



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:50 PM GMT

PDB ID : 4AP1
Title : Oxidized steroid monooxygenase bound to NADP
Authors : Franceschini, S.; Van Beek, H.L.; Martinoli, C.; Pennetta, A.; Fraaije, M.W.;
Mattevi, A.
Deposited on : 2012-03-30
Resolution : 2.95 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

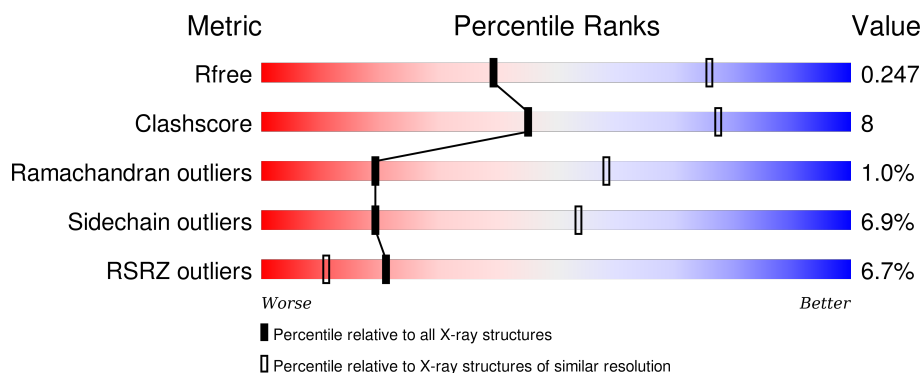
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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}	91344	2184 (3.00-2.92)
Clashscore	102246	2552 (3.00-2.92)
Ramachandran outliers	100387	2468 (3.00-2.92)
Sidechain outliers	100360	2471 (3.00-2.92)
RSRZ outliers	91569	2201 (3.00-2.92)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 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	549	

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	NAP	A	1002	-	-	-	X

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4106 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 STEROID MONOOXYGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	523	Total	C	N	O	S	0	1	0
			3982	2525	694	756	7			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	295	ALA	LYS	CONFLICT	UNP O50641

- 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		

- Molecule 3 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		

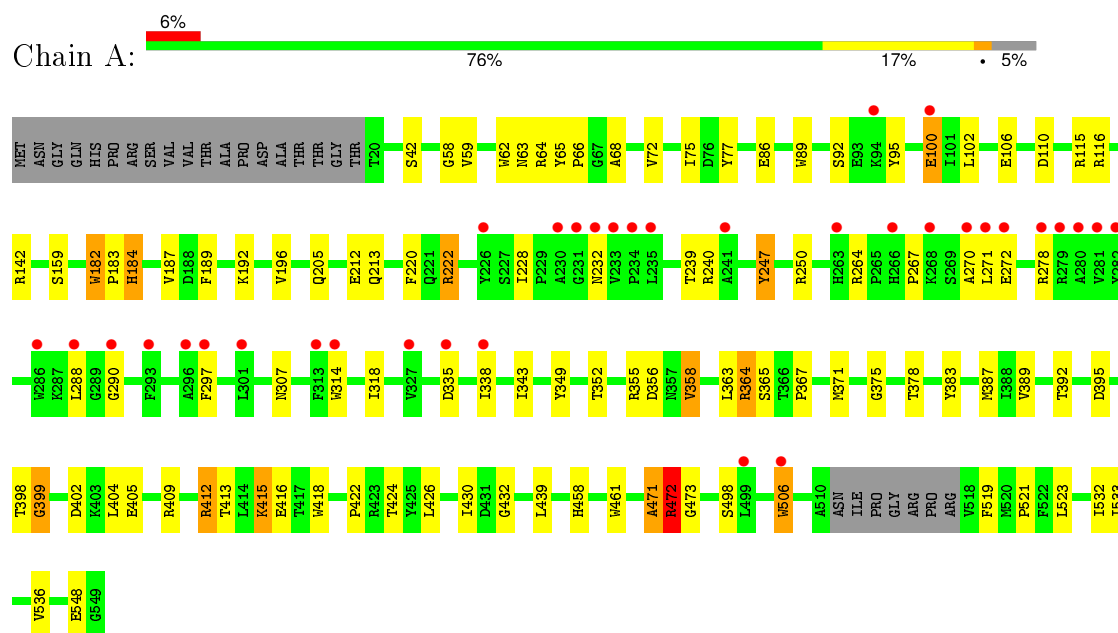
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	18	Total	O	0	0
			18	18		

