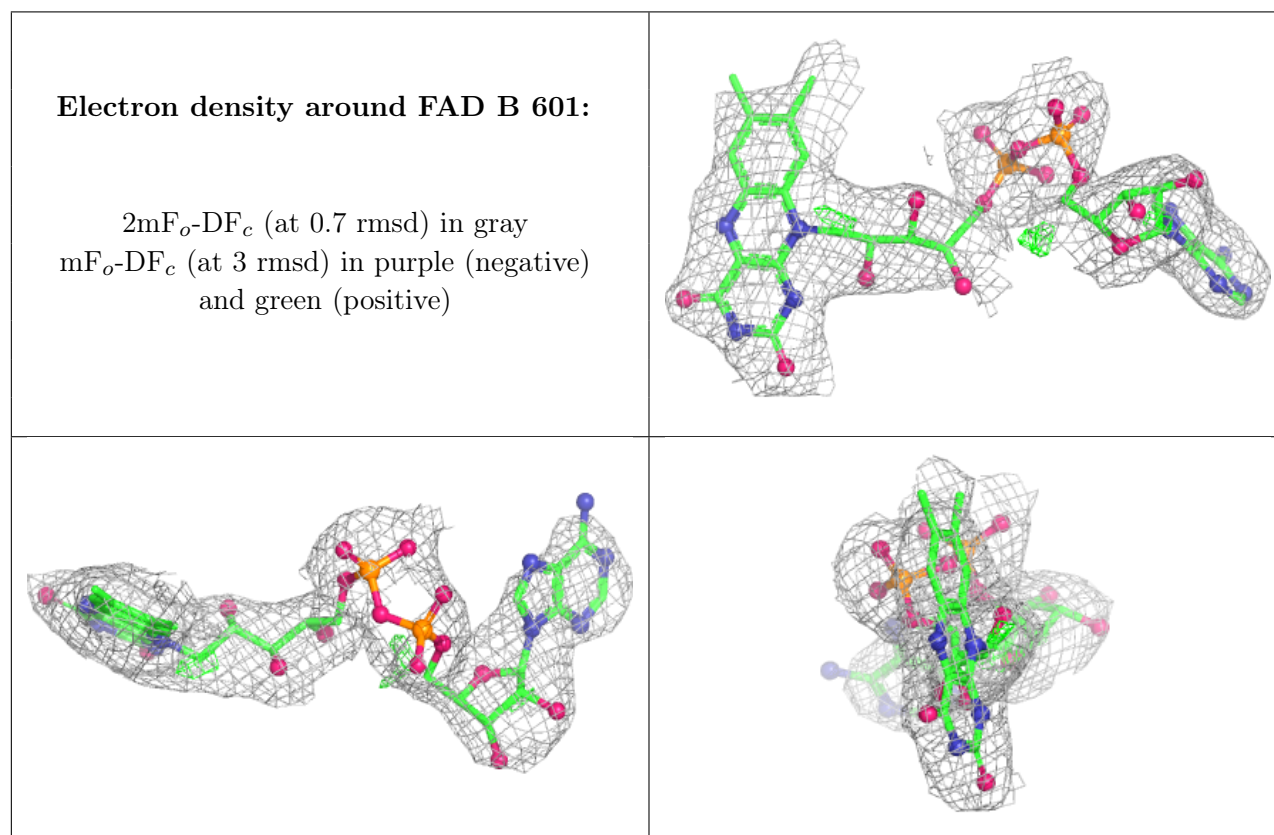
There are no oligosaccharides in this entry.

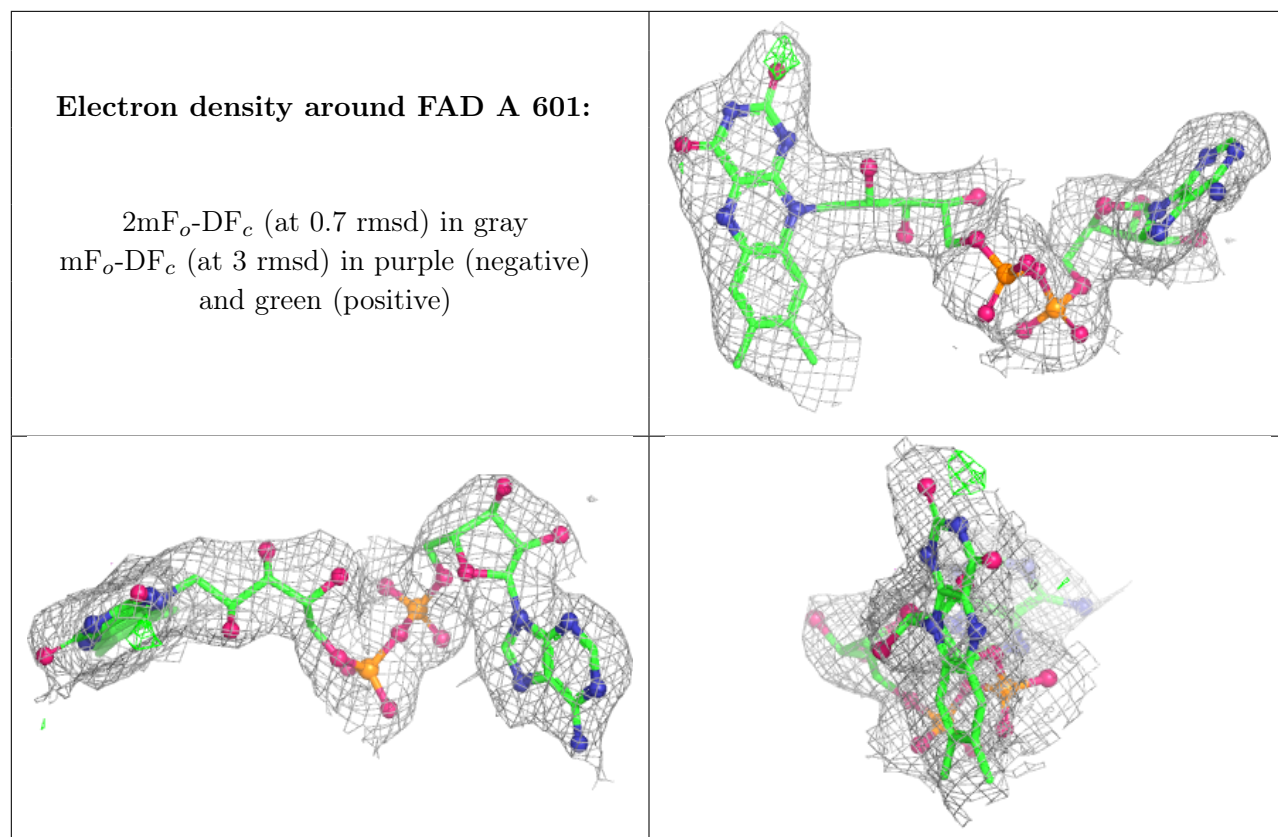
6.4 Ligands [i](#)

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($\text{\AA}^2$)	Q<0.9
3	NAG	A	602	14/15	0.70	0.16	58,62,72,72	0
3	NAG	A	603	14/15	0.78	0.13	45,53,58,60	0
2	FAD	B	601	53/53	0.87	0.14	47,53,58,60	0
2	FAD	A	601	53/53	0.91	0.10	30,36,40,41	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.