Full wwPDB X-ray Structure Validation Report (i)

Aug 28, 2023 – 02:58 AM EDT

PDB ID	:	3K7T
Title	:	Crystal structure of apo-form 6-hydroxy-L-nicotine oxidase, crystal form P3121
Authors	:	Bourenkov, G.P.; Kachalova, G.S.; Bartunik, H.D.
Deposited on	:	2009-10-13
Resolution	:	2.85 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 (i) 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 (i)) were used in the production of this report:

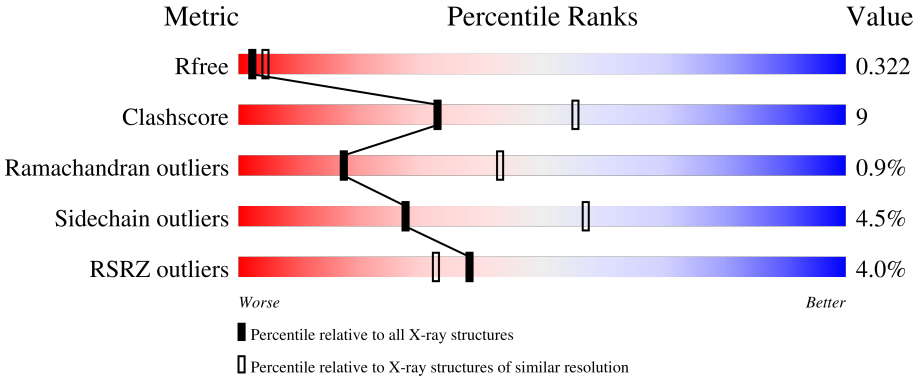
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.85 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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 <=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	425	2% 86% 12% •
1	B	425	6% 83% 14% •

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
3	GP7	B	435	-	-	X	-

2 Entry composition (i)

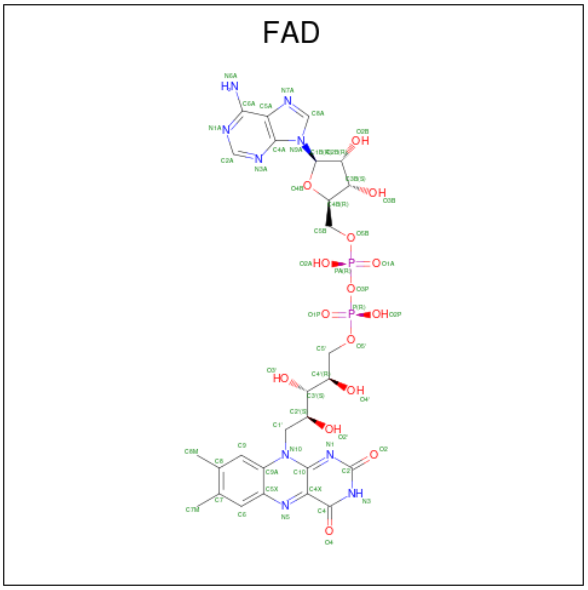
There are 4 unique types of molecules in this entry. The entry contains 6774 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 6-hydroxy-L-nicotine oxidase.

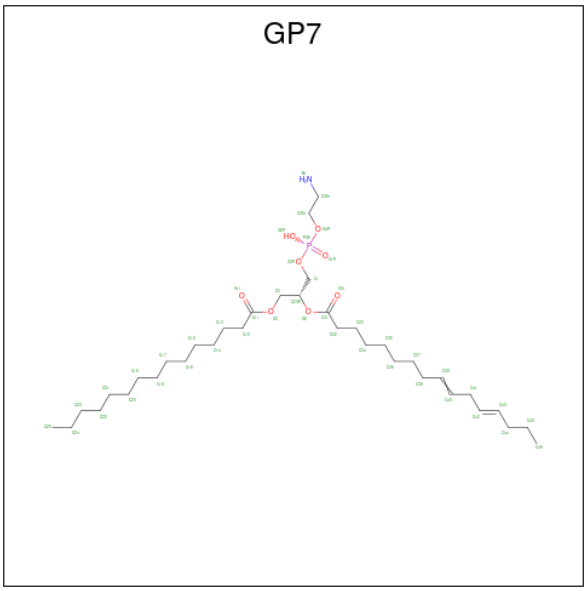
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	425	3270	2077	567	618	8	0	0	0
1	B	425	3270	2077	567	618	8	0	0	0

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



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

- Molecule 3 is (1R)-2-{[(S)-(2-aminoethoxy)(hydroxy)phosphoryl]oxy}-1-[(pentadecanoyloxy)methyl]ethyl (12E)-hexadeca-9,12-dienoate (three-letter code: GP7) (formula: $C_{36}H_{68}NO_8P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
3	A	1	43	34	8	1	0	0
			Total	C	O	P		
3	B	1	43	34	8	1	0	0

- Molecule 4 is water.

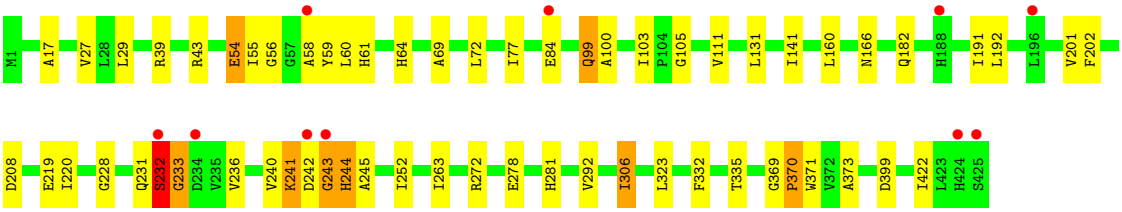
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	19	19	19	0	0
			Total	O		
4	B	23	23	23	0	3

