



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 26, 2017 – 01:28 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 : unknown  
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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20030345

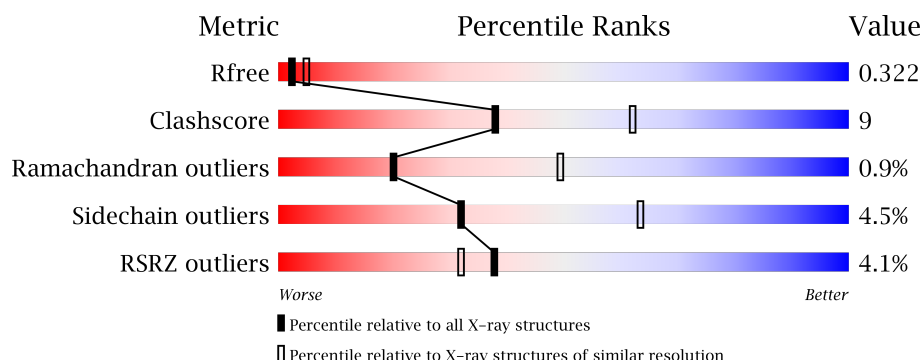
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.85 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))
$R_{free}$	100719	2469 (2.90-2.82)
Clashscore	112137	2749 (2.90-2.82)
Ramachandran outliers	110173	2687 (2.90-2.82)
Sidechain outliers	110143	2690 (2.90-2.82)
RSRZ outliers	101464	2487 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	425	
1	B	425	

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	A	435	-	-	-	X
3	GP7	B	435	-	-	X	X

## 2 Entry composition [i](#)

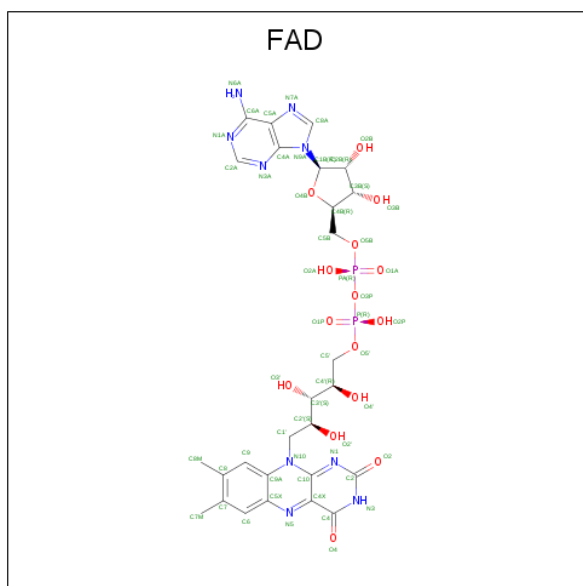
There are 4 unique types of molecules in this entry. The entry contains 6774 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

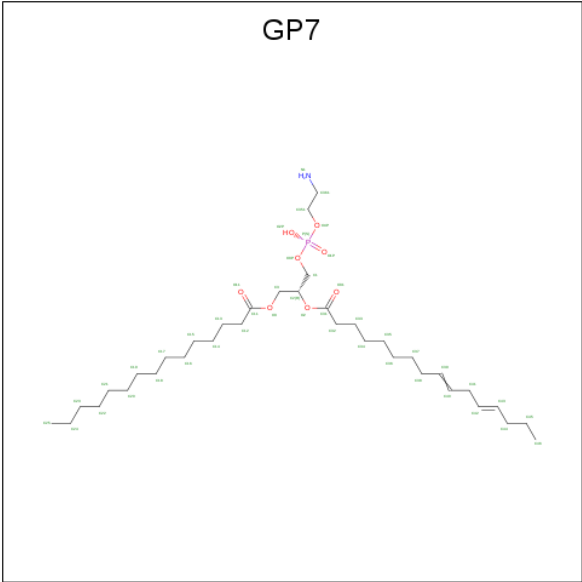
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	425	Total	C	N	O	S	0	0	0
			3270	2077	567	618	8			
1	B	425	Total	C	N	O	S	0	0	0
			3270	2077	567	618	8			

- 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
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 (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
3	A	1	Total	C	O	P	0	0
			43	34	8	1		
3	B	1	Total	C	O	P	0	0
			43	34	8	1		

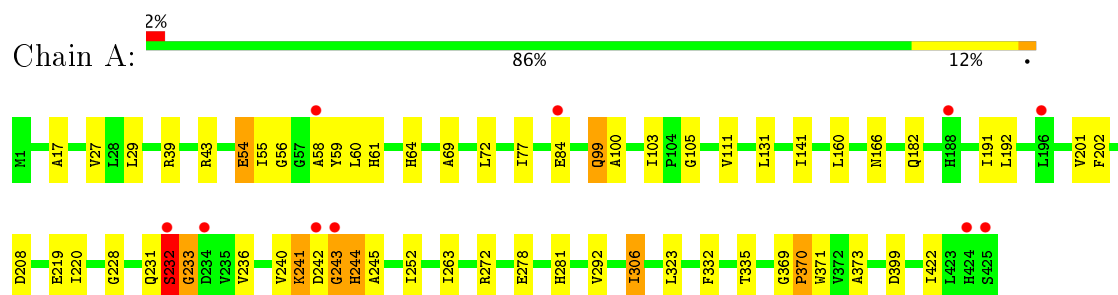
- Molecule 4 is water.

