WORLDWIDE PDB

PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:18 PM GMT

PDB ID	:	4XC7
Title	:	Isobutyryl-CoA mutase fused with bound butyryl-CoA and without cobalamin or GDP (apo-IcmF)
Authors	:	Jost, M.; Drennan, C.L.
Deposited on	:	2014-12-17
Resolution	:	3.45 Å(reported)

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
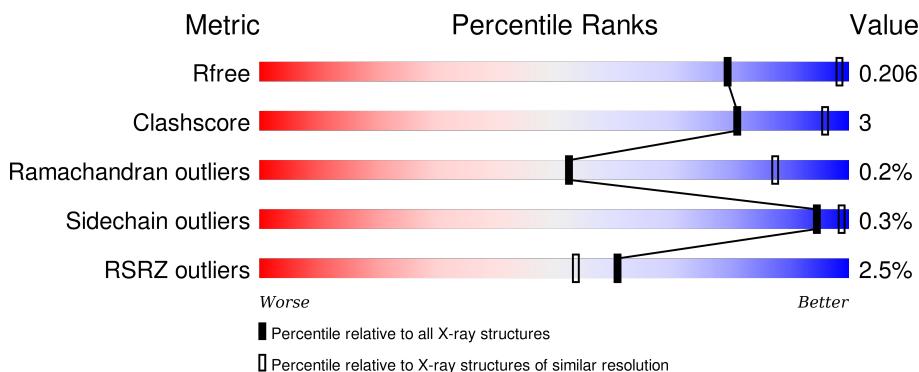
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.45 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	1000 (3.56-3.36)
Clashscore	102246	1090 (3.56-3.36)
Ramachandran outliers	100387	1057 (3.56-3.36)
Sidechain outliers	100360	1058 (3.56-3.36)
RSRZ outliers	91569	1005 (3.56-3.36)

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 <=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	1113	
1	B	1113	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 16179 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 Isobutyryl-CoA mutase fused.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1053	Total 7951	C 4974	N 1413	O 1528	S 36	0	0	0
1	B	1063	Total 8128	C 5075	N 1455	O 1562	S 36	0	0	0

There are 40 discrepancies between the modelled and reference sequences:
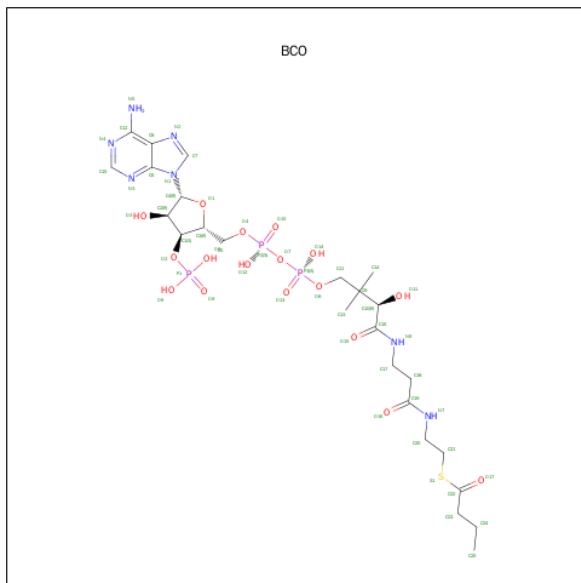
Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP Q1LRY0
A	-18	GLY	-	expression tag	UNP Q1LRY0
A	-17	SER	-	expression tag	UNP Q1LRY0
A	-16	SER	-	expression tag	UNP Q1LRY0
A	-15	HIS	-	expression tag	UNP Q1LRY0
A	-14	HIS	-	expression tag	UNP Q1LRY0
A	-13	HIS	-	expression tag	UNP Q1LRY0
A	-12	HIS	-	expression tag	UNP Q1LRY0
A	-11	HIS	-	expression tag	UNP Q1LRY0
A	-10	HIS	-	expression tag	UNP Q1LRY0
A	-9	SER	-	expression tag	UNP Q1LRY0
A	-8	SER	-	expression tag	UNP Q1LRY0
A	-7	GLY	-	expression tag	UNP Q1LRY0
A	-6	LEU	-	expression tag	UNP Q1LRY0
A	-5	VAL	-	expression tag	UNP Q1LRY0
A	-4	PRO	-	expression tag	UNP Q1LRY0
A	-3	ARG	-	expression tag	UNP Q1LRY0
A	-2	GLY	-	expression tag	UNP Q1LRY0
A	-1	SER	-	expression tag	UNP Q1LRY0
A	0	HIS	-	expression tag	UNP Q1LRY0
B	-19	MET	-	initiating methionine	UNP Q1LRY0
B	-18	GLY	-	expression tag	UNP Q1LRY0
B	-17	SER	-	expression tag	UNP Q1LRY0
B	-16	SER	-	expression tag	UNP Q1LRY0
B	-15	HIS	-	expression tag	UNP Q1LRY0

