



# Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 11:36 pm BST

PDB ID : 3TJG  
Title : Crystal Structure of human peroxiredoxin IV C51A mutant in oxidized form  
Authors : Cao, Z.; Tavender, T.J.; Roszak, A.W.; Cogdell, R.J.; Bulleid, N.J.  
Deposited on : 2011-08-24  
Resolution : 2.24 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](mailto: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  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

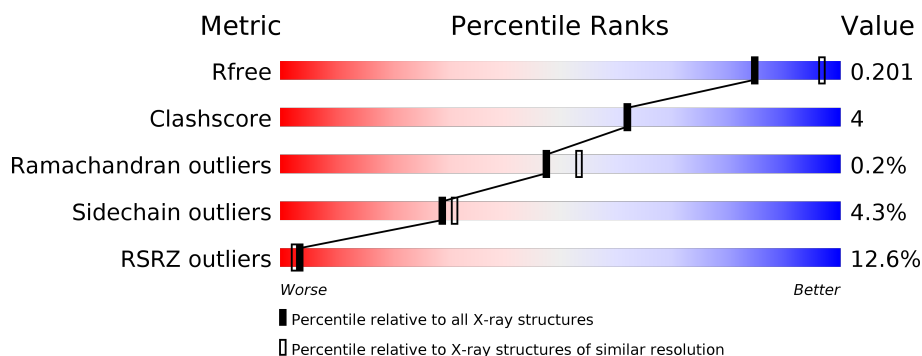
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.24 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	2391 (2.26-2.22)
Clashscore	141614	2539 (2.26-2.22)
Ramachandran outliers	138981	2489 (2.26-2.22)
Sidechain outliers	138945	2490 (2.26-2.22)
RSRZ outliers	127900	2353 (2.26-2.22)

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  $\geq 3$ , 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	254	<div> <div>7%</div> <div>58%</div> <div>7%</div> <div>34%</div> </div>
1	B	254	<div> <div>8%</div> <div>58%</div> <div>7%</div> <div>33%</div> </div>
1	C	254	<div> <div>9%</div> <div>60%</div> <div>6%</div> <div>33%</div> </div>
1	D	254	<div> <div>9%</div> <div>57%</div> <div>8%</div> <div>33%</div> </div>
1	E	254	<div> <div>8%</div> <div>57%</div> <div>8%</div> <div>34%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7811 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 Peroxiredoxin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	167	Total	C	N	O	S	0	9	0
			1402	907	234	259	2			
1	B	170	Total	C	N	O	S	0	6	0
			1407	908	235	260	4			
1	C	170	Total	C	N	O	S	0	6	0
			1414	913	236	262	3			
1	D	169	Total	C	N	O	S	0	9	0
			1424	920	239	262	3			
1	E	167	Total	C	N	O	S	0	11	0
			1425	920	238	264	3			

There are 105 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	18	MET	-	EXPRESSION TAG	UNP Q13162
A	19	GLY	-	EXPRESSION TAG	UNP Q13162
A	20	SER	-	EXPRESSION TAG	UNP Q13162
A	21	SER	-	EXPRESSION TAG	UNP Q13162
A	22	HIS	-	EXPRESSION TAG	UNP Q13162
A	23	HIS	-	EXPRESSION TAG	UNP Q13162
A	24	HIS	-	EXPRESSION TAG	UNP Q13162
A	25	HIS	-	EXPRESSION TAG	UNP Q13162
A	26	HIS	-	EXPRESSION TAG	UNP Q13162
A	27	HIS	-	EXPRESSION TAG	UNP Q13162
A	28	SER	-	EXPRESSION TAG	UNP Q13162
A	29	GLN	-	EXPRESSION TAG	UNP Q13162
A	30	ASP	-	EXPRESSION TAG	UNP Q13162
A	31	PRO	-	EXPRESSION TAG	UNP Q13162
A	32	LEU	-	EXPRESSION TAG	UNP Q13162
A	33	VAL	-	EXPRESSION TAG	UNP Q13162
A	34	PRO	-	EXPRESSION TAG	UNP Q13162
A	35	ARG	-	EXPRESSION TAG	UNP Q13162
A	36	GLY	-	EXPRESSION TAG	UNP Q13162