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

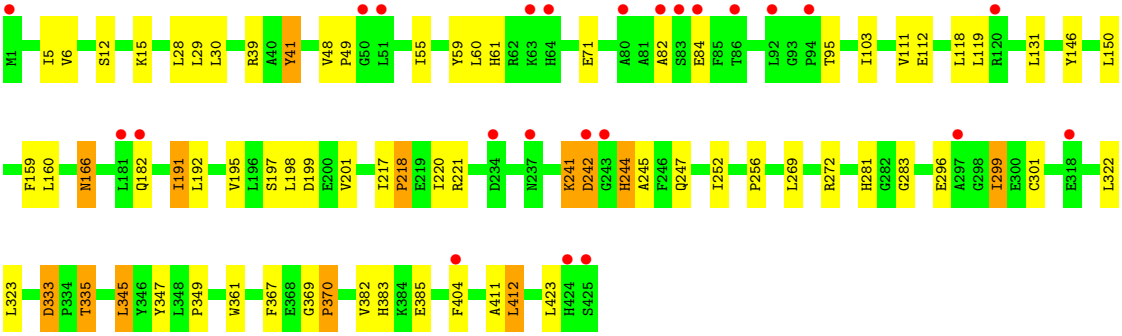
- Molecule 1: 6-hydroxy-L-nicotine oxidase

Chain A:



- Molecule 1: 6-hydroxy-L-nicotine oxidase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	122.96Å 122.96Å 199.92Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	16.60 – 2.85 19.73 – 2.85	Depositor EDS
% Data completeness (in resolution range)	98.1 (16.60-2.85) 98.1 (19.73-2.85)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	2.86 (at 2.83Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.275 , 0.321 0.317 , 0.322	Depositor DCC
R_{free} test set	2039 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	81.4	Xtriage
Anisotropy	0.427	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 33.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.56$, $< L^2 > = 0.40$	Xtriage
Estimated twinning fraction	0.000 for -h,-k,l	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	6774	wwPDB-VP
Average B, all atoms (Å^2)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.31% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: GP7, 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	0.31	0/3346	0.45	1/4555 (0.0%)
1	B	0.31	0/3346	0.47	2/4555 (0.0%)
All	All	0.31	0/6692	0.46	3/9110 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	54	GLU	O-C-N	5.27	131.13	122.70
1	B	242	ASP	CB-CG-OD2	5.25	123.03	118.30
1	B	333	ASP	CB-CG-OD2	5.23	123.01	118.30

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	3270	0	3204	60	0
1	B	3270	0	3204	48	0
2	A	53	0	31	0	0
2	B	53	0	31	1	0
3	A	43	0	61	19	0
3	B	43	0	61	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	19	0	0	0	0
4	B	23	0	0	0	0
All	All	6774	0	6592	116	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 9.