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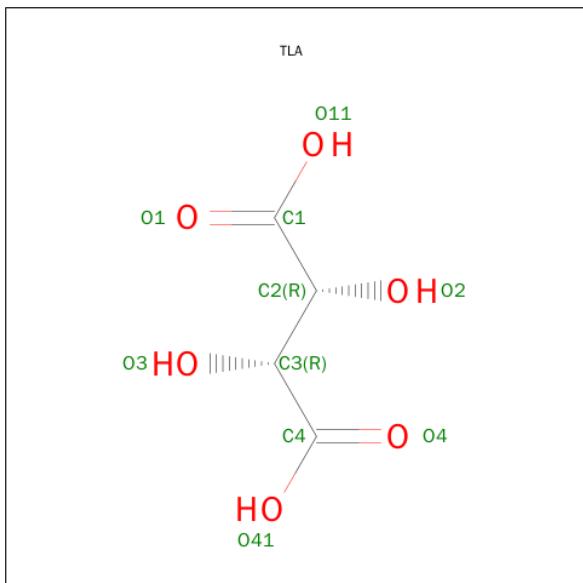
Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	HIS	-	expression tag	UNP Q1LRY0
B	-13	HIS	-	expression tag	UNP Q1LRY0
B	-12	HIS	-	expression tag	UNP Q1LRY0
B	-11	HIS	-	expression tag	UNP Q1LRY0
B	-10	HIS	-	expression tag	UNP Q1LRY0
B	-9	SER	-	expression tag	UNP Q1LRY0
B	-8	SER	-	expression tag	UNP Q1LRY0
B	-7	GLY	-	expression tag	UNP Q1LRY0
B	-6	LEU	-	expression tag	UNP Q1LRY0
B	-5	VAL	-	expression tag	UNP Q1LRY0
B	-4	PRO	-	expression tag	UNP Q1LRY0
B	-3	ARG	-	expression tag	UNP Q1LRY0
B	-2	GLY	-	expression tag	UNP Q1LRY0
B	-1	SER	-	expression tag	UNP Q1LRY0
B	0	HIS	-	expression tag	UNP Q1LRY0

- Molecule 2 is Butyryl Coenzyme A (three-letter code: BCO) (formula: $C_{25}H_{42}N_7O_{17}P_3S$).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	0
			53	25	7	17	3	1		
2	B	1	Total	C	N	O	P		0	0
			27	10	5	10	2			

