



Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2017 – 08:38 AM EDT

PDB ID : 5X1W
Title : PKM2 in complex with compound 5
Authors : Matsui, Y.; Hanzawa, H.
Deposited on : 2017-01-27
Resolution : 3.00 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

<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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029077
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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-20029077

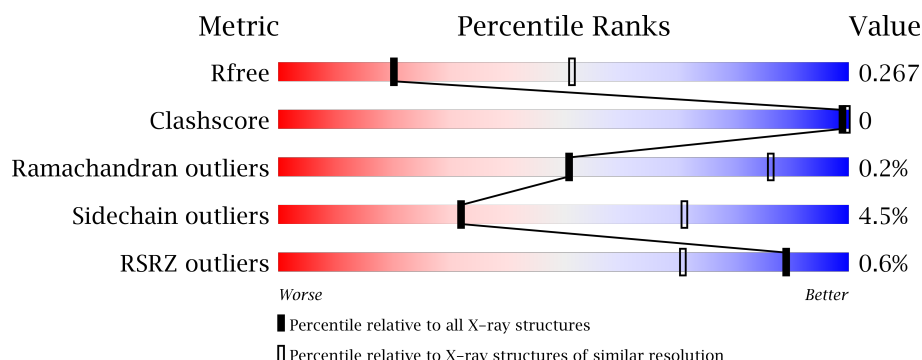
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION





The reported resolution of this entry is 3.00 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}	100719	1692 (3.00-3.00)
Clashscore	112137	2037 (3.00-3.00)
Ramachandran outliers	110173	1973 (3.00-3.00)
Sidechain outliers	110143	1976 (3.00-3.00)
RSRZ outliers	101464	1716 (3.00-3.00)

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	550	 89% 5% 6%
1	B	550	 87% 9%
1	C	550	 89% 5% 6%
1	D	550	 88% 5% 7%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15907 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 Pyruvate kinase PKM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	518	Total	C	N	O	S	0	0	0
			3965	2492	704	744	25			
1	B	501	Total	C	N	O	S	0	0	0
			3836	2416	684	713	23			
1	C	518	Total	C	N	O	S	0	0	0
			3965	2492	704	744	25			
1	D	511	Total	C	N	O	S	0	0	0
			3919	2463	696	735	25			

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MET	-	expression tag	UNP P14618
A	-17	GLY	-	expression tag	UNP P14618
A	-16	SER	-	expression tag	UNP P14618
A	-15	SER	-	expression tag	UNP P14618
A	-14	HIS	-	expression tag	UNP P14618
A	-13	HIS	-	expression tag	UNP P14618
A	-12	HIS	-	expression tag	UNP P14618
A	-11	HIS	-	expression tag	UNP P14618
A	-10	HIS	-	expression tag	UNP P14618
A	-9	HIS	-	expression tag	UNP P14618
A	-8	SER	-	expression tag	UNP P14618
A	-7	SER	-	expression tag	UNP P14618
A	-6	GLY	-	expression tag	UNP P14618
A	-5	LEU	-	expression tag	UNP P14618
A	-4	VAL	-	expression tag	UNP P14618
A	-3	PRO	-	expression tag	UNP P14618
A	-2	ARG	-	expression tag	UNP P14618
A	-1	GLY	-	expression tag	UNP P14618
A	0	SER	-	expression tag	UNP P14618
B	-18	MET	-	expression tag	UNP P14618
B	-17	GLY	-	expression tag	UNP P14618

