



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2026 – 11:46 PM UTC

PDB ID : 9H8J / pdb_00009h8j
Title : Crystal Structure of Polyphosphate kinase 2-II (PPK2-II) from *Lysinibacillus fusiformis* in apo form
Authors : Friedrich, F.; Kuge, M.; Keppler, M.; Gerhardt, S.; Einsle, O.; Andexer, J.N.
Deposited on : 2024-10-29
Resolution : 2.20 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

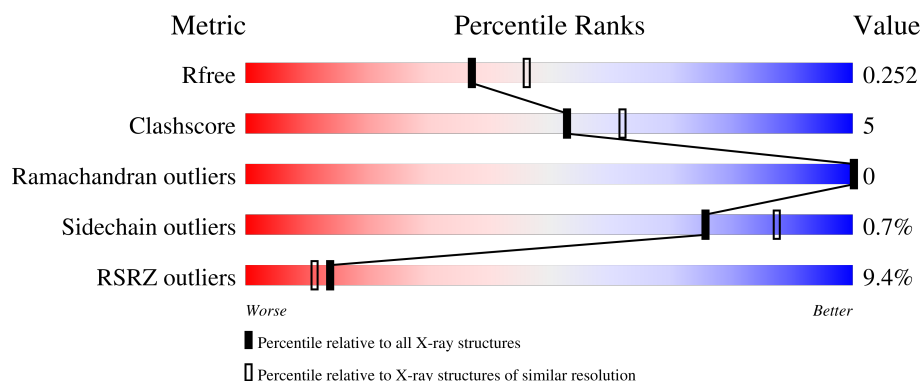
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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 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	269	10% 77% 13% 9%
1	B	269	7% 80% 12% 9%
1	C	269	7% 78% 9% 12%
1	D	269	9% 77% 10% 12%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8601 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 Polyphosphate kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	246	Total	C	N	O	S	0	1	0
			2071	1330	368	368	5			
1	A	244	Total	C	N	O	S	0	0	0
			2051	1319	364	363	5			
1	C	236	Total	C	N	O	S	0	0	0
			1981	1272	353	352	4			
1	D	237	Total	C	N	O	S	0	0	0
			1984	1270	355	355	4			

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



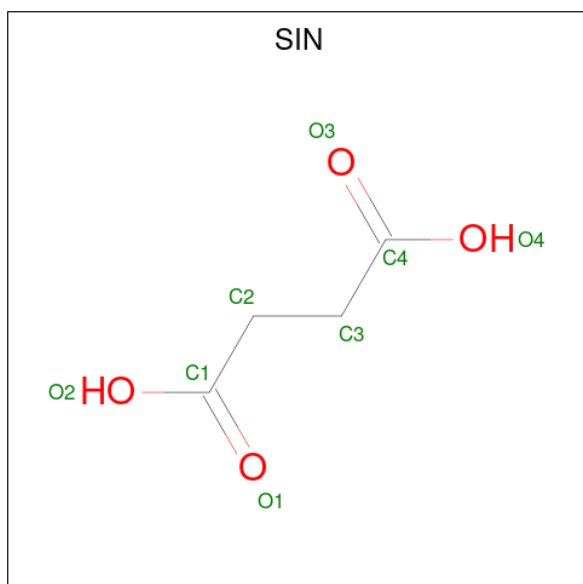
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is SUCCINIC ACID (CCD ID: SIN) (formula: C₄H₆O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	4	4		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	163	Total	O	0	0
			163	163		
4	A	136	Total	O	0	0
			136	136		

