Full wwPDB X-ray Structure Validation Report (i)

Nov 14, 2023 – 05:42 PM JST

PDB ID	:	5ZVL
Title	:	Crystal Structure of Wheat Glutarredoxin
Authors	:	Hu, S.Q.; Sun, X.M.; Chen, M.R.
Deposited on	:	2018-05-11
Resolution	:	2.96 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

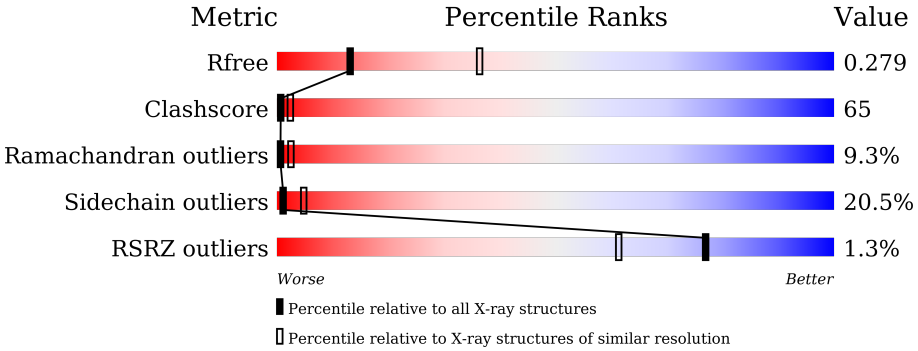
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.96 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	3104 (3.00-2.92)
Clashscore	141614	3462 (3.00-2.92)
Ramachandran outliers	138981	3340 (3.00-2.92)
Sidechain outliers	138945	3343 (3.00-2.92)
RSRZ outliers	127900	2986 (3.00-2.92)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	171	% 19% 30% 11% • 39%
1	B	171	% 25% 27% 8% • 37%
1	C	171	2% 22% 30% 8% • 38%
1	D	171	23% 29% 8% • 38%
1	E	171	% 15% 30% 13% • 40%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3961 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 Glutaredoxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	104	766	488	126	148	4	0	0	0
1	B	108	792	505	130	152	5	0	0	0
1	C	106	782	500	128	150	4	0	0	0
1	D	106	782	500	128	150	4	0	0	0
1	E	103	760	485	125	146	4	0	0	0