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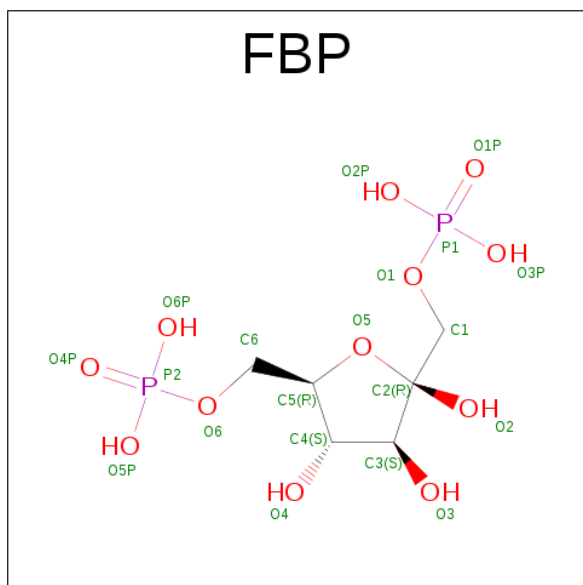
Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	SER	-	expression tag	UNP P14618
B	-15	SER	-	expression tag	UNP P14618
B	-14	HIS	-	expression tag	UNP P14618
B	-13	HIS	-	expression tag	UNP P14618
B	-12	HIS	-	expression tag	UNP P14618
B	-11	HIS	-	expression tag	UNP P14618
B	-10	HIS	-	expression tag	UNP P14618
B	-9	HIS	-	expression tag	UNP P14618
B	-8	SER	-	expression tag	UNP P14618
B	-7	SER	-	expression tag	UNP P14618
B	-6	GLY	-	expression tag	UNP P14618
B	-5	LEU	-	expression tag	UNP P14618
B	-4	VAL	-	expression tag	UNP P14618
B	-3	PRO	-	expression tag	UNP P14618
B	-2	ARG	-	expression tag	UNP P14618
B	-1	GLY	-	expression tag	UNP P14618
B	0	SER	-	expression tag	UNP P14618
C	-18	MET	-	expression tag	UNP P14618
C	-17	GLY	-	expression tag	UNP P14618
C	-16	SER	-	expression tag	UNP P14618
C	-15	SER	-	expression tag	UNP P14618
C	-14	HIS	-	expression tag	UNP P14618
C	-13	HIS	-	expression tag	UNP P14618
C	-12	HIS	-	expression tag	UNP P14618
C	-11	HIS	-	expression tag	UNP P14618
C	-10	HIS	-	expression tag	UNP P14618
C	-9	HIS	-	expression tag	UNP P14618
C	-8	SER	-	expression tag	UNP P14618
C	-7	SER	-	expression tag	UNP P14618
C	-6	GLY	-	expression tag	UNP P14618
C	-5	LEU	-	expression tag	UNP P14618
C	-4	VAL	-	expression tag	UNP P14618
C	-3	PRO	-	expression tag	UNP P14618
C	-2	ARG	-	expression tag	UNP P14618
C	-1	GLY	-	expression tag	UNP P14618
C	0	SER	-	expression tag	UNP P14618
D	-18	MET	-	expression tag	UNP P14618
D	-17	GLY	-	expression tag	UNP P14618
D	-16	SER	-	expression tag	UNP P14618
D	-15	SER	-	expression tag	UNP P14618
D	-14	HIS	-	expression tag	UNP P14618
D	-13	HIS	-	expression tag	UNP P14618

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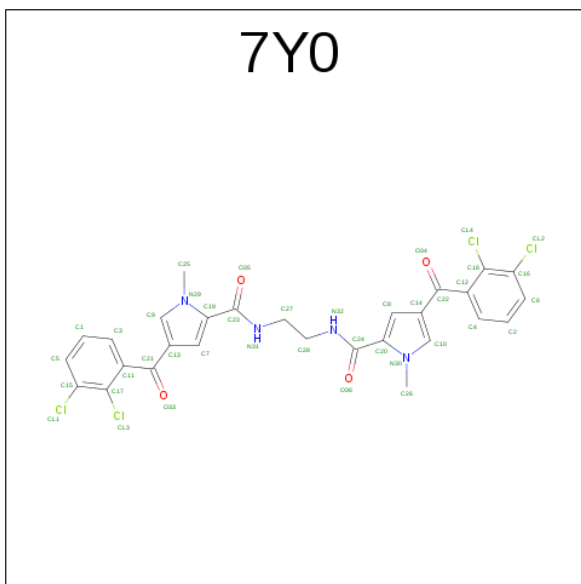
Chain	Residue	Modelled	Actual	Comment	Reference
D	-12	HIS	-	expression tag	UNP P14618
D	-11	HIS	-	expression tag	UNP P14618
D	-10	HIS	-	expression tag	UNP P14618
D	-9	HIS	-	expression tag	UNP P14618
D	-8	SER	-	expression tag	UNP P14618
D	-7	SER	-	expression tag	UNP P14618
D	-6	GLY	-	expression tag	UNP P14618
D	-5	LEU	-	expression tag	UNP P14618
D	-4	VAL	-	expression tag	UNP P14618
D	-3	PRO	-	expression tag	UNP P14618
D	-2	ARG	-	expression tag	UNP P14618
D	-1	GLY	-	expression tag	UNP P14618
D	0	SER	-	expression tag	UNP P14618

