



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 12:18 pm BST

PDB ID : 5ZI0
Title : Ketoreductase LbCR mutant - M8
Authors : Gong, X.M.; Zheng, G.W.; Xu, J.H.
Deposited on : 2018-03-14
Resolution : 2.30 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtrriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

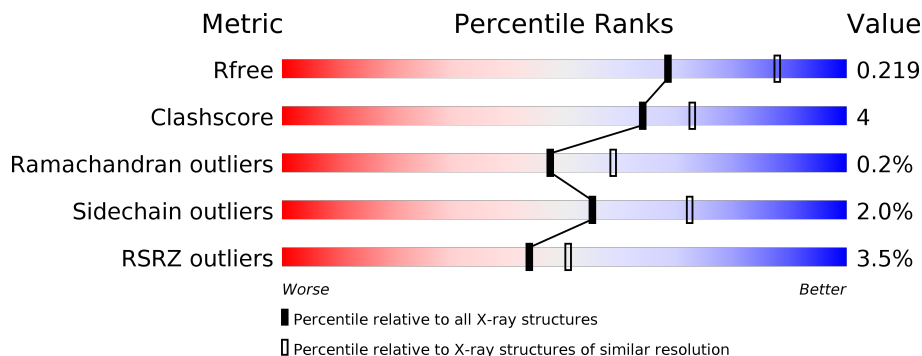
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 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	281	 5% 77% 11% • 12%
1	B	281	 7% 77% 11% • 12%
1	C	281	 83% 5% 12%
1	D	281	 80% 8% 12%

2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 7972 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 3-oxoacyl-acyl carrier protein reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	248	1830	1145	324	357	4	0	0	0
1	B	248	1830	1145	324	357	4	0	0	0
1	C	248	1830	1145	324	357	4	0	0	0
1	D	248	1830	1145	324	357	4	0	0	0

