



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 7, 2020 – 02:24 PM BST

PDB ID : 4MH3
Title : Crystal structure of Bovine Mitochondrial Peroxiredoxin III
Authors : Cao, Z.; McGow, D.P.; Shepherd, C.; Lindsay, J.G.
Deposited on : 2013-08-29
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

<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
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.14.2
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) : 2.14.2

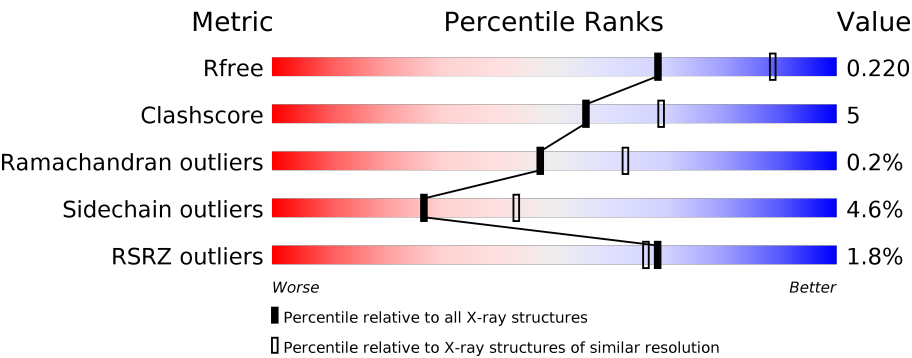
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (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 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	220	<div><div></div><div><div></div><div></div><div></div><div></div></div><div>70%5%•25%</div></div>
1	B	220	<div><div>3%</div><div></div><div></div><div></div><div></div></div> <div>66%10%24%</div>
1	C	220	<div><div>%</div><div></div><div></div><div></div><div></div></div> <div>64%11%•23%</div>
1	D	220	<div><div></div><div></div><div></div><div></div><div></div></div> <div>64%10%•24%</div>
1	E	220	<div><div>2%</div><div></div><div></div><div></div><div></div></div> <div>67%7%•25%</div>
1	F	220	<div><div>3%</div><div></div><div></div><div></div><div></div></div> <div>69%7%24%</div>

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Mol	Chain	Length	Quality of chain
1	G	220	<div><div><div></div><div></div><div></div></div><div><div>2%</div><div>64%</div><div>12%</div><div>24%</div></div></div>
1	H	220	<div><div><div></div><div></div><div></div></div><div><div>3%</div><div>62%</div><div>12%</div><div>24%</div></div></div>
1	I	220	<div><div><div></div><div></div><div></div></div><div><div></div><div>65%</div><div>10%</div><div>24%</div></div></div>
1	J	220	<div><div><div></div><div></div><div></div></div><div><div></div><div>63%</div><div>12%</div><div>25%</div></div></div>
1	K	220	<div><div><div></div><div></div><div></div></div><div><div>%</div><div>65%</div><div>10%</div><div>24%</div></div></div>
1	L	220	<div><div><div></div><div></div><div></div></div><div><div>%</div><div>69%</div><div>6%</div><div>24%</div></div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16286 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 Thioredoxin-dependent peroxide reductase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	166	Total	C	N	O	S	0	6	0
			1338	869	222	244	3			
1	B	168	Total	C	N	O	S	0	4	0
			1335	868	220	243	4			
1	C	169	Total	C	N	O	S	0	2	0
			1329	863	222	240	4			
1	D	168	Total	C	N	O	S	0	4	0
			1339	870	223	242	4			
1	E	164	Total	C	N	O	S	0	3	0
			1300	846	216	235	3			
1	F	168	Total	C	N	O	S	0	3	0
			1326	861	218	243	4			
1	G	168	Total	C	N	O	S	0	3	0
			1328	864	220	241	3			
1	H	167	Total	C	N	O	S	0	7	0
			1350	877	223	246	4			
1	I	167	Total	C	N	O	S	0	6	0
			1350	875	224	247	4			
1	J	166	Total	C	N	O	S	0	2	0
			1310	851	216	239	4			
1	K	168	Total	C	N	O	S	0	4	0
			1339	868	222	245	4			
1	L	167	Total	C	N	O	S	0	6	0
			1340	871	220	245	4			

There are 312 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-24	MET	-	expression tag	UNP P35705
A	-23	GLY	-	expression tag	UNP P35705
A	-22	SER	-	expression tag	UNP P35705
A	-21	SER	-	expression tag	UNP P35705
A	-20	HIS	-	expression tag	UNP P35705

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	HIS	-	expression tag	UNP P35705
A	-18	HIS	-	expression tag	UNP P35705
A	-17	HIS	-	expression tag	UNP P35705
A	-16	HIS	-	expression tag	UNP P35705
A	-15	HIS	-	expression tag	UNP P35705
A	-14	SER	-	expression tag	UNP P35705
A	-13	SER	-	expression tag	UNP P35705
A	-12	GLY	-	expression tag	UNP P35705
A	-11	LEU	-	expression tag	UNP P35705
A	-10	VAL	-	expression tag	UNP P35705
A	-9	PRO	-	expression tag	UNP P35705
A	-8	ARG	-	expression tag	UNP P35705
A	-7	GLY	-	expression tag	UNP P35705
A	-6	SER	-	expression tag	UNP P35705
A	-5	HIS	-	expression tag	UNP P35705
A	-4	MET	-	expression tag	UNP P35705
A	-3	LEU	-	expression tag	UNP P35705
A	-2	GLU	-	expression tag	UNP P35705
A	-1	ASP	-	expression tag	UNP P35705
A	0	PRO	-	expression tag	UNP P35705
A	190	LEU	PHE	engineered mutation	UNP P35705
B	-24	MET	-	expression tag	UNP P35705
B	-23	GLY	-	expression tag	UNP P35705
B	-22	SER	-	expression tag	UNP P35705
B	-21	SER	-	expression tag	UNP P35705
B	-20	HIS	-	expression tag	UNP P35705
B	-19	HIS	-	expression tag	UNP P35705
B	-18	HIS	-	expression tag	UNP P35705
B	-17	HIS	-	expression tag	UNP P35705
B	-16	HIS	-	expression tag	UNP P35705
B	-15	HIS	-	expression tag	UNP P35705
B	-14	SER	-	expression tag	UNP P35705
B	-13	SER	-	expression tag	UNP P35705
B	-12	GLY	-	expression tag	UNP P35705
B	-11	LEU	-	expression tag	UNP P35705
B	-10	VAL	-	expression tag	UNP P35705
B	-9	PRO	-	expression tag	UNP P35705
B	-8	ARG	-	expression tag	UNP P35705
B	-7	GLY	-	expression tag	UNP P35705
B	-6	SER	-	expression tag	UNP P35705
B	-5	HIS	-	expression tag	UNP P35705
B	-4	MET	-	expression tag	UNP P35705

