



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 9, 2024 – 12:09 PM JST

PDB ID : 8XG9
Title : Crystal structure of phenylacetone monooxygenase mutant PM3 bound to FAD and NADP
Authors : Li, X.; Sun, Z.T.
Deposited on : 2023-12-15
Resolution : 2.00 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.21
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.004 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

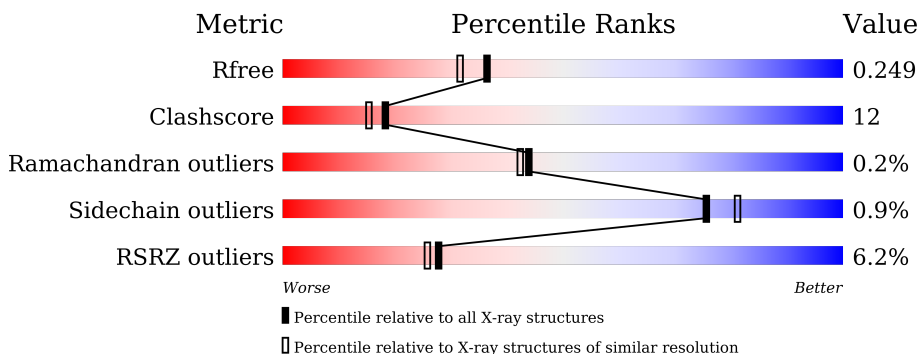
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	164625	9409 (2.00-2.00)
Clashscore	180529	10737 (2.00-2.00)
Ramachandran outliers	177936	10628 (2.00-2.00)
Sidechain outliers	177891	10627 (2.00-2.00)
RSRZ outliers	164620	9409 (2.00-2.00)

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	546	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 4528 atoms, of which 83 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.

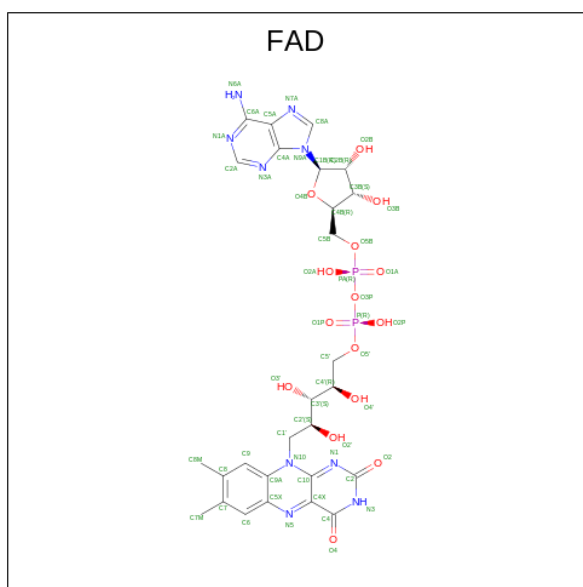
- Molecule 1 is a protein called Phenylacetone monooxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	514	4140	2637	719	775	9	0	1	0

There are 10 discrepancies between the modelled and reference sequences:

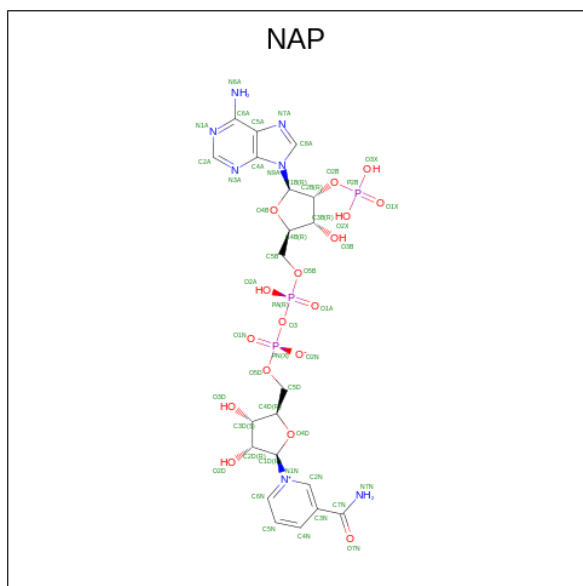
Chain	Residue	Modelled	Actual	Comment	Reference
A	441	GLY	SER	conflict	UNP Q47PU3
A	442	ILE	ALA	conflict	UNP Q47PU3
A	?	-	LEU	deletion	UNP Q47PU3
A	?	-	SER	deletion	UNP Q47PU3
A	541	HIS	-	expression tag	UNP Q47PU3
A	542	HIS	-	expression tag	UNP Q47PU3
A	543	HIS	-	expression tag	UNP Q47PU3
A	544	HIS	-	expression tag	UNP Q47PU3
A	545	HIS	-	expression tag	UNP Q47PU3
A	546	HIS	-	expression tag	UNP Q47PU3

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$) (labeled as "Ligand of Interest" by depositor).