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

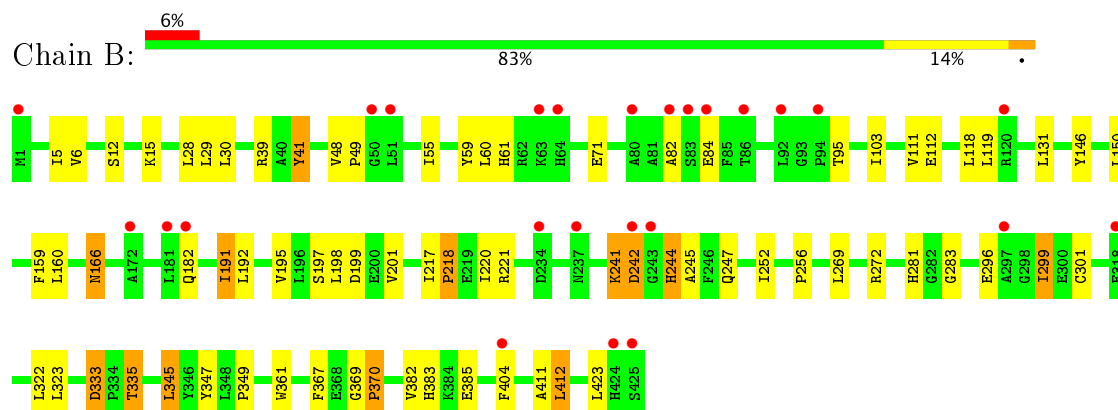
### 3 Residue-property plots

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 ( $\text{RSRZ} > 2$ ). 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



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



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	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
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.86 (at 2.83Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.275 , 0.321 0.316 , 0.322	Depositor DCC
$R_{free}$ test set	2035 reflections (5.02%)	DCC
Wilson B-factor (Å <sup>2</sup> )	81.4	Xtriage
Anisotropy	0.427	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 33.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.56$ , $\langle L^2 \rangle = 0.40$	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 <sup>2</sup> )	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.*

<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: 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(°)	Ideal(°)
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:B:39:ARG:HD3	1:B:370:PRO:O	1.93	0.69
1:A:191:ILE:O	3:A:435:GP7:H42	1.93	0.69
3:B:435:GP7:H32	3:B:435:GP7:O3	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:O1P	3:B:435:GP7:C31	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:OD1	1:A:242:ASP:O	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
3:A:435:GP7:H17	3:B:435:GP7:H17	1.97	0.46
1:A:191:ILE:HG13	1:B:112:GLU:OE2	2.15	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:30:LEU:HD23	1:B:221:ARG:HB2	2.02	0.42
1:B:12:SER:HB2	1:B:411:ALA:HB1	2.01	0.42
1:B:272:ARG:HG2	1:B:272:ARG:H	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:335:THR:O	1:A:335:THR:CG2	2.65	0.41
1:A:99:GLN:HB2	1:A:99:GLN:HE21	1.62	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%)	13	37
1	B	423/425 (100%)	401 (95%)	20 (5%)	2 (0%)	32	64
All	All	846/850 (100%)	801 (95%)	37 (4%)	8 (1%)	20	49

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%)	48	78
1	B	341/342 (100%)	320 (94%)	21 (6%)	21	48
All	All	682/684 (100%)	651 (96%)	31 (4%)	32	63

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

Some 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 carbohydrates 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	$\# Z  > 2$
2	FAD	A	434	-	51,58,58	1.35	7 (13%)	54,89,89	1.87	5 (9%)
3	GP7	A	435	-	42,42,45	1.38	4 (9%)	46,47,50	1.40	6 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	FAD	B	434	-	51,58,58	1.34	7 (13%)	54,89,89	1.89	5 (9%)
3	GP7	B	435	-	42,42,45	1.26	4 (9%)	46,47,50	1.36	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
2	FAD	A	434	-	-	0/28/50/50	0/6/6/6
3	GP7	A	435	-	-	0/44/44/49	0/0/0/0
2	FAD	B	434	-	-	0/28/50/50	0/6/6/6
3	GP7	B	435	-	-	2/44/44/49	0/0/0/0

