



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:35 PM UTC

PDB ID : 4JX6 / pdb_00004jx6
Title : Structure of the carboxyl transferase domain Y628A from *Rhizobium etli* pyruvate carboxylase with pyruvate
Authors : Lietzan, A.D.; St Maurice, M.
Deposited on : 2013-03-27
Resolution : 2.78 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

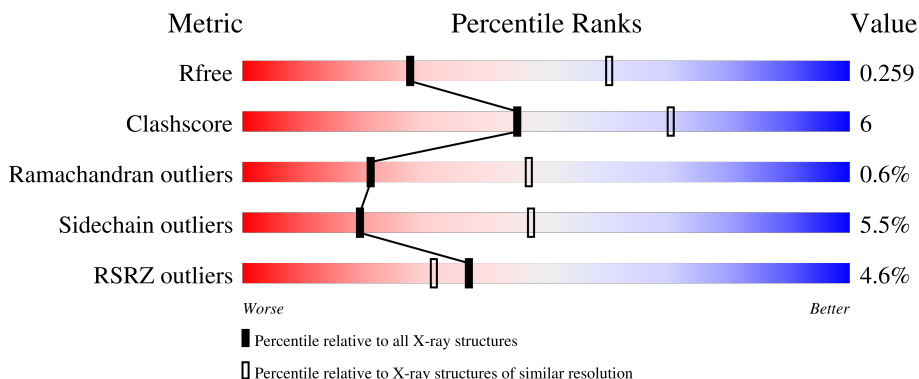
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.78 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	5248 (2.80-2.76)
Clashscore	190562	5693 (2.80-2.76)
Ramachandran outliers	187476	5590 (2.80-2.76)
Sidechain outliers	187428	5592 (2.80-2.76)
RSRZ outliers	180081	5251 (2.80-2.76)

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	632	
1	B	632	
1	C	632	
1	D	632	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 17344 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 carboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	595	Total	C	N	O	S	0	1	0
			4456	2841	739	853	23			
1	B	593	Total	C	N	O	S	0	0	0
			4342	2745	729	846	22			
1	C	588	Total	C	N	O	S	0	1	0
			4247	2691	712	822	22			
1	D	584	Total	C	N	O	S	0	0	0
			4213	2665	706	820	22			

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	436	MET	-	expression tag	UNP Q2K340
A	437	GLY	-	expression tag	UNP Q2K340
A	438	SER	-	expression tag	UNP Q2K340
A	439	SER	-	expression tag	UNP Q2K340
A	440	HIS	-	expression tag	UNP Q2K340
A	441	HIS	-	expression tag	UNP Q2K340
A	442	HIS	-	expression tag	UNP Q2K340
A	443	HIS	-	expression tag	UNP Q2K340
A	444	HIS	-	expression tag	UNP Q2K340
A	445	HIS	-	expression tag	UNP Q2K340
A	446	HIS	-	expression tag	UNP Q2K340
A	447	HIS	-	expression tag	UNP Q2K340
A	448	ASP	-	expression tag	UNP Q2K340
A	449	TYR	-	expression tag	UNP Q2K340
A	450	ASP	-	expression tag	UNP Q2K340
A	451	ILE	-	expression tag	UNP Q2K340
A	452	PRO	-	expression tag	UNP Q2K340
A	453	THR	-	expression tag	UNP Q2K340
A	454	SER	-	expression tag	UNP Q2K340
A	455	GLU	-	expression tag	UNP Q2K340
A	456	ASN	-	expression tag	UNP Q2K340

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Chain	Residue	Modelled	Actual	Comment	Reference
A	457	LEU	-	expression tag	UNP Q2K340
A	458	TYR	-	expression tag	UNP Q2K340
A	459	PHE	-	expression tag	UNP Q2K340
A	460	GLN	-	expression tag	UNP Q2K340
A	461	GLY	-	expression tag	UNP Q2K340
A	462	LEU	-	expression tag	UNP Q2K340
A	463	LEU	-	expression tag	UNP Q2K340
A	464	HIS	-	expression tag	UNP Q2K340
A	628	ALA	TYR	engineered mutation	UNP Q2K340
B	436	MET	-	expression tag	UNP Q2K340
B	437	GLY	-	expression tag	UNP Q2K340
B	438	SER	-	expression tag	UNP Q2K340
B	439	SER	-	expression tag	UNP Q2K340
B	440	HIS	-	expression tag	UNP Q2K340
B	441	HIS	-	expression tag	UNP Q2K340
B	442	HIS	-	expression tag	UNP Q2K340
B	443	HIS	-	expression tag	UNP Q2K340
B	444	HIS	-	expression tag	UNP Q2K340
B	445	HIS	-	expression tag	UNP Q2K340
B	446	HIS	-	expression tag	UNP Q2K340
B	447	HIS	-	expression tag	UNP Q2K340
B	448	ASP	-	expression tag	UNP Q2K340
B	449	TYR	-	expression tag	UNP Q2K340
B	450	ASP	-	expression tag	UNP Q2K340
B	451	ILE	-	expression tag	UNP Q2K340
B	452	PRO	-	expression tag	UNP Q2K340
B	453	THR	-	expression tag	UNP Q2K340
B	454	SER	-	expression tag	UNP Q2K340
B	455	GLU	-	expression tag	UNP Q2K340
B	456	ASN	-	expression tag	UNP Q2K340
B	457	LEU	-	expression tag	UNP Q2K340
B	458	TYR	-	expression tag	UNP Q2K340
B	459	PHE	-	expression tag	UNP Q2K340
B	460	GLN	-	expression tag	UNP Q2K340
B	461	GLY	-	expression tag	UNP Q2K340
B	462	LEU	-	expression tag	UNP Q2K340
B	463	LEU	-	expression tag	UNP Q2K340
B	464	HIS	-	expression tag	UNP Q2K340
B	628	ALA	TYR	engineered mutation	UNP Q2K340
C	436	MET	-	expression tag	UNP Q2K340
C	437	GLY	-	expression tag	UNP Q2K340
C	438	SER	-	expression tag	UNP Q2K340