There are 148 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-31	MET	-	expression tag	UNP Q03TH6
A	-30	GLY	-	expression tag	UNP Q03TH6
A	-29	SER	-	expression tag	UNP Q03TH6
A	-28	SER	-	expression tag	UNP Q03TH6
A	-27	HIS	-	expression tag	UNP Q03TH6
A	-26	HIS	-	expression tag	UNP Q03TH6
A	-25	HIS	-	expression tag	UNP Q03TH6
A	-24	HIS	-	expression tag	UNP Q03TH6
A	-23	HIS	-	expression tag	UNP Q03TH6
A	-22	HIS	-	expression tag	UNP Q03TH6
A	-21	SER	-	expression tag	UNP Q03TH6
A	-20	SER	-	expression tag	UNP Q03TH6
A	-19	GLY	-	expression tag	UNP Q03TH6
A	-18	LEU	-	expression tag	UNP Q03TH6
A	-17	VAL	-	expression tag	UNP Q03TH6
A	-16	PRO	-	expression tag	UNP Q03TH6
A	-15	ARG	-	expression tag	UNP Q03TH6
A	-14	GLY	-	expression tag	UNP Q03TH6
A	-13	SER	-	expression tag	UNP Q03TH6
A	-12	HIS	-	expression tag	UNP Q03TH6
A	-11	MET	-	expression tag	UNP Q03TH6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	ALA	-	expression tag	UNP Q03TH6
A	-9	SER	-	expression tag	UNP Q03TH6
A	-8	MET	-	expression tag	UNP Q03TH6
A	-7	THR	-	expression tag	UNP Q03TH6
A	-6	GLY	-	expression tag	UNP Q03TH6
A	-5	GLY	-	expression tag	UNP Q03TH6
A	-4	GLN	-	expression tag	UNP Q03TH6
A	-3	GLN	-	expression tag	UNP Q03TH6
A	-2	MET	-	expression tag	UNP Q03TH6
A	-1	GLY	-	expression tag	UNP Q03TH6
A	0	ARG	-	expression tag	UNP Q03TH6
A	154	ILE	MET	engineered mutation	UNP Q03TH6
A	155	ASP	ALA	engineered mutation	UNP Q03TH6
A	198	ILE	VAL	engineered mutation	UNP Q03TH6
A	201	ASP	ALA	engineered mutation	UNP Q03TH6
A	202	LEU	ALA	engineered mutation	UNP Q03TH6
B	-31	MET	-	expression tag	UNP Q03TH6
B	-30	GLY	-	expression tag	UNP Q03TH6
B	-29	SER	-	expression tag	UNP Q03TH6
B	-28	SER	-	expression tag	UNP Q03TH6
B	-27	HIS	-	expression tag	UNP Q03TH6
B	-26	HIS	-	expression tag	UNP Q03TH6
B	-25	HIS	-	expression tag	UNP Q03TH6
B	-24	HIS	-	expression tag	UNP Q03TH6
B	-23	HIS	-	expression tag	UNP Q03TH6
B	-22	HIS	-	expression tag	UNP Q03TH6
B	-21	SER	-	expression tag	UNP Q03TH6
B	-20	SER	-	expression tag	UNP Q03TH6
B	-19	GLY	-	expression tag	UNP Q03TH6
B	-18	LEU	-	expression tag	UNP Q03TH6
B	-17	VAL	-	expression tag	UNP Q03TH6
B	-16	PRO	-	expression tag	UNP Q03TH6
B	-15	ARG	-	expression tag	UNP Q03TH6
B	-14	GLY	-	expression tag	UNP Q03TH6
B	-13	SER	-	expression tag	UNP Q03TH6
B	-12	HIS	-	expression tag	UNP Q03TH6
B	-11	MET	-	expression tag	UNP Q03TH6
B	-10	ALA	-	expression tag	UNP Q03TH6
B	-9	SER	-	expression tag	UNP Q03TH6
B	-8	MET	-	expression tag	UNP Q03TH6
B	-7	THR	-	expression tag	UNP Q03TH6
B	-6	GLY	-	expression tag	UNP Q03TH6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	GLY	-	expression tag	UNP Q03TH6
B	-4	GLN	-	expression tag	UNP Q03TH6
B	-3	GLN	-	expression tag	UNP Q03TH6
B	-2	MET	-	expression tag	UNP Q03TH6
B	-1	GLY	-	expression tag	UNP Q03TH6
B	0	ARG	-	expression tag	UNP Q03TH6
B	154	ILE	MET	engineered mutation	UNP Q03TH6
B	155	ASP	ALA	engineered mutation	UNP Q03TH6
B	198	ILE	VAL	engineered mutation	UNP Q03TH6
B	201	ASP	ALA	engineered mutation	UNP Q03TH6
