



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 19, 2016 – 11:07 PM GMT

PDB ID : 5F2V
Title : Crystal structure of the small alarmone synthetase 1 from *Bacillus subtilis* bound to AMPCPP
Authors : Steinchen, W.; Schuhmacher, J.S.; Altegoer, F.; Bange, G.
Deposited on : 2015-12-02
Resolution : 2.80 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 : 1.7.1 (RC1), CSD as537be (2016)
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

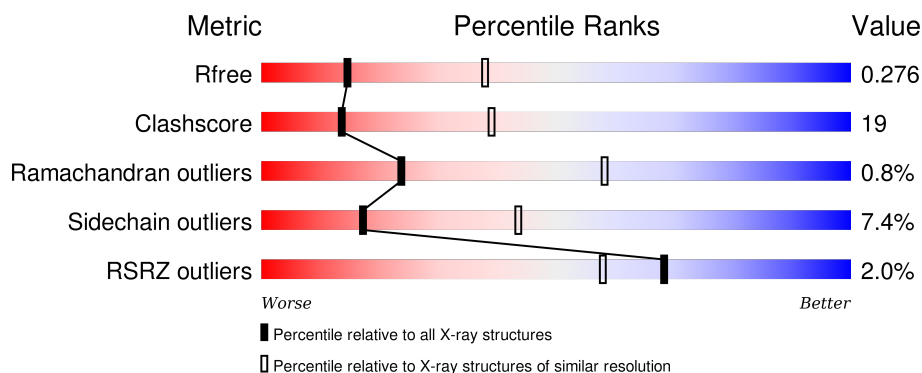
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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	O	209	<div> <div>4%</div> <div>52% 31% 6% 12%</div> </div>
1	P	209	<div> <div>2%</div> <div>58% 26% • 12%</div> </div>
1	Q	209	<div> <div>3%</div> <div>53% 29% • 14%</div> </div>
1	R	209	<div> <div>57% 29% • 12%</div> </div>
1	S	209	<div> <div>57% 28% • 13%</div> </div>

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Mol	Chain	Length	Quality of chain
1	T	209	
1	U	209	
1	V	209	
1	W	209	
1	X	209	
1	Y	209	
1	Z	209	

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
2	APC	T	301	-	-	X	-
3	MG	P	302	-	-	-	X
3	MG	S	301	-	-	-	X

