



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:39 PM UTC

PDB ID : 7ZZK / pdb_00007zzk
Title : Structure of the N-acetyl-D-glucosamine oxidase from Ralstonia Solanacearum
Authors : Boverio, A.; Rozeboom, H.J.; Fraaije, M.W.
Deposited on : 2022-05-25
Resolution : 1.50 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

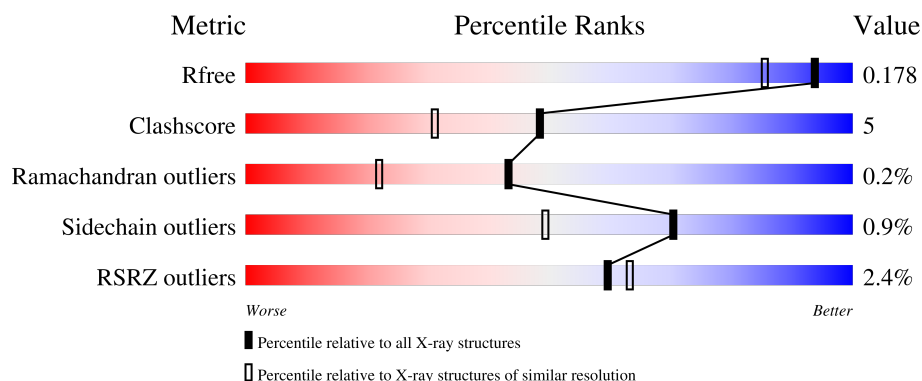
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

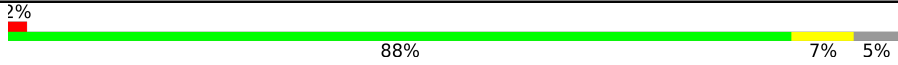
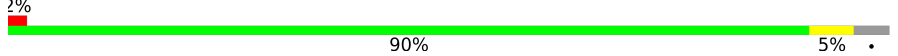
The reported resolution of this entry is 1.50 Å.

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	4037 (1.50-1.50)
Clashscore	190562	4235 (1.50-1.50)
Ramachandran outliers	187476	4153 (1.50-1.50)
Sidechain outliers	187428	4150 (1.50-1.50)
RSRZ outliers	180081	4039 (1.50-1.50)

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	511	
1	B	511	

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
5	PEG	A	605	-	-	X	-
5	PEG	B	601	-	-	X	-
5	PEG	B	604	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 9058 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.

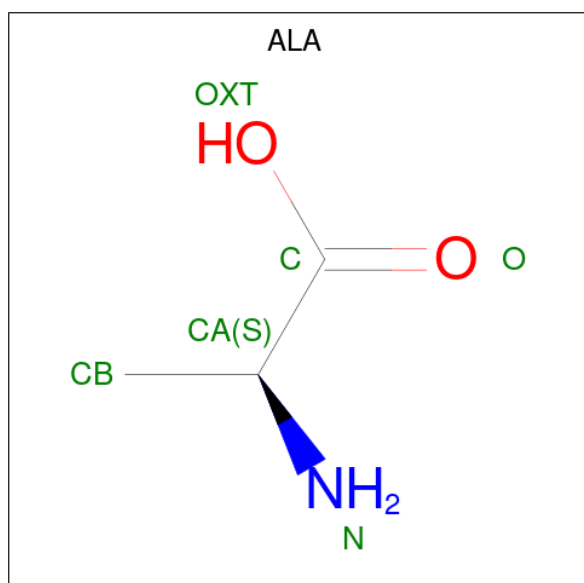
- Molecule 1 is a protein called N-acetyl-D-hexosamine oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	486	Total	C	N	O	S	0	6	0
			3845	2423	687	715	20			
1	B	489	Total	C	N	O	S	0	5	0
			3839	2421	686	713	19			

There are 6 discrepancies between the modelled and reference sequences:

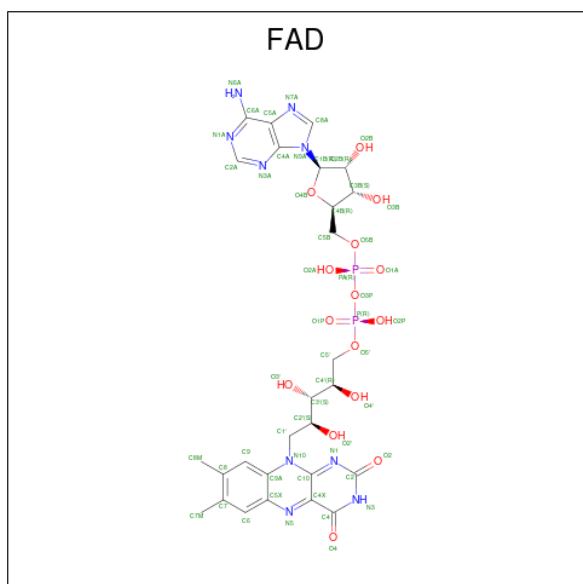
Chain	Residue	Modelled	Actual	Comment	Reference
A	509	ALA	-	expression tag	UNP A3RXB7
A	510	ALA	-	expression tag	UNP A3RXB7
A	511	ALA	-	expression tag	UNP A3RXB7
B	509	ALA	-	expression tag	UNP A3RXB7
B	510	ALA	-	expression tag	UNP A3RXB7
B	511	ALA	-	expression tag	UNP A3RXB7

- Molecule 2 is ALANINE (CCD ID: ALA) (formula: $C_3H_7NO_2$).



