Full wwPDB X-ray Structure Validation Report (i)

Aug 20, 2023 – 07:35 AM EDT

PDB ID	:	2I81
Title	:	Crystal Structure of Plasmodium vivax 2-Cys Peroxiredoxin, Reduced
Authors	:	Artz, J.D.; Qiu, W.; Dong, A.; Lew, J.; Ren, H.; Zhao, Y.; Kozieradski, I.; Edwards, A.M.; Arrowsmith, C.H.; Weigelt, J.; Sundstrom, M.; Bochkarev, A.; Hui, R.; Structural Genomics Consortium (SGC)
Deposited on	:	2006-08-31
Resolution	:	2.45 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:

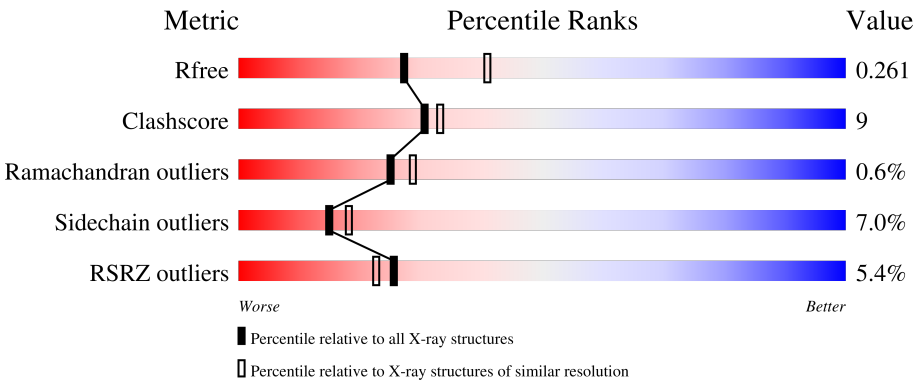
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.45 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	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

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	213	2%, 73%, 15%, •, 9%
1	B	213	6%, 69%, 20%, •, 9%
1	C	213	8%, 68%, 21%, •, 9%
1	D	213	%, 66%, 8%, •, 23%
1	E	213	5%, 58%, 17%, •, 22%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 7270 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 2-Cys Peroxiredoxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	193	1522	986	249	282	5	0	0	0
1	B	193	1523	987	249	282	5	0	0	0
1	C	193	1522	986	249	282	5	0	0	0
1	D	163	1298	845	212	238	3	0	0	0
1	E	167	1325	862	216	244	3	0	0	0

- Molecule 2 is water.

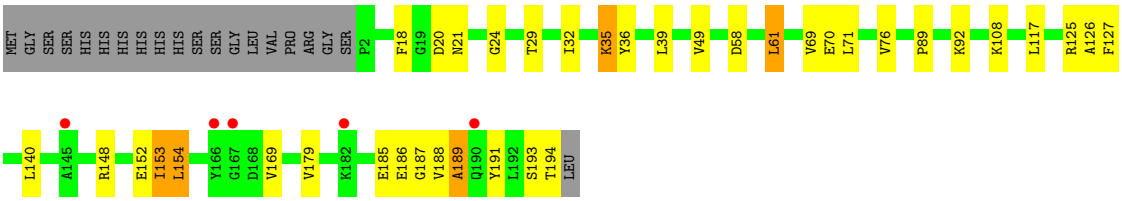
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	26	26	26	0	0
2	B	19	19	19	0	0
2	C	16	16	16	0	0
2	D	11	11	11	0	0
2	E	8	8	8	0	0

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.

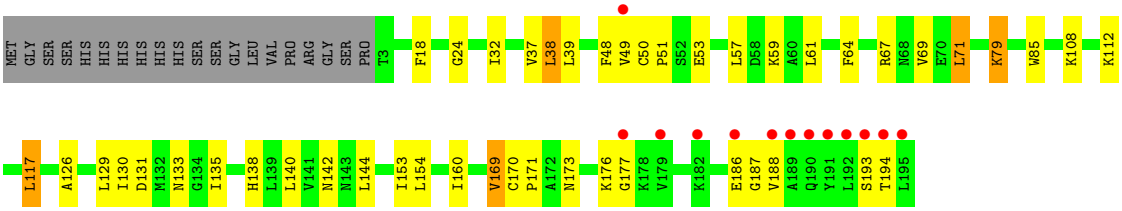
• Molecule 1: 2-Cys Peroxiredoxin

Chain A:



