



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 10, 2018 – 04:06 PM EST

PDB ID : 6F73
Title : Crystal structure of VAO-type flavoprotein MtVAO615 at pH 5.0 from Myceliophthora thermophila C1
Authors : Rozeboom, H.J.; Fraaije, M.W.
Deposited on : 2017-12-07
Resolution : 2.22 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030736
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-20030736

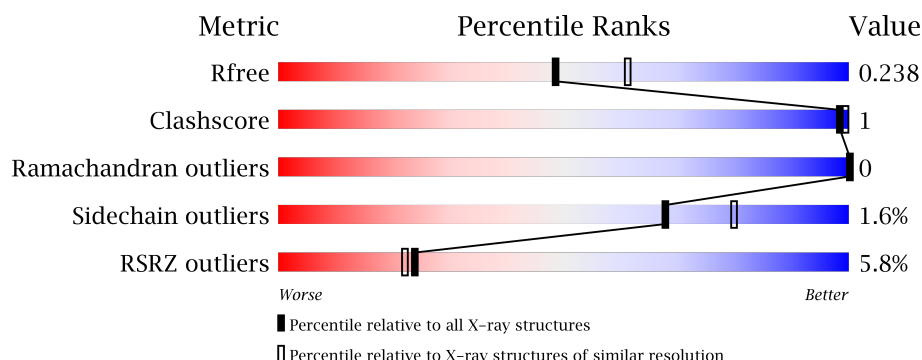
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.22 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	4744 (2.24-2.20)
Clashscore	112137	5509 (2.24-2.20)
Ramachandran outliers	110173	5427 (2.24-2.20)
Sidechain outliers	110143	5428 (2.24-2.20)
RSRZ outliers	101464	4776 (2.24-2.20)

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	574	<div> <div>11%</div> <div> <div></div> <div>91%</div> <div>5%</div> </div> </div>
1	B	574	<div> <div>94%</div> <div>5%</div> </div>



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	265	Total	O	0	0
			265	265		

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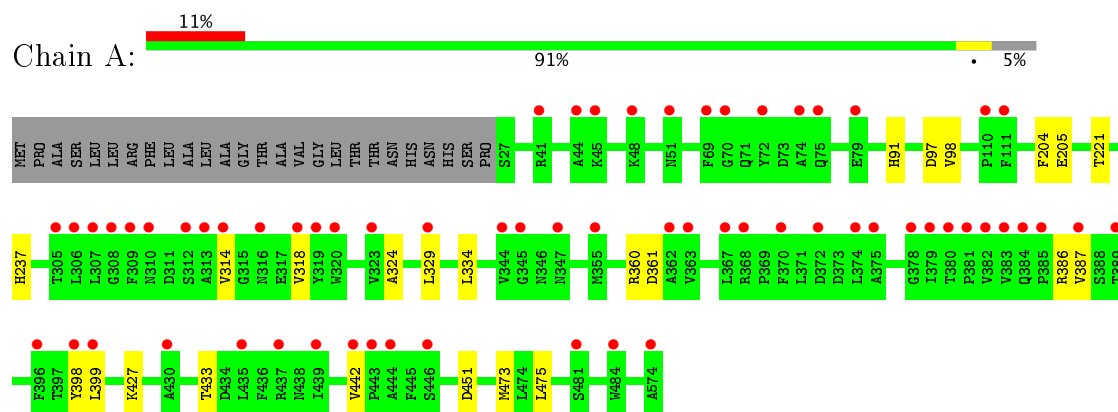
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	579	Total	O	0	0
			579	579		

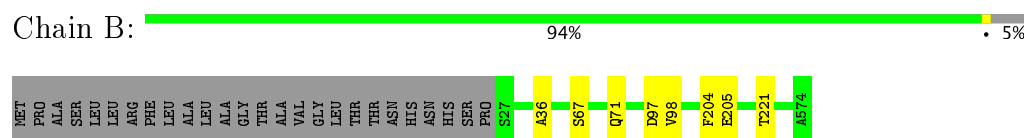
3 Residue-property plots [i](#)

