



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 06:29 PM UTC

PDB ID : 6GG5 / pdb_00006gg5
Title : Crystal structure of M2 PYK in complex with Tryptophan.
Authors : McNae, I.W.; Yuan, M.; Walkinshaw, M.D.
Deposited on : 2018-05-02
Resolution : 3.20 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

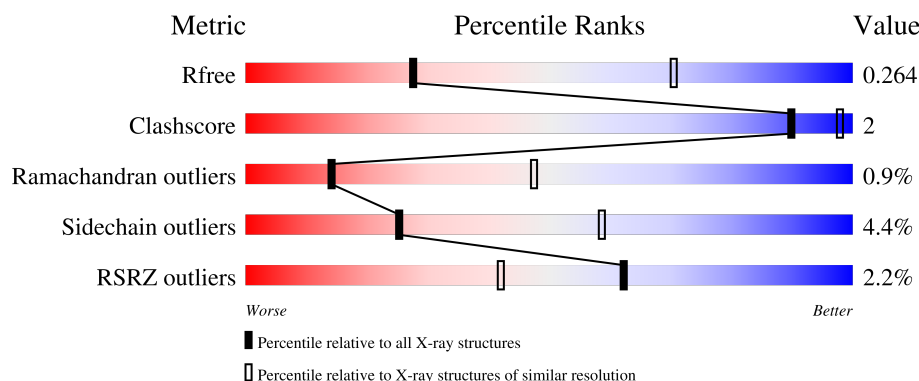
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	551	85% 7% 8%
1	B	551	3% 85% 7% 8%
1	C	551	2% 69% 5% 26%
1	D	551	2% 68% 5% 26%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14263 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	509	Total	C	N	O	S	0	0	0
			3896	2450	690	732	24			
1	B	509	Total	C	N	O	S	0	1	0
			3904	2455	693	732	24			
1	C	410	Total	C	N	O	S	0	2	0
			3169	1990	571	587	21			
1	D	410	Total	C	N	O	S	0	1	0
			3163	1986	571	585	21			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP P14618
A	-18	GLY	-	expression tag	UNP P14618
A	-17	SER	-	expression tag	UNP P14618
A	-16	SER	-	expression tag	UNP P14618
A	-15	HIS	-	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	SER	-	expression tag	UNP P14618
A	-8	SER	-	expression tag	UNP P14618
A	-7	GLY	-	expression tag	UNP P14618
A	-6	LEU	-	expression tag	UNP P14618
A	-5	VAL	-	expression tag	UNP P14618
A	-4	PRO	-	expression tag	UNP P14618
A	-3	ARG	-	expression tag	UNP P14618
A	-2	GLY	-	expression tag	UNP P14618
A	-1	SER	-	expression tag	UNP P14618
A	0	HIS	-	expression tag	UNP P14618
B	-19	MET	-	initiating methionine	UNP P14618