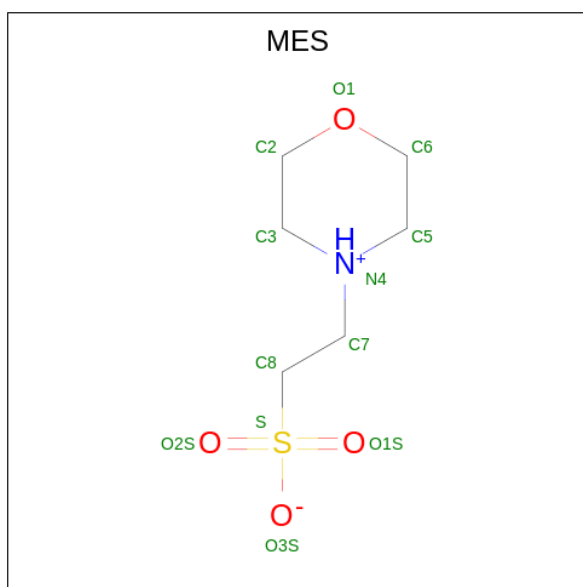
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	H	N	O			P
2	A	1	84	27	31	9	15	2	0	0

- Molecule 3 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$) (labeled as "Ligand of Interest" by depositor).



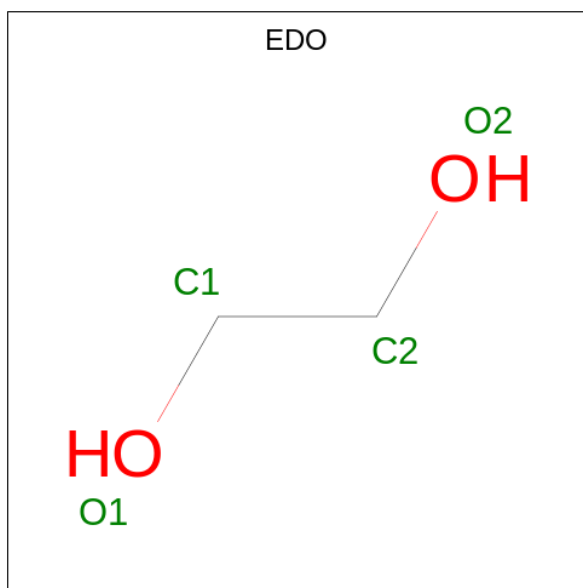
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	H	N	O			P
3	A	1	73	21	25	7	17	3	0	0

- Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	H	N	O			S
4	A	1	25	6	13	1	4	1	0	0

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
			Total	C	H			O
5	A	1	10	2	6	2	0	0

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
6	A	1	14	3	8	3	0	0

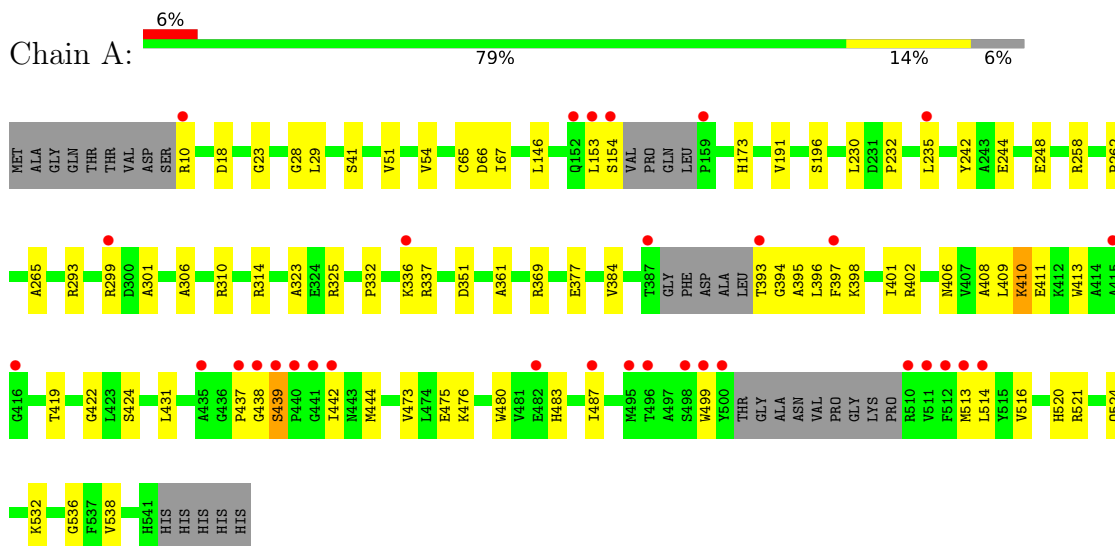
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	182	182	182	0	0

