



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:38 PM GMT

PDB ID : 4M6V
Title : Structure of the carboxyl transferase domain from *Rhizobium etli* pyruvate carboxylase with pyruvate and biocytin
Authors : Lietzan, A.D.; St. Maurice, M.
Deposited on : 2013-08-11
Resolution : 2.40 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

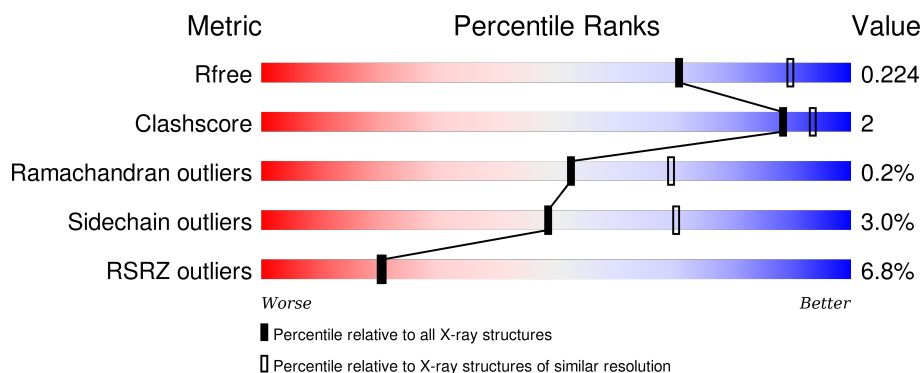
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	632	<div> <div>2%</div> <div>87% 6% • 6%</div> </div>
1	B	632	<div> <div>8%</div> <div>88% 5% • 6%</div> </div>
1	C	632	<div> <div>6%</div> <div>89% 5% • 6%</div> </div>
1	D	632	<div> <div>10%</div> <div>88% 5% 6%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	PYR	D	1104	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 18461 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	597	Total	C	N	O	S	0	2	0
			4564	2901	769	871	23			
1	B	593	Total	C	N	O	S	0	2	0
			4435	2822	742	848	23			
1	C	596	Total	C	N	O	S	0	3	0
			4491	2859	750	859	23			
1	D	593	Total	C	N	O	S	0	2	0
			4404	2801	739	841	23			

There are 116 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

Continued on next page...

Continued from previous page...

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
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
C	436	MET	-	EXPRESSION TAG	UNP Q2K340
C	437	GLY	-	EXPRESSION TAG	UNP Q2K340
C	438	SER	-	EXPRESSION TAG	UNP Q2K340
C	439	SER	-	EXPRESSION TAG	UNP Q2K340
C	440	HIS	-	EXPRESSION TAG	UNP Q2K340

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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
C	454	SER	-	EXPRESSION TAG	UNP Q2K340
C	455	GLU	-	EXPRESSION TAG	UNP Q2K340
C	456	ASN	-	EXPRESSION TAG	UNP Q2K340
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
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
D	451	ILE	-	EXPRESSION TAG	UNP Q2K340
D	452	PRO	-	EXPRESSION TAG	UNP Q2K340
D	453	THR	-	EXPRESSION TAG	UNP Q2K340

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

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

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

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

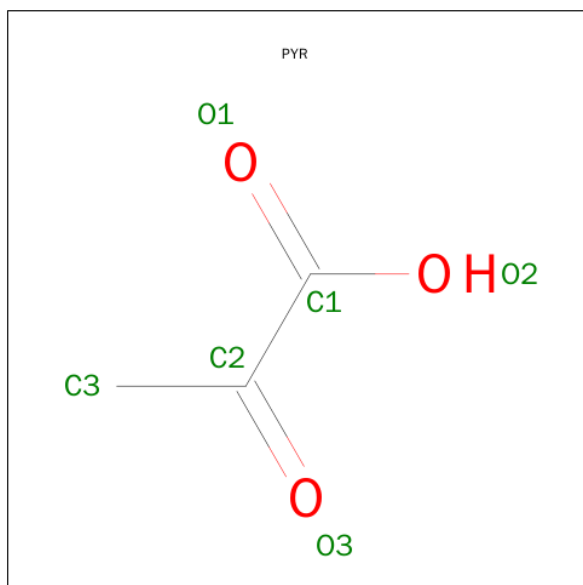
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Cl 1 1	0	0

Continued on next page...

Continued from previous page...

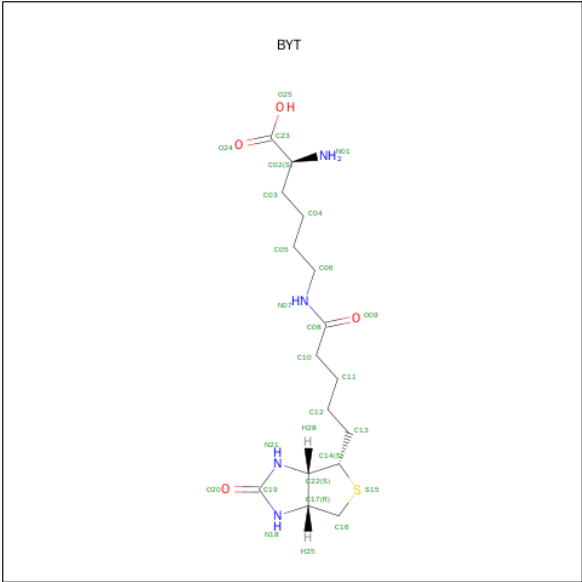
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		
4	D	1	Total	Cl	0	0
			1	1		
4	C	1	Total	Cl	0	0
			1	1		

- Molecule 5 is PYRUVIC ACID (three-letter code: PYR) (formula: $C_3H_4O_3$).