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	LEU	-	expression tag	UNP P35705
B	-2	GLU	-	expression tag	UNP P35705
B	-1	ASP	-	expression tag	UNP P35705
B	0	PRO	-	expression tag	UNP P35705
B	190	LEU	PHE	engineered mutation	UNP P35705
C	-24	MET	-	expression tag	UNP P35705
C	-23	GLY	-	expression tag	UNP P35705
C	-22	SER	-	expression tag	UNP P35705
C	-21	SER	-	expression tag	UNP P35705
C	-20	HIS	-	expression tag	UNP P35705
C	-19	HIS	-	expression tag	UNP P35705
C	-18	HIS	-	expression tag	UNP P35705
C	-17	HIS	-	expression tag	UNP P35705
C	-16	HIS	-	expression tag	UNP P35705
C	-15	HIS	-	expression tag	UNP P35705
C	-14	SER	-	expression tag	UNP P35705
C	-13	SER	-	expression tag	UNP P35705
C	-12	GLY	-	expression tag	UNP P35705
C	-11	LEU	-	expression tag	UNP P35705
C	-10	VAL	-	expression tag	UNP P35705
C	-9	PRO	-	expression tag	UNP P35705
C	-8	ARG	-	expression tag	UNP P35705
C	-7	GLY	-	expression tag	UNP P35705
C	-6	SER	-	expression tag	UNP P35705
C	-5	HIS	-	expression tag	UNP P35705
C	-4	MET	-	expression tag	UNP P35705
C	-3	LEU	-	expression tag	UNP P35705
C	-2	GLU	-	expression tag	UNP P35705
C	-1	ASP	-	expression tag	UNP P35705
C	0	PRO	-	expression tag	UNP P35705
C	190	LEU	PHE	engineered mutation	UNP P35705
D	-24	MET	-	expression tag	UNP P35705
D	-23	GLY	-	expression tag	UNP P35705
D	-22	SER	-	expression tag	UNP P35705
D	-21	SER	-	expression tag	UNP P35705
D	-20	HIS	-	expression tag	UNP P35705
D	-19	HIS	-	expression tag	UNP P35705
D	-18	HIS	-	expression tag	UNP P35705
D	-17	HIS	-	expression tag	UNP P35705
D	-16	HIS	-	expression tag	UNP P35705
D	-15	HIS	-	expression tag	UNP P35705
D	-14	SER	-	expression tag	UNP P35705

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-13	SER	-	expression tag	UNP P35705
D	-12	GLY	-	expression tag	UNP P35705
D	-11	LEU	-	expression tag	UNP P35705
D	-10	VAL	-	expression tag	UNP P35705
D	-9	PRO	-	expression tag	UNP P35705
D	-8	ARG	-	expression tag	UNP P35705
D	-7	GLY	-	expression tag	UNP P35705
D	-6	SER	-	expression tag	UNP P35705
D	-5	HIS	-	expression tag	UNP P35705
D	-4	MET	-	expression tag	UNP P35705
D	-3	LEU	-	expression tag	UNP P35705
D	-2	GLU	-	expression tag	UNP P35705
D	-1	ASP	-	expression tag	UNP P35705
D	0	PRO	-	expression tag	UNP P35705
D	190	LEU	PHE	engineered mutation	UNP P35705
E	-24	MET	-	expression tag	UNP P35705
E	-23	GLY	-	expression tag	UNP P35705
E	-22	SER	-	expression tag	UNP P35705
E	-21	SER	-	expression tag	UNP P35705
E	-20	HIS	-	expression tag	UNP P35705
E	-19	HIS	-	expression tag	UNP P35705
E	-18	HIS	-	expression tag	UNP P35705
E	-17	HIS	-	expression tag	UNP P35705
E	-16	HIS	-	expression tag	UNP P35705
E	-15	HIS	-	expression tag	UNP P35705
E	-14	SER	-	expression tag	UNP P35705
E	-13	SER	-	expression tag	UNP P35705
E	-12	GLY	-	expression tag	UNP P35705
E	-11	LEU	-	expression tag	UNP P35705
E	-10	VAL	-	expression tag	UNP P35705
E	-9	PRO	-	expression tag	UNP P35705
E	-8	ARG	-	expression tag	UNP P35705
E	-7	GLY	-	expression tag	UNP P35705
E	-6	SER	-	expression tag	UNP P35705
E	-5	HIS	-	expression tag	UNP P35705
E	-4	MET	-	expression tag	UNP P35705
E	-3	LEU	-	expression tag	UNP P35705
E	-2	GLU	-	expression tag	UNP P35705
E	-1	ASP	-	expression tag	UNP P35705
E	0	PRO	-	expression tag	UNP P35705
E	190	LEU	PHE	engineered mutation	UNP P35705
F	-24	MET	-	expression tag	UNP P35705

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-23	GLY	-	expression tag	UNP P35705
F	-22	SER	-	expression tag	UNP P35705
F	-21	SER	-	expression tag	UNP P35705
F	-20	HIS	-	expression tag	UNP P35705
F	-19	HIS	-	expression tag	UNP P35705
F	-18	HIS	-	expression tag	UNP P35705
F	-17	HIS	-	expression tag	UNP P35705
F	-16	HIS	-	expression tag	UNP P35705
F	-15	HIS	-	expression tag	UNP P35705
F	-14	SER	-	expression tag	UNP P35705
F	-13	SER	-	expression tag	UNP P35705
F	-12	GLY	-	expression tag	UNP P35705
F	-11	LEU	-	expression tag	UNP P35705
F	-10	VAL	-	expression tag	UNP P35705
F	-9	PRO	-	expression tag	UNP P35705
F	-8	ARG	-	expression tag	UNP P35705
F	-7	GLY	-	expression tag	UNP P35705
F	-6	SER	-	expression tag	UNP P35705
F	-5	HIS	-	expression tag	UNP P35705
F	-4	MET	-	expression tag	UNP P35705
F	-3	LEU	-	expression tag	UNP P35705
F	-2	GLU	-	expression tag	UNP P35705
F	-1	ASP	-	expression tag	UNP P35705
F	0	PRO	-	expression tag	UNP P35705
F	190	LEU	PHE	engineered mutation	UNP P35705
G	-24	MET	-	expression tag	UNP P35705
G	-23	GLY	-	expression tag	UNP P35705
G	-22	SER	-	expression tag	UNP P35705
G	-21	SER	-	expression tag	UNP P35705
G	-20	HIS	-	expression tag	UNP P35705
G	-19	HIS	-	expression tag	UNP P35705
G	-18	HIS	-	expression tag	UNP P35705
G	-17	HIS	-	expression tag	UNP P35705
G	-16	HIS	-	expression tag	UNP P35705
G	-15	HIS	-	expression tag	UNP P35705
G	-14	SER	-	expression tag	UNP P35705
G	-13	SER	-	expression tag	UNP P35705
G	-12	GLY	-	expression tag	UNP P35705
G	-11	LEU	-	expression tag	UNP P35705
G	-10	VAL	-	expression tag	UNP P35705
G	-9	PRO	-	expression tag	UNP P35705
G	-8	ARG	-	expression tag	UNP P35705