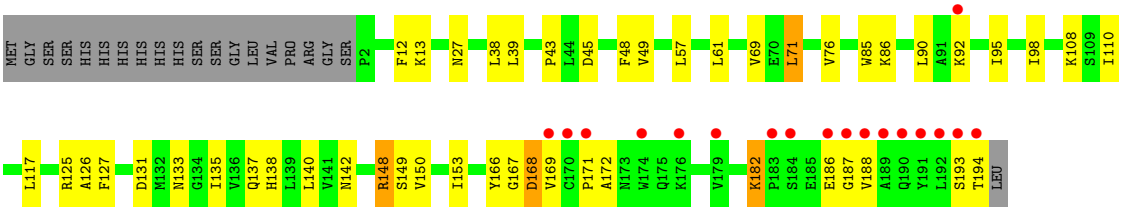
• Molecule 1: 2-Cys Peroxiredoxin

Chain B:



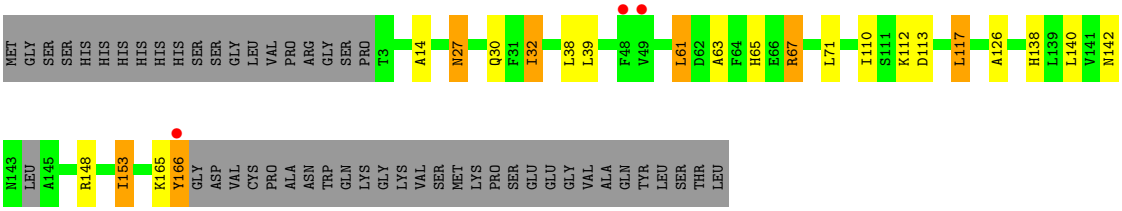
• Molecule 1: 2-Cys Peroxiredoxin

Chain C:



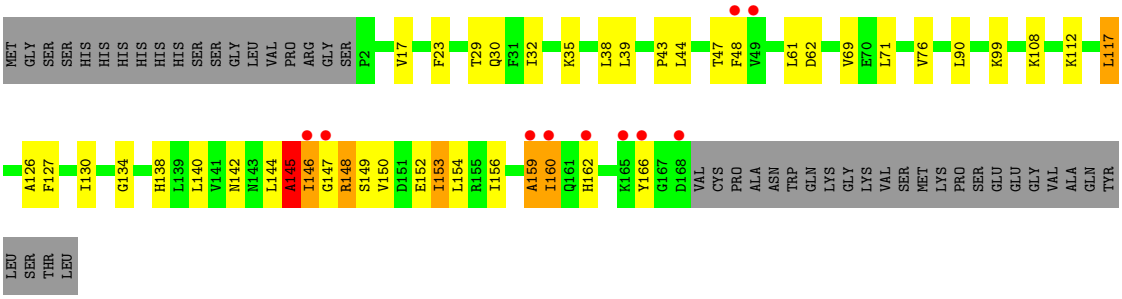
• Molecule 1: 2-Cys Peroxiredoxin

Chain D:



- Molecule 1: 2-Cys Peroxiredoxin

Chain E:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	91.35Å 212.57Å 115.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.56 – 2.45 36.56 – 2.45	Depositor EDS
% Data completeness (in resolution range)	100.0 (36.56-2.45) 99.9 (36.56-2.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	1.96 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.217 , 0.265 0.232 , 0.261	Depositor DCC
R_{free} test set	2107 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	43.4	Xtriage
Anisotropy	0.022	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 31.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	7270	wwPDB-VP
Average B, all atoms (Å^2)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.88% 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	0.45	0/1557	0.66	2/2108 (0.1%)
1	B	0.35	0/1557	0.54	0/2108
1	C	0.35	0/1557	0.54	0/2108
1	D	0.39	0/1326	0.55	0/1793
1	E	0.46	2/1355 (0.1%)	0.65	4/1834 (0.2%)
All	All	0.40	2/7352 (0.0%)	0.59	6/9951 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	E	0	2
All	All	0	4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	44	LEU	C-N	-8.45	1.14	1.34
1	E	35	LYS	CE-NZ	6.10	1.64	1.49

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	189	ALA	N-CA-C	-8.97	86.78	111.00
1	E	43	PRO	O-C-N	-7.38	110.90	122.70
1	E	43	PRO	CA-C-N	5.54	129.40	117.20
1	E	43	PRO	C-N-CA	5.42	135.26	121.70
1	E	145	ALA	N-CA-C	-5.30	96.68	111.00
1	A	154	LEU	CB-CG-CD1	5.14	119.73	111.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	188	VAL	Peptide
1	A	193	SER	Peptide
1	E	145	ALA	Peptide
1	E	146	ILE	Peptide