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A	37	SER	-	EXPRESSION TAG	UNP Q13162
A	51	ALA	CYS	ENGINEERED MUTATION	UNP Q13162
B	18	MET	-	EXPRESSION TAG	UNP Q13162
B	19	GLY	-	EXPRESSION TAG	UNP Q13162
B	20	SER	-	EXPRESSION TAG	UNP Q13162
B	21	SER	-	EXPRESSION TAG	UNP Q13162
B	22	HIS	-	EXPRESSION TAG	UNP Q13162
B	23	HIS	-	EXPRESSION TAG	UNP Q13162
B	24	HIS	-	EXPRESSION TAG	UNP Q13162
B	25	HIS	-	EXPRESSION TAG	UNP Q13162
B	26	HIS	-	EXPRESSION TAG	UNP Q13162
B	27	HIS	-	EXPRESSION TAG	UNP Q13162
B	28	SER	-	EXPRESSION TAG	UNP Q13162
B	29	GLN	-	EXPRESSION TAG	UNP Q13162
B	30	ASP	-	EXPRESSION TAG	UNP Q13162
B	31	PRO	-	EXPRESSION TAG	UNP Q13162
B	32	LEU	-	EXPRESSION TAG	UNP Q13162
B	33	VAL	-	EXPRESSION TAG	UNP Q13162
B	34	PRO	-	EXPRESSION TAG	UNP Q13162
B	35	ARG	-	EXPRESSION TAG	UNP Q13162
B	36	GLY	-	EXPRESSION TAG	UNP Q13162
B	37	SER	-	EXPRESSION TAG	UNP Q13162
B	51	ALA	CYS	ENGINEERED MUTATION	UNP Q13162
C	18	MET	-	EXPRESSION TAG	UNP Q13162
C	19	GLY	-	EXPRESSION TAG	UNP Q13162
C	20	SER	-	EXPRESSION TAG	UNP Q13162
C	21	SER	-	EXPRESSION TAG	UNP Q13162
C	22	HIS	-	EXPRESSION TAG	UNP Q13162
C	23	HIS	-	EXPRESSION TAG	UNP Q13162
C	24	HIS	-	EXPRESSION TAG	UNP Q13162
C	25	HIS	-	EXPRESSION TAG	UNP Q13162
C	26	HIS	-	EXPRESSION TAG	UNP Q13162
C	27	HIS	-	EXPRESSION TAG	UNP Q13162
C	28	SER	-	EXPRESSION TAG	UNP Q13162
C	29	GLN	-	EXPRESSION TAG	UNP Q13162
C	30	ASP	-	EXPRESSION TAG	UNP Q13162
C	31	PRO	-	EXPRESSION TAG	UNP Q13162
C	32	LEU	-	EXPRESSION TAG	UNP Q13162
C	33	VAL	-	EXPRESSION TAG	UNP Q13162
C	34	PRO	-	EXPRESSION TAG	UNP Q13162
C	35	ARG	-	EXPRESSION TAG	UNP Q13162
C	36	GLY	-	EXPRESSION TAG	UNP Q13162