There are 305 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP B5A8A6
A	2	HIS	-	expression tag	UNP B5A8A6
A	3	HIS	-	expression tag	UNP B5A8A6
A	4	HIS	-	expression tag	UNP B5A8A6
A	5	HIS	-	expression tag	UNP B5A8A6
A	6	HIS	-	expression tag	UNP B5A8A6
A	7	HIS	-	expression tag	UNP B5A8A6
A	8	SER	-	expression tag	UNP B5A8A6
A	9	SER	-	expression tag	UNP B5A8A6
A	10	GLY	-	expression tag	UNP B5A8A6
A	11	LEU	-	expression tag	UNP B5A8A6
A	12	VAL	-	expression tag	UNP B5A8A6
A	13	PRO	-	expression tag	UNP B5A8A6
A	14	ARG	-	expression tag	UNP B5A8A6
A	15	GLY	-	expression tag	UNP B5A8A6
A	16	SER	-	expression tag	UNP B5A8A6
A	17	GLY	-	expression tag	UNP B5A8A6
A	18	MET	-	expression tag	UNP B5A8A6
A	19	LYS	-	expression tag	UNP B5A8A6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	20	GLU	-	expression tag	UNP B5A8A6
A	21	THR	-	expression tag	UNP B5A8A6
A	22	ALA	-	expression tag	UNP B5A8A6
A	23	ALA	-	expression tag	UNP B5A8A6
A	24	ALA	-	expression tag	UNP B5A8A6
A	25	LYS	-	expression tag	UNP B5A8A6
A	26	PHE	-	expression tag	UNP B5A8A6
A	27	GLU	-	expression tag	UNP B5A8A6
A	28	ARG	-	expression tag	UNP B5A8A6
A	29	GLN	-	expression tag	UNP B5A8A6
A	30	HIS	-	expression tag	UNP B5A8A6
A	31	MET	-	expression tag	UNP B5A8A6
A	32	ASP	-	expression tag	UNP B5A8A6
A	33	SER	-	expression tag	UNP B5A8A6
A	34	PRO	-	expression tag	UNP B5A8A6
A	35	ASP	-	expression tag	UNP B5A8A6
A	36	LEU	-	expression tag	UNP B5A8A6
A	37	GLY	-	expression tag	UNP B5A8A6
A	38	THR	-	expression tag	UNP B5A8A6
A	39	ASP	-	expression tag	UNP B5A8A6
A	40	ASP	-	expression tag	UNP B5A8A6
A	41	ASP	-	expression tag	UNP B5A8A6
A	42	ASP	-	expression tag	UNP B5A8A6
A	43	LYS	-	expression tag	UNP B5A8A6
A	44	ALA	-	expression tag	UNP B5A8A6
A	45	MET	-	expression tag	UNP B5A8A6
A	46	ALA	-	expression tag	UNP B5A8A6
A	47	ILE	-	expression tag	UNP B5A8A6
A	48	SER	-	expression tag	UNP B5A8A6
A	49	ASP	-	expression tag	UNP B5A8A6
A	50	PRO	-	expression tag	UNP B5A8A6
A	102	THR	PRO	conflict	UNP B5A8A6
A	134	ILE	VAL	conflict	UNP B5A8A6
A	143	VAL	ILE	conflict	UNP B5A8A6
A	164	LEU	-	expression tag	UNP B5A8A6
A	165	GLU	-	expression tag	UNP B5A8A6
A	166	HIS	-	expression tag	UNP B5A8A6
A	167	HIS	-	expression tag	UNP B5A8A6
A	168	HIS	-	expression tag	UNP B5A8A6
A	169	HIS	-	expression tag	UNP B5A8A6
A	170	HIS	-	expression tag	UNP B5A8A6
A	171	HIS	-	expression tag	UNP B5A8A6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	expression tag	UNP B5A8A6
B	2	HIS	-	expression tag	UNP B5A8A6
B	3	HIS	-	expression tag	UNP B5A8A6
B	4	HIS	-	expression tag	UNP B5A8A6
B	5	HIS	-	expression tag	UNP B5A8A6
B	6	HIS	-	expression tag	UNP B5A8A6
B	7	HIS	-	expression tag	UNP B5A8A6
B	8	SER	-	expression tag	UNP B5A8A6
B	9	SER	-	expression tag	UNP B5A8A6
B	10	GLY	-	expression tag	UNP B5A8A6
B	11	LEU	-	expression tag	UNP B5A8A6
B	12	VAL	-	expression tag	UNP B5A8A6
B	13	PRO	-	expression tag	UNP B5A8A6
B	14	ARG	-	expression tag	UNP B5A8A6
B	15	GLY	-	expression tag	UNP B5A8A6
B	16	SER	-	expression tag	UNP B5A8A6
B	17	GLY	-	expression tag	UNP B5A8A6
B	18	MET	-	expression tag	UNP B5A8A6
B	19	LYS	-	expression tag	UNP B5A8A6
B	20	GLU	-	expression tag	UNP B5A8A6
B	21	THR	-	expression tag	UNP B5A8A6
B	22	ALA	-	expression tag	UNP B5A8A6
B	23	ALA	-	expression tag	UNP B5A8A6
B	24	ALA	-	expression tag	UNP B5A8A6
B	25	LYS	-	expression tag	UNP B5A8A6
B	26	PHE	-	expression tag	UNP B5A8A6
B	27	GLU	-	expression tag	UNP B5A8A6
B	28	ARG	-	expression tag	UNP B5A8A6
B	29	GLN	-	expression tag	UNP B5A8A6
B	30	HIS	-	expression tag	UNP B5A8A6
B	31	MET	-	expression tag	UNP B5A8A6
B	32	ASP	-	expression tag	UNP B5A8A6
B	33	SER	-	expression tag	UNP B5A8A6
B	34	PRO	-	expression tag	UNP B5A8A6
B	35	ASP	-	expression tag	UNP B5A8A6
B	36	LEU	-	expression tag	UNP B5A8A6
B	37	GLY	-	expression tag	UNP B5A8A6
B	38	THR	-	expression tag	UNP B5A8A6
B	39	ASP	-	expression tag	UNP B5A8A6
B	40	ASP	-	expression tag	UNP B5A8A6
B	41	ASP	-	expression tag	UNP B5A8A6
B	42	ASP	-	expression tag	UNP B5A8A6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	43	LYS	-	expression tag	UNP B5A8A6
B	44	ALA	-	expression tag	UNP B5A8A6
B	45	MET	-	expression tag	UNP B5A8A6
B	46	ALA	-	expression tag	UNP B5A8A6
B	47	ILE	-	expression tag	UNP B5A8A6
B	48	SER	-	expression tag	UNP B5A8A6
B	49	ASP	-	expression tag	UNP B5A8A6
B	50	PRO	-	expression tag	UNP B5A8A6
B	102	THR	PRO	conflict	UNP B5A8A6
B	134	ILE	VAL	conflict	UNP B5A8A6
B	143	VAL	ILE	conflict	UNP B5A8A6
B	164	LEU	-	expression tag	UNP B5A8A6
B	165	GLU	-	expression tag	UNP B5A8A6
B	166	HIS	-	expression tag	UNP B5A8A6
B	167	HIS	-	expression tag	UNP B5A8A6
B	168	HIS	-	expression tag	UNP B5A8A6
B	169	HIS	-	expression tag	UNP B5A8A6
B	170	HIS	-	expression tag	UNP B5A8A6
B	171	HIS	-	expression tag	UNP B5A8A6
C	1	MET	-	expression tag	UNP B5A8A6
C	2	HIS	-	expression tag	UNP B5A8A6
C	3	HIS	-	expression tag	UNP B5A8A6
C	4	HIS	-	expression tag	UNP B5A8A6
C	5	HIS	-	expression tag	UNP B5A8A6
C	6	HIS	-	expression tag	UNP B5A8A6
C	7	HIS	-	expression tag	UNP B5A8A6
C	8	SER	-	expression tag	UNP B5A8A6
C	9	SER	-	expression tag	UNP B5A8A6
C	10	GLY	-	expression tag	UNP B5A8A6
C	11	LEU	-	expression tag	UNP B5A8A6
C	12	VAL	-	expression tag	UNP B5A8A6
C	13	PRO	-	expression tag	UNP B5A8A6
C	14	ARG	-	expression tag	UNP B5A8A6
C	15	GLY	-	expression tag	UNP B5A8A6
C	16	SER	-	expression tag	UNP B5A8A6
C	17	GLY	-	expression tag	UNP B5A8A6
C	18	MET	-	expression tag	UNP B5A8A6
C	19	LYS	-	expression tag	UNP B5A8A6
C	20	GLU	-	expression tag	UNP B5A8A6
C	21	THR	-	expression tag	UNP B5A8A6
C	22	ALA	-	expression tag	UNP B5A8A6
C	23	ALA	-	expression tag	UNP B5A8A6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	24	ALA	-	expression tag	UNP B5A8A6
C	25	LYS	-	expression tag	UNP B5A8A6
C	26	PHE	-	expression tag	UNP B5A8A6
C	27	GLU	-	expression tag	UNP B5A8A6
C	28	ARG	-	expression tag	UNP B5A8A6
C	29	GLN	-	expression tag	UNP B5A8A6
C	30	HIS	-	expression tag	UNP B5A8A6
C	31	MET	-	expression tag	UNP B5A8A6
C	32	ASP	-	expression tag	UNP B5A8A6
C	33	SER	-	expression tag	UNP B5A8A6
C	34	PRO	-	expression tag	UNP B5A8A6
C	35	ASP	-	expression tag	UNP B5A8A6
C	36	LEU	-	expression tag	UNP B5A8A6
C	37	GLY	-	expression tag	UNP B5A8A6
C	38	THR	-	expression tag	UNP B5A8A6
C	39	ASP	-	expression tag	UNP B5A8A6
C	40	ASP	-	expression tag	UNP B5A8A6
C	41	ASP	-	expression tag	UNP B5A8A6
C	42	ASP	-	expression tag	UNP B5A8A6
C	43	LYS	-	expression tag	UNP B5A8A6
C	44	ALA	-	expression tag	UNP B5A8A6
C	45	MET	-	expression tag	UNP B5A8A6
C	46	ALA	-	expression tag	UNP B5A8A6
C	47	ILE	-	expression tag	UNP B5A8A6
C	48	SER	-	expression tag	UNP B5A8A6
C	49	ASP	-	expression tag	UNP B5A8A6
C	50	PRO	-	expression tag	UNP B5A8A6
C	102	THR	PRO	conflict	UNP B5A8A6
C	134	ILE	VAL	conflict	UNP B5A8A6
C	143	VAL	ILE	conflict	UNP B5A8A6
C	164	LEU	-	expression tag	UNP B5A8A6
C	165	GLU	-	expression tag	UNP B5A8A6
C	166	HIS	-	expression tag	UNP B5A8A6
C	167	HIS	-	expression tag	UNP B5A8A6
C	168	HIS	-	expression tag	UNP B5A8A6
C	169	HIS	-	expression tag	UNP B5A8A6
C	170	HIS	-	expression tag	UNP B5A8A6
C	171	HIS	-	expression tag	UNP B5A8A6
D	1	MET	-	expression tag	UNP B5A8A6
D	2	HIS	-	expression tag	UNP B5A8A6
D	3	HIS	-	expression tag	UNP B5A8A6
D	4	HIS	-	expression tag	UNP B5A8A6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	5	HIS	-	expression tag	UNP B5A8A6
D	6	HIS	-	expression tag	UNP B5A8A6
D	7	HIS	-	expression tag	UNP B5A8A6
D	8	SER	-	expression tag	UNP B5A8A6
D	9	SER	-	expression tag	UNP B5A8A6
D	10	GLY	-	expression tag	UNP B5A8A6
D	11	LEU	-	expression tag	UNP B5A8A6
D	12	VAL	-	expression tag	UNP B5A8A6
D	13	PRO	-	expression tag	UNP B5A8A6
D	14	ARG	-	expression tag	UNP B5A8A6
D	15	GLY	-	expression tag	UNP B5A8A6
D	16	SER	-	expression tag	UNP B5A8A6
D	17	GLY	-	expression tag	UNP B5A8A6
D	18	MET	-	expression tag	UNP B5A8A6
D	19	LYS	-	expression tag	UNP B5A8A6
D	20	GLU	-	expression tag	UNP B5A8A6
D	21	THR	-	expression tag	UNP B5A8A6
D	22	ALA	-	expression tag	UNP B5A8A6
D	23	ALA	-	expression tag	UNP B5A8A6
D	24	ALA	-	expression tag	UNP B5A8A6
D	25	LYS	-	expression tag	UNP B5A8A6
D	26	PHE	-	expression tag	UNP B5A8A6
D	27	GLU	-	expression tag	UNP B5A8A6
D	28	ARG	-	expression tag	UNP B5A8A6
D	29	GLN	-	expression tag	UNP B5A8A6
D	30	HIS	-	expression tag	UNP B5A8A6
D	31	MET	-	expression tag	UNP B5A8A6
D	32	ASP	-	expression tag	UNP B5A8A6
D	33	SER	-	expression tag	UNP B5A8A6
D	34	PRO	-	expression tag	UNP B5A8A6
D	35	ASP	-	expression tag	UNP B5A8A6
D	36	LEU	-	expression tag	UNP B5A8A6
D	37	GLY	-	expression tag	UNP B5A8A6
D	38	THR	-	expression tag	UNP B5A8A6
D	39	ASP	-	expression tag	UNP B5A8A6
D	40	ASP	-	expression tag	UNP B5A8A6
D	41	ASP	-	expression tag	UNP B5A8A6
D	42	ASP	-	expression tag	UNP B5A8A6
D	43	LYS	-	expression tag	UNP B5A8A6
D	44	ALA	-	expression tag	UNP B5A8A6
D	45	MET	-	expression tag	UNP B5A8A6
D	46	ALA	-	expression tag	UNP B5A8A6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	47	ILE	-	expression tag	UNP B5A8A6
D	48	SER	-	expression tag	UNP B5A8A6
D	49	ASP	-	expression tag	UNP B5A8A6
D	50	PRO	-	expression tag	UNP B5A8A6
D	102	THR	PRO	conflict	UNP B5A8A6
D	134	ILE	VAL	conflict	UNP B5A8A6
D	143	VAL	ILE	conflict	UNP B5A8A6
D	164	LEU	-	expression tag	UNP B5A8A6
D	165	GLU	-	expression tag	UNP B5A8A6
D	166	HIS	-	expression tag	UNP B5A8A6
D	167	HIS	-	expression tag	UNP B5A8A6
D	168	HIS	-	expression tag	UNP B5A8A6
D	169	HIS	-	expression tag	UNP B5A8A6
D	170	HIS	-	expression tag	UNP B5A8A6
D	171	HIS	-	expression tag	UNP B5A8A6
E	1	MET	-	expression tag	UNP B5A8A6
E	2	HIS	-	expression tag	UNP B5A8A6
E	3	HIS	-	expression tag	UNP B5A8A6
E	4	HIS	-	expression tag	UNP B5A8A6
E	5	HIS	-	expression tag	UNP B5A8A6
E	6	HIS	-	expression tag	UNP B5A8A6
E	7	HIS	-	expression tag	UNP B5A8A6
E	8	SER	-	expression tag	UNP B5A8A6
E	9	SER	-	expression tag	UNP B5A8A6
E	10	GLY	-	expression tag	UNP B5A8A6
E	11	LEU	-	expression tag	UNP B5A8A6
E	12	VAL	-	expression tag	UNP B5A8A6
E	13	PRO	-	expression tag	UNP B5A8A6
E	14	ARG	-	expression tag	UNP B5A8A6
E	15	GLY	-	expression tag	UNP B5A8A6
E	16	SER	-	expression tag	UNP B5A8A6
E	17	GLY	-	expression tag	UNP B5A8A6
E	18	MET	-	expression tag	UNP B5A8A6
E	19	LYS	-	expression tag	UNP B5A8A6
E	20	GLU	-	expression tag	UNP B5A8A6
E	21	THR	-	expression tag	UNP B5A8A6
E	22	ALA	-	expression tag	UNP B5A8A6
E	23	ALA	-	expression tag	UNP B5A8A6
E	24	ALA	-	expression tag	UNP B5A8A6
E	25	LYS	-	expression tag	UNP B5A8A6
E	26	PHE	-	expression tag	UNP B5A8A6
E	27	GLU	-	expression tag	UNP B5A8A6