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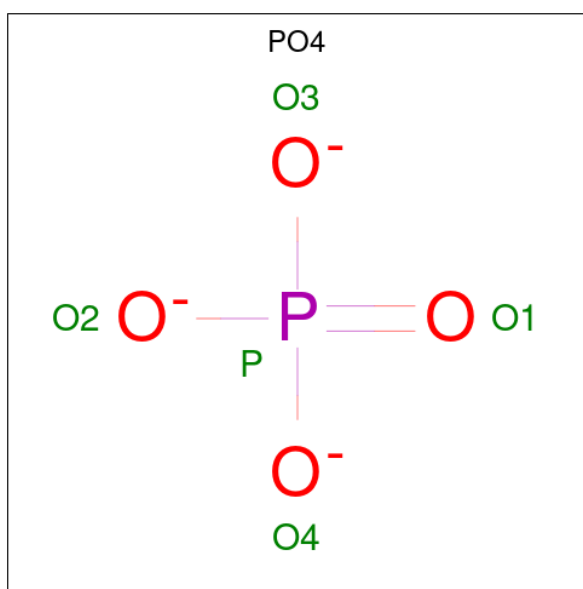
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	expression tag	UNP P14618
B	-17	SER	-	expression tag	UNP P14618
B	-16	SER	-	expression tag	UNP P14618
B	-15	HIS	-	expression tag	UNP P14618
B	-14	HIS	-	expression tag	UNP P14618
B	-13	HIS	-	expression tag	UNP P14618
B	-12	HIS	-	expression tag	UNP P14618
B	-11	HIS	-	expression tag	UNP P14618
B	-10	HIS	-	expression tag	UNP P14618
B	-9	SER	-	expression tag	UNP P14618
B	-8	SER	-	expression tag	UNP P14618
B	-7	GLY	-	expression tag	UNP P14618
B	-6	LEU	-	expression tag	UNP P14618
B	-5	VAL	-	expression tag	UNP P14618
B	-4	PRO	-	expression tag	UNP P14618
B	-3	ARG	-	expression tag	UNP P14618
B	-2	GLY	-	expression tag	UNP P14618
B	-1	SER	-	expression tag	UNP P14618
B	0	HIS	-	expression tag	UNP P14618
C	-19	MET	-	initiating methionine	UNP P14618
C	-18	GLY	-	expression tag	UNP P14618
C	-17	SER	-	expression tag	UNP P14618
C	-16	SER	-	expression tag	UNP P14618
C	-15	HIS	-	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	SER	-	expression tag	UNP P14618
C	-8	SER	-	expression tag	UNP P14618
C	-7	GLY	-	expression tag	UNP P14618
C	-6	LEU	-	expression tag	UNP P14618
C	-5	VAL	-	expression tag	UNP P14618
C	-4	PRO	-	expression tag	UNP P14618
C	-3	ARG	-	expression tag	UNP P14618
C	-2	GLY	-	expression tag	UNP P14618
C	-1	SER	-	expression tag	UNP P14618
C	0	HIS	-	expression tag	UNP P14618
D	-19	MET	-	initiating methionine	UNP P14618
D	-18	GLY	-	expression tag	UNP P14618
D	-17	SER	-	expression tag	UNP P14618

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

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



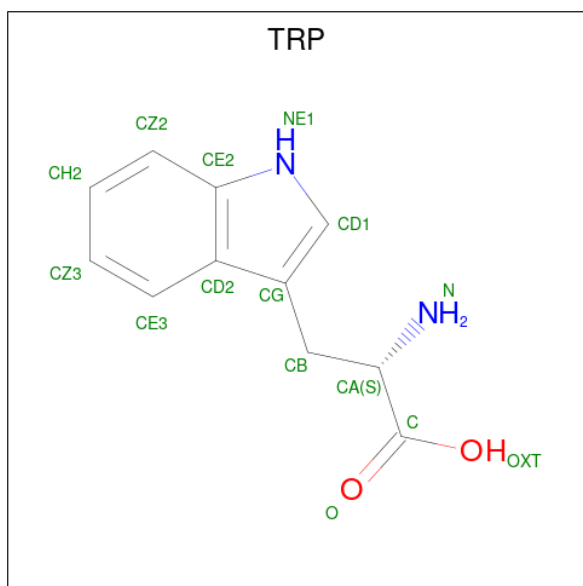
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		

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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		
2	B	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		

- Molecule 3 is TRYPTOPHAN (CCD ID: TRP) (formula: $C_{11}H_{12}N_2O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			15	11	2	2		
3	B	1	Total	C	N	O	0	0
			15	11	2	2		
3	C	1	Total	C	N	O	0	0
			15	11	2	2		
3	D	1	Total	C	N	O	0	0
			15	11	2	2		

- Molecule 4 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total K 1 1	0	0
4	B	1	Total K 1 1	0	0
4	C	1	Total K 1 1	0	0
4	D	1	Total K 1 1	0	0

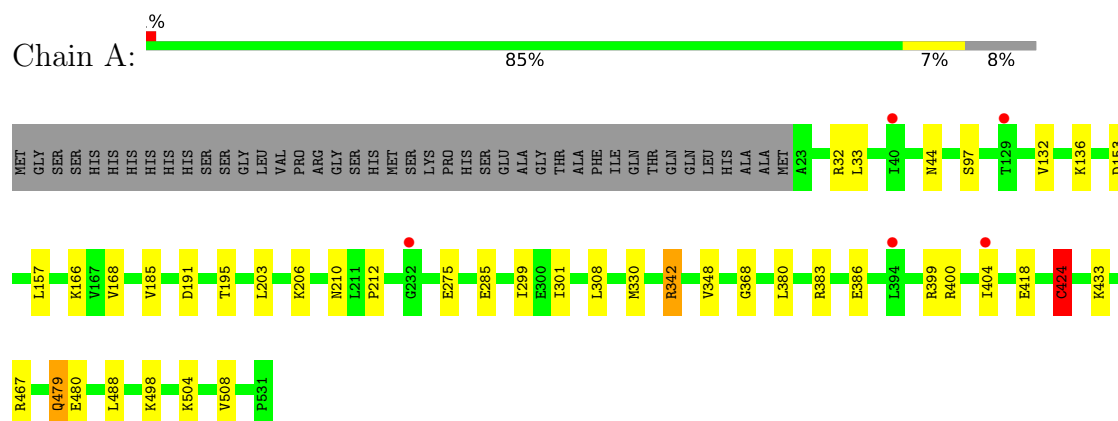
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	9	Total O 9 9	0	0
5	B	3	Total O 3 3	0	0
5	C	11	Total O 11 11	0	0
5	D	4	Total O 4 4	0	0