All (116) 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:105:GLY:HA3	3:B:435:GP7:O4P	1.26	1.27
1:A:244:HIS:CD2	1:A:245:ALA:H	1.59	1.20
1:A:191:ILE:HD11	3:A:435:GP7:H20A	1.29	1.12
1:A:244:HIS:HD2	1:A:245:ALA:N	1.53	1.06
3:B:435:GP7:O31	3:B:435:GP7:H34A	1.54	1.03
1:A:191:ILE:HD11	3:A:435:GP7:C20	1.92	1.00
1:B:166:ASN:C	1:B:166:ASN:HD22	1.62	0.98
1:A:244:HIS:CD2	1:A:245:ALA:N	2.30	0.96
1:A:61:HIS:HB3	1:A:64:HIS:HB2	1.55	0.89
1:B:333:ASP:OD1	1:B:335:THR:HG23	1.72	0.88
1:A:192:LEU:HD11	3:A:435:GP7:H18A	1.58	0.85
1:B:159:PHE:CE2	3:B:435:GP7:H39	2.11	0.85
1:B:61:HIS:CD2	1:B:199:ASP:HB2	2.15	0.81
1:A:105:GLY:CA	3:B:435:GP7:O4P	2.21	0.78
1:B:166:ASN:C	1:B:166:ASN:ND2	2.34	0.78
3:B:435:GP7:O31	3:B:435:GP7:C34	2.30	0.77
1:B:160:LEU:HD13	3:B:435:GP7:H24	1.68	0.74
1:A:39:ARG:HD3	1:A:370:PRO:O	1.88	0.74
1:B:361:TRP:HB3	1:B:369:GLY:O	1.90	0.71
1:A:244:HIS:HD2	1:A:245:ALA:H	0.77	0.69
1:A:191:ILE:O	3:A:435:GP7:H42	1.93	0.69
1:B:39:ARG:HD3	1:B:370:PRO:O	1.93	0.69
3:B:435:GP7:O3	3:B:435:GP7:H32	1.93	0.68
1:A:242:ASP:O	1:A:244:HIS:N	2.24	0.68
1:A:191:ILE:HD13	3:A:435:GP7:H22A	1.77	0.67
1:B:159:PHE:CZ	3:B:435:GP7:H39	2.29	0.67
1:B:159:PHE:HE2	3:B:435:GP7:H39	1.61	0.66
1:A:99:GLN:HE22	3:A:435:GP7:H1	1.61	0.65
1:B:192:LEU:HD22	3:B:435:GP7:H36A	1.78	0.64
1:B:241:LYS:O	1:B:242:ASP:OD1	2.16	0.63
1:A:232:SER:OG	1:A:233:GLY:N	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:LEU:HD13	3:A:435:GP7:H25B	1.81	0.62
1:A:39:ARG:CD	1:A:370:PRO:O	2.48	0.62
1:A:191:ILE:CD1	3:A:435:GP7:C21	2.78	0.61
1:A:191:ILE:CD1	3:A:435:GP7:C20	2.76	0.61
1:A:191:ILE:CD1	3:A:435:GP7:H20A	2.20	0.60
1:B:5:ILE:HG12	1:B:28:LEU:HB3	1.85	0.58
1:B:192:LEU:CD2	3:B:435:GP7:H36A	2.33	0.58
1:A:59:TYR:CD1	1:A:201:VAL:HG12	2.39	0.58
1:A:281:HIS:CD2	1:A:373:ALA:H	2.22	0.57
1:A:191:ILE:HD13	3:A:435:GP7:C22	2.35	0.56
1:A:99:GLN:NE2	3:A:435:GP7:H1	2.21	0.55
1:A:58:ALA:HB1	1:A:202:PHE:HB2	1.88	0.55
1:B:39:ARG:CD	1:B:370:PRO:O	2.55	0.55
1:A:99:GLN:HE22	3:A:435:GP7:C1	2.19	0.54
1:B:71:GLU:HG3	1:B:412:LEU:HD11	1.89	0.54
1:A:306:ILE:HD12	1:A:332:PHE:HB2	1.89	0.53
1:A:240:VAL:O	1:A:241:LYS:C	2.46	0.53
1:A:191:ILE:CD1	3:A:435:GP7:H21	2.39	0.53
1:A:191:ILE:HD11	3:A:435:GP7:C21	2.38	0.52
1:B:191:ILE:HG22	3:B:435:GP7:C42	2.38	0.52
1:A:242:ASP:OD1	1:A:242:ASP:C	2.48	0.52
1:B:59:TYR:HA	1:B:201:VAL:HG12	1.92	0.52
1:B:192:LEU:HD23	3:B:435:GP7:H38	1.90	0.51
3:A:435:GP7:H32	3:A:435:GP7:O3	2.10	0.51
1:B:61:HIS:HD2	1:B:197:SER:HA	1.76	0.51
1:B:361:TRP:CB	1:B:369:GLY:O	2.57	0.51
1:B:15:LYS:HD2	1:B:412:LEU:HD13	1.93	0.51
3:B:435:GP7:C31	3:B:435:GP7:O1P	2.59	0.50
1:A:39:ARG:O	1:A:56:GLY:HA3	2.11	0.50
1:A:232:SER:O	1:A:233:GLY:O	2.30	0.50
3:B:435:GP7:O31	3:B:435:GP7:O1P	2.30	0.50
1:B:256:PRO:HD3	2:B:434:FAD:H51A	1.94	0.50
1:A:242:ASP:O	1:A:242:ASP:OD1	2.30	0.50
1:A:243:GLY:O	1:A:244:HIS:O	2.30	0.49
1:B:195:VAL:HG21	3:B:435:GP7:H38A	1.94	0.49
1:A:100:ALA:HB3	3:A:435:GP7:O2	2.13	0.49
1:B:41:TYR:HB3	1:B:55:ILE:HB	1.94	0.48
1:B:191:ILE:HG22	3:B:435:GP7:H42	1.94	0.48
3:B:435:GP7:H32	3:B:435:GP7:C3	2.43	0.48
3:B:435:GP7:H33	3:B:435:GP7:H36	1.44	0.48
1:B:256:PRO:HG2	1:B:367:PHE:HA	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:58:ALA:O	1:A:202:PHE:HD2	1.97	0.47
1:B:192:LEU:HD11	3:B:435:GP7:H18	1.95	0.47
1:A:281:HIS:HD2	1:A:373:ALA:H	1.60	0.47
1:A:244:HIS:CD2	1:A:245:ALA:O	2.68	0.46
1:A:292:VAL:HG11	1:A:323:LEU:HD12	1.97	0.46
1:A:191:ILE:HG13	1:B:112:GLU:OE2	2.15	0.46
3:A:435:GP7:H17	3:B:435:GP7:H17	1.97	0.46
1:B:296:GLU:HB2	1:B:299:ILE:HG12	1.97	0.46
1:A:103:ILE:HG21	1:A:111:VAL:HG21	1.96	0.46
1:B:103:ILE:HG21	1:B:111:VAL:HG21	1.98	0.46
1:A:131:LEU:HD21	1:A:182:GLN:HE21	1.80	0.46
1:A:370:PRO:HG2	1:A:371:TRP:H	1.81	0.45
1:B:345:LEU:HD22	1:B:349:PRO:HA	1.99	0.45
1:A:231:GLN:HB3	1:A:236:VAL:HG13	1.98	0.45
1:A:191:ILE:CD1	3:A:435:GP7:H22A	2.46	0.44
1:B:299:ILE:HD12	1:B:323:LEU:HD21	2.00	0.44
1:A:69:ALA:HA	1:A:72:LEU:HD12	1.99	0.44
1:A:59:TYR:CD1	1:A:201:VAL:CG1	3.01	0.44
1:A:43:ARG:HE	1:A:55:ILE:HG13	1.83	0.43
1:A:29:LEU:HD22	1:A:220:ILE:HG23	2.01	0.43
1:B:146:TYR:O	1:B:150:LEU:HD12	2.18	0.43
1:B:301:CYS:HB3	1:B:347:TYR:CD1	2.54	0.43
1:B:281:HIS:HD2	1:B:283:GLY:H	1.67	0.43
1:B:244:HIS:HA	1:B:245:ALA:HA	1.69	0.43
1:A:17:ALA:HA	1:A:27:VAL:HG11	2.01	0.43
1:A:77:ILE:HD12	1:A:208:ASP:HB3	2.00	0.42
1:B:29:LEU:HB3	1:B:220:ILE:HA	2.00	0.42
1:B:6:VAL:HG22	1:B:252:ILE:HD12	2.01	0.42
1:B:12:SER:HB2	1:B:411:ALA:HB1	2.01	0.42
1:B:30:LEU:HD23	1:B:221:ARG:HB2	2.02	0.42
1:B:272:ARG:H	1:B:272:ARG:HG2	1.70	0.42
1:A:252:ILE:HD11	1:A:422:ILE:HD11	2.01	0.42
1:B:82:ALA:HB2	1:B:199:ASP:O	2.20	0.42
1:A:166:ASN:OD1	1:A:166:ASN:C	2.58	0.41
1:B:48:VAL:HA	1:B:49:PRO:HD3	1.93	0.41
1:B:382:VAL:HG23	1:B:385:GLU:HB2	2.02	0.41
1:A:54:GLU:HG3	1:A:58:ALA:HB2	2.02	0.41
1:B:217:ILE:HA	1:B:218:PRO:HD3	1.91	0.41
1:B:131:LEU:H	1:B:383:HIS:CD2	2.38	0.41
1:A:99:GLN:HE21	1:A:99:GLN:HB2	1.62	0.41
1:A:335:THR:O	1:A:335:THR:CG2	2.65	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:195:VAL:CG2	3:B:435:GP7:H38A	2.51	0.41
1:A:369:GLY:HA2	1:A:370:PRO:HD3	1.94	0.40
1:A:228:GLY:HA2	1:A:263:ILE:HG23	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	423/425 (100%)	400 (95%)	17 (4%)	6 (1%)	11	31
1	B	423/425 (100%)	401 (95%)	20 (5%)	2 (0%)	29	57
All	All	846/850 (100%)	801 (95%)	37 (4%)	8 (1%)	17	43

