



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 19, 2016 – 06:43 PM GMT

PDB ID : 3WXX
Title : Crystal Structure of a T3SS complex from *Aeromonas hydrophila*
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Deposited on : 2014-08-12
Resolution : 2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
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) : rb-20026982

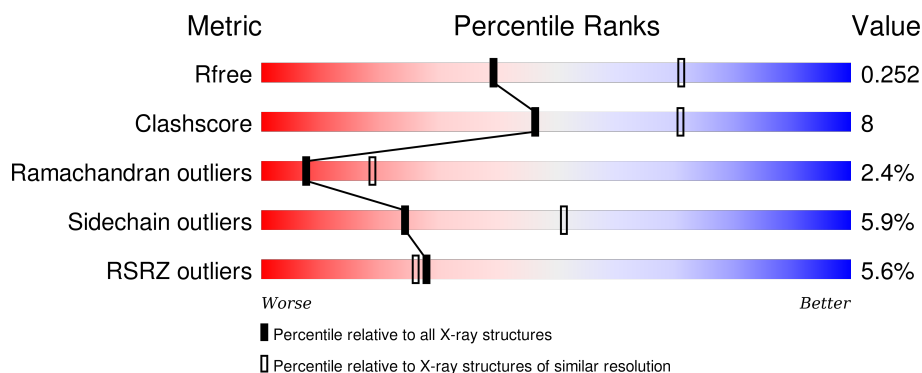
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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 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	151	<div> <div>%</div> <div> <div></div> <div>93%</div> <div>5% ..</div> </div> </div>
1	C	151	<div> <div>2%</div> <div> <div></div> <div>87%</div> <div>10% ...</div> </div> </div>
1	E	151	<div> <div>%</div> <div> <div></div> <div>93%</div> <div>5% .</div> </div> </div>
1	G	151	<div> <div>3%</div> <div> <div></div> <div>89%</div> <div>8% .</div> </div> </div>
2	B	219	<div> <div>7%</div> <div> <div></div> <div>64%</div> <div>16% . 16%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	D	219	
2	F	219	
2	H	219	

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	MG	G	201	-	-	-	X

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9737 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 AcrH.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	150	Total	C	N	O	S	Se	0	1	0
			1161	739	193	220	3	6			
1	C	150	Total	C	N	O	S	Se	0	1	0
			1161	739	193	220	3	6			
1	E	151	Total	C	N	O	S	Se	0	1	0
			1158	738	194	217	3	6			
1	G	151	Total	C	N	O	S	Se	0	1	0
			1166	742	194	221	3	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	HIS	ARG	ENGINEERED MUTATION	UNP Q6TLM1
C	107	HIS	ARG	ENGINEERED MUTATION	UNP Q6TLM1
E	107	HIS	ARG	ENGINEERED MUTATION	UNP Q6TLM1
G	107	HIS	ARG	ENGINEERED MUTATION	UNP Q6TLM1

- Molecule 2 is a protein called AopB.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	183	Total	C	N	O	S	Se	0	0	0
			1253	793	215	236	9				
2	D	183	Total	C	N	O	S	Se	0	0	0
			1259	799	215	236	9				
2	F	183	Total	C	N	O	S	Se	0	0	0
			1259	799	215	236	9				
2	H	183	Total	C	N	O	S	Se	0	0	0
			1263	801	215	238	9				

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

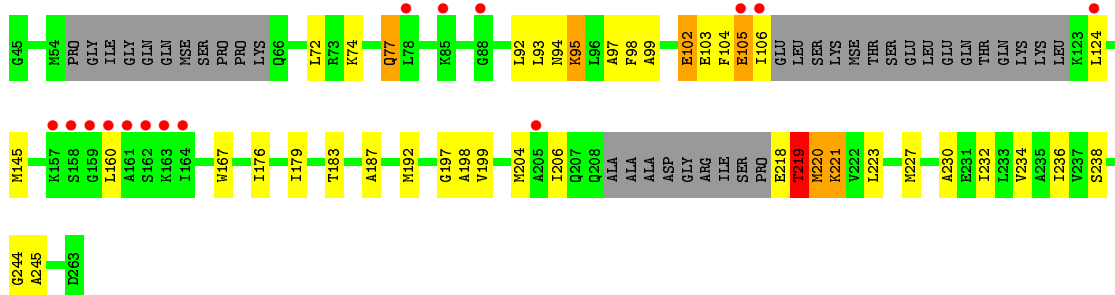
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	G	1	Total Mg 1 1	0	0

- Molecule 4 is water.

