Full wwPDB X-ray Structure Validation Report ⓘ

Nov 21, 2023 – 11:12 PM JST

PDB ID	:	7YVT
Title	:	S-formylglutathione hydrolase from Variovorax sp. PAMC 28711
Authors	:	Hwang, J.; Do, H.; Lee, J.H.
Deposited on	:	2022-08-19
Resolution	:	2.38 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:

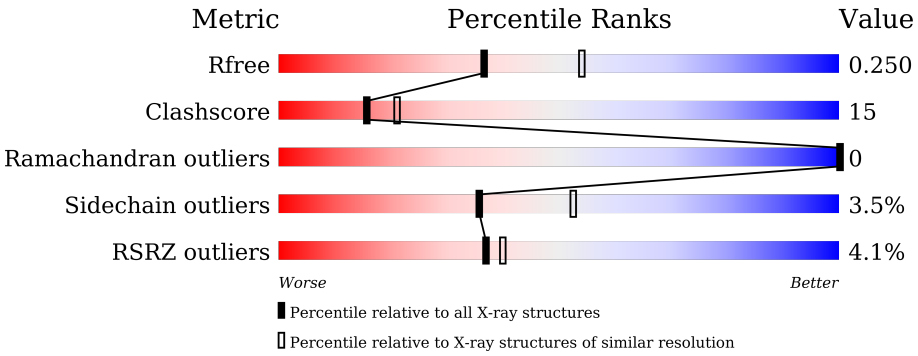
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 2.38 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	5509 (2.40-2.36)
Clashscore	141614	6082 (2.40-2.36)
Ramachandran outliers	138981	5973 (2.40-2.36)
Sidechain outliers	138945	5975 (2.40-2.36)
RSRZ outliers	127900	5397 (2.40-2.36)

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	295	73% 22% • •
1	B	295	76% 19% • •
1	C	295	12% 62% 30% • 5%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6715 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 S-formylglutathione hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	283	Total	C	N	O	S	0	0	0
			2180	1398	383	389	10			
1	B	284	Total	C	N	O	S	0	0	0
			2188	1403	384	390	11			
1	C	280	Total	C	N	O	S	0	0	0
			2157	1386	379	382	10			

- Molecule 2 is water.

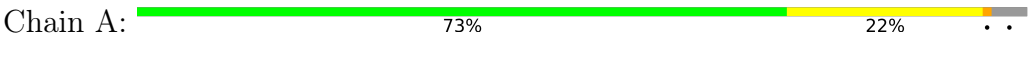
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	94	Total	O	0	0
			94	94		
2	B	80	Total	O	0	0
			80	80		
2	C	16	Total	O	0	0
			16	16		

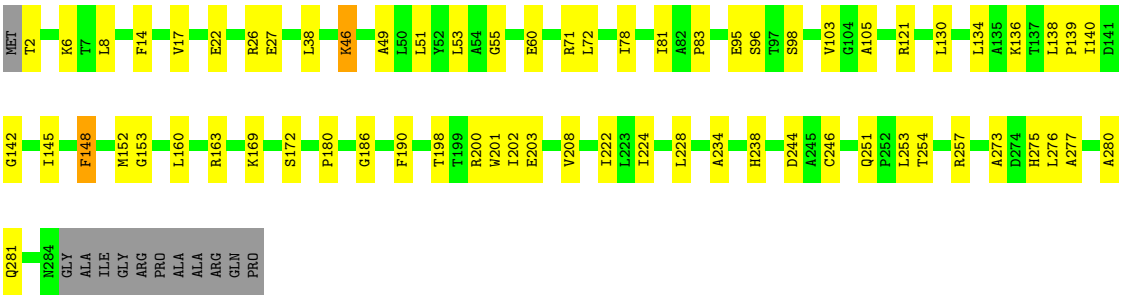
3 Residue-property plots (i)

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: S-formylglutathione hydrolase