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 errors 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: STEROID MONOOXYGENASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	82.17Å 82.17Å 228.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	58.10 – 2.95 58.10 – 2.95	Depositor EDS
% Data completeness (in resolution range)	99.9 (58.10-2.95) 99.9 (58.10-2.95)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.58 (at 2.96Å)	Xtriage
Refinement program	REFMAC 5.6.0119	Depositor
R, R_{free}	0.200 , 0.249 0.198 , 0.247	Depositor DCC
R_{free} test set	890 reflections (5.42%)	DCC
Wilson B-factor (Å ²)	61.0	Xtriage
Anisotropy	0.200	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 52.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 17306 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4106	wwPDB-VP
Average B, all atoms (Å ²)	63.0	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.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: NAP, SO4, 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	0.62	7/4082 (0.2%)	0.70	0/5563

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	272	GLU	CD-OE1	6.54	1.32	1.25
1	A	272	GLU	CD-OE2	5.82	1.32	1.25
1	A	89	TRP	CD2-CE2	5.71	1.48	1.41
1	A	506	TRP	CD2-CE2	5.40	1.47	1.41
1	A	182	TRP	CD2-CE2	5.28	1.47	1.41
1	A	62	TRP	CD2-CE2	5.17	1.47	1.41
1	A	461	TRP	CD2-CE2	5.10	1.47	1.41

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3982	0	3776	62	0
2	A	53	0	31	1	0
3	A	48	0	25	0	0
4	A	5	0	0	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	18	0	0	0	0
All	All	4106	0	3832	62	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 8.

All (62) 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:412:ARG:HG3	1:A:412:ARG:HH11	1.12	1.09
1:A:189:PHE:H	1:A:213:GLN:NE2	1.64	0.93
1:A:413:THR:HB	1:A:416:GLU:HG3	1.49	0.92
1:A:100:GLU:HA	1:A:100:GLU:OE1	1.69	0.90
1:A:472:ARG:HG2	1:A:472:ARG:HH11	1.40	0.86
1:A:189:PHE:H	1:A:213:GLN:HE21	1.21	0.85
1:A:412:ARG:CG	1:A:412:ARG:HH11	1.90	0.84
1:A:222:ARG:HG3	1:A:364:ARG:HH21	1.45	0.81
1:A:412:ARG:HG3	1:A:412:ARG:NH1	1.85	0.79
1:A:532:ILE:O	1:A:536:VAL:HG23	1.92	0.69
1:A:228:ILE:HD13	1:A:343:ILE:HG21	1.76	0.66
1:A:307:ASN:HD21	1:A:338:ILE:H	1.43	0.66
1:A:110:ASP:OD1	1:A:115:ARG:NH2	2.29	0.65
1:A:102:LEU:O	1:A:106:GLU:HG3	1.99	0.62
1:A:159:SER:OG	1:A:395:ASP:HB3	1.99	0.61
1:A:471:ALA:O	1:A:473:GLY:N	2.35	0.59
1:A:472:ARG:HG2	1:A:472:ARG:NH1	2.17	0.59
1:A:228:ILE:CD1	1:A:343:ILE:HG21	2.36	0.56
1:A:116:ARG:HB3	4:A:1551:SO4:O4	2.06	0.56
1:A:86:GLU:HG2	1:A:247:TYR:CE2	2.40	0.56
1:A:63:ASN:ND2	1:A:65:TYR:HE2	2.04	0.56
1:A:402:ASP:O	1:A:415:LYS:NZ	2.40	0.55
1:A:189:PHE:N	1:A:213:GLN:NE2	2.46	0.54
1:A:398:THR:OG1	1:A:399:GLY:N	2.41	0.54
1:A:68:ALA:HA	1:A:205:GLN:NE2	2.24	0.53
1:A:142:ARG:HH11	1:A:142:ARG:HG3	1.74	0.53
1:A:189:PHE:N	1:A:213:GLN:HE21	2.01	0.53
1:A:278:ARG:HG3	1:A:297:PHE:CE2	2.45	0.52
1:A:192:LYS:HD3	1:A:387:MET:HE3	1.90	0.52
1:A:395:ASP:O	1:A:506:TRP:HZ2	1.94	0.51
1:A:189:PHE:HB2	1:A:213:GLN:HG3	1.92	0.51
1:A:183:PRO:HG2	1:A:187:VAL:CG2	2.40	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:TYR:OH	1:A:288:LEU:O	2.30	0.50
1:A:220:PHE:HB3	1:A:363:LEU:HD21	1.94	0.50
1:A:222:ARG:CG	1:A:364:ARG:HH21	2.21	0.49
1:A:86:GLU:HG2	1:A:247:TYR:CD2	2.48	0.49
1:A:412:ARG:CG	1:A:412:ARG:NH1	2.59	0.49
1:A:66:PRO:HD3	1:A:182:TRP:CE2	2.47	0.49
1:A:314:TRP:CH2	1:A:318:ILE:HG12	2.48	0.49
1:A:75:ILE:HD11	1:A:250:ARG:CZ	2.43	0.48
1:A:196:VAL:HG22	1:A:389:VAL:HB	1.96	0.48
1:A:58:GLY:HA2	2:A:1001:FAD:O3B	2.14	0.47
1:A:100:GLU:OE1	1:A:100:GLU:CA	2.47	0.47
1:A:439:LEU:O	1:A:458:HIS:ND1	2.46	0.47
1:A:72:VAL:HG12	1:A:77:TYR:HB2	1.96	0.46
1:A:426:LEU:HD13	1:A:533:ILE:HG22	1.96	0.46
1:A:72:VAL:CG1	1:A:77:TYR:HB2	2.45	0.45
1:A:375:GLY:HA3	1:A:383:TYR:O	2.16	0.45
1:A:472:ARG:HH11	1:A:472:ARG:CG	2.20	0.45
1:A:424:THR:HG22	1:A:430:ILE:HG12	1.99	0.44
1:A:472:ARG:HG2	1:A:472:ARG:H	1.55	0.44
1:A:519:PHE:CE2	1:A:521:PRO:HD2	2.53	0.44
1:A:355:ARG:HB2	1:A:358:VAL:HG13	1.99	0.43
1:A:409:ARG:HG3	1:A:432:GLY:HA2	2.00	0.43
1:A:418:TRP:CG	1:A:422:PRO:HA	2.54	0.42
1:A:349:TYR:O	1:A:352:THR:HB	2.19	0.42
1:A:439:LEU:HD23	1:A:439:LEU:HA	1.86	0.41
1:A:270:ALA:HA	1:A:297:PHE:CD1	2.55	0.41
1:A:367:PRO:O	1:A:378:THR:HA	2.21	0.41
1:A:95:TYR:H	1:A:232:ASN:HD21	1.69	0.41
1:A:64:ARG:HD2	1:A:184:HIS:CE1	2.56	0.40
1:A:222:ARG:HA	1:A:363:LEU:HB2	2.04	0.40