- Molecule 3 is L(+)-TARTARIC ACID (three-letter code: TLA) (formula: $C_4H_6O_6$).
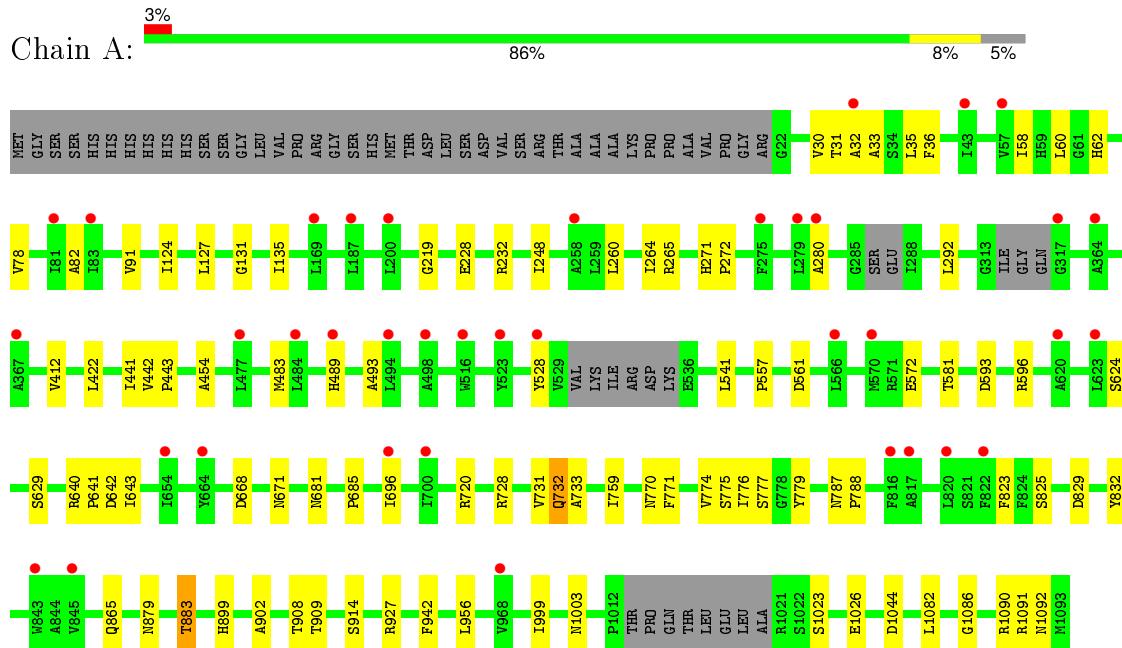
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			10	4	6		
3	B	1	Total	C	O	0	0
			10	4	6		
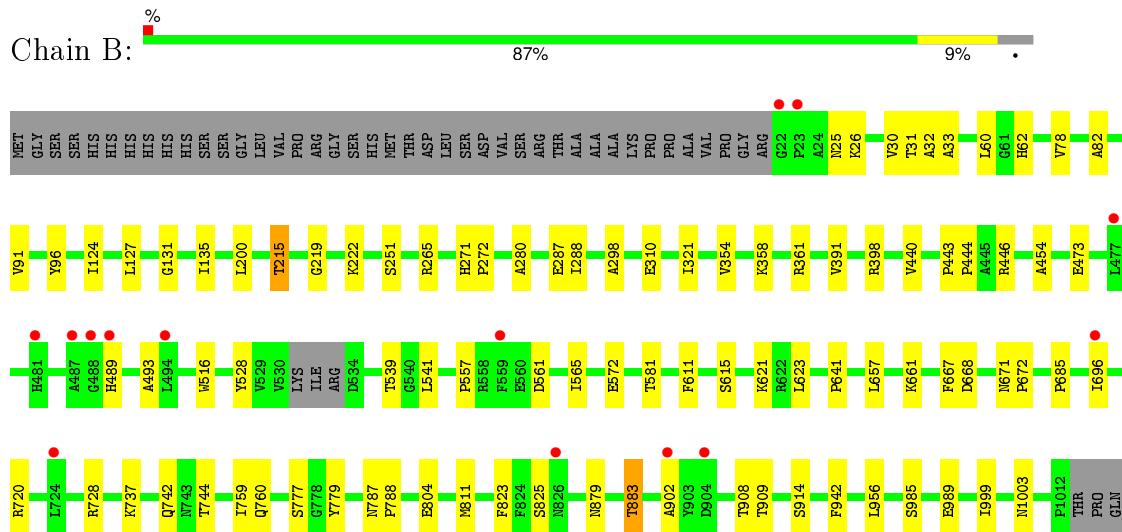
3 Residue-property plots ⓘ
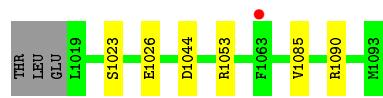
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Isobutyryl-CoA mutase fused

- Molecule 1: Isobutyryl-CoA mutase fused

4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α, β, γ	318.18Å 318.18Å 344.71Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	91.85 – 3.45 91.85 – 3.45	Depositor EDS
% Data completeness (in resolution range)	95.7 (91.85-3.45) 95.7 (91.85-3.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.19	Depositor
$< I/\sigma(I) >$ [1]	3.70 (at 3.49Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1760)	Depositor
R, R_{free}	0.186 , 0.203 0.194 , 0.206	Depositor DCC
R_{free} test set	4218 reflections (5.29%)	DCC
Wilson B-factor (Å^2)	92.7	Xtriage
Anisotropy	0.557	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 73.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< |L| > = 0.48, < L^2 > = 0.31$	Xtriage
Outliers	0 of 84003 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	16179	wwPDB-VP
Average B, all atoms (Å^2)	106.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.02% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: TLA, BCO