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: Phenylacetone monooxygenase



4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	83.25Å 84.75Å 92.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.98 – 2.00 34.98 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.2 (34.98-2.00) 99.2 (34.98-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.01 (at 2.00Å)	Xtrriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.221 , 0.251 0.221 , 0.249	Depositor DCC
R_{free} test set	42932 reflections (4.48%)	wwPDB-VP
Wilson B-factor (Å ²)	33.6	Xtrriage
Anisotropy	0.168	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 39.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtrriage
Estimated twinning fraction	0.000 for k,h,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4528	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.26% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, NAP, FAD, MES, GOL

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	0.29	0/4250	0.46	0/5773

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 [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	4140	0	3988	95	0
2	A	53	31	31	11	0
3	A	48	25	25	6	0
4	A	12	13	13	2	0
5	A	4	6	6	1	0
6	A	6	8	8	0	0
7	A	182	0	0	16	0
All	All	4445	83	4071	99	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 12.

All (99) 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:258:ARG:HD2	7:A:857:HOH:O	1.42	1.18
1:A:532:LYS:HE3	7:A:774:HOH:O	1.41	1.17
1:A:395:ALA:HA	1:A:398:LYS:CE	1.78	1.13
1:A:395:ALA:CA	1:A:398:LYS:HE3	1.77	1.13
1:A:408:ALA:HB3	1:A:411:GLU:HG3	1.37	1.06
1:A:410:LYS:HE3	7:A:803:HOH:O	1.58	1.03
1:A:154:SER:HA	7:A:791:HOH:O	1.61	0.99
1:A:393:THR:HG21	1:A:397:PHE:CE2	1.97	0.98
1:A:410:LYS:HE2	1:A:410:LYS:H	1.28	0.98
1:A:480:TRP:HE3	4:A:603:MES:H21	1.31	0.95
1:A:299:ARG:HH12	1:A:332:PRO:HG3	1.36	0.89
1:A:395:ALA:HA	1:A:398:LYS:HE3	0.89	0.84
1:A:480:TRP:CE3	4:A:603:MES:H21	2.14	0.81
1:A:406:ASN:O	1:A:406:ASN:OD1	2.00	0.80
1:A:153:LEU:HD12	2:A:601:FAD:H1'1	1.63	0.78
1:A:393:THR:CG2	1:A:397:PHE:CE2	2.68	0.76
1:A:410:LYS:H	1:A:410:LYS:CE	2.00	0.75
1:A:475:GLU:HB2	7:A:788:HOH:O	1.86	0.74
1:A:336:LYS:HE3	1:A:337:ARG:H	1.54	0.73
1:A:258:ARG:HH22	1:A:442:ILE:HD11	1.56	0.71
1:A:258:ARG:NH2	1:A:442:ILE:HD11	2.06	0.70
1:A:299:ARG:HH11	1:A:299:ARG:HG3	1.61	0.66
1:A:475:GLU:CB	7:A:788:HOH:O	2.42	0.65
1:A:419:THR:HG21	1:A:437:PRO:HG3	1.78	0.64
1:A:299:ARG:NH1	1:A:332:PRO:HG3	2.12	0.63
1:A:154:SER:CB	7:A:791:HOH:O	2.46	0.63
1:A:351:ASP:H	5:A:604:EDO:H12	1.63	0.63
1:A:422:GLY:HA2	1:A:437:PRO:HG2	1.81	0.62
1:A:66[B]:ASP:OD2	3:A:602:NAP:N7N	2.32	0.61
2:A:601:FAD:HM73	3:A:602:NAP:C5N	2.30	0.61
1:A:483:HIS:O	1:A:487:ILE:HG13	2.00	0.61
1:A:336:LYS:HE3	1:A:337:ARG:N	2.15	0.61
1:A:408:ALA:HB3	1:A:411:GLU:CG	2.25	0.60
1:A:483:HIS:NE2	1:A:487:ILE:HD11	2.16	0.60
1:A:393:THR:HG23	1:A:397:PHE:CD2	2.38	0.58