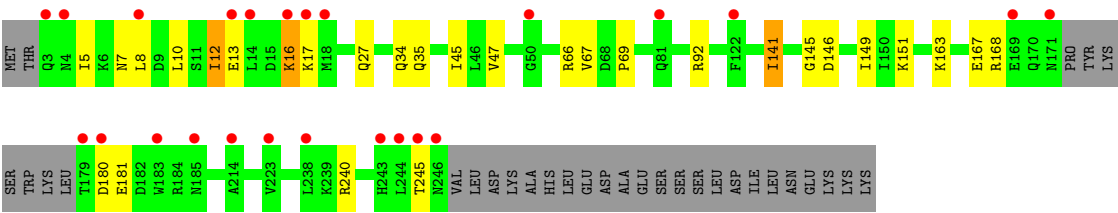
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	85	Total	O	0	0
			85	85		
4	D	82	Total	O	0	0
			82	82		

- Molecule 1: Polyphosphate kinase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	86.11Å 71.93Å 97.69Å 90.00° 92.59° 90.00°	Depositor
Resolution (Å)	63.13 – 2.20 63.13 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.6 (63.13-2.20) 98.6 (63.13-2.20)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 2.20Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.205 , 0.253 0.204 , 0.252	Depositor DCC
R_{free} test set	2988 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	31.8	Xtriage
Anisotropy	0.265	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 41.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.021 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8601	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.59% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SIN, PO4

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	0.30	0/2098	0.55	0/2823
1	B	0.31	0/2121	0.55	0/2856
1	C	0.24	0/2025	0.49	0/2724
1	D	0.24	0/2026	0.48	0/2725
All	All	0.28	0/8270	0.52	0/11128

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 [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	2051	0	2070	26	0
1	B	2071	0	2089	25	0
1	C	1981	0	1987	17	0
1	D	1984	0	1991	20	0
2	A	10	0	0	0	0
2	B	10	0	0	1	0
2	C	10	0	0	0	0
2	D	10	0	0	1	0
3	A	8	0	4	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	136	0	0	3	0
4	B	163	0	0	4	0
4	C	85	0	0	1	0
4	D	82	0	0	1	0
All	All	8601	0	8141	82	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 5.