- Molecule 2 is BETA-FRUCTOSE-1,6-DIPHOSPHATE (three-letter code: FBP) (formula: $C_6H_{14}O_{12}P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			20	6	12	2		
2	B	1	Total	C	O	P	0	0
			20	6	12	2		
2	C	1	Total	C	O	P	0	0
			20	6	12	2		
2	D	1	Total	C	O	P	0	0
			20	6	12	2		

- Molecule 3 is 4-[2,3-bis(chloranyl)phenyl]carbonyl-N-[2-[[4-[2,3-bis(chloranyl)phenyl]carbonyl-1-methyl-pyrrol-2-yl]carbonylamino]ethyl]-1-methyl-pyrrole-2-carboxamide (three-letter code: 7Y0) (formula: $\text{C}_{28}\text{H}_{22}\text{Cl}_4\text{N}_4\text{O}_4$).



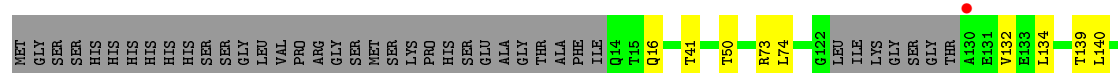
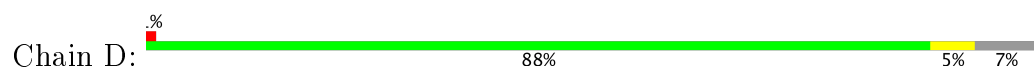
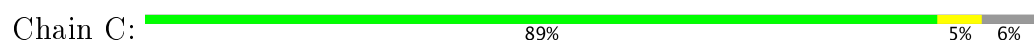
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total 40	C 28	Cl 4	N 4	O 4	0	0
3	C	1	Total 40	C 28	Cl 4	N 4	O 4	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	16	Total O 16 16	0	0
4	B	18	Total O 18 18	0	0
4	C	12	Total O 12 12	0	0
4	D	16	Total O 16 16	0	0

These plots are drawn for all protein, RNA and DNA 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.

Chain A: 89% 5% 6%





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	80.82Å 153.49Å 94.21Å 90.00° 103.52° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00 26.99 – 2.99	Depositor EDS
% Data completeness (in resolution range)	92.6 (20.00-3.00) 92.3 (26.99-2.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 3.00Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.237 , 0.290 0.215 , 0.267	Depositor DCC
R_{free} test set	4088 reflections (10.98%)	DCC
Wilson B-factor (Å ²)	40.7	Xtriage
Anisotropy	0.375	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 31.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	15907	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% 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: FBP, 7Y0

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	0.43	0/4029	0.75	0/5441
1	B	0.43	0/3897	0.75	0/5262
1	C	0.43	0/4029	0.75	0/5441
1	D	0.43	0/3982	0.74	0/5377
All	All	0.43	0/15937	0.75	0/21521

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	3965	0	4049	4	0
1	B	3836	0	3932	2	0
1	C	3965	0	4049	7	0
1	D	3919	0	3995	4	0
2	A	20	0	10	0	0
2	B	20	0	10	0	0
2	C	20	0	10	0	0
2	D	20	0	10	0	0
3	B	40	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	40	0	0	0	0
4	A	16	0	0	0	0
4	B	18	0	0	0	0
4	C	12	0	0	0	0
4	D	16	0	0	0	0
All	All	15907	0	16065	16	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 0.

