



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 07:21 AM UTC

PDB ID : 8QD1 / pdb_00008qd1
Title : Ayglp from *A. fumigatus* catalyzes polyketide shortening in the biosynthesis of DHN-melanin
Authors : Schmalhofer, M.; Vagstad, A.L.; Zhou, Q.; Bode, H.B.; Groll, M.
Deposited on : 2023-08-28
Resolution : 1.70 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
Xtriage (Phenix) : 2.0
EDS : 3.0
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

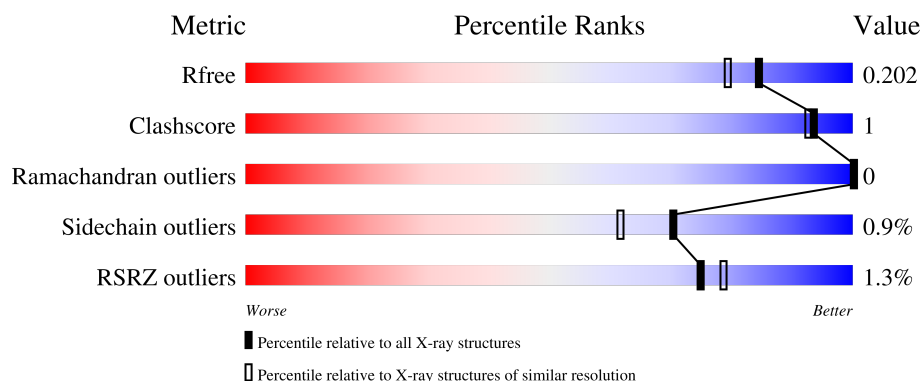
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	423	0% 90% 6%
1	B	423	0% 90% 6%
1	C	423	2% 90% 6%
1	D	423	0% 91% 6%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14233 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 Pigment biosynthesis protein yellowish-green 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	398	Total	C	N	O	S	0	3	0
			3142	2014	542	577	9			
1	B	398	Total	C	N	O	S	0	4	0
			3127	2004	539	575	9			
1	C	398	Total	C	N	O	S	0	4	0
			3090	1991	526	564	9			
1	D	398	Total	C	N	O	S	0	5	0
			3131	2009	538	575	9			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	MET	-	initiating methionine	UNP Q9UVV1
A	-15	ARG	-	expression tag	UNP Q9UVV1
A	-14	GLY	-	expression tag	UNP Q9UVV1
A	-13	SER	-	expression tag	UNP Q9UVV1
A	-12	HIS	-	expression tag	UNP Q9UVV1
A	-11	HIS	-	expression tag	UNP Q9UVV1
A	-10	HIS	-	expression tag	UNP Q9UVV1
A	-9	HIS	-	expression tag	UNP Q9UVV1
A	-8	HIS	-	expression tag	UNP Q9UVV1
A	-7	HIS	-	expression tag	UNP Q9UVV1
A	-6	GLU	-	expression tag	UNP Q9UVV1
A	-5	ASN	-	expression tag	UNP Q9UVV1
A	-4	LEU	-	expression tag	UNP Q9UVV1
A	-3	TYR	-	expression tag	UNP Q9UVV1
A	-2	PHE	-	expression tag	UNP Q9UVV1
A	-1	GLN	-	expression tag	UNP Q9UVV1
A	0	GLY	-	expression tag	UNP Q9UVV1
A	1	SER	-	expression tag	UNP Q9UVV1
B	-16	MET	-	initiating methionine	UNP Q9UVV1
B	-15	ARG	-	expression tag	UNP Q9UVV1
B	-14	GLY	-	expression tag	UNP Q9UVV1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-13	SER	-	expression tag	UNP Q9UVV1
B	-12	HIS	-	expression tag	UNP Q9UVV1
B	-11	HIS	-	expression tag	UNP Q9UVV1
B	-10	HIS	-	expression tag	UNP Q9UVV1
B	-9	HIS	-	expression tag	UNP Q9UVV1
B	-8	HIS	-	expression tag	UNP Q9UVV1
B	-7	HIS	-	expression tag	UNP Q9UVV1
B	-6	GLU	-	expression tag	UNP Q9UVV1
B	-5	ASN	-	expression tag	UNP Q9UVV1
B	-4	LEU	-	expression tag	UNP Q9UVV1
B	-3	TYR	-	expression tag	UNP Q9UVV1
B	-2	PHE	-	expression tag	UNP Q9UVV1
B	-1	GLN	-	expression tag	UNP Q9UVV1
B	0	GLY	-	expression tag	UNP Q9UVV1
B	1	SER	-	expression tag	UNP Q9UVV1
C	-16	MET	-	initiating methionine	UNP Q9UVV1
C	-15	ARG	-	expression tag	UNP Q9UVV1
C	-14	GLY	-	expression tag	UNP Q9UVV1
C	-13	SER	-	expression tag	UNP Q9UVV1
C	-12	HIS	-	expression tag	UNP Q9UVV1
C	-11	HIS	-	expression tag	UNP Q9UVV1
C	-10	HIS	-	expression tag	UNP Q9UVV1
C	-9	HIS	-	expression tag	UNP Q9UVV1
C	-8	HIS	-	expression tag	UNP Q9UVV1
C	-7	HIS	-	expression tag	UNP Q9UVV1
C	-6	GLU	-	expression tag	UNP Q9UVV1
C	-5	ASN	-	expression tag	UNP Q9UVV1
C	-4	LEU	-	expression tag	UNP Q9UVV1
C	-3	TYR	-	expression tag	UNP Q9UVV1
C	-2	PHE	-	expression tag	UNP Q9UVV1
C	-1	GLN	-	expression tag	UNP Q9UVV1
C	0	GLY	-	expression tag	UNP Q9UVV1
C	1	SER	-	expression tag	UNP Q9UVV1
D	-16	MET	-	initiating methionine	UNP Q9UVV1
D	-15	ARG	-	expression tag	UNP Q9UVV1
D	-14	GLY	-	expression tag	UNP Q9UVV1
D	-13	SER	-	expression tag	UNP Q9UVV1
D	-12	HIS	-	expression tag	UNP Q9UVV1
D	-11	HIS	-	expression tag	UNP Q9UVV1
D	-10	HIS	-	expression tag	UNP Q9UVV1
D	-9	HIS	-	expression tag	UNP Q9UVV1
D	-8	HIS	-	expression tag	UNP Q9UVV1