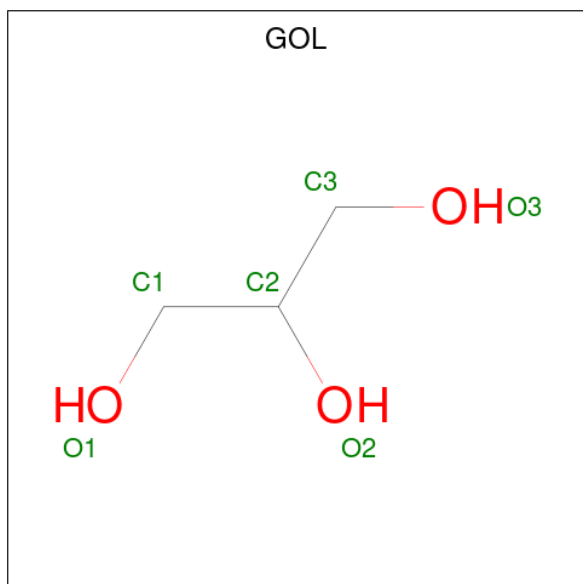
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			5	3	1	1		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $\text{C}_{27}\text{H}_{33}\text{N}_9\text{O}_{15}\text{P}_2$).



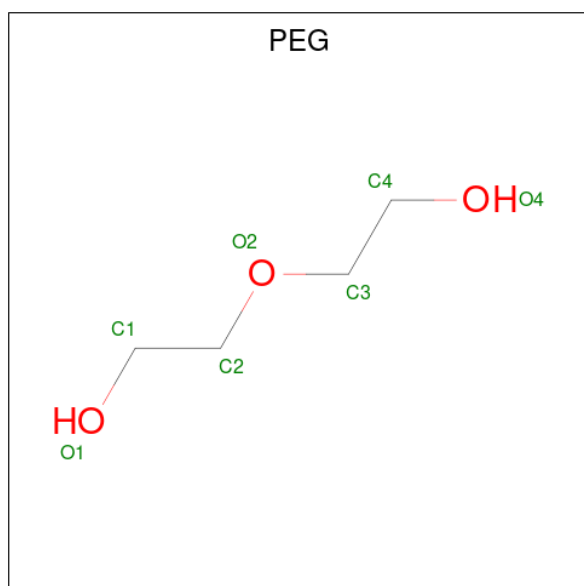
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 53	C 27	N 9	O 15	P 2	0	0
3	B	1	Total 53	C 27	N 9	O 15	P 2	0	0

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $\text{C}_3\text{H}_8\text{O}_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 7 4 3	0	0
5	A	1	Total C O 7 4 3	0	0
5	B	1	Total C O 7 4 3	0	0
5	B	1	Total C O 7 4 3	0	0

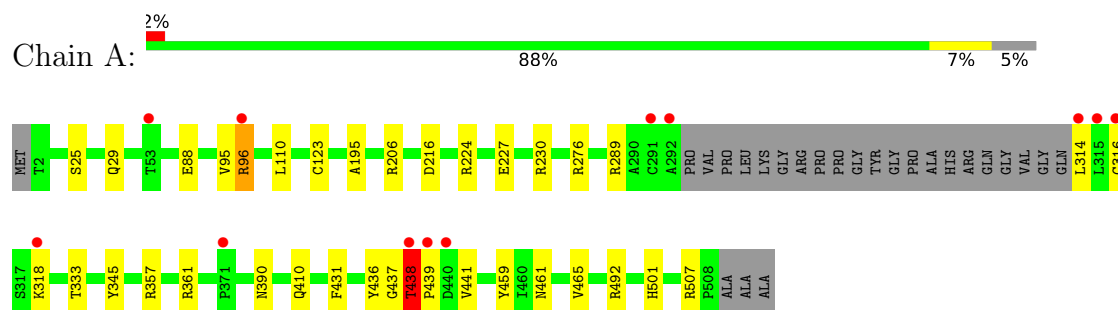
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	557	Total 574	O 574	0	17
6	B	605	Total 619	O 619	0	14

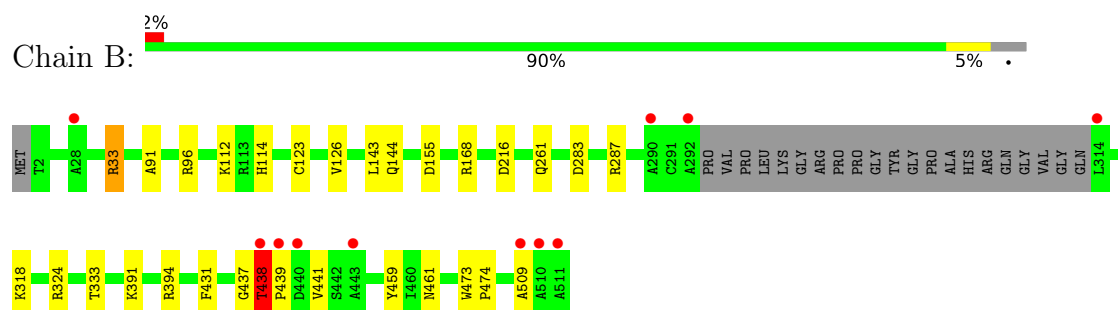
3 Residue-property plots [i](#)