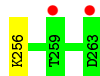
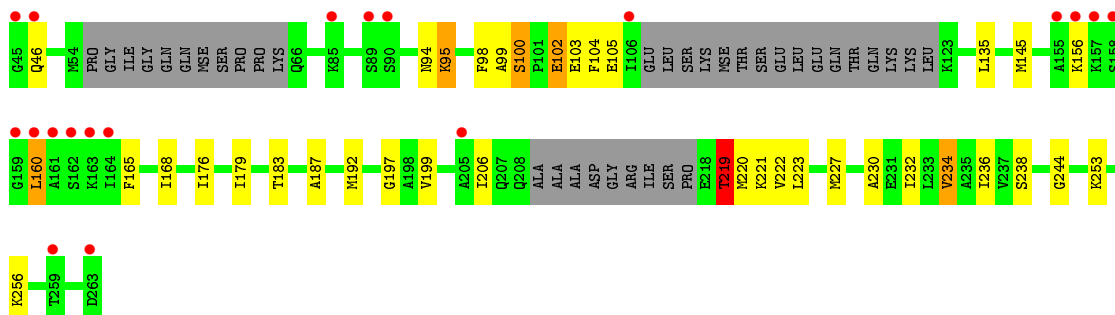
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	9	Total O 9 9	0	0
4	B	5	Total O 5 5	0	0
4	C	8	Total O 8 8	0	0
4	D	6	Total O 6 6	0	0
4	E	11	Total O 11 11	0	0
4	F	5	Total O 5 5	0	0
4	G	8	Total O 8 8	0	0
4	H	4	Total O 4 4	0	0



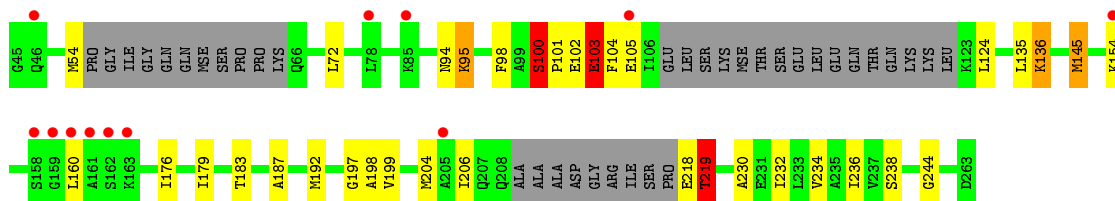
- Molecule 2: AopB



- Molecule 2: AopB



- Molecule 2: AopB



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	124.66Å 151.94Å 106.25Å 90.00° 104.95° 90.00°	Depositor
Resolution (Å)	15.00 – 2.70 36.40 – 2.49	Depositor EDS
% Data completeness (in resolution range)	93.2 (15.00-2.70) 85.3 (36.40-2.49)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	9.36 (at 2.48Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.213 , 0.252 0.216 , 0.252	Depositor DCC
R_{free} test set	2634 reflections (5.68%)	DCC
Wilson B-factor (Å ²)	50.7	Xtriage
Anisotropy	0.469	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 51.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 62144 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9737	wwPDB-VP
Average B, all atoms (Å ²)	69.0	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 39.32 % 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 3.2287e-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, 0.375 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: MG

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	0.64	0/1181	0.74	1/1583 (0.1%)
1	C	0.65	0/1181	0.79	3/1583 (0.2%)
1	E	0.67	0/1178	0.75	1/1580 (0.1%)
1	G	0.66	0/1186	0.79	1/1590 (0.1%)
2	B	0.60	0/1250	0.86	2/1669 (0.1%)
2	D	0.60	0/1257	0.86	3/1678 (0.2%)
2	F	0.64	0/1257	0.84	2/1678 (0.1%)
2	H	0.62	0/1261	0.82	2/1683 (0.1%)
All	All	0.64	0/9751	0.81	15/13044 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	F	0	1

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	160	LEU	CA-CB-CG	7.41	132.35	115.30
1	A	78	ARG	CG-CD-NE	7.12	126.76	111.80
1	C	156	LYS	CA-CB-CG	6.91	128.60	113.40
2	B	129	ARG	CA-CB-CG	6.27	127.20	113.40
2	D	192	MSE	CG-SE-CE	-6.17	85.32	98.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	F	221	LYS	Peptide