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Chain	Residue	Modelled	Actual	Comment	Reference
E	28	ARG	-	expression tag	UNP B5A8A6
E	29	GLN	-	expression tag	UNP B5A8A6
E	30	HIS	-	expression tag	UNP B5A8A6
E	31	MET	-	expression tag	UNP B5A8A6
E	32	ASP	-	expression tag	UNP B5A8A6
E	33	SER	-	expression tag	UNP B5A8A6
E	34	PRO	-	expression tag	UNP B5A8A6
E	35	ASP	-	expression tag	UNP B5A8A6
E	36	LEU	-	expression tag	UNP B5A8A6
E	37	GLY	-	expression tag	UNP B5A8A6
E	38	THR	-	expression tag	UNP B5A8A6
E	39	ASP	-	expression tag	UNP B5A8A6
E	40	ASP	-	expression tag	UNP B5A8A6
E	41	ASP	-	expression tag	UNP B5A8A6
E	42	ASP	-	expression tag	UNP B5A8A6
E	43	LYS	-	expression tag	UNP B5A8A6
E	44	ALA	-	expression tag	UNP B5A8A6
E	45	MET	-	expression tag	UNP B5A8A6
E	46	ALA	-	expression tag	UNP B5A8A6
E	47	ILE	-	expression tag	UNP B5A8A6
E	48	SER	-	expression tag	UNP B5A8A6
E	49	ASP	-	expression tag	UNP B5A8A6
E	50	PRO	-	expression tag	UNP B5A8A6
E	102	THR	PRO	conflict	UNP B5A8A6
E	134	ILE	VAL	conflict	UNP B5A8A6
E	143	VAL	ILE	conflict	UNP B5A8A6
E	164	LEU	-	expression tag	UNP B5A8A6
E	165	GLU	-	expression tag	UNP B5A8A6
E	166	HIS	-	expression tag	UNP B5A8A6
E	167	HIS	-	expression tag	UNP B5A8A6
E	168	HIS	-	expression tag	UNP B5A8A6
E	169	HIS	-	expression tag	UNP B5A8A6
E	170	HIS	-	expression tag	UNP B5A8A6
E	171	HIS	-	expression tag	UNP B5A8A6

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	11	11	11	0	0
			Total	O		
2	B	15	15	15	0	0

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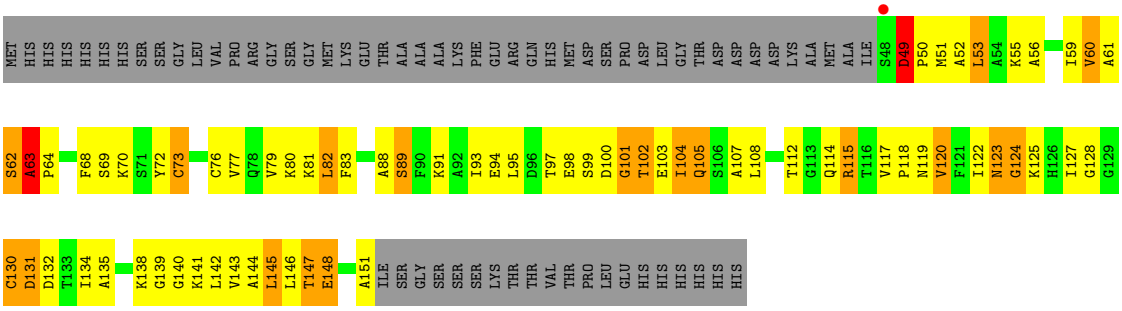
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	C	21	21	21	0	0
			Total	O		
2	D	18	18	18	0	0
			Total	O		
2	E	14	14	14	0	0

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.

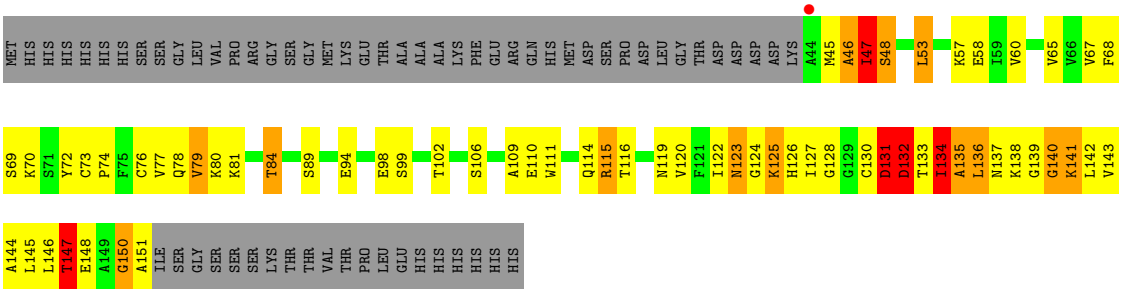
- Molecule 1: Glutaredoxin

Chain A:



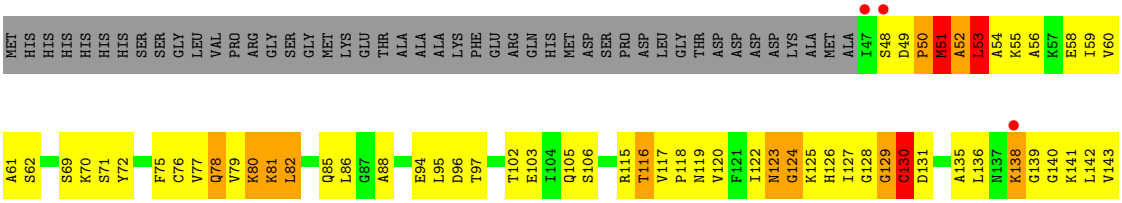
- Molecule 1: Glutaredoxin

Chain B:

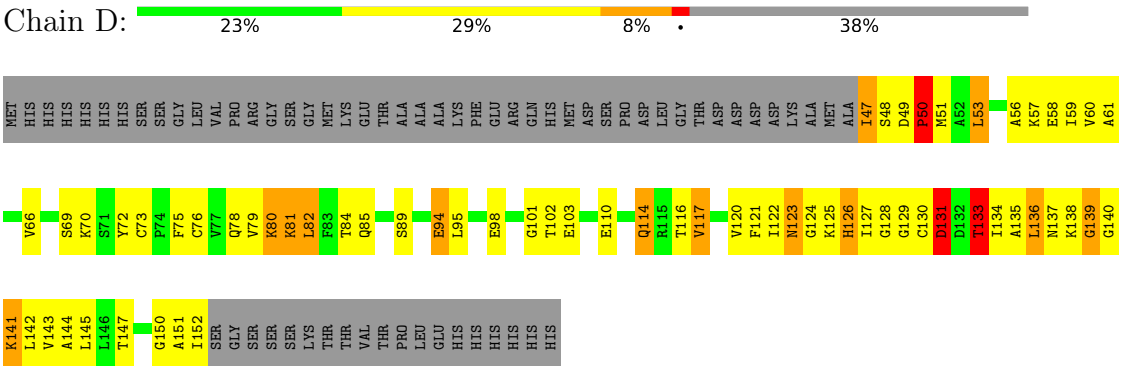


- Molecule 1: Glutaredoxin

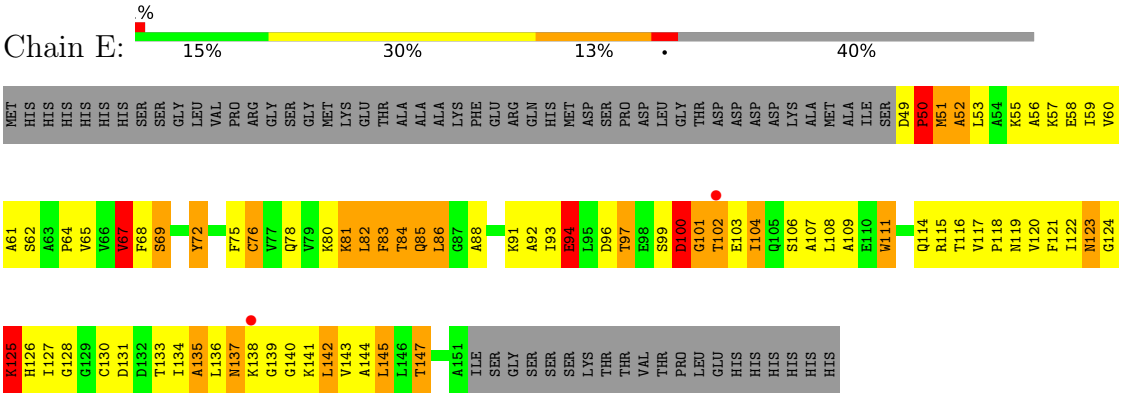
Chain C:



• Molecule 1: Glutaredoxin



• Molecule 1: Glutaredoxin



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	92.56Å 173.64Å 175.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.86 – 2.96 31.86 – 2.96	Depositor EDS
% Data completeness (in resolution range)	88.4 (31.86-2.96) 85.8 (31.86-2.96)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.67 (at 2.95Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.254 , 0.279 0.254 , 0.279	Depositor DCC
R_{free} test set	1810 reflections (6.84%)	wwPDB-VP
Wilson B-factor (Å^2)	49.8	Xtriage
Anisotropy	0.187	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 63.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.022 for -h,-l,-k	Xtriage
F_o,F_c correlation	0.87	EDS
Total number of atoms	3961	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.73% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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	1.35	7/778 (0.9%)	1.01	3/1053 (0.3%)
1	B	1.03	3/804 (0.4%)	1.00	4/1088 (0.4%)
1	C	1.44	1/794 (0.1%)	1.08	4/1075 (0.4%)
1	D	1.04	1/794 (0.1%)	1.04	3/1075 (0.3%)
1	E	1.33	9/772 (1.2%)	0.91	1/1045 (0.1%)
All	All	1.25	21/3942 (0.5%)	1.01	15/5336 (0.3%)

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	50	PRO	N-CD	29.12	1.88	1.47
1	E	50	PRO	N-CD	15.27	1.69	1.47
1	D	50	PRO	N-CD	11.77	1.64	1.47
1	E	94	GLU	CD-OE2	-8.35	1.16	1.25
1	E	72	TYR	CD2-CE2	-6.95	1.28	1.39
1	E	72	TYR	CD1-CE1	-6.59	1.29	1.39
1	E	72	TYR	CE1-CZ	-6.31	1.30	1.38
1	A	72	TYR	CE2-CZ	-6.26	1.30	1.38
1	A	60	VAL	CA-CB	-6.15	1.41	1.54
1	E	67	VAL	CB-CG2	-5.93	1.40	1.52
1	B	79	VAL	CB-CG2	-5.68	1.41	1.52
1	B	79	VAL	CB-CG1	-5.44	1.41	1.52
1	A	60	VAL	CB-CG2	-5.41	1.41	1.52
1	A	60	VAL	CB-CG1	-5.41	1.41	1.52
1	E	67	VAL	CA-CB	-5.33	1.43	1.54
1	A	72	TYR	CD2-CE2	-5.29	1.31	1.39
1	A	120	VAL	CB-CG2	-5.16	1.42	1.52
1	B	79	VAL	CA-CB	-5.11	1.44	1.54
1	E	104	ILE	CA-CB	-5.05	1.43	1.54
1	E	72	TYR	CE2-CZ	-5.03	1.32	1.38
1	A	72	TYR	CE1-CZ	-5.02	1.32	1.38