B	202	LEU	ALA	engineered mutation	UNP Q03TH6
C	-31	MET	-	expression tag	UNP Q03TH6
C	-30	GLY	-	expression tag	UNP Q03TH6
C	-29	SER	-	expression tag	UNP Q03TH6
C	-28	SER	-	expression tag	UNP Q03TH6
C	-27	HIS	-	expression tag	UNP Q03TH6
C	-26	HIS	-	expression tag	UNP Q03TH6
C	-25	HIS	-	expression tag	UNP Q03TH6
C	-24	HIS	-	expression tag	UNP Q03TH6
C	-23	HIS	-	expression tag	UNP Q03TH6
C	-22	HIS	-	expression tag	UNP Q03TH6
C	-21	SER	-	expression tag	UNP Q03TH6
C	-20	SER	-	expression tag	UNP Q03TH6
C	-19	GLY	-	expression tag	UNP Q03TH6
C	-18	LEU	-	expression tag	UNP Q03TH6
C	-17	VAL	-	expression tag	UNP Q03TH6
C	-16	PRO	-	expression tag	UNP Q03TH6
C	-15	ARG	-	expression tag	UNP Q03TH6
C	-14	GLY	-	expression tag	UNP Q03TH6
C	-13	SER	-	expression tag	UNP Q03TH6
C	-12	HIS	-	expression tag	UNP Q03TH6
C	-11	MET	-	expression tag	UNP Q03TH6
C	-10	ALA	-	expression tag	UNP Q03TH6
C	-9	SER	-	expression tag	UNP Q03TH6
C	-8	MET	-	expression tag	UNP Q03TH6
C	-7	THR	-	expression tag	UNP Q03TH6
C	-6	GLY	-	expression tag	UNP Q03TH6
C	-5	GLY	-	expression tag	UNP Q03TH6
C	-4	GLN	-	expression tag	UNP Q03TH6
C	-3	GLN	-	expression tag	UNP Q03TH6
C	-2	MET	-	expression tag	UNP Q03TH6
C	-1	GLY	-	expression tag	UNP Q03TH6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	0	ARG	-	expression tag	UNP Q03TH6
C	154	ILE	MET	engineered mutation	UNP Q03TH6
C	155	ASP	ALA	engineered mutation	UNP Q03TH6
C	198	ILE	VAL	engineered mutation	UNP Q03TH6
C	201	ASP	ALA	engineered mutation	UNP Q03TH6
C	202	LEU	ALA	engineered mutation	UNP Q03TH6
D	-31	MET	-	expression tag	UNP Q03TH6
D	-30	GLY	-	expression tag	UNP Q03TH6
D	-29	SER	-	expression tag	UNP Q03TH6
D	-28	SER	-	expression tag	UNP Q03TH6
D	-27	HIS	-	expression tag	UNP Q03TH6
D	-26	HIS	-	expression tag	UNP Q03TH6
D	-25	HIS	-	expression tag	UNP Q03TH6
D	-24	HIS	-	expression tag	UNP Q03TH6
D	-23	HIS	-	expression tag	UNP Q03TH6
D	-22	HIS	-	expression tag	UNP Q03TH6
D	-21	SER	-	expression tag	UNP Q03TH6
D	-20	SER	-	expression tag	UNP Q03TH6
D	-19	GLY	-	expression tag	UNP Q03TH6
D	-18	LEU	-	expression tag	UNP Q03TH6
D	-17	VAL	-	expression tag	UNP Q03TH6
D	-16	PRO	-	expression tag	UNP Q03TH6
D	-15	ARG	-	expression tag	UNP Q03TH6
D	-14	GLY	-	expression tag	UNP Q03TH6
D	-13	SER	-	expression tag	UNP Q03TH6
D	-12	HIS	-	expression tag	UNP Q03TH6
D	-11	MET	-	expression tag	UNP Q03TH6
D	-10	ALA	-	expression tag	UNP Q03TH6
D	-9	SER	-	expression tag	UNP Q03TH6
D	-8	MET	-	expression tag	UNP Q03TH6
D	-7	THR	-	expression tag	UNP Q03TH6
D	-6	GLY	-	expression tag	UNP Q03TH6
D	-5	GLY	-	expression tag	UNP Q03TH6
D	-4	GLN	-	expression tag	UNP Q03TH6
D	-3	GLN	-	expression tag	UNP Q03TH6
D	-2	MET	-	expression tag	UNP Q03TH6
D	-1	GLY	-	expression tag	UNP Q03TH6
D	0	ARG	-	expression tag	UNP Q03TH6
D	154	ILE	MET	engineered mutation	UNP Q03TH6
D	155	ASP	ALA	engineered mutation	UNP Q03TH6
D	198	ILE	VAL	engineered mutation	UNP Q03TH6
D	201	ASP	ALA	engineered mutation	UNP Q03TH6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	202	LEU	ALA	engineered mutation	UNP Q03TH6