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-7	GLY	-	expression tag	UNP P35705
G	-6	SER	-	expression tag	UNP P35705
G	-5	HIS	-	expression tag	UNP P35705
G	-4	MET	-	expression tag	UNP P35705
G	-3	LEU	-	expression tag	UNP P35705
G	-2	GLU	-	expression tag	UNP P35705
G	-1	ASP	-	expression tag	UNP P35705
G	0	PRO	-	expression tag	UNP P35705
G	190	LEU	PHE	engineered mutation	UNP P35705
H	-24	MET	-	expression tag	UNP P35705
H	-23	GLY	-	expression tag	UNP P35705
H	-22	SER	-	expression tag	UNP P35705
H	-21	SER	-	expression tag	UNP P35705
H	-20	HIS	-	expression tag	UNP P35705
H	-19	HIS	-	expression tag	UNP P35705
H	-18	HIS	-	expression tag	UNP P35705
H	-17	HIS	-	expression tag	UNP P35705
H	-16	HIS	-	expression tag	UNP P35705
H	-15	HIS	-	expression tag	UNP P35705
H	-14	SER	-	expression tag	UNP P35705
H	-13	SER	-	expression tag	UNP P35705
H	-12	GLY	-	expression tag	UNP P35705
H	-11	LEU	-	expression tag	UNP P35705
H	-10	VAL	-	expression tag	UNP P35705
H	-9	PRO	-	expression tag	UNP P35705
H	-8	ARG	-	expression tag	UNP P35705
H	-7	GLY	-	expression tag	UNP P35705
H	-6	SER	-	expression tag	UNP P35705
H	-5	HIS	-	expression tag	UNP P35705
H	-4	MET	-	expression tag	UNP P35705
H	-3	LEU	-	expression tag	UNP P35705
H	-2	GLU	-	expression tag	UNP P35705
H	-1	ASP	-	expression tag	UNP P35705
H	0	PRO	-	expression tag	UNP P35705
H	190	LEU	PHE	engineered mutation	UNP P35705
I	-24	MET	-	expression tag	UNP P35705
I	-23	GLY	-	expression tag	UNP P35705
I	-22	SER	-	expression tag	UNP P35705
I	-21	SER	-	expression tag	UNP P35705
I	-20	HIS	-	expression tag	UNP P35705
I	-19	HIS	-	expression tag	UNP P35705
I	-18	HIS	-	expression tag	UNP P35705

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-17	HIS	-	expression tag	UNP P35705
I	-16	HIS	-	expression tag	UNP P35705
I	-15	HIS	-	expression tag	UNP P35705
I	-14	SER	-	expression tag	UNP P35705
I	-13	SER	-	expression tag	UNP P35705
I	-12	GLY	-	expression tag	UNP P35705
I	-11	LEU	-	expression tag	UNP P35705
I	-10	VAL	-	expression tag	UNP P35705
I	-9	PRO	-	expression tag	UNP P35705
I	-8	ARG	-	expression tag	UNP P35705
I	-7	GLY	-	expression tag	UNP P35705
I	-6	SER	-	expression tag	UNP P35705
I	-5	HIS	-	expression tag	UNP P35705
I	-4	MET	-	expression tag	UNP P35705
I	-3	LEU	-	expression tag	UNP P35705
I	-2	GLU	-	expression tag	UNP P35705
I	-1	ASP	-	expression tag	UNP P35705
I	0	PRO	-	expression tag	UNP P35705
I	190	LEU	PHE	engineered mutation	UNP P35705
J	-24	MET	-	expression tag	UNP P35705
J	-23	GLY	-	expression tag	UNP P35705
J	-22	SER	-	expression tag	UNP P35705
J	-21	SER	-	expression tag	UNP P35705
J	-20	HIS	-	expression tag	UNP P35705
J	-19	HIS	-	expression tag	UNP P35705
J	-18	HIS	-	expression tag	UNP P35705
J	-17	HIS	-	expression tag	UNP P35705
J	-16	HIS	-	expression tag	UNP P35705
J	-15	HIS	-	expression tag	UNP P35705
J	-14	SER	-	expression tag	UNP P35705
J	-13	SER	-	expression tag	UNP P35705
J	-12	GLY	-	expression tag	UNP P35705
J	-11	LEU	-	expression tag	UNP P35705
J	-10	VAL	-	expression tag	UNP P35705
J	-9	PRO	-	expression tag	UNP P35705
J	-8	ARG	-	expression tag	UNP P35705
J	-7	GLY	-	expression tag	UNP P35705
J	-6	SER	-	expression tag	UNP P35705
J	-5	HIS	-	expression tag	UNP P35705
J	-4	MET	-	expression tag	UNP P35705
J	-3	LEU	-	expression tag	UNP P35705
J	-2	GLU	-	expression tag	UNP P35705

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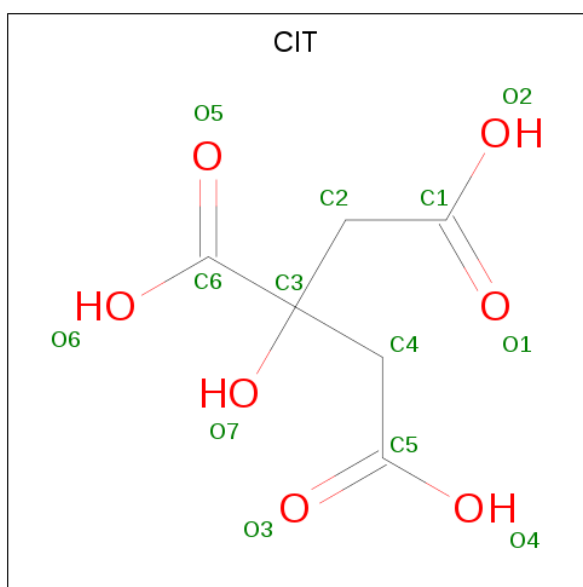
Chain	Residue	Modelled	Actual	Comment	Reference
J	-1	ASP	-	expression tag	UNP P35705
J	0	PRO	-	expression tag	UNP P35705
J	190	LEU	PHE	engineered mutation	UNP P35705
K	-24	MET	-	expression tag	UNP P35705
K	-23	GLY	-	expression tag	UNP P35705
K	-22	SER	-	expression tag	UNP P35705
K	-21	SER	-	expression tag	UNP P35705
K	-20	HIS	-	expression tag	UNP P35705
K	-19	HIS	-	expression tag	UNP P35705
K	-18	HIS	-	expression tag	UNP P35705
K	-17	HIS	-	expression tag	UNP P35705
K	-16	HIS	-	expression tag	UNP P35705
K	-15	HIS	-	expression tag	UNP P35705
K	-14	SER	-	expression tag	UNP P35705
K	-13	SER	-	expression tag	UNP P35705
K	-12	GLY	-	expression tag	UNP P35705
K	-11	LEU	-	expression tag	UNP P35705
K	-10	VAL	-	expression tag	UNP P35705
K	-9	PRO	-	expression tag	UNP P35705
K	-8	ARG	-	expression tag	UNP P35705
K	-7	GLY	-	expression tag	UNP P35705
K	-6	SER	-	expression tag	UNP P35705
K	-5	HIS	-	expression tag	UNP P35705
K	-4	MET	-	expression tag	UNP P35705
K	-3	LEU	-	expression tag	UNP P35705
K	-2	GLU	-	expression tag	UNP P35705
K	-1	ASP	-	expression tag	UNP P35705
K	0	PRO	-	expression tag	UNP P35705
K	190	LEU	PHE	engineered mutation	UNP P35705
L	-24	MET	-	expression tag	UNP P35705
L	-23	GLY	-	expression tag	UNP P35705
L	-22	SER	-	expression tag	UNP P35705
L	-21	SER	-	expression tag	UNP P35705
L	-20	HIS	-	expression tag	UNP P35705
L	-19	HIS	-	expression tag	UNP P35705
L	-18	HIS	-	expression tag	UNP P35705
L	-17	HIS	-	expression tag	UNP P35705
L	-16	HIS	-	expression tag	UNP P35705
L	-15	HIS	-	expression tag	UNP P35705
L	-14	SER	-	expression tag	UNP P35705
L	-13	SER	-	expression tag	UNP P35705
L	-12	GLY	-	expression tag	UNP P35705