All (82) 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:3:GLN:NE2	4:B:401:HOH:O	2.06	0.87
1:C:16:LYS:HE3	1:C:18:MET:HB2	1.61	0.81
1:D:5:ILE:HG22	1:D:7:ASN:H	1.49	0.77
1:B:171:ASN:HB3	1:B:174:LYS:HB2	1.72	0.71
1:B:17:LYS:C	1:B:19:TYR:H	2.00	0.68
1:C:13:GLU:OE2	1:C:214:ALA:HB3	1.95	0.66
1:C:27:GLN:OE1	1:C:66:ARG:NH1	2.29	0.65
1:B:27:GLN:OE1	1:B:66:ARG:NH1	2.30	0.64
1:D:10:LEU:HD11	1:D:12:ILE:HG12	1.81	0.61
1:A:62:ARG:HG3	1:A:222:ARG:HD3	1.82	0.61
1:B:164:ARG:HA	1:B:167:GLU:HG2	1.83	0.60
1:C:211:VAL:HG11	1:C:228:GLU:HG3	1.85	0.58
1:B:168:ARG:NH2	2:B:302:PO4:O1	2.36	0.56
1:B:5:ILE:CG2	1:B:8:LEU:HG	2.35	0.56
1:A:164:ARG:O	1:A:167:GLU:HG2	2.06	0.56
1:D:180:ASP:OD1	1:D:181:GLU:N	2.39	0.55
1:C:27:GLN:HB2	1:C:66:ARG:HH11	1.71	0.55
1:D:145:GLY:O	1:D:240:ARG:NH2	2.38	0.54
1:B:17:LYS:C	1:B:19:TYR:N	2.65	0.54
1:C:62:ARG:HG3	1:C:222:ARG:HD3	1.89	0.53
1:D:45:ILE:HB	1:D:149:ILE:HG12	1.92	0.52
1:D:146:ASP:HA	1:D:240:ARG:NH2	2.25	0.52
1:A:130:ARG:NH1	4:A:403:HOH:O	2.42	0.52
1:C:137:ASN:O	1:C:141:ILE:HG13	2.10	0.52
1:B:191:GLN:HG3	4:B:516:HOH:O	2.10	0.52
1:C:16:LYS:HG3	1:C:18:MET:H	1.75	0.51
1:A:27:GLN:OE1	1:A:66:ARG:NH1	2.43	0.51
1:A:14:LEU:CD2	1:A:217:ASP:HB2	2.41	0.50
1:C:47:VAL:HB	1:C:151:LYS:HG2	1.91	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:LEU:HD22	1:A:217:ASP:HB2	1.93	0.50
1:D:16:LYS:HZ2	1:D:17:LYS:HG2	1.76	0.50
1:A:5:ILE:HG23	1:A:8:LEU:HG	1.93	0.50
1:B:111:TYR:CE2	1:B:151:LYS:HD2	2.47	0.50
1:B:5:ILE:HG22	1:B:8:LEU:HG	1.94	0.50
1:B:96:LYS:HE3	4:B:470:HOH:O	2.12	0.49
1:B:5:ILE:HG13	1:B:197:ASN:CG	2.38	0.49
1:A:236:GLU:HB3	1:A:240:ARG:HH12	1.78	0.49
1:A:45:ILE:HB	1:A:149:ILE:HG12	1.95	0.49
1:B:10:LEU:HD11	1:B:12:ILE:HB	1.95	0.49
1:D:47:VAL:HB	1:D:151:LYS:HG2	1.96	0.48
1:C:17:LYS:C	1:C:19:TYR:H	2.22	0.48
1:A:62:ARG:HH22	3:A:303:SIN:H22	1.78	0.47
1:A:10:LEU:HD11	1:A:12:ILE:HG12	1.95	0.47
1:D:168:ARG:NH2	2:D:302:PO4:O1	2.48	0.46
1:A:47:VAL:HB	1:A:151:LYS:HG2	1.97	0.45
1:C:5:ILE:HG23	1:C:8:LEU:HG	1.99	0.45
1:B:159:GLU:H	1:B:159:GLU:CD	2.25	0.45
1:B:14:LEU:CD2	1:B:217:ASP:HB2	2.46	0.45
1:A:63:LEU:HD12	1:A:225:VAL:HG12	1.99	0.44
1:D:5:ILE:HB	1:D:8:LEU:HD13	1.99	0.44
1:C:220:TYR:C	1:C:220:TYR:CD2	2.96	0.44
1:A:8:LEU:HD12	4:A:515:HOH:O	2.17	0.44
1:A:16:LYS:HB2	1:A:17:LYS:H	1.58	0.44
1:B:137:ASN:O	1:B:141:ILE:HG13	2.18	0.43
1:C:3:GLN:NE2	1:C:4:ASN:O	2.51	0.43
1:C:61:LYS:HE2	1:D:69:PRO:HD3	2.00	0.43
1:C:111:TYR:CE2	1:C:151:LYS:HD2	2.53	0.43
1:B:61:LYS:NZ	1:A:65:GLU:O	2.47	0.43
1:B:134:GLU:CD	1:D:141:ILE:HD12	2.43	0.43
1:D:163:LYS:O	1:D:167:GLU:HG3	2.19	0.43
1:C:126:ASP:HB3	4:C:485:HOH:O	2.19	0.43
1:B:14:LEU:HD23	1:B:217:ASP:HB2	2.01	0.43
1:B:70:ARG:NH1	1:A:107:ASP:OD2	2.37	0.43
1:A:98:PRO:HG2	1:A:147:TYR:HE2	1.83	0.42
1:D:27:GLN:OE1	1:D:66:ARG:NH1	2.51	0.42
1:A:211:VAL:HG11	1:A:228:GLU:HG3	2.01	0.42
1:A:19:TYR:CD1	1:A:219:LYS:HB3	2.54	0.42
1:A:169:GLU:HG3	1:A:178:LEU:HD13	2.02	0.42
1:A:164:ARG:HA	1:A:167:GLU:HG2	2.02	0.42
1:D:10:LEU:O	1:D:13:GLU:HG2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:16:LYS:HB2	1:D:17:LYS:H	1.69	0.41
1:B:5:ILE:HG13	1:B:197:ASN:OD1	2.19	0.41
1:B:35:GLN:OE1	1:A:176:TRP:NE1	2.45	0.41
1:B:108:ARG:HD3	4:B:473:HOH:O	2.20	0.41
1:A:236:GLU:HB3	1:A:240:ARG:NH1	2.35	0.41
1:A:214:ALA:HB1	4:A:490:HOH:O	2.21	0.41
1:D:34:GLN:CD	1:D:67:VAL:HG13	2.46	0.41
1:D:16:LYS:HB2	1:D:16:LYS:NZ	2.33	0.41
1:A:8:LEU:HA	1:A:8:LEU:HD23	1.56	0.41
1:D:92:ARG:NH2	4:D:414:HOH:O	2.55	0.40
1:C:173:TYR:CD2	1:D:35:GLN:HG3	2.55	0.40
1:B:189:SER:OG	1:B:190:PRO:HD3	2.22	0.40