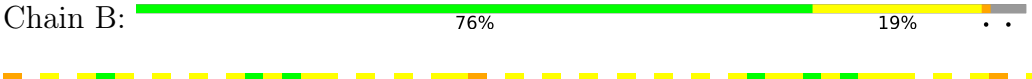
Chain A:

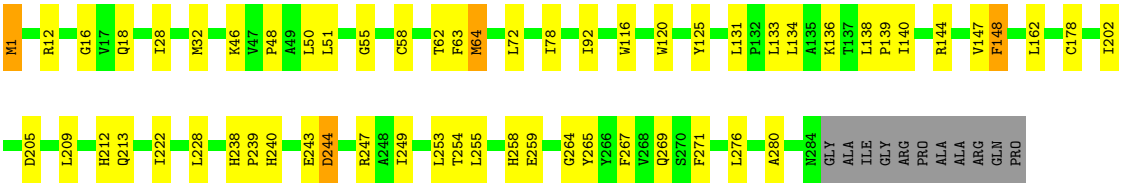




• Molecule 1: S-formylglutathione hydrolase

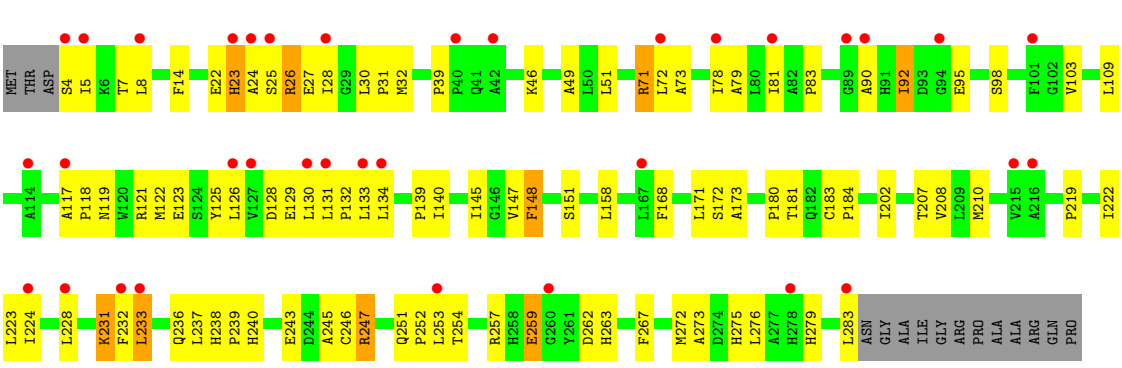
Chain B:





• Molecule 1: S-formylglutathione hydrolase

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	53.20Å 76.44Å 199.87Å 90.00° 91.19° 90.00°	Depositor
Resolution (Å)	43.66 – 2.38 43.66 – 2.38	Depositor EDS
% Data completeness (in resolution range)	95.6 (43.66-2.38) 95.6 (43.66-2.38)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.34 (at 2.37Å)	Xtriage
Refinement program	REFMAC 1.14_3260	Depositor
R, R_{free}	0.204 , 0.245 0.207 , 0.250	Depositor DCC
R_{free} test set	1509 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å^2)	36.3	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 52.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.035 for -h,-k,l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6715	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.54% 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

5.1 Standard geometry

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	0.63	2/2249 (0.1%)	0.74	0/3065
1	B	0.50	0/2257	0.66	0/3075
1	C	0.44	0/2226	0.69	2/3033 (0.1%)
All	All	0.53	2/6732 (0.0%)	0.70	2/9173 (0.0%)

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	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	95	GLU	CD-OE2	-5.40	1.19	1.25
1	A	60	GLU	CD-OE1	-5.02	1.20	1.25

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	233	LEU	CA-CB-CG	5.58	128.14	115.30
1	C	92	ILE	C-N-CA	-5.38	108.24	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	26	ARG	Mainchain

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	2180	0	2107	46	0
1	B	2188	0	2119	46	1
1	C	2157	0	2090	100	0
2	A	94	0	0	1	0
2	B	80	0	0	3	0
2	C	16	0	0	1	0
All	All	6715	0	6316	189	1

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 15.