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: N-acetyl-D-hexosamine oxidase



- Molecule 1: N-acetyl-D-hexosamine oxidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.96Å 105.01Å 120.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.00 – 1.50 45.00 – 1.50	Depositor EDS
% Data completeness (in resolution range)	99.7 (45.00-1.50) 99.6 (45.00-1.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.151 , 0.178 0.151 , 0.178	Depositor DCC
R_{free} test set	8912 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	13.9	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 39.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	9058	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% 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: GOL, PEG, 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	1.03	0/3946	1.16	3/5373 (0.1%)
1	B	1.02	0/3940	1.17	3/5368 (0.1%)
All	All	1.03	0/7886	1.16	6/10741 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	1
All	All	0	3

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	33	ARG	CG-CD-NE	-8.50	93.30	112.00
1	B	168	ARG	CG-CD-NE	7.58	128.66	112.00
1	A	507	ARG	CG-CD-NE	-6.53	97.64	112.00
1	A	438	THR	CB-CA-C	5.87	121.73	110.17
1	B	431	PHE	CA-CB-CG	5.83	119.63	113.80
1	A	431	PHE	CA-CB-CG	5.09	118.89	113.80

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	436	TYR	Sidechain
1	A	438	THR	Peptide
1	B	438	THR	Peptide

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	3845	0	3690	35	0
1	B	3839	0	3680	33	0
2	A	5	0	4	0	0
3	A	53	0	29	4	0
3	B	53	0	29	0	0
4	A	30	0	40	6	0
4	B	12	0	16	0	0
5	A	14	0	20	11	0
5	B	14	0	20	9	0
6	A	574	0	0	19	0
6	B	619	0	0	12	0
All	All	9058	0	7528	84	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 5.

