



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 12, 2020 – 11:20 AM EDT

PDB ID : 6E6Y
Title : Dieckmann cyclase, NcmC
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Deposited on : 2018-07-25
Resolution : 1.60 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 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)
Xtriage (Phenix) : 1.13
EDS : 2.14.6
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.14.6

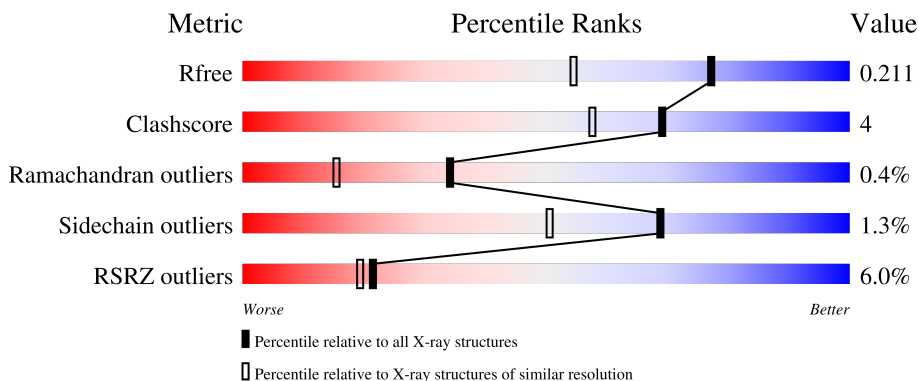
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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}	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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 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	275	 3% 90% 7% •
1	B	275	 9% 89% 7% ••

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4474 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 Dieckmann cyclase, NcmC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	268	1994	1252	358	380	4	0	1	0
1	B	268	1989	1249	355	381	4	0	1	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP A0A1X9WEN9
A	-1	ASN	-	expression tag	UNP A0A1X9WEN9
A	0	ALA	-	expression tag	UNP A0A1X9WEN9
B	-2	SER	-	expression tag	UNP A0A1X9WEN9
B	-1	ASN	-	expression tag	UNP A0A1X9WEN9
B	0	ALA	-	expression tag	UNP A0A1X9WEN9

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

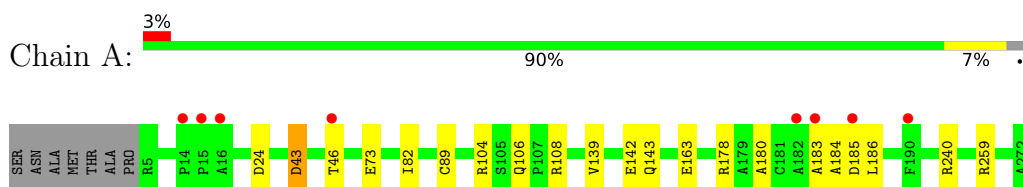
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	270	Total	O	0	0
			270	270		
3	B	211	Total	O	0	0
			211	211		

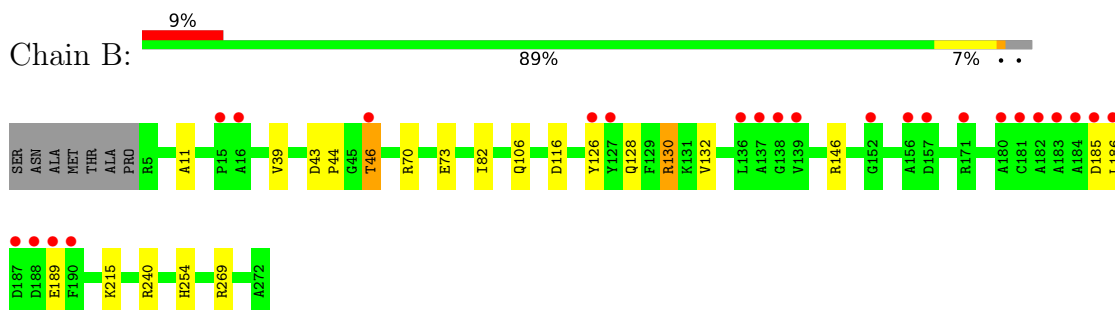
3 Residue-property plots [i](#)