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
C	37	SER	-	EXPRESSION TAG	UNP Q13162
C	51	ALA	CYS	ENGINEERED MUTATION	UNP Q13162
D	18	MET	-	EXPRESSION TAG	UNP Q13162
D	19	GLY	-	EXPRESSION TAG	UNP Q13162
D	20	SER	-	EXPRESSION TAG	UNP Q13162
D	21	SER	-	EXPRESSION TAG	UNP Q13162
D	22	HIS	-	EXPRESSION TAG	UNP Q13162
D	23	HIS	-	EXPRESSION TAG	UNP Q13162
D	24	HIS	-	EXPRESSION TAG	UNP Q13162
D	25	HIS	-	EXPRESSION TAG	UNP Q13162
D	26	HIS	-	EXPRESSION TAG	UNP Q13162
D	27	HIS	-	EXPRESSION TAG	UNP Q13162
D	28	SER	-	EXPRESSION TAG	UNP Q13162
D	29	GLN	-	EXPRESSION TAG	UNP Q13162
D	30	ASP	-	EXPRESSION TAG	UNP Q13162
D	31	PRO	-	EXPRESSION TAG	UNP Q13162
D	32	LEU	-	EXPRESSION TAG	UNP Q13162
D	33	VAL	-	EXPRESSION TAG	UNP Q13162
D	34	PRO	-	EXPRESSION TAG	UNP Q13162
D	35	ARG	-	EXPRESSION TAG	UNP Q13162
D	36	GLY	-	EXPRESSION TAG	UNP Q13162
D	37	SER	-	EXPRESSION TAG	UNP Q13162
D	51	ALA	CYS	ENGINEERED MUTATION	UNP Q13162
E	18	MET	-	EXPRESSION TAG	UNP Q13162
E	19	GLY	-	EXPRESSION TAG	UNP Q13162
E	20	SER	-	EXPRESSION TAG	UNP Q13162
E	21	SER	-	EXPRESSION TAG	UNP Q13162
E	22	HIS	-	EXPRESSION TAG	UNP Q13162
E	23	HIS	-	EXPRESSION TAG	UNP Q13162
E	24	HIS	-	EXPRESSION TAG	UNP Q13162
E	25	HIS	-	EXPRESSION TAG	UNP Q13162
E	26	HIS	-	EXPRESSION TAG	UNP Q13162
E	27	HIS	-	EXPRESSION TAG	UNP Q13162
E	28	SER	-	EXPRESSION TAG	UNP Q13162
E	29	GLN	-	EXPRESSION TAG	UNP Q13162
E	30	ASP	-	EXPRESSION TAG	UNP Q13162
E	31	PRO	-	EXPRESSION TAG	UNP Q13162
E	32	LEU	-	EXPRESSION TAG	UNP Q13162
E	33	VAL	-	EXPRESSION TAG	UNP Q13162
E	34	PRO	-	EXPRESSION TAG	UNP Q13162
E	35	ARG	-	EXPRESSION TAG	UNP Q13162
E	36	GLY	-	EXPRESSION TAG	UNP Q13162

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
E	37	SER	-	EXPRESSION TAG	UNP Q13162
E	51	ALA	CYS	ENGINEERED MUTATION	UNP Q13162

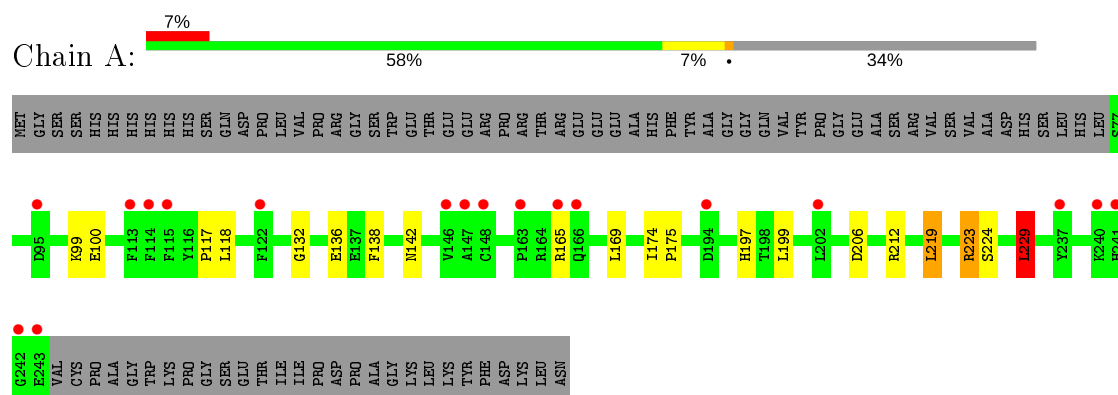
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	131	Total O 131 131	0	0
2	B	168	Total O 168 168	0	0
2	C	136	Total O 136 136	0	0
2	D	156	Total O 156 156	0	0
2	E	148	Total O 148 148	0	0