1:A:153:LEU:CD1	2:A:601:FAD:H1'1	2.30	0.58
1:A:514:LEU:HD12	1:A:516:VAL:HG12	1.87	0.57
1:A:369:ARG:HH12	1:A:377:GLU:HG2	1.70	0.57
1:A:54:VAL:HB	2:A:601:FAD:HM82	1.90	0.54
1:A:396:LEU:HD23	1:A:413:TRP:HZ3	1.73	0.54
1:A:244:GLU:O	1:A:248:GLU:HG3	2.08	0.53
1:A:422:GLY:CA	1:A:437:PRO:HG2	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:401:ILE:H	1:A:410:LYS:HZ2	1.56	0.53
1:A:65:CYS:SG	2:A:601:FAD:O4	2.63	0.53
1:A:67:ILE:HG12	2:A:601:FAD:HN3	1.74	0.52
1:A:173:HIS:HB3	7:A:729:HOH:O	2.10	0.52
1:A:397:PHE:CD1	1:A:410:LYS:HG3	2.45	0.51
1:A:361:ALA:HB3	7:A:723:HOH:O	2.09	0.51
1:A:258:ARG:HH22	1:A:442:ILE:CD1	2.23	0.51
1:A:393:THR:CG2	1:A:397:PHE:CD2	2.94	0.51
1:A:476:LYS:HG3	1:A:536:GLY:HA2	1.92	0.51
1:A:18:ASP:HB2	1:A:41:SER:O	2.11	0.50
1:A:154:SER:CA	7:A:791:HOH:O	2.32	0.50
1:A:439:SER:HB3	1:A:514:LEU:CD2	2.41	0.50
1:A:401:ILE:H	1:A:410:LYS:NZ	2.10	0.50
1:A:401:ILE:N	1:A:410:LYS:HZ2	2.09	0.50
1:A:520:HIS:HB3	7:A:843:HOH:O	2.11	0.49
1:A:235:LEU:HD13	7:A:718:HOH:O	2.12	0.49
1:A:499:TRP:HA	1:A:513:MET:HE2	1.95	0.49
2:A:601:FAD:HM73	3:A:602:NAP:C4N	2.43	0.49
1:A:402:ARG:HD2	1:A:406:ASN:OD1	2.13	0.49
1:A:438:GLY:O	1:A:439:SER:C	2.51	0.48
1:A:54:VAL:HG12	7:A:814:HOH:O	2.13	0.48
2:A:601:FAD:O2'	2:A:601:FAD:H5'1	2.14	0.48
1:A:520:HIS:NE2	1:A:524:GLN:NE2	2.62	0.47
1:A:401:ILE:O	1:A:410:LYS:NZ	2.46	0.47
1:A:337:ARG:HD3	3:A:602:NAP:O2D	2.13	0.47
1:A:191:VAL:HG22	1:A:384:VAL:HB	1.97	0.47
1:A:336:LYS:CE	1:A:337:ARG:H	2.26	0.47
1:A:265:ALA:HB3	1:A:301:ALA:HB1	1.98	0.46
1:A:397:PHE:CE1	1:A:410:LYS:HA	2.51	0.46
1:A:10:ARG:HH11	1:A:10:ARG:HG2	1.81	0.46
1:A:244:GLU:HB2	7:A:830:HOH:O	2.15	0.45
1:A:314:ARG:HA	1:A:323:ALA:HB1	1.99	0.45
1:A:299:ARG:HH12	1:A:332:PRO:CG	2.20	0.45
1:A:10:ARG:HG2	1:A:10:ARG:NH1	2.32	0.45
1:A:410:LYS:H	1:A:410:LYS:CD	2.30	0.45
1:A:409:LEU:HD11	1:A:413:TRP:CE2	2.53	0.44
1:A:396:LEU:HD23	1:A:413:TRP:CZ3	2.51	0.44
1:A:299:ARG:HG3	1:A:299:ARG:NH1	2.30	0.43
1:A:393:THR:HG21	1:A:397:PHE:CZ	2.48	0.43
1:A:521:ARG:HD2	1:A:521:ARG:O	2.19	0.43
1:A:532:LYS:CE	7:A:774:HOH:O	2.24	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:29:LEU:HD11	1:A:51:VAL:HB	2.01	0.42
1:A:306:ALA:O	1:A:310:ARG:HG3	2.19	0.42
1:A:262:PRO:O	1:A:293:ARG:HD3	2.20	0.42
1:A:23:GLY:O	1:A:28:GLY:HA3	2.19	0.42
1:A:146:LEU:HD23	1:A:431:LEU:HD13	2.01	0.42
1:A:473:VAL:HG22	1:A:538:VAL:HG23	2.02	0.42
2:A:601:FAD:N5	3:A:602:NAP:N7N	2.66	0.41
1:A:54:VAL:HB	2:A:601:FAD:C8M	2.49	0.41
1:A:196:SER:N	3:A:602:NAP:O2N	2.52	0.41
1:A:410:LYS:CD	1:A:410:LYS:N	2.83	0.41
1:A:394:GLY:O	1:A:398:LYS:HE2	2.21	0.41
1:A:395:ALA:CA	1:A:398:LYS:CE	2.63	0.41
1:A:230:LEU:O	1:A:232:PRO:HD3	2.20	0.41
1:A:521:ARG:NE	7:A:702:HOH:O	2.23	0.41
1:A:444:MET:HG2	2:A:601:FAD:O2	2.21	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	507/546 (93%)	493 (97%)	13 (3%)	1 (0%)	44 42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	439	SER