All (189) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:233:LEU:CD2	1:C:237:LEU:HD22	1.70	1.20
1:C:30:LEU:CD1	1:C:90:ALA:HB2	1.77	1.13
1:C:30:LEU:HD11	1:C:90:ALA:HB2	1.05	1.03
1:C:134:LEU:HB3	1:C:140:ILE:HD11	1.44	1.00
1:C:233:LEU:HD23	1:C:237:LEU:HD22	1.41	0.99
1:C:72:LEU:HB2	1:C:276:LEU:HD12	1.48	0.95
1:B:72:LEU:HB2	1:B:276:LEU:HD23	1.48	0.93
1:C:90:ALA:O	1:C:92:ILE:HD12	1.69	0.92
1:C:237:LEU:CD2	1:C:239:PRO:HD3	2.09	0.83
1:B:92:ILE:HD12	1:B:120:TRP:CZ3	2.15	0.82
1:C:246:CYS:HB3	1:C:251:GLN:HB3	1.62	0.80
1:C:30:LEU:HD11	1:C:90:ALA:CB	2.01	0.79
1:C:233:LEU:HD21	1:C:237:LEU:HD22	1.64	0.79
1:C:26:ARG:HG2	1:C:129:GLU:OE2	1.82	0.79
1:C:237:LEU:HD23	1:C:239:PRO:HD3	1.62	0.79
1:C:233:LEU:HD23	1:C:237:LEU:CD2	2.13	0.78
1:B:131:LEU:HA	1:B:134:LEU:HD12	1.67	0.75
1:C:223:LEU:HA	1:C:254:THR:OG1	1.87	0.75
1:B:202:ILE:HD12	1:C:202:ILE:CD1	2.17	0.75
1:B:222:ILE:HB	1:B:253:LEU:HD23	1.68	0.74
1:C:233:LEU:HD23	1:C:237:LEU:HD13	1.69	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:212:HIS:ND1	2:B:301:HOH:O	2.23	0.72
1:C:231:LYS:CD	1:C:231:LYS:H	2.04	0.70
1:C:228:LEU:HD21	1:C:257:ARG:HB3	1.72	0.70
1:C:243:GLU:HB3	1:C:247:ARG:HH11	1.56	0.69
1:C:14:PHE:CE2	1:C:71:ARG:HG3	2.30	0.67
1:C:228:LEU:HB2	1:C:259:GLU:HA	1.76	0.67
1:B:138:LEU:HB2	1:B:140:ILE:HG12	1.74	0.67
1:B:50:LEU:HD22	1:B:148:PHE:CD1	2.30	0.66
1:C:231:LYS:HE2	1:C:262:ASP:HB2	1.77	0.66
1:A:134:LEU:HA	1:A:138:LEU:CD1	2.26	0.66
1:B:202:ILE:HD12	1:C:202:ILE:HD12	1.78	0.66
1:C:24:ALA:HA	1:C:31:PRO:HA	1.77	0.66
1:C:109:LEU:HD12	1:C:109:LEU:C	2.15	0.66
1:B:62:THR:HG23	2:B:342:HOH:O	1.96	0.65
1:A:17:VAL:HG12	1:A:38:LEU:HB2	1.78	0.65
1:C:72:LEU:HB2	1:C:276:LEU:CD1	2.26	0.65
1:C:72:LEU:CB	1:C:276:LEU:HD12	2.25	0.65
1:A:72:LEU:HB2	1:A:276:LEU:HD23	1.78	0.64
1:A:8:LEU:HD11	1:A:22:GLU:HB2	1.80	0.63
1:B:265:TYR:O	1:B:269:GLN:HG2	1.98	0.63
1:B:253:LEU:HD11	1:B:255:LEU:HB2	1.79	0.63
1:C:28:ILE:HD12	1:C:32:MET:SD	2.39	0.63
1:C:158:LEU:HD23	1:C:171:LEU:HD11	1.82	0.61
1:C:237:LEU:HD22	1:C:239:PRO:HD3	1.82	0.61
1:C:49:ALA:HB1	1:C:81:ILE:CD1	2.32	0.60