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

- Molecule 6 is BIOCYTIN (three-letter code: BYT) (formula: $C_{16}H_{28}N_4O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	S	0	0
			25	16	4	4	1		
6	A	1	Total	C	N	O	S	0	0
			18	12	3	2	1		
6	B	1	Total	C	N	O	S	0	0
			25	16	4	4	1		
6	B	1	Total	C	N	O	S	0	0
			14	10	2	1	1		
6	C	1	Total	C	N	O	S	0	0
			25	16	4	4	1		
6	C	1	Total	C	N	O	S	0	0
			16	10	3	2	1		
6	D	1	Total	C	N	O	S	0	0
			25	16	4	4	1		
6	D	1	Total	C	N	O	S	0	0
			10	6	2	1	1		

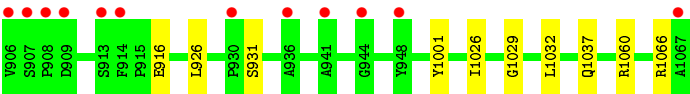
- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



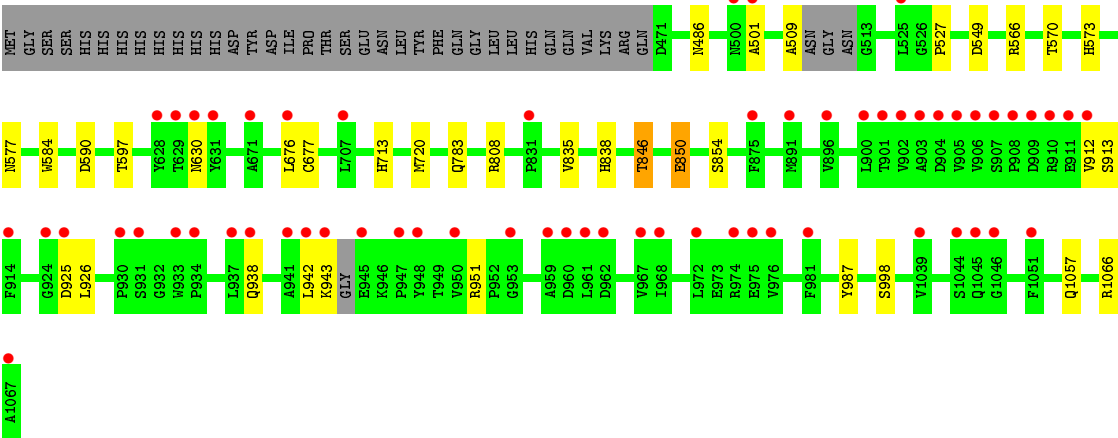
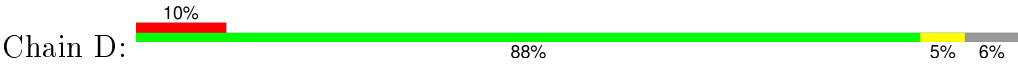
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			6	3	3		
7	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	143	Total	O	0	0
			143	143		
8	B	85	Total	O	0	0
			85	85		
8	C	77	Total	O	0	0
			77	77		
8	D	56	Total	O	0	0
			56	56		



● Molecule 1: PYRUVATE CARBOXYLASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	84.64Å 157.83Å 244.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.66 – 2.40 49.61 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.6 (49.66-2.40) 99.6 (49.61-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.57 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.184 , 0.223 0.189 , 0.224	Depositor DCC
R_{free} test set	6448 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	49.7	Xtriage
Anisotropy	0.083	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 37.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 128194 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	18461	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.39% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, MG, PYR, CL, BYT, ZN, KCX

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	0.64	0/4655	0.75	5/6330 (0.1%)
1	B	0.55	0/4524	0.69	4/6166 (0.1%)
1	C	0.52	0/4585	0.68	2/6246 (0.0%)
1	D	0.45	0/4493	0.61	0/6134
All	All	0.54	0/18257	0.69	11/24876 (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	C	0	1

