



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:25 PM UTC

PDB ID : 3TJG / pdb_00003tjg
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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

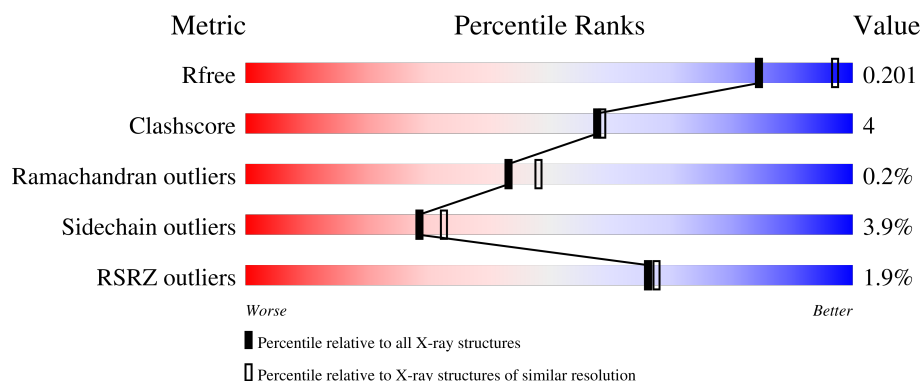
1 Overall quality at a glance

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}	180053	3416 (2.26-2.22)
Clashscore	190562	3556 (2.26-2.22)
Ramachandran outliers	187476	3500 (2.26-2.22)
Sidechain outliers	187428	3501 (2.26-2.22)
RSRZ outliers	180081	3415 (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 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 $\leq 5\%$. 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	57% 7% . 34%
1	B	254	% 58% 7% . 33%
1	C	254	2% 60% 6% . 33%
1	D	254	2% 57% 8% . 33%
1	E	254	% 58% 7% 34%

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

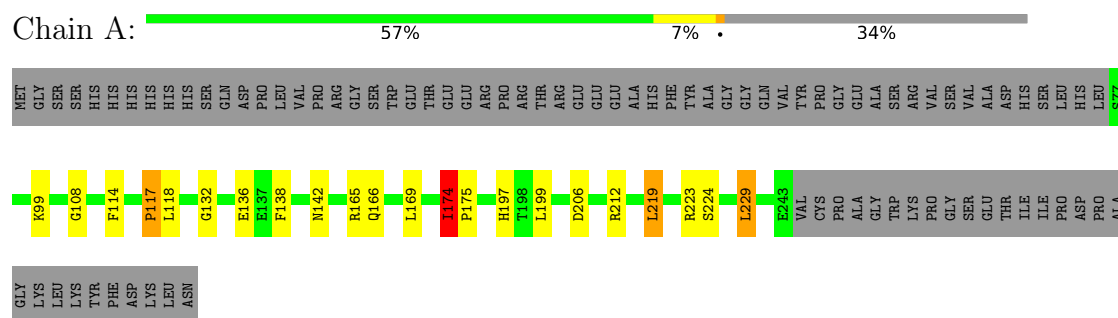
- Molecule 2 is water.

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

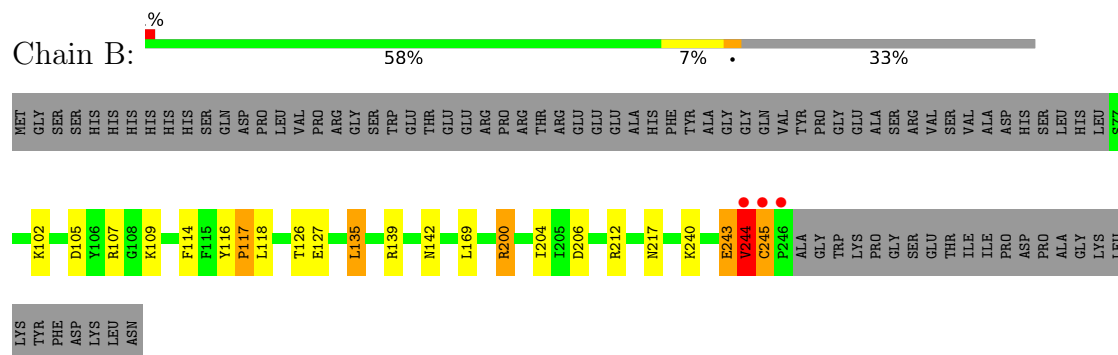
3 Residue-property plots

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.