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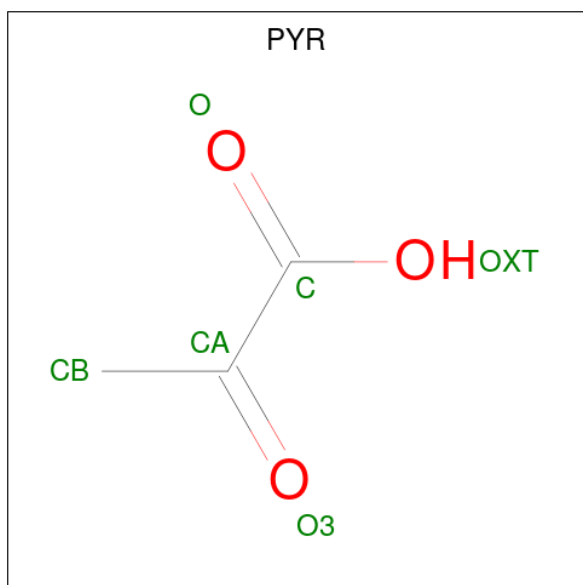
Chain	Residue	Modelled	Actual	Comment	Reference
C	439	SER	-	expression tag	UNP Q2K340
C	440	HIS	-	expression tag	UNP Q2K340
C	441	HIS	-	expression tag	UNP Q2K340
C	442	HIS	-	expression tag	UNP Q2K340
C	443	HIS	-	expression tag	UNP Q2K340
C	444	HIS	-	expression tag	UNP Q2K340
C	445	HIS	-	expression tag	UNP Q2K340
C	446	HIS	-	expression tag	UNP Q2K340
C	447	HIS	-	expression tag	UNP Q2K340
C	448	ASP	-	expression tag	UNP Q2K340
C	449	TYR	-	expression tag	UNP Q2K340
C	450	ASP	-	expression tag	UNP Q2K340
C	451	ILE	-	expression tag	UNP Q2K340
C	452	PRO	-	expression tag	UNP Q2K340
C	453	THR	-	expression tag	UNP Q2K340
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C	457	LEU	-	expression tag	UNP Q2K340
C	458	TYR	-	expression tag	UNP Q2K340
C	459	PHE	-	expression tag	UNP Q2K340
C	460	GLN	-	expression tag	UNP Q2K340
C	461	GLY	-	expression tag	UNP Q2K340
C	462	LEU	-	expression tag	UNP Q2K340
C	463	LEU	-	expression tag	UNP Q2K340
C	464	HIS	-	expression tag	UNP Q2K340
C	628	ALA	TYR	engineered mutation	UNP Q2K340
D	436	MET	-	expression tag	UNP Q2K340
D	437	GLY	-	expression tag	UNP Q2K340
D	438	SER	-	expression tag	UNP Q2K340
D	439	SER	-	expression tag	UNP Q2K340
D	440	HIS	-	expression tag	UNP Q2K340
D	441	HIS	-	expression tag	UNP Q2K340
D	442	HIS	-	expression tag	UNP Q2K340
D	443	HIS	-	expression tag	UNP Q2K340
D	444	HIS	-	expression tag	UNP Q2K340
D	445	HIS	-	expression tag	UNP Q2K340
D	446	HIS	-	expression tag	UNP Q2K340
D	447	HIS	-	expression tag	UNP Q2K340
D	448	ASP	-	expression tag	UNP Q2K340
D	449	TYR	-	expression tag	UNP Q2K340
D	450	ASP	-	expression tag	UNP Q2K340

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Chain	Residue	Modelled	Actual	Comment	Reference
D	451	ILE	-	expression tag	UNP Q2K340
D	452	PRO	-	expression tag	UNP Q2K340
D	453	THR	-	expression tag	UNP Q2K340
D	454	SER	-	expression tag	UNP Q2K340
D	455	GLU	-	expression tag	UNP Q2K340
D	456	ASN	-	expression tag	UNP Q2K340
D	457	LEU	-	expression tag	UNP Q2K340
D	458	TYR	-	expression tag	UNP Q2K340
D	459	PHE	-	expression tag	UNP Q2K340
D	460	GLN	-	expression tag	UNP Q2K340
D	461	GLY	-	expression tag	UNP Q2K340
D	462	LEU	-	expression tag	UNP Q2K340
D	463	LEU	-	expression tag	UNP Q2K340
D	464	HIS	-	expression tag	UNP Q2K340
D	628	ALA	TYR	engineered mutation	UNP Q2K340

- Molecule 2 is PYRUVIC ACID (CCD ID: PYR) (formula: $C_3H_4O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		

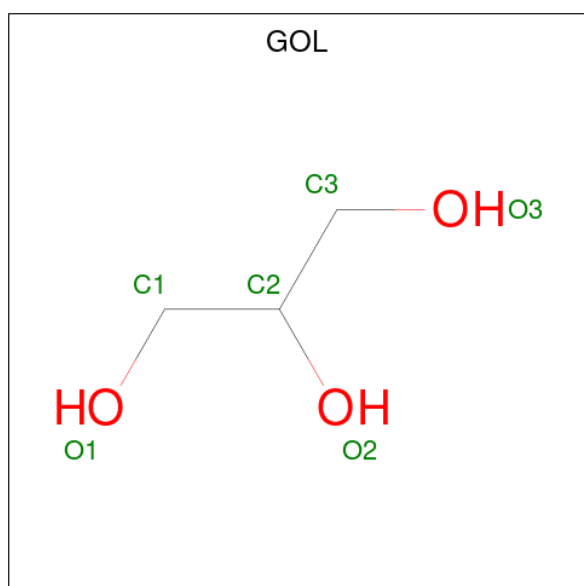
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		
3	B	1	Total	Zn	0	0
			1	1		
3	C	1	Total	Zn	0	0
			1	1		
3	D	1	Total	Zn	0	0
			1	1		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is water.