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	0.21	0/8091	0.36	0/10968
1	B	0.21	0/8270	0.37	0/11199
All	All	0.21	0/16361	0.36	0/22167

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7951	0	7616	55	0
1	B	8128	0	7885	55	0
2	A	53	0	36	1	0
2	B	27	0	13	0	0
3	A	10	0	4	1	0
3	B	10	0	4	0	0
All	All	16179	0	15558	104	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 3.

All (104) close contacts within the same asymmetric unit are listed below, sorted by their clash

magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1053:ARG:HG2	1:B:1085:VAL:HB	1.72	0.72
1:A:732:GLN:HA	1:A:775:SER:HB3	1.75	0.68
1:A:248:ILE:HD11	1:A:292:LEU:HD13	1.80	0.63
1:A:561:ASP:HB2	1:B:561:ASP:HB2	1.82	0.62
1:A:777:SER:HA	1:A:823:PHE:HB3	1.80	0.62
1:A:728:ARG:NH2	2:A:1101:BCO:O14	2.33	0.61
1:B:615:SER:O	1:B:621:LYS:NZ	2.35	0.60
1:A:731:VAL:HG12	1:A:771:PHE:HE1	1.67	0.60
1:B:454:ALA:HA	1:B:956:LEU:HD22	1.84	0.59
1:A:30:VAL:HG23	1:A:78:VAL:HG11	1.86	0.57
1:A:696:ILE:HD13	1:A:720:ARG:HG3	1.87	0.57
1:B:30:VAL:HG23	1:B:78:VAL:HG11	1.87	0.57
1:A:31:THR:HG22	1:A:82:ALA:HB3	1.88	0.56
1:B:696:ILE:HD13	1:B:720:ARG:HG3	1.87	0.56
1:B:742:GLN:HB3	1:B:744:THR:OG1	2.07	0.54
1:A:260:LEU:HD21	1:A:280:ALA:HB2	1.90	0.54
1:B:31:THR:HG22	1:B:82:ALA:HB3	1.89	0.53
1:A:908:THR:OG1	1:A:909:THR:N	2.42	0.53
1:B:685:PRO:HB3	1:B:759:ILE:HD11	1.91	0.52
1:B:760:GLN:HG3	1:B:811:MET:HE1	1.91	0.52
1:A:454:ALA:HA	1:A:956:LEU:HD22	1.92	0.52
1:A:787:ASN:HB2	1:A:788:PRO:HD2	1.93	0.51
1:A:685:PRO:HB3	1:A:759:ILE:HD11	1.92	0.51
1:A:58:ILE:HG13	1:A:260:LEU:HD12	1.92	0.51
1:B:999:ILE:N	1:B:1003:ASN:OD1	2.42	0.51
1:A:572:GLU:HG2	1:A:581:THR:HG21	1.94	0.50
1:B:879:ASN:O	1:B:883:THR:OG1	2.25	0.50
1:A:36:PHE:HE2	1:A:643:ILE:HG23	1.77	0.50
1:B:787:ASN:HB2	1:B:788:PRO:HD2	1.92	0.50
1:A:1082:LEU:O	1:A:1086:GLY:N	2.44	0.49
1:B:572:GLU:HG2	1:B:581:THR:HG21	1.93	0.49
1:A:999:ILE:N	1:A:1003:ASN:OD1	2.44	0.48
1:B:33:ALA:HB3	1:B:62:HIS:HA	1.94	0.48
1:A:33:ALA:HB3	1:A:62:HIS:HA	1.94	0.48
1:A:35:LEU:HD22	1:A:642:ASP:HB3	1.95	0.48
1:B:777:SER:HA	1:B:823:PHE:HB3	1.96	0.47
1:B:26:LYS:HD3	1:B:26:LYS:HA	1.82	0.47
1:B:908:THR:OG1	1:B:909:THR:N	2.47	0.47
1:A:942:PHE:CZ	1:B:557:PRO:HB3	2.49	0.47
1:A:902:ALA:HB1	1:A:914:SER:OG	2.14	0.47
1:A:1023:SER:HB3	1:A:1026:GLU:HG3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:672:PRO:O	1:B:728:ARG:NH2	2.45	0.47
1:B:215:THR:HB	1:B:321:ILE:HG21	1.96	0.47
1:B:737:LYS:HD3	1:B:777:SER:HB3	1.97	0.46
1:B:1023:SER:HB3	1:B:1026:GLU:HG3	1.97	0.46
1:A:557:PRO:HB3	1:B:942:PHE:CZ	2.52	0.45
1:A:36:PHE:HB3	1:A:629:SER:HB2	1.99	0.45
1:A:228:GLU:OE1	1:A:232:ARG:NH2	2.50	0.45