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	241	LYS
1	A	370	PRO
1	B	370	PRO
1	A	232	SER
1	A	243	GLY
1	A	244	HIS
1	A	233	GLY
1	B	218	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	341/342 (100%)	331 (97%)	10 (3%)	42	72
1	B	341/342 (100%)	320 (94%)	21 (6%)	18	43
All	All	682/684 (100%)	651 (96%)	31 (4%)	27	57

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	LEU
1	A	84	GLU
1	A	99	GLN
1	A	141	ILE
1	A	219	GLU
1	A	232	SER
1	A	272	ARG
1	A	278	GLU
1	A	306	ILE
1	A	399	ASP
1	B	41	TYR
1	B	60	LEU
1	B	84	GLU
1	B	95	THR
1	B	118	LEU
1	B	119	LEU
1	B	166	ASN
1	B	182	GLN
1	B	191	ILE
1	B	198	LEU
1	B	241	LYS
1	B	244	HIS
1	B	247	GLN
1	B	269	LEU
1	B	299	ILE
1	B	322	LEU
1	B	335	THR
1	B	345	LEU
1	B	404	PHE
1	B	412	LEU
1	B	423	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	HIS
1	A	99	GLN
1	A	182	GLN
1	A	244	HIS
1	A	284	GLN
1	B	61	HIS
1	B	166	ASN
1	B	182	GLN
1	B	281	HIS
1	B	359	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

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	GP7	B	435	-	42,42,45	1.26	4 (9%)	46,47,50	1.26	3 (6%)
2	FAD	A	434	-	53,58,58	1.15	4 (7%)	68,89,89	1.37	10 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	FAD	B	434	-	53,58,58	1.15	4 (7%)	68,89,89	1.39	10 (14%)
3	GP7	A	435	-	42,42,45	1.38	4 (9%)	46,47,50	1.31	5 (10%)

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	GP7	B	435	-	-	27/44/44/49	-
2	FAD	A	434	-	-	4/30/50/50	0/6/6/6
2	FAD	B	434	-	-	17/30/50/50	0/6/6/6
3	GP7	A	435	-	-	20/44/44/49	-

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	435	GP7	O2-C31	4.61	1.47	1.34
3	A	435	GP7	O3-C11	4.56	1.46	1.33
3	B	435	GP7	O3-C11	4.29	1.45	1.33
2	B	434	FAD	C2A-N3A	4.16	1.38	1.32
2	A	434	FAD	C2A-N3A	4.16	1.38	1.32
2	A	434	FAD	C4X-N5	4.06	1.38	1.30
3	B	435	GP7	O2-C31	4.01	1.45	1.34
2	B	434	FAD	C4X-N5	3.99	1.38	1.30
3	A	435	GP7	C40-C39	3.92	1.54	1.31
3	B	435	GP7	C40-C39	3.53	1.52	1.31
3	B	435	GP7	C43-C42	3.53	1.52	1.31
3	A	435	GP7	C43-C42	3.50	1.52	1.31
2	A	434	FAD	C10-N1	2.90	1.39	1.33
2	B	434	FAD	C10-N1	2.88	1.39	1.33
2	A	434	FAD	C2A-N1A	2.61	1.38	1.33
2	B	434	FAD	C2A-N1A	2.57	1.38	1.33

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	434	FAD	N3A-C2A-N1A	-5.69	119.78	128.68
2	B	434	FAD	N3A-C2A-N1A	-5.68	119.80	128.68
3	A	435	GP7	O2-C31-C32	4.55	121.30	111.50
3	B	435	GP7	O2-C31-C32	3.64	119.34	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	434	FAD	P-O3P-PA	-3.09	122.22	132.83
3	B	435	GP7	O3-C11-C12	3.04	121.45	111.91
2	A	434	FAD	C4-N3-C2	-3.02	120.06	125.64
2	B	434	FAD	C4-N3-C2	-3.00	120.09	125.64
2	A	434	FAD	P-O3P-PA	-2.97	122.63	132.83
3	A	435	GP7	O3-C11-C12	2.94	121.12	111.91
3	B	435	GP7	C2-O2-C31	-2.82	110.84	117.79
2	A	434	FAD	C4X-C4-N3	2.75	120.18	113.19
2	B	434	FAD	C4X-C10-N10	2.75	120.50	116.48
2	B	434	FAD	C4X-C4-N3	2.70	120.05	113.19
2	A	434	FAD	C4X-C10-N10	2.69	120.41	116.48
2	B	434	FAD	C4X-C10-N1	-2.48	118.97	124.73
3	A	435	GP7	C2-O2-C31	-2.47	111.71	117.79
2	A	434	FAD	C4X-C10-N1	-2.42	119.11	124.73
2	B	434	FAD	O4-C4-C4X	-2.37	120.30	126.60
2	A	434	FAD	O4-C4-C4X	-2.37	120.30	126.60
2	A	434	FAD	C10-C4X-N5	-2.33	119.91	124.86
2	B	434	FAD	C10-C4X-N5	-2.30	119.98	124.86
2	A	434	FAD	C9A-C5X-N5	-2.29	119.94	122.43
2	B	434	FAD	C5X-C9A-N10	2.29	120.31	117.95
2	A	434	FAD	C5X-C9A-N10	2.25	120.28	117.95
3	A	435	GP7	P-O3P-C1	2.12	124.13	118.30
2	B	434	FAD	C9A-C5X-N5	-2.10	120.15	122.43
3	A	435	GP7	O2-C31-O31	-2.03	118.79	123.70

There are no chirality outliers.