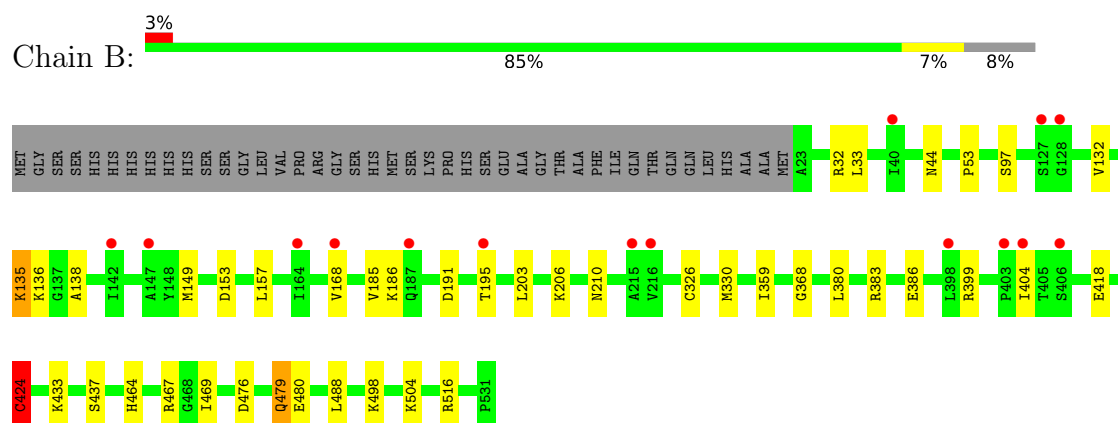
3 Residue-property plots [i](#)

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.