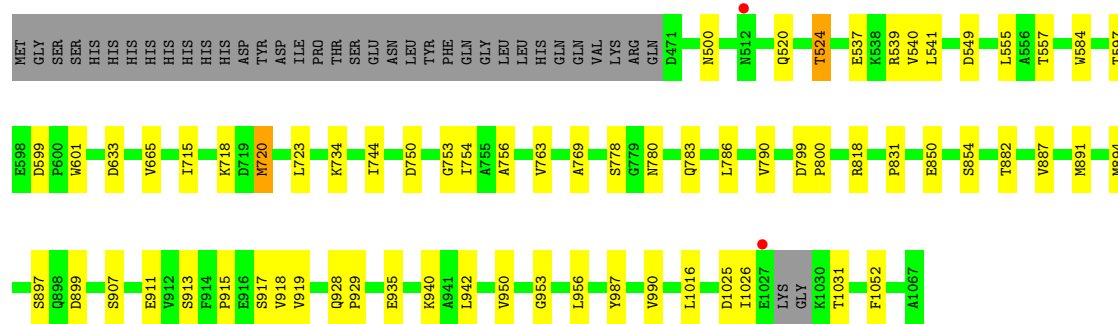
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	28	Total 28	O 28	0	0
6	B	12	Total 12	O 12	0	0
6	C	12	Total 12	O 12	0	0
6	D	8	Total 8	O 8	0	0

3 Residue-property plots

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.

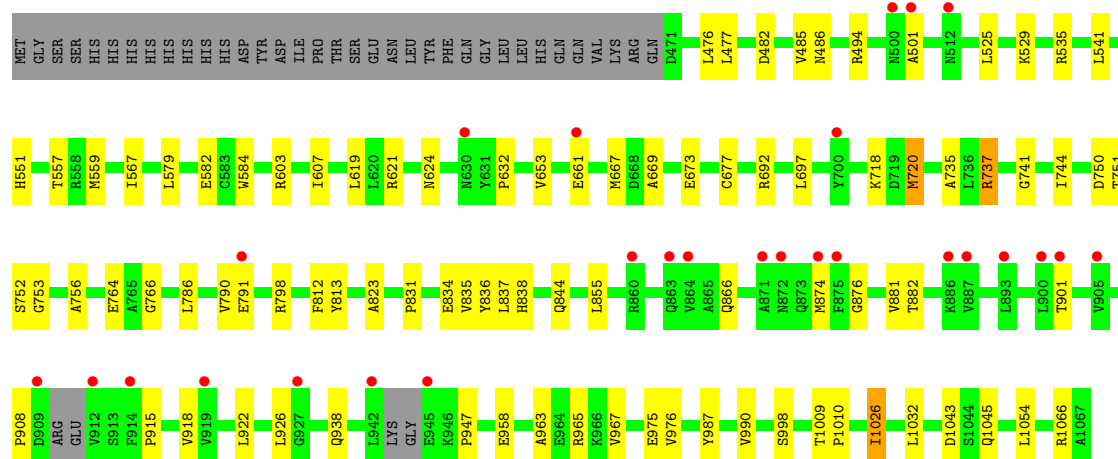
• Molecule 1: Pyruvate carboxylase

Chain A: 



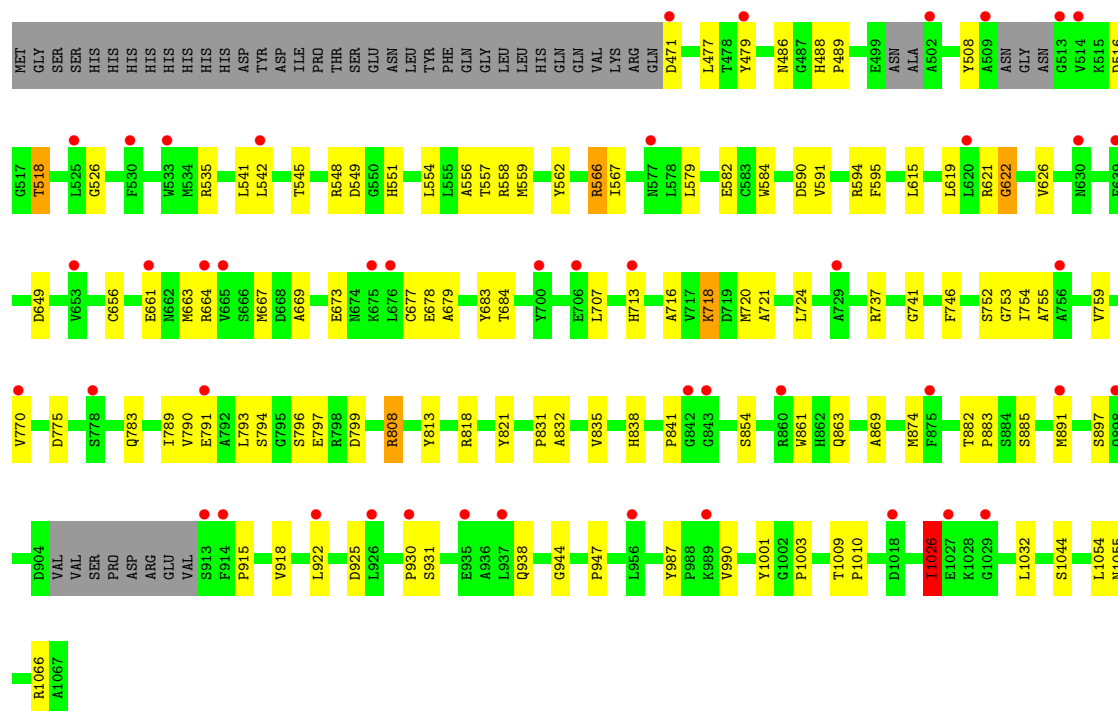
• Molecule 1: Pyruvate carboxylase

Chain B: 



• Molecule 1: Pyruvate carboxylase

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	84.81Å 157.28Å 245.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.78 50.00 – 2.78	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.00-2.78) 99.9 (50.00-2.78)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.01 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.209 , 0.258 0.211 , 0.259	Depositor DCC
R_{free} test set	4195 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	61.2	Xtriage
Anisotropy	0.023	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 75.3	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	0.94	EDS
Total number of atoms	17344	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.28% 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: GOL, MG, ZN, KCX, PYR

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	0.84	0/4542	1.01	3/6192 (0.0%)
1	B	0.73	0/4420	0.97	0/6040
1	C	0.78	1/4329 (0.0%)	0.98	8/5919 (0.1%)
1	D	0.69	0/4292	0.96	6/5872 (0.1%)
All	All	0.77	1/17583 (0.0%)	0.98	17/24023 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	573	HIS	CG-CD2	5.34	1.41	1.35