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	1522	0	1524	21	0
1	B	1523	0	1527	49	0
1	C	1522	0	1524	47	0
1	D	1298	0	1301	14	0
1	E	1325	0	1327	31	0
2	A	26	0	0	1	0
2	B	19	0	0	0	0
2	C	16	0	0	0	0
2	D	11	0	0	2	0
2	E	8	0	0	0	0
All	All	7270	0	7203	132	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 9.

All (132) 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:49:VAL:HG23	1:C:169:VAL:CG1	1.69	1.21
1:B:49:VAL:CG2	1:C:169:VAL:CG1	2.27	1.13
1:E:159:ALA:HB2	1:E:162:HIS:HB3	1.24	1.09
1:B:49:VAL:HG23	1:C:169:VAL:HG11	1.52	0.89
1:A:191:TYR:O	1:A:194:THR:HB	1.73	0.88
1:B:49:VAL:CG2	1:C:169:VAL:HG12	2.00	0.88
1:C:186:GLU:N	1:C:187:GLY:HA3	1.90	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:49:VAL:CG2	1:C:169:VAL:HG13	2.05	0.84
1:B:188:VAL:CG2	1:C:48:PHE:HD1	1.98	0.77
1:B:49:VAL:HG13	1:C:171:PRO:HA	1.69	0.74
1:C:186:GLU:H	1:C:187:GLY:HA3	1.49	0.74
1:B:169:VAL:HG13	1:C:49:VAL:HG22	1.68	0.72
1:B:173:ASN:HD21	1:C:150:VAL:H	1.36	0.72
1:B:49:VAL:HG21	1:C:169:VAL:HG13	1.70	0.71
1:C:166:TYR:C	1:C:168:ASP:H	1.93	0.70
1:A:76:VAL:HG11	1:A:108:LYS:HZ3	1.56	0.69
1:D:142:ASN:OD1	1:E:138:HIS:HD2	1.77	0.67
1:C:127:PHE:CE1	1:C:148:ARG:HG3	2.29	0.67
1:A:186:GLU:N	1:A:187:GLY:HA3	2.10	0.67
1:C:182:LYS:HG3	1:C:187:GLY:HA2	1.77	0.66
1:C:193:SER:HA	1:C:194:THR:C	2.15	0.66
1:D:138:HIS:HD2	1:E:142:ASN:OD1	1.79	0.65
1:E:159:ALA:HA	1:E:160:ILE:C	2.17	0.65
1:B:188:VAL:CG2	1:C:48:PHE:HA	2.27	0.64
1:B:138:HIS:HD2	1:C:142:ASN:OD1	1.83	0.62
1:D:165:LYS:HB3	1:D:166:TYR:CG	2.34	0.61
1:B:129:LEU:HD23	1:B:160:ILE:CD1	2.32	0.60
1:E:159:ALA:H	1:E:162:HIS:H	1.50	0.60
1:B:188:VAL:HG21	1:C:48:PHE:HD1	1.65	0.60
1:C:12:PHE:HB2	1:C:110:ILE:HD12	1.84	0.59
1:B:48:PHE:O	1:B:51:PRO:HD2	2.02	0.59
1:B:53:GLU:HA	1:C:172:ALA:HB2	1.83	0.59
1:A:89:PRO:HG2	1:A:92:LYS:HD3	1.85	0.59
1:B:48:PHE:HA	1:C:188:VAL:HG21	1.85	0.58
1:C:131:ASP:HB3	1:C:133:ASN:H	1.68	0.58
1:B:188:VAL:HG22	1:C:48:PHE:HA	1.86	0.57
1:C:166:TYR:C	1:C:168:ASP:N	2.55	0.57
1:B:186:GLU:N	1:B:187:GLY:HA3	2.20	0.56
1:E:159:ALA:HB2	1:E:162:HIS:CB	2.15	0.56
1:B:131:ASP:HB2	1:B:135:ILE:H	1.71	0.56
1:E:145:ALA:H	1:E:146:ILE:HG23	1.72	0.54