All (68) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	434	FAD	O4B-C4B-C5B-O5B
2	B	434	FAD	C5B-O5B-PA-O2A
2	B	434	FAD	N10-C1'-C2'-O2'
2	B	434	FAD	N10-C1'-C2'-C3'
2	B	434	FAD	C1'-C2'-C3'-C4'
2	B	434	FAD	C2'-C3'-C4'-C5'
2	B	434	FAD	O3'-C3'-C4'-O4'
2	B	434	FAD	O3'-C3'-C4'-C5'
3	A	435	GP7	C2-C1-O3P-P
3	A	435	GP7	O31-C31-O2-C2
3	A	435	GP7	C32-C31-O2-C2
3	B	435	GP7	C1-O3P-P-O2P
3	B	435	GP7	C1-O3P-P-O4P

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Mol	Chain	Res	Type	Atoms
3	B	435	GP7	C2-C1-O3P-P
3	B	435	GP7	O31-C31-O2-C2
3	B	435	GP7	C32-C31-O2-C2
3	B	435	GP7	C33-C34-C35-C36
2	A	434	FAD	C3B-C4B-C5B-O5B
2	B	434	FAD	O4B-C4B-C5B-O5B
2	B	434	FAD	C2'-C3'-C4'-O4'
3	B	435	GP7	C15-C16-C17-C18
3	B	435	GP7	C11-C12-C13-C14
2	B	434	FAD	C3B-C4B-C5B-O5B
3	B	435	GP7	C12-C11-O3-C3
3	B	435	GP7	C31-C32-C33-C34
3	B	435	GP7	O11-C11-O3-C3
3	B	435	GP7	C38-C39-C40-C41
3	B	435	GP7	C17-C18-C19-C20
3	A	435	GP7	C16-C17-C18-C19
3	B	435	GP7	C36-C37-C38-C39
3	A	435	GP7	C12-C13-C14-C15
3	B	435	GP7	C35-C36-C37-C38
3	B	435	GP7	C18-C19-C20-C21
3	B	435	GP7	C22-C23-C24-C25
3	A	435	GP7	C19-C20-C21-C22
3	A	435	GP7	C15-C16-C17-C18
3	B	435	GP7	C1-C2-C3-O3
3	B	435	GP7	C1-O3P-P-O1P
3	A	435	GP7	O3P-C1-C2-C3
3	A	435	GP7	C40-C41-C42-C43
3	B	435	GP7	C40-C41-C42-C43
3	A	435	GP7	O3P-C1-C2-O2
2	B	434	FAD	O2'-C2'-C3'-O3'
3	A	435	GP7	C21-C22-C23-C24
2	B	434	FAD	O2'-C2'-C3'-C4'
2	B	434	FAD	C4'-C5'-O5'-P
3	B	435	GP7	O3P-C1-C2-O2
2	A	434	FAD	C5B-O5B-PA-O3P
2	B	434	FAD	C5B-O5B-PA-O3P
3	A	435	GP7	C18-C19-C20-C21
2	A	434	FAD	C5B-O5B-PA-O1A
2	B	434	FAD	C5B-O5B-PA-O1A
2	B	434	FAD	C1'-C2'-C3'-O3'
3	B	435	GP7	O2-C2-C3-O3
3	A	435	GP7	C17-C18-C19-C20

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Mol	Chain	Res	Type	Atoms
3	B	435	GP7	C19-C20-C21-C22
2	B	434	FAD	C4B-C5B-O5B-PA
3	A	435	GP7	C42-C43-C44-C45
3	B	435	GP7	C39-C40-C41-C42
3	B	435	GP7	C34-C35-C36-C37
3	A	435	GP7	C1-O3P-P-O2P
3	B	435	GP7	C37-C38-C39-C40
3	A	435	GP7	C34-C35-C36-C37
3	A	435	GP7	O3-C11-C12-C13
3	A	435	GP7	C37-C38-C39-C40
3	A	435	GP7	O11-C11-C12-C13
3	B	435	GP7	C13-C14-C15-C16
3	A	435	GP7	O2-C31-C32-C33

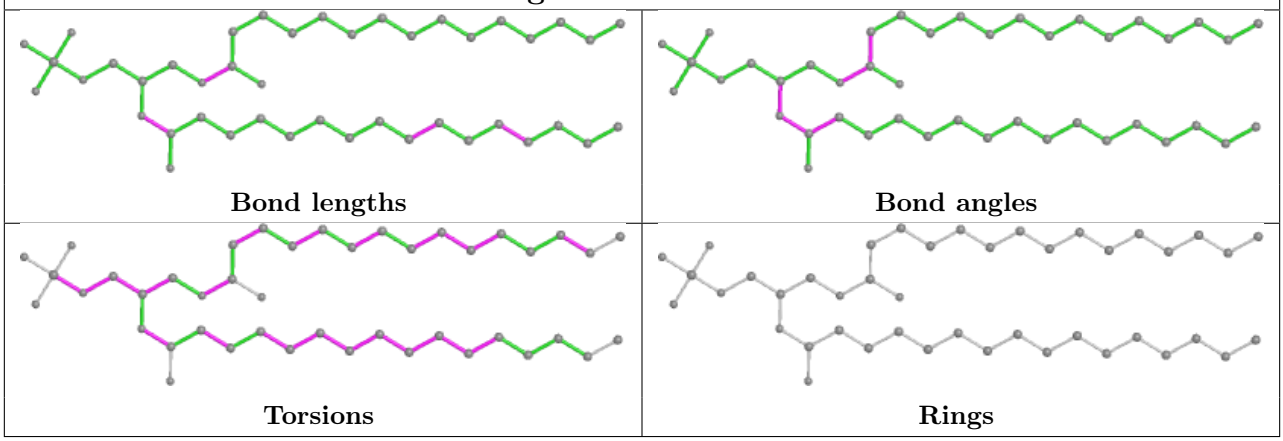
There are no ring outliers.