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	433/457 (95%)	429 (99%)	4 (1%)	75 81

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	242	TYR
1	A	325	ARG
1	A	410	LYS
1	A	424	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

5 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	MES	A	603	-	12,12,12	0.68	0	14,16,16	0.37	0
3	NAP	A	602	-	45,52,52	2.84	18 (40%)	56,80,80	1.60	11 (19%)
6	GOL	A	605	-	5,5,5	0.09	0	5,5,5	0.25	0
2	FAD	A	601	-	53,58,58	0.64	0	68,89,89	0.75	2 (2%)
5	EDO	A	604	-	3,3,3	0.40	0	2,2,2	0.38	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
4	MES	A	603	-	-	0/6/14/14	0/1/1/1
3	NAP	A	602	-	-	5/31/67/67	0/5/5/5
6	GOL	A	605	-	-	2/4/4/4	-
2	FAD	A	601	-	-	3/30/50/50	0/6/6/6
5	EDO	A	604	-	-	0/1/1/1	-

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	602	NAP	O4B-C1B	8.73	1.53	1.41
3	A	602	NAP	O4D-C1D	8.46	1.52	1.41
3	A	602	NAP	C7N-N7N	5.81	1.44	1.33
3	A	602	NAP	C4N-C3N	4.95	1.47	1.39
3	A	602	NAP	C2N-N1N	4.74	1.40	1.35
3	A	602	NAP	P2B-O2B	4.07	1.67	1.59
3	A	602	NAP	C5N-C4N	3.96	1.47	1.38
3	A	602	NAP	O4D-C4D	3.76	1.53	1.45
3	A	602	NAP	C6A-N6A	3.39	1.46	1.34
3	A	602	NAP	O4B-C4B	3.06	1.51	1.45
3	A	602	NAP	C3N-C7N	2.49	1.54	1.50
3	A	602	NAP	PN-O5D	2.41	1.69	1.59
3	A	602	NAP	C2D-C3D	-2.23	1.47	1.53
3	A	602	NAP	C3B-C2B	-2.13	1.48	1.52
3	A	602	NAP	O7N-C7N	-2.13	1.20	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	602	NAP	C6N-N1N	2.09	1.40	1.35
3	A	602	NAP	PA-O5B	2.08	1.67	1.59
3	A	602	NAP	C5A-N7A	2.00	1.47	1.39

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	NAP	C3D-C2D-C1D	4.63	107.95	100.98
3	A	602	NAP	N3A-C2A-N1A	-4.42	121.77	128.68
3	A	602	NAP	O7N-C7N-N7N	-4.03	116.85	122.58
3	A	602	NAP	O2N-PN-O1N	-3.60	94.46	112.24
3	A	602	NAP	O7N-C7N-C3N	2.64	122.79	119.63
3	A	602	NAP	C2D-C3D-C4D	2.56	107.61	102.64
3	A	602	NAP	C4A-C5A-N7A	-2.49	106.80	109.40
3	A	602	NAP	C1B-N9A-C4A	-2.38	122.45	126.64
3	A	602	NAP	N6A-C6A-N1A	2.22	123.18	118.57
3	A	602	NAP	C3N-C7N-N7N	2.16	120.35	117.75
3	A	602	NAP	O4D-C4D-C3D	2.15	109.36	105.11
2	A	601	FAD	O4B-C1B-C2B	-2.09	103.87	106.93
2	A	601	FAD	O2A-PA-O1A	2.06	122.43	112.24