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	951	ARG	CA-C-N	6.96	127.26	119.32
1	C	951	ARG	C-N-CA	6.96	127.26	119.32
1	C	878	ILE	N-CA-C	6.72	118.51	108.96
1	C	599	ASP	CA-C-N	-6.32	113.26	119.64
1	C	599	ASP	C-N-CA	-6.32	113.26	119.64
1	D	755	ALA	N-CA-C	6.13	118.75	111.33
1	D	591	VAL	N-CA-C	5.96	116.74	110.72
1	A	723	LEU	N-CA-C	-5.87	106.66	113.88
1	A	1052	PHE	N-CA-C	5.62	119.25	110.32
1	D	925	ASP	N-CA-C	5.59	117.46	111.36
1	C	768	ASP	N-CA-C	5.40	117.25	111.36
1	A	720	MET	N-CA-C	5.39	117.91	111.71
1	C	542	LEU	N-CA-C	5.24	117.79	109.24
1	D	526	GLY	CA-C-N	5.19	124.37	118.97
1	D	526	GLY	C-N-CA	5.19	124.37	118.97
1	D	626	VAL	N-CA-C	-5.04	108.21	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	712	ALA	N-CA-C	5.00	117.42	109.96

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	A	4456	0	4275	30	0
1	B	4342	0	4040	51	0
1	C	4247	0	3886	58	0
1	D	4213	0	3833	66	0
2	A	6	0	0	0	0
2	B	6	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	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	C	6	0	8	3	0
6	A	28	0	0	0	0
6	B	12	0	0	3	0
6	C	12	0	0	0	0
6	D	8	0	0	0	0
All	All	17344	0	16042	198	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 6.