2 Entry composition

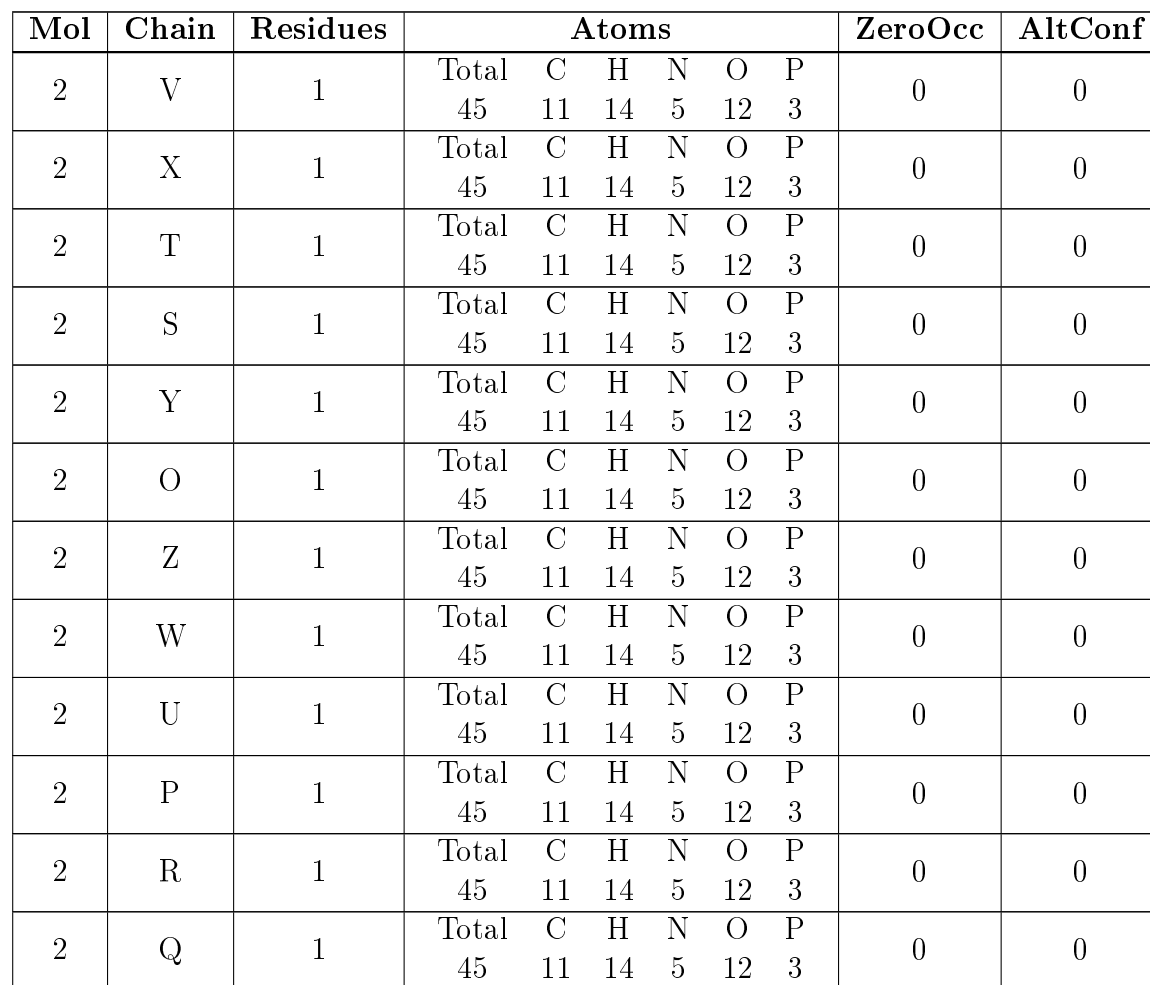
There are 4 unique types of molecules in this entry. The entry contains 18753 atoms, of which 168 are hydrogens and 0 are deuteriums.

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 GTP pyrophosphokinase YjbM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	V	180	Total	C	N	O	S	0	0	0
			1476	942	259	269	6			
1	X	181	Total	C	N	O	S	0	0	0
			1491	952	260	273	6			
1	T	195	Total	C	N	O	S	0	0	0
			1611	1025	281	299	6			
1	S	182	Total	C	N	O	S	0	0	0
			1488	950	259	273	6			
1	Y	182	Total	C	N	O	S	0	0	0
			1479	946	256	271	6			
1	O	184	Total	C	N	O	S	0	0	0
			1504	961	261	276	6			
1	Z	179	Total	C	N	O	S	0	0	0
			1474	942	257	269	6			
1	W	187	Total	C	N	O	S	0	0	0
			1534	980	266	282	6			
1	U	186	Total	C	N	O	S	0	0	0
			1526	973	264	283	6			
1	P	183	Total	C	N	O	S	0	0	0
			1490	952	260	272	6			
1	R	184	Total	C	N	O	S	0	0	0
			1497	955	261	275	6			
1	Q	179	Total	C	N	O	S	0	0	0
			1468	938	256	268	6			

- Molecule 2 is DIPHOSPHOMETHYLPHOSPHONIC ACID ADENOSYL ESTER (three-letter code: APC) (formula: C₁₁H₁₈N₅O₁₂P₃).