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	50	PRO	N-CD-CG	-15.17	80.44	103.20
1	D	49	ASP	N-CA-C	-10.36	83.03	111.00
1	A	63	ALA	C-N-CD	-7.47	104.16	120.60
1	D	131	ASP	CB-CG-OD2	7.47	125.02	118.30
1	D	50	PRO	CA-N-CD	-7.31	101.26	111.50
1	B	47	ILE	N-CA-C	-7.24	91.44	111.00
1	B	46	ALA	C-N-CA	6.00	136.69	121.70
1	A	63	ALA	C-N-CA	5.86	146.60	122.00
1	B	140	GLY	N-CA-C	-5.76	98.71	113.10
1	B	139	GLY	N-CA-C	-5.26	99.94	113.10
1	C	129	GLY	C-N-CA	5.25	134.83	121.70
1	C	86	LEU	CB-CG-CD2	-5.22	102.12	111.00
1	C	130	CYS	CA-CB-SG	5.17	123.30	114.00
1	E	67	VAL	CB-CA-C	-5.16	101.60	111.40
1	A	49	ASP	C-N-CD	5.04	138.99	128.40

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	766	0	777	90	0
1	B	792	0	810	83	0
1	C	782	0	802	97	0
1	D	782	0	802	112	0
1	E	760	0	773	133	0
2	A	11	0	0	14	0
2	B	15	0	0	8	0
2	C	21	0	0	20	0
2	D	18	0	0	13	0
2	E	14	0	0	37	0
All	All	3961	0	3964	508	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 65.