All (198) 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:677:CYS:H	1:D:713:HIS:CD2	1.81	0.97
1:C:883:PRO:HG2	1:C:926:LEU:HD21	1.45	0.95
1:C:566:ARG:CG	1:C:566:ARG:HH11	1.80	0.93
1:D:677:CYS:H	1:D:713:HIS:HD2	0.94	0.93
1:C:677:CYS:H	1:C:713:HIS:HD2	1.16	0.91
1:A:891[B]:MET:CE	1:A:918:VAL:HG21	2.01	0.89
1:C:566:ARG:HH11	1:C:566:ARG:HG2	1.35	0.89
1:A:891[B]:MET:HE3	1:A:918:VAL:HG21	1.61	0.80
1:D:793:LEU:O	1:D:796:SER:HB3	1.82	0.79
1:C:790:VAL:HG13	1:C:800:PRO:HG2	1.64	0.78
1:D:619:LEU:HD11	1:D:718:KCX:HE2	1.71	0.73
1:D:677:CYS:N	1:D:713:HIS:HD2	1.78	0.72
1:C:566:ARG:HG2	1:C:566:ARG:NH1	1.97	0.70
1:C:679:ALA:HB1	1:C:707:LEU:HD13	1.74	0.69
1:C:562:TYR:O	1:C:566:ARG:HG3	1.93	0.68
1:C:677:CYS:H	1:C:713:HIS:CD2	2.06	0.68
1:A:953:GLY:HA2	1:A:956:LEU:HD12	1.74	0.68
1:B:764:GLU:HA	1:B:764:GLU:OE1	1.93	0.68
1:B:938:GLN:HE22	1:B:947:PRO:HG3	1.58	0.67
1:B:482:ASP:OD2	1:B:1066:ARG:NH2	2.28	0.67
1:B:619:LEU:HD13	6:B:1211:HOH:O	1.94	0.67
1:B:1043:ASP:OD1	1:B:1043:ASP:C	2.39	0.66
1:A:891[B]:MET:HA	1:A:891[B]:MET:HE2	1.77	0.64
1:D:549:ASP:HB3	1:D:783:GLN:HE22	1.63	0.64
1:C:520:GLN:O	1:C:524:THR:CG2	2.46	0.64
1:C:901:THR:O	1:C:904:ASP:HB2	1.97	0.63
1:C:664:ARG:HH21	1:C:710:ALA:HA	1.62	0.63
1:A:780:ASN:H	5:C:1101:GOL:H12	1.64	0.62
1:D:548:ARG:HB3	1:D:582:GLU:OE1	2.00	0.62
1:C:629:THR:OG1	1:C:630:ASN:N	2.32	0.61
1:D:679:ALA:HB1	1:D:707:LEU:HD22	1.81	0.61
1:C:621:ARG:O	1:C:623:ALA:N	2.34	0.61
1:D:486:ASN:HD21	1:D:1066:ARG:H	1.49	0.61
1:B:756:ALA:CB	1:D:754:ILE:HG22	2.32	0.60
1:C:928:GLN:NE2	1:C:949:THR:HA	2.17	0.59
1:B:1026:ILE:HG12	1:B:1032:LEU:CD1	2.32	0.59
1:D:558:ARG:O	1:D:821:TYR:HE1	1.86	0.59
1:D:535:ARG:HD3	1:D:741:GLY:O	2.02	0.59
1:C:679:ALA:CB	1:C:707:LEU:HD13	2.32	0.58
1:A:555:LEU:HD11	1:A:818:ARG:HG3	1.85	0.58
1:B:486:ASN:ND2	1:B:1066:ARG:H	2.01	0.58
1:D:566:ARG:HH11	1:D:566:ARG:CG	2.16	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:844:GLN:O	1:B:844:GLN:HG2	2.03	0.57
1:A:894:MET:HE1	1:A:913:SER:O	2.05	0.57
1:B:567:ILE:HD13	1:B:813:TYR:CD2	2.40	0.56
1:C:566:ARG:HH11	1:C:566:ARG:HG3	1.65	0.56
1:A:799:ASP:OD1	1:A:800:PRO:HD2	2.06	0.56
1:B:1026:ILE:HG12	1:B:1032:LEU:HD11	1.87	0.55
1:C:597:THR:HB	1:C:1004:VAL:HG21	1.89	0.55
1:A:778:SER:OG	1:C:831:PRO:HG2	2.07	0.55
1:C:664:ARG:NH2	1:C:710:ALA:HA	2.22	0.55
1:C:520:GLN:O	1:C:524:THR:HG23	2.06	0.54
1:B:836:TYR:CD2	1:D:791:GLU:HG2	2.42	0.54
1:B:744:ILE:HG13	6:B:1207:HOH:O	2.07	0.54
1:B:922:LEU:HB3	1:B:938:GLN:HG3	1.90	0.53
1:D:488:HIS:ND1	1:D:489:PRO:HD2	2.23	0.53
1:B:915:PRO:HB2	1:B:918:VAL:HG23	1.90	0.53
1:D:938:GLN:NE2	1:D:947:PRO:HB3	2.24	0.53
1:D:518:THR:HB	1:D:615:LEU:HG	1.92	0.52
1:B:720:MET:HG3	1:B:881:VAL:HG23	1.92	0.52
1:C:549:ASP:HB3	1:C:783:GLN:HE22	1.74	0.52
1:C:554:LEU:HD12	1:C:777:LEU:HD23	1.92	0.52
1:A:919:VAL:HG13	1:A:942:LEU:HD23	1.91	0.52
1:A:633:ASP:OD1	1:A:665:VAL:HG21	2.09	0.52
1:A:750:ASP:OD2	5:C:1101:GOL:O1	2.26	0.52
1:B:535:ARG:HD3	1:B:741:GLY:O	2.09	0.52
1:C:618:MET:HB3	1:C:648:ILE:HD12	1.92	0.52
1:B:494:ARG:HD2	1:B:823:ALA:O	2.09	0.51
1:A:891[B]:MET:HE1	1:A:915:PRO:HD2	1.92	0.51
1:C:520:GLN:O	1:C:524:THR:HG22	2.09	0.51
1:D:479:TYR:HB2	1:D:1001:TYR:HB3	1.92	0.51
1:C:1021:GLU:CG	1:C:1035:VAL:HG22	2.41	0.51
1:D:615:LEU:HA	1:D:649:ASP:OD2	2.11	0.51
1:A:549:ASP:HB3	1:A:783:GLN:HE22	1.76	0.51
1:B:874:MET:C	1:B:876:GLY:H	2.20	0.50
1:B:535:ARG:HD2	1:B:737:ARG:NH1	2.27	0.50
1:C:660:VAL:HG13	1:C:707:LEU:HD23	1.93	0.50
1:B:621:ARG:HB2	1:B:624:ASN:HB2	1.93	0.49
1:D:753:GLY:HA3	1:D:831:PRO:HB3	1.94	0.49
1:B:632:PRO:HB3	1:B:958:GLU:HA	1.93	0.49
1:A:907:SER:O	1:A:940:LYS:NZ	2.37	0.49
1:C:539:ARG:HG3	1:C:539:ARG:O	2.12	0.49
1:D:566:ARG:CG	1:D:566:ARG:NH1	2.74	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:697:LEU:HD11	1:B:735:ALA:CB	2.43	0.49
1:D:683:TYR:CE1	1:D:724:LEU:HD13	2.48	0.49
1:C:987:TYR:HB3	1:C:990:VAL:HB	1.94	0.48
1:D:542:LEU:HD13	1:D:770:VAL:HG23	1.95	0.48
1:D:554:LEU:HD13	1:D:818:ARG:HH21	1.79	0.48
1:D:545:THR:HA	1:D:582:GLU:HB3	1.96	0.48
1:A:891[B]:MET:HE2	1:A:891[B]:MET:CA	2.39	0.48
1:A:987:TYR:HB3	1:A:990:VAL:HB	1.93	0.48
1:B:835:VAL:HA	1:B:838:HIS:CE1	2.49	0.48
1:C:692:ARG:HH22	1:C:839:GLU:CD	2.22	0.48
1:B:482:ASP:CG	1:B:1066:ARG:HH21	2.21	0.48
1:B:744:ILE:CG1	6:B:1207:HOH:O	2.60	0.48
1:B:965:ARG:NH2	1:B:976:VAL:O	2.47	0.47
1:C:661:GLU:HA	1:C:664:ARG:HG3	1.96	0.47
1:A:753:GLY:HA3	1:A:831:PRO:HB3	1.96	0.47
1:D:535:ARG:HH22	1:D:737:ARG:HB3	1.80	0.47
1:A:1025:ASP:OD2	1:A:1031:THR:OG1	2.26	0.47
1:B:753:GLY:HA3	1:B:831:PRO:HB3	1.96	0.47