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	FAD	N10-C1'-C2'-O2'
2	A	601	FAD	N10-C1'-C2'-C3'
3	A	602	NAP	C2B-O2B-P2B-O2X
3	A	602	NAP	C5D-O5D-PN-O1N
6	A	605	GOL	O1-C1-C2-C3
6	A	605	GOL	O1-C1-C2-O2
3	A	602	NAP	O4B-C4B-C5B-O5B
3	A	602	NAP	C5B-O5B-PA-O3
2	A	601	FAD	O4B-C4B-C5B-O5B
3	A	602	NAP	PN-O3-PA-O2A

There are no ring outliers.

4 monomers are involved in 17 short contacts:

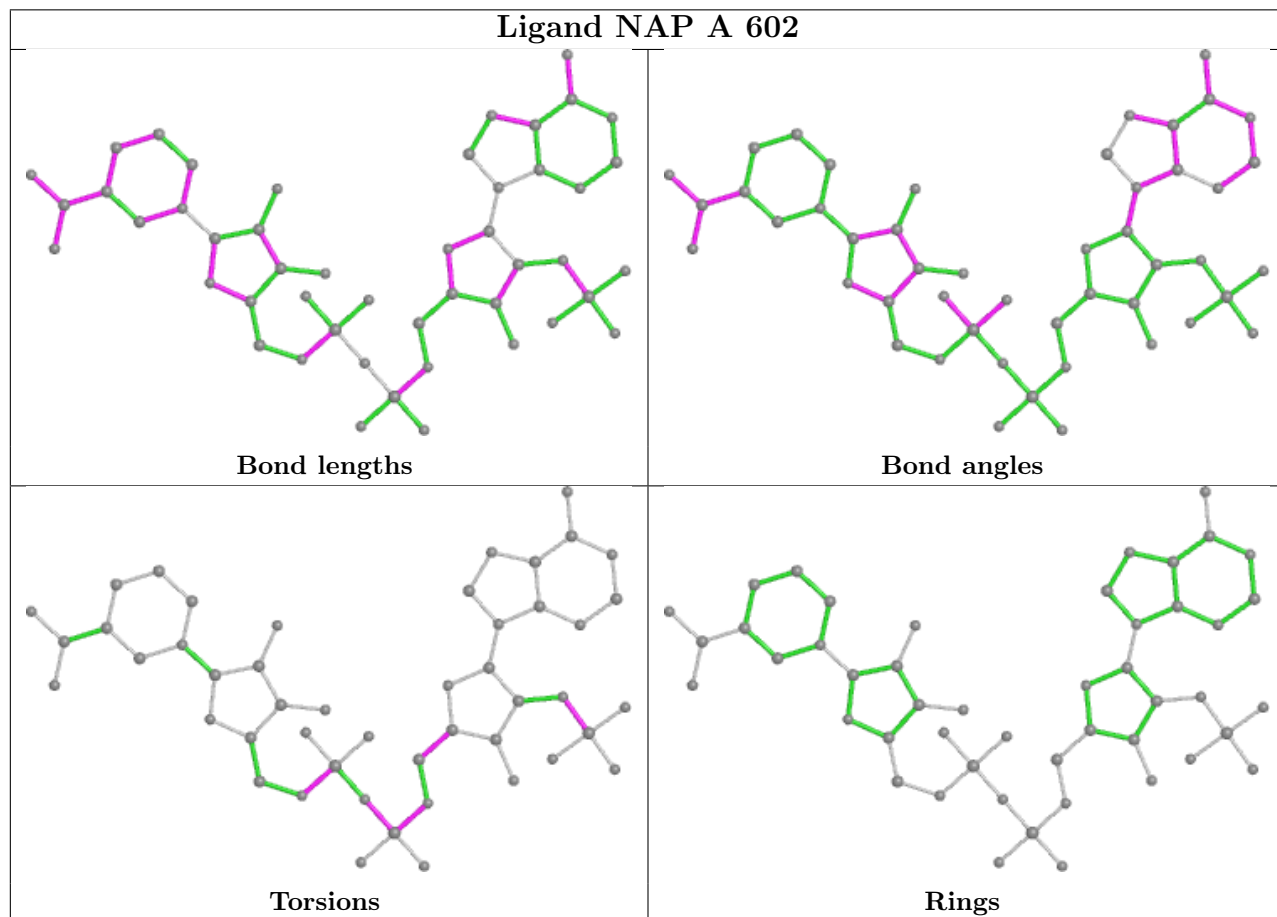
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	603	MES	2	0