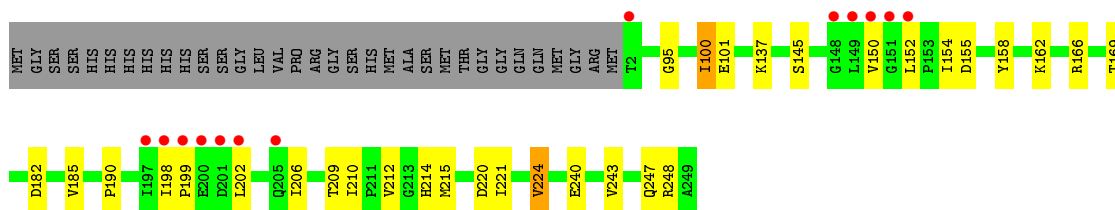
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	157	Total O 157 157	0	0
2	B	109	Total O 109 109	0	0
2	C	201	Total O 201 201	0	0
2	D	185	Total O 185 185	0	0

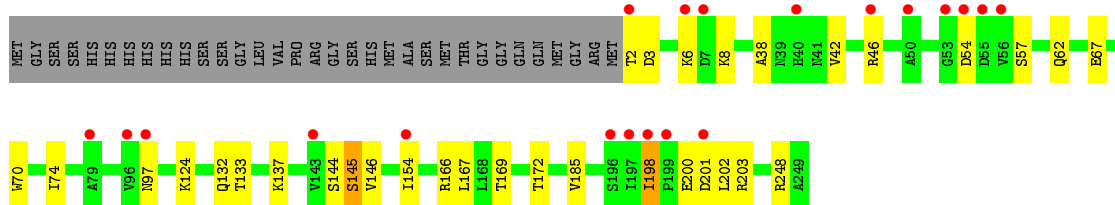
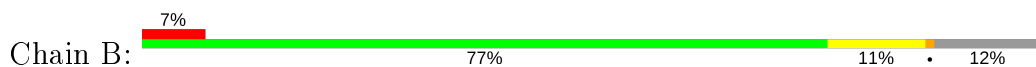
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

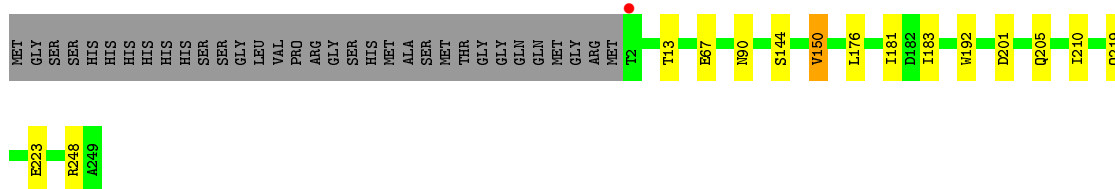
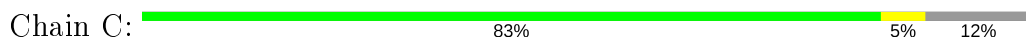
- Molecule 1: 3-oxoacyl-acyl carrier protein reductase



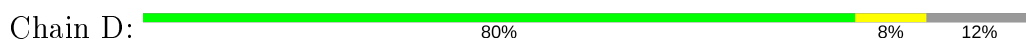
- Molecule 1: 3-oxoacyl-acyl carrier protein reductase

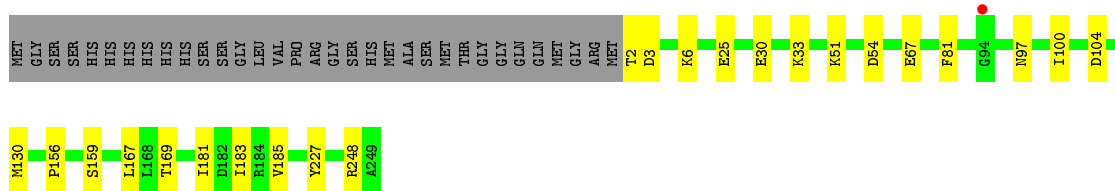


- Molecule 1: 3-oxoacyl-acyl carrier protein reductase



- Molecule 1: 3-oxoacyl-acyl carrier protein reductase





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	71.93Å 118.19Å 248.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.01 – 2.30 31.11 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.4 (31.01-2.30) 97.4 (31.11-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	17.70 (at 2.31Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.168 , 0.220 0.168 , 0.219	Depositor DCC
R_{free} test set	2321 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	19.7	Xtriage
Anisotropy	0.252	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 40.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.019 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.035 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7972	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.07% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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	0.39	0/1854	0.54	0/2513
1	B	0.35	0/1854	0.53	0/2513
1	C	0.38	0/1854	0.54	0/2513
1	D	0.40	0/1854	0.55	0/2513
All	All	0.38	0/7416	0.54	0/10052

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

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	1830	0	1845	25	0
1	B	1830	0	1845	19	0
1	C	1830	0	1845	9	0
1	D	1830	0	1845	13	0
2	A	157	0	0	5	0
2	B	109	0	0	4	0
2	C	201	0	0	3	0
2	D	185	0	0	4	0
All	All	7972	0	7380	62	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 4.