1:D:562:TYR:O	1:D:566:ARG:HG3	2.15	0.47
1:D:615:LEU:HD22	1:D:649:ASP:HB3	1.97	0.47
1:A:537:GLU:HG3	1:A:539:ARG:HG2	1.97	0.46
1:C:1021:GLU:HG2	1:C:1035:VAL:HG22	1.96	0.46
1:C:615:LEU:HD22	1:C:649:ASP:HB3	1.96	0.46
1:D:656:CYS:SG	1:D:883:PRO:HD2	2.56	0.46
1:C:655:ASP:HB2	1:C:663:MET:HG2	1.97	0.46
1:A:887:VAL:HG13	1:A:918:VAL:HA	1.97	0.46
1:B:551:HIS:CE1	1:B:559:MET:HB3	2.51	0.46
1:D:566:ARG:HH11	1:D:566:ARG:HG3	1.79	0.46
1:D:594:ARG:HD3	1:D:595:PHE:CE2	2.50	0.46
1:B:1026:ILE:HD13	1:B:1026:ILE:HA	1.58	0.46
1:D:1026:ILE:HD11	1:D:1032:LEU:CG	2.45	0.46
1:D:922:LEU:O	1:D:938:GLN:NE2	2.49	0.46
1:A:520:GLN:O	1:A:524:THR:HG23	2.16	0.46
1:D:558:ARG:NH1	1:D:595:PHE:CD2	2.84	0.46
1:D:549:ASP:HB3	1:D:783:GLN:NE2	2.30	0.45
1:D:752:SER:HB2	1:D:754:ILE:HG12	1.99	0.45
1:D:619:LEU:HD11	1:D:718:KCX:CE	2.45	0.45
1:D:838:HIS:HA	1:D:869:ALA:HB2	1.99	0.45
1:A:599:ASP:OD1	1:A:601:TRP:N	2.48	0.45
1:A:786:LEU:O	1:A:790:VAL:HG23	2.16	0.45
1:A:715:ILE:HB	1:A:744:ILE:HD13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:549:ASP:HB2	1:D:582:GLU:OE1	2.17	0.45
1:D:663:MET:O	1:D:664:ARG:C	2.60	0.44
1:D:746:PHE:HB3	1:D:770:VAL:HG12	1.99	0.44
1:C:716:ALA:HA	1:C:745:HIS:O	2.17	0.44
1:D:678:GLU:OE2	1:D:716:ALA:HB2	2.17	0.44
1:D:759:VAL:HG11	1:D:789:ILE:HD13	2.00	0.44
1:C:678:GLU:OE1	1:C:745:HIS:ND1	2.44	0.44
1:B:837:LEU:HD21	1:B:866:GLN:OE1	2.18	0.44
1:C:655:ASP:OD1	1:C:662:ASN:HB3	2.18	0.44
1:B:541:LEU:HB3	1:B:579:LEU:HB2	1.99	0.44
1:C:676:LEU:HD22	1:C:714:ILE:HD11	1.99	0.44
1:D:915:PRO:HD2	1:D:918:VAL:HB	1.99	0.44
1:C:541:LEU:O	1:C:769:ALA:HA	2.18	0.43
1:C:627:GLY:HA3	1:C:631:TYR:HE2	1.83	0.43
1:B:987:TYR:HB3	1:B:990:VAL:HB	2.00	0.43
1:A:541:LEU:O	1:A:769:ALA:HA	2.17	0.43
1:B:667:MET:HG2	1:B:677:CYS:SG	2.58	0.43
1:D:554:LEU:HD13	1:D:818:ARG:NH2	2.32	0.43
1:B:485:VAL:HG12	1:B:486:ASN:ND2	2.34	0.43
1:B:525:LEU:O	1:B:529:LYS:HB2	2.18	0.43
1:B:750:ASP:O	1:B:751:THR:C	2.61	0.43
1:C:584:TRP:HB3	1:C:618:MET:HB2	2.01	0.43
1:B:812:PHE:N	1:B:812:PHE:CD1	2.86	0.43
1:C:841:PRO:O	1:C:842:GLY:C	2.62	0.43
1:C:951:ARG:HA	1:C:952:PRO:HD3	1.76	0.43
1:B:963:ALA:O	1:B:967:VAL:HG23	2.18	0.43
1:C:476:LEU:O	1:C:479:TYR:N	2.52	0.43
1:C:926:LEU:HD12	1:C:926:LEU:HA	1.74	0.43
1:D:558:ARG:O	1:D:821:TYR:CE1	2.68	0.43
1:B:766:GLY:HA2	1:B:798:ARG:NH1	2.34	0.43
1:D:590:ASP:HB2	1:D:987:TYR:CZ	2.53	0.43
1:D:567:ILE:HB	1:D:813:TYR:CE2	2.54	0.42
1:B:535:ARG:CZ	1:B:737:ARG:HD3	2.49	0.42
1:B:874:MET:C	1:B:876:GLY:N	2.77	0.42
1:B:669:ALA:O	1:B:673:GLU:HG2	2.19	0.42
1:C:477:LEU:HD11	1:C:1054:LEU:HD22	2.01	0.42
1:D:861:TRP:O	1:D:861:TRP:CG	2.70	0.42
1:D:794:SER:HA	1:D:799:ASP:OD2	2.19	0.42
1:A:778:SER:HG	1:C:831:PRO:HG2	1.85	0.42
1:C:793:LEU:HD23	1:C:793:LEU:HA	1.76	0.42
1:D:621:ARG:O	1:D:622:GLY:C	2.63	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:603:ARG:O	1:B:607:ILE:HG13	2.19	0.42
1:D:667:MET:HE3	1:D:679:ALA:HB2	2.00	0.42
1:C:743:PRO:HA	1:C:768:ASP:OD2	2.20	0.42
1:D:874:MET:HE1	1:D:891:MET:HE3	2.01	0.42
1:B:486:ASN:HD21	1:B:1066:ARG:H	1.68	0.42
1:D:486:ASN:ND2	1:D:1066:ARG:H	2.14	0.42
1:D:987:TYR:HB3	1:D:990:VAL:HB	2.00	0.41
1:B:1009:THR:O	1:B:1010:PRO:C	2.63	0.41
1:B:485:VAL:HG12	1:B:486:ASN:CG	2.46	0.41
1:D:721:ALA:HA	1:D:841:PRO:HA	2.01	0.41
1:D:541:LEU:HB3	1:D:579:LEU:HB2	2.02	0.41
1:D:1054:LEU:O	1:D:1055:ASN:C	2.64	0.41
1:B:834:GLU:HA	1:D:808:ARG:HD2	2.03	0.41
1:B:477:LEU:HD11	1:B:1054:LEU:HD22	2.03	0.41
1:C:981:PHE:O	1:C:985:LEU:HG	2.21	0.41
1:C:750:ASP:OD2	5:C:1101:GOL:C3	2.69	0.41
1:D:1009:THR:HB	1:D:1010:PRO:HD3	2.03	0.41
1:A:540:VAL:HG21	1:A:763:VAL:HG22	2.03	0.41
1:A:756:ALA:CB	1:C:754:ILE:HG22	2.51	0.41
1:C:535:ARG:HD3	1:C:741:GLY:O	2.21	0.41
1:B:756:ALA:HB1	1:D:754:ILE:HG22	2.03	0.41
1:B:1043:ASP:OD1	1:B:1045:GLN:N	2.54	0.41
1:D:832:ALA:O	1:D:835:VAL:HG12	2.21	0.41
1:A:928:GLN:HA	1:A:929:PRO:HD3	1.88	0.40
1:C:656:CYS:HA	1:C:881:VAL:CG1	2.52	0.40
1:D:556:ALA:O	1:D:558:ARG:HD3	2.22	0.40
1:C:753:GLY:HA3	1:C:831:PRO:HB3	2.03	0.40
1:C:872:ASN:O	1:C:876:GLY:O	2.39	0.40
1:D:477:LEU:HD11	1:D:1054:LEU:HD22	2.02	0.40
1:C:891:MET:HA	1:C:891:MET:HE3	2.04	0.40
1:C:901:THR:N	1:C:904:ASP:HB2	2.36	0.40
1:D:551:HIS:CG	1:D:559:MET:HB2	2.56	0.40
1:D:669:ALA:O	1:D:673:GLU:HG2	2.21	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	591/632 (94%)	563 (95%)	27 (5%)	1 (0%)	43	70
1	B	586/632 (93%)	549 (94%)	35 (6%)	2 (0%)	36	63
1	C	582/632 (92%)	533 (92%)	44 (8%)	5 (1%)	14	37
1	D	575/632 (91%)	542 (94%)	27 (5%)	6 (1%)	12	35
All	All	2334/2528 (92%)	2187 (94%)	133 (6%)	14 (1%)	21	47