1:A:412:VAL:HG13	1:A:422:LEU:HD13	1.99	0.45
1:A:264:ILE:HG12	1:A:1091:ARG:HB2	1.98	0.45
1:B:446:ARG:NH2	1:B:804:GLU:OE2	2.50	0.44
1:B:32:ALA:HB2	1:B:60:LEU:HB2	1.99	0.44
1:A:879:ASN:O	1:A:883:THR:OG1	2.30	0.43
1:A:681:ASN:HA	1:A:733:ALA:HA	1.98	0.43
1:A:640:ARG:NH2	1:A:642:ASP:OD2	2.51	0.43
1:B:611:PHE:CD1	1:B:623:LEU:HD22	2.53	0.43
1:B:287:GLU:HG2	1:B:288:ILE:HG23	2.01	0.43
1:B:398:ARG:NH1	1:B:440:VAL:HA	2.34	0.43
1:B:443:PRO:HA	1:B:444:PRO:HD3	1.85	0.43
1:B:358:LYS:O	1:B:361:ARG:HG2	2.19	0.43
1:B:96:TYR:HB2	1:B:641:PRO:HB2	2.00	0.43
1:A:32:ALA:HB2	1:A:60:LEU:HB2	2.00	0.42
1:A:596:ARG:HG2	1:A:624:SER:HB2	2.00	0.42
1:A:528:TYR:HB2	1:A:541:LEU:HD21	2.02	0.42
1:B:902:ALA:HB1	1:B:914:SER:OG	2.19	0.42
1:A:1044:ASP:N	1:A:1044:ASP:OD1	2.53	0.42
1:B:779:TYR:CD1	1:B:825:SER:HB2	2.55	0.42
1:B:265:ARG:HE	1:B:1090:ARG:HD3	1.83	0.41
1:A:668:ASP:HB3	1:A:671:ASN:HB2	2.02	0.41
1:A:489:HIS:CE1	1:B:493:ALA:HB1	2.55	0.41
1:B:219:GLY:O	1:B:358:LYS:NZ	2.46	0.41
1:A:728:ARG:HG2	1:A:770:ASN:HB3	2.02	0.41
1:B:528:TYR:HB2	1:B:541:LEU:HD21	2.01	0.41
1:B:222:LYS:HD2	1:B:310:GLU:HB2	2.02	0.41
1:B:985:SER:O	1:B:989:GLU:HG2	2.20	0.41
1:A:441:ILE:HG22	1:A:442:VAL:HG23	2.03	0.41
1:A:779:TYR:CD1	1:A:825:SER:HB2	2.56	0.41
1:A:593:ASP:OD1	1:A:927:ARG:NH2	2.53	0.41
1:B:1044:ASP:N	1:B:1044:ASP:OD1	2.53	0.41
1:B:668:ASP:HB3	1:B:671:ASN:HB2	2.03	0.41
1:B:251:SER:HB3	1:B:280:ALA:HB1	2.02	0.41
1:B:271:HIS:CG	1:B:272:PRO:HD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:265:ARG:NH1	1:A:1092:ASN:OD1	2.53	0.41
1:B:516:TRP:CE2	1:B:565:ILE:HD12	2.56	0.41
1:A:829:ASP:HB2	1:A:832:TYR:CE2	2.56	0.41
1:A:219:GLY:HA2	3:A:1102:TLA:O2	2.21	0.41
1:A:640:ARG:HA	1:A:641:PRO:HD3	1.93	0.41
1:B:528:TYR:HB3	1:B:539:THR:HB	2.03	0.41
1:B:354:VAL:HB	1:B:391:VAL:HG22	2.03	0.41
1:B:200:LEU:HD11	1:B:298:ALA:HA	2.01	0.41
1:A:91:VAL:HA	1:A:127:LEU:HD11	2.03	0.41
1:A:493:ALA:HB1	1:B:489:HIS:CD2	2.55	0.41
1:B:446:ARG:HH11	1:B:446:ARG:HA	1.86	0.41
1:A:927:ARG:HA	1:A:927:ARG:HD3	1.82	0.41
1:B:124:ILE:HG23	1:B:135:ILE:HB	2.02	0.40
1:B:611:PHE:HB3	1:B:667:PHE:CZ	2.57	0.40
1:A:265:ARG:O	1:A:1090:ARG:NH2	2.51	0.40
1:A:442:VAL:HA	1:A:443:PRO:HD2	1.93	0.40
1:A:124:ILE:HG23	1:A:135:ILE:HB	2.03	0.40
1:B:91:VAL:HA	1:B:127:LEU:HD11	2.03	0.40
1:A:865:GLN:HG3	1:A:899:HIS:HD2	1.86	0.40
1:A:483:MET:HE1	1:B:473:GLU:HB3	2.04	0.40
1:B:657:LEU:HG	1:B:661:LYS:HE3	2.04	0.40
1:A:271:HIS:CG	1:A:272:PRO:HD2	2.56	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	1043/1113 (94%)	997 (96%)	43 (4%)	3 (0%)	46	84
1	B	1057/1113 (95%)	1013 (96%)	43 (4%)	1 (0%)	56	90
All	All	2100/2226 (94%)	2010 (96%)	86 (4%)	4 (0%)	52	87