1:B:18:GLN:NE2	1:B:64:MET:HG2	2.16	0.60
1:B:238:HIS:HA	1:B:240:HIS:CE1	2.37	0.60
1:C:202:ILE:HB	1:C:208:VAL:HG11	1.83	0.59
1:A:234:ALA:O	1:A:238:HIS:CE1	2.55	0.59
1:C:95:GLU:O	1:C:103:VAL:HG22	2.03	0.59
1:C:51:LEU:HD11	1:C:83:PRO:HD3	1.85	0.59
1:C:233:LEU:HD23	1:C:237:LEU:CD1	2.33	0.58
1:C:223:LEU:HA	1:C:254:THR:HG1	1.67	0.58
1:A:49:ALA:HB1	1:A:81:ILE:HD12	1.85	0.58
1:B:78:ILE:HD11	1:B:280:ALA:HB2	1.85	0.58
1:B:213:GLN:HB2	1:B:249:ILE:HD13	1.86	0.58
1:C:27:GLU:O	1:C:121:ARG:HD3	2.02	0.58
1:C:49:ALA:HB1	1:C:81:ILE:HD11	1.86	0.58
1:C:28:ILE:HD12	1:C:32:MET:HG3	1.84	0.57
1:A:2:THR:OG1	1:A:136:LYS:HD2	2.04	0.57
1:A:224:ILE:HD12	1:A:253:LEU:HD11	1.87	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:VAL:CG1	1:A:38:LEU:HB2	2.34	0.57
1:C:109:LEU:HD12	1:C:109:LEU:O	2.05	0.57
1:B:243:GLU:O	1:B:247:ARG:HG2	2.04	0.57
1:C:231:LYS:H	1:C:231:LYS:HD3	1.69	0.56
1:C:231:LYS:HD3	1:C:231:LYS:N	2.20	0.56
1:A:234:ALA:O	1:A:238:HIS:HE1	1.88	0.56
1:B:138:LEU:CB	1:B:140:ILE:HG12	2.35	0.56
1:C:171:LEU:C	1:C:171:LEU:HD13	2.26	0.56
1:B:92:ILE:HG21	1:B:116:TRP:CZ3	2.41	0.56
1:C:8:LEU:HD11	1:C:22:GLU:HB2	1.87	0.56
1:C:109:LEU:HA	1:C:123:GLU:HB2	1.88	0.55
1:C:25:SER:HG	1:C:125:TYR:HE1	1.52	0.55
1:C:233:LEU:CD2	1:C:237:LEU:CD2	2.63	0.54
1:C:23:HIS:O	1:C:31:PRO:HA	2.06	0.54
1:B:92:ILE:HD12	1:B:120:TRP:HZ3	1.66	0.54
1:C:133:LEU:HD23	1:C:134:LEU:HD12	1.88	0.54
1:A:198:THR:HA	1:A:201:TRP:HB2	1.89	0.54
1:C:28:ILE:HD12	1:C:32:MET:CG	2.37	0.53
1:C:25:SER:HB3	1:C:129:GLU:OE1	2.07	0.53
1:C:222:ILE:O	1:C:253:LEU:HD12	2.09	0.53
1:A:228:LEU:HD21	1:A:257:ARG:HB3	1.91	0.53
1:C:128:ASP:O	1:C:132:PRO:HG2	2.09	0.53
1:A:172:SER:HB3	1:A:275:HIS:ND1	2.23	0.53
1:C:210:MET:HG2	1:C:246:CYS:SG	2.49	0.53
1:A:246:CYS:HB3	1:A:251:GLN:HB3	1.91	0.53
1:C:72:LEU:HD13	1:C:273:ALA:HA	1.91	0.53
1:B:178:CYS:SG	1:B:239:PRO:HA	2.49	0.52
1:C:147:VAL:HG13	1:C:171:LEU:HD23	1.92	0.52
1:C:233:LEU:HD22	1:C:237:LEU:HB3	1.90	0.52
1:A:254:THR:HG23	2:A:359:HOH:O	2.09	0.52
1:A:53:LEU:O	1:A:153:GLY:HA3	2.09	0.52
1:A:2:THR:N	1:A:136:LYS:O	2.43	0.52
1:C:233:LEU:HD23	1:C:237:LEU:CG	2.40	0.51