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Chain	Residue	Modelled	Actual	Comment	Reference
L	-11	LEU	-	expression tag	UNP P35705
L	-10	VAL	-	expression tag	UNP P35705
L	-9	PRO	-	expression tag	UNP P35705
L	-8	ARG	-	expression tag	UNP P35705
L	-7	GLY	-	expression tag	UNP P35705
L	-6	SER	-	expression tag	UNP P35705
L	-5	HIS	-	expression tag	UNP P35705
L	-4	MET	-	expression tag	UNP P35705
L	-3	LEU	-	expression tag	UNP P35705
L	-2	GLU	-	expression tag	UNP P35705
L	-1	ASP	-	expression tag	UNP P35705
L	0	PRO	-	expression tag	UNP P35705
L	190	LEU	PHE	engineered mutation	UNP P35705

- Molecule 2 is CITRIC ACID (three-letter code: CIT) (formula: C₆H₈O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			13	6	7		
2	C	1	Total	C	O	0	0
			13	6	7		
2	H	1	Total	C	O	0	0
			13	6	7		

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	J	1	Total	O	P	0	0
			5	4	1		
3	K	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	49	Total	O	0	0
			49	49		
4	B	13	Total	O	0	0
			13	13		
4	C	19	Total	O	0	0
			19	19		
4	D	20	Total	O	0	0
			20	20		
4	E	20	Total	O	0	0
			20	20		
4	F	7	Total	O	0	0
			7	7		
4	G	9	Total	O	0	0
			9	9		
4	H	25	Total	O	0	0
			25	25		
4	I	20	Total	O	0	0
			20	20		
4	J	13	Total	O	0	0
			13	13		

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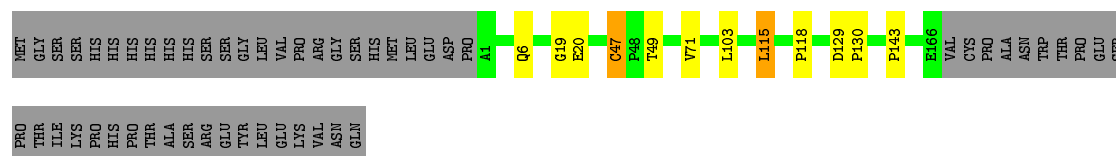
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	K	15	Total	O	0	0
			15	15		
4	L	43	Total	O	0	0
			43	43		

3 Residue-property plots [i](#)

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

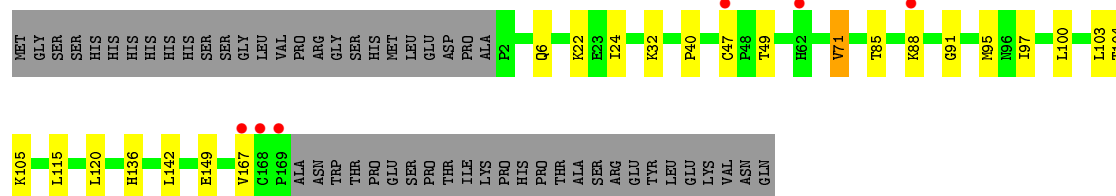
- Molecule 1: Thioredoxin-dependent peroxide reductase, mitochondrial

Chain A: 



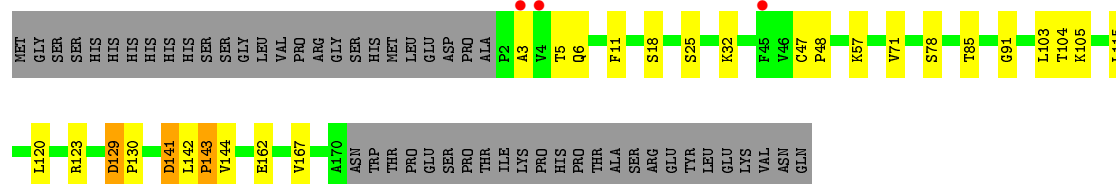
- Molecule 1: Thioredoxin-dependent peroxide reductase, mitochondrial

Chain B: 



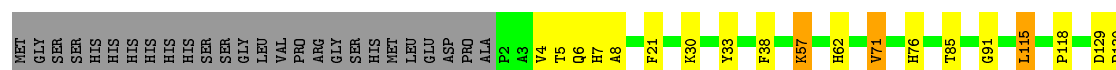
- Molecule 1: Thioredoxin-dependent peroxide reductase, mitochondrial

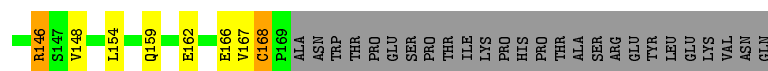
Chain C: 



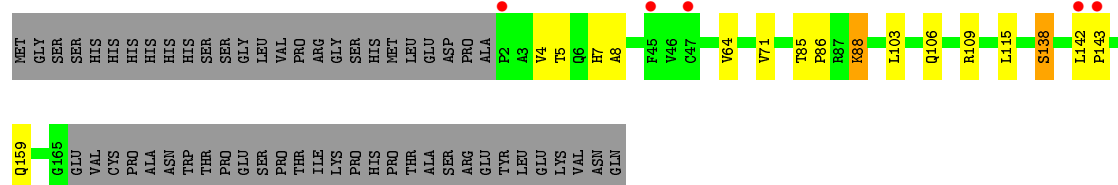
- Molecule 1: Thioredoxin-dependent peroxide reductase, mitochondrial

Chain D: 

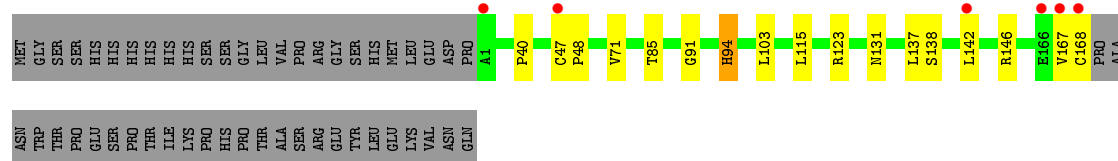




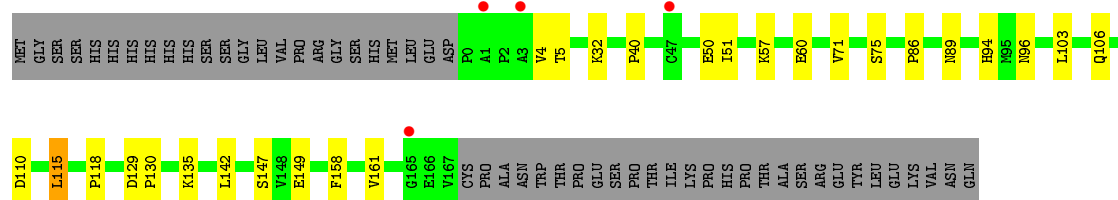
- Molecule 1: Thioredoxin-dependent peroxide reductase, mitochondrial



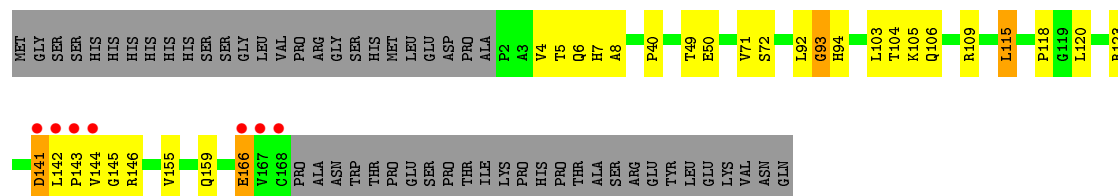
- Molecule 1: Thioredoxin-dependent peroxide reductase, mitochondrial