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	776	ILE
1	A	732	GLN
1	A	131	GLY
1	B	131	GLY

5.3.2 Protein sidechains (i)

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	795/906 (88%)	793 (100%)	2 (0%)	94	99
1	B	830/906 (92%)	827 (100%)	3 (0%)	93	98
All	All	1625/1812 (90%)	1620 (100%)	5 (0%)	94	99

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	774	VAL
1	A	883	THR
1	B	25	ASN
1	B	215	THR
1	B	883	THR

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

Mol	Chain	Res	Type
1	A	475	GLN
1	A	865	GLN
1	A	899	HIS
1	B	475	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#$|Z| > 2$	Counts	RMSZ	#$|Z| > 2$
2	BCO	A	1101	-	43,55,55	2.64	8 (18%)	55,81,81	2.56	16 (29%)
3	TLA	A	1102	-	3,9,9	0.44	0	6,12,12	0.85	0
2	BCO	B	1101	-	24,29,55	1.73	4 (16%)	28,45,81	2.34	3 (10%)
3	TLA	B	1102	-	3,9,9	0.37	0	6,12,12	1.48	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
2	BCO	A	1101	-	-	0/49/70/70	0/3/3/3
3	TLA	A	1102	-	-	0/4/12/12	0/0/0/0
2	BCO	B	1101	-	-	0/11/31/70	0/3/3/3
3	TLA	B	1102	-	-	0/4/12/12	0/0/0/0

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	BCO	C2-C1	-4.91	1.41	1.53
2	B	1101	BCO	C2-C1	-4.76	1.42	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1101	BCO	O1-C3	-2.26	1.39	1.45
2	A	1101	BCO	O1-C3	-2.26	1.39	1.45
2	A	1101	BCO	O17-C22	2.12	1.26	1.21
2	B	1101	BCO	P2-O10	3.67	1.63	1.51
2	A	1101	BCO	C17-C18	3.70	1.51	1.36
2	B	1101	BCO	C12-N5	4.17	1.47	1.34
2	A	1101	BCO	C12-N5	4.18	1.47	1.34
2	A	1101	BCO	C23-C24	5.57	1.50	1.30
2	A	1101	BCO	C19-N7	8.69	1.46	1.34
2	A	1101	BCO	C16-N6	10.14	1.46	1.34