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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	P	1	Total Mg 1 1	0	0
3	Q	1	Total Mg 1 1	0	0
3	V	1	Total Mg 1 1	0	0
3	W	1	Total Mg 1 1	0	0
3	Z	1	Total Mg 1 1	0	0
3	T	1	Total Mg 1 1	0	0
3	U	1	Total Mg 1 1	0	0
3	X	1	Total Mg 1 1	0	0
3	O	1	Total Mg 1 1	0	0
3	R	1	Total Mg 1 1	0	0
3	Y	1	Total Mg 1 1	0	0
3	S	1	Total Mg 1 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	V	22	Total O 22 22	0	0
4	X	18	Total O 18 18	0	0
4	T	21	Total O 21 21	0	0
4	S	19	Total O 19 19	0	0
4	Y	19	Total O 19 19	0	0
4	O	3	Total O 3 3	0	0
4	Z	9	Total O 9 9	0	0
4	W	20	Total O 20 20	0	0

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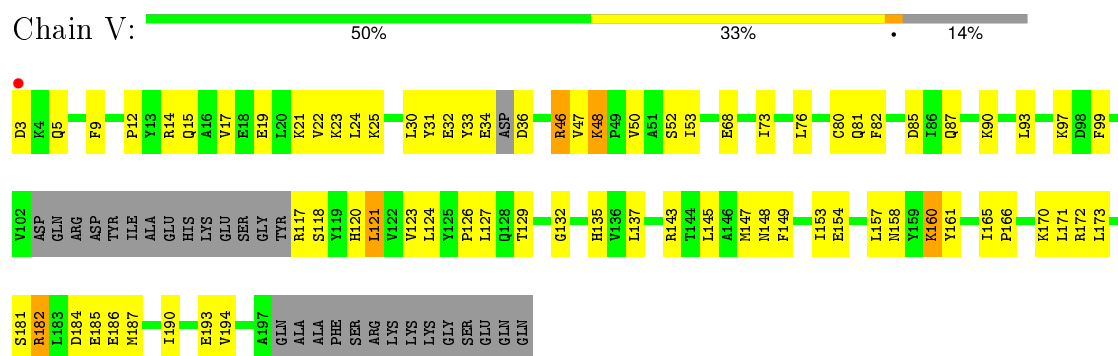
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	U	6	Total 6	O 6	0	0
4	P	7	Total 7	O 7	0	0
4	R	14	Total 14	O 14	0	0
4	Q	5	Total 5	O 5	0	0

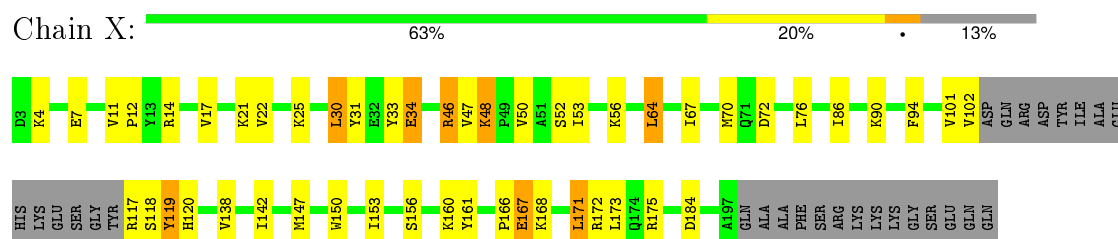
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

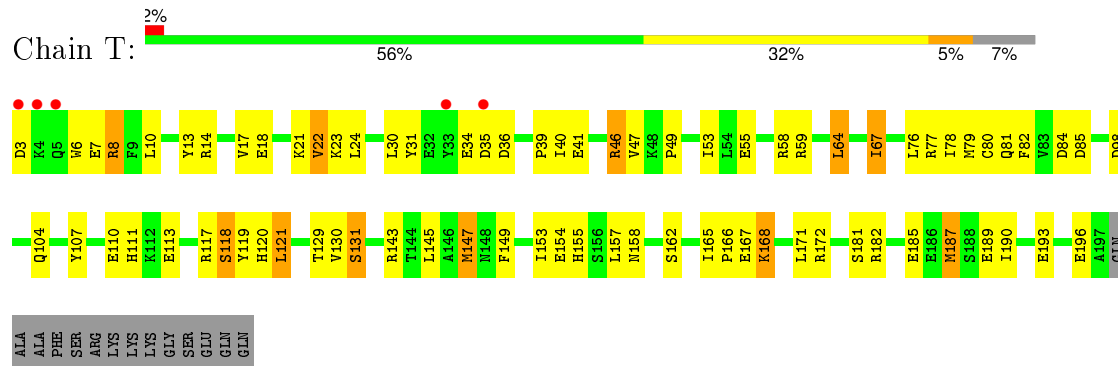
• Molecule 1: GTP pyrophosphokinase YjbM