1:B:205:ASP:O	1:B:209:LEU:HG	2.11	0.51
1:C:14:PHE:CZ	1:C:71:ARG:HB2	2.46	0.51
1:A:134:LEU:HA	1:A:138:LEU:HD12	1.92	0.51
1:C:26:ARG:HG2	1:C:129:GLU:CD	2.30	0.51
1:C:219:PRO:O	1:C:252:PRO:HG2	2.11	0.50
1:B:253:LEU:HD13	1:B:255:LEU:N	2.26	0.50
1:A:78:ILE:HD11	1:A:280:ALA:HA	1.94	0.49
1:A:190:PHE:HB3	1:A:201:TRP:CE2	2.47	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:253:LEU:HD13	1:B:253:LEU:C	2.32	0.49
1:C:7:THR:HG22	1:C:7:THR:O	2.11	0.49
1:C:172:SER:HB3	1:C:275:HIS:ND1	2.26	0.49
1:C:158:LEU:CD2	1:C:171:LEU:HD11	2.42	0.49
1:A:222:ILE:HB	1:A:253:LEU:HD12	1.94	0.49
1:C:184:PRO:HD2	1:C:236:GLN:HG3	1.94	0.49
1:A:27:GLU:HA	1:A:27:GLU:OE1	2.13	0.49
1:C:145:ILE:O	1:C:168:PHE:HA	2.12	0.48
1:C:180:PRO:HA	1:C:183:CYS:SG	2.54	0.48
1:C:207:THR:HG23	1:C:245:ALA:HB2	1.95	0.48
1:C:39:PRO:HD3	1:C:79:ALA:HA	1.96	0.48
1:A:202:ILE:HB	1:A:208:VAL:HG11	1.96	0.47
1:C:5:ILE:HD12	1:C:5:ILE:N	2.28	0.47
1:A:46:LYS:HE3	1:A:139:PRO:HA	1.95	0.47
1:B:133:LEU:HD12	1:B:136:LYS:HB2	1.96	0.47
1:B:18:GLN:HE22	1:B:64:MET:HG2	1.79	0.47
1:A:72:LEU:HB2	1:A:276:LEU:CD2	2.42	0.47
1:B:63:PHE:HD2	1:B:64:MET:SD	2.37	0.47
1:C:181:THR:HG21	1:C:202:ILE:HG22	1.97	0.47
1:A:130:LEU:O	1:A:134:LEU:HG	2.15	0.47
1:B:253:LEU:HD22	1:B:254:THR:N	2.29	0.46
1:C:73:ALA:HB1	1:C:78:ILE:O	2.16	0.46
1:C:51:LEU:HD12	1:C:81:ILE:O	2.16	0.46
1:A:169:LYS:N	1:A:169:LYS:HD2	2.30	0.46
1:C:183:CYS:HB2	1:C:236:GLN:HA	1.97	0.46
1:C:228:LEU:CD2	1:C:257:ARG:HB3	2.44	0.45
1:C:243:GLU:O	1:C:247:ARG:HB2	2.16	0.45
1:B:12:ARG:HD3	1:B:16:GLY:O	2.17	0.45
1:C:109:LEU:C	1:C:109:LEU:CD1	2.85	0.45
1:C:98:SER:O	2:C:301:HOH:O	2.20	0.45
1:C:272:MET:O	1:C:276:LEU:HG	2.16	0.44
1:A:180:PRO:O	1:A:186:GLY:HA3	2.17	0.44
1:C:238:HIS:HB3	1:C:240:HIS:CE1	2.53	0.44
1:B:92:ILE:CD1	1:B:120:TRP:HZ3	2.30	0.44
1:B:247:ARG:CD	2:B:322:HOH:O	2.65	0.44
1:C:183:CYS:HB2	1:C:236:GLN:HG3	2.00	0.44
1:A:148:PHE:CB	1:A:172:SER:HB2	2.48	0.44
1:C:117:ALA:N	1:C:118:PRO:HD2	2.33	0.44
1:C:148:PHE:HB3	1:C:172:SER:HB2	2.00	0.44
1:C:121:ARG:HG2	1:C:121:ARG:HH11	1.83	0.44