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	775	ASP	CB-CG-OD1	7.04	124.64	118.30
1	B	737	ARG	NE-CZ-NH1	-6.96	116.82	120.30
1	B	809	ARG	NE-CZ-NH1	6.32	123.46	120.30
1	A	951	ARG	NE-CZ-NH1	-6.19	117.21	120.30
1	A	750	ASP	CB-CG-OD1	6.00	123.70	118.30
1	C	494	ARG	NE-CZ-NH2	5.96	123.28	120.30
1	A	590	ASP	N-CA-CB	-5.95	99.90	110.60
1	A	1032	LEU	CA-CB-CG	5.91	128.89	115.30
1	A	951	ARG	NE-CZ-NH2	5.33	122.97	120.30
1	C	535	ARG	NE-CZ-NH2	-5.21	117.69	120.30
1	B	737	ARG	NE-CZ-NH2	5.07	122.83	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	1029	GLY	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	4564	0	4461	33	0
1	B	4435	0	4224	18	0
1	C	4491	0	4302	23	0
1	D	4404	0	4180	17	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	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	A	6	0	3	0	0
5	B	6	0	3	0	0
5	C	6	0	3	0	0
5	D	6	0	3	0	0
6	A	43	0	45	3	0
6	B	39	0	42	2	0
6	C	41	0	42	7	0
6	D	35	0	34	2	0
7	B	6	0	8	3	0
7	C	6	0	8	0	0
8	A	143	0	0	7	0
8	B	85	0	0	2	0
8	C	77	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	D	56	0	0	2	0
All	All	18461	0	17358	88	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 (88) 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:C:850:GLU:HG3	6:C:1107:BYT:H28	1.56	0.87
1:A:472:ARG:HB3	1:A:1026:ILE:HD11	1.57	0.86
1:A:850:GLU:HG3	6:A:1106:BYT:H28	1.59	0.85
1:A:1060:ARG:NH1	1:C:1037:GLN:OE1	2.10	0.84
1:C:1001:TYR:CE2	6:C:1106:BYT:H18	2.16	0.81
1:B:577:ASN:HB2	8:B:1229:HOH:O	1.81	0.79
1:C:500:ASN:HD22	1:C:501:ALA:H	1.29	0.79
1:C:850:GLU:CG	6:C:1107:BYT:H28	2.17	0.75
1:A:850:GLU:HG2	8:A:1322:HOH:O	1.87	0.74
1:A:853:ARG:NE	8:A:1321:HOH:O	2.19	0.74
1:A:472:ARG:CB	1:A:1026:ILE:HD11	2.20	0.72
1:C:500:ASN:ND2	1:C:501:ALA:H	1.88	0.70
1:A:780:ASN:H	7:B:1101:GOL:H11	1.58	0.68
1:A:677:CYS:H	1:A:713:HIS:HD2	1.42	0.67
1:A:633:ASP:OD1	1:A:951:ARG:NH1	2.28	0.66
1:A:1026:ILE:HB	1:A:1032:LEU:HD11	1.76	0.66
1:C:677:CYS:H	1:C:713:HIS:HD2	1.44	0.64
1:A:891[B]:MET:HE2	1:A:918:VAL:HG11	1.79	0.64
1:A:808:ARG:HD3	8:A:1336:HOH:O	1.99	0.63
1:A:549:ASP:HB3	1:A:783:GLN:HE22	1.64	0.62
1:A:829:LYS:NZ	8:B:1201:HOH:O	2.34	0.61
1:D:942:LEU:O	1:D:943:LYS:CB	2.49	0.59
1:B:509:ALA:HA	1:B:573[B]:HIS:CE1	2.37	0.59
1:C:500:ASN:HD22	1:C:501:ALA:N	2.00	0.59
1:C:846:THR:HG22	6:C:1107:BYT:O20	2.02	0.58
1:A:1024:ALA:O	1:A:1032:LEU:HD12	2.04	0.58
1:A:730:LYS:HG3	8:A:1333:HOH:O	2.04	0.57
1:A:812:PHE:HE1	1:B:862:HIS:CD2	2.23	0.56
1:C:549:ASP:HB3	1:C:783:GLN:HE22	1.69	0.56
1:D:808:ARG:HD3	8:D:1213:HOH:O	2.04	0.56
1:A:812:PHE:CE1	1:B:862:HIS:CD2	2.93	0.56
8:A:1316:HOH:O	7:B:1101:GOL:H11	2.06	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:527:PRO:HB2	1:D:713:HIS:CD2	2.41	0.55
1:C:486:ASN:ND2	1:C:1066:ARG:H	2.05	0.53
1:C:486:ASN:HD21	1:C:1066:ARG:H	1.56	0.53
1:B:549:ASP:HB3	1:B:783:GLN:HE22	1.74	0.53
1:D:509:ALA:HA	1:D:573[B]:HIS:CE1	2.44	0.53
1:B:698:LYS:HE2	1:B:699:TYR:N	2.24	0.52
1:C:850:GLU:HG3	6:C:1107:BYT:C22	2.36	0.52
1:D:912:VAL:HG12	1:D:913:SER:N	2.26	0.51
1:C:551:HIS:CE1	1:C:559:MET:HB3	2.46	0.50
1:A:943:LYS:NZ	8:A:1340:HOH:O	2.42	0.50
1:C:500:ASN:ND2	1:C:500:ASN:H	2.09	0.50
1:B:1001:TYR:CE2	6:B:1106:BYT:H19	2.47	0.50
1:D:846:THR:HG21	8:D:1239:HOH:O	2.11	0.50
1:C:1001:TYR:HE2	6:C:1106:BYT:H18	1.75	0.49
1:C:500:ASN:ND2	1:C:500:ASN:N	2.60	0.49
1:A:846:THR:CG2	6:A:1106:BYT:O20	2.60	0.49
1:A:486:ASN:HD21	1:A:1066:ARG:H	1.59	0.49
1:A:677:CYS:H	1:A:713:HIS:CD2	2.25	0.49
1:C:500:ASN:N	1:C:500:ASN:HD22	2.10	0.49
1:A:486:ASN:ND2	1:A:1066:ARG:H	2.11	0.49
1:A:750:ASP:OD2	7:B:1101:GOL:O1	2.24	0.48
1:B:566:ARG:CG	1:B:566:ARG:HH11	2.26	0.48
1:D:677:CYS:H	1:D:713:HIS:CD2	2.31	0.48
1:D:630:ASN:OD1	1:D:925:ASP:O	2.32	0.48
1:B:551:HIS:CE1	1:B:559:MET:HB3	2.49	0.48
1:B:987:TYR:HB3	1:B:990:VAL:HB	1.96	0.47
1:D:570:THR:HA	1:D:573[B]:HIS:CD2	2.50	0.47
1:A:510:ASN:HD22	1:A:511:GLY:H	1.63	0.46
1:A:850:GLU:OE2	1:A:853:ARG:NE	2.49	0.46
1:D:676:LEU:HA	1:D:713:HIS:HD2	1.79	0.46
1:C:509:ALA:HA	1:C:573[B]:HIS:CE1	2.51	0.45
1:B:494:ARG:HD2	6:B:1107:BYT:H16	1.98	0.45
1:A:551:HIS:CE1	1:A:559:MET:HB3	2.52	0.44
1:A:677:CYS:N	1:A:713:HIS:HD2	2.14	0.44
1:B:509:ALA:HA	1:B:573[B]:HIS:NE2	2.33	0.43
1:A:630:ASN:ND2	8:A:1270:HOH:O	2.50	0.43
1:B:656:CYS:HA	1:B:881:VAL:CG1	2.48	0.43
1:A:846:THR:HG22	6:A:1106:BYT:O20	2.19	0.43
1:A:894:MET:HE3	1:A:894:MET:HB2	1.92	0.43
1:D:835:VAL:HA	1:D:838:HIS:CE1	2.53	0.43
1:B:566:ARG:CG	1:B:566:ARG:NH1	2.82	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:622:GLY:O	1:A:666:SER:OG	2.33	0.42
1:B:557:THR:O	1:B:557:THR:HG22	2.19	0.42
1:C:677:CYS:H	1:C:713:HIS:CD2	2.30	0.42
1:D:850:GLU:HG3	6:D:1106:BYT:H28	2.01	0.42
1:C:482:ASP:HB3	6:C:1106:BYT:H25	2.01	0.42
1:D:486:ASN:ND2	1:D:1066:ARG:H	2.16	0.42
1:A:836:TYR:CD2	1:B:791:GLU:HG2	2.55	0.42
1:B:963:ALA:O	1:B:967:VAL:HG23	2.20	0.42
1:D:938:GLN:HG2	1:D:942:LEU:HD12	2.01	0.42
1:B:835:VAL:HA	1:B:838:HIS:CE1	2.56	0.41
1:D:846:THR:HG23	6:D:1106:BYT:O20	2.21	0.41
1:C:1026:ILE:HD12	1:C:1032:LEU:HD11	2.03	0.41
1:D:590:ASP:HB3	1:D:987:TYR:CZ	2.56	0.41
1:D:549:ASP:HB3	1:D:783:GLN:HE22	1.85	0.40
1:C:835:VAL:HA	1:C:838:HIS:CE1	2.57	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	596/632 (94%)	583 (98%)	11 (2%)	2 (0%)	46	63
1	B	588/632 (93%)	574 (98%)	14 (2%)	0	100	100
1	C	594/632 (94%)	579 (98%)	14 (2%)	1 (0%)	52	69
1	D	588/632 (93%)	570 (97%)	17 (3%)	1 (0%)	52	69
All	All	2366/2528 (94%)	2306 (98%)	56 (2%)	4 (0%)	52	69