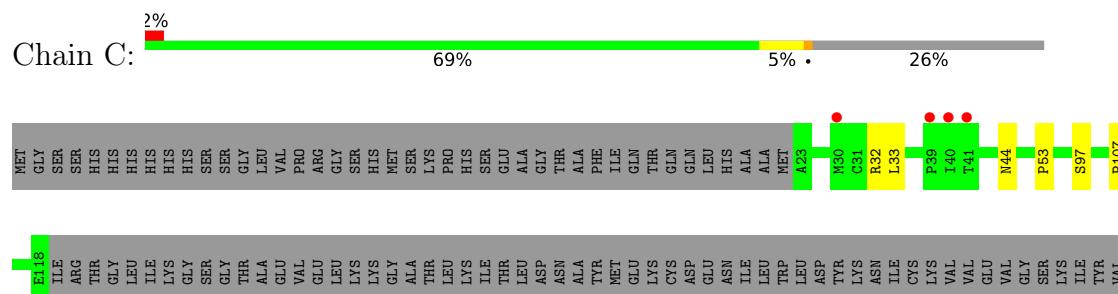
• Molecule 1: Pyruvate kinase PKM

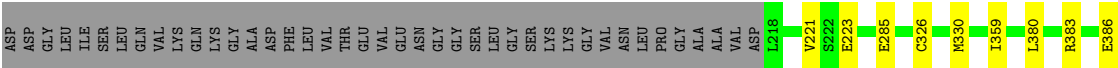


• Molecule 1: Pyruvate kinase PKM

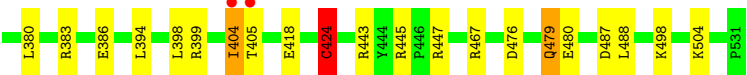
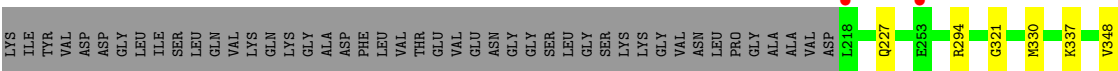
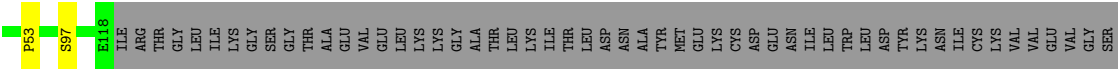
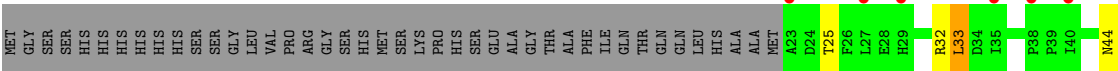


• Molecule 1: Pyruvate kinase PKM





● Molecule 1: Pyruvate kinase PKM



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	96.88Å 70.58Å 168.50Å 90.00° 106.02° 90.00°	Depositor
Resolution (Å)	72.54 – 3.20 72.54 – 3.20	Depositor EDS
% Data completeness (in resolution range)	97.8 (72.54-3.20) 97.8 (72.54-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.56 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.228 , 0.265 0.227 , 0.264	Depositor DCC
R_{free} test set	1769 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	50.7	Xtriage
Anisotropy	0.951	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 39.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.019 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	14263	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.87% 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

5.1 Standard geometry

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

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	0.82	1/3951 (0.0%)	0.97	2/5334 (0.0%)
1	B	0.77	1/3962 (0.0%)	0.94	1/5349 (0.0%)
1	C	0.81	2/3222 (0.1%)	0.97	2/4351 (0.0%)
1	D	0.76	1/3213 (0.0%)	0.95	0/4339
All	All	0.79	5/14348 (0.0%)	0.96	5/19373 (0.0%)

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
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
All	All	0	4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	424	CYS	N-CA	6.19	1.54	1.46
1	A	424	CYS	N-CA	6.18	1.54	1.46
1	C	515	TRP	CA-C	6.05	1.60	1.53
1	D	424	CYS	N-CA	5.82	1.53	1.46
1	B	424	CYS	N-CA	5.50	1.53	1.46

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	368	GLY	N-CA-C	6.26	119.22	112.33
1	B	368	GLY	N-CA-C	5.65	118.55	112.33
1	C	515	TRP	N-CA-C	5.43	119.86	111.56
1	C	500	ARG	CB-CG-CD	5.32	123.54	111.30
1	A	301	ILE	N-CA-CB	-5.29	108.18	111.83

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	424	CYS	Peptide
1	B	424	CYS	Peptide
1	C	424	CYS	Peptide
1	D	424	CYS	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	3896	0	3980	15	0
1	B	3904	0	3994	16	0
1	C	3169	0	3228	12	0
1	D	3163	0	3222	14	0
2	A	15	0	0	0	0
2	B	15	0	0	1	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
3	A	15	0	9	0	0
3	B	15	0	9	2	0
3	C	15	0	9	0	0
3	D	15	0	9	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	9	0	0	0	0
5	B	3	0	0	0	0
5	C	11	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	4	0	0	0	0
All	All	14263	0	14460	51	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 2.