- Molecule 1: Thioredoxin-dependent peroxide reductase, mitochondrial

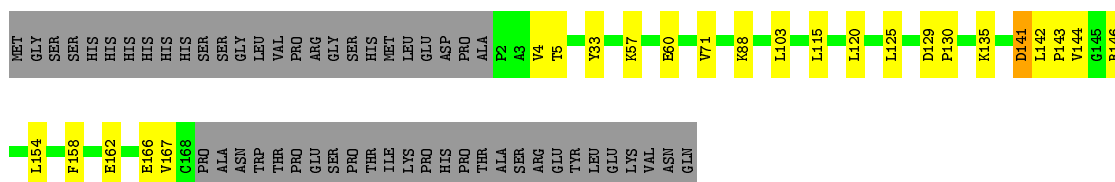


- Molecule 1: Thioredoxin-dependent peroxide reductase, mitochondrial



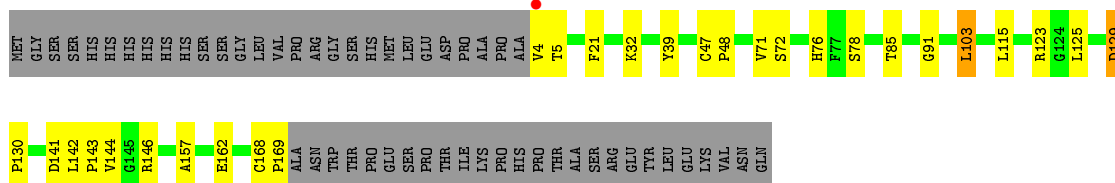
- Molecule 1: Thioredoxin-dependent peroxide reductase, mitochondrial





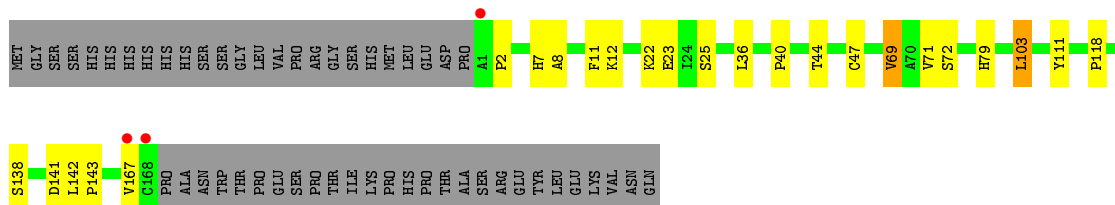
- Molecule 1: Thioredoxin-dependent peroxide reductase, mitochondrial

Chain J: 63% 12% 25%



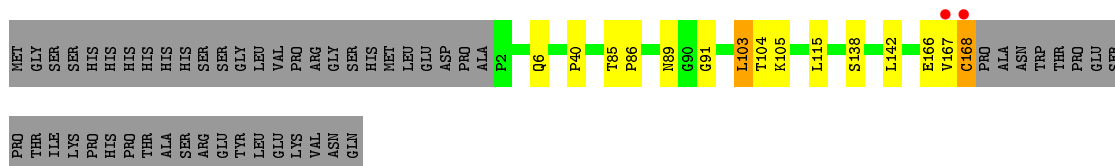
- Molecule 1: Thioredoxin-dependent peroxide reductase, mitochondrial

Chain K: 65% 10% 24%



- Molecule 1: Thioredoxin-dependent peroxide reductase, mitochondrial

Chain L: 69% 6% 24%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	142.90 Å 290.88 Å 81.14 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	102.14 – 2.40 96.96 – 2.40	Depositor EDS
% Data completeness (in resolution range)	97.9 (102.14-2.40) 97.9 (96.96-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 2.40 Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, R_{free}	0.182 , 0.221 0.182 , 0.220	Depositor DCC
R_{free} test set	6556 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	51.1	Xtriage
Anisotropy	0.074	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 43.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	16286	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.15% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	0.72	0/1385	0.82	0/1879
1	B	0.65	0/1383	0.75	0/1878
1	C	0.65	0/1370	0.78	1/1860 (0.1%)
1	D	0.63	0/1383	0.76	0/1876
1	E	0.58	0/1344	0.71	0/1824
1	F	0.61	0/1369	0.74	1/1859 (0.1%)
1	G	0.55	0/1373	0.70	0/1865
1	H	0.62	0/1404	0.75	0/1905
1	I	0.65	0/1395	0.76	0/1893
1	J	0.59	0/1350	0.75	3/1833 (0.2%)
1	K	0.64	0/1380	0.76	1/1874 (0.1%)
1	L	0.69	0/1393	0.80	1/1890 (0.1%)
All	All	0.63	0/16529	0.76	7/22436 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	129	ASP	CB-CG-OD1	5.81	123.53	118.30
1	J	123	ARG	NE-CZ-NH1	5.71	123.16	120.30
1	J	123	ARG	NE-CZ-NH2	-5.43	117.58	120.30
1	K	103	LEU	CB-CG-CD2	5.39	120.16	111.00
1	L	103	LEU	CB-CG-CD2	5.34	120.08	111.00
1	J	129	ASP	CB-CG-OD1	5.27	123.05	118.30
1	F	94	HIS	CB-CA-C	-5.12	100.16	110.40

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	1338	0	1328	5	0
1	B	1335	0	1323	10	0
1	C	1329	0	1321	15	0
1	D	1339	0	1334	20	0
1	E	1300	0	1290	14	0
1	F	1326	0	1316	9	0
1	G	1328	0	1319	17	0
1	H	1350	0	1336	27	0
1	I	1350	0	1326	18	0
1	J	1310	0	1296	24	0
1	K	1339	0	1320	17	0
1	L	1340	0	1329	9	0
2	B	13	0	5	2	0
2	C	13	0	5	1	0
2	H	13	0	5	0	0
3	J	5	0	0	0	0
3	K	5	0	0	0	0
4	A	49	0	0	1	0
4	B	13	0	0	0	0
4	C	19	0	0	3	0
4	D	20	0	0	0	0
4	E	20	0	0	1	0
4	F	7	0	0	0	0
4	G	9	0	0	0	0
4	H	25	0	0	0	0
4	I	20	0	0	0	0
4	J	13	0	0	0	0
4	K	15	0	0	0	0
4	L	43	0	0	0	0
All	All	16286	0	15853	163	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 5.