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	501	ALA
1	A	625	GLY
1	C	501	ALA
1	D	501	ALA

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	468/519 (90%)	454 (97%)	14 (3%)	48	70
1	B	438/519 (84%)	426 (97%)	12 (3%)	52	73
1	C	448/519 (86%)	433 (97%)	15 (3%)	45	66
1	D	435/519 (84%)	423 (97%)	12 (3%)	51	72
All	All	1789/2076 (86%)	1736 (97%)	53 (3%)	48	70

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	510	ASN
1	A	584	TRP
1	A	597	THR
1	A	672	GLU
1	A	720	MET
1	A	730	LYS
1	A	764	GLU
1	A	775	ASP
1	A	846	THR
1	A	850	GLU
1	A	854	SER
1	A	926	LEU
1	A	1027	GLU
1	A	1032	LEU
1	B	521	LEU
1	B	566	ARG
1	B	577	ASN
1	B	584	TRP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	594	ARG
1	B	698	LYS
1	B	720	MET
1	B	775	ASP
1	B	854	SER
1	B	899	ASP
1	B	926	LEU
1	B	931	SER
1	C	476	LEU
1	C	494	ARG
1	C	500	ASN
1	C	557	THR
1	C	584	TRP
1	C	597	THR
1	C	720	MET
1	C	775	ASP
1	C	794	SER
1	C	849	LYS
1	C	850	GLU
1	C	916	GLU
1	C	926	LEU
1	C	931	SER
1	C	1060	ARG
1	D	566	ARG
1	D	577	ASN
1	D	584	TRP
1	D	597	THR
1	D	720	MET
1	D	846	THR
1	D	850	GLU
1	D	854	SER
1	D	926	LEU
1	D	951	ARG
1	D	998	SER
1	D	1057	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	486	ASN
1	A	510	ASN
1	A	577	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	624	ASN
1	A	630	ASN
1	A	713	HIS
1	A	783	GLN
1	B	486	ASN
1	B	624	ASN
1	B	783	GLN
1	B	928	GLN
1	C	486	ASN
1	C	500	ASN
1	C	577	ASN
1	C	713	HIS
1	C	783	GLN
1	C	938	GLN
1	D	486	ASN
1	D	713	HIS
1	D	783	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	A	718	1,2	7,11,12	0.60	0	7,12,14	1.20	0
1	KCX	B	718	1,2	7,11,12	0.46	0	7,12,14	0.82	0
1	KCX	C	718	1,2	7,11,12	0.51	0	7,12,14	0.98	1 (14%)
1	KCX	D	718	1,2	7,11,12	0.71	0	7,12,14	1.46	1 (14%)