All (51) 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:D:330:MET:HE3	1:D:348:VAL:HG22	1.52	0.88
1:A:330:MET:HE3	1:A:348:VAL:HG22	1.53	0.88
1:A:399:ARG:NH1	1:A:418:GLU:OE1	2.22	0.72
1:B:399:ARG:NH1	1:B:418:GLU:OE1	2.23	0.72
1:A:157:LEU:HD13	1:A:203:LEU:HD21	1.71	0.71
1:D:399:ARG:NH1	1:D:418:GLU:OE1	2.24	0.70
1:A:508:VAL:HG21	1:C:406:SER:HB2	1.72	0.70
1:C:399:ARG:NH1	1:C:418:GLU:OE1	2.25	0.69
1:C:479:GLN:HE21	1:C:479:GLN:HA	1.59	0.67
1:C:482:TRP:CH2	1:C:515:TRP:O	2.47	0.67
1:B:157:LEU:HD13	1:B:203:LEU:HD21	1.75	0.65
1:D:479:GLN:HA	1:D:479:GLN:HE21	1.61	0.63
1:B:479:GLN:HE21	1:B:479:GLN:HA	1.65	0.62
1:B:330:MET:HE3	1:B:359:ILE:HG23	1.86	0.58
1:D:321:GLY:HA3	1:D:443:ARG:HD2	1.86	0.58
1:C:330:MET:HE3	1:C:359:ILE:HG23	1.86	0.56
1:C:326:CYS:HB3	1:C:330:MET:HE1	1.88	0.55
1:B:464:HIS:HD1	3:B:603:TRP:N	2.04	0.55
1:B:326:CYS:HB3	1:B:330:MET:HE1	1.89	0.53
1:A:308:LEU:HD22	1:D:33:LEU:HD13	1.93	0.50
1:C:107:PRO:O	1:C:464:HIS:HE1	1.94	0.49
1:D:394:LEU:HD23	1:D:445[B]:ARG:NH1	2.28	0.49
1:C:480:GLU:HG2	1:C:481:ALA:N	2.26	0.49
1:A:212:PRO:HG3	1:A:299:ILE:HG22	1.95	0.48
1:C:482:TRP:CZ3	1:C:515:TRP:O	2.66	0.48
1:D:330:MET:CE	1:D:348:VAL:HG22	2.36	0.48
1:B:185:VAL:HA	1:B:195:THR:HG22	1.96	0.48
1:A:330:MET:CE	1:A:348:VAL:HG22	2.37	0.47
1:A:185:VAL:HA	1:A:195:THR:HG22	1.97	0.46
1:A:342:ARG:HD2	1:D:294:ARG:HB3	1.97	0.45
1:B:469:ILE:O	3:B:603:TRP:N	2.50	0.45
1:C:386:GLU:OE1	1:C:467:ARG:NH2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:LEU:CD1	1:A:203:LEU:HD21	2.44	0.45
1:B:326:CYS:HB3	1:B:330:MET:CE	2.47	0.44
1:C:476:ASP:OD2	1:C:488:LEU:HD21	2.17	0.44
1:D:476:ASP:OD2	1:D:488:LEU:HD21	2.18	0.43
1:B:476:ASP:OD2	1:B:488:LEU:HD21	2.18	0.43
1:B:386:GLU:OE1	1:B:467:ARG:NH2	2.50	0.43
1:A:479:GLN:HE21	1:A:479:GLN:HB3	1.64	0.42
1:C:326:CYS:HB3	1:C:330:MET:CE	2.48	0.42
1:B:516:ARG:NH1	1:D:487:ASP:OD2	2.52	0.42
1:D:386:GLU:OE1	1:D:467:ARG:NH2	2.51	0.42
1:A:308:LEU:CD2	1:D:33:LEU:HD13	2.49	0.42
1:B:157:LEU:CD1	1:B:203:LEU:HD21	2.46	0.42
1:B:437:SER:OG	2:B:601:PO4:O1	2.30	0.41
1:A:400:ARG:NH2	1:D:25:THR:HG22	2.34	0.41
1:A:386:GLU:OE1	1:A:467:ARG:NH2	2.50	0.41
1:A:132:VAL:HG11	1:A:153:ASP:HA	2.03	0.41
1:D:394:LEU:O	1:D:398:LEU:HD12	2.21	0.41
1:B:135:LYS:HD3	1:B:138:ALA:HB2	2.03	0.41
1:B:132:VAL:HG11	1:B:153:ASP:HA	2.04	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	506/551 (92%)	485 (96%)	17 (3%)	4 (1%)	16	50
1	B	507/551 (92%)	483 (95%)	19 (4%)	5 (1%)	12	45
1	C	407/551 (74%)	392 (96%)	12 (3%)	3 (1%)	18	52
1	D	406/551 (74%)	392 (97%)	10 (2%)	4 (1%)	12	45
All	All	1826/2204 (83%)	1752 (96%)	58 (3%)	16 (1%)	14	47

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	424	CYS
1	B	424	CYS
1	C	424	CYS
1	D	424	CYS
1	A	33	LEU
1	B	33	LEU
1	C	33	LEU
1	D	33	LEU
1	D	404	ILE
1	A	206	LYS
1	B	206	LYS
1	B	404	ILE
1	A	404	ILE
1	C	53	PRO
1	B	53	PRO
1	D	53	PRO

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	418/452 (92%)	398 (95%)	20 (5%)	23	56
1	B	419/452 (93%)	401 (96%)	18 (4%)	26	59
1	C	339/452 (75%)	325 (96%)	14 (4%)	27	60
1	D	338/452 (75%)	323 (96%)	15 (4%)	25	59
All	All	1514/1808 (84%)	1447 (96%)	67 (4%)	25	59