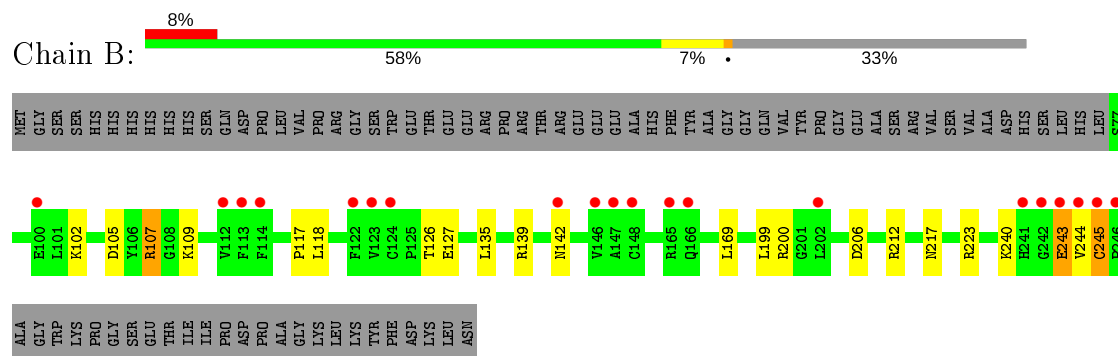
### 3 Residue-property plots [i](#)