All (508) 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:E:122:ILE:HG13	1:E:127:ILE:CD1	1.16	1.55
1:E:50:PRO:N	1:E:50:PRO:CD	1.69	1.43
1:A:55:LYS:NZ	1:A:100:ASP:OD2	1.59	1.34
1:A:135:ALA:O	1:A:138:LYS:HG2	1.29	1.29
1:E:122:ILE:CG1	1:E:127:ILE:CD1	2.08	1.29
1:C:50:PRO:CD	1:C:50:PRO:N	1.88	1.27
1:B:130:CYS:O	1:B:134:ILE:HG12	1.11	1.26
1:D:80:LYS:NZ	1:D:94:GLU:OE2	1.70	1.25
1:A:76:CYS:O	1:A:79:VAL:HG22	1.24	1.24
1:A:76:CYS:O	1:A:79:VAL:CG2	1.93	1.16
1:B:46:ALA:HB3	1:B:47:ILE:HG12	1.18	1.15
1:E:131:ASP:O	1:E:134:ILE:HG13	1.45	1.14
1:D:81:LYS:HD2	1:D:82:LEU:N	1.62	1.14
1:A:117:VAL:HG12	1:A:118:PRO:HA	1.21	1.12
1:B:123:ASN:HB3	1:B:124:GLY:HA3	1.24	1.12
1:E:78:GLN:HB2	2:E:201:HOH:O	1.49	1.12
1:A:151:ALA:HA	2:A:205:HOH:O	1.49	1.11
1:B:136:LEU:HB3	1:B:142:LEU:HB2	1.17	1.11
1:E:122:ILE:HG13	1:E:127:ILE:HD12	1.31	1.10
1:E:122:ILE:HG13	1:E:127:ILE:HD13	1.20	1.10
1:E:122:ILE:CG1	1:E:127:ILE:HD11	1.76	1.09
1:E:122:ILE:CB	1:E:127:ILE:HD11	1.84	1.08
1:D:81:LYS:HD2	1:D:82:LEU:H	1.01	1.07
1:A:114:GLN:NE2	1:A:119:ASN:OD1	1.85	1.07
1:A:138:LYS:HG3	1:A:139:GLY:H	1.16	1.07
1:D:81:LYS:CD	1:D:82:LEU:H	1.67	1.06
1:E:122:ILE:HG13	1:E:127:ILE:HD11	1.21	1.05
1:D:81:LYS:CD	1:D:82:LEU:N	2.21	1.03
1:E:108:LEU:HD13	1:E:119:ASN:HD21	1.18	1.02
1:B:130:CYS:O	1:B:134:ILE:CG1	2.08	1.01
1:A:100:ASP:O	1:A:102:THR:N	1.94	1.01
1:A:117:VAL:CG1	1:A:118:PRO:HA	1.91	1.01
1:C:51:MET:HA	1:C:53:LEU:N	1.76	1.00
1:D:69:SER:CA	2:D:204:HOH:O	2.07	1.00
1:E:68:PHE:HB2	1:E:119:ASN:OD1	1.62	1.00
1:E:62:SER:N	2:E:202:HOH:O	1.92	1.00
1:E:51:MET:HA	2:E:203:HOH:O	1.62	1.00
1:C:76:CYS:O	1:C:80:LYS:HG3	1.61	0.99
1:D:145:LEU:H	1:D:145:LEU:HD12	1.27	0.99
1:E:131:ASP:N	2:E:204:HOH:O	1.94	0.99
1:C:53:LEU:HA	2:C:201:HOH:O	1.63	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:ASP:OD1	1:A:101:GLY:N	1.94	0.99
1:B:46:ALA:CB	1:B:47:ILE:HG12	1.92	0.99
1:E:75:PHE:HA	2:E:201:HOH:O	1.64	0.96
1:D:47:ILE:O	2:D:201:HOH:O	1.84	0.96
1:A:135:ALA:O	1:A:138:LYS:CG	2.13	0.96
1:E:51:MET:SD	2:E:209:HOH:O	2.22	0.96
1:D:50:PRO:HD2	1:D:51:MET:H	1.32	0.95
1:C:50:PRO:C	1:C:51:MET:HG2	1.83	0.95
1:D:47:ILE:HB	2:D:201:HOH:O	1.67	0.95
1:B:151:ALA:O	2:B:201:HOH:O	1.85	0.95
1:C:52:ALA:C	2:C:201:HOH:O	2.03	0.94
1:E:108:LEU:HD13	1:E:119:ASN:ND2	1.82	0.94
1:C:53:LEU:CA	2:C:201:HOH:O	2.15	0.94
1:E:131:ASP:CB	2:E:204:HOH:O	2.14	0.94
1:C:130:CYS:O	2:C:202:HOH:O	1.85	0.93
1:E:86:LEU:HD11	2:E:207:HOH:O	1.67	0.93
1:D:69:SER:HB2	2:D:204:HOH:O	1.67	0.93
1:E:75:PHE:O	2:E:201:HOH:O	1.87	0.93
1:C:52:ALA:O	2:C:201:HOH:O	1.85	0.93
1:D:122:ILE:HB	1:D:127:ILE:HD11	1.49	0.92
1:D:47:ILE:HA	1:D:110:GLU:OE1	1.69	0.92
1:D:69:SER:CB	2:D:204:HOH:O	2.18	0.91
1:D:69:SER:HA	2:D:204:HOH:O	1.67	0.91
1:B:123:ASN:HB3	1:B:124:GLY:CA	2.01	0.90
1:B:46:ALA:HB3	1:B:47:ILE:CG1	2.01	0.90
1:C:139:GLY:O	1:C:141:LYS:N	2.04	0.90
1:E:131:ASP:O	1:E:134:ILE:CG1	2.19	0.90
1:C:78:GLN:O	1:C:81:LYS:HB2	1.70	0.90
1:D:138:LYS:HD2	1:D:138:LYS:O	1.73	0.89
1:C:125:LYS:HD2	2:C:205:HOH:O	1.71	0.89
1:D:123:ASN:O	1:D:125:LYS:N	2.06	0.89
1:A:139:GLY:O	1:A:141:LYS:N	2.06	0.88
1:E:122:ILE:HB	1:E:127:ILE:HD11	1.53	0.88
1:A:59:ILE:O	2:A:202:HOH:O	1.91	0.88
1:E:50:PRO:O	2:E:203:HOH:O	1.92	0.87
1:A:79:VAL:HG23	1:A:80:LYS:N	1.87	0.87
1:E:122:ILE:CG2	2:E:205:HOH:O	2.20	0.87
1:C:130:CYS:O	2:C:203:HOH:O	1.91	0.86
1:A:62:SER:O	2:A:202:HOH:O	1.92	0.86
1:C:125:LYS:CD	2:C:205:HOH:O	2.23	0.86
1:E:101:GLY:O	1:E:103:GLU:N	2.07	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:ARG:H	1:A:115:ARG:NE	1.74	0.85
1:C:143:VAL:O	1:C:147:THR:OG1	1.93	0.85
1:A:138:LYS:HG3	1:A:139:GLY:N	1.90	0.84
1:A:49:ASP:HB3	1:A:50:PRO:CD	2.06	0.84
1:B:131:ASP:OD1	1:B:131:ASP:N	2.08	0.84
1:E:82:LEU:O	1:E:84:THR:N	2.10	0.84
1:E:122:ILE:CA	2:E:205:HOH:O	2.25	0.84
1:C:53:LEU:N	2:C:201:HOH:O	2.11	0.83
1:A:131:ASP:OD1	1:A:131:ASP:N	2.09	0.83
1:A:52:ALA:O	2:A:201:HOH:O	1.94	0.82
1:B:123:ASN:CB	1:B:124:GLY:HA3	2.02	0.82
1:E:64:PRO:O	2:E:205:HOH:O	1.97	0.82
1:B:76:CYS:O	1:B:80:LYS:HG3	1.79	0.82
1:B:60:VAL:O	2:B:203:HOH:O	1.97	0.82
1:E:123:ASN:N	2:E:205:HOH:O	2.13	0.81
1:D:47:ILE:CA	1:D:110:GLU:OE1	2.28	0.81
1:D:126:HIS:O	1:D:127:ILE:HB	1.79	0.81
1:E:133:THR:HG22	1:E:133:THR:O	1.80	0.81
1:A:76:CYS:C	1:A:79:VAL:HG22	2.01	0.80
1:D:69:SER:HB2	1:D:76:CYS:HG	1.44	0.80
1:E:76:CYS:O	1:E:80:LYS:HG3	1.81	0.80
1:E:137:ASN:ND2	2:E:208:HOH:O	2.15	0.80
1:E:78:GLN:CB	2:E:201:HOH:O	2.17	0.80
1:E:122:ILE:HA	2:E:205:HOH:O	1.81	0.80
1:B:146:LEU:O	1:B:148:GLU:N	2.13	0.80
1:C:142:LEU:HD22	1:C:146:LEU:HD11	1.63	0.80
1:E:61:ALA:C	2:E:202:HOH:O	2.18	0.80
1:E:86:LEU:CD1	2:E:207:HOH:O	2.25	0.79
1:A:51:MET:O	2:A:201:HOH:O	1.99	0.78
1:D:70:LYS:N	2:D:204:HOH:O	2.16	0.78
1:B:67:VAL:HG22	1:B:120:VAL:HG22	1.64	0.78
1:D:69:SER:OG	1:D:94:GLU:OE2	2.01	0.78
1:A:79:VAL:HG23	1:A:80:LYS:H	1.45	0.78
1:B:78:GLN:O	1:B:81:LYS:HB3	1.83	0.78
1:E:139:GLY:O	1:E:141:LYS:N	2.13	0.78
1:E:122:ILE:HG23	2:E:205:HOH:O	1.82	0.78
1:C:51:MET:HA	1:C:52:ALA:C	1.99	0.77
1:E:131:ASP:HB2	2:E:204:HOH:O	1.80	0.77
1:A:70:LYS:O	2:A:203:HOH:O	2.01	0.77
1:A:115:ARG:H	1:A:115:ARG:HE	1.28	0.76
1:D:126:HIS:O	1:D:127:ILE:CB	2.30	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:69:SER:OG	1:C:94:GLU:OE1	2.01	0.76
1:B:125:LYS:HG3	1:B:126:HIS:H	1.50	0.76
1:A:76:CYS:HA	1:A:118:PRO:HG3	1.68	0.76
1:A:131:ASP:OD2	2:A:204:HOH:O	2.03	0.76
1:B:123:ASN:O	2:B:203:HOH:O	2.04	0.75
1:C:51:MET:HB3	1:C:54:ALA:N	2.02	0.75
1:D:122:ILE:CB	1:D:127:ILE:HD11	2.17	0.75
1:A:77:VAL:O	1:A:81:LYS:HG2	1.86	0.74
1:A:94:GLU:HB2	1:A:97:THR:CG2	2.17	0.74
1:A:143:VAL:O	1:A:147:THR:OG1	2.04	0.74
1:A:49:ASP:HB3	1:A:50:PRO:HD2	1.68	0.74
1:D:144:ALA:N	2:D:202:HOH:O	2.21	0.73
1:D:47:ILE:HD13	1:D:47:ILE:N	2.04	0.73
1:E:69:SER:HB2	1:E:76:CYS:HB3	1.70	0.73
1:D:69:SER:HB2	1:D:76:CYS:SG	2.28	0.73
1:E:85:GLN:HB3	1:E:86:LEU:HD23	1.70	0.73
1:E:50:PRO:HD2	1:E:52:ALA:HB2	1.69	0.73
1:E:50:PRO:HG2	1:E:51:MET:H	1.52	0.72
1:B:143:VAL:O	1:B:147:THR:HG22	1.90	0.72
1:D:145:LEU:HD12	1:D:145:LEU:N	2.03	0.72
1:D:138:LYS:O	1:D:138:LYS:CD	2.38	0.72
1:C:51:MET:C	2:C:208:HOH:O	2.28	0.71
1:A:115:ARG:H	1:A:115:ARG:CD	2.02	0.71
1:E:91:LYS:O	2:E:206:HOH:O	2.07	0.71
1:D:144:ALA:O	1:D:147:THR:HG22	1.90	0.71
1:E:137:ASN:HA	2:E:208:HOH:O	1.90	0.71
1:B:134:ILE:O	1:B:136:LEU:N	2.23	0.71
1:A:80:LYS:NZ	1:A:94:GLU:OE2	2.24	0.70
1:B:131:ASP:OD2	2:B:204:HOH:O	2.09	0.70
1:E:86:LEU:HD23	1:E:86:LEU:N	2.04	0.70
1:C:50:PRO:O	1:C:51:MET:HG2	1.91	0.70
1:D:145:LEU:H	1:D:145:LEU:CD1	2.01	0.70
1:E:85:GLN:C	1:E:86:LEU:HD23	2.12	0.70
1:D:117:VAL:HG13	2:D:204:HOH:O	1.91	0.70
1:E:67:VAL:HG23	2:E:206:HOH:O	1.91	0.70
1:C:142:LEU:HD23	1:C:146:LEU:HG	1.74	0.69
1:D:138:LYS:O	1:D:138:LYS:CG	2.38	0.69
1:A:79:VAL:CG2	1:A:80:LYS:N	2.55	0.69
1:B:133:THR:O	1:B:134:ILE:O	2.09	0.69
1:C:53:LEU:O	1:C:53:LEU:HD22	1.92	0.69
1:C:142:LEU:CD2	1:C:146:LEU:HD11	2.23	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:52:ALA:N	2:C:208:HOH:O	2.26	0.69
1:E:92:ALA:HA	2:E:206:HOH:O	1.92	0.69
1:E:137:ASN:OD1	2:E:207:HOH:O	2.10	0.69
1:B:147:THR:H	1:B:151:ALA:HB1	1.57	0.68
1:E:82:LEU:O	1:E:85:GLN:N	2.26	0.68
1:A:79:VAL:CG2	1:A:80:LYS:H	2.06	0.68
1:D:140:GLY:O	2:D:202:HOH:O	2.12	0.68
1:A:89:SER:OG	2:A:205:HOH:O	2.11	0.67