• Molecule 1: GTP pyrophosphokinase YjbM

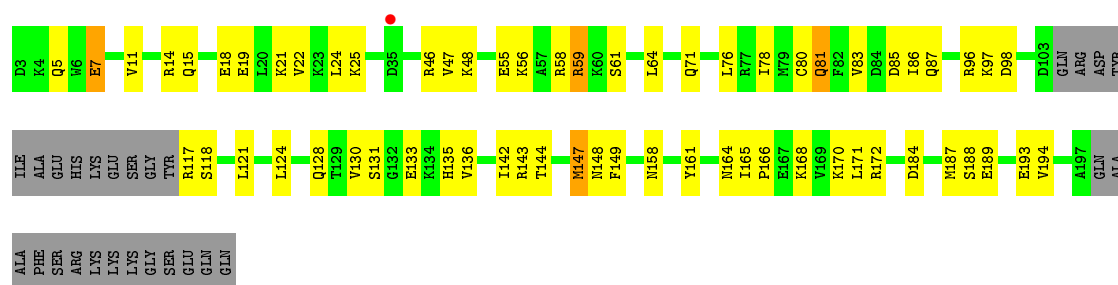


• Molecule 1: GTP pyrophosphokinase YjbM



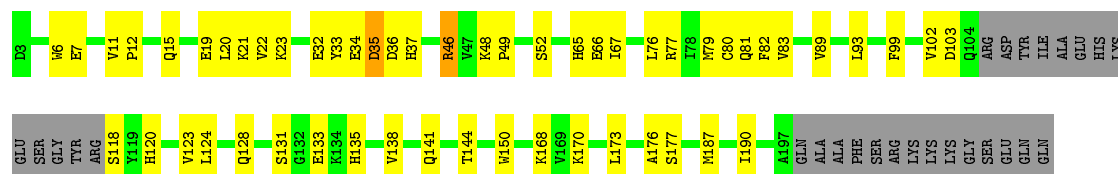
• Molecule 1: GTP pyrophosphokinase YjbM





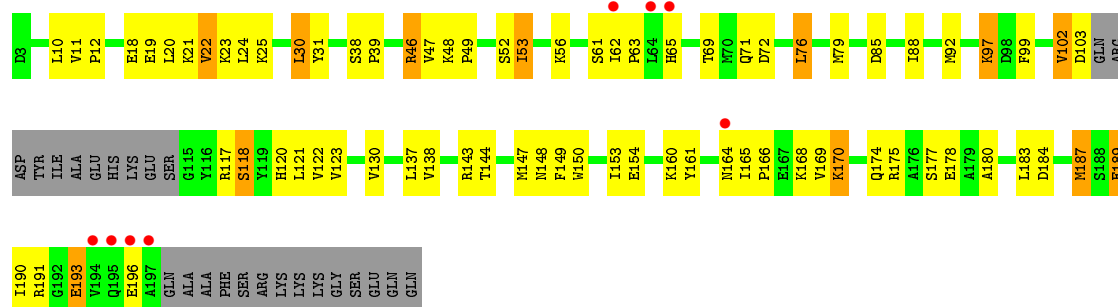
• Molecule 1: GTP pyrophosphokinase YjbM