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	501	ALA
1	C	622	GLY
1	C	943	LYS
1	D	622	GLY
1	B	908	PRO
1	C	1041	ALA
1	C	1055	ASN
1	D	508	TYR
1	D	944	GLY
1	A	500	ASN
1	D	1026	ILE
1	D	930	PRO
1	C	492	LYS
1	D	1003	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	443/518 (86%)	425 (96%)	18 (4%)	27	59
1	B	419/518 (81%)	399 (95%)	20 (5%)	23	53
1	C	394/518 (76%)	362 (92%)	32 (8%)	11	30
1	D	395/518 (76%)	374 (95%)	21 (5%)	20	49
All	All	1651/2072 (80%)	1560 (94%)	91 (6%)	19	47

All (91) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	524	THR
1	A	557	THR
1	A	584	TRP
1	A	597	THR
1	A	720	MET
1	A	734	LYS
1	A	754	ILE
1	A	850	GLU
1	A	854	SER
1	A	882	THR
1	A	897	SER
1	A	899	ASP
1	A	911	GLU
1	A	917	SER
1	A	935	GLU
1	A	950	VAL
1	A	1016	LEU
1	A	1026	ILE
1	B	476	LEU
1	B	557	THR
1	B	582	GLU
1	B	584	TRP
1	B	653	VAL
1	B	661	GLU
1	B	692	ARG
1	B	720	MET
1	B	737	ARG
1	B	752	SER
1	B	786	LEU
1	B	790	VAL
1	B	791	GLU
1	B	855	LEU
1	B	882	THR

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Mol	Chain	Res	Type
1	B	901	THR
1	B	926	LEU
1	B	975	GLU
1	B	998	SER
1	B	1026	ILE
1	C	510	ASN
1	C	514	VAL
1	C	521	LEU
1	C	524	THR
1	C	546	THR
1	C	553	SER
1	C	557	THR
1	C	566	ARG
1	C	577	ASN
1	C	584	TRP
1	C	597	THR
1	C	618	MET
1	C	629	THR
1	C	661	GLU
1	C	664	ARG
1	C	689	ASN
1	C	732	LEU
1	C	767	VAL
1	C	777	LEU
1	C	794	SER
1	C	808[A]	ARG
1	C	808[B]	ARG
1	C	848	LEU
1	C	881	VAL
1	C	882	THR
1	C	894	MET
1	C	899	ASP
1	C	926	LEU
1	C	951	ARG
1	C	1005	SER
1	C	1021	GLU
1	C	1047	MET
1	D	471	ASP
1	D	516	ASP
1	D	518	THR
1	D	557	THR
1	D	566	ARG

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Mol	Chain	Res	Type
1	D	584	TRP
1	D	661	GLU
1	D	684	THR
1	D	720	MET
1	D	775	ASP
1	D	790	VAL
1	D	797	GLU
1	D	808	ARG
1	D	854	SER
1	D	863	GLN
1	D	882	THR
1	D	885	SER
1	D	897	SER
1	D	931	SER
1	D	1026	ILE
1	D	1044	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	486	ASN
1	A	624	ASN
1	A	630	ASN
1	A	783	GLN
1	A	863	GLN
1	B	486	ASN
1	B	624	ASN
1	B	630	ASN
1	B	780	ASN
1	B	783	GLN
1	B	938	GLN
1	C	630	ASN
1	C	713	HIS
1	C	1057	GLN
1	D	486	ASN
1	D	624	ASN
1	D	630	ASN
1	D	713	HIS
1	D	783	GLN
1	D	847	ASN
1	D	938	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	KCX	D	718	1,3	10,11,12	0.59	0	6,12,14	1.87	2 (33%)
1	KCX	A	718	1,3	10,11,12	0.63	0	6,12,14	3.81	2 (33%)
1	KCX	C	718	1,3	10,11,12	0.70	0	6,12,14	1.06	0
1	KCX	B	718	1,3	10,11,12	0.58	0	6,12,14	2.16	2 (33%)

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	KCX	D	718	1,3	-	5/9/10/12	-
1	KCX	A	718	1,3	-	5/9/10/12	-
1	KCX	C	718	1,3	-	4/9/10/12	-
1	KCX	B	718	1,3	-	1/9/10/12	-

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	718	KCX	CE-NZ-CX	8.50	136.41	121.98
1	B	718	KCX	OQ1-CX-NZ	-4.26	118.45	124.92
1	A	718	KCX	CD-CE-NZ	3.43	121.81	112.20
1	D	718	KCX	CE-NZ-CX	3.03	127.12	121.98
1	B	718	KCX	CE-NZ-CX	2.83	126.78	121.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	718	KCX	OQ1-CX-NZ	-2.40	121.27	124.92

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	718	KCX	C-CA-CB-CG
1	A	718	KCX	O-C-CA-CB
1	A	718	KCX	CD-CE-NZ-CX
1	B	718	KCX	O-C-CA-CB
1	C	718	KCX	N-CA-CB-CG
1	C	718	KCX	C-CA-CB-CG
1	C	718	KCX	O-C-CA-CB
1	D	718	KCX	O-C-CA-CB
1	D	718	KCX	CD-CE-NZ-CX
1	A	718	KCX	CG-CD-CE-NZ
1	D	718	KCX	CG-CD-CE-NZ
1	C	718	KCX	CE-CD-CG-CB
1	A	718	KCX	CA-CB-CG-CD
1	D	718	KCX	CE-CD-CG-CB
1	D	718	KCX	N-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	718	KCX	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 8 are monoatomic - leaving 3 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
5	GOL	C	1101	-	5,5,5	0.37	0	5,5,5	1.48	1 (20%)
2	PYR	B	1101	-	5,5,5	1.20	0	3,6,6	1.67	1 (33%)
2	PYR	A	1101	-	5,5,5	1.36	0	3,6,6	1.07	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
5	GOL	C	1101	-	-	0/4/4/4	-
2	PYR	B	1101	-	-	2/4/4/4	-
2	PYR	A	1101	-	-	4/4/4/4	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1101	PYR	OXT-C-CA	2.46	120.40	113.59
5	C	1101	GOL	C3-C2-C1	-2.22	103.67	111.80