1:B:132:ASP:H	1:B:134:ILE:HG12	1.59	0.67
1:E:100:ASP:C	1:E:103:GLU:OE2	2.33	0.67
1:D:81:LYS:CG	1:D:82:LEU:H	2.08	0.67
1:C:151:ALA:O	2:C:206:HOH:O	2.13	0.67
1:D:78:GLN:CG	1:D:81:LYS:HE3	2.25	0.67
1:A:62:SER:H	1:B:74:PRO:HG3	1.60	0.66
1:D:50:PRO:CD	1:D:51:MET:H	2.07	0.66
1:E:137:ASN:ND2	1:E:137:ASN:O	2.28	0.66
1:B:137:ASN:HB2	1:B:142:LEU:HD23	1.78	0.66
1:C:51:MET:CB	1:C:54:ALA:HB2	2.25	0.66
1:A:100:ASP:HA	1:A:103:GLU:OE1	1.95	0.66
1:C:142:LEU:HD22	1:C:146:LEU:CD1	2.25	0.66
1:B:58:GLU:OE1	2:B:205:HOH:O	2.13	0.65
1:D:76:CYS:O	1:D:80:LYS:HG3	1.96	0.65
1:A:55:LYS:CB	2:A:201:HOH:O	2.45	0.65
1:E:122:ILE:C	2:E:205:HOH:O	2.31	0.65
1:D:125:LYS:O	1:D:127:ILE:HG13	1.97	0.65
1:D:136:LEU:N	1:D:136:LEU:HD23	2.12	0.65
1:C:82:LEU:O	1:C:85:GLN:HB2	1.96	0.65
1:E:80:LYS:O	1:E:84:THR:OG1	2.14	0.65
1:D:131:ASP:OD2	2:D:203:HOH:O	2.14	0.64
1:C:129:GLY:CA	1:C:130:CYS:HB3	2.27	0.64
1:E:122:ILE:O	1:E:124:GLY:N	2.30	0.64
1:E:134:ILE:HD12	1:E:135:ALA:N	2.12	0.64
1:D:78:GLN:HG2	1:D:81:LYS:HE3	1.78	0.64
1:B:132:ASP:H	1:B:134:ILE:CG1	2.11	0.63
1:C:48:SER:HA	1:C:50:PRO:CD	2.28	0.63
1:A:94:GLU:HB2	1:A:97:THR:HG23	1.79	0.63
1:A:117:VAL:HG12	1:A:118:PRO:CA	2.12	0.63
1:E:85:GLN:HB3	1:E:86:LEU:CD2	2.28	0.63
1:D:122:ILE:HG13	1:D:127:ILE:HD12	1.81	0.63
1:D:50:PRO:HD2	1:D:51:MET:N	2.10	0.63
1:A:94:GLU:HB2	1:A:97:THR:HG21	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:79:VAL:HG23	1:D:130:CYS:HB2	1.81	0.62
1:D:120:VAL:HG21	1:D:133:THR:HG21	1.80	0.62
1:D:137:ASN:C	1:D:139:GLY:H	2.02	0.62
1:D:81:LYS:HD2	1:D:82:LEU:CA	2.28	0.62
1:D:141:LYS:O	1:D:144:ALA:HB3	2.00	0.62
1:A:76:CYS:O	1:A:80:LYS:HG3	1.99	0.62
1:D:78:GLN:O	1:D:81:LYS:HE3	2.00	0.61
1:E:51:MET:CA	2:E:203:HOH:O	2.29	0.61
1:C:69:SER:HB2	1:C:76:CYS:HB3	1.83	0.61
1:D:122:ILE:H	1:D:127:ILE:CD1	2.14	0.61
1:B:46:ALA:N	1:B:47:ILE:HB	2.16	0.61
1:D:136:LEU:O	1:D:142:LEU:N	2.32	0.60
1:D:81:LYS:O	1:D:82:LEU:C	2.39	0.60
1:C:51:MET:HB3	1:C:54:ALA:HB2	1.82	0.60
1:A:144:ALA:O	1:A:147:THR:OG1	2.18	0.60
1:E:134:ILE:C	1:E:136:LEU:H	2.05	0.60
1:C:144:ALA:O	1:C:147:THR:OG1	2.20	0.60
1:A:83:PHE:HB3	1:A:88:ALA:HB3	1.83	0.59
1:C:142:LEU:CD2	1:C:146:LEU:CD1	2.80	0.59
1:C:75:PHE:O	1:C:78:GLN:HB2	2.02	0.59
1:D:122:ILE:CG1	1:D:127:ILE:CD1	2.81	0.59
1:D:122:ILE:HG13	1:D:127:ILE:CD1	2.33	0.59
1:E:78:GLN:O	1:E:81:LYS:HB2	2.02	0.59
1:C:88:ALA:HA	1:C:151:ALA:HB1	1.85	0.59
1:E:51:MET:O	1:E:53:LEU:N	2.35	0.59
1:D:122:ILE:HD12	1:D:127:ILE:HD13	1.85	0.58
1:A:144:ALA:O	1:A:147:THR:N	2.33	0.58
1:E:50:PRO:C	2:E:203:HOH:O	2.38	0.58
1:B:73:CYS:O	1:B:77:VAL:HG23	2.04	0.58
1:E:100:ASP:CA	1:E:103:GLU:OE2	2.52	0.58
1:C:124:GLY:O	2:C:205:HOH:O	2.16	0.58
1:E:75:PHE:CA	2:E:201:HOH:O	2.32	0.57
1:E:137:ASN:HB2	1:E:142:LEU:HD12	1.84	0.57
1:C:49:ASP:O	1:C:51:MET:N	2.37	0.57
1:C:129:GLY:HA2	1:C:130:CYS:HB3	1.86	0.57
1:C:142:LEU:N	2:C:204:HOH:O	2.37	0.57
1:E:82:LEU:C	1:E:84:THR:H	2.08	0.57
1:E:100:ASP:OD1	1:E:100:ASP:N	2.37	0.57
1:E:134:ILE:C	1:E:136:LEU:N	2.57	0.57
1:A:97:THR:OG1	1:A:98:GLU:N	2.38	0.57
1:D:79:VAL:O	1:D:81:LYS:N	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:117:VAL:CG1	2:D:204:HOH:O	2.51	0.56
1:D:138:LYS:O	1:D:138:LYS:HG3	2.03	0.56
1:D:82:LEU:O	1:D:85:GLN:HB2	2.05	0.56
1:C:142:LEU:CD2	1:C:146:LEU:HG	2.34	0.56
1:B:150:GLY:CA	1:B:151:ALA:HB3	2.36	0.56
1:C:51:MET:CB	1:C:54:ALA:CB	2.84	0.56
1:C:141:LYS:O	1:C:144:ALA:HB3	2.06	0.56
1:E:117:VAL:HG13	1:E:118:PRO:HA	1.87	0.56
1:E:122:ILE:CG1	1:E:127:ILE:HD13	2.05	0.56
1:B:65:VAL:HG22	1:B:122:ILE:HD13	1.88	0.55
1:C:51:MET:HB3	1:C:54:ALA:CB	2.36	0.55
1:B:150:GLY:N	1:B:151:ALA:HB3	2.21	0.55
1:E:52:ALA:HB1	1:E:107:ALA:HB2	1.86	0.55
1:C:51:MET:HA	1:C:53:LEU:H	1.67	0.55
1:E:134:ILE:O	1:E:136:LEU:N	2.40	0.55
1:A:55:LYS:N	2:A:201:HOH:O	1.88	0.55
1:D:122:ILE:CB	1:D:127:ILE:CD1	2.85	0.55
1:D:126:HIS:C	1:D:127:ILE:HG13	2.27	0.55
1:B:111:TRP:CZ2	1:B:125:LYS:HE2	2.42	0.54
1:E:114:GLN:O	1:E:114:GLN:HG3	2.06	0.54
1:C:105:GLN:NE2	1:C:115:ARG:O	2.40	0.54
1:B:131:ASP:OD1	2:B:204:HOH:O	2.18	0.54
1:E:57:LYS:NZ	1:E:111:TRP:CE2	2.75	0.54
1:E:121:PHE:CD1	1:E:126:HIS:HA	2.42	0.54
1:D:122:ILE:H	1:D:127:ILE:HD11	1.73	0.54
1:B:131:ASP:CG	2:B:204:HOH:O	2.44	0.54
1:A:52:ALA:C	2:A:201:HOH:O	2.40	0.54
1:A:135:ALA:C	1:A:138:LYS:HG2	2.21	0.54
1:B:114:GLN:HE22	1:B:128:GLY:HA2	1.73	0.54
1:E:67:VAL:O	2:E:206:HOH:O	2.18	0.54
1:E:141:LYS:O	1:E:145:LEU:HD12	2.08	0.53
1:E:143:VAL:HG23	2:E:208:HOH:O	2.08	0.53
1:C:95:LEU:HD13	1:C:105:GLN:HB2	1.89	0.53
1:E:133:THR:O	1:E:133:THR:CG2	2.52	0.53
1:C:59:ILE:O	1:C:62:SER:OG	2.25	0.53
1:A:104:ILE:HG22	1:A:108:LEU:HD12	1.91	0.53
1:B:125:LYS:HD3	1:C:72:TYR:CE1	2.44	0.53
1:A:95:LEU:HD23	1:A:101:GLY:O	2.08	0.53
1:D:56:ALA:O	1:D:60:VAL:HG23	2.09	0.52
1:A:104:ILE:O	1:A:107:ALA:N	2.41	0.52
1:B:53:LEU:HD22	1:B:57:LYS:HE2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:141:LYS:O	1:E:144:ALA:HB3	2.09	0.52
1:A:115:ARG:HE	1:A:115:ARG:N	2.04	0.52
1:C:143:VAL:N	2:C:204:HOH:O	1.95	0.52
1:D:76:CYS:SG	2:D:204:HOH:O	2.01	0.52
1:E:50:PRO:HG2	1:E:51:MET:N	2.22	0.52
1:B:136:LEU:HB3	1:B:142:LEU:CB	2.12	0.52
1:A:79:VAL:HG11	1:A:118:PRO:HG2	1.92	0.52
1:A:49:ASP:CB	1:A:50:PRO:CD	2.84	0.52
1:D:48:SER:N	1:D:110:GLU:OE1	2.42	0.52
1:C:78:GLN:OE1	2:C:207:HOH:O	2.18	0.52
1:D:78:GLN:HA	1:D:81:LYS:HG2	1.90	0.52
1:C:71:SER:N	1:C:96:ASP:OD2	2.38	0.52
1:D:81:LYS:CG	1:D:82:LEU:N	2.64	0.52
1:C:152:ILE:O	1:C:152:ILE:HG23	2.10	0.52
1:E:78:GLN:OE1	1:E:130:CYS:SG	2.67	0.52
1:B:48:SER:OG	1:B:110:GLU:OE2	2.22	0.51
1:D:114:GLN:HE22	1:D:128:GLY:C	2.14	0.51
1:B:133:THR:O	1:B:134:ILE:C	2.49	0.51
1:D:122:ILE:HB	1:D:127:ILE:CD1	2.31	0.51
1:A:144:ALA:O	1:A:148:GLU:HG2	2.09	0.51
1:D:78:GLN:HG3	1:D:81:LYS:HE3	1.92	0.51
1:B:143:VAL:O	1:B:147:THR:CG2	2.57	0.51
1:A:115:ARG:CD	1:A:115:ARG:N	2.72	0.51
1:C:78:GLN:O	1:C:81:LYS:CB	2.53	0.51
1:A:122:ILE:O	1:A:124:GLY:N	2.44	0.51
1:C:51:MET:HB3	1:C:54:ALA:H	1.76	0.51
1:D:136:LEU:N	1:D:136:LEU:CD2	2.74	0.50
1:A:123:ASN:O	1:A:125:LYS:N	2.44	0.50
1:D:78:GLN:C	1:D:81:LYS:HG3	2.31	0.50
1:E:56:ALA:HB1	1:E:108:LEU:HD21	1.92	0.50
1:E:114:GLN:O	1:E:114:GLN:CG	2.59	0.50
1:E:52:ALA:O	2:E:209:HOH:O	2.19	0.50
1:A:82:LEU:HD12	1:A:82:LEU:O	2.11	0.50
1:C:79:VAL:C	1:C:81:LYS:H	2.15	0.50
1:E:57:LYS:NZ	1:E:111:TRP:CZ2	2.78	0.50
1:B:53:LEU:O	1:B:57:LYS:HG3	2.12	0.50
1:A:73:CYS:O	1:A:77:VAL:HG23	2.11	0.50
1:C:142:LEU:CD2	1:C:146:LEU:CG	2.89	0.49
1:B:57:LYS:HB3	1:C:72:TYR:HB3	1.94	0.49
1:C:123:ASN:O	1:C:125:LYS:N	2.46	0.49
1:D:122:ILE:N	1:D:127:ILE:CD1	2.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:69:SER:OG	1:B:70:LYS:N	2.46	0.49
1:B:111:TRP:HZ2	1:B:125:LYS:HE2	1.77	0.49
1:D:120:VAL:HG12	1:D:121:PHE:N	2.28	0.49
1:D:50:PRO:CD	1:D:51:MET:N	2.73	0.49
1:E:76:CYS:O	1:E:80:LYS:NZ	2.44	0.49
1:B:68:PHE:HB2	1:B:119:ASN:HB3	1.94	0.49
1:E:83:PHE:N	1:E:83:PHE:CD1	2.74	0.49
1:A:93:ILE:O	1:A:95:LEU:HD12	2.13	0.49
1:D:47:ILE:C	1:D:110:GLU:OE1	2.50	0.49
1:B:141:LYS:O	1:B:145:LEU:HG	2.13	0.49
1:C:61:ALA:HB2	1:D:72:TYR:HA	1.94	0.49
1:C:150:GLY:O	1:C:151:ALA:HB2	2.13	0.49
1:A:130:CYS:SG	1:A:134:ILE:HD11	2.53	0.48
1:D:123:ASN:C	1:D:125:LYS:H	2.15	0.48
1:D:73:CYS:SG	1:D:76:CYS:SG	3.11	0.48
1:C:79:VAL:C	1:C:81:LYS:N	2.66	0.48