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 ($RSRZ > 2$). 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: MtVAO615



• Molecule 1: MtVAO615



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	62.42Å 115.96Å 198.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	58.00 – 2.22 57.98 – 2.22	Depositor EDS
% Data completeness (in resolution range)	99.5 (58.00-2.22) 99.5 (57.98-2.22)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.86 (at 2.22Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.193 , 0.235 0.199 , 0.238	Depositor DCC
R_{free} test set	3610 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	22.1	Xtriage
Anisotropy	0.576	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 43.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9468	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% 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: NAG, 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	0.40	0/4303	0.64	0/5874
1	B	0.46	0/4303	0.64	0/5874
All	All	0.43	0/8606	0.64	0/11748

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 ⓘ

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	4182	0	3988	8	0
1	B	4182	0	3985	3	0
2	A	53	0	28	0	0
2	B	53	0	29	0	0
3	A	56	0	51	0	0
3	B	98	0	90	0	0
4	A	265	0	0	0	0
4	B	579	0	0	1	0
All	All	9468	0	8171	11	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 1.

All (11) 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:324:ALA:HB2	1:A:433:THR:HG21	1.60	0.81
1:A:314:VAL:HB	1:A:318:VAL:HG11	1.69	0.75
1:A:334:LEU:HD12	1:A:473:MET:HE2	1.80	0.63
1:A:237:HIS:CD2	1:A:475:LEU:HD23	2.42	0.54
1:A:334:LEU:HD12	1:A:473:MET:CE	2.40	0.51
1:A:398:TYR:HB2	1:A:399:LEU:HD22	1.95	0.49
1:B:71:GLN:N	1:B:71:GLN:OE1	2.45	0.48
1:A:360:ARG:HE	1:A:387:VAL:HG22	1.82	0.45
1:A:204:PHE:CE1	1:A:205:GLU:HG3	2.54	0.43
1:B:36:ALA:HB1	4:B:709:HOH:O	2.19	0.42
1:B:204:PHE:CE1	1:B:205:GLU:HG3	2.55	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	546/574 (95%)	529 (97%)	17 (3%)	0	100	100
1	B	546/574 (95%)	529 (97%)	17 (3%)	0	100	100
All	All	1092/1148 (95%)	1058 (97%)	34 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	437/458 (95%)	427 (98%)	10 (2%)	56	68
1	B	437/458 (95%)	433 (99%)	4 (1%)	82	90
All	All	874/916 (95%)	860 (98%)	14 (2%)	68	80

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	91	HIS
1	A	97	ASP
1	A	98	VAL
1	A	221	THR
1	A	329	LEU
1	A	361	ASP
1	A	386	ARG
1	A	427	LYS
1	A	442	VAL
1	A	451	ASP
1	B	67	SER
1	B	97	ASP
1	B	98	VAL
1	B	221	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	184	ASN
1	A	211	ASN
1	A	535	ASN
1	B	429	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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

13 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	600	1	51,58,58	1.51	6 (11%)	54,89,89	2.28	11 (20%)
3	NAG	A	601	1	14,14,15	0.37	0	15,19,21	0.89	0
3	NAG	A	602	1,3	14,14,15	0.44	0	15,19,21	1.13	1 (6%)
3	NAG	A	603	3	14,14,15	0.39	0	15,19,21	0.88	1 (6%)
3	NAG	A	604	1	14,14,15	0.28	0	15,19,21	0.93	2 (13%)
2	FAD	B	601	1	51,58,58	1.53	6 (11%)	54,89,89	2.32	11 (20%)
3	NAG	B	602	1	14,14,15	0.50	0	15,19,21	1.18	1 (6%)
3	NAG	B	603	1,3	14,14,15	0.34	0	15,19,21	0.85	0
3	NAG	B	604	3	14,14,15	0.34	0	15,19,21	1.11	1 (6%)
3	NAG	B	605	1	14,14,15	0.34	0	15,19,21	1.10	1 (6%)
3	NAG	B	606	1	14,14,15	0.36	0	15,19,21	0.80	0
3	NAG	B	607	1	14,14,15	0.33	0	15,19,21	1.29	2 (13%)
3	NAG	B	608	1	14,14,15	0.36	0	15,19,21	1.21	2 (13%)