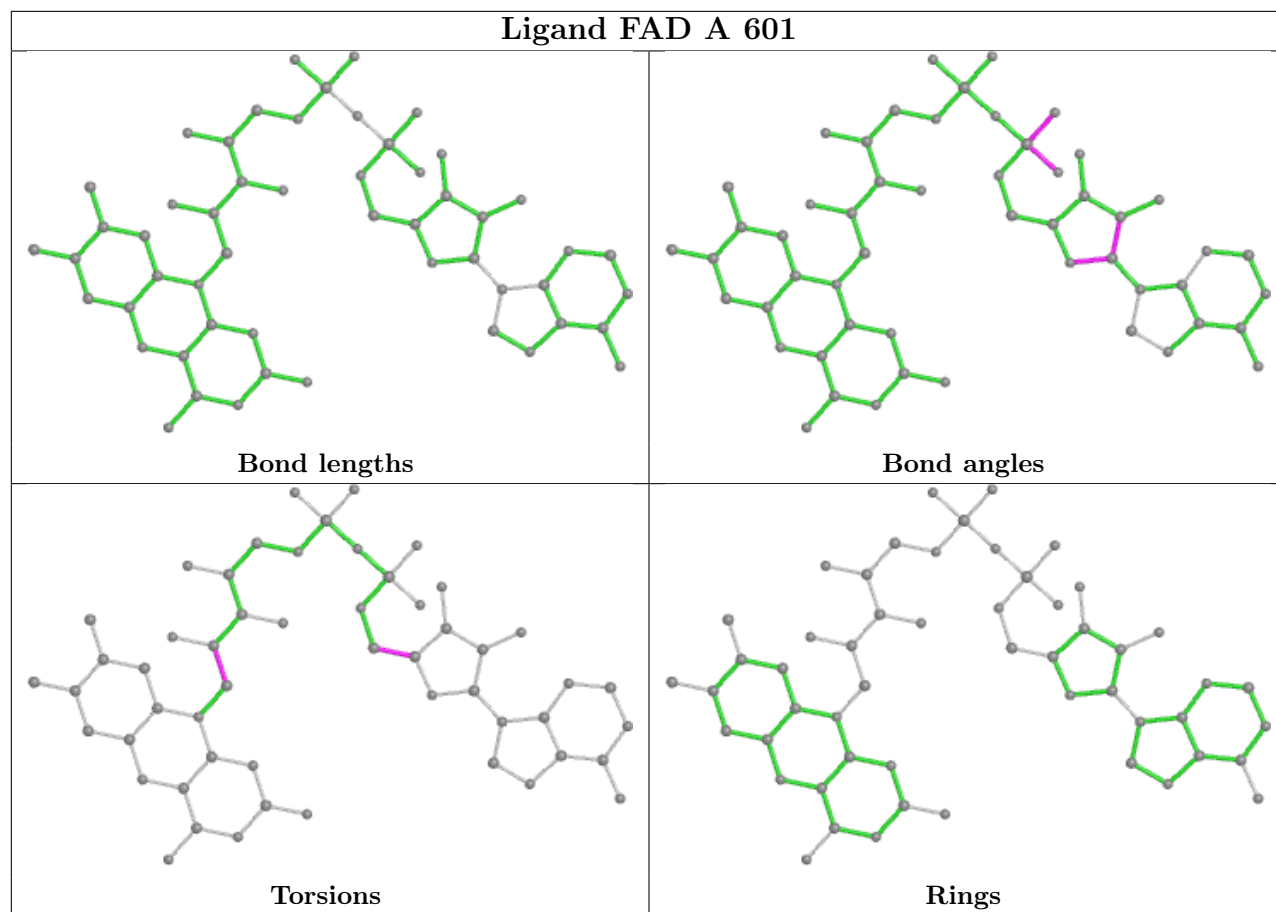
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	602	NAP	6	0
2	A	601	FAD	11	0
5	A	604	EDO	1	0

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	514/546 (94%)	0.36	32 (6%) 28 26	22, 38, 68, 124	1 (0%)