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-7	HIS	-	expression tag	UNP Q9UVV1
D	-6	GLU	-	expression tag	UNP Q9UVV1
D	-5	ASN	-	expression tag	UNP Q9UVV1
D	-4	LEU	-	expression tag	UNP Q9UVV1
D	-3	TYR	-	expression tag	UNP Q9UVV1
D	-2	PHE	-	expression tag	UNP Q9UVV1
D	-1	GLN	-	expression tag	UNP Q9UVV1
D	0	GLY	-	expression tag	UNP Q9UVV1
D	1	SER	-	expression tag	UNP Q9UVV1

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	433	Total O 433 433	0	0
2	B	460	Total O 460 460	0	0
2	C	394	Total O 394 394	0	0
2	D	456	Total O 456 456	0	0

- Molecule 1: Pigment biosynthesis protein yellowish-green 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.83Å 108.48Å 91.89Å 90.00° 90.03° 90.00°	Depositor
Resolution (Å)	46.71 – 1.70 46.71 – 1.70	Depositor EDS
% Data completeness (in resolution range)	97.1 (46.71-1.70) 99.5 (46.71-1.70)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.82 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.166 , 0.199 0.171 , 0.202	Depositor DCC
R_{free} test set	9170 reflections (4.06%)	wwPDB-VP
Wilson B-factor (Å ²)	22.6	Xtriage
Anisotropy	0.284	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 34.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.54$, $\langle L^2 \rangle = 0.38$	Xtriage
Estimated twinning fraction	0.044 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14233	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 43.41 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.7710e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² 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

5.1 Standard geometry

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	0.98	0/3239	1.33	3/4422 (0.1%)
1	B	0.97	0/3226	1.32	1/4406 (0.0%)
1	C	0.99	0/3193	1.38	7/4366 (0.2%)
1	D	0.98	0/3236	1.34	1/4419 (0.0%)
All	All	0.98	0/12894	1.35	12/17613 (0.1%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	41	ASP	CA-CB-CG	6.72	119.32	112.60
1	C	41	ASP	CA-CB-CG	6.45	119.05	112.60
1	A	41	ASP	CA-CB-CG	6.07	118.67	112.60
1	C	371[A]	GLU	CA-C-N	-5.70	112.77	121.09
1	C	371[A]	GLU	C-N-CA	-5.70	112.77	121.09
1	C	371[B]	GLU	CA-C-N	-5.70	112.77	121.09
1	C	371[B]	GLU	C-N-CA	-5.70	112.77	121.09
1	C	380	HIS	CA-C-N	5.25	131.56	121.54
1	C	380	HIS	C-N-CA	5.25	131.56	121.54
1	A	380	HIS	CA-C-N	5.21	131.49	121.54
1	A	380	HIS	C-N-CA	5.21	131.49	121.54
1	B	41	ASP	CA-CB-CG	5.16	117.76	112.60