3 monomers are involved in 41 short contacts:

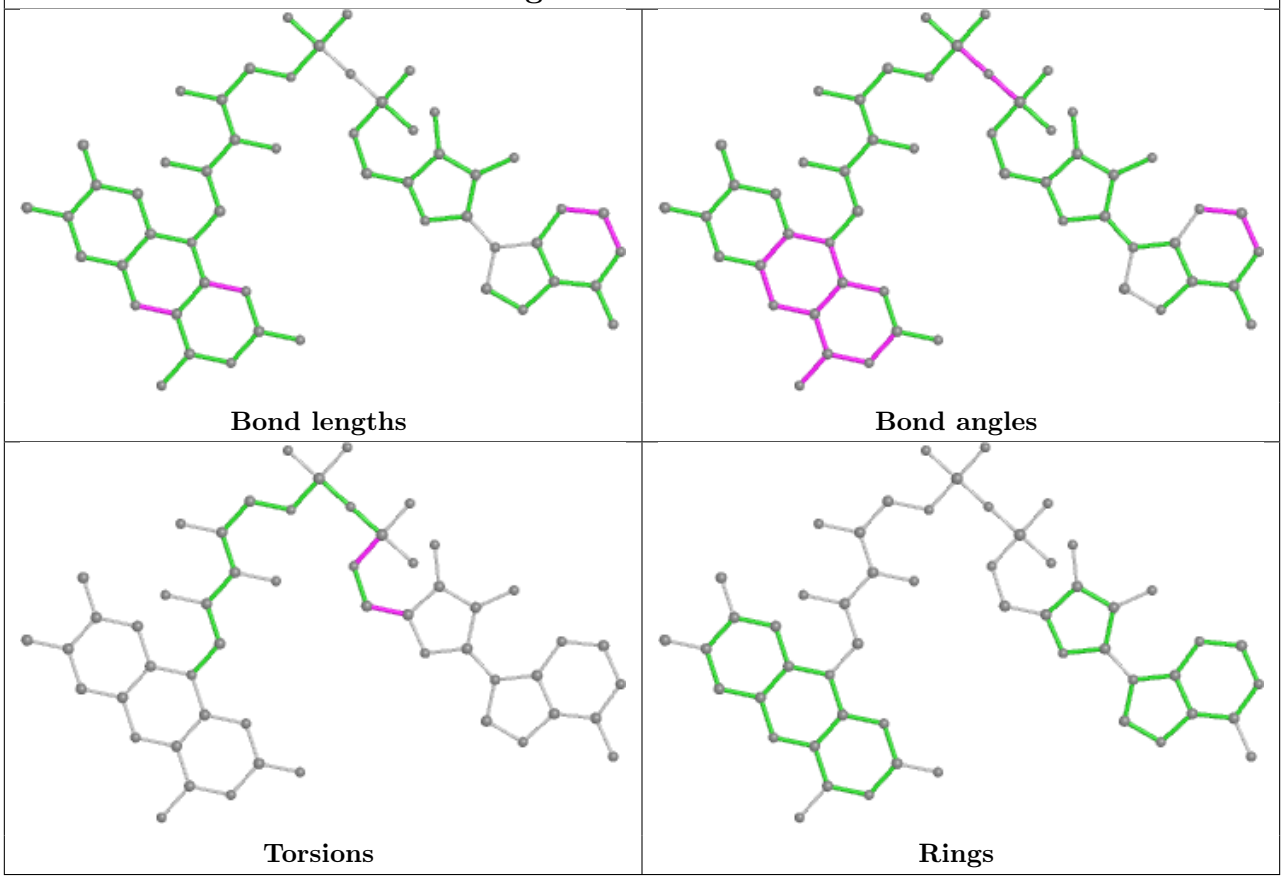
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	435	GP7	22	0
2	B	434	FAD	1	0
3	A	435	GP7	19	0

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 then 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.