Chain Y: 61% 25% 13%



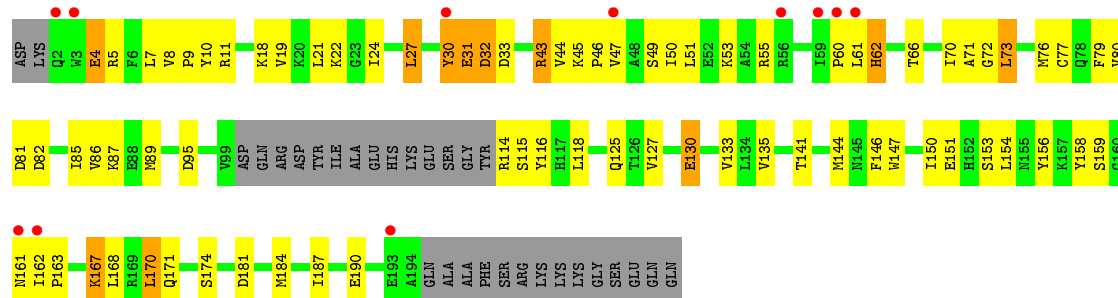
• Molecule 1: GTP pyrophosphokinase YjbM

Chain O: 4% 52% 31% 6% 12%



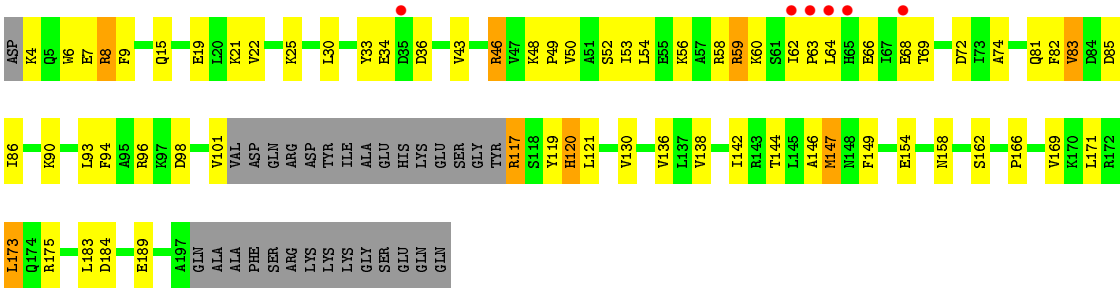
• Molecule 1: GTP pyrophosphokinase YjbM

Chain Z: 5% 48% 32% 5% 14%



• Molecule 1: GTP pyrophosphokinase YjbM

Chain W: 62% 24% 11%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	116.67Å 103.63Å 138.29Å 90.00° 104.84° 90.00°	Depositor
Resolution (Å)	48.31 – 2.80 48.31 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.31-2.80) 95.2 (48.31-2.80)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.07 (at 2.81Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1685)	Depositor
R, R_{free}	0.193 , 0.264 0.209 , 0.276	Depositor DCC
R_{free} test set	2000 reflections (2.74%)	DCC
Wilson B-factor (Å ²)	50.0	Xtriage
Anisotropy	0.565	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 38.7	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 78602 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18753	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% 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: APC, 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	O	0.39	0/1531	0.54	0/2064
1	P	0.45	0/1516	0.56	0/2044
1	Q	0.42	0/1494	0.55	0/2013
1	R	0.41	0/1523	0.57	0/2053
1	S	0.49	0/1514	0.59	0/2041
1	T	0.44	0/1641	0.58	0/2211
1	U	0.43	0/1553	0.55	0/2092
1	V	0.45	0/1500	0.58	0/2018
1	W	0.48	0/1561	0.59	0/2104
1	X	0.47	0/1517	0.60	0/2043
1	Y	0.46	0/1505	0.59	0/2030
1	Z	0.43	0/1500	0.56	0/2021
All	All	0.44	0/18355	0.57	0/24734