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	3142	0	3037	13	0
1	B	3127	0	3014	13	0
1	C	3090	0	2953	7	0
1	D	3131	0	3031	6	0
2	A	433	0	0	1	0
2	B	460	0	0	1	0
2	C	394	0	0	0	0
2	D	456	0	0	0	0
All	All	14233	0	12035	34	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 (34) 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:371[A]:GLU:HG2	1:B:371[A]:GLU:CG	1.61	1.31
1:A:371[A]:GLU:CG	1:B:371[A]:GLU:HG2	1.62	1.28
1:A:371[A]:GLU:HG2	1:B:371[A]:GLU:HG2	0.91	0.91
1:A:371[A]:GLU:HG3	1:B:371[A]:GLU:HG2	1.73	0.69
1:A:371[A]:GLU:HG2	1:B:371[A]:GLU:HG3	1.72	0.67
1:B:174:GLN:HG3	1:B:244:PRO:HB3	1.82	0.61
1:B:145:ARG:HG2	2:B:808:HOH:O	2.04	0.57
1:C:387:LEU:HB3	1:C:388:PRO:HD3	1.89	0.54
1:C:180:ILE:HD11	1:C:246:LEU:HB3	1.90	0.54
1:C:228:SER:N	1:C:229:PRO:HD2	2.23	0.54
1:B:387:LEU:HB3	1:B:388:PRO:HD3	1.90	0.53
1:B:228:SER:N	1:B:229:PRO:HD2	2.22	0.53
1:A:228:SER:N	1:A:229:PRO:HD2	2.24	0.52
1:D:387:LEU:HB3	1:D:388:PRO:HD3	1.92	0.52
1:D:147:VAL:HG11	1:D:239:TYR:CZ	2.44	0.52
1:D:228:SER:N	1:D:229:PRO:HD2	2.26	0.49
1:A:387:LEU:HB3	1:A:388:PRO:HD3	1.95	0.48
1:B:233:TRP:O	1:B:237:LEU:HG	2.13	0.48
1:C:191:ARG:N	1:C:192:PRO:CD	2.78	0.47
1:B:185:THR:HB	1:B:189:GLY:O	2.16	0.46
1:A:185:THR:HB	1:A:189:GLY:O	2.16	0.45
1:A:233:TRP:O	1:A:237:LEU:HG	2.16	0.45
1:A:191:ARG:N	1:A:192:PRO:CD	2.80	0.45
1:B:191:ARG:N	1:B:192:PRO:CD	2.80	0.44
1:C:75:ALA:HB1	1:C:105:TYR:CZ	2.53	0.44
1:D:191:ARG:N	1:D:192:PRO:CD	2.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:27[A]:ARG:NH2	1:D:300:GLU:O	2.47	0.43
1:A:27[A]:ARG:NH2	1:A:300:GLU:O	2.51	0.42
1:C:182:LEU:HB2	1:C:251:MET:HE3	2.01	0.42
1:D:185:THR:HB	1:D:189:GLY:O	2.20	0.42
1:A:371[B]:GLU:OE1	2:A:501:HOH:O	2.20	0.41
1:B:75:ALA:HB1	1:B:105:TYR:CZ	2.55	0.41
1:A:75:ALA:HB1	1:A:105:TYR:CZ	2.55	0.41
1:C:147:VAL:HG11	1:C:239:TYR:CZ	2.56	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	399/423 (94%)	384 (96%)	15 (4%)	0	100	100
1	B	400/423 (95%)	383 (96%)	17 (4%)	0	100	100
1	C	400/423 (95%)	387 (97%)	13 (3%)	0	100	100
1	D	401/423 (95%)	386 (96%)	15 (4%)	0	100	100
All	All	1600/1692 (95%)	1540 (96%)	60 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	327/354 (92%)	325 (99%)	2 (1%)	78	72
1	B	324/354 (92%)	320 (99%)	4 (1%)	63	51
1	C	313/354 (88%)	311 (99%)	2 (1%)	78	72
1	D	326/354 (92%)	323 (99%)	3 (1%)	70	62
All	All	1290/1416 (91%)	1279 (99%)	11 (1%)	70	62

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	ASP
1	A	280	HIS
1	B	41	ASP
1	B	144	ILE
1	B	174	GLN
1	B	333	GLU
1	C	41	ASP
1	C	280	HIS
1	D	41	ASP
1	D	144	ILE
1	D	280	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	142	GLN
1	B	326	GLN
1	C	96	ASN
1	C	131	GLN
1	C	142	GLN
1	C	326	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	398/423 (94%)	0.29	4 (1%) 79 82	9, 23, 34, 41	3 (0%)
1	B	398/423 (94%)	0.29	4 (1%) 79 82	9, 23, 35, 43	4 (1%)
1	C	398/423 (94%)	0.39	10 (2%) 58 62	10, 26, 39, 46	4 (1%)
1	D	398/423 (94%)	0.29	3 (0%) 82 85	14, 23, 33, 45	5 (1%)
All	All	1592/1692 (94%)	0.32	21 (1%) 75 79	9, 24, 36, 46	16 (1%)

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	63	ALA	3.2
1	D	11	ASP	3.1
1	C	30[A]	PHE	2.9
1	C	63	ALA	2.9
1	C	89	GLY	2.9
1	C	25	GLU	2.8
1	A	139	LEU	2.8
1	D	400	SER	2.6
1	A	400	SER	2.6
1	C	11	ASP	2.6
1	A	63	ALA	2.6
1	C	86	LEU	2.5
1	C	58	ASN	2.3
1	B	88	ALA	2.3
1	B	61	ASP	2.3
1	C	61	ASP	2.3
1	B	30	PHE	2.2
1	C	175	SER	2.2
1	D	318	VAL	2.1
1	A	272	ASP	2.1
1	C	59	ILE	2.1

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.