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	A	718	1,2	-	0/6/10/12	0/0/0/0
1	KCX	B	718	1,2	-	0/6/10/12	0/0/0/0
1	KCX	C	718	1,2	-	0/6/10/12	0/0/0/0
1	KCX	D	718	1,2	-	0/6/10/12	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	718	KCX	O-C-CA	-2.01	120.24	125.49
1	D	718	KCX	CE-NZ-CX	3.34	127.27	123.49

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 26 ligands modelled in this entry, 12 are monoatomic - leaving 14 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	PYR	A	1104	-	2,5,5	0.43	0	2,6,6	0.08	0
6	BYT	A	1105	-	21,26,26	2.91	6 (28%)	21,34,34	3.86	7 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	BYT	A	1106	-	17,19,26	3.95	7 (41%)	18,25,34	5.46	8 (44%)
7	GOL	B	1101	-	5,5,5	0.43	0	5,5,5	0.98	0
5	PYR	B	1105	-	2,5,5	0.25	0	2,6,6	0.31	0
6	BYT	B	1106	-	21,26,26	3.08	6 (28%)	21,34,34	4.22	9 (42%)
6	BYT	B	1107	-	13,15,26	4.27	5 (38%)	13,20,34	5.46	8 (61%)
7	GOL	C	1102	-	5,5,5	0.16	0	5,5,5	0.34	0
5	PYR	C	1105	-	2,5,5	0.60	0	2,6,6	0.10	0
6	BYT	C	1106	-	21,26,26	3.45	8 (38%)	21,34,34	4.36	10 (47%)
6	BYT	C	1107	-	15,17,26	3.91	7 (46%)	16,23,34	4.52	6 (37%)
5	PYR	D	1104	-	2,5,5	0.43	0	2,6,6	0.28	0
6	BYT	D	1105	-	21,26,26	3.17	6 (28%)	21,34,34	3.84	9 (42%)
6	BYT	D	1106	-	9,11,26	4.15	4 (44%)	8,16,34	7.15	8 (100%)

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	PYR	A	1104	-	-	0/0/4/4	0/0/0/0
6	BYT	A	1105	-	-	0/15/40/40	0/2/2/2
6	BYT	A	1106	-	-	0/10/31/40	0/2/2/2
7	GOL	B	1101	-	-	0/4/4/4	0/0/0/0
5	PYR	B	1105	-	-	0/0/4/4	0/0/0/0
6	BYT	B	1106	-	-	0/15/40/40	0/2/2/2
6	BYT	B	1107	-	-	0/5/26/40	0/2/2/2
7	GOL	C	1102	-	-	0/4/4/4	0/0/0/0
5	PYR	C	1105	-	-	0/0/4/4	0/0/0/0
6	BYT	C	1106	-	-	0/15/40/40	0/2/2/2
6	BYT	C	1107	-	-	0/7/28/40	0/2/2/2
5	PYR	D	1104	-	-	0/0/4/4	0/0/0/0
6	BYT	D	1105	-	-	0/15/40/40	0/2/2/2
6	BYT	D	1106	-	-	0/0/21/40	0/2/2/2

All (49) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	1106	BYT	C14-S15	-11.63	1.64	1.82
6	B	1107	BYT	C14-S15	-8.94	1.68	1.82
6	A	1105	BYT	C14-S15	-8.59	1.68	1.82
6	C	1107	BYT	C14-S15	-8.09	1.69	1.82

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1106	BYT	C14-S15	-8.04	1.69	1.82
6	B	1106	BYT	C14-S15	-7.97	1.69	1.82
6	D	1105	BYT	C14-S15	-7.87	1.70	1.82
6	C	1106	BYT	C16-S15	-5.68	1.64	1.81
6	A	1106	BYT	C16-S15	-5.15	1.65	1.81
6	B	1107	BYT	C16-S15	-4.69	1.67	1.81
6	C	1107	BYT	C16-S15	-4.46	1.67	1.81
6	B	1106	BYT	C16-S15	-4.44	1.68	1.81
6	D	1106	BYT	C16-S15	-4.39	1.68	1.81
6	A	1105	BYT	C16-S15	-4.27	1.68	1.81
6	D	1105	BYT	C16-S15	-4.05	1.69	1.81
6	C	1106	BYT	O09-C08	-2.30	1.18	1.23
6	C	1106	BYT	O20-C19	-2.10	1.19	1.23
6	A	1106	BYT	C17-N18	2.19	1.49	1.45
6	C	1107	BYT	C13-C14	2.31	1.57	1.52
6	A	1105	BYT	C19-N18	3.12	1.39	1.35
6	C	1106	BYT	C19-N21	3.44	1.40	1.35
6	C	1107	BYT	C08-N07	3.63	1.44	1.32
6	C	1106	BYT	C08-N07	3.64	1.42	1.33
6	C	1106	BYT	C19-N18	3.65	1.40	1.35
6	A	1105	BYT	C19-N21	3.85	1.40	1.35
6	B	1106	BYT	C19-N21	4.37	1.41	1.35
6	B	1106	BYT	C08-N07	4.44	1.44	1.33
6	A	1106	BYT	C19-N21	4.62	1.41	1.35
6	D	1105	BYT	C08-N07	4.66	1.44	1.33
6	A	1105	BYT	C08-N07	4.81	1.44	1.33
6	C	1106	BYT	C17-C22	5.08	1.64	1.56
6	A	1106	BYT	C08-N07	5.16	1.45	1.33
6	B	1106	BYT	C19-N18	5.20	1.42	1.35
6	D	1105	BYT	C19-N18	5.21	1.42	1.35
6	A	1105	BYT	C17-C22	5.42	1.64	1.56
6	C	1107	BYT	C19-N21	5.49	1.42	1.35
6	D	1106	BYT	C19-N18	5.86	1.43	1.35
6	B	1107	BYT	C19-N21	6.00	1.43	1.35
6	D	1105	BYT	C17-C22	6.10	1.65	1.56
6	D	1105	BYT	C19-N21	6.16	1.43	1.35
6	B	1107	BYT	C19-N18	6.24	1.44	1.35
6	B	1106	BYT	C17-C22	6.41	1.66	1.56
6	D	1106	BYT	C19-N21	6.42	1.44	1.35
6	C	1107	BYT	C17-C22	6.70	1.66	1.56
6	C	1107	BYT	C19-N18	6.79	1.44	1.35
6	A	1106	BYT	C19-N18	7.22	1.45	1.35