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	O	1504	0	1518	79	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	P	1490	0	1506	66	0
1	Q	1468	0	1491	68	0
1	R	1497	0	1511	61	0
1	S	1488	0	1506	52	0
1	T	1611	0	1625	64	0
1	U	1526	0	1542	83	0
1	V	1476	0	1509	68	0
1	W	1534	0	1554	54	0
1	X	1491	0	1521	46	0
1	Y	1479	0	1493	41	0
1	Z	1474	0	1504	81	0
2	O	31	14	14	5	0
2	P	31	14	14	4	0
2	Q	31	14	14	4	0
2	R	31	14	14	2	0
2	S	31	14	14	2	0
2	T	31	14	14	9	0
2	U	31	14	14	2	0
2	V	31	14	14	3	0
2	W	31	14	14	2	0
2	X	31	14	14	3	0
2	Y	31	14	14	3	0
2	Z	31	14	14	7	0
3	O	1	0	0	0	0
3	P	1	0	0	0	0
3	Q	1	0	0	0	0
3	R	1	0	0	0	0
3	S	1	0	0	0	0
3	T	1	0	0	0	0
3	U	1	0	0	0	0
3	V	1	0	0	0	0
3	W	1	0	0	0	0
3	X	1	0	0	0	0
3	Y	1	0	0	0	0
3	Z	1	0	0	0	0
4	O	3	0	0	4	0
4	P	7	0	0	2	0
4	Q	5	0	0	1	0
4	R	14	0	0	2	0
4	S	19	0	0	3	0
4	T	21	0	0	3	0
4	U	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	V	22	0	0	3	0
4	W	20	0	0	0	0
4	X	18	0	0	1	0
4	Y	19	0	0	1	0
4	Z	9	0	0	1	0
All	All	18585	168	18448	684	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 19.

The worst 5 of 684 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:X:22:VAL:HG21	1:Y:22:VAL:HG21	1.25	1.12
1:O:22:VAL:HG11	1:R:22:VAL:HG21	1.39	1.00
1:Z:19:VAL:HG21	1:W:22:VAL:HG21	1.41	0.99
1:Z:43:ARG:HH21	1:Z:45:LYS:HD3	1.26	0.98
1:R:48:LYS:HG2	1:R:53:ILE:HG12	1.48	0.96

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	O	180/209 (86%)	168 (93%)	12 (7%)	0	100	100
1	P	179/209 (86%)	166 (93%)	11 (6%)	2 (1%)	17	50
1	Q	175/209 (84%)	155 (89%)	19 (11%)	1 (1%)	30	65
1	R	180/209 (86%)	168 (93%)	11 (6%)	1 (1%)	30	65
1	S	178/209 (85%)	170 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	T	193/209 (92%)	182 (94%)	11 (6%)	0	100	100
1	U	182/209 (87%)	175 (96%)	5 (3%)	2 (1%)	17	50
1	V	174/209 (83%)	161 (92%)	11 (6%)	2 (1%)	17	50
1	W	183/209 (88%)	170 (93%)	10 (6%)	3 (2%)	12	38
1	X	177/209 (85%)	160 (90%)	14 (8%)	3 (2%)	11	36
1	Y	178/209 (85%)	174 (98%)	3 (2%)	1 (1%)	30	65
1	Z	175/209 (84%)	158 (90%)	14 (8%)	3 (2%)	11	36
All	All	2154/2508 (86%)	2007 (93%)	129 (6%)	18 (1%)	24	58

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	V	32	GLU
1	Y	35	ASP
1	V	160	LYS
1	Z	32	ASP
1	Z	61	LEU

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	O	163/187 (87%)	147 (90%)	16 (10%)	10	28
1	P	161/187 (86%)	150 (93%)	11 (7%)	20	49
1	Q	160/187 (86%)	149 (93%)	11 (7%)	19	48
1	R	162/187 (87%)	153 (94%)	9 (6%)	26	59
1	S	162/187 (87%)	150 (93%)	12 (7%)	17	43
1	T	176/187 (94%)	155 (88%)	21 (12%)	6	19
1	U	167/187 (89%)	155 (93%)	12 (7%)	18	45
1	V	162/187 (87%)	153 (94%)	9 (6%)	26	59
1	W	167/187 (89%)	159 (95%)	8 (5%)	31	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	X	164/187 (88%)	154 (94%)	10 (6%)	23	55
1	Y	160/187 (86%)	151 (94%)	9 (6%)	26	59
1	Z	162/187 (87%)	145 (90%)	17 (10%)	8	24
All	All	1966/2244 (88%)	1821 (93%)	145 (7%)	17	43