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	434	FAD	C5X-N5	2.01	1.38	1.35
2	A	434	FAD	C5X-N5	2.15	1.38	1.35
2	A	434	FAD	C1'-N10	2.45	1.50	1.48
2	B	434	FAD	C2A-N1A	2.54	1.38	1.33
2	A	434	FAD	C2A-N1A	2.58	1.38	1.33
2	B	434	FAD	C1'-N10	2.67	1.51	1.48
2	B	434	FAD	C4-N3	3.08	1.38	1.33
2	A	434	FAD	C4-N3	3.10	1.38	1.33
2	B	434	FAD	C4X-N5	3.59	1.38	1.33
3	A	435	GP7	C43-C42	3.63	1.52	1.31
3	B	435	GP7	C43-C42	3.66	1.52	1.31
3	B	435	GP7	C40-C39	3.66	1.52	1.31
2	A	434	FAD	C4X-N5	3.69	1.38	1.33
3	B	435	GP7	O2-C31	3.90	1.45	1.34
2	A	434	FAD	C2A-N3A	3.98	1.38	1.32
2	B	434	FAD	C2A-N3A	3.98	1.38	1.32
3	A	435	GP7	C40-C39	4.06	1.54	1.31
2	B	434	FAD	C10-N1	4.18	1.39	1.33
2	A	434	FAD	C10-N1	4.20	1.39	1.33
3	B	435	GP7	O3-C11	4.26	1.45	1.33
3	A	435	GP7	O2-C31	4.49	1.47	1.34
3	A	435	GP7	O3-C11	4.53	1.46	1.33

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	434	FAD	N3A-C2A-N1A	-10.42	119.78	128.86
2	B	434	FAD	N3A-C2A-N1A	-10.40	119.80	128.86
3	B	435	GP7	C2-O2-C31	-2.98	110.84	117.88
3	A	435	GP7	C41-C42-C43	-2.69	109.01	124.90
3	A	435	GP7	C2-O2-C31	-2.61	111.71	117.88
3	B	435	GP7	C41-C40-C39	-2.41	110.62	124.90
2	B	434	FAD	C4X-C4-N3	-2.41	120.05	123.48
3	B	435	GP7	C41-C42-C43	-2.37	110.87	124.90
2	A	434	FAD	C4X-C4-N3	-2.32	120.18	123.48
3	A	435	GP7	C3-O3-C11	2.05	123.31	117.13
3	A	435	GP7	P-O3P-C1	2.12	124.13	118.30
3	A	435	GP7	O3-C11-C12	3.17	121.12	111.90
2	B	434	FAD	C4X-N5-C5X	3.19	120.13	116.76
3	B	435	GP7	O3-C11-C12	3.28	121.45	111.90
2	A	434	FAD	C4X-N5-C5X	3.35	120.30	116.76
2	A	434	FAD	C5X-C9A-N10	3.53	120.28	117.66
2	B	434	FAD	C5X-C9A-N10	3.58	120.31	117.66
3	B	435	GP7	O2-C31-C32	3.75	119.34	111.55
3	A	435	GP7	O2-C31-C32	4.70	121.30	111.55
2	A	434	FAD	C4-N3-C2	5.60	120.06	115.16
2	B	434	FAD	C4-N3-C2	5.64	120.09	115.16

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	435	GP7	C2-O2-C31-O31
3	B	435	GP7	C2-O2-C31-C32

There are no ring outliers.

3 monomers are involved in 41 short contacts:

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

## 5.7 Other polymers ⓘ

There are no such residues in this entry.



## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	425/425 (100%)	0.10	10 (2%) 59 55	24, 63, 90, 96	0
1	B	425/425 (100%)	0.34	25 (5%) 23 18	25, 74, 94, 98	0
All	All	850/850 (100%)	0.22	35 (4%) 38 32	24, 68, 94, 98	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	80	ALA	5.5
1	B	1	MET	4.7
1	B	84	GLU	4.2
1	B	64	HIS	3.9
1	B	242	ASP	3.8
1	B	425	SER	3.7
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	B	63	LYS	2.9
1	A	425	SER	2.8
1	B	297	ALA	2.7
1	A	188	HIS	2.6
1	B	94	PRO	2.6
1	B	86	THR	2.6
1	B	92	LEU	2.5
1	B	424	HIS	2.5
1	B	237	ASN	2.4
1	B	83	SER	2.4
1	B	404	PHE	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	318	GLU	2.2
1	B	120	ARG	2.2
1	B	50	GLY	2.2
1	A	243	GLY	2.1
1	B	172	ALA	2.0
1	A	84	GLU	2.0
1	B	243	GLY	2.0
1	B	51	LEU	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	GP7	B	435	43/46	0.79	0.34	3.77	57,68,72,74	16
3	GP7	A	435	43/46	0.77	0.40	2.86	59,77,83,85	16
2	FAD	A	434	53/53	0.92	0.22	0.06	33,56,84,94	0
2	FAD	B	434	53/53	0.90	0.19	-0.77	24,51,75,83	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.