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

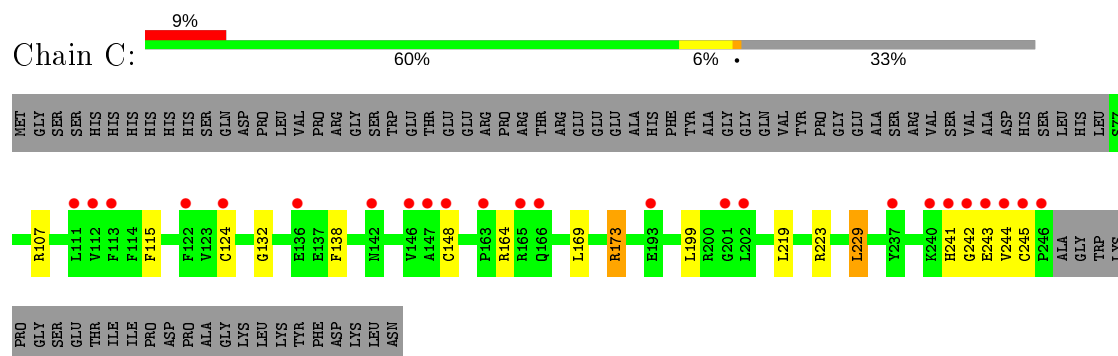
#### • Molecule 1: Peroxiredoxin-4



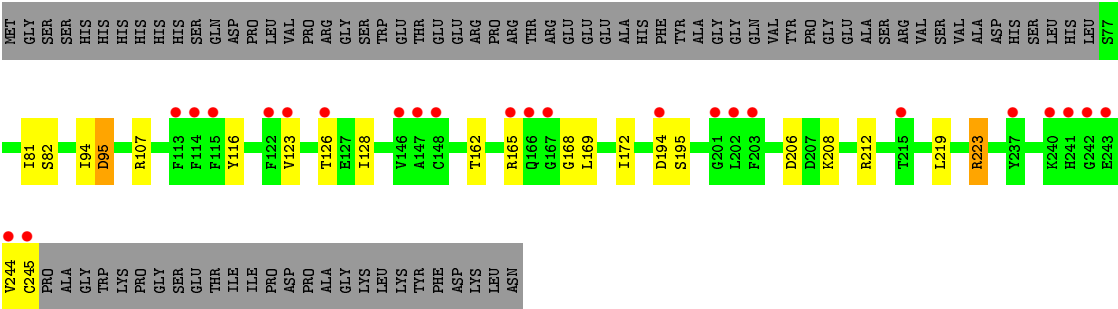
#### • Molecule 1: Peroxiredoxin-4



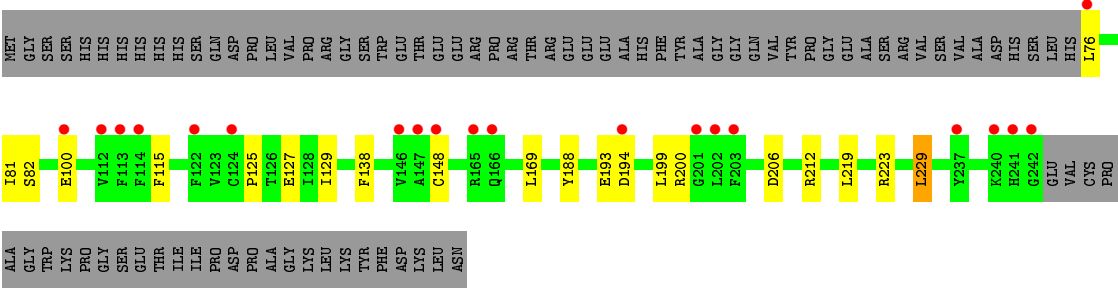
#### • Molecule 1: Peroxiredoxin-4



#### • Molecule 1: Peroxiredoxin-4



● Molecule 1: Peroxiredoxin-4





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	107.16Å 139.07Å 95.14Å 90.00° 102.29° 90.00°	Depositor
Resolution (Å)	28.96 – 2.24 28.96 – 2.24	Depositor EDS
% Data completeness (in resolution range)	100.0 (28.96-2.24) 99.8 (28.96-2.24)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.93 (at 2.24Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, $R_{free}$	0.158 , 0.201 0.159 , 0.201	Depositor DCC
$R_{free}$ test set	3285 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	46.9	Xtriage
Anisotropy	0.105	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 69.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	7811	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [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	0.97	1/1459 (0.1%)	0.86	1/1976 (0.1%)
1	B	0.88	0/1453	0.82	2/1970 (0.1%)
1	C	0.75	0/1457	0.72	0/1973
1	D	0.83	0/1475	0.81	2/1997 (0.1%)
1	E	0.92	1/1473 (0.1%)	0.84	0/1996
All	All	0.88	2/7317 (0.0%)	0.81	5/9912 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	188	TYR	CD2-CE2	5.88	1.48	1.39
1	A	100	GLU	CG-CD	5.26	1.59	1.51

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	107[A]	ARG	NE-CZ-NH2	-5.85	117.37	120.30
1	D	107[B]	ARG	NE-CZ-NH2	-5.85	117.37	120.30
1	A	229	LEU	CA-CB-CG	5.78	128.59	115.30
1	B	107[A]	ARG	NE-CZ-NH2	-5.71	117.44	120.30
1	B	107[B]	ARG	NE-CZ-NH2	-5.71	117.44	120.30