5 of 145 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	O	69	THR
1	Z	32	ASP
1	Q	8	ARG
1	O	97	LYS
1	O	189	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	T	120	HIS
1	W	195	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 12 are monoatomic - leaving 12 for Mogul analysis.

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	APC	O	301	3	29,33,33	1.89	11 (37%)	29,52,52	2.20	8 (27%)
2	APC	P	301	3	29,33,33	1.83	13 (44%)	29,52,52	2.05	6 (20%)
2	APC	Q	301	3	29,33,33	1.97	11 (37%)	29,52,52	2.48	7 (24%)
2	APC	R	301	3	29,33,33	1.74	8 (27%)	29,52,52	2.29	12 (41%)
2	APC	S	302	3	29,33,33	1.80	10 (34%)	29,52,52	1.88	5 (17%)
2	APC	T	301	3	29,33,33	3.16	9 (31%)	29,52,52	2.54	15 (51%)
2	APC	U	301	3	29,33,33	1.81	11 (37%)	29,52,52	2.00	7 (24%)
2	APC	V	301	3	29,33,33	1.89	11 (37%)	29,52,52	2.10	7 (24%)
2	APC	W	301	3	29,33,33	1.88	10 (34%)	29,52,52	2.35	9 (31%)
2	APC	X	301	3	29,33,33	1.72	10 (34%)	29,52,52	2.42	7 (24%)
2	APC	Y	301	3	29,33,33	1.77	8 (27%)	29,52,52	2.37	9 (31%)
2	APC	Z	301	3	29,33,33	2.03	10 (34%)	29,52,52	2.08	7 (24%)

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	APC	O	301	3	-	0/15/38/38	0/3/3/3
2	APC	P	301	3	-	0/15/38/38	0/3/3/3
2	APC	Q	301	3	-	0/15/38/38	0/3/3/3
2	APC	R	301	3	-	0/15/38/38	0/3/3/3
2	APC	S	302	3	-	0/15/38/38	0/3/3/3
2	APC	T	301	3	-	0/15/38/38	0/3/3/3
2	APC	U	301	3	-	0/15/38/38	0/3/3/3
2	APC	V	301	3	-	0/15/38/38	0/3/3/3
2	APC	W	301	3	-	0/15/38/38	0/3/3/3
2	APC	X	301	3	-	0/15/38/38	0/3/3/3
2	APC	Y	301	3	-	0/15/38/38	0/3/3/3
2	APC	Z	301	3	-	0/15/38/38	0/3/3/3

The worst 5 of 122 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	T	301	APC	C2'-C1'	-4.05	1.47	1.53
2	T	301	APC	PA-O2A	-3.29	1.48	1.56
2	V	301	APC	C2'-C1'	-2.86	1.49	1.53
2	Q	301	APC	C2'-C1'	-2.80	1.49	1.53
2	P	301	APC	C2'-C3'	-2.67	1.46	1.53

The worst 5 of 99 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	W	301	APC	N3-C2-N1	-8.48	122.21	128.87
2	X	301	APC	N3-C2-N1	-8.40	122.27	128.87
2	O	301	APC	N3-C2-N1	-7.90	122.67	128.87
2	Q	301	APC	N3-C2-N1	-7.75	122.78	128.87
2	Y	301	APC	N3-C2-N1	-7.53	122.95	128.87