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	ARG
1	A	44	ASN
1	A	97	SER
1	A	136	LYS

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Mol	Chain	Res	Type
1	A	166	LYS
1	A	168	VAL
1	A	191	ASP
1	A	210	ASN
1	A	275	GLU
1	A	285	GLU
1	A	342	ARG
1	A	380	LEU
1	A	383	ARG
1	A	424	CYS
1	A	433	LYS
1	A	479	GLN
1	A	480	GLU
1	A	488	LEU
1	A	498	LYS
1	A	504	LYS
1	B	32	ARG
1	B	44	ASN
1	B	97	SER
1	B	135	LYS
1	B	136	LYS
1	B	149	MET
1	B	168	VAL
1	B	186	LYS
1	B	191	ASP
1	B	210	ASN
1	B	380	LEU
1	B	383	ARG
1	B	424	CYS
1	B	433	LYS
1	B	479	GLN
1	B	480	GLU
1	B	498	LYS
1	B	504	LYS
1	C	32	ARG
1	C	44	ASN
1	C	97	SER
1	C	221	VAL
1	C	223	GLU
1	C	285	GLU
1	C	380	LEU
1	C	383	ARG

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Mol	Chain	Res	Type
1	C	418	GLU
1	C	424	CYS
1	C	443	ARG
1	C	479	GLN
1	C	480	GLU
1	C	504	LYS
1	D	32	ARG
1	D	44	ASN
1	D	97	SER
1	D	227	GLN
1	D	337	LYS
1	D	380	LEU
1	D	383	ARG
1	D	404	ILE
1	D	405	THR
1	D	424	CYS
1	D	447	ARG
1	D	479	GLN
1	D	480	GLU
1	D	498	LYS
1	D	504	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	184	GLN
1	A	318	ASN
1	A	393	GLN
1	A	479	GLN
1	B	184	GLN
1	B	199	ASN
1	B	210	ASN
1	B	393	GLN
1	B	479	GLN
1	C	393	GLN
1	C	464	HIS
1	C	479	GLN
1	D	479	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	CSO	B	474	1	3,6,7	0.58	0	1,6,8	0.23	0
1	CSO	A	474	1	3,6,7	0.76	0	1,6,8	0.78	0
1	CSO	D	474	1	3,6,7	0.73	0	1,6,8	0.23	0
1	CSO	C	474	1	3,6,7	0.70	0	1,6,8	0.53	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
1	CSO	B	474	1	-	0/1/5/7	-
1	CSO	A	474	1	-	0/1/5/7	-
1	CSO	D	474	1	-	0/1/5/7	-
1	CSO	C	474	1	-	0/1/5/7	-

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.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 4 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	$\# Z > 2$
3	TRP	C	602	-	15,16,16	0.98	1 (6%)	18,22,22	1.06	1 (5%)
2	PO4	D	601	-	4,4,4	0.72	0	6,6,6	1.53	2 (33%)
2	PO4	A	602	-	4,4,4	0.76	0	6,6,6	0.97	0
2	PO4	C	601	-	4,4,4	1.03	0	6,6,6	0.85	0
3	TRP	D	602	-	15,16,16	1.04	2 (13%)	18,22,22	0.97	1 (5%)
2	PO4	B	604	-	4,4,4	1.23	0	6,6,6	0.56	0
2	PO4	B	601	-	4,4,4	0.94	0	6,6,6	0.69	0
3	TRP	A	603	-	15,16,16	0.80	1 (6%)	18,22,22	1.03	1 (5%)
2	PO4	A	604	-	4,4,4	0.81	0	6,6,6	0.56	0
2	PO4	A	601	-	4,4,4	1.43	0	6,6,6	1.20	0
2	PO4	B	602	-	4,4,4	0.82	0	6,6,6	0.52	0
3	TRP	B	603	-	15,16,16	1.11	1 (6%)	18,22,22	1.06	2 (11%)

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	TRP	C	602	-	-	0/8/8/8	0/2/2/2
3	TRP	D	602	-	-	0/8/8/8	0/2/2/2
3	TRP	B	603	-	-	0/8/8/8	0/2/2/2
3	TRP	A	603	-	-	0/8/8/8	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	603	TRP	OXT-C	-2.91	1.21	1.30
3	A	603	TRP	OXT-C	-2.31	1.23	1.30
3	D	602	TRP	CB-CG	-2.31	1.45	1.50
3	D	602	TRP	OXT-C	-2.20	1.23	1.30
3	C	602	TRP	OXT-C	-2.11	1.23	1.30