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	1402	0	1411	15	0
1	B	1407	0	1402	17	0
1	C	1414	0	1407	8	0
1	D	1424	0	1428	14	0
1	E	1425	0	1423	9	0
2	A	131	0	0	2	0
2	B	168	0	0	3	0
2	C	136	0	0	2	0
2	D	156	0	0	2	0
2	E	148	0	0	1	0
All	All	7811	0	7071	61	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (61) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:244:VAL:HG12	1:B:245:CYS:HB3	1.57	0.85
1:B:135:LEU:HD21	1:B:139:ARG:NH1	1.96	0.81
1:A:199:LEU:HA	1:A:219[A]:LEU:HD11	1.67	0.76
1:A:199:LEU:HA	1:A:219[A]:LEU:CD1	2.16	0.75
1:B:117:PRO:O	1:B:118:LEU:HG	1.91	0.70
1:B:244:VAL:HG12	1:B:245:CYS:N	2.06	0.70
1:D:94:ILE:O	1:D:95:ASP:HB2	1.95	0.66
1:D:94:ILE:O	1:D:95:ASP:CB	2.45	0.64
1:B:243:GLU:H	1:B:243:GLU:CD	2.02	0.62
1:E:206:ASP:OD2	1:E:212:ARG:HD3	2.00	0.62
1:B:243:GLU:CD	1:B:243:GLU:N	2.53	0.60
1:A:117:PRO:O	1:A:118:LEU:HG	2.01	0.60
1:B:135:LEU:HD21	1:B:139:ARG:HH12	1.65	0.60
1:A:165[A]:ARG:HB3	1:A:165[A]:ARG:CZ	2.33	0.59
1:A:165[A]:ARG:HB3	1:A:165[A]:ARG:NH1	2.20	0.56
1:A:197:HIS:HE1	1:A:219[A]:LEU:HD21	1.70	0.56
2:C:403:HOH:O	1:D:223:ARG:HD2	2.04	0.56
1:D:208[A]:LYS:NZ	2:D:455:HOH:O	2.41	0.54
1:A:223:ARG:HD2	2:B:422:HOH:O	2.09	0.52
1:D:244:VAL:O	1:D:245:CYS:HB3	2.10	0.51
1:C:124:CYS:SG	1:D:245:CYS:C	2.90	0.50
1:E:100[B]:GLU:HG3	2:E:322:HOH:O	2.10	0.50
1:A:132:GLY:HA2	1:A:174:ILE:HD12	1.94	0.50
1:B:117:PRO:O	1:B:118:LEU:CG	2.59	0.50