All (16) 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:175:TYR:HB3	1:B:179:GLY:HA2	1.90	0.54
1:B:328:THR:HG22	1:B:329:GLN:HG3	1.96	0.48
1:C:328:THR:HG22	1:C:329:GLN:HG3	1.95	0.48
1:A:157:LEU:HD13	1:A:203:LEU:HD21	1.96	0.47
1:C:40:ILE:HD12	1:C:42:ALA:HB3	1.96	0.46
1:C:246:ARG:HG2	1:C:273:ASN:HD21	1.81	0.45
1:D:157:LEU:HD13	1:D:203:LEU:HD21	1.99	0.44
1:D:50:THR:OG1	1:D:73:ARG:NH1	2.46	0.44
1:D:134:LEU:HD21	1:D:140:LEU:HD13	1.99	0.43
1:C:48:ILE:HB	1:C:360:MET:HG3	2.00	0.42
1:D:409:THR:HG22	1:D:522:THR:HB	2.01	0.42
1:C:482:TRP:CD1	1:C:517:PRO:HG3	2.55	0.42
1:A:392:LEU:HD21	1:C:400:ARG:HE	1.85	0.41
1:A:48:ILE:HB	1:A:360:MET:HG3	2.03	0.41
1:A:346:SER:O	1:A:350:ASN:ND2	2.54	0.40
1:C:268:ILE:HG21	1:C:325:ILE:HD12	2.04	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	516/550 (94%)	500 (97%)	15 (3%)	1 (0%)	51	86
1	B	495/550 (90%)	482 (97%)	12 (2%)	1 (0%)	51	86
1	C	516/550 (94%)	502 (97%)	13 (2%)	1 (0%)	51	86
1	D	507/550 (92%)	490 (97%)	16 (3%)	1 (0%)	51	86
All	All	2034/2200 (92%)	1974 (97%)	56 (3%)	4 (0%)	51	86

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	328	THR
1	A	328	THR
1	C	328	THR
1	D	328	THR

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	426/452 (94%)	405 (95%)	21 (5%)	29	68
1	B	412/452 (91%)	393 (95%)	19 (5%)	31	70
1	C	426/452 (94%)	409 (96%)	17 (4%)	36	74
1	D	421/452 (93%)	403 (96%)	18 (4%)	33	72
All	All	1685/1808 (93%)	1610 (96%)	75 (4%)	32	71

All (75) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	THR
1	A	43	ARG
1	A	64	MET
1	A	120	ARG

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Mol	Chain	Res	Type
1	A	153	ASP
1	A	156	ILE
1	A	164	ILE
1	A	170	VAL
1	A	186	LYS
1	A	223	GLU
1	A	273	ASN
1	A	285	GLU
1	A	318	ASN
1	A	323	PRO
1	A	346	SER
1	A	401	LEU
1	A	412	THR
1	A	480	GLU
1	A	500	ARG
1	A	508	VAL
1	A	513	THR
1	B	74	LEU
1	B	134	LEU
1	B	136	LYS
1	B	164	ILE
1	B	185	VAL
1	B	191	ASP
1	B	195	THR
1	B	203	LEU
1	B	260	GLU
1	B	285	GLU
1	B	328	THR
1	B	339	ARG
1	B	353	LEU
1	B	371	PRO
1	B	399	ARG
1	B	409	THR
1	B	414	VAL
1	B	454	THR
1	B	513	THR
1	C	14	GLN
1	C	106	ARG
1	C	135	LYS
1	C	162	LYS
1	C	173	LYS
1	C	260	GLU