All (84) 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:B:391:LYS:HE3	6:B:818:HOH:O	1.44	1.18
1:B:144:GLN:HG2	5:B:604:PEG:H32	1.28	1.13
1:A:227[B]:GLU:CD	1:A:230:ARG:HH12	1.57	1.11
5:B:601:PEG:O4	5:B:601:PEG:H11	1.50	1.10
1:B:439:PRO:CD	6:B:774:HOH:O	2.04	1.06
1:B:439:PRO:HD2	6:B:774:HOH:O	1.59	1.02
1:B:144:GLN:HG2	5:B:604:PEG:C3	1.90	1.00
1:A:227[B]:GLU:OE1	1:A:230:ARG:NH1	1.93	1.00
1:A:227[B]:GLU:CD	1:A:230:ARG:NH1	2.25	0.92
1:B:287[B]:ARG:HH11	1:B:287[B]:ARG:HG3	1.35	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:ARG:HG2	1:A:96:ARG:HH11	1.39	0.87
1:B:144:GLN:NE2	6:B:701:HOH:O	2.07	0.87
1:A:345:TYR:HE2	5:A:605:PEG:H42	1.40	0.85
1:B:438:THR:HB	1:B:439:PRO:HD3	1.57	0.85
1:A:96:ARG:HG2	1:A:96:ARG:NH1	1.94	0.81
1:B:144:GLN:CG	5:B:604:PEG:H32	2.12	0.79
1:A:410:GLN:HE22	5:A:605:PEG:H12	1.48	0.78
5:B:601:PEG:O4	5:B:601:PEG:C1	2.31	0.77
1:A:390:ASN:HB2	4:A:608:GOL:H31	1.66	0.77
1:A:96:ARG:HH11	1:A:96:ARG:CG	1.98	0.76
1:B:287[A]:ARG:NH1	6:B:704:HOH:O	2.20	0.75
1:A:345:TYR:CE2	5:A:605:PEG:H42	2.21	0.74
5:B:604:PEG:O1	6:B:702:HOH:O	2.08	0.72
1:B:283:ASP:O	1:B:287[B]:ARG:NH1	2.25	0.69
1:B:287[B]:ARG:HH11	1:B:287[B]:ARG:CG	2.04	0.66
1:A:276:ARG:NH1	6:A:705:HOH:O	2.28	0.66
1:B:439:PRO:HD3	6:B:774:HOH:O	1.81	0.66
1:B:216:ASP:OD1	6:B:703:HOH:O	2.15	0.64
1:A:492:ARG:NE	6:A:703:HOH:O	2.27	0.64
1:A:88:GLU:HG3	6:A:889:HOH:O	1.98	0.63
1:A:357:ARG:HD3	1:A:361:ARG:NH2	2.13	0.63
5:A:609:PEG:H32	6:A:849:HOH:O	1.99	0.61
1:A:501:HIS:HE1	6:A:1168:HOH:O	1.83	0.61
3:A:602:FAD:C7	5:A:605:PEG:H32	2.31	0.60
1:B:287[B]:ARG:NH1	1:B:287[B]:ARG:CG	2.62	0.60
1:A:438:THR:O	1:A:441:VAL:O	2.20	0.59
1:A:224:ARG:HE	1:A:314:LEU:HG	1.67	0.59
1:A:216:ASP:OD1	6:A:702:HOH:O	2.16	0.58
1:B:112:LYS:NZ	6:B:1071[B]:HOH:O	2.36	0.58
1:A:318:LYS:HE2	6:A:1204:HOH:O	2.03	0.58
1:B:438:THR:O	1:B:441:VAL:O	2.21	0.58
1:B:438:THR:HB	1:B:439:PRO:CD	2.29	0.57
3:A:602:FAD:C5X	5:A:605:PEG:H11	2.34	0.56
5:A:609:PEG:C4	6:A:731:HOH:O	2.53	0.55
1:A:459:TYR:CZ	1:A:461:ASN:HB2	2.41	0.55
1:B:287[B]:ARG:HG3	1:B:287[B]:ARG:NH1	2.11	0.55
4:A:603:GOL:H31	6:A:1195:HOH:O	2.05	0.55
1:B:144:GLN:HG2	5:B:604:PEG:O2	2.08	0.54
1:B:143:LEU:HD12	6:B:980:HOH:O	2.08	0.53
1:B:509:ALA:HB3	6:B:1164:HOH:O	2.08	0.53
1:A:95:VAL:HG11	1:A:110[A]:LEU:HD21	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:410:GLN:HE22	5:A:605:PEG:C1	2.18	0.53
1:B:459:TYR:CZ	1:B:461:ASN:HB2	2.45	0.52
1:A:501:HIS:HD2	6:A:1145:HOH:O	1.93	0.52
3:A:602:FAD:C6	5:A:605:PEG:H32	2.40	0.51
1:B:438:THR:O	1:B:439:PRO:C	2.54	0.51
1:A:361:ARG:NH1	6:A:718:HOH:O	2.44	0.51
1:A:438:THR:O	1:A:439:PRO:C	2.54	0.50
1:B:96:ARG:NH2	1:B:155:ASP:OD2	2.44	0.50
4:A:607:GOL:H12	6:A:1020:HOH:O	2.13	0.49
6:A:941:HOH:O	5:B:601:PEG:H21	2.12	0.48
1:B:391:LYS:HZ3	1:B:394:ARG:HH11	1.62	0.48
4:A:608:GOL:H2	6:A:715:HOH:O	2.14	0.47
1:B:123[B]:CYS:HB3	1:B:126:VAL:HG23	1.97	0.46
1:A:227[B]:GLU:OE2	1:A:230:ARG:NH1	2.38	0.46
5:B:601:PEG:H11	5:B:601:PEG:C4	2.39	0.46
3:A:602:FAD:N5	5:A:605:PEG:H11	2.32	0.46
1:A:25:SER:HB2	1:A:29:GLN:OE1	2.16	0.45
1:B:391:LYS:CE	6:B:818:HOH:O	2.27	0.45
1:A:345:TYR:CE2	5:A:605:PEG:C4	2.97	0.44
1:A:123[B]:CYS:HB2	6:A:1036:HOH:O	2.18	0.43
1:A:289:ARG:O	1:A:316:CYS:HA	2.18	0.43
1:A:357:ARG:HG2	1:A:361:ARG:CZ	2.49	0.42
1:B:261:GLN:HE22	1:B:318:LYS:NZ	2.16	0.42
4:A:607:GOL:H31	6:A:1108:HOH:O	2.18	0.42
1:B:473:TRP:CG	1:B:474:PRO:HD3	2.54	0.42
1:B:391:LYS:NZ	1:B:394:ARG:HH11	2.18	0.42
1:A:437:GLY:O	1:A:438:THR:C	2.63	0.42
4:A:608:GOL:C2	6:A:715:HOH:O	2.68	0.41
1:A:465:VAL:HG11	6:A:894:HOH:O	2.19	0.41
1:A:96:ARG:HD2	1:A:195:ALA:HB1	2.01	0.41
1:B:91:ALA:O	1:B:114:HIS:HE1	2.04	0.41
1:B:437:GLY:O	1:B:438:THR:C	2.63	0.41
1:A:206:ARG:HD3	6:A:1071:HOH:O	2.20	0.41

There are no symmetry-related clashes.