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	1161	0	1124	8	0
1	C	1161	0	1124	12	0
1	E	1158	0	1118	11	0
1	G	1166	0	1126	19	0
2	B	1253	0	1279	28	0
2	D	1259	0	1286	31	0
2	F	1259	0	1286	28	0
2	H	1263	0	1290	27	0
3	G	1	0	0	0	0
4	A	9	0	0	0	0
4	B	5	0	0	0	0
4	C	8	0	0	0	0
4	D	6	0	0	1	0
4	E	11	0	0	1	0
4	F	5	0	0	0	0
4	G	8	0	0	2	0
4	H	4	0	0	0	0
All	All	9737	0	9633	147	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.

The worst 5 of 147 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:G:157:ASP:O	1:G:158:MSE:HG2	1.64	0.96
2:H:103:GLU:CB	2:H:104:PHE:HA	2.00	0.91
2:H:103:GLU:HB2	2:H:104:PHE:HA	1.56	0.87
2:F:145:MSE:HE2	2:F:179:ILE:HG23	1.59	0.85
1:G:158:MSE:HB3	1:G:159:GLU:HA	1.58	0.84

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	149/151 (99%)	144 (97%)	5 (3%)	0	100	100
1	C	149/151 (99%)	145 (97%)	3 (2%)	1 (1%)	26	55
1	E	150/151 (99%)	145 (97%)	4 (3%)	1 (1%)	26	55
1	G	150/151 (99%)	144 (96%)	5 (3%)	1 (1%)	26	55
2	B	175/219 (80%)	145 (83%)	23 (13%)	7 (4%)	4	8
2	D	175/219 (80%)	145 (83%)	25 (14%)	5 (3%)	6	14
2	F	175/219 (80%)	147 (84%)	21 (12%)	7 (4%)	4	8
2	H	175/219 (80%)	142 (81%)	24 (14%)	9 (5%)	2	4
All	All	1298/1480 (88%)	1157 (89%)	110 (8%)	31 (2%)	7	19

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	105	GLU
2	B	219	THR
2	B	221	LYS
1	C	157	ASP
2	D	105	GLU

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	116/112 (104%)	115 (99%)	1 (1%)	84	95
1	C	116/112 (104%)	112 (97%)	4 (3%)	44	75
1	E	114/112 (102%)	113 (99%)	1 (1%)	84	95
1	G	116/112 (104%)	111 (96%)	5 (4%)	35	66
2	B	115/152 (76%)	101 (88%)	14 (12%)	6	14
2	D	116/152 (76%)	108 (93%)	8 (7%)	19	43
2	F	116/152 (76%)	105 (90%)	11 (10%)	11	24
2	H	117/152 (77%)	106 (91%)	11 (9%)	11	25
All	All	926/1056 (88%)	871 (94%)	55 (6%)	24	51

5 of 55 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	220	MSE
2	F	135	LEU
2	H	136	LYS
2	D	221	LYS
1	E	155	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	52	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	145/151 (96%)	-0.14	2 (1%) 78 77	30, 53, 88, 110	0
1	C	145/151 (96%)	-0.10	3 (2%) 67 68	33, 52, 87, 130	0
1	E	146/151 (96%)	-0.07	1 (0%) 89 90	32, 56, 94, 113	0
1	G	146/151 (96%)	-0.17	4 (2%) 58 58	37, 54, 90, 125	0
2	B	174/219 (79%)	0.30	16 (9%) 11 9	37, 76, 143, 194	0
2	D	174/219 (79%)	0.26	15 (8%) 13 10	36, 78, 128, 159	0
2	F	174/219 (79%)	0.33	19 (10%) 7 5	32, 75, 134, 156	0
2	H	174/219 (79%)	0.24	12 (6%) 20 18	32, 70, 136, 158	0
All	All	1278/1480 (86%)	0.10	72 (5%) 28 26	30, 62, 127, 194	0

The worst 5 of 72 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	159	GLY	9.2
2	F	163	LYS	5.5
2	D	161	ALA	5.4
2	B	160	LEU	5.3
2	D	159	GLY	5.3

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(\AA^2)	Q<0.9
3	MG	G	201	1/1	0.91	0.43	7.80	55,55,55,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.