1:C:46:LYS:HD3	1:C:139:PRO:HA	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:ARG:HD2	1:A:203:GLU:O	2.17	0.43
1:B:51:LEU:HD23	1:B:147:VAL:HG23	1.99	0.43
1:C:90:ALA:O	1:C:95:GLU:OE1	2.37	0.43
1:A:14:PHE:CZ	1:A:71:ARG:HB2	2.52	0.43
1:A:121:ARG:HH11	1:A:121:ARG:HG2	1.83	0.43
1:C:222:ILE:HB	1:C:253:LEU:HD12	2.00	0.43
1:B:28:ILE:HD13	1:B:32:MET:SD	2.59	0.43
1:A:51:LEU:HD11	1:A:83:PRO:HG3	2.00	0.43
1:C:279:HIS:O	1:C:283:LEU:HD12	2.18	0.43
1:A:55:GLY:HA2	1:A:152:MET:HB3	1.99	0.43
1:B:28:ILE:HD11	1:B:125:TYR:CG	2.54	0.43
1:A:105:ALA:HA	1:A:152:MET:SD	2.59	0.42
1:A:134:LEU:O	1:A:138:LEU:HD12	2.19	0.42
1:C:51:LEU:HD22	1:C:131:LEU:HD21	2.01	0.42
1:B:253:LEU:CD1	1:B:255:LEU:HB2	2.48	0.42
1:A:72:LEU:HD22	1:A:273:ALA:HA	2.00	0.42
1:C:51:LEU:CD1	1:C:83:PRO:HD3	2.48	0.42
1:C:202:ILE:H	1:C:202:ILE:HG13	1.70	0.42
1:A:246:CYS:CB	1:A:251:GLN:HB3	2.50	0.42
1:B:264:GLY:O	1:B:267:PHE:HB3	2.20	0.42
1:A:142:GLY:O	1:A:145:ILE:HD12	2.20	0.42
1:B:55:GLY:O	1:B:58:CYS:HB2	2.19	0.42
1:B:202:ILE:HD12	1:C:202:ILE:HD13	1.95	0.42
1:C:147:VAL:HB	1:C:168:PHE:CD1	2.55	0.42
1:A:142:GLY:HA2	1:A:145:ILE:HD11	2.02	0.41
1:A:148:PHE:HB3	1:A:172:SER:HB2	2.02	0.41
1:B:162:LEU:HD23	1:B:162:LEU:HA	1.86	0.41
1:B:92:ILE:CD1	1:B:120:TRP:CZ3	2.94	0.41
1:C:173:ALA:HB3	1:C:224:ILE:HG12	2.02	0.41
1:B:46:LYS:HD2	1:B:139:PRO:HA	2.02	0.41
1:A:38:LEU:HD23	1:A:38:LEU:HA	1.92	0.41
1:C:130:LEU:HD13	1:C:134:LEU:HD13	2.02	0.41
1:C:151:SER:HB2	1:C:263:HIS:HE1	1.85	0.41
1:B:72:LEU:HB2	1:B:276:LEU:CD2	2.34	0.41
1:B:258:HIS:CE1	1:B:271:PHE:CE1	3.09	0.41
1:A:277:ALA:O	1:A:281:GLN:HG3	2.21	0.41
1:B:58:CYS:SG	1:B:62:THR:HG21	2.61	0.41
1:B:228:LEU:HD12	1:B:259:GLU:OE1	2.21	0.41
1:A:160:LEU:HD23	1:A:160:LEU:HA	1.89	0.41
1:A:81:ILE:HD13	1:A:134:LEU:HD13	2.03	0.40
1:A:49:ALA:HB2	1:A:140:ILE:HD12	2.03	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:259:GLU:H	1:C:259:GLU:CD	2.23	0.40
1:C:122:MET:O	1:C:126:LEU:HG	2.22	0.40
1:B:48:PRO:HG3	1:B:144:ARG:NH1	2.36	0.40
1:C:147:VAL:CG1	1:C:171:LEU:HD23	2.51	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1:MET:N	1:B:244:ASP:OD2[3_445]	2.15	0.05