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	520/549 (95%)	493 (95%)	22 (4%)	5 (1%)	19	58

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	471	ALA
1	A	472	ARG
1	A	290	GLY
1	A	399	GLY
1	A	267	PRO

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	392/435 (90%)	365 (93%)	27 (7%)	19	54

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	SER
1	A	59	VAL
1	A	92	SER
1	A	100	GLU
1	A	184	HIS
1	A	212	GLU
1	A	222	ARG
1	A	239	THR
1	A	240	ARG
1	A	247	TYR
1	A	264	ARG
1	A	271	LEU
1	A	335	ASP
1	A	356	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	358	VAL
1	A	364	ARG
1	A	365	SER
1	A	371	MET
1	A	392	THR
1	A	404	LEU
1	A	405	GLU
1	A	412	ARG
1	A	415	LYS
1	A	472	ARG
1	A	498	SER
1	A	523	LEU
1	A	548	GLU

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	63	ASN
1	A	87	GLN
1	A	98	GLN
1	A	160	ASN
1	A	178	HIS
1	A	205	GLN
1	A	213	GLN
1	A	225	ASN
1	A	232	ASN
1	A	307	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

3 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	1001	-	48,58,58	1.46	8 (16%)	54,89,89	2.16	14 (25%)
3	NAP	A	1002	-	42,52,52	1.04	2 (4%)	54,80,80	1.56	8 (14%)
4	SO4	A	1551	-	4,4,4	0.55	0	6,6,6	0.35	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
2	FAD	A	1001	-	-	0/30/50/50	0/6/6/6
3	NAP	A	1002	-	-	0/27/67/67	0/5/5/5
4	SO4	A	1551	-	-	0/0/0/0	0/0/0/0