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: Dieckmann cyclase, NcmC



- Molecule 1: Dieckmann cyclase, NcmC



4 Data and refinement statistics i

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	80.44Å 80.44Å 77.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	80.43 – 1.60 35.74 – 1.60	Depositor EDS
% Data completeness (in resolution range)	98.7 (80.43-1.60) 98.8 (35.74-1.60)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 1.60Å)	Xtrriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.169 , 0.204 0.182 , 0.211	Depositor DCC
R_{free} test set	3275 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	12.9	Xtrriage
Anisotropy	0.084	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 57.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.006 for -h,-l,-k 0.000 for -h,l,k 0.000 for l,-k,h 0.007 for -l,-k,-h 0.034 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4474	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 20.88 % 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 7.9007e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: SO4

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	1.13	1/2035 (0.0%)	1.17	8/2779 (0.3%)
1	B	1.10	1/2030 (0.0%)	1.07	6/2773 (0.2%)
All	All	1.11	2/4065 (0.0%)	1.12	14/5552 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	73	GLU	CD-OE2	-8.76	1.16	1.25
1	A	108	ARG	C-O	-5.31	1.13	1.23

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	240	ARG	NE-CZ-NH1	9.07	124.84	120.30
1	A	108	ARG	NE-CZ-NH2	8.61	124.60	120.30
1	B	240	ARG	NE-CZ-NH1	-8.39	116.11	120.30
1	A	108	ARG	NE-CZ-NH1	-7.86	116.37	120.30
1	A	104	ARG	NE-CZ-NH2	7.52	124.06	120.30
1	A	104	ARG	NE-CZ-NH1	-7.11	116.75	120.30
1	B	46	THR	CA-C-N	7.02	132.64	117.20
1	B	240	ARG	NE-CZ-NH2	6.78	123.69	120.30
1	B	46	THR	CA-C-O	-6.73	105.97	120.10
1	B	70	ARG	NE-CZ-NH2	-6.39	117.11	120.30
1	A	259	ARG	NE-CZ-NH2	-5.88	117.36	120.30
1	A	259	ARG	NE-CZ-NH1	5.73	123.17	120.30
1	B	46	THR	N-CA-CB	-5.16	100.50	110.30
1	A	24	ASP	CB-CG-OD2	-5.08	113.73	118.30

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	1994	0	1964	14	0
1	B	1989	0	1956	16	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	270	0	0	5	0
3	B	211	0	0	7	0
All	All	4474	0	3920	29	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 4.