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	1107	BYT	C17-C22	7.33	1.67	1.56
6	D	1106	BYT	C17-C22	7.51	1.67	1.56
6	A	1106	BYT	C17-C22	7.78	1.68	1.56

All (65) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1106	BYT	C17-N18-C19	-9.62	105.29	112.49
6	A	1106	BYT	O20-C19-N21	-9.62	114.74	125.90
6	D	1106	BYT	C17-N18-C19	-9.22	105.59	112.49
6	B	1107	BYT	C17-N18-C19	-9.14	105.65	112.49
6	B	1106	BYT	C17-N18-C19	-8.96	105.79	112.49
6	C	1106	BYT	C17-N18-C19	-8.66	106.00	112.49
6	A	1106	BYT	C22-N21-C19	-8.12	104.89	112.66
6	D	1105	BYT	C17-N18-C19	-8.04	106.47	112.49
6	A	1105	BYT	C17-N18-C19	-8.01	106.50	112.49
6	D	1106	BYT	C22-N21-C19	-7.54	105.45	112.66
6	C	1107	BYT	C22-N21-C19	-7.47	105.52	112.66
6	B	1107	BYT	C22-N21-C19	-7.41	105.57	112.66
6	C	1106	BYT	C22-N21-C19	-7.10	105.87	112.66
6	D	1105	BYT	C22-N21-C19	-6.74	106.21	112.66
6	C	1107	BYT	C17-N18-C19	-6.57	107.57	112.49
6	B	1106	BYT	C22-N21-C19	-6.34	106.60	112.66
6	A	1105	BYT	C22-N21-C19	-6.28	106.65	112.66
6	C	1107	BYT	O20-C19-N21	-5.97	118.98	125.90
6	B	1106	BYT	O20-C19-N21	-5.72	119.26	125.90
6	B	1107	BYT	O20-C19-N21	-5.47	119.56	125.90
6	D	1106	BYT	O20-C19-N21	-4.52	120.66	125.90
6	C	1106	BYT	O20-C19-N21	-4.13	121.11	125.90
6	A	1105	BYT	O20-C19-N18	-4.01	121.25	125.90
6	D	1105	BYT	O20-C19-N18	-3.94	121.33	125.90
6	C	1106	BYT	O20-C19-N18	-3.94	121.33	125.90
6	A	1105	BYT	O20-C19-N21	-3.86	121.43	125.90
6	D	1106	BYT	O20-C19-N18	-3.84	121.45	125.90
6	D	1105	BYT	O20-C19-N21	-3.17	122.22	125.90
6	B	1107	BYT	O20-C19-N18	-2.72	122.75	125.90
6	A	1106	BYT	O09-C08-N07	-2.65	117.68	122.94
6	D	1105	BYT	C12-C13-C14	-2.52	107.85	113.70
6	C	1106	BYT	C06-N07-C08	-2.21	118.44	122.79
6	B	1106	BYT	C11-C10-C08	-2.14	107.58	113.24
6	B	1106	BYT	O20-C19-N18	-2.13	123.43	125.90
6	C	1106	BYT	O09-C08-C10	-2.13	118.31	121.98