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	242/269 (90%)	235 (97%)	7 (3%)	0	100	100
1	B	245/269 (91%)	238 (97%)	7 (3%)	0	100	100
1	C	232/269 (86%)	225 (97%)	7 (3%)	0	100	100
1	D	233/269 (87%)	227 (97%)	6 (3%)	0	100	100
All	All	952/1076 (88%)	925 (97%)	27 (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	215/239 (90%)	213 (99%)	2 (1%)	70	84
1	B	218/239 (91%)	218 (100%)	0	100	100
1	C	207/239 (87%)	207 (100%)	0	100	100
1	D	208/239 (87%)	204 (98%)	4 (2%)	50	66
All	All	848/956 (89%)	842 (99%)	6 (1%)	76	87

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	ILE
1	A	194	GLU
1	D	12	ILE
1	D	16	LYS
1	D	141	ILE
1	D	245	THR

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

Mol	Chain	Res	Type
1	A	243	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 oligosaccharides in this entry.

5.6 Ligand geometry

9 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	PO4	C	302	-	4,4,4	0.90	0	6,6,6	0.40	0
2	PO4	D	302	-	4,4,4	0.93	0	6,6,6	0.48	0
2	PO4	B	302	-	4,4,4	0.93	0	6,6,6	0.49	0
2	PO4	A	302	-	4,4,4	0.94	0	6,6,6	0.51	0
2	PO4	B	301	-	4,4,4	0.89	0	6,6,6	0.52	0
2	PO4	C	301	-	4,4,4	0.97	0	6,6,6	0.52	0
3	SIN	A	303	-	7,7,7	1.05	0	8,8,8	1.62	2 (25%)
2	PO4	D	301	-	4,4,4	1.13	0	6,6,6	0.47	0
2	PO4	A	301	-	4,4,4	1.11	0	6,6,6	0.66	0

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
3	SIN	A	303	-	-	4/5/5/5	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	303	SIN	O2-C1-C2	2.21	120.98	114.00
3	A	303	SIN	O4-C4-C3	2.14	120.77	114.00

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	303	SIN	C2-C3-C4-O3

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Mol	Chain	Res	Type	Atoms
3	A	303	SIN	C2-C3-C4-O4
3	A	303	SIN	O2-C1-C2-C3
3	A	303	SIN	O1-C1-C2-C3

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	302	PO4	1	0
2	B	302	PO4	1	0
3	A	303	SIN	1	0

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	244/269 (90%)	0.54	27 (11%) 10 8	19, 32, 66, 83	0
1	B	246/269 (91%)	0.39	20 (8%) 18 15	18, 29, 64, 76	1 (0%)
1	C	236/269 (87%)	0.62	20 (8%) 16 14	24, 46, 83, 108	0
1	D	237/269 (88%)	0.70	24 (10%) 12 10	25, 45, 79, 102	0
All	All	963/1076 (89%)	0.56	91 (9%) 14 11	18, 37, 75, 108	1 (0%)