All (29) 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:82:ILE:H	1:B:106:GLN:HE22	1.18	0.89
1:A:82:ILE:H	1:A:106:GLN:HE22	1.17	0.88
1:B:11:ALA:HB2	1:B:39:VAL:HG11	1.70	0.73
1:A:139:VAL:HG22	1:A:186:LEU:HD13	1.75	0.69
1:A:143:GLN:HB2	3:A:453:HOH:O	1.93	0.69
1:B:46:THR:HG22	3:B:546:HOH:O	1.96	0.65
1:A:43:ASP:O	1:A:46:THR:HG23	1.96	0.65
1:B:254:HIS:HE1	3:B:572:HOH:O	1.80	0.65
1:B:116:ASP:OD2	1:B:254:HIS:HD2	1.81	0.64
1:A:183:ALA:O	1:A:185:ASP:N	2.30	0.64
1:B:215:LYS:NZ	3:B:402:HOH:O	2.26	0.60
1:A:139:VAL:CG2	1:A:186:LEU:HD13	2.32	0.59
1:A:82:ILE:H	1:A:106:GLN:NE2	1.97	0.59
1:B:269:ARG:NH2	3:B:403:HOH:O	2.35	0.59
1:A:163:GLU:HG2	1:B:44:PRO:HG3	1.85	0.58
1:A:178:ARG:NH1	3:A:401:HOH:O	2.37	0.58
1:A:89:CYS:SG	3:A:635:HOH:O	2.38	0.52
1:B:11:ALA:CB	1:B:39:VAL:HG11	2.37	0.52
1:B:126:TYR:OH	1:B:130:ARG:NH1	2.43	0.51
1:B:46:THR:HG23	1:B:46:THR:O	2.10	0.51
1:B:146:ARG:NH1	3:B:407:HOH:O	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:THR:HG21	3:A:593:HOH:O	2.13	0.48
1:B:269:ARG:NH1	3:B:401:HOH:O	2.22	0.48
1:B:128:GLN:O	1:B:132:VAL:HG23	2.16	0.46
1:A:73:GLU:HG3	3:A:403:HOH:O	2.15	0.46
1:A:82:ILE:N	1:A:106:GLN:HE22	1.99	0.45
1:B:186:LEU:HA	3:B:410:HOH:O	2.16	0.44
1:B:82:ILE:H	1:B:106:GLN:NE2	2.00	0.44
1:A:180:ALA:O	1:A:183:ALA:O	2.38	0.41

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	267/275 (97%)	261 (98%)	5 (2%)	1 (0%)	34	15
1	B	267/275 (97%)	261 (98%)	5 (2%)	1 (0%)	34	15
All	All	534/550 (97%)	522 (98%)	10 (2%)	2 (0%)	34	15

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	184	ALA
1	B	185	ASP

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	195/199 (98%)	193 (99%)	2 (1%)	76	61
1	B	195/199 (98%)	192 (98%)	3 (2%)	65	44
All	All	390/398 (98%)	385 (99%)	5 (1%)	69	50

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	ASP
1	A	142	GLU
1	B	43	ASP
1	B	130	ARG
1	B	189	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	106	GLN
1	A	233	ASN
1	B	106	GLN
1	B	233	ASN
1	B	254	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	SO4	B	301	-	4,4,4	0.57	0	6,6,6	0.63	0
2	SO4	A	301	-	4,4,4	0.29	0	6,6,6	0.99	0

There are no bond length outliers.

There are no bond angle outliers.

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	268/275 (97%)	-0.06	8 (2%) 50 48	6, 13, 32, 57	0
1	B	268/275 (97%)	0.35	24 (8%) 9 8	6, 15, 47, 90	0
All	All	536/550 (97%)	0.14	32 (5%) 21 19	6, 14, 40, 90	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	184	ALA	8.5
1	B	185	ASP	6.9
1	A	15	PRO	6.6
1	B	186	LEU	5.8
1	B	15	PRO	5.7
1	B	16	ALA	5.6
1	B	190	PHE	5.4
1	A	16	ALA	4.9
1	B	187	ASP	4.4
1	B	127	TYR	4.1
1	B	181	CYS	3.8
1	B	183	ALA	3.8
1	B	182	ALA	3.7
1	B	188	ASP	3.6
1	B	126	TYR	3.5
1	B	138	GLY	3.2
1	B	189	GLU	3.1
1	B	152	GLY	2.9
1	A	185	ASP	2.8
1	B	156	ALA	2.8
1	B	46	THR	2.7
1	A	190	PHE	2.5
1	B	137	ALA	2.5
1	B	139	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	157	ASP	2.5
1	A	14	PRO	2.4
1	A	183	ALA	2.4
1	A	182	ALA	2.4
1	B	171	ARG	2.2
1	B	136	LEU	2.1
1	B	180	ALA	2.1
1	A	46	THR	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 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
2	SO4	B	301	5/5	0.97	0.09	24,24,27,32	0
2	SO4	A	301	5/5	0.98	0.07	19,21,24,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.