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Mol	Chain	Res	Type
1	C	261	LYS
1	C	272	GLU
1	C	318	ASN
1	C	328	THR
1	C	339	ARG
1	C	367	LYS
1	C	405	THR
1	C	436	ARG
1	C	458	GLN
1	C	480	GLU
1	C	519	SER
1	D	16	GLN
1	D	41	THR
1	D	74	LEU
1	D	132	VAL
1	D	139	THR
1	D	144	LEU
1	D	154	GLU
1	D	180	LEU
1	D	194	VAL
1	D	196	GLU
1	D	261	LYS
1	D	285	GLU
1	D	318	ASN
1	D	336	LYS
1	D	376	ARG
1	D	401	LEU
1	D	409	THR
1	D	436	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	199	ASN
1	C	14	GLN
1	C	44	ASN
1	C	273	ASN

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 ⓘ

6 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	FBP	A	601	-	18,20,20	0.63	0	23,32,32	1.05	0
3	7Y0	B	601	-	37,43,43	0.77	1 (2%)	46,62,62	1.05	1 (2%)
2	FBP	B	602	-	18,20,20	0.66	0	23,32,32	1.06	0
3	7Y0	C	601	-	37,43,43	0.87	1 (2%)	46,62,62	1.13	4 (8%)
2	FBP	C	602	-	18,20,20	0.60	0	23,32,32	0.96	0
2	FBP	D	601	-	18,20,20	0.71	1 (5%)	23,32,32	1.05	1 (4%)

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	FBP	A	601	-	-	0/13/32/32	0/1/1/1
3	7Y0	B	601	-	-	0/17/31/31	0/4/4/4
2	FBP	B	602	-	-	0/13/32/32	0/1/1/1
3	7Y0	C	601	-	-	0/17/31/31	0/4/4/4
2	FBP	C	602	-	-	0/13/32/32	0/1/1/1
2	FBP	D	601	-	-	0/13/32/32	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	601	FBP	O2-C2	2.16	1.44	1.40
3	B	601	7Y0	C24-N32	2.18	1.38	1.33
3	C	601	7Y0	C24-N32	2.82	1.40	1.33

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	601	FBP	P2-O6-C6	2.05	123.94	118.30
3	B	601	7Y0	C11-C17-CL3	2.09	121.95	119.71
3	C	601	7Y0	C8-C14-C22	2.10	131.76	125.34
3	C	601	7Y0	C7-C13-C21	2.10	131.76	125.34
3	C	601	7Y0	C12-C18-CL4	2.14	122.01	119.71
3	C	601	7Y0	C11-C17-CL3	2.26	122.14	119.71

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	518/550 (94%)	-0.31	2 (0%) 92 77	33, 40, 85, 98	0
1	B	501/550 (91%)	-0.33	6 (1%) 79 53	33, 42, 94, 109	1 (0%)
1	C	518/550 (94%)	-0.36	1 (0%) 94 85	33, 42, 65, 88	0
1	D	511/550 (92%)	-0.35	4 (0%) 86 64	33, 42, 87, 103	0
All	All	2048/2200 (93%)	-0.34	13 (0%) 89 71	33, 42, 85, 109	1 (0%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	205	SER	3.6
1	B	123	LEU	3.2
1	D	202	SER	3.1
1	D	147	ALA	2.8
1	B	403	PRO	2.8
1	D	130	ALA	2.4
1	B	156	ILE	2.4
1	B	122	GLY	2.2
1	A	480	GLU	2.2
1	C	217	ASP	2.2
1	D	148	TYR	2.1
1	B	200	GLY	2.1
1	A	217	ASP	2.0

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 [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	7Y0	C	601	40/40	0.95	0.15	-0.61	29,31,39,41	0
3	7Y0	B	601	40/40	0.96	0.14	-0.99	31,32,35,36	0
2	FBP	C	602	20/20	0.97	0.14	-1.05	33,34,37,37	0
2	FBP	A	601	20/20	0.97	0.13	-1.37	31,35,38,38	0
2	FBP	D	601	20/20	0.97	0.12	-1.38	33,35,37,37	0
2	FBP	B	602	20/20	0.97	0.11	-1.56	27,33,38,40	0

6.5 Other polymers [i](#)

There are no such residues in this entry.