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136[B]:GLU:H	1:A:136[B]:GLU:CD	2.15	0.49
1:B:127:GLU:OE1	1:B:200:ARG:NH1	2.36	0.49
1:B:240:LYS:HG3	2:B:404:HOH:O	2.13	0.49
2:D:373:HOH:O	1:E:76:LEU:N	2.45	0.49
1:B:109:LYS:HD3	1:B:142[A]:ASN:OD1	2.13	0.48
1:C:132:GLY:O	1:C:173:ARG:NH1	2.46	0.48
1:A:138:PHE:CE2	1:A:229:LEU:HD13	2.49	0.48
1:C:107[B]:ARG:NE	2:C:340:HOH:O	2.43	0.47
1:D:208[A]:LYS:HE3	1:D:208[A]:LYS:HB2	1.25	0.47
1:D:206:ASP:OD2	1:D:212:ARG:HD3	2.15	0.47
1:A:224:SER:OG	2:A:353:HOH:O	2.21	0.46
1:C:138:PHE:CE2	1:C:229:LEU:HD13	2.51	0.46
1:C:138:PHE:CZ	1:C:229:LEU:HD13	2.52	0.45
1:E:125:PRO:HG2	1:E:129:ILE:HD11	1.98	0.45
1:E:138:PHE:CE2	1:E:229:LEU:HD13	2.52	0.45
1:E:81:ILE:O	1:E:82:SER:HB2	2.16	0.45
1:B:102:LYS:O	1:B:105:ASP:HB2	2.18	0.45
1:D:81:ILE:O	1:D:82:SER:HB2	2.17	0.44
1:B:107[A]:ARG:NH2	2:B:420:HOH:O	2.51	0.43
1:D:116:TYR:CG	1:D:128:ILE:HD11	2.54	0.43
1:A:206:ASP:OD2	1:A:212:ARG:HD3	2.18	0.43
1:B:206:ASP:OD2	1:B:212:ARG:HD3	2.18	0.43
1:C:241:HIS:O	1:C:243:GLU:N	2.47	0.43
1:E:115:PHE:HA	1:E:148:CYS:O	2.19	0.43
1:A:165[A]:ARG:NH1	1:A:165[A]:ARG:CB	2.82	0.42
1:B:244:VAL:CG1	1:B:245:CYS:HB3	2.39	0.42
1:D:116:TYR:CD2	1:D:128:ILE:HD11	2.54	0.42
1:B:243:GLU:O	1:B:243:GLU:OE1	2.37	0.42
1:A:174:ILE:HA	1:A:175:PRO:HD3	1.98	0.41
1:C:244:VAL:HB	1:D:123:VAL:HG11	2.03	0.41
1:C:115:PHE:HA	1:C:148:CYS:O	2.21	0.41
1:D:162:THR:HG22	1:D:168:GLY:HA3	2.03	0.40
1:B:200:ARG:HB2	1:B:217:ASN:HB2	2.04	0.40
1:A:142[A]:ASN:ND2	2:A:339:HOH:O	2.45	0.40
1:E:127:GLU:OE1	1:E:200:ARG:NH1	2.53	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	174/254 (68%)	169 (97%)	5 (3%)	0	100	100
1	B	174/254 (68%)	169 (97%)	5 (3%)	0	100	100
1	C	174/254 (68%)	168 (97%)	5 (3%)	1 (1%)	25	23
1	D	176/254 (69%)	166 (94%)	9 (5%)	1 (1%)	25	23
1	E	176/254 (69%)	170 (97%)	6 (3%)	0	100	100
All	All	874/1270 (69%)	842 (96%)	30 (3%)	2 (0%)	47	53

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	242	GLY
1	D	165	ARG

### 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	156/220 (71%)	150 (96%)	6 (4%)	33	36
1	B	156/220 (71%)	150 (96%)	6 (4%)	33	36
1	C	156/220 (71%)	148 (95%)	8 (5%)	24	23
1	D	158/220 (72%)	151 (96%)	7 (4%)	28	30
1	E	158/220 (72%)	150 (95%)	8 (5%)	24	23
All	All	784/1100 (71%)	749 (96%)	35 (4%)	29	29

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	99	LYS
1	A	169	LEU
1	A	219[A]	LEU
1	A	219[B]	LEU
1	A	223	ARG
1	A	229	LEU
1	B	126	THR
1	B	169	LEU
1	B	199	LEU
1	B	223	ARG
1	B	243	GLU
1	B	245	CYS
1	C	164	ARG
1	C	169	LEU
1	C	173	ARG
1	C	199	LEU
1	C	219	LEU
1	C	223	ARG
1	C	229	LEU
1	C	245	CYS
1	D	95	ASP
1	D	126	THR
1	D	169	LEU
1	D	172	ILE
1	D	195	SER
1	D	219	LEU
1	D	223	ARG
1	E	169	LEU
1	E	193[A]	GLU
1	E	193[B]	GLU
1	E	199	LEU
1	E	219[A]	LEU
1	E	219[B]	LEU
1	E	223	ARG
1	E	229	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	166	GLN
1	C	233	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	D	166	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	167/254 (65%)	0.20	18 (10%)	5 5	32, 46, 77, 99	0
1	B	170/254 (66%)	0.25	20 (11%)	4 3	36, 50, 82, 113	0
1	C	170/254 (66%)	0.48	24 (14%)	2 2	43, 58, 91, 117	0
1	D	169/254 (66%)	0.31	24 (14%)	2 2	36, 51, 82, 116	0
1	E	167/254 (65%)	0.26	20 (11%)	4 3	31, 48, 74, 101	0
All	All	843/1270 (66%)	0.30	106 (12%)	3 2	31, 51, 82, 117	0