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	437	PRO	7.7
1	A	440	PRO	6.4
1	A	438	GLY	6.0
1	A	499	TRP	5.7
1	A	153	LEU	5.1
1	A	511	VAL	4.4
1	A	159	PRO	4.4
1	A	336	LYS	3.9
1	A	152	GLN	3.7
1	A	439	SER	3.6
1	A	154	SER	3.6
1	A	442	ILE	3.6
1	A	393	THR	3.5
1	A	500	TYR	3.5
1	A	513	MET	3.3
1	A	514	LEU	3.2
1	A	441	GLY	3.1
1	A	299	ARG	3.0
1	A	387	THR	3.0
1	A	397	PHE	3.0
1	A	498	SER	2.8
1	A	235	LEU	2.6
1	A	512	PHE	2.5
1	A	10	ARG	2.4
1	A	495	MET	2.3
1	A	510	ARG	2.2
1	A	487	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	496	THR	2.1
1	A	435	ALA	2.1
1	A	482	GLU	2.1
1	A	415	ALA	2.0
1	A	416	GLY	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](#)

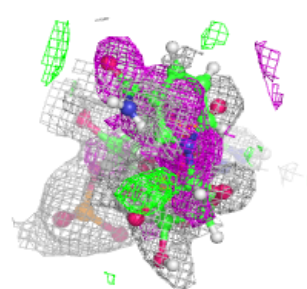
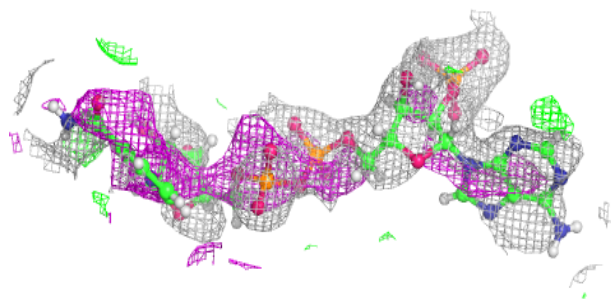
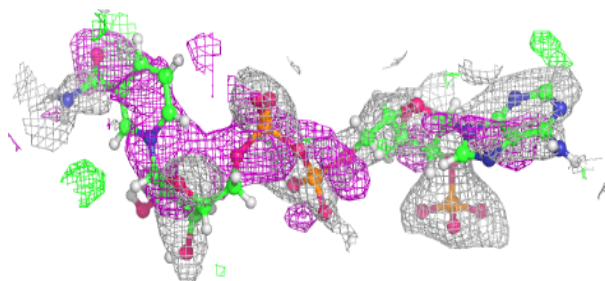
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	EDO	A	604	4/4	0.55	0.19	52,67,81,90	0
3	NAP	A	602	48/48	0.68	0.17	48,74,100,103	0
6	GOL	A	605	6/6	0.70	0.22	50,62,79,79	0
4	MES	A	603	12/12	0.78	0.12	54,69,85,100	0
2	FAD	A	601	53/53	0.94	0.10	22,39,78,82	0

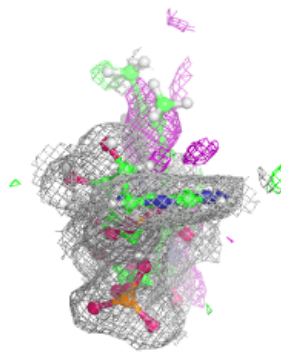
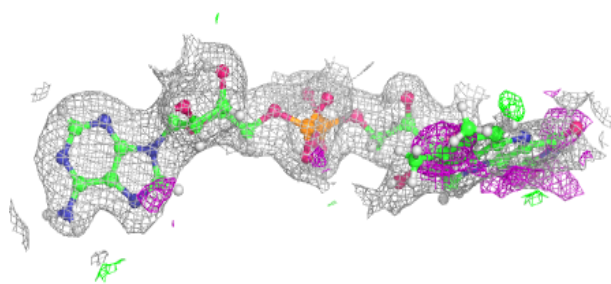
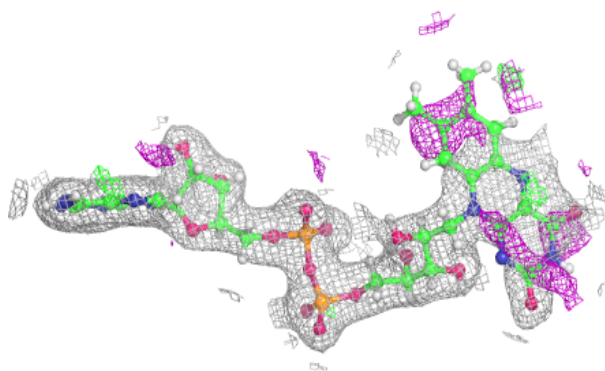
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NAP 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)

**Electron density around FAD A 601:**

$2mF_o-DF_c$ (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.