1:C:76:VAL:HG11	1:C:108:LYS:HZ3	1.72	0.54
1:A:185:GLU:O	1:A:189:ALA:HB2	2.07	0.54
1:B:112:LYS:HG3	1:B:117:LEU:HD12	1.88	0.54
1:E:127:PHE:CE1	1:E:148:ARG:HG3	2.43	0.54
1:A:186:GLU:H	1:A:187:GLY:HA3	1.72	0.54
1:B:188:VAL:CG2	1:C:48:PHE:CD1	2.86	0.53
1:B:188:VAL:HG23	1:C:48:PHE:HD1	1.70	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:LYS:HE3	1:A:70:GLU:HB2	1.91	0.53
1:C:126:ALA:HA	1:C:140:LEU:O	2.08	0.53
1:B:142:ASN:OD1	1:C:138:HIS:HD2	1.91	0.53
1:B:188:VAL:HG21	1:C:48:PHE:HA	1.91	0.53
1:B:48:PHE:HA	1:C:188:VAL:CG2	2.39	0.52
1:C:45:ASP:O	1:C:85:TRP:CZ2	2.62	0.52
1:D:112:LYS:HG3	1:D:117:LEU:HD12	1.91	0.52
1:E:150:VAL:HA	1:E:153:ILE:HD11	1.92	0.52
1:B:169:VAL:HG13	1:C:49:VAL:CG2	2.37	0.52
1:B:50:CYS:HB2	1:B:51:PRO:HD3	1.92	0.52
1:C:49:VAL:HB	1:C:125:ARG:NH2	2.24	0.52
1:E:144:LEU:HA	1:E:145:ALA:HB2	1.92	0.52
1:B:51:PRO:HG3	1:B:85:TRP:HZ2	1.76	0.51
1:B:49:VAL:HG22	1:C:169:VAL:HG12	1.87	0.51
1:E:149:SER:HB3	1:E:152:GLU:HB2	1.94	0.50
1:B:144:LEU:HG	1:C:137:GLN:OE1	2.11	0.49
1:E:47:THR:HG22	1:E:48:PHE:H	1.77	0.49
1:E:153:ILE:HA	1:E:156:ILE:HG13	1.94	0.49
1:D:165:LYS:HB3	1:D:166:TYR:CD2	2.48	0.49
1:B:188:VAL:HG23	1:C:48:PHE:CD1	2.48	0.48
1:B:131:ASP:HB3	1:B:133:ASN:H	1.76	0.48
1:B:18:PHE:HE1	1:B:24:GLY:HA3	1.77	0.48
1:B:129:LEU:HD23	1:B:160:ILE:HD12	1.95	0.48
1:A:18:PHE:HE1	1:A:24:GLY:HA3	1.78	0.48
1:D:113:ASP:OD2	2:D:200:HOH:O	2.20	0.48
1:A:108:LYS:HE2	1:B:108:LYS:HE2	1.96	0.47
1:E:159:ALA:N	1:E:162:HIS:H	2.12	0.47
1:B:126:ALA:HA	1:B:140:LEU:O	2.14	0.47
1:D:14:ALA:HB2	1:D:110:ILE:HD11	1.95	0.47
1:E:159:ALA:CB	1:E:162:HIS:HB3	2.17	0.46
1:D:61:LEU:HD22	1:D:65:HIS:CE1	2.50	0.46
1:D:63:ALA:HB1	1:D:67:ARG:HH21	1.81	0.46
1:B:176:LYS:HA	1:B:177:GLY:HA2	1.57	0.46
1:B:51:PRO:HG3	1:B:85:TRP:CZ2	2.50	0.46
1:C:86:LYS:HE3	1:C:98:ILE:HG13	1.97	0.46
1:E:76:VAL:HG11	1:E:108:LYS:NZ	2.31	0.46
1:A:126:ALA:HA	1:A:140:LEU:O	2.16	0.45
1:C:166:TYR:O	1:C:168:ASP:N	2.49	0.45
1:E:47:THR:HG22	1:E:48:PHE:N	2.31	0.45
1:A:29:THR:O	1:A:32:ILE:HG22	2.16	0.45
1:E:144:LEU:HD12	1:E:144:LEU:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:VAL:HB	1:A:125:ARG:CZ	2.47	0.45