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	1106	BYT	C22-C17-N18	2.16	104.81	102.37
6	B	1107	BYT	C22-C17-N18	2.19	104.83	102.37
6	D	1106	BYT	C22-C17-N18	2.19	104.84	102.37
6	D	1105	BYT	C22-C17-N18	2.34	105.01	102.37
6	C	1106	BYT	C10-C08-N07	2.73	121.21	116.46
6	A	1105	BYT	C16-S15-C14	2.77	96.43	90.33
6	A	1105	BYT	C17-C22-N21	2.81	105.35	102.52
6	B	1106	BYT	C17-C22-N21	2.93	105.47	102.52
6	D	1105	BYT	C17-C22-N21	3.26	105.81	102.52
6	C	1106	BYT	C17-C22-N21	3.47	106.03	102.52
6	D	1106	BYT	C17-C22-N21	3.55	106.10	102.52
6	B	1107	BYT	C17-C22-N21	3.65	106.21	102.52
6	A	1106	BYT	C10-C08-N07	3.96	123.34	116.46
6	A	1106	BYT	C17-C22-N21	4.86	107.43	102.52
6	C	1107	BYT	C17-C22-N21	5.09	107.66	102.52
6	D	1105	BYT	C16-S15-C14	5.35	102.11	90.33
6	A	1106	BYT	C16-S15-C14	5.44	102.30	90.33
6	B	1107	BYT	C16-S15-C14	5.55	102.55	90.33
6	B	1106	BYT	C16-S15-C14	6.16	103.89	90.33
6	C	1106	BYT	C16-S15-C14	6.50	104.63	90.33
6	D	1106	BYT	C16-S15-C14	6.78	105.36	90.39
6	C	1107	BYT	C16-S15-C14	7.10	105.97	90.33
6	C	1107	BYT	N18-C19-N21	10.50	116.14	108.88
6	D	1105	BYT	N18-C19-N21	10.91	116.42	108.88
6	B	1106	BYT	N18-C19-N21	12.20	117.30	108.88
6	A	1105	BYT	N18-C19-N21	12.21	117.31	108.88
6	C	1106	BYT	N18-C19-N21	12.51	117.52	108.88
6	B	1107	BYT	N18-C19-N21	12.73	117.67	108.88
6	D	1106	BYT	N18-C19-N21	12.99	117.85	108.88
6	A	1106	BYT	N18-C19-N21	14.17	118.67	108.88

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1106	BYT	3	0
7	B	1101	GOL	3	0
6	B	1106	BYT	1	0
6	B	1107	BYT	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	1106	BYT	3	0
6	C	1107	BYT	4	0
6	D	1106	BYT	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	596/632 (94%)	-0.20	15 (2%)	61 60	30, 45, 68, 130	19 (3%)
1	B	592/632 (93%)	0.25	51 (8%)	13 13	31, 65, 122, 168	13 (2%)
1	C	595/632 (94%)	0.10	35 (5%)	26 26	38, 60, 118, 170	15 (2%)
1	D	592/632 (93%)	0.39	61 (10%)	9 8	46, 77, 115, 158	14 (2%)
All	All	2375/2528 (93%)	0.13	162 (6%)	20 20	30, 60, 113, 170	61 (2%)