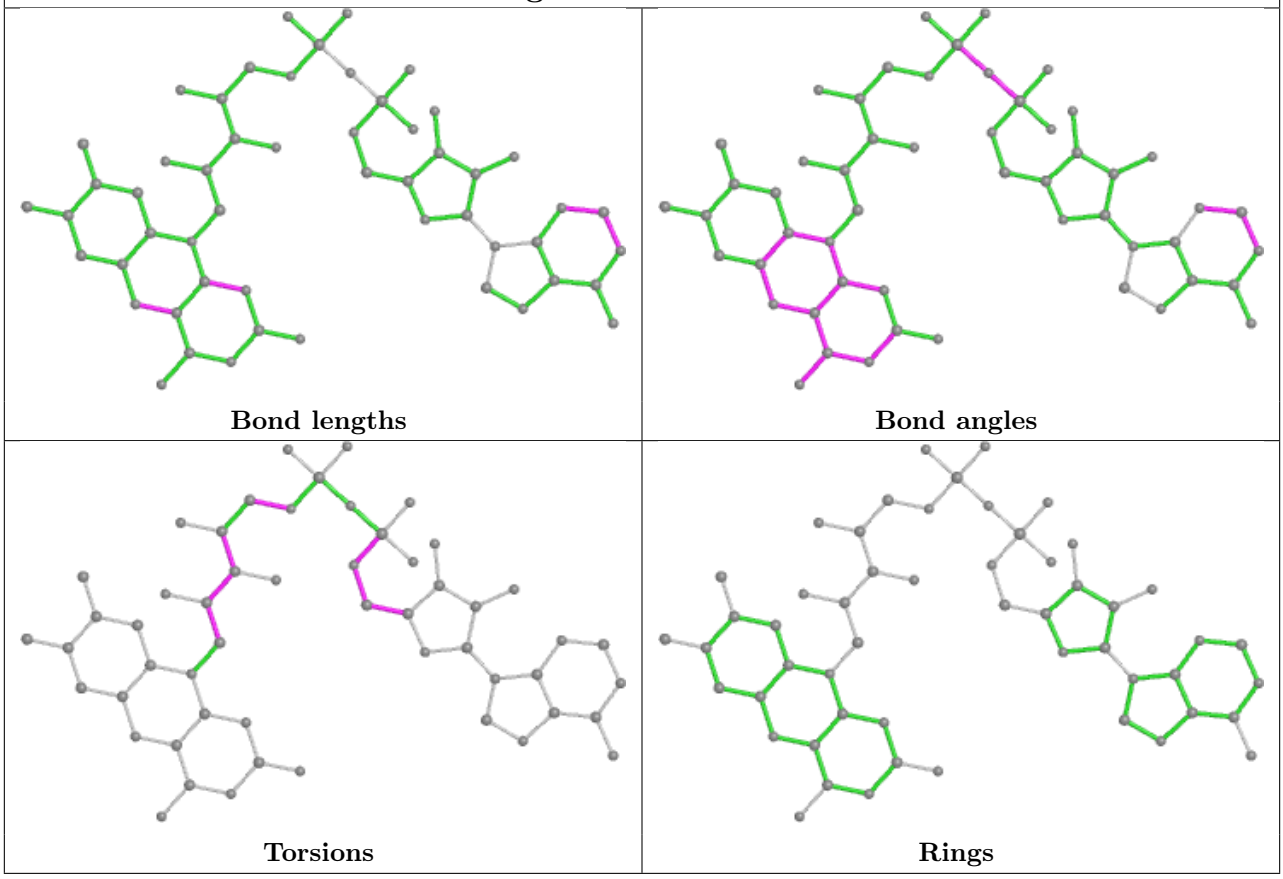
Ligand GP7 B 435



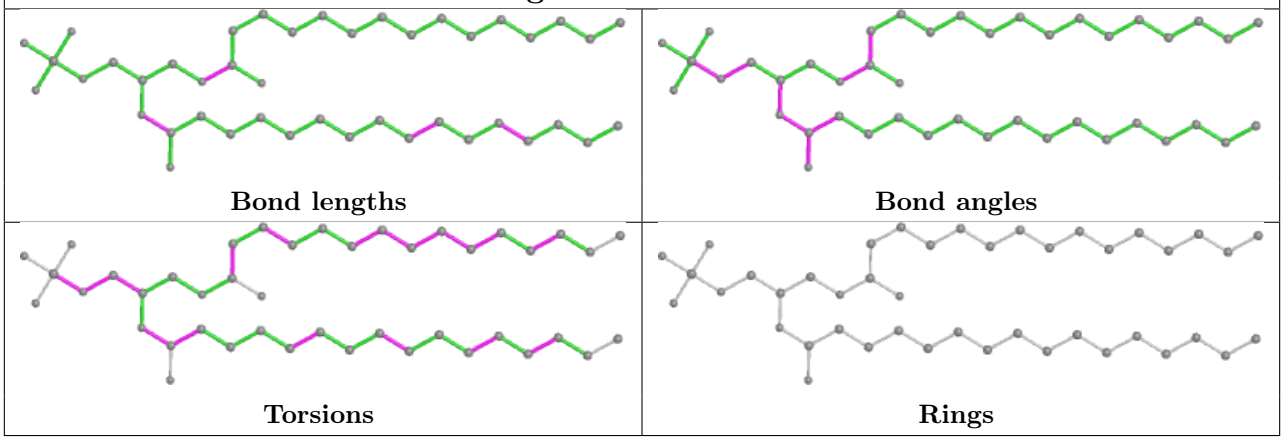
Ligand FAD A 434



Ligand FAD B 434



Ligand GP7 A 435



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	425/425 (100%)	0.10	10 (2%)	59	56	24, 63, 90, 96	0
1	B	425/425 (100%)	0.34	24 (5%)	24	20	25, 74, 94, 98	0
All	All	850/850 (100%)	0.22	34 (4%)	38	32	24, 68, 94, 98	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	80	ALA	5.6
1	B	1	MET	4.7
1	B	84	GLU	4.2
1	B	64	HIS	4.0
1	B	242	ASP	3.9
1	B	425	SER	3.9
1	A	232	SER	3.5
1	A	234	ASP	3.5
1	A	58	ALA	3.4
1	A	242	ASP	3.2
1	B	234	ASP	3.0
1	B	82	ALA	2.9
1	A	425	SER	2.9
1	B	63	LYS	2.9
1	B	297	ALA	2.7
1	A	188	HIS	2.6
1	B	86	THR	2.6
1	B	94	PRO	2.5
1	B	424	HIS	2.5
1	B	92	LEU	2.5
1	B	83	SER	2.4
1	B	404	PHE	2.4
1	B	237	ASN	2.4
1	A	196	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	424	HIS	2.2
1	B	181	LEU	2.2
1	B	182	GLN	2.2
1	B	50	GLY	2.2
1	B	120	ARG	2.2
1	A	243	GLY	2.2
1	B	318	GLU	2.2
1	B	243	GLY	2.0
1	B	51	LEU	2.0
1	A	84	GLU	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

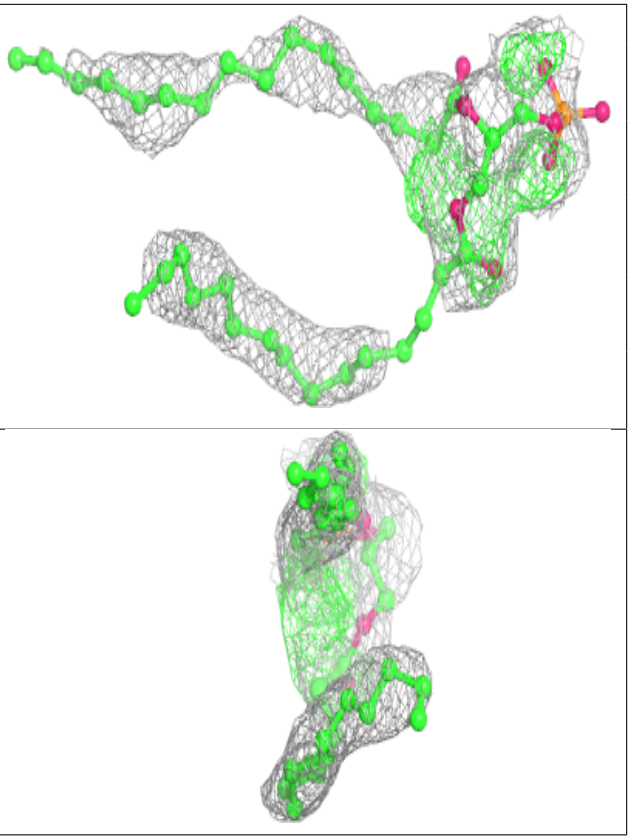
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