1:D:32:ILE:HA	2:D:205:HOH:O	2.17	0.45
1:A:76:VAL:HG11	1:A:108:LYS:NZ	2.28	0.45
1:A:179:VAL:HG13	1:A:191:TYR:HE1	1.81	0.45
1:D:27:ASN:H	1:D:30:GLN:NE2	2.15	0.45
1:C:57:LEU:HB3	1:C:71:LEU:HD11	1.99	0.45
1:E:90:LEU:H	1:E:90:LEU:HD12	1.82	0.45
1:E:149:SER:O	1:E:153:ILE:HD13	2.16	0.45
1:B:18:PHE:CE1	1:B:24:GLY:HA3	2.52	0.45
1:E:156:ILE:O	1:E:160:ILE:HG22	2.16	0.44
1:E:112:LYS:HG2	1:E:117:LEU:HD12	2.00	0.44
1:A:20:ASP:O	1:A:21:ASN:HB2	2.18	0.44
1:B:57:LEU:HB3	1:B:71:LEU:HD11	2.00	0.44
1:A:36:TYR:HB2	1:A:69:VAL:HG12	2.00	0.44
1:C:13:LYS:HG3	1:C:27:ASN:HB3	2.00	0.44
1:B:173:ASN:ND2	1:C:150:VAL:H	2.09	0.44
1:E:126:ALA:HA	1:E:140:LEU:O	2.18	0.44
1:B:193:SER:HA	1:B:194:THR:HA	1.68	0.44
1:D:126:ALA:HA	1:D:140:LEU:O	2.18	0.43
1:E:150:VAL:O	1:E:154:LEU:HG	2.18	0.43
1:A:58:ASP:O	1:A:61:LEU:HB2	2.18	0.43
1:B:37:VAL:HB	1:B:130:ILE:HB	2.00	0.43
1:E:29:THR:O	1:E:32:ILE:HG22	2.19	0.43
1:B:170:CYS:HA	1:B:171:PRO:HD3	1.82	0.43
1:D:166:TYR:CD1	1:D:166:TYR:N	2.85	0.43
1:B:129:LEU:HD23	1:B:160:ILE:HD13	2.01	0.43
1:B:79:LYS:H	1:B:79:LYS:HG3	1.64	0.42
1:E:159:ALA:CA	1:E:160:ILE:C	2.87	0.42
1:A:152:GLU:HG3	2:A:206:HOH:O	2.19	0.42
1:E:147:GLY:HA2	1:E:148:ARG:HA	1.85	0.42
1:C:95:ILE:HD12	1:C:98:ILE:HG12	2.02	0.42
1:E:76:VAL:HG11	1:E:108:LYS:HZ3	1.84	0.42
1:A:18:PHE:CE1	1:A:24:GLY:HA3	2.55	0.41
1:C:131:ASP:HB2	1:C:135:ILE:H	1.84	0.41
1:A:127:PHE:CE1	1:A:153:ILE:HG12	2.55	0.41
1:B:38:LEU:HD12	1:B:64:PHE:CE2	2.55	0.41
1:E:130:ILE:CG2	1:E:134:GLY:HA2	2.50	0.41
1:B:173:ASN:HD22	1:C:149:SER:HA	1.85	0.41
1:E:162:HIS:HD2	1:E:166:TYR:CD2	2.38	0.41
1:A:153:ILE:H	1:A:153:ILE:HG13	1.75	0.41
1:C:153:ILE:H	1:C:153:ILE:HG13	1.73	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:153:ILE:H	1:D:153:ILE:HG13	1.62	0.40
1:E:17:VAL:HG22	1:E:23:PHE:HE2	1.87	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	191/213 (90%)	183 (96%)	8 (4%)	0	100	100
1	B	191/213 (90%)	182 (95%)	9 (5%)	0	100	100
1	C	191/213 (90%)	176 (92%)	13 (7%)	2 (1%)	15	16
1	D	159/213 (75%)	154 (97%)	5 (3%)	0	100	100
1	E	165/213 (78%)	154 (93%)	8 (5%)	3 (2%)	8	6
All	All	897/1065 (84%)	849 (95%)	43 (5%)	5 (1%)	25	29