All (163) 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:141:ASP:HB3	1:D:4:VAL:CG1	1.97	0.94
1:H:106:GLN:HE22	1:H:109:ARG:HH11	1.05	0.92
1:E:142:LEU:HB3	1:E:143:PRO:HD2	1.52	0.89
1:E:142:LEU:HB3	1:E:143:PRO:CD	2.05	0.86
1:C:141:ASP:HB3	1:D:4:VAL:HG13	1.56	0.86
1:I:142:LEU:HB3	1:I:143:PRO:HD2	1.60	0.84
1:E:106:GLN:HE22	1:E:109:ARG:HH11	1.21	0.83
1:G:135:LYS:CD	1:H:141:ASP:OD2	2.28	0.82
1:L:167:VAL:O	1:L:168:CYS:HB2	1.80	0.81
1:G:135:LYS:HD2	1:H:141:ASP:OD2	1.81	0.80
1:J:142:LEU:HB3	1:J:143:PRO:HD2	1.64	0.79
1:G:158:PHE:HE1	1:H:141:ASP:HB2	1.49	0.78
1:H:4:VAL:O	1:H:5:THR:HB	1.85	0.75
1:L:86:PRO:HG2	1:L:89:ASN:HD22	1.51	0.74
1:H:123:ARG:HB3	1:H:146:ARG:HH22	1.54	0.72
1:B:47:CYS:HB3	1:B:49:THR:HG23	1.72	0.72
1:E:143:PRO:HA	4:E:206:HOH:O	1.90	0.70
1:D:7[B]:HIS:HD2	1:D:8:ALA:O	1.75	0.69
1:J:4:VAL:O	1:J:5:THR:OG1	2.10	0.68
1:D:4:VAL:O	1:D:5:THR:HB	1.93	0.67
1:H:143:PRO:O	1:H:144:VAL:HG23	1.95	0.66
1:K:7[B]:HIS:HD2	1:K:8:ALA:O	1.79	0.65
1:I:141:ASP:OD1	1:J:4:VAL:HG12	1.98	0.64
1:H:143:PRO:O	1:H:144:VAL:CG2	2.47	0.63
1:I:141:ASP:OD1	1:J:5:THR:HG23	1.99	0.63
1:F:167:VAL:HG23	1:F:168:CYS:H	1.64	0.62
1:A:115:LEU:HB3	1:A:118:PRO:HD2	1.81	0.62
1:G:135:LYS:HD3	1:H:141:ASP:OD2	2.00	0.62
1:I:142:LEU:HB3	1:I:143:PRO:CD	2.32	0.60
1:J:129:ASP:HB2	1:J:130:PRO:CD	2.32	0.60
1:K:36:LEU:HD12	1:K:69:VAL:HG22	1.82	0.60
1:H:144:VAL:HG12	1:H:145:GLY:N	2.15	0.59
1:E:86:PRO:HB3	1:E:88:LYS:HE3	1.85	0.59
1:F:94:HIS:O	1:F:94:HIS:CG	2.56	0.59
1:G:129:ASP:HB2	1:G:130:PRO:HD2	1.83	0.59
1:B:40:PRO:HG3	1:B:142:LEU:HD22	1.86	0.58
1:I:141:ASP:OD1	1:J:4:VAL:CG1	2.51	0.58
1:C:143:PRO:HG3	1:D:166:GLU:HB3	1.85	0.58
1:H:123:ARG:NE	1:H:142:LEU:O	2.38	0.56
1:B:95:MET:HE3	1:B:97:ILE:HG12	1.88	0.56
1:H:106:GLN:NE2	1:H:109:ARG:HH11	1.89	0.56
2:C:201:CIT:O3	2:C:201:CIT:O7	2.23	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:5:THR:HG22	1:J:141:ASP:OD1	2.08	0.53
1:D:5:THR:HG22	1:D:6:GLN:HE21	1.74	0.53
1:E:142:LEU:CB	1:E:143:PRO:CD	2.77	0.53
1:G:57:LYS:HD2	1:G:60:GLU:OE2	2.09	0.53
1:E:7[B]:HIS:HD2	1:E:8:ALA:O	1.91	0.53
1:H:40:PRO:HG3	1:H:142:LEU:HD23	1.90	0.53
1:G:158:PHE:CE1	1:H:141:ASP:HB2	2.38	0.52
1:E:64:VAL:O	1:E:159:GLN:NE2	2.42	0.52
1:C:141:ASP:CB	1:D:4:VAL:CG1	2.79	0.52
1:H:144:VAL:CG1	1:H:145:GLY:N	2.73	0.52
1:G:115:LEU:HB3	1:G:118:PRO:HD2	1.92	0.52
1:D:115:LEU:HB3	1:D:118:PRO:HD2	1.92	0.52
1:E:106:GLN:HE22	1:E:109:ARG:NH1	2.01	0.52
1:H:7[B]:HIS:HD2	1:H:8:ALA:O	1.93	0.51
1:G:94[A]:HIS:CE1	1:G:96:ASN:OD1	2.63	0.51
1:F:40:PRO:HG3	1:F:142:LEU:HD22	1.92	0.51
1:G:161:VAL:HG11	1:H:143:PRO:CG	2.41	0.51
1:H:143:PRO:C	1:H:144:VAL:HG23	2.30	0.50
1:I:141:ASP:HB3	1:I:142:LEU:HG	1.93	0.50
1:B:136:HIS:CE1	2:B:201:CIT:H21	2.46	0.50
1:D:167:VAL:HG12	1:D:168:CYS:N	2.26	0.50
1:L:40:PRO:HG3	1:L:142:LEU:HD22	1.92	0.50
1:B:85:THR:HB	1:B:91:GLY:HA3	1.94	0.50
1:A:129:ASP:HB2	1:A:130:PRO:HD2	1.94	0.49
1:C:11:PHE:O	1:C:25:SER:HB2	2.12	0.49
1:H:166:GLU:HG2	1:H:166:GLU:O	2.11	0.49
1:C:142:LEU:C	1:C:144:VAL:H	2.15	0.49
1:J:142:LEU:CB	1:J:143:PRO:HD2	2.33	0.49
1:K:36:LEU:CD1	1:K:69:VAL:HG22	2.42	0.49
1:C:129:ASP:HB2	1:C:130:PRO:CD	2.43	0.49
1:C:167:VAL:HB	4:C:317:HOH:O	2.13	0.49
1:B:71:VAL:HB	1:B:100:LEU:HB3	1.95	0.48
1:C:120:LEU:HD12	1:C:120:LEU:C	2.33	0.48
1:K:167:VAL:HG12	1:K:167:VAL:O	2.13	0.48
1:H:106:GLN:HE22	1:H:109:ARG:NH1	1.89	0.48
1:I:125:LEU:HD13	1:I:146:ARG:HD3	1.95	0.48
1:D:33:TYR:CE1	1:D:159:GLN:HG2	2.49	0.47
1:F:137:LEU:HD12	1:F:137:LEU:C	2.35	0.47
1:G:94[A]:HIS:HE1	1:G:96:ASN:OD1	1.97	0.47
1:A:143:PRO:HG2	4:A:231:HOH:O	2.13	0.47
1:H:155:VAL:O	1:H:159:GLN:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:57:LYS:NZ	1:G:149:GLU:OE2	2.48	0.47
1:K:72:SER:OG	1:K:79:HIS:HE1	1.98	0.47
1:D:38:PHE:HA	1:D:71:VAL:O	2.15	0.47
1:I:135:LYS:HE2	1:I:162:GLU:OE2	2.15	0.47