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	FAD	C2A-N3A	2.07	1.35	1.32
2	A	1001	FAD	C10-N10	2.31	1.41	1.39
2	A	1001	FAD	C9A-N10	2.55	1.42	1.38
3	A	1002	NAP	O4D-C1D	2.67	1.44	1.41
2	A	1001	FAD	C5A-C4A	3.20	1.47	1.40
2	A	1001	FAD	C4-C4X	3.49	1.48	1.41
3	A	1002	NAP	C5A-C4A	3.54	1.48	1.40
2	A	1001	FAD	C8-C7	3.56	1.50	1.41
2	A	1001	FAD	C9A-C5X	3.85	1.50	1.42
2	A	1001	FAD	C4X-C10	4.15	1.48	1.41

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	FAD	N3A-C2A-N1A	-6.74	123.74	128.89
3	A	1002	NAP	N3A-C2A-N1A	-6.64	123.81	128.89
2	A	1001	FAD	C4-C4X-C10	-5.13	116.66	119.94
2	A	1001	FAD	C4X-C4-N3	-3.67	118.58	123.59
2	A	1001	FAD	C2B-C1B-N9A	-3.53	108.90	114.29
3	A	1002	NAP	C4A-C5A-N7A	-3.46	106.30	109.48
2	A	1001	FAD	C1B-N9A-C4A	-3.09	122.28	126.94
2	A	1001	FAD	C4X-C10-N10	-2.60	118.98	120.52
3	A	1002	NAP	PN-O3-PA	-2.56	125.54	132.73
2	A	1001	FAD	C4B-O4B-C1B	-2.53	106.94	109.72
3	A	1002	NAP	C1B-N9A-C4A	-2.48	123.19	126.94
3	A	1002	NAP	O7N-C7N-N7N	-2.41	119.20	122.59
2	A	1001	FAD	O2'-C2'-C1'	-2.20	104.53	109.94
2	A	1001	FAD	P-O3P-PA	-2.08	126.89	132.73
2	A	1001	FAD	C5X-C9A-N10	2.16	119.26	117.62
2	A	1001	FAD	O4B-C1B-N9A	2.39	113.10	108.10
2	A	1001	FAD	C1'-N10-C9A	2.54	121.72	118.86
3	A	1002	NAP	C4D-O4D-C1D	2.67	112.66	109.72
3	A	1002	NAP	O4B-C1B-N9A	2.72	113.79	108.10
3	A	1002	NAP	O4D-C1D-N1N	2.86	111.28	108.13
2	A	1001	FAD	C4X-N5-C5X	2.94	120.14	116.76
2	A	1001	FAD	C4-N3-C2	8.02	122.18	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	FAD	1	0
4	A	1551	SO4	1	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, 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	523/549 (95%)	0.38	35 (6%) 21 11	30, 55, 117, 170	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	234	PRO	8.5
1	A	232	ASN	7.2
1	A	235	LEU	6.4
1	A	293	PHE	5.2
1	A	231	GLY	4.9
1	A	271	LEU	4.3
1	A	233	VAL	4.1
1	A	281	VAL	3.7
1	A	270	ALA	3.5
1	A	296	ALA	3.4
1	A	282	TYR	3.1
1	A	226	TYR	3.1
1	A	230	ALA	3.0
1	A	272	GLU	3.0
1	A	314	TRP	2.9
1	A	288	LEU	2.9
1	A	506	TRP	2.9
1	A	268	LYS	2.9
1	A	286	TRP	2.8
1	A	313	PHE	2.8
1	A	241	ALA	2.7
1	A	278	ARG	2.7
1	A	338	ILE	2.6
1	A	266	HIS	2.6
1	A	335	ASP	2.5
1	A	297	PHE	2.5
1	A	499	LEU	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	290	GLY	2.4
1	A	263	HIS	2.4
1	A	327	VAL	2.4
1	A	279	ARG	2.2
1	A	94	LYS	2.2
1	A	100	GLU	2.1
1	A	280	ALA	2.1
1	A	301	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, 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	LLDF	B-factors(Å ²)	Q<0.9
3	NAP	A	1002	48/48	0.71	0.56	6.11	91,125,154,157	0
2	FAD	A	1001	53/53	0.97	0.18	-0.48	26,33,50,52	0
4	SO4	A	1551	5/5	0.96	0.18	-	56,59,60,65	0

6.5 Other polymers [i](#)

There are no such residues in this entry.