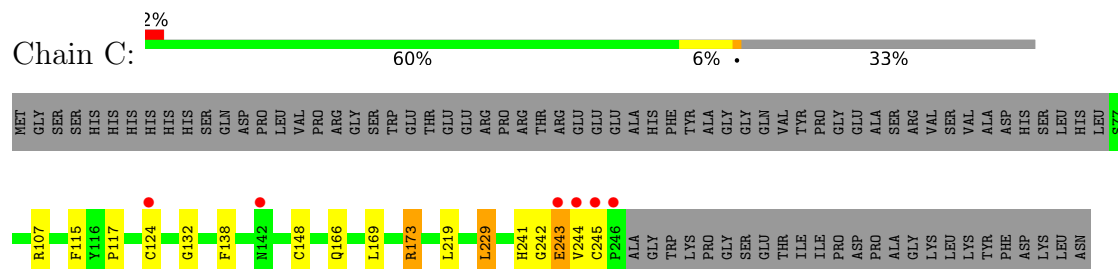
• Molecule 1: Peroxiredoxin-4



• Molecule 1: Peroxiredoxin-4

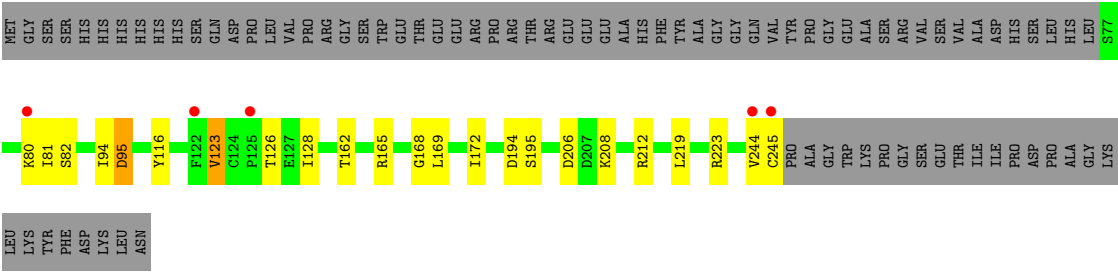


• Molecule 1: Peroxiredoxin-4

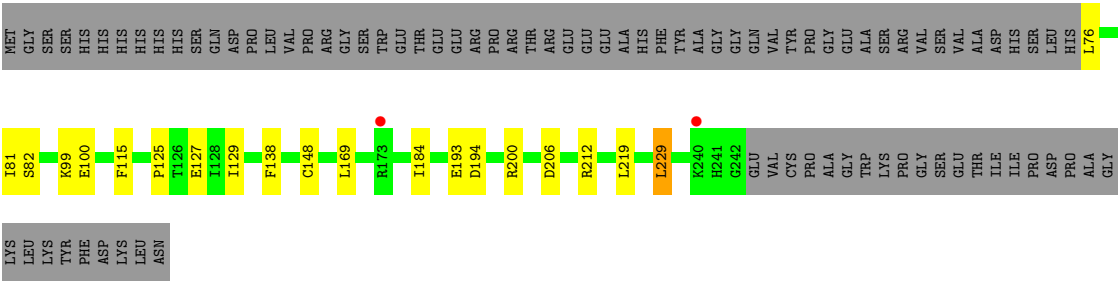


• Molecule 1: Peroxiredoxin-4





● Molecule 1: Peroxiredoxin-4



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	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) 99.7 (28.96-2.24)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	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 ²)	46.9	Xtriage
Anisotropy	0.105	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 77.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	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 ²)	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.*

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 [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	1.11	0/1459	1.05	4/1976 (0.2%)
1	B	1.01	2/1453 (0.1%)	1.05	7/1970 (0.4%)
1	C	0.84	0/1457	0.93	2/1973 (0.1%)
1	D	0.96	0/1475	0.96	0/1997
1	E	1.02	1/1473 (0.1%)	1.02	0/1996
All	All	0.99	3/7317 (0.0%)	1.00	13/9912 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	184	ILE	CA-CB	5.29	1.60	1.54
1	B	204	ILE	C-O	-5.01	1.18	1.24
1	B	116	TYR	C-O	-5.00	1.18	1.24

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	244	VAL	CB-CA-C	-7.39	102.51	111.97
1	B	244	VAL	N-CA-C	6.73	116.88	110.42
1	A	117	PRO	N-CA-C	6.22	122.36	113.47
1	B	117	PRO	N-CA-C	6.06	121.96	113.53
1	B	200	ARG	CA-C-N	-5.44	117.52	122.80
1	B	200	ARG	C-N-CA	-5.44	117.52	122.80
1	B	114	PHE	N-CA-C	5.44	118.09	109.50
1	B	135	LEU	N-CA-C	5.39	117.85	111.33
1	C	117	PRO	N-CA-C	5.39	121.18	113.47
1	A	114	PHE	N-CA-C	5.32	117.91	109.50
1	C	243	GLU	N-CA-C	5.24	117.48	110.35
1	A	174	ILE	CB-CA-C	5.21	115.95	110.37
1	A	108	GLY	N-CA-C	-5.01	108.41	114.92