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	488/511 (96%)	476 (98%)	11 (2%)	1 (0%)	43	22
1	B	490/511 (96%)	479 (98%)	10 (2%)	1 (0%)	43	22
All	All	978/1022 (96%)	955 (98%)	21 (2%)	2 (0%)	43	22

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	438	THR
1	B	438	THR

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	398/410 (97%)	395 (99%)	3 (1%)	73	54
1	B	394/410 (96%)	390 (99%)	4 (1%)	68	45
All	All	792/820 (97%)	785 (99%)	7 (1%)	70	49

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	96	ARG
1	A	333	THR
1	A	438	THR
1	B	33	ARG

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Mol	Chain	Res	Type
1	B	324	ARG
1	B	333	THR
1	B	438	THR

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

Mol	Chain	Res	Type
1	A	49	HIS
1	A	105	ASN
1	A	261	GLN
1	A	320	HIS
1	A	341	GLN
1	A	377	GLN
1	A	410	GLN
1	A	501	HIS
1	B	105	ASN
1	B	261	GLN
1	B	341	GLN
1	B	377	GLN
1	B	410	GLN
1	B	445	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

14 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	GOL	A	607	-	5,5,5	0.13	0	5,5,5	0.32	0
4	GOL	A	608	-	5,5,5	0.13	0	5,5,5	0.54	0
5	PEG	A	605	-	6,6,6	0.57	0	5,5,5	0.41	0
4	GOL	B	603	-	5,5,5	0.14	0	5,5,5	0.37	0
3	FAD	A	602	1	58,58,58	0.97	2 (3%)	85,89,89	0.99	5 (5%)
4	GOL	B	605	-	5,5,5	0.15	0	5,5,5	0.59	0
3	FAD	B	602	1	58,58,58	1.03	4 (6%)	85,89,89	0.94	2 (2%)
4	GOL	A	604	-	5,5,5	0.10	0	5,5,5	0.52	0
4	GOL	A	603	-	5,5,5	0.14	0	5,5,5	0.27	0
5	PEG	B	604	-	6,6,6	0.31	0	5,5,5	0.37	0
5	PEG	A	609	-	6,6,6	0.48	0	5,5,5	0.66	0
5	PEG	B	601	-	6,6,6	1.06	0	5,5,5	0.93	0
4	GOL	A	606	-	5,5,5	0.10	0	5,5,5	0.47	0
2	ALA	A	601	-	3,4,5	1.12	0	2,4,6	1.87	1 (50%)

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
4	GOL	A	607	-	-	2/4/4/4	-
4	GOL	A	608	-	-	4/4/4/4	-
5	PEG	A	605	-	-	2/4/4/4	-
4	GOL	B	603	-	-	0/4/4/4	-
3	FAD	A	602	1	-	6/34/50/50	0/6/6/6
4	GOL	B	605	-	-	2/4/4/4	-
3	FAD	B	602	1	-	5/34/50/50	0/6/6/6
4	GOL	A	604	-	-	3/4/4/4	-
4	GOL	A	603	-	-	0/4/4/4	-
5	PEG	B	604	-	-	4/4/4/4	-
5	PEG	A	609	-	-	3/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PEG	B	601	-	-	2/4/4/4	-
4	GOL	A	606	-	-	2/4/4/4	-
2	ALA	A	601	-	-	1/1/2/4	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	602	FAD	C1'-C2'	-3.69	1.47	1.52
3	B	602	FAD	P-O3P	3.17	1.62	1.59
3	A	602	FAD	P-O3P	2.84	1.62	1.59
3	B	602	FAD	C6-C5X	2.69	1.44	1.40
3	B	602	FAD	C8-C7	2.64	1.47	1.40
3	B	602	FAD	C5'-C4'	-2.16	1.48	1.51

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	602	FAD	C9A-C5X-N5	-3.23	119.02	122.45
2	A	601	ALA	O-C-CA	-2.61	115.87	124.23
3	A	602	FAD	C5X-C9A-N10	2.56	120.28	117.97
3	A	602	FAD	N3A-C2A-N1A	2.51	132.39	128.58
3	A	602	FAD	C9A-C5X-N5	-2.51	119.79	122.45
3	A	602	FAD	O3P-P-O1P	-2.43	103.41	110.70
3	A	602	FAD	C6-C5X-C9A	2.26	122.16	119.05
3	B	602	FAD	C5X-C9A-N10	2.02	119.80	117.97

There are no chirality outliers.

All (36) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	ALA	O-C-CA-CB
4	A	604	GOL	O1-C1-C2-C3
4	A	608	GOL	O1-C1-C2-C3
4	A	608	GOL	O2-C2-C3-O3
4	B	605	GOL	O1-C1-C2-C3
5	B	601	PEG	C4-C3-O2-C2
3	A	602	FAD	O3'-C3'-C4'-C5'
5	B	604	PEG	C4-C3-O2-C2
5	B	601	PEG	C1-C2-O2-C3
4	A	608	GOL	O1-C1-C2-O2
3	A	602	FAD	O3'-C3'-C4'-O4'

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Mol	Chain	Res	Type	Atoms
3	B	602	FAD	O3'-C3'-C4'-O4'
5	A	605	PEG	O2-C3-C4-O4
5	B	604	PEG	O1-C1-C2-O2
4	A	606	GOL	C1-C2-C3-O3
4	A	607	GOL	O1-C1-C2-C3
4	A	608	GOL	C1-C2-C3-O3
4	A	604	GOL	O1-C1-C2-O2
4	A	607	GOL	O1-C1-C2-O2
3	B	602	FAD	O3'-C3'-C4'-C5'
3	A	602	FAD	C2'-C3'-C4'-C5'
3	A	602	FAD	C2'-C3'-C4'-O4'
3	B	602	FAD	C2'-C3'-C4'-O4'
4	B	605	GOL	O1-C1-C2-O2
3	B	602	FAD	C2'-C3'-C4'-C5'
5	B	604	PEG	C1-C2-O2-C3
3	A	602	FAD	C5B-O5B-PA-O1A
5	A	609	PEG	O2-C3-C4-O4
3	A	602	FAD	PA-O3P-P-O2P
4	A	606	GOL	O2-C2-C3-O3
5	B	604	PEG	O2-C3-C4-O4
4	A	604	GOL	O2-C2-C3-O3
5	A	609	PEG	C1-C2-O2-C3
5	A	609	PEG	O1-C1-C2-O2
5	A	605	PEG	O1-C1-C2-O2
3	B	602	FAD	PA-O3P-P-O2P