All (106) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	245	CYS	8.9
1	C	246	PRO	8.4
1	A	165[A]	ARG	6.5
1	C	243	GLU	6.0
1	B	246	PRO	5.9
1	D	245	CYS	5.8
1	D	122	PHE	5.4
1	D	165	ARG	5.4
1	C	244	VAL	5.3
1	B	122	PHE	5.2
1	B	244	VAL	5.0
1	B	245	CYS	4.6
1	B	242	GLY	4.4
1	C	242	GLY	4.3
1	D	167	GLY	4.2
1	B	165	ARG	4.1
1	D	244	VAL	4.1
1	C	165	ARG	4.0
1	B	243	GLU	3.8
1	C	166	GLN	3.6

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	C	124	CYS	3.6
1	A	122	PHE	3.6
1	D	242	GLY	3.5
1	C	240	LYS	3.4
1	C	163	PRO	3.4
1	D	241	HIS	3.4
1	D	243	GLU	3.3
1	E	237	TYR	3.3
1	B	241	HIS	3.3
1	E	76	LEU	3.3
1	C	113	PHE	3.2
1	D	166	GLN	3.2
1	B	123	VAL	3.2
1	D	194[A]	ASP	3.2
1	C	146	VAL	3.1
1	A	243	GLU	3.1
1	D	146	VAL	3.1
1	E	165	ARG	3.1
1	E	122	PHE	3.1
1	E	202	LEU	3.1
1	E	241	HIS	3.1
1	D	202	LEU	3.0
1	E	146	VAL	2.9
1	C	202	LEU	2.8
1	C	112	VAL	2.8
1	B	148	CYS	2.8
1	A	202	LEU	2.8
1	E	148	CYS	2.8
1	B	146	VAL	2.8
1	D	123	VAL	2.8
1	A	166	GLN	2.7
1	E	124[A]	CYS	2.7
1	D	113	PHE	2.7
1	B	100[A]	GLU	2.6
1	C	237	TYR	2.6
1	D	114	PHE	2.6
1	E	242	GLY	2.6
1	E	114	PHE	2.6
1	A	163	PRO	2.6
1	D	148	CYS	2.6
1	E	240[A]	LYS	2.6
1	A	148	CYS	2.6

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	C	147	ALA	2.6
1	D	240	LYS	2.5
1	B	124[A]	CYS	2.5
1	D	215	THR	2.5
1	A	146	VAL	2.5
1	B	113	PHE	2.5
1	A	147	ALA	2.5
1	D	237	TYR	2.4
1	D	126	THR	2.4
1	B	112	VAL	2.4
1	A	114	PHE	2.3
1	B	114	PHE	2.3
1	B	166	GLN	2.3
1	E	147	ALA	2.3
1	C	142	ASN	2.3
1	D	201	GLY	2.2
1	A	241	HIS	2.2
1	A	95	ASP	2.2
1	A	242	GLY	2.2
1	B	202	LEU	2.2
1	E	113	PHE	2.2
1	B	147	ALA	2.2
1	C	136[A]	GLU	2.2
1	E	203	PHE	2.1
1	A	240[A]	LYS	2.1
1	A	237	TYR	2.1
1	E	100[A]	GLU	2.1
1	D	147	ALA	2.1
1	B	142[A]	ASN	2.1
1	D	203	PHE	2.1
1	A	194[A]	ASP	2.1
1	E	166	GLN	2.1
1	A	115	PHE	2.1
1	C	193	GLU	2.1
1	E	201	GLY	2.1
1	C	111	LEU	2.1
1	C	148	CYS	2.1
1	C	122	PHE	2.1
1	C	201	GLY	2.1
1	C	241	HIS	2.0
1	A	113	PHE	2.0
1	E	112	VAL	2.0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	D	115	PHE	2.0
1	E	194[A]	ASP	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.