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

12 monomers are involved in 46 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	O	301	APC	5	0
2	P	301	APC	4	0
2	Q	301	APC	4	0
2	R	301	APC	2	0
2	S	302	APC	2	0
2	T	301	APC	9	0
2	U	301	APC	2	0
2	V	301	APC	3	0
2	W	301	APC	2	0
2	X	301	APC	3	0
2	Y	301	APC	3	0
2	Z	301	APC	7	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	O	184/209 (88%)	-0.00	8 (4%)	39	27	42, 61, 103, 116	0
1	P	183/209 (87%)	-0.08	4 (2%)	65	54	35, 51, 98, 117	0
1	Q	179/209 (85%)	-0.04	6 (3%)	49	36	43, 62, 109, 124	0
1	R	184/209 (88%)	-0.30	1 (0%)	91	88	38, 54, 81, 102	0
1	S	182/209 (87%)	-0.20	1 (0%)	91	88	28, 46, 78, 100	0
1	T	195/209 (93%)	-0.28	5 (2%)	59	47	30, 46, 83, 98	0
1	U	186/209 (88%)	-0.04	4 (2%)	65	54	36, 56, 96, 112	0
1	V	180/209 (86%)	-0.29	1 (0%)	90	86	33, 45, 81, 89	0
1	W	187/209 (89%)	-0.23	2 (1%)	82	74	29, 47, 78, 99	0
1	X	181/209 (86%)	-0.26	0	100	100	31, 47, 80, 96	0
1	Y	182/209 (87%)	-0.39	0	100	100	30, 45, 78, 98	0
1	Z	179/209 (85%)	-0.01	11 (6%)	25	15	37, 58, 103, 120	0
All	All	2202/2508 (87%)	-0.18	43 (1%)	68	58	28, 52, 94, 124	0

The worst 5 of 43 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Z	61	LEU	5.9
1	O	195	GLN	5.5
1	O	196	GLU	5.3
1	T	33	TYR	4.9
1	Z	30	TYR	4.3

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	MG	P	302	1/1	0.99	0.28	5.28	39,39,39,39	0
3	MG	S	301	1/1	0.97	0.25	2.05	39,39,39,39	0
3	MG	X	302	1/1	0.92	0.18	1.15	39,39,39,39	0
3	MG	O	302	1/1	0.92	0.24	0.92	63,63,63,63	0
2	APC	T	301	31/31	0.92	0.17	0.09	23,37,54,60	0
2	APC	V	301	31/31	0.95	0.14	-0.32	33,47,55,56	0
2	APC	U	301	31/31	0.95	0.16	-0.32	44,58,73,75	0
3	MG	V	302	1/1	0.95	0.13	-0.46	44,44,44,44	0
2	APC	Y	301	31/31	0.97	0.15	-0.56	30,40,50,52	0
2	APC	Q	301	31/31	0.95	0.15	-0.57	52,71,85,92	0
2	APC	Z	301	31/31	0.93	0.14	-0.81	45,66,84,89	0
2	APC	O	301	31/31	0.95	0.15	-0.88	47,62,77,82	0
2	APC	R	301	31/31	0.96	0.13	-0.92	34,49,56,61	0
2	APC	P	301	31/31	0.98	0.14	-0.97	35,46,55,62	0
2	APC	S	302	31/31	0.98	0.15	-0.98	30,44,55,56	0
2	APC	X	301	31/31	0.97	0.13	-1.06	35,46,58,63	0
2	APC	W	301	31/31	0.98	0.13	-1.53	32,42,51,56	0
3	MG	W	302	1/1	0.95	0.10	-1.75	45,45,45,45	0
3	MG	Y	302	1/1	0.96	0.14	-	39,39,39,39	0
3	MG	Q	302	1/1	0.89	0.10	-	62,62,62,62	0
3	MG	T	302	1/1	0.97	0.18	-	52,52,52,52	0
3	MG	R	302	1/1	0.98	0.09	-	46,46,46,46	0
3	MG	Z	302	1/1	0.81	0.21	-	59,59,59,59	0
3	MG	U	302	1/1	0.91	0.15	-	75,75,75,75	0

6.5 Other polymers ⓘ

There are no such residues in this entry.