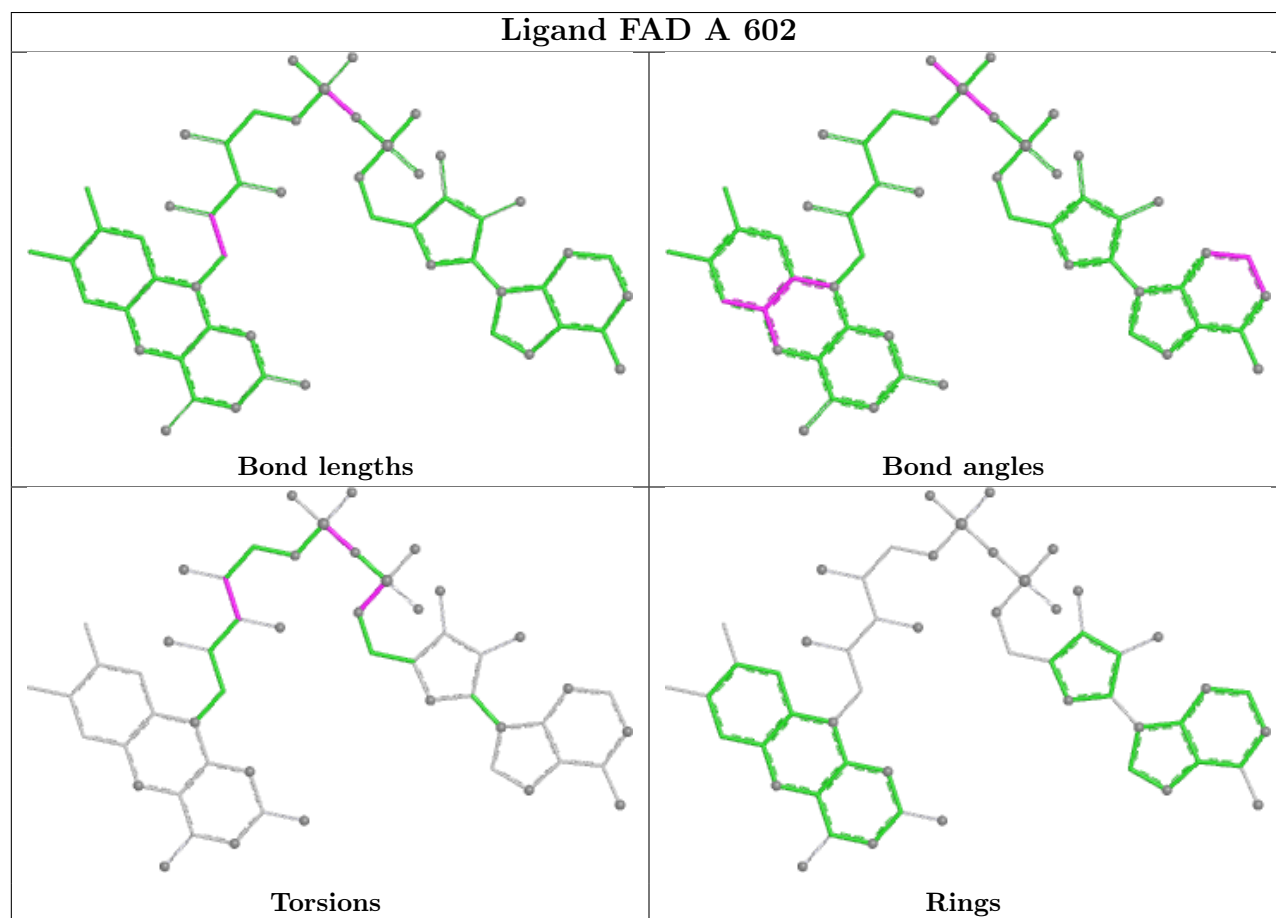
There are no ring outliers.