All (62) 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:67:GLU:OE1	2:C:301:HOH:O	1.98	0.80
1:D:97:ASN:OD1	2:D:301:HOH:O	1.99	0.80
1:A:166:ARG:NH1	1:A:240:GLU:OE2	2.17	0.77
1:B:132:GLN:NE2	2:B:302:HOH:O	2.17	0.77
1:A:224:VAL:HG11	1:A:243:VAL:HG21	1.67	0.76
1:A:209:THR:O	2:A:301:HOH:O	2.06	0.73
1:B:198:ILE:HD11	1:B:203:ARG:HH11	1.54	0.72
1:B:67:GLU:O	2:B:301:HOH:O	2.08	0.70
1:C:150:VAL:O	2:C:302:HOH:O	2.10	0.69
1:A:150:VAL:HG11	1:A:202:LEU:HG	1.74	0.69
1:B:132:GLN:HG3	1:B:133:THR:HG23	1.78	0.66
1:D:54:ASP:OD1	2:D:302:HOH:O	2.14	0.65
1:D:67:GLU:OE2	2:D:303:HOH:O	2.15	0.65
1:A:220:ASP:O	2:A:302:HOH:O	2.14	0.64
1:A:198:ILE:HG13	1:A:199:PRO:HD2	1.82	0.62
1:C:181:ILE:HG22	1:C:183:ILE:HG12	1.82	0.61
1:B:2:THR:OG1	1:B:3:ASP:N	2.30	0.59
1:A:247:GLN:NE2	2:A:303:HOH:O	2.14	0.58
1:A:224:VAL:HG12	1:D:227:TYR:OH	2.07	0.54
1:A:202:LEU:O	1:A:206:ILE:N	2.41	0.54
1:A:101:GLU:HA	1:B:124:LYS:HG2	1.89	0.53
1:D:181:ILE:HG22	1:D:183:ILE:HG12	1.90	0.53
1:A:137:LYS:HG2	1:A:182:ASP:HB3	1.91	0.52
1:B:201:ASP:OD1	1:B:202:LEU:N	2.43	0.52
1:B:3:ASP:HB3	1:B:6:LYS:HD2	1.90	0.52
1:B:57:SER:N	2:B:307:HOH:O	2.31	0.51
1:C:13:THR:O	1:C:90:ASN:HB3	2.11	0.50
1:A:95:GLY:HA2	1:A:155:ASP:OD2	2.12	0.50
1:C:144:SER:HB2	2:C:471:HOH:O	2.13	0.49
1:A:152:LEU:O	2:A:305:HOH:O	2.20	0.49
1:A:169:THR:HG23	1:A:185:VAL:HG12	1.93	0.49
1:D:25:GLU:OE2	1:D:51:LYS:NZ	2.46	0.49
1:A:162:LYS:HE2	2:A:307:HOH:O	2.13	0.48
1:C:192:TRP:HB2	1:C:210:ILE:HD11	1.96	0.48
1:B:167:LEU:HD23	1:B:167:LEU:HA	1.82	0.46
1:B:97:ASN:HA	1:B:154:ILE:O	2.15	0.46
1:A:206:ILE:HG21	1:A:215:MET:HE2	1.96	0.45
1:B:70:TRP:O	1:B:74:ILE:HG12	2.16	0.45
1:C:219:GLN:O	1:C:223:GLU:HG2	2.17	0.45
1:B:169:THR:HG23	1:B:185:VAL:HG12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2:THR:HB	1:D:30:GLU:OE1	2.17	0.44
1:A:166:ARG:HH21	1:B:166:ARG:HH21	1.65	0.44
1:B:198:ILE:HD11	1:B:203:ARG:NH1	2.27	0.44
1:D:169:THR:HG23	1:D:185:VAL:HG12	1.99	0.43
1:C:176:LEU:HD13	1:C:183:ILE:HB	2.01	0.43
1:D:100:ILE:HD13	1:D:156:PRO:HG2	2.00	0.43
1:A:152:LEU:O	1:A:154:ILE:HG23	2.18	0.43
1:A:152:LEU:O	1:A:154:ILE:N	2.51	0.42
1:A:145:SER:HB2	1:A:158:TYR:OH	2.19	0.42
1:A:210:ILE:HG22	1:A:212:VAL:HG22	2.01	0.42
1:D:3:ASP:HB3	1:D:6:LYS:HB2	2.02	0.42
1:B:137:LYS:O	2:B:303:HOH:O	2.21	0.42
1:D:130:MET:SD	1:D:183:ILE:HD12	2.59	0.42
1:D:167:LEU:HA	1:D:167:LEU:HD23	1.81	0.42
1:B:145:SER:OG	1:B:146:VAL:N	2.53	0.42
1:C:201:ASP:O	1:C:205:GLN:HG3	2.20	0.41
1:A:100:ILE:HD13	1:B:172:THR:HG23	2.01	0.41
1:A:214:HIS:HE1	2:D:420:HOH:O	2.04	0.41
1:A:221:ILE:O	1:A:224:VAL:HG22	2.21	0.41
1:B:38:ALA:O	1:B:62:GLN:N	2.38	0.41
1:A:145:SER:HA	1:A:190:PRO:HD2	2.03	0.40
1:D:33:LYS:HD3	1:D:81:PHE:CD1	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	246/281 (88%)	236 (96%)	10 (4%)	0	100	100
1	B	246/281 (88%)	236 (96%)	8 (3%)	2 (1%)	19	23
1	C	246/281 (88%)	240 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	246/281 (88%)	239 (97%)	7 (3%)	0	100	100
All	All	984/1124 (88%)	951 (97%)	31 (3%)	2 (0%)	47	58