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1101	BCO	N3-C15-N4	-10.94	120.52	128.89
2	A	1101	BCO	N3-C15-N4	-10.72	120.69	128.89
2	A	1101	BCO	P3-O7-P2	-4.08	121.27	132.73
2	A	1101	BCO	C25-C24-C23	-4.05	117.69	125.27
2	A	1101	BCO	O15-C16-N6	-3.99	119.68	123.94
2	A	1101	BCO	C24-C23-C22	-3.18	117.74	123.68
3	B	1102	TLA	C4-C3-C2	-2.95	107.30	113.35
2	A	1101	BCO	C17-N6-C16	-2.12	120.02	123.80
3	B	1102	TLA	C1-C2-C3	-2.01	109.23	113.35
2	A	1101	BCO	C1-C2-C4	2.04	104.87	99.98
2	A	1101	BCO	C18-C19-N7	2.20	119.94	114.87
2	B	1101	BCO	O4-C5-C3	2.26	117.44	109.12
2	A	1101	BCO	C20-C21-S1	2.34	117.62	111.36
2	A	1101	BCO	O4-C5-C3	2.38	117.90	109.12
2	A	1101	BCO	O7-P3-O8	2.59	109.82	102.94
2	A	1101	BCO	O7-P2-O4	2.70	110.10	102.94
2	B	1101	BCO	C1-C2-C4	2.75	106.58	99.98
2	A	1101	BCO	C21-C20-N7	3.15	118.66	112.36
2	A	1101	BCO	C10-C16-N6	3.88	119.68	115.58
2	A	1101	BCO	O8-C11-C9	4.27	117.41	110.55
2	A	1101	BCO	C21-S1-C22	8.30	110.15	99.59

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1101	BCO	1	0
3	A	1102	TLA	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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	1053/1113 (94%)	0.42	38 (3%) 46	40	72, 114, 169, 224	0
1	B	1063/1113 (95%)	0.26	15 (1%) 78	71	56, 89, 156, 209	0
All	All	2116/2226 (95%)	0.34	53 (2%) 61	54	56, 102, 162, 224	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	22	GLY	3.9
1	A	570	MET	3.9
1	B	494	LEU	3.7
1	B	489	HIS	3.6
1	A	494	LEU	3.3
1	B	487	ALA	3.2
1	A	700	ILE	3.0
1	A	620	ALA	2.9
1	B	902	ALA	2.8
1	A	280	ALA	2.8
1	A	279	LEU	2.8
1	A	32	ALA	2.7
1	A	816	PHE	2.7
1	B	904	ASP	2.7
1	B	696	ILE	2.7
1	A	498	ALA	2.7
1	A	817	ALA	2.7
1	A	258	ALA	2.6
1	B	488	GLY	2.5
1	A	484	LEU	2.5
1	A	83	ILE	2.5
1	A	489	HIS	2.5
1	A	822	PHE	2.5
1	A	623	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	724	LEU	2.5
1	A	696	ILE	2.4
1	A	200	LEU	2.4
1	A	57	VAL	2.4
1	A	317	GLY	2.4
1	A	43	ILE	2.4
1	A	169	LEU	2.4
1	A	654	ILE	2.4
1	A	477	LEU	2.4
1	B	481	HIS	2.4
1	A	367	ALA	2.3
1	B	477	LEU	2.3
1	A	523	TYR	2.3
1	B	559	PHE	2.3
1	A	843	TRP	2.3
1	B	826	ASN	2.2
1	A	664	TYR	2.2
1	A	275	PHE	2.2
1	B	1063	PHE	2.2
1	A	820	LEU	2.2
1	A	968	VAL	2.2
1	A	528	TYR	2.1
1	A	516	TRP	2.1
1	A	187	LEU	2.1
1	A	566	LEU	2.1
1	B	23	PRO	2.0
1	A	845	VAL	2.0
1	A	81	ILE	2.0
1	A	364	ALA	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no 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($Å^2$)	Q<0.9
3	TLA	A	1102	10/10	0.72	0.22	-0.22	135,140,141,142	0
3	TLA	B	1102	10/10	0.94	0.21	-0.79	93,98,100,102	0
2	BCO	A	1101	53/53	0.93	0.23	-0.88	72,114,148,163	0
2	BCO	B	1101	27/53	0.85	0.15	-1.74	118,152,198,199	0

6.5 Other polymers (i)

There are no such residues in this entry.