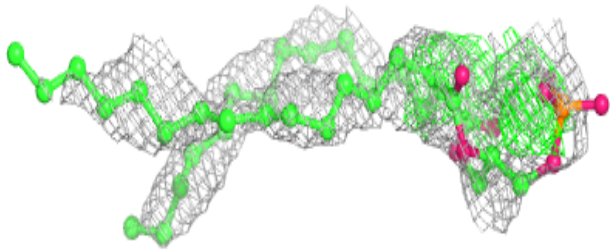
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	GP7	A	435	43/46	0.77	0.40	59,77,83,85	16
3	GP7	B	435	43/46	0.79	0.34	57,68,72,74	16
2	FAD	B	434	53/53	0.90	0.19	24,51,75,83	0
2	FAD	A	434	53/53	0.92	0.22	33,56,84,94	0

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

Electron density around GP7 A 435:

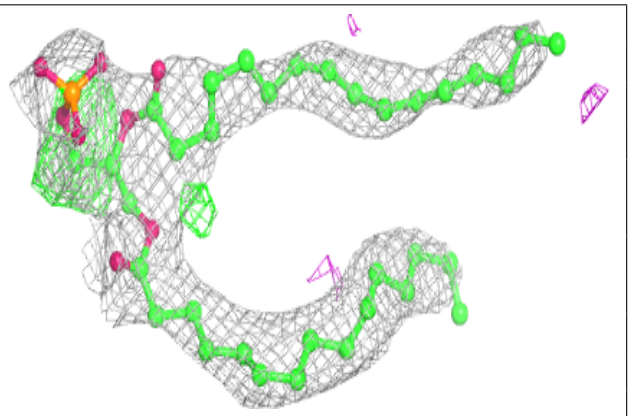
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

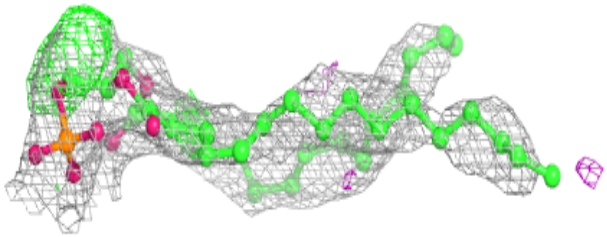


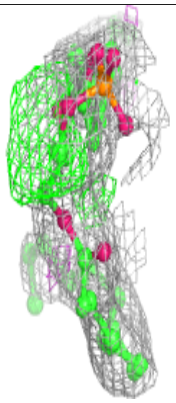


Electron density around GP7 B 435:

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

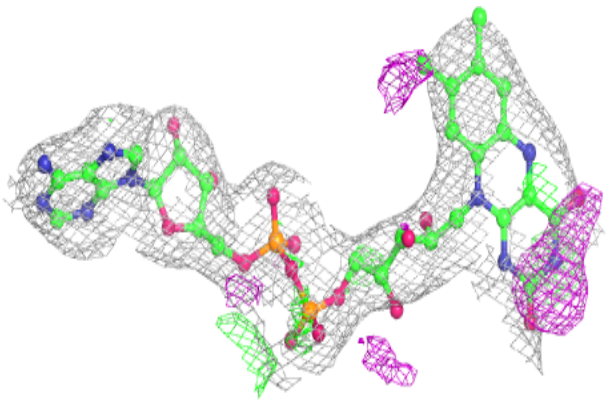


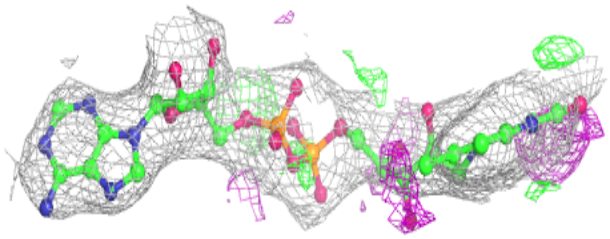


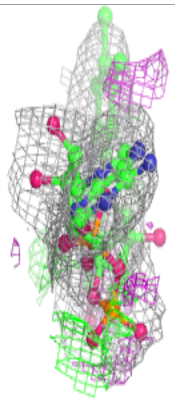


Electron density around FAD B 434:

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

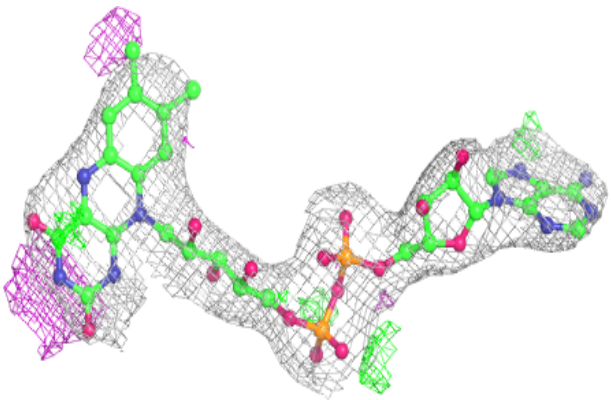


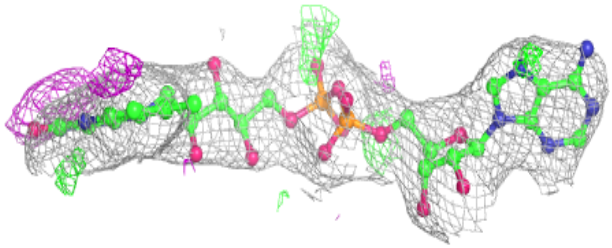


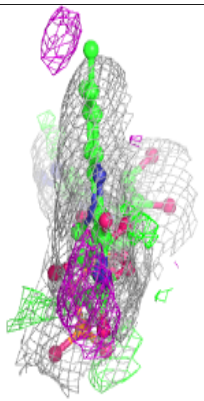


Electron density around FAD A 434:

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







6.5 Other polymers (i)

There are no such residues in this entry.