1:K:2:PRO:HG3	1:K:111:TYR:HA	1.97	0.47
1:L:86:PRO:HG2	1:L:89:ASN:ND2	2.26	0.47
1:J:85:THR:O	1:J:91:GLY:HA3	2.16	0.46
1:K:142:LEU:N	1:K:143:PRO:HD3	2.30	0.46
1:G:4:VAL:HG12	1:G:5:THR:HG23	1.97	0.46
1:A:47:CYS:HB3	1:A:49:THR:HG23	1.98	0.46
1:I:154:LEU:HD23	1:J:144:VAL:HG11	1.98	0.46
1:K:143:PRO:HB3	1:L:166:GLU:HG2	1.97	0.46
1:J:125:LEU:HD13	1:J:146:ARG:CD	2.46	0.46
1:D:57:LYS:HG3	1:D:148:VAL:HG11	1.97	0.46
1:I:144:VAL:HG13	1:J:157:ALA:HB3	1.97	0.45
1:I:4:VAL:HG12	1:I:5:THR:HG23	1.98	0.45
1:J:142:LEU:O	1:J:144:VAL:N	2.42	0.45
1:E:4:VAL:HG12	1:E:5:THR:HG23	1.97	0.45
1:D:21:PHE:CE1	1:D:76:HIS:HD2	2.35	0.45
1:B:136:HIS:HE1	2:B:201:CIT:H21	1.82	0.45
1:J:129:ASP:CB	1:J:130:PRO:CD	2.94	0.45
1:K:141:ASP:C	1:K:143:PRO:CD	2.85	0.45
1:G:106:GLN:NE2	1:G:110:ASP:OD1	2.48	0.45
1:G:50[B]:GLU:OE2	1:G:51:ILE:HG13	2.17	0.45
1:I:144:VAL:HG13	1:J:157:ALA:CB	2.47	0.45
1:E:138:SER:HB3	1:F:138:SER:HB2	2.00	0.44
1:J:47:CYS:HA	1:J:48:PRO:HD3	1.80	0.44
1:K:11:PHE:O	1:K:25:SER:HB2	2.17	0.44
1:G:40:PRO:HG3	1:G:142:LEU:HD22	1.98	0.44
1:J:142:LEU:C	1:J:144:VAL:H	2.20	0.44
1:C:104:THR:O	1:C:105:LYS:HB2	2.17	0.44
1:K:12:LYS:HE2	1:K:23[A]:GLU:CG	2.48	0.44
1:I:129:ASP:HB2	1:I:130:PRO:CD	2.48	0.44
1:J:103:LEU:HD13	1:K:118:PRO:O	2.18	0.44
1:H:115:LEU:HB3	1:H:118:PRO:HD2	1.99	0.44
1:H:50:GLU:CD	1:H:146:ARG:HE	2.21	0.43
1:B:95:MET:CE	1:B:97:ILE:CG1	2.96	0.43
1:C:123[B]:ARG:NH1	4:C:311:HOH:O	2.48	0.43
1:C:3:ALA:O	1:C:6:GLN:HB2	2.17	0.43
1:F:85:THR:HB	1:F:91:GLY:HA3	2.01	0.43
1:L:85:THR:O	1:L:91:GLY:HA3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:104:THR:O	1:B:105:LYS:HB2	2.17	0.43
1:H:92:LEU:C	1:H:93:GLY:O	2.57	0.43
1:I:33:TYR:CE1	1:I:130:PRO:HD3	2.54	0.43
1:K:142:LEU:N	1:K:143:PRO:CD	2.83	0.42
1:K:138:SER:CB	1:L:138:SER:HB3	2.49	0.42
1:I:57:LYS:HD3	1:I:60:GLU:OE2	2.19	0.42
1:E:85:THR:HA	1:E:86:PRO:HD2	1.88	0.42
1:E:138:SER:HB3	1:F:138:SER:CB	2.50	0.42
1:H:141:ASP:O	1:H:144:VAL:HG23	2.20	0.42
1:E:106:GLN:NE2	1:E:109:ARG:HH11	2.03	0.42
1:I:135:LYS:HB3	1:I:158:PHE:CE1	2.54	0.42
1:D:21:PHE:CZ	1:D:76:HIS:HD2	2.38	0.42
1:J:125:LEU:HD13	1:J:146:ARG:HD2	2.02	0.42
1:D:167:VAL:CG1	1:D:168:CYS:N	2.83	0.42
1:I:120:LEU:HD12	1:I:120:LEU:C	2.40	0.42
1:K:12:LYS:HE2	1:K:23[A]:GLU:HG3	2.02	0.41
1:C:85:THR:O	1:C:91:GLY:HA3	2.20	0.41
1:F:123:ARG:O	1:F:146:ARG:NH2	2.53	0.41
1:H:104:THR:O	1:H:105:LYS:HB2	2.21	0.41
1:K:138:SER:HB2	1:L:138:SER:HB3	2.03	0.41
1:F:47:CYS:HA	1:F:48:PRO:HD2	1.89	0.41
1:G:86:PRO:HD2	1:G:89:ASN:HD22	1.84	0.41
1:J:39:TYR:CZ	1:J:72:SER:HB3	2.55	0.41
1:L:104:THR:O	1:L:105:LYS:HB2	2.20	0.41
1:A:19:GLY:O	1:A:20[B]:GLU:OE2	2.38	0.41
1:C:123[B]:ARG:NH2	4:C:311:HOH:O	2.48	0.41
1:D:129:ASP:OD1	1:D:129:ASP:C	2.59	0.41
1:J:21:PHE:CE1	1:J:76:HIS:HD2	2.38	0.41
1:K:40:PRO:HG3	1:K:142:LEU:HD22	2.03	0.40
1:B:95:MET:CE	1:B:97:ILE:HG12	2.50	0.40
1:J:32:LYS:O	1:J:130:PRO:HA	2.22	0.40
1:D:129:ASP:HB2	1:D:130:PRO:CD	2.52	0.40
1:J:168:CYS:HA	1:J:169:PRO:HD3	1.95	0.40
1:C:47:CYS:HA	1:C:48:PRO:HD3	1.75	0.40
1:D:154:LEU:HD23	1:D:154:LEU:HA	1.76	0.40
1:J:129:ASP:HB2	1:J:130:PRO:HD3	2.01	0.40
1:D:85:THR:HB	1:D:91:GLY:HA3	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	170/220 (77%)	163 (96%)	7 (4%)	0	100	100
1	B	170/220 (77%)	158 (93%)	11 (6%)	1 (1%)	25	36
1	C	169/220 (77%)	162 (96%)	6 (4%)	1 (1%)	25	36
1	D	170/220 (77%)	162 (95%)	8 (5%)	0	100	100
1	E	165/220 (75%)	154 (93%)	11 (7%)	0	100	100
1	F	169/220 (77%)	157 (93%)	12 (7%)	0	100	100
1	G	169/220 (77%)	158 (94%)	11 (6%)	0	100	100
1	H	172/220 (78%)	161 (94%)	10 (6%)	1 (1%)	25	36
1	I	171/220 (78%)	158 (92%)	13 (8%)	0	100	100
1	J	166/220 (76%)	158 (95%)	8 (5%)	0	100	100
1	K	170/220 (77%)	158 (93%)	12 (7%)	0	100	100
1	L	171/220 (78%)	162 (95%)	9 (5%)	0	100	100
All	All	2032/2640 (77%)	1911 (94%)	118 (6%)	3 (0%)	47	68