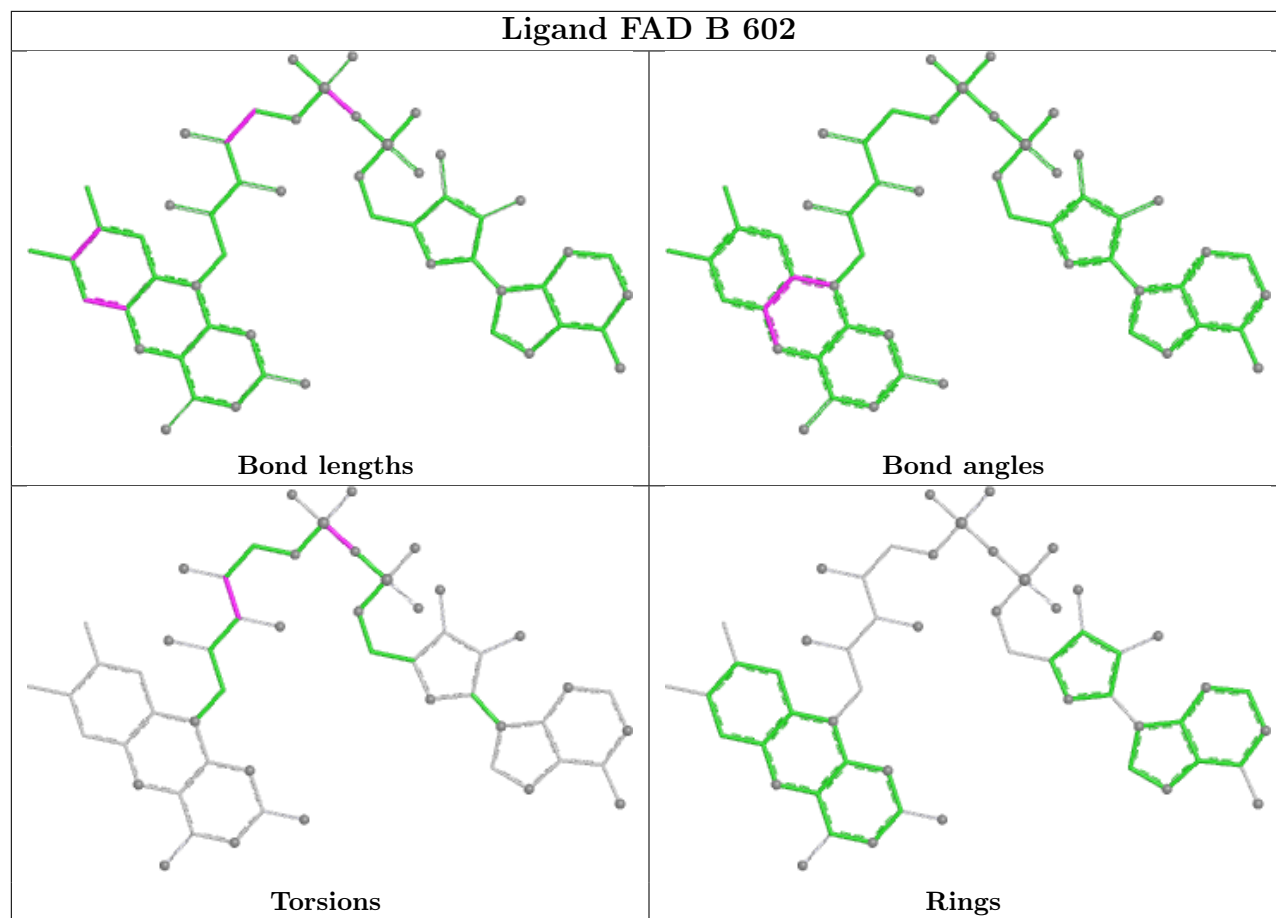
8 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	607	GOL	2	0
4	A	608	GOL	3	0
5	A	605	PEG	9	0
3	A	602	FAD	4	0
4	A	603	GOL	1	0
5	B	604	PEG	5	0
5	A	609	PEG	2	0
5	B	601	PEG	4	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	486/511 (95%)	-0.16	12 (2%) 58 62	5, 14, 29, 56	6 (1%)
1	B	489/511 (95%)	-0.19	11 (2%) 62 66	6, 13, 28, 54	5 (1%)
All	All	975/1022 (95%)	-0.17	23 (2%) 59 63	5, 13, 29, 56	11 (1%)

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	314	LEU	8.0
1	B	509	ALA	5.5
1	A	438	THR	5.5
1	A	439	PRO	5.0
1	B	438	THR	4.9
1	A	292	ALA	4.4
1	B	292	ALA	4.3
1	A	291	CYS	4.3
1	B	314	LEU	4.1
1	B	439	PRO	3.8
1	A	315	LEU	3.6
1	B	443	ALA	2.8
1	B	511	ALA	2.8
1	A	440	ASP	2.7
1	B	440	ASP	2.7
1	B	510	ALA	2.5
1	A	316	CYS	2.4
1	B	290	ALA	2.3
1	A	96	ARG	2.2
1	A	318	LYS	2.2
1	A	371	PRO	2.2
1	A	53	THR	2.1
1	B	28	ALA	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