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1101	PYR	O-C-CA-O3
2	A	1101	PYR	OXT-C-CA-O3
2	B	1101	PYR	OXT-C-CA-CB
2	A	1101	PYR	O-C-CA-CB
2	B	1101	PYR	O-C-CA-CB
2	A	1101	PYR	OXT-C-CA-CB

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	1101	GOL	3	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	594/632 (93%)	-0.35	2 (0%)	90	88	24, 51, 74, 124	19 (3%)
1	B	592/632 (93%)	0.24	27 (4%)	37	31	40, 71, 136, 196	19 (3%)
1	C	587/632 (92%)	0.32	34 (5%)	29	24	23, 83, 158, 199	16 (2%)
1	D	583/632 (92%)	0.59	46 (7%)	18	15	58, 88, 126, 147	15 (2%)
All	All	2356/2528 (93%)	0.20	109 (4%)	37	31	23, 71, 135, 199	69 (2%)

All (109) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	843	GLY	5.3
1	C	1055	ASN	4.3
1	D	630	ASN	4.3
1	C	1045	GLN	4.0
1	C	1032	LEU	3.6
1	B	909	ASP	3.6
1	B	942	LEU	3.5
1	C	915	PRO	3.4
1	C	940	LYS	3.4
1	D	675	LYS	3.3
1	B	887	VAL	3.3
1	C	472	ARG	3.3
1	B	872	ASN	3.3
1	D	713	HIS	3.3
1	B	893	LEU	3.2
1	B	860	ARG	3.2
1	D	922	LEU	3.2
1	B	875	PHE	3.2
1	B	905	VAL	3.1
1	D	1029	GLY	3.1
1	C	502	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	639	PHE	3.0
1	D	661	GLU	3.0
1	D	1027	GLU	2.9
1	C	919	VAL	2.9
1	C	876	GLY	2.9
1	C	893	LEU	2.9
1	D	956	LEU	2.9
1	B	791	GLU	2.9
1	B	630	ASN	2.9
1	D	729	ALA	2.8
1	D	875	PHE	2.8
1	A	512	ASN	2.8
1	D	513	GLY	2.8
1	D	935	GLU	2.8
1	C	500	ASN	2.7
1	D	842	GLY	2.7
1	C	1043	ASP	2.7
1	B	700	TYR	2.7
1	B	863	GLN	2.6
1	B	900	LEU	2.6
1	D	479	TYR	2.6
1	B	661	GLU	2.6
1	C	902	VAL	2.6
1	C	906	VAL	2.6
1	C	937	LEU	2.6
1	D	676	LEU	2.6
1	D	926	LEU	2.6
1	D	770	VAL	2.6
1	D	913	SER	2.6
1	C	999	ASP	2.6
1	D	620	LEU	2.6
1	D	937	LEU	2.6
1	D	700	TYR	2.6
1	B	914	PHE	2.6
1	D	756	ALA	2.6
1	D	542	LEU	2.5
1	D	914	PHE	2.5
1	B	886	LYS	2.5
1	D	502	ALA	2.5
1	D	509	ALA	2.5
1	A	1027	GLU	2.4
1	C	512	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	972	LEU	2.4
1	D	1018	ASP	2.4
1	B	945	GLU	2.4
1	D	891	MET	2.4
1	C	685	GLY	2.4
1	B	919	VAL	2.4
1	D	653	VAL	2.4
1	B	912	VAL	2.4
1	D	860	ARG	2.4
1	D	791	GLU	2.4
1	B	864	VAL	2.4
1	D	471	ASP	2.3
1	D	778	SER	2.3
1	D	930	PRO	2.3
1	D	664	ARG	2.3
1	C	988	PRO	2.3
1	C	944	GLY	2.3
1	B	501	ALA	2.3
1	D	706	GLU	2.3
1	C	625	GLY	2.3
1	C	1037	GLN	2.2
1	C	1044	SER	2.2
1	D	525	LEU	2.2
1	B	874	MET	2.2
1	B	901	THR	2.2
1	D	898	GLN	2.2
1	C	981	PHE	2.2
1	C	1018	ASP	2.2
1	D	533	TRP	2.1
1	B	500	ASN	2.1
1	B	512	ASN	2.1
1	D	577	ASN	2.1
1	C	962	ASP	2.1
1	B	927	GLY	2.1
1	C	864	VAL	2.1
1	D	665	VAL	2.1
1	C	936	ALA	2.1
1	D	530	PHE	2.1
1	B	871	ALA	2.1
1	C	659	TRP	2.1
1	D	514	VAL	2.1
1	C	897	SER	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	930	PRO	2.0
1	C	622	GLY	2.0
1	C	791	GLU	2.0
1	D	989	LYS	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	KCX	D	718	12/13	0.90	0.13	73,77,87,90	0
1	KCX	C	718	12/13	0.94	0.09	64,67,76,77	0
1	KCX	A	718	12/13	0.96	0.08	40,42,58,59	0
1	KCX	B	718	12/13	0.96	0.10	68,71,78,81	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
5	GOL	C	1101	6/6	0.81	0.38	22,24,24,25	6
2	PYR	B	1101	6/6	0.94	0.18	74,80,88,91	0
2	PYR	A	1101	6/6	0.94	0.14	24,26,26,27	6
4	MG	A	1103	1/1	0.95	0.05	71,71,71,71	0
4	MG	C	1103	1/1	0.96	0.06	55,55,55,55	0
3	ZN	D	1101	1/1	0.98	0.07	77,77,77,77	0
3	ZN	C	1102	1/1	0.98	0.04	72,72,72,72	0
4	MG	B	1103	1/1	0.99	0.03	54,54,54,54	0
3	ZN	B	1102	1/1	0.99	0.06	78,78,78,78	0
4	MG	D	1102	1/1	0.99	0.04	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	ZN	A	1102	1/1	0.99	0.02	58,58,58,58	0

6.5 Other polymers [i](#)

There are no such residues in this entry.