1:E:67:VAL:N	2:E:206:HOH:O	2.33	0.48
1:A:132:ASP:O	2:A:206:HOH:O	2.20	0.48
1:C:51:MET:HB2	1:C:54:ALA:CB	2.44	0.48
1:A:145:LEU:HA	1:A:148:GLU:HG3	1.96	0.48
1:B:79:VAL:O	1:B:81:LYS:N	2.46	0.48
1:E:102:THR:HG23	1:E:103:GLU:N	2.29	0.48
1:A:61:ALA:HB2	1:B:72:TYR:HA	1.96	0.48
1:D:135:ALA:HA	1:D:138:LYS:HB3	1.96	0.48
1:C:58:GLU:O	1:C:58:GLU:HG2	2.14	0.48
1:E:143:VAL:O	1:E:147:THR:OG1	2.32	0.48
1:E:122:ILE:N	1:E:127:ILE:CD1	2.77	0.47
1:B:144:ALA:O	1:B:146:LEU:O	2.31	0.47
1:C:77:VAL:O	1:C:81:LYS:HB2	2.13	0.47
1:D:141:LYS:O	1:D:145:LEU:HD12	2.14	0.47
1:D:143:VAL:HG12	1:D:143:VAL:O	2.15	0.47
1:B:115:ARG:HB3	1:B:115:ARG:HH21	1.79	0.47
1:C:70:LYS:HA	1:C:96:ASP:OD2	2.13	0.47
1:C:131:ASP:OD1	1:C:131:ASP:N	2.46	0.47
1:E:75:PHE:O	1:E:78:GLN:N	2.47	0.47
1:B:132:ASP:N	1:B:134:ILE:CG1	2.76	0.47
1:D:142:LEU:C	1:D:144:ALA:N	2.66	0.47
1:C:129:GLY:HA3	1:C:131:ASP:OD1	2.15	0.46
1:D:125:LYS:HA	1:D:125:LYS:HD2	1.50	0.46
1:E:50:PRO:CG	1:E:51:MET:H	2.20	0.46
1:E:59:ILE:HG21	1:E:93:ILE:CD1	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:103:GLU:N	1:C:103:GLU:OE1	2.48	0.46
1:A:120:VAL:HG23	1:A:128:GLY:O	2.15	0.46
1:D:78:GLN:O	1:D:81:LYS:HG3	2.16	0.46
1:E:78:GLN:O	1:E:81:LYS:N	2.35	0.46
1:E:121:PHE:HD1	1:E:126:HIS:HA	1.79	0.46
1:B:123:ASN:CB	1:B:124:GLY:CA	2.77	0.46
1:D:47:ILE:N	1:D:47:ILE:CD1	2.73	0.46
1:A:49:ASP:O	1:A:52:ALA:HB3	2.15	0.46
1:A:55:LYS:HB2	2:A:201:HOH:O	2.12	0.46
1:B:125:LYS:N	2:B:202:HOH:O	1.91	0.46
1:B:140:GLY:C	1:B:142:LEU:H	2.19	0.46
1:A:132:ASP:C	2:A:206:HOH:O	2.53	0.46
1:D:141:LYS:O	1:D:145:LEU:CD1	2.63	0.46
1:E:69:SER:OG	1:E:94:GLU:OE2	2.28	0.46
1:E:82:LEU:HD23	1:E:82:LEU:HA	1.77	0.46
1:A:69:SER:HA	1:A:117:VAL:CG1	2.46	0.46
1:D:150:GLY:HA2	1:D:151:ALA:C	2.37	0.46
1:E:76:CYS:SG	1:E:117:VAL:HG12	2.56	0.46
1:A:139:GLY:O	1:A:141:LYS:HG2	2.17	0.46
1:A:120:VAL:HG23	1:A:120:VAL:H	1.46	0.45
1:B:94:GLU:OE1	1:B:94:GLU:HA	2.15	0.45
1:B:120:VAL:HG12	1:B:127:ILE:HG13	1.97	0.45
1:B:146:LEU:HB3	1:B:151:ALA:HB1	1.98	0.45
1:E:68:PHE:HD2	1:E:119:ASN:ND2	2.14	0.45
1:E:68:PHE:O	1:E:117:VAL:HG13	2.16	0.45
1:E:120:VAL:HG23	1:E:128:GLY:O	2.16	0.45
1:A:63:ALA:HB3	1:B:74:PRO:HG3	1.97	0.45
1:D:82:LEU:HD12	1:D:134:ILE:HD13	1.98	0.45
1:C:79:VAL:O	1:C:81:LYS:N	2.50	0.45
1:C:50:PRO:O	1:C:51:MET:CG	2.64	0.45
1:D:78:GLN:HG3	1:D:81:LYS:CE	2.46	0.45
1:D:126:HIS:C	1:D:127:ILE:CG1	2.82	0.45
1:A:103:GLU:O	1:A:104:ILE:C	2.55	0.45
1:B:147:THR:N	1:B:151:ALA:HB1	2.30	0.45
1:C:52:ALA:C	1:C:54:ALA:H	2.20	0.45
1:C:52:ALA:O	1:C:55:LYS:N	2.42	0.45
1:C:143:VAL:HG23	2:C:204:HOH:O	2.16	0.45
1:D:136:LEU:O	1:D:142:LEU:HB2	2.17	0.45
1:B:79:VAL:C	1:B:81:LYS:N	2.68	0.45
1:B:134:ILE:O	1:B:135:ALA:C	2.55	0.45
1:C:125:LYS:NZ	2:C:205:HOH:O	2.02	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:50:PRO:C	1:C:51:MET:CG	2.67	0.45
1:E:50:PRO:CG	1:E:51:MET:N	2.77	0.45
1:E:53:LEU:N	1:E:53:LEU:HD12	2.32	0.44
1:A:56:ALA:O	1:A:60:VAL:HG23	2.17	0.44
1:B:142:LEU:O	1:B:142:LEU:HD12	2.18	0.44
1:C:120:VAL:HG23	1:C:128:GLY:O	2.18	0.44
1:E:76:CYS:HA	1:E:118:PRO:HG3	1.99	0.44
1:C:51:MET:HB2	1:C:54:ALA:HB2	1.99	0.44
1:E:86:LEU:C	1:E:88:ALA:H	2.21	0.44
1:B:47:ILE:O	1:B:47:ILE:HG22	2.16	0.44
1:C:135:ALA:O	1:C:138:LYS:HB2	2.17	0.44
1:E:125:LYS:HG3	1:E:126:HIS:N	2.33	0.44
1:C:125:LYS:HD2	1:C:125:LYS:HA	1.36	0.44
1:E:106:SER:O	1:E:109:ALA:HB3	2.18	0.44
1:A:69:SER:HA	1:A:117:VAL:HG11	1.98	0.44
1:A:100:ASP:C	1:A:102:THR:H	2.11	0.44
1:C:147:THR:C	1:C:149:ALA:N	2.70	0.44
1:D:137:ASN:C	1:D:139:GLY:N	2.69	0.44
1:B:122:ILE:O	1:B:124:GLY:HA3	2.17	0.43
1:D:126:HIS:O	1:D:127:ILE:HG13	2.18	0.43
1:E:61:ALA:CA	2:E:202:HOH:O	2.65	0.43
1:E:131:ASP:CA	2:E:204:HOH:O	2.38	0.43
1:D:61:ALA:HB2	1:E:72:TYR:C	2.37	0.43
1:E:50:PRO:HD2	1:E:52:ALA:CB	2.41	0.43
1:E:59:ILE:O	1:E:62:SER:OG	2.19	0.43
1:E:100:ASP:HA	1:E:103:GLU:OE2	2.18	0.43
1:E:55:LYS:HE2	1:E:100:ASP:OD2	2.18	0.43
1:C:52:ALA:O	1:C:54:ALA:N	2.52	0.43
1:D:75:PHE:O	1:D:78:GLN:N	2.51	0.43
1:D:142:LEU:O	1:D:144:ALA:N	2.51	0.43
1:A:79:VAL:HG23	1:A:80:LYS:HG3	2.01	0.43
1:A:53:LEU:HD23	1:A:53:LEU:O	2.19	0.43
1:A:122:ILE:HG13	1:A:127:ILE:HG13	2.00	0.43
1:E:134:ILE:CD1	1:E:135:ALA:N	2.82	0.43
1:B:73:CYS:HA	1:B:74:PRO:HD3	1.85	0.43
1:C:48:SER:HA	1:C:49:ASP:C	2.39	0.43
1:E:49:ASP:HA	1:E:50:PRO:HA	1.78	0.43
1:A:138:LYS:CG	1:A:139:GLY:N	2.68	0.42
1:B:125:LYS:HG3	1:B:126:HIS:N	2.26	0.42
1:B:140:GLY:C	1:B:142:LEU:N	2.72	0.42
1:C:69:SER:HB2	1:C:76:CYS:SG	2.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:147:THR:H	1:B:151:ALA:CB	2.27	0.42
1:C:122:ILE:HG13	1:C:127:ILE:HG13	2.01	0.42
1:D:95:LEU:O	1:D:101:GLY:HA3	2.19	0.42
1:A:68:PHE:HB2	1:A:119:ASN:HB2	2.01	0.42
1:B:81:LYS:O	1:B:84:THR:OG1	2.36	0.42
1:E:137:ASN:O	1:E:138:LYS:C	2.58	0.42
1:C:116:THR:HG23	2:C:213:HOH:O	2.19	0.42
1:E:56:ALA:O	1:E:60:VAL:HG23	2.19	0.42
1:E:134:ILE:CG1	1:E:135:ALA:N	2.83	0.42
1:B:147:THR:N	1:B:151:ALA:CB	2.83	0.42
1:D:59:ILE:O	1:D:66:VAL:HG21	2.20	0.42
1:E:104:ILE:HD13	1:E:104:ILE:HG21	1.71	0.42
1:B:135:ALA:O	1:B:138:LYS:HB3	2.20	0.42
1:C:142:LEU:CA	2:C:204:HOH:O	2.68	0.42
1:C:97:THR:HG22	1:C:97:THR:O	2.18	0.42
1:E:68:PHE:HD2	1:E:119:ASN:HD21	1.68	0.42
1:A:130:CYS:N	1:A:131:ASP:OD1	2.53	0.41
1:D:125:LYS:HD2	1:D:126:HIS:H	1.86	0.41
1:C:52:ALA:C	1:C:54:ALA:N	2.73	0.41
1:E:97:THR:O	1:E:97:THR:OG1	2.35	0.41
1:E:102:THR:HG23	1:E:103:GLU:H	1.85	0.41
1:B:140:GLY:O	1:B:142:LEU:N	2.53	0.41
1:C:69:SER:HB2	1:C:76:CYS:CB	2.49	0.41
1:C:117:VAL:HB	1:C:118:PRO:HA	2.02	0.41
1:C:125:LYS:HD2	1:C:126:HIS:H	1.85	0.41
1:D:57:LYS:O	1:D:58:GLU:C	2.59	0.41
1:E:122:ILE:CG1	1:E:127:ILE:HD12	2.14	0.41
1:B:69:SER:OG	1:B:94:GLU:OE1	2.33	0.41
1:B:115:ARG:HB3	1:B:115:ARG:NH2	2.35	0.41
1:D:81:LYS:HG3	1:D:81:LYS:H	1.62	0.41
1:D:129:GLY:O	1:D:133:THR:HG22	2.19	0.41
1:A:120:VAL:HB	1:A:127:ILE:HB	2.02	0.41
1:D:53:LEU:HD22	1:D:53:LEU:O	2.20	0.41
1:E:123:ASN:O	1:E:125:LYS:N	2.52	0.41
1:D:144:ALA:HB3	1:D:145:LEU:HD12	2.02	0.41
1:D:145:LEU:C	1:D:147:THR:N	2.72	0.41
1:A:104:ILE:O	1:A:105:GLN:C	2.57	0.41
1:B:80:LYS:O	1:B:84:THR:OG1	2.37	0.41
1:B:81:LYS:C	1:B:81:LYS:HD2	2.40	0.41
1:C:150:GLY:O	1:C:151:ALA:CB	2.69	0.41
1:D:79:VAL:C	1:D:81:LYS:N	2.72	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:122:ILE:N	1:D:127:ILE:HD11	2.35	0.41
1:D:125:LYS:CD	1:D:126:HIS:H	2.34	0.41
1:E:124:GLY:O	1:E:125:LYS:C	2.59	0.41
1:B:46:ALA:H	1:B:47:ILE:HB	1.86	0.41
1:C:76:CYS:O	1:C:80:LYS:CG	2.50	0.41
1:E:122:ILE:HG22	2:E:205:HOH:O	2.06	0.41
1:D:126:HIS:O	1:D:127:ILE:CG1	2.68	0.40
1:E:134:ILE:HG13	1:E:135:ALA:H	1.85	0.40
1:B:47:ILE:HD13	1:B:47:ILE:HA	1.81	0.40
1:A:142:LEU:O	1:A:146:LEU:HD12	2.20	0.40
1:C:56:ALA:O	1:C:60:VAL:HG23	2.21	0.40
1:E:124:GLY:O	1:E:125:LYS:O	2.39	0.40
1:A:141:LYS:O	1:A:144:ALA:N	2.55	0.40
1:B:106:SER:O	1:B:109:ALA:HB3	2.21	0.40
1:B:142:LEU:O	1:B:146:LEU:HD13	2.22	0.40
1:D:142:LEU:O	1:D:143:VAL:C	2.58	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	102/171 (60%)	79 (78%)	14 (14%)	9 (9%)	1 3
1	B	106/171 (62%)	85 (80%)	11 (10%)	10 (9%)	0 2
1	C	104/171 (61%)	83 (80%)	13 (12%)	8 (8%)	1 4
1	D	104/171 (61%)	75 (72%)	21 (20%)	8 (8%)	1 4
1	E	101/171 (59%)	72 (71%)	16 (16%)	13 (13%)	0 1
All	All	517/855 (60%)	394 (76%)	75 (14%)	48 (9%)	0 2