All (162) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	628	TYR	9.7
1	D	906	VAL	8.1
1	D	909	ASP	7.1
1	D	907	SER	7.0
1	B	912	VAL	6.4
1	D	905	VAL	6.3
1	C	896	VAL	5.0
1	D	1044	SER	4.9
1	D	908	PRO	4.7
1	D	891[A]	MET	4.7
1	C	900	LEU	4.7
1	A	1029	GLY	4.7
1	C	893	LEU	4.1
1	D	896	VAL	4.0
1	D	937	LEU	4.0
1	A	1028	LYS	4.0
1	D	1067	ALA	4.0
1	D	501	ALA	4.0
1	C	874	MET	3.9
1	C	914	PHE	3.9
1	B	934	PRO	3.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	1067	ALA	3.9
1	B	942	LEU	3.9
1	D	525	LEU	3.9
1	B	900	LEU	3.8
1	D	903	ALA	3.7
1	B	909	ASP	3.7
1	D	941	ALA	3.7
1	D	961	LEU	3.7
1	D	942	LEU	3.7
1	B	963	ALA	3.6
1	D	950	VAL	3.6
1	B	904	ASP	3.6
1	C	906	VAL	3.5
1	D	914	PHE	3.5
1	D	910	ARG	3.5
1	A	512	ASN	3.5
1	D	875	PHE	3.5
1	B	907	SER	3.4
1	D	912	VAL	3.4
1	C	908	PRO	3.4
1	C	904	ASP	3.4
1	B	914	PHE	3.3
1	C	902	VAL	3.3
1	B	1067	ALA	3.3
1	D	900	LEU	3.3
1	A	779	GLY	3.2
1	D	1051	PHE	3.2
1	C	905	VAL	3.2
1	C	875	PHE	3.2
1	B	933	TRP	3.2
1	D	630	ASN	3.2
1	B	509	ALA	3.1
1	C	948	TYR	3.1
1	D	901	THR	3.1
1	B	905	VAL	3.1
1	C	909	ASP	3.0
1	B	908	PRO	3.0
1	C	907	SER	3.0
1	B	906	VAL	3.0
1	D	911	GLU	3.0
1	B	919	VAL	2.9
1	D	933	TRP	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	941	ALA	2.9
1	B	962	ASP	2.9
1	B	944	GLY	2.9
1	D	671	ALA	2.9
1	B	1051	PHE	2.8
1	A	828	LEU	2.8
1	B	897	SER	2.8
1	C	936	ALA	2.8
1	A	554	LEU	2.7
1	B	485	VAL	2.7
1	B	896	VAL	2.7
1	B	913	SER	2.7
1	A	835	VAL	2.7
1	B	910	ARG	2.7
1	A	778	SER	2.6
1	D	904	ASP	2.6
1	B	936	ALA	2.6
1	B	961	LEU	2.6
1	C	785	CYS	2.6
1	D	967	VAL	2.6
1	B	659	TRP	2.5
1	C	891[A]	MET	2.5
1	D	924	GLY	2.5
1	C	913	SER	2.5
1	B	831	PRO	2.5
1	D	831	PRO	2.5
1	C	751	THR	2.5
1	B	941	ALA	2.5
1	D	959	ALA	2.5
1	D	931	SER	2.5
1	D	975	GLU	2.5
1	D	676	LEU	2.5
1	B	968	ILE	2.5
1	D	500	ASN	2.5
1	B	782	SER	2.4
1	C	782	SER	2.4
1	B	903	ALA	2.4
1	D	938	GLN	2.4
1	C	857	LEU	2.4
1	B	891[A]	MET	2.4
1	B	950	VAL	2.3
1	A	751	THR	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	831	PRO	2.3
1	D	629	THR	2.3
1	D	960	ASP	2.3
1	B	554	LEU	2.3
1	D	976	VAL	2.3
1	B	911	GLU	2.3
1	B	938	GLN	2.3
1	D	968	ILE	2.3
1	D	948	TYR	2.3
1	A	753	GLY	2.3
1	D	930	PRO	2.3
1	C	897	SER	2.3
1	B	781	THR	2.3
1	B	948	TYR	2.3
1	C	784	PRO	2.3
1	D	934	PRO	2.3
1	B	981	PHE	2.2
1	B	893	LEU	2.2
1	C	944	GLY	2.2
1	D	1039	VAL	2.2
1	D	972	LEU	2.2
1	B	899	ASP	2.2
1	A	782	SER	2.2
1	D	947	PRO	2.2
1	D	925	ASP	2.2
1	C	554	LEU	2.2
1	C	894	MET	2.2
1	D	943	LYS	2.2
1	B	1063	VAL	2.1
1	D	902	VAL	2.1
1	D	1046	GLY	2.1
1	D	631	TYR	2.1
1	D	974	ARG	2.1
1	D	981	PHE	2.1
1	C	553	SER	2.1
1	A	781	THR	2.1
1	B	1048	VAL	2.1
1	D	1045	GLN	2.1
1	B	828	LEU	2.1
1	D	953	GLY	2.1
1	B	785	CYS	2.1
1	B	830	GLY	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	513	GLY	2.1
1	C	693	PRO	2.1
1	D	962	ASP	2.1
1	B	776	ALA	2.0
1	A	785	CYS	2.0
1	B	901	THR	2.0
1	C	903	ALA	2.0
1	C	895	MET	2.0
1	B	784	PRO	2.0
1	C	930	PRO	2.0
1	D	707	LEU	2.0
1	C	509	ALA	2.0
1	A	750	ASP	2.0
1	B	898	GLN	2.0
1	D	945	GLU	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
1	KCX	C	718	12/13	0.99	0.17	-	49,52,53,55	0
1	KCX	A	718	12/13	0.98	0.16	-	34,37,39,39	0
1	KCX	D	718	12/13	0.98	0.17	-	56,62,65,66	0
1	KCX	B	718	12/13	0.98	0.15	-	45,48,50,51	0

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
5	PYR	D	1104	6/6	0.92	0.22	2.00	70,77,77,78	0
7	GOL	B	1101	6/6	0.95	0.33	1.70	48,48,50,53	0
6	BYT	B	1107	14/25	0.89	0.18	1.05	63,75,85,85	1
5	PYR	C	1105	6/6	0.96	0.18	0.58	56,62,65,65	0
6	BYT	A	1105	25/25	0.98	0.12	0.06	40,45,47,48	0
6	BYT	D	1106	10/25	0.89	0.16	-0.05	78,81,83,84	0
6	BYT	A	1106	18/25	0.92	0.15	-0.11	37,46,82,83	1
6	BYT	D	1105	25/25	0.96	0.12	-0.55	67,70,76,76	0
5	PYR	B	1105	6/6	0.94	0.15	-0.56	63,64,66,67	0
5	PYR	A	1104	6/6	0.95	0.15	-0.62	41,44,47,47	0
6	BYT	B	1106	25/25	0.93	0.12	-0.68	71,77,83,84	0
6	BYT	C	1106	25/25	0.96	0.11	-0.73	51,55,61,61	0
7	GOL	C	1102	6/6	0.96	0.21	-0.84	60,63,69,72	0
3	MG	A	1102	1/1	0.81	0.09	-1.15	60,60,60,60	0
6	BYT	C	1107	16/25	0.93	0.12	-1.36	72,78,83,84	0
3	MG	D	1102	1/1	0.89	0.09	-1.36	82,82,82,82	0
2	ZN	C	1101	1/1	1.00	0.15	-1.54	49,49,49,49	0
2	ZN	D	1101	1/1	1.00	0.14	-1.98	57,57,57,57	0
2	ZN	A	1101	1/1	0.99	0.14	-2.22	37,37,37,37	0
2	ZN	B	1102	1/1	1.00	0.12	-2.40	46,46,46,46	0
3	MG	B	1103	1/1	0.97	0.06	-3.23	43,43,43,43	0
3	MG	C	1103	1/1	0.99	0.07	-6.53	56,56,56,56	0
4	CL	B	1104	1/1	0.96	0.11	-	86,86,86,86	0
4	CL	A	1103	1/1	0.97	0.10	-	47,47,47,47	0
4	CL	D	1103	1/1	0.87	0.09	-	83,83,83,83	0
4	CL	C	1104	1/1	0.94	0.09	-	70,70,70,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.