All (91) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	178	LEU	5.4
1	A	176	TRP	5.3
1	A	180	ASP	5.0
1	A	178	LEU	4.8
1	A	13	GLU	4.5
1	B	173	TYR	4.5
1	B	9	ASP	4.0
1	B	179	THR	3.7
1	D	185	ASN	3.7
1	C	237	ALA	3.5
1	D	14	LEU	3.5
1	A	2	THR	3.4
1	A	173	TYR	3.3
1	C	10	LEU	3.3
1	C	183	TRP	3.3
1	C	173	TYR	3.3
1	D	238	LEU	3.2
1	B	12	ILE	3.2
1	C	13	GLU	3.1
1	A	172	PRO	3.1
1	A	17	LYS	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	15	ASP	3.0
1	A	175	SER	3.0
1	A	14	LEU	3.0
1	B	2	THR	3.0
1	D	179	THR	3.0
1	B	133	GLU	3.0
1	D	4	ASN	2.9
1	C	8	LEU	2.8
1	A	16	LYS	2.8
1	A	1	MET	2.8
1	B	8	LEU	2.8
1	C	14	LEU	2.8
1	A	12	ILE	2.8
1	D	18	MET	2.7
1	A	181	GLU	2.7
1	D	243	HIS	2.7
1	B	172	PRO	2.7
1	D	214	ALA	2.6
1	D	122	PHE	2.6
1	B	18	MET	2.6
1	D	16	LYS	2.6
1	B	7	ASN	2.6
1	A	4	ASN	2.6
1	A	244	LEU	2.6
1	B	17	LYS	2.6
1	A	174	LYS	2.6
1	C	238	LEU	2.6
1	A	15	ASP	2.5
1	C	165	PHE	2.5
1	A	21	LYS	2.5
1	C	158	ASP	2.5
1	D	17	LYS	2.5
1	A	3	GLN	2.5
1	B	180	ASP	2.5
1	C	224	GLN	2.5
1	B	3	GLN	2.4
1	C	12	ILE	2.4
1	C	243	HIS	2.4
1	D	223	VAL	2.4
1	A	18	MET	2.4
1	B	16	LYS	2.3
1	A	179	THR	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	16	LYS	2.3
1	D	13	GLU	2.3
1	D	81	GLN	2.3
1	D	244	LEU	2.3
1	C	244	LEU	2.2
1	D	171	ASN	2.2
1	A	168	ARG	2.2
1	A	169	GLU	2.2
1	D	169	GLU	2.2
1	B	176	TRP	2.2
1	C	5	ILE	2.2
1	D	8	LEU	2.2
1	D	246	ASN	2.2
1	C	101	GLY	2.2
1	D	245	THR	2.2
1	B	171	ASN	2.1
1	A	177	LYS	2.1
1	B	1	MET	2.1
1	C	239	LYS	2.1
1	B	13	GLU	2.1
1	D	183	TRP	2.1
1	D	3	GLN	2.1
1	D	180	ASP	2.1
1	D	50	GLY	2.1
1	C	180	ASP	2.0
1	A	159	GLU	2.0
1	B	246	ASN	2.0
1	A	7	ASN	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 oligosaccharides 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
3	SIN	A	303	8/8	0.75	0.16	57,60,64,71	0
2	PO4	C	302	5/5	0.95	0.11	48,49,57,58	0
2	PO4	B	302	5/5	0.97	0.07	32,32,34,34	0
2	PO4	D	301	5/5	0.97	0.06	32,33,38,39	0
2	PO4	D	302	5/5	0.97	0.06	54,55,57,59	0
2	PO4	A	301	5/5	0.97	0.06	27,29,31,34	0
2	PO4	A	302	5/5	0.98	0.06	31,35,40,43	0
2	PO4	C	301	5/5	0.98	0.05	23,28,31,31	0
2	PO4	B	301	5/5	0.98	0.06	25,27,27,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.