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	600	1	-	0/28/50/50	0/6/6/6
3	NAG	A	601	1	-	0/6/23/26	0/1/1/1
3	NAG	A	602	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	603	3	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	604	1	-	0/6/23/26	0/1/1/1
2	FAD	B	601	1	-	0/28/50/50	0/6/6/6
3	NAG	B	602	1	-	0/6/23/26	0/1/1/1
3	NAG	B	603	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	604	3	-	0/6/23/26	0/1/1/1
3	NAG	B	605	1	-	0/6/23/26	0/1/1/1
3	NAG	B	606	1	-	0/6/23/26	0/1/1/1
3	NAG	B	607	1	-	0/6/23/26	0/1/1/1
3	NAG	B	608	1	-	0/6/23/26	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	FAD	C9A-N10	2.68	1.42	1.38
2	A	600	FAD	C5A-C4A	2.84	1.46	1.40
2	A	600	FAD	C9A-N10	2.84	1.42	1.38
2	B	601	FAD	C5A-C4A	2.85	1.46	1.40
2	A	600	FAD	C9A-C5X	3.96	1.50	1.42
2	B	601	FAD	C9A-C5X	4.03	1.50	1.42
2	B	601	FAD	C8-C7	4.05	1.51	1.41
2	A	600	FAD	C4-C4X	4.09	1.49	1.41
2	A	600	FAD	C8-C7	4.11	1.51	1.41
2	B	601	FAD	C4-C4X	4.14	1.49	1.41
2	B	601	FAD	C4X-C10	4.43	1.48	1.41
2	A	600	FAD	C4X-C10	4.58	1.49	1.41