All (48) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	49	ASP
1	A	64	PRO
1	A	101	GLY
1	A	140	GLY
1	B	45	MET
1	B	47	ILE
1	B	131	ASP
1	B	132	ASP
1	B	134	ILE
1	B	135	ALA
1	B	147	THR
1	C	130	CYS
1	C	140	GLY
1	C	151	ALA
1	D	124	GLY
1	E	50	PRO
1	E	52	ALA
1	E	83	PHE
1	E	102	THR
1	E	125	LYS
1	E	140	GLY
1	A	124	GLY
1	B	150	GLY
1	C	124	GLY
1	D	80	LYS
1	D	131	ASP
1	E	76	CYS
1	E	82	LEU
1	E	100	ASP
1	E	111	TRP
1	E	123	ASN
1	A	123	ASN
1	B	123	ASN
1	C	51	MET
1	C	53	LEU
1	D	123	ASN
1	A	62	SER
1	C	52	ALA
1	C	123	ASN
1	D	133	THR
1	E	135	ALA
1	D	126	HIS
1	E	101	GLY

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Mol	Chain	Res	Type
1	A	63	ALA
1	B	125	LYS
1	D	139	GLY
1	A	104	ILE
1	D	50	PRO

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	82/139 (59%)	67 (82%)	15 (18%)	1 7
1	B	84/139 (60%)	68 (81%)	16 (19%)	1 6
1	C	84/139 (60%)	69 (82%)	15 (18%)	2 7
1	D	84/139 (60%)	67 (80%)	17 (20%)	1 5
1	E	81/139 (58%)	59 (73%)	22 (27%)	0 1
All	All	415/695 (60%)	330 (80%)	85 (20%)	1 5

All (85) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	LEU
1	A	73	CYS
1	A	82	LEU
1	A	89	SER
1	A	91	LYS
1	A	99	SER
1	A	102	THR
1	A	105	GLN
1	A	112	THR
1	A	115	ARG
1	A	130	CYS
1	A	131	ASP
1	A	145	LEU
1	A	147	THR

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Mol	Chain	Res	Type
1	A	148	GLU
1	B	47	ILE
1	B	48	SER
1	B	53	LEU
1	B	84	THR
1	B	89	SER
1	B	98	GLU
1	B	99	SER
1	B	102	THR
1	B	115	ARG
1	B	116	THR
1	B	131	ASP
1	B	132	ASP
1	B	134	ILE
1	B	136	LEU
1	B	141	LYS
1	B	147	THR
1	C	51	MET
1	C	53	LEU
1	C	78	GLN
1	C	80	LYS
1	C	81	LYS
1	C	82	LEU
1	C	102	THR
1	C	106	SER
1	C	116	THR
1	C	119	ASN
1	C	130	CYS
1	C	136	LEU
1	C	138	LYS
1	C	147	THR
1	C	152	ILE
1	D	47	ILE
1	D	53	LEU
1	D	81	LYS
1	D	82	LEU
1	D	84	THR
1	D	89	SER
1	D	94	GLU
1	D	98	GLU
1	D	102	THR
1	D	103	GLU

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Mol	Chain	Res	Type
1	D	114	GLN
1	D	116	THR
1	D	117	VAL
1	D	133	THR
1	D	136	LEU
1	D	141	LYS
1	D	152	ILE
1	E	50	PRO
1	E	51	MET
1	E	58	GLU
1	E	65	VAL
1	E	67	VAL
1	E	69	SER
1	E	81	LYS
1	E	84	THR
1	E	85	GLN
1	E	86	LEU
1	E	94	GLU
1	E	96	ASP
1	E	97	THR
1	E	99	SER
1	E	100	ASP
1	E	115	ARG
1	E	116	THR
1	E	125	LYS
1	E	137	ASN
1	E	142	LEU
1	E	145	LEU
1	E	147	THR

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

Mol	Chain	Res	Type
1	E	137	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 monosaccharides 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 (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	104/171 (60%)	-0.02	1 (0%)	82	68	39, 53, 75, 84	0
1	B	108/171 (63%)	-0.29	1 (0%)	84	71	18, 44, 76, 89	0
1	C	106/171 (61%)	-0.11	3 (2%)	53	36	16, 34, 63, 90	0
1	D	106/171 (61%)	-0.24	0	100	100	18, 37, 65, 85	0
1	E	103/171 (60%)	0.13	2 (1%)	66	49	28, 51, 74, 85	0
All	All	527/855 (61%)	-0.11	7 (1%)	77	61	16, 45, 73, 90	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	47	ILE	5.3
1	C	48	SER	4.0
1	A	48	SER	3.8
1	C	138	LYS	2.7
1	B	44	ALA	2.6
1	E	138	LYS	2.4
1	E	102	THR	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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.