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	145	ALA
1	E	159	ALA
1	C	43	PRO
1	C	167	GLY
1	E	160	ILE

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	167/184 (91%)	158 (95%)	9 (5%)	22	28
1	B	167/184 (91%)	154 (92%)	13 (8%)	12	15
1	C	167/184 (91%)	156 (93%)	11 (7%)	16	20
1	D	142/184 (77%)	131 (92%)	11 (8%)	13	15
1	E	145/184 (79%)	134 (92%)	11 (8%)	13	15
All	All	788/920 (86%)	733 (93%)	55 (7%)	15	18

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	LYS
1	A	39	LEU
1	A	61	LEU
1	A	71	LEU
1	A	117	LEU
1	A	148	ARG
1	A	153	ILE
1	A	154	LEU
1	A	169	VAL
1	B	32	ILE
1	B	38	LEU
1	B	39	LEU
1	B	59	LYS
1	B	61	LEU
1	B	67	ARG
1	B	69	VAL
1	B	71	LEU
1	B	79	LYS
1	B	117	LEU
1	B	153	ILE
1	B	154	LEU
1	B	169	VAL
1	C	38	LEU
1	C	39	LEU
1	C	61	LEU
1	C	69	VAL
1	C	71	LEU
1	C	90	LEU

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Mol	Chain	Res	Type
1	C	92	LYS
1	C	117	LEU
1	C	148	ARG
1	C	168	ASP
1	C	182	LYS
1	D	27	ASN
1	D	32	ILE
1	D	38	LEU
1	D	39	LEU
1	D	61	LEU
1	D	67	ARG
1	D	71	LEU
1	D	117	LEU
1	D	148	ARG
1	D	153	ILE
1	D	166	TYR
1	E	30	GLN
1	E	38	LEU
1	E	39	LEU
1	E	61	LEU
1	E	62	ASP
1	E	69	VAL
1	E	71	LEU
1	E	99	LYS
1	E	117	LEU
1	E	148	ARG
1	E	153	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	68	ASN
1	A	97	ASN
1	A	133	ASN
1	A	173	ASN
1	B	27	ASN
1	B	68	ASN
1	B	133	ASN
1	B	138	HIS
1	B	173	ASN
1	C	68	ASN
1	C	138	HIS

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Mol	Chain	Res	Type
1	D	27	ASN
1	D	30	GLN
1	D	65	HIS
1	D	68	ASN
1	D	115	ASN
1	D	138	HIS
1	D	162	HIS
1	D	163	HIS
1	E	27	ASN
1	E	30	GLN
1	E	68	ASN
1	E	138	HIS
1	E	143	ASN
1	E	161	GLN
1	E	162	HIS

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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	E	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	44:LEU	C	45:ASP	N	1.14

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	193/213 (90%)	-0.17	5 (2%)	56	52	17, 30, 53, 63	0
1	B	193/213 (90%)	0.21	13 (6%)	17	14	17, 34, 74, 92	0
1	C	193/213 (90%)	0.51	18 (9%)	8	5	19, 36, 92, 102	0
1	D	163/213 (76%)	-0.04	3 (1%)	68	65	20, 33, 64, 70	0
1	E	167/213 (78%)	0.17	10 (5%)	21	18	21, 42, 68, 94	0
All	All	909/1065 (85%)	0.14	49 (5%)	25	23	17, 35, 70, 102	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	194	THR	7.5
1	C	193	SER	7.4
1	C	188	VAL	7.0
1	C	170	CYS	6.6
1	B	49	VAL	6.2
1	C	179	VAL	6.1
1	E	168	ASP	5.9
1	B	189	ALA	5.5
1	B	193	SER	4.7
1	C	194	THR	4.4
1	C	191	TYR	4.3
1	D	48	PHE	4.2
1	E	166	TYR	4.1
1	B	188	VAL	4.1
1	E	165	LYS	3.9
1	C	190	GLN	3.9
1	C	189	ALA	3.8
1	B	186	GLU	3.8
1	C	183	PRO	3.5
1	C	192	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
1	E	146	ILE	3.5
1	B	190	GLN	3.5
1	C	184	SER	3.5
1	B	192	LEU	3.3
1	E	49	VAL	3.3
1	C	187	GLY	3.2
1	C	169	VAL	3.2
1	A	182	LYS	3.2
1	D	49	VAL	3.1
1	E	48	PHE	3.0
1	D	166	TYR	3.0
1	B	182	LYS	2.9
1	B	195	LEU	2.9
1	C	174	TRP	2.8
1	C	186	GLU	2.8
1	C	176	LYS	2.8
1	C	171	PRO	2.8
1	A	166	TYR	2.8
1	E	147	GLY	2.6
1	A	190	GLN	2.5
1	E	160	ILE	2.5
1	B	191	TYR	2.4
1	E	162	HIS	2.2
1	E	159	ALA	2.1
1	B	179	VAL	2.1
1	B	177	GLY	2.1
1	C	92	LYS	2.0
1	A	167	GLY	2.0
1	A	145	ALA	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.