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	600	FAD	N3A-C2A-N1A	-6.77	122.97	128.86
2	B	601	FAD	N3A-C2A-N1A	-6.42	123.26	128.86
2	A	600	FAD	C4-C4X-C10	-4.90	116.00	119.96
2	B	601	FAD	C4-C4X-C10	-4.87	116.03	119.96
2	B	601	FAD	C4X-C4-N3	-3.69	118.23	123.48
3	A	602	NAG	O5-C1-C2	-3.61	106.44	111.47
2	A	600	FAD	C4X-C4-N3	-3.49	118.52	123.48
2	A	600	FAD	C8M-C8-C9	-3.01	112.79	120.34
2	B	601	FAD	C8M-C8-C9	-2.93	113.00	120.34
3	B	607	NAG	O5-C1-C2	-2.38	108.16	111.47
2	A	600	FAD	C4A-C5A-N7A	-2.27	107.22	109.41
3	B	608	NAG	O5-C1-C2	-2.16	108.46	111.47
3	A	604	NAG	O5-C1-C2	-2.14	108.49	111.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	FAD	C2A-N1A-C6A	2.06	122.37	118.77
3	A	603	NAG	C1-O5-C5	2.06	115.01	112.17
3	A	604	NAG	C1-O5-C5	2.22	115.23	112.17
2	A	600	FAD	C5X-C9A-N10	2.38	119.42	117.66
2	B	601	FAD	N6A-C6A-N1A	2.47	123.66	118.77
3	B	604	NAG	C1-O5-C5	2.70	115.89	112.17
3	B	605	NAG	C1-O5-C5	2.81	116.03	112.17
2	B	601	FAD	C8M-C8-C7	3.07	127.15	120.72
2	A	600	FAD	C8M-C8-C7	3.23	127.49	120.72
3	B	608	NAG	C1-O5-C5	3.40	116.85	112.17
3	B	602	NAG	C1-O5-C5	3.41	116.87	112.17
3	B	607	NAG	C1-O5-C5	3.72	117.30	112.17
2	A	600	FAD	C4-C4X-N5	3.91	122.97	118.68
2	B	601	FAD	C4-C4X-N5	4.22	123.31	118.68
2	A	600	FAD	C4X-N5-C5X	4.45	121.46	116.76
2	B	601	FAD	C4X-N5-C5X	4.80	121.83	116.76
2	B	601	FAD	C1'-N10-C9A	4.99	122.92	118.35
2	A	600	FAD	C1'-N10-C9A	5.01	122.94	118.35
2	A	600	FAD	C4-N3-C2	8.73	122.80	115.16
2	B	601	FAD	C4-N3-C2	9.05	123.08	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	548/574 (95%)	0.46	64 (11%) 5 4	21, 49, 91, 134	0
1	B	548/574 (95%)	-0.48	0 100 100	12, 21, 37, 66	0
All	All	1096/1148 (95%)	-0.01	64 (5%) 24 22	12, 29, 80, 134	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	320	TRP	6.7
1	A	70	GLY	6.4
1	A	323	VAL	6.2
1	A	437	ARG	4.4
1	A	380	THR	4.3
1	A	319	TYR	4.1
1	A	51	ASN	4.1
1	A	439	ILE	4.0
1	A	430	ALA	4.0
1	A	111	PHE	3.9
1	A	442	VAL	3.9
1	A	398	TYR	3.6
1	A	312	SER	3.4
1	A	305	THR	3.4
1	A	368	ARG	3.4
1	A	444	ALA	3.4
1	A	313	ALA	3.3
1	A	306	LEU	3.3
1	A	345	GLY	3.3
1	A	443	PRO	3.3
1	A	383	VAL	3.2
1	A	79	GLU	3.2
1	A	385	PRO	3.2
1	A	378	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	384	GLN	3.1
1	A	382	VAL	3.1
1	A	399	LEU	3.1
1	A	381	PRO	3.1
1	A	370	PHE	3.1
1	A	375	ALA	3.0
1	A	41	ARG	3.0
1	A	484	TRP	3.0
1	A	362	ALA	2.9
1	A	435	LEU	2.9
1	A	379	ILE	2.9
1	A	367	LEU	2.9
1	A	396	PHE	2.8
1	A	309	PHE	2.7
1	A	446	SER	2.7
1	A	389	THR	2.7
1	A	75	GLN	2.7
1	A	574	ALA	2.7
1	A	69	PHE	2.7
1	A	308	GLY	2.6
1	A	72	TYR	2.6
1	A	48	LYS	2.6
1	A	347	ASN	2.6
1	A	374	LEU	2.5
1	A	44	ALA	2.4
1	A	110	PRO	2.4
1	A	307	LEU	2.4
1	A	316	ASN	2.3
1	A	363	VAL	2.2
1	A	318	VAL	2.2
1	A	481	SER	2.2
1	A	45	LYS	2.2
1	A	74	ALA	2.2
1	A	372	ASP	2.1
1	A	387	VAL	2.1
1	A	310	ASN	2.1
1	A	344	VAL	2.1
1	A	355	MET	2.0
1	A	314	VAL	2.0
1	A	329	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	NAG	B	607	14/15	0.92	0.13	1.85	30,42,62,75	0
3	NAG	B	608	14/15	0.93	0.12	1.52	24,48,63,78	0
3	NAG	A	604	14/15	0.93	0.20	1.26	24,46,58,64	0
2	FAD	B	601	53/53	0.97	0.12	0.94	6,16,50,74	0
3	NAG	A	601	14/15	0.93	0.21	0.70	35,46,67,88	0
3	NAG	B	605	14/15	0.94	0.11	0.56	17,26,32,39	0
3	NAG	A	602	14/15	0.93	0.12	0.34	35,49,59,59	0
2	FAD	A	600	53/53	0.96	0.12	0.11	13,29,78,128	0
3	NAG	B	602	14/15	0.94	0.11	-0.42	19,24,38,48	0
3	NAG	B	603	14/15	0.97	0.07	-2.05	13,25,33,37	0
3	NAG	A	603	14/15	0.84	0.17	-	50,66,91,94	0
3	NAG	B	606	14/15	0.93	0.17	-	34,39,70,79	0
3	NAG	B	604	14/15	0.88	0.12	-	38,51,61,67	0

6.5 Other polymers [i](#)

There are no such residues in this entry.