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	167	VAL
1	H	93	GLY
1	C	143	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	147/190 (77%)	142 (97%)	5 (3%)	37	56
1	B	148/190 (78%)	137 (93%)	11 (7%)	13	22
1	C	146/190 (77%)	136 (93%)	10 (7%)	16	25
1	D	148/190 (78%)	139 (94%)	9 (6%)	18	30
1	E	143/190 (75%)	138 (96%)	5 (4%)	36	55
1	F	146/190 (77%)	142 (97%)	4 (3%)	44	65
1	G	146/190 (77%)	140 (96%)	6 (4%)	30	48
1	H	150/190 (79%)	140 (93%)	10 (7%)	16	26
1	I	149/190 (78%)	142 (95%)	7 (5%)	26	42
1	J	145/190 (76%)	139 (96%)	6 (4%)	30	48
1	K	147/190 (77%)	141 (96%)	6 (4%)	30	48
1	L	149/190 (78%)	145 (97%)	4 (3%)	44	65
All	All	1764/2280 (77%)	1681 (95%)	83 (5%)	27	42

All (83) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	47	CYS
1	A	71	VAL
1	A	103	LEU
1	A	115	LEU
1	B	6	GLN
1	B	22	LYS
1	B	24	ILE
1	B	32	LYS
1	B	71	VAL
1	B	88	LYS
1	B	103	LEU
1	B	115	LEU
1	B	120	LEU
1	B	149[A]	GLU
1	B	149[B]	GLU
1	C	5	THR
1	C	18	SER
1	C	32	LYS
1	C	57	LYS
1	C	71	VAL
1	C	78	SER

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Mol	Chain	Res	Type
1	C	103	LEU
1	C	115	LEU
1	C	141	ASP
1	C	162	GLU
1	D	30[A]	LYS
1	D	30[B]	LYS
1	D	57	LYS
1	D	62	HIS
1	D	71	VAL
1	D	115	LEU
1	D	146	ARG
1	D	162	GLU
1	D	168	CYS
1	E	71	VAL
1	E	88	LYS
1	E	103	LEU
1	E	115	LEU
1	E	138	SER
1	F	71	VAL
1	F	103	LEU
1	F	115	LEU
1	F	131	ASN
1	G	32	LYS
1	G	71	VAL
1	G	75	SER
1	G	103	LEU
1	G	115	LEU
1	G	147	SER
1	H	49	THR
1	H	71	VAL
1	H	72	SER
1	H	94[A]	HIS
1	H	94[B]	HIS
1	H	103	LEU
1	H	115	LEU
1	H	120	LEU
1	H	141	ASP
1	H	166	GLU
1	I	71	VAL
1	I	88	LYS
1	I	103	LEU
1	I	115	LEU

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Mol	Chain	Res	Type
1	I	141	ASP
1	I	166	GLU
1	I	167	VAL
1	J	71	VAL
1	J	78	SER
1	J	103	LEU
1	J	115	LEU
1	J	162[A]	GLU
1	J	162[B]	GLU
1	K	22	LYS
1	K	44	THR
1	K	47	CYS
1	K	69	VAL
1	K	71	VAL
1	K	103	LEU
1	L	6	GLN
1	L	103	LEU
1	L	115	LEU
1	L	168	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	89	ASN
1	D	6	GLN
1	D	76	HIS
1	D	164	HIS
1	E	89	ASN
1	E	106	GLN
1	G	89	ASN
1	H	106	GLN
1	I	65	ASN
1	J	76	HIS
1	K	89	ASN
1	L	89	ASN

5.3.3 RNA ⓘ

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

5 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	CIT	B	201	-	3,12,12	0.52	0	3,17,17	1.12	0
3	PO4	K	201	-	4,4,4	0.74	0	6,6,6	0.63	0
3	PO4	J	201	-	4,4,4	0.72	0	6,6,6	0.72	0
2	CIT	H	201	-	3,12,12	0.40	0	3,17,17	0.66	0
2	CIT	C	201	-	3,12,12	1.29	1 (33%)	3,17,17	1.16	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
2	CIT	B	201	-	-	1/6/16/16	-
2	CIT	H	201	-	-	3/6/16/16	-
2	CIT	C	201	-	-	3/6/16/16	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	201	CIT	C2-C3	-2.12	1.51	1.54

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	H	201	CIT	C1-C2-C3-O7
2	H	201	CIT	C1-C2-C3-C4
2	H	201	CIT	C1-C2-C3-C6
2	C	201	CIT	C2-C3-C4-C5
2	C	201	CIT	O7-C3-C4-C5
2	C	201	CIT	C6-C3-C4-C5
2	B	201	CIT	C1-C2-C3-C4

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	201	CIT	2	0
2	C	201	CIT	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 ⓘ

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	166/220 (75%)	0.06	0 100 100	27, 37, 69, 98	0
1	B	168/220 (76%)	0.15	6 (3%) 42 42	31, 51, 87, 133	0
1	C	169/220 (76%)	0.12	3 (1%) 68 66	33, 50, 83, 101	0
1	D	168/220 (76%)	0.04	0 100 100	32, 48, 78, 123	1 (0%)
1	E	164/220 (74%)	0.19	5 (3%) 50 49	35, 55, 98, 120	0
1	F	168/220 (76%)	0.16	6 (3%) 42 42	39, 55, 93, 146	0
1	G	168/220 (76%)	0.22	4 (2%) 59 57	40, 62, 106, 126	0
1	H	167/220 (75%)	0.28	7 (4%) 36 35	31, 49, 96, 152	1 (0%)
1	I	167/220 (75%)	0.06	0 100 100	30, 47, 81, 134	1 (0%)
1	J	166/220 (75%)	0.00	1 (0%) 89 88	34, 54, 85, 102	1 (0%)
1	K	168/220 (76%)	0.10	3 (1%) 68 66	32, 52, 91, 126	0
1	L	167/220 (75%)	0.11	2 (1%) 79 77	29, 38, 69, 141	1 (0%)
All	All	2006/2640 (75%)	0.12	37 (1%) 68 66	27, 50, 90, 152	5 (0%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	143	PRO	7.5
1	G	1	ALA	5.9
1	B	169	PRO	5.5
1	H	168	CYS	5.1
1	H	167	VAL	5.0
1	H	142	LEU	4.9
1	K	167	VAL	4.5
1	F	142	LEU	3.9
1	C	3	ALA	3.9
1	G	47	CYS	3.9
1	E	143	PRO	3.8

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Mol	Chain	Res	Type	RSRZ
1	B	168	CYS	3.8
1	G	3	ALA	3.7
1	E	45	PHE	3.7
1	H	141	ASP	3.6
1	H	144	VAL	3.5
1	F	168	CYS	3.1
1	F	47	CYS	3.1
1	E	142	LEU	3.0
1	G	165	GLY	3.0
1	F	166	GLU	2.9
1	K	1	ALA	2.8
1	B	167	VAL	2.6
1	B	47	CYS	2.5
1	H	166	GLU	2.5
1	E	2	PRO	2.5
1	B	88	LYS	2.4
1	B	62[A]	HIS	2.4
1	K	168	CYS	2.3
1	J	4	VAL	2.3
1	F	1	ALA	2.3
1	L	168	CYS	2.3
1	E	47	CYS	2.3
1	L	167	VAL	2.2
1	C	45	PHE	2.0
1	C	4	VAL	2.0
1	F	167	VAL	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 monosaccharides 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(\AA^2)	Q<0.9
2	CIT	H	201	13/13	0.75	0.28	85,108,119,129	0
2	CIT	B	201	13/13	0.78	0.27	88,94,104,105	0
2	CIT	C	201	13/13	0.86	0.31	80,103,114,119	0
3	PO4	K	201	5/5	0.90	0.27	101,102,115,116	0
3	PO4	J	201	5/5	0.92	0.14	85,86,96,101	0

6.5 Other polymers [i](#)

There are no such residues in this entry.