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	144	SER
1	B	198	ILE

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	190/216 (88%)	187 (98%)	3 (2%)	62	78
1	B	190/216 (88%)	183 (96%)	7 (4%)	34	48
1	C	190/216 (88%)	188 (99%)	2 (1%)	73	86
1	D	190/216 (88%)	187 (98%)	3 (2%)	62	78
All	All	760/864 (88%)	745 (98%)	15 (2%)	55	72

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	100	ILE
1	A	224	VAL
1	A	248	ARG
1	B	8	LYS
1	B	42	VAL
1	B	46	ARG
1	B	54	ASP
1	B	145	SER
1	B	200	GLU
1	B	248	ARG
1	C	150	VAL
1	C	248	ARG

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Mol	Chain	Res	Type
1	D	104	ASP
1	D	159	SER
1	D	248	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	119	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	248/281 (88%)	-0.17	13 (5%) 27 34	5, 14, 44, 72	0
1	B	248/281 (88%)	0.12	20 (8%) 12 16	8, 22, 45, 63	0
1	C	248/281 (88%)	-0.47	1 (0%) 92 95	5, 12, 24, 55	0
1	D	248/281 (88%)	-0.37	1 (0%) 92 95	5, 12, 27, 39	0
All	All	992/1124 (88%)	-0.22	35 (3%) 44 51	5, 14, 38, 72	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	2	THR	6.5
1	A	149	LEU	5.9
1	A	202	LEU	5.9
1	A	2	THR	5.7
1	A	201	ASP	5.0
1	A	150	VAL	4.8
1	B	96	VAL	4.7
1	A	148	GLY	4.3
1	B	197	ILE	4.3
1	B	2	THR	3.9
1	D	94	GLY	3.4
1	B	201	ASP	3.4
1	B	53	GLY	3.3
1	B	198	ILE	3.2
1	B	97	ASN	2.9
1	B	46	ARG	2.8
1	B	50	ALA	2.7
1	A	197	ILE	2.6
1	B	196	SER	2.6
1	A	199	PRO	2.6
1	B	40	HIS	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	6	LYS	2.4
1	B	154	ILE	2.4
1	A	151	GLY	2.3
1	B	143	VAL	2.3
1	A	205	GLN	2.3
1	B	54	ASP	2.2
1	B	199	PRO	2.2
1	A	152	LEU	2.2
1	A	200	GLU	2.2
1	B	79	ALA	2.1
1	B	55	ASP	2.1
1	B	56	VAL	2.1
1	B	7	ASP	2.0
1	A	198	ILE	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.