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	1402	0	1411	15	0
1	B	1407	0	1402	18	0
1	C	1414	0	1407	8	0
1	D	1424	0	1428	15	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	3	0
2	E	148	0	0	1	0
All	All	7811	0	7071	63	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 (63) 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:B:243:GLU:H	1:B:243:GLU:CD	2.02	0.66
1:D:94:ILE:O	1:D:95:ASP:HB2	1.95	0.66
1:B:243:GLU:CD	1:B:243:GLU:N	2.53	0.65
1:D:94:ILE:O	1:D:95:ASP:CB	2.45	0.64
1:E:206:ASP:OD2	1:E:212:ARG:HD3	2.00	0.62
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:CZ	1:A:165[A]:ARG:HB3	2.33	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:C:124:CYS:SG	1:D:245:CYS:C	2.90	0.55
1:A:136[B]:GLU:H	1:A:136[B]:GLU:CD	2.15	0.54
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: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
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:HB2	1:D:208[A]:LYS:HE3	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:D:80[B]:LYS:NZ	2:D:425:HOH:O	2.53	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

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:117:PRO:C	1:B:118:LEU:HG	2.44	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 [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	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%)	21	20
1	D	176/254 (69%)	166 (94%)	9 (5%)	1 (1%)	21	20
1	E	176/254 (69%)	170 (97%)	6 (3%)	0	100	100
All	All	874/1270 (69%)	842 (96%)	30 (3%)	2 (0%)	43	48

All (2) Ramachandran outliers are listed below:

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

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	156/220 (71%)	149 (96%)	7 (4%)	24	26
1	B	156/220 (71%)	151 (97%)	5 (3%)	34	40
1	C	156/220 (71%)	150 (96%)	6 (4%)	29	34
1	D	158/220 (72%)	151 (96%)	7 (4%)	25	27
1	E	158/220 (72%)	151 (96%)	7 (4%)	25	27
All	All	784/1100 (71%)	752 (96%)	32 (4%)	28	30

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	99	LYS
1	A	166	GLN
1	A	169	LEU
1	A	174	ILE
1	A	219[A]	LEU
1	A	219[B]	LEU
1	A	229	LEU
1	B	126	THR
1	B	169	LEU
1	B	243	GLU
1	B	244	VAL
1	B	245	CYS
1	C	166	GLN
1	C	169	LEU
1	C	173	ARG
1	C	219	LEU
1	C	229	LEU
1	C	245	CYS
1	D	95	ASP
1	D	123	VAL
1	D	126	THR
1	D	169	LEU
1	D	172	ILE
1	D	195	SER
1	D	219	LEU
1	E	99	LYS
1	E	169	LEU
1	E	193[A]	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	193[B]	GLU
1	E	219[A]	LEU
1	E	219[B]	LEU
1	E	229	LEU

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

Mol	Chain	Res	Type
1	C	233	GLN
1	D	166	GLN
1	E	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 oligosaccharides 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	167/254 (65%)	-0.40	0 100 100	23, 44, 73, 94	9 (5%)
1	B	170/254 (66%)	-0.28	3 (1%) 67 69	27, 48, 82, 113	6 (3%)
1	C	170/254 (66%)	-0.24	6 (3%) 47 46	26, 56, 91, 117	6 (3%)
1	D	169/254 (66%)	-0.35	5 (2%) 52 52	27, 50, 82, 116	9 (5%)
1	E	167/254 (65%)	-0.39	2 (1%) 76 78	21, 45, 73, 101	11 (6%)
All	All	843/1270 (66%)	-0.33	16 (1%) 66 68	21, 49, 82, 117	41 (4%)

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	244	VAL	4.1
1	B	244	VAL	4.1
1	C	246	PRO	4.1
1	C	244	VAL	4.1
1	C	245	CYS	3.6
1	B	245	CYS	3.1
1	D	245	CYS	2.7
1	B	246	PRO	2.7
1	C	124	CYS	2.5
1	E	173[A]	ARG	2.5
1	D	122	PHE	2.4
1	E	240[A]	LYS	2.3
1	D	80[A]	LYS	2.2
1	C	243	GLU	2.1
1	C	142	ASN	2.1
1	D	125	PRO	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 oligosaccharides 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.