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	281/295 (95%)	267 (95%)	14 (5%)	0	100	100
1	B	282/295 (96%)	271 (96%)	11 (4%)	0	100	100
1	C	278/295 (94%)	256 (92%)	22 (8%)	0	100	100
All	All	841/885 (95%)	794 (94%)	47 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	219/226 (97%)	211 (96%)	8 (4%)	34	50
1	B	220/226 (97%)	216 (98%)	4 (2%)	59	75
1	C	216/226 (96%)	205 (95%)	11 (5%)	24	36
All	All	655/678 (97%)	632 (96%)	23 (4%)	36	52

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LYS
1	A	46	LYS
1	A	96	SER
1	A	98	SER
1	A	103	VAL
1	A	148	PHE
1	A	200	ARG
1	A	244	ASP
1	B	1	MET
1	B	64	MET
1	B	148	PHE
1	B	244	ASP
1	C	4	SER
1	C	23	HIS
1	C	26	ARG
1	C	71	ARG
1	C	119	ASN
1	C	148	PHE
1	C	231	LYS
1	C	232	PHE
1	C	247	ARG
1	C	259	GLU
1	C	267	PHE

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

Mol	Chain	Res	Type
1	A	155	HIS
1	B	240	HIS
1	C	21	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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^{th} 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	283/295 (95%)	-0.18	0 100 100	25, 33, 48, 66	0
1	B	284/295 (96%)	-0.19	0 100 100	24, 36, 52, 88	0
1	C	280/295 (94%)	0.72	35 (12%) 3 4	34, 58, 79, 154	0
All	All	847/885 (95%)	0.11	35 (4%) 37 40	24, 40, 71, 154	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	228	LEU	4.0
1	C	134	LEU	3.9
1	C	42	ALA	3.8
1	C	4	SER	3.7
1	C	94	GLY	3.4
1	C	81	ILE	3.3
1	C	215	VAL	3.1
1	C	224	ILE	2.9
1	C	78	ILE	2.9
1	C	8	LEU	2.8
1	C	253	LEU	2.8
1	C	117	ALA	2.7
1	C	126	LEU	2.7
1	C	28	ILE	2.6
1	C	130	LEU	2.6
1	C	233	LEU	2.6
1	C	232	PHE	2.5
1	C	25	SER	2.5
1	C	5	ILE	2.4
1	C	23	HIS	2.4
1	C	283	LEU	2.4
1	C	89	GLY	2.3
1	C	127	VAL	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	101	PHE	2.3
1	C	167	LEU	2.2
1	C	278	HIS	2.2
1	C	216	ALA	2.2
1	C	72	LEU	2.2
1	C	131	LEU	2.1
1	C	40	PRO	2.1
1	C	133	LEU	2.0
1	C	114	ALA	2.0
1	C	260	GLY	2.0
1	C	24	ALA	2.0
1	C	90	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.