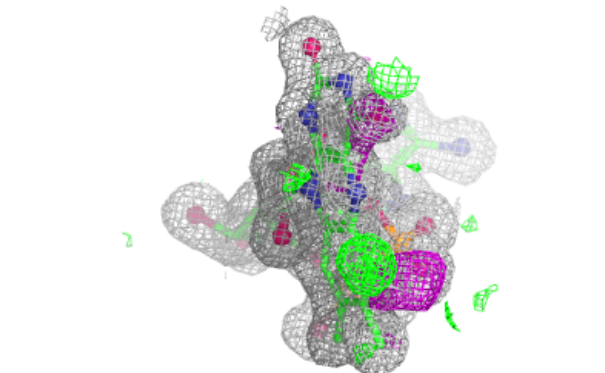
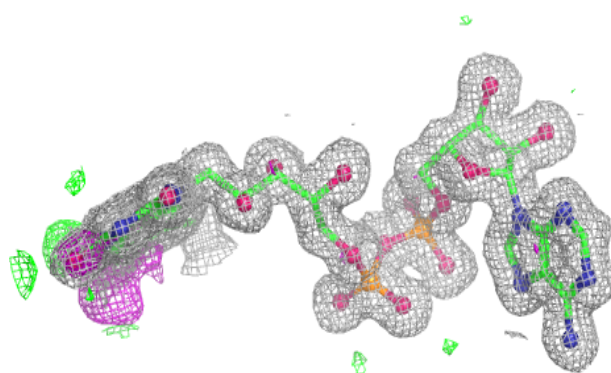
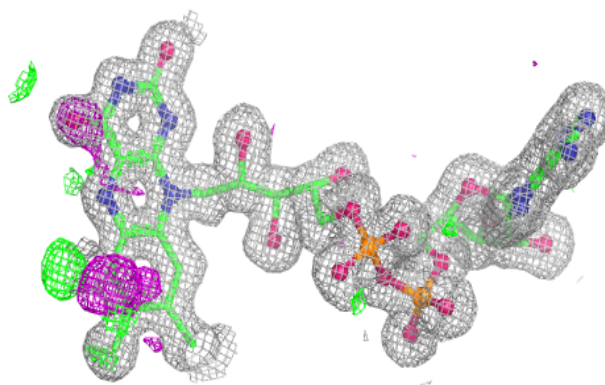
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	PEG	B	604	7/7	0.58	0.29	52,53,73,79	0
2	ALA	A	601	5/6	0.68	0.20	41,46,47,49	0
5	PEG	A	609	7/7	0.73	0.21	24,28,35,44	0
4	GOL	A	607	6/6	0.75	0.18	44,47,48,48	0
4	GOL	B	603	6/6	0.80	0.15	29,38,42,45	0
4	GOL	A	608	6/6	0.81	0.16	31,47,48,55	0
5	PEG	A	605	7/7	0.82	0.17	24,34,38,42	0
5	PEG	B	601	7/7	0.84	0.19	20,35,38,38	0
4	GOL	A	603	6/6	0.84	0.14	27,41,43,44	0
4	GOL	B	605	6/6	0.85	0.15	31,39,42,44	0
4	GOL	A	604	6/6	0.88	0.12	28,34,37,38	0
4	GOL	A	606	6/6	0.94	0.10	22,30,32,34	0
3	FAD	B	602	53/53	0.98	0.04	7,10,16,18	0
3	FAD	A	602	53/53	0.98	0.04	7,11,15,17	0

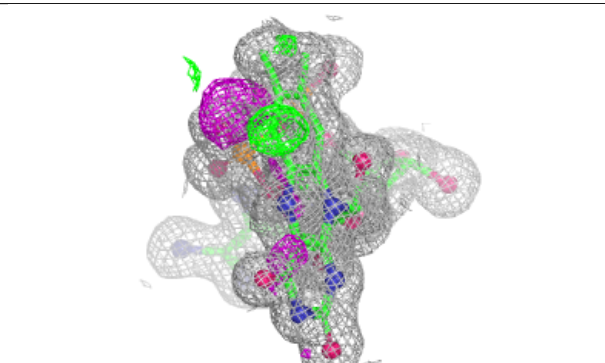
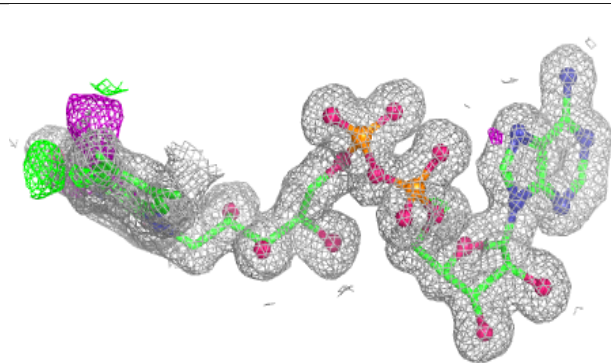
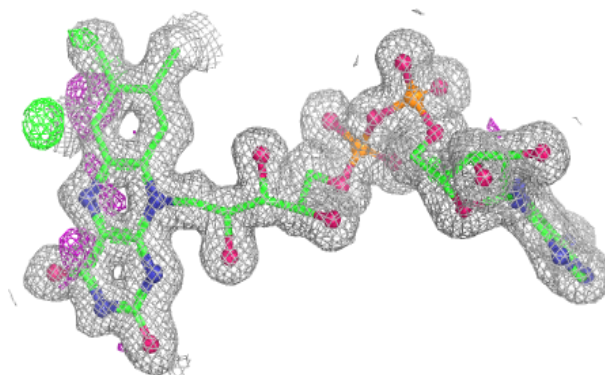
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around FAD B 602:

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

**Electron density around FAD A 602:**

$2mF_o-DF_c$ (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.