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	603	TRP	OXT-C-O	-3.79	115.47	124.08
3	C	602	TRP	OXT-C-O	-3.67	115.76	124.08
3	D	602	TRP	OXT-C-O	-3.45	116.25	124.08
3	B	603	TRP	OXT-C-O	-2.83	117.67	124.08
2	D	601	PO4	O4-P-O1	-2.71	101.38	110.95
2	D	601	PO4	O4-P-O2	2.56	115.88	107.91
3	B	603	TRP	CA-CB-CG	2.56	118.35	113.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	PO4	1	0
3	B	603	TRP	2	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	508/551 (92%)	0.14	5 (0%) 79 63	36, 51, 89, 110	0
1	B	508/551 (92%)	0.34	15 (2%) 52 33	30, 60, 111, 137	1 (0%)
1	C	409/551 (74%)	0.09	11 (2%) 56 36	21, 46, 91, 118	2 (0%)
1	D	409/551 (74%)	0.14	10 (2%) 59 40	27, 54, 103, 125	1 (0%)
All	All	1834/2204 (83%)	0.19	41 (2%) 62 42	21, 53, 103, 137	4 (0%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	127	SER	3.9
1	B	128	GLY	3.7
1	C	39	PRO	3.1
1	B	215	ALA	3.1
1	B	404	ILE	3.1
1	C	404	ILE	2.8
1	D	404	ILE	2.8
1	A	394	LEU	2.7
1	A	40	ILE	2.7
1	D	405	THR	2.7
1	B	187	GLN	2.6
1	B	164	ILE	2.6
1	B	406	SER	2.6
1	C	406	SER	2.6
1	C	41	THR	2.6
1	B	403	PRO	2.5
1	B	168	VAL	2.5
1	B	142	ILE	2.5
1	D	218	LEU	2.5
1	B	147	ALA	2.5
1	A	404	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	40	ILE	2.4
1	C	40	ILE	2.3
1	C	30	MET	2.2
1	C	402	ALA	2.2
1	A	129	THR	2.2
1	D	35	ILE	2.2
1	A	232	GLY	2.2
1	C	392	LEU	2.2
1	B	216	VAL	2.2
1	D	23	ALA	2.2
1	C	394	LEU	2.1
1	C	403	PRO	2.1
1	D	29	HIS	2.1
1	B	40	ILE	2.1
1	D	27	LEU	2.1
1	D	253	GLU	2.1
1	D	38	PRO	2.1
1	B	195	THR	2.1
1	C	424	CYS	2.1
1	B	398	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	CSO	B	474	7/8	0.86	0.11	58,62,64,64	0
1	CSO	A	474	7/8	0.87	0.13	47,49,52,52	0
1	CSO	D	474	7/8	0.95	0.08	53,54,57,57	0
1	CSO	C	474	7/8	0.96	0.07	40,42,43,44	0

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
2	PO4	B	604	5/5	0.75	0.17	93,94,94,94	0
4	K	C	603	1/1	0.78	0.12	66,66,66,66	0
2	PO4	B	602	5/5	0.79	0.13	99,99,101,101	0
2	PO4	A	602	5/5	0.82	0.12	80,81,81,82	0
2	PO4	A	604	5/5	0.84	0.12	93,95,96,97	0
4	K	D	603	1/1	0.86	0.09	79,79,79,79	0
3	TRP	D	602	15/15	0.93	0.10	48,49,50,50	0
3	TRP	A	603	15/15	0.93	0.12	42,42,43,43	0
3	TRP	B	603	15/15	0.93	0.10	45,46,46,46	0
3	TRP	C	602	15/15	0.94	0.11	29,29,30,30	0
4	K	B	605	1/1	0.94	0.05	61,61,61,61	0
2	PO4	A	601	5/5	0.95	0.08	48,48,48,48	0
2	PO4	D	601	5/5	0.96	0.08	39,40,40,40	0
2	PO4	B	601	5/5	0.96	0.08	51,51,52,52	0
4	K	A	605	1/1	0.98	0.04	45,45,45,45	0
2	PO4	C	601	5/5	0.98	0.06	34,35,35,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.