



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2020 – 12:06 PM BST

PDB ID : 6IVA
Title : Crystal structure of the *S. typhimurium* oxaloacetate decarboxylase beta-gamma sub-complex
Authors : Xu, X.; Xiang, S.
Deposited on : 2018-12-03
Resolution : 4.40 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 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	:	2.13.1
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)	:	2.13.1

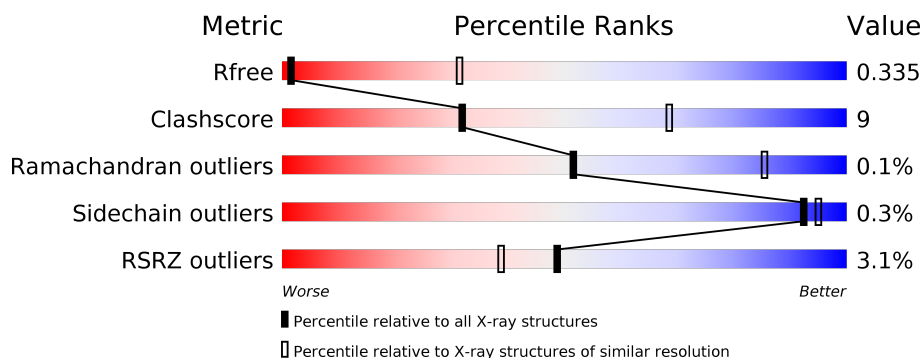
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.40 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	1043 (5.00-3.80)
Clashscore	141614	1111 (5.00-3.80)
Ramachandran outliers	138981	1059 (5.00-3.80)
Sidechain outliers	138945	1041 (5.00-3.80)
RSRZ outliers	127900	1095 (5.08-3.70)

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 ≥ 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	433	<div> <div>2%</div> <div> <div></div> <div>75%</div> <div>22%</div> <div>.</div> </div> </div>
1	C	433	<div> <div>4%</div> <div> <div></div> <div>75%</div> <div>21%</div> <div>..</div> </div> </div>
1	E	433	<div> <div>3%</div> <div> <div></div> <div>77%</div> <div>20%</div> <div>.</div> </div> </div>
2	B	104	<div> <div>2%</div> <div> <div></div> <div>37%</div> <div>60%</div> <div>.</div> </div> </div>
2	D	104	<div> <div>%</div> <div> <div></div> <div>31%</div> <div>10%</div> <div>60%</div> </div> </div>
2	F	104	<div> <div></div> <div> <div></div> <div>33%</div> <div>8%</div> <div>60%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10122 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 Oxaloacetate decarboxylase beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	420	Total	C	N	O	S	0	0	0
			3054	2005	501	528	20			
1	C	420	Total	C	N	O	S	0	0	0
			3054	2005	501	528	20			
1	E	420	Total	C	N	O	S	0	0	0
			3054	2005	501	528	20			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	GLY	SER	see sequence details	UNP A0A0F7JAV8
C	107	GLY	SER	see sequence details	UNP A0A0F7JAV8
E	107	GLY	SER	see sequence details	UNP A0A0F7JAV8

- Molecule 2 is a protein called Probable oxaloacetate decarboxylase gamma chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	42	Total	C	N	O	S	0	0	0
			320	218	50	49	3			
2	D	42	Total	C	N	O	S	0	0	0
			320	218	50	49	3			
2	F	42	Total	C	N	O	S	0	0	0
			320	218	50	49	3			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	initiating methionine	UNP A0A0F7JC72
B	-18	GLY	-	expression tag	UNP A0A0F7JC72
B	-17	SER	-	expression tag	UNP A0A0F7JC72
B	-16	SER	-	expression tag	UNP A0A0F7JC72
B	-15	HIS	-	expression tag	UNP A0A0F7JC72

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	HIS	-	expression tag	UNP A0A0F7JC72
B	-13	HIS	-	expression tag	UNP A0A0F7JC72
B	-12	HIS	-	expression tag	UNP A0A0F7JC72
B	-11	HIS	-	expression tag	UNP A0A0F7JC72
B	-10	HIS	-	expression tag	UNP A0A0F7JC72
B	-9	SER	-	expression tag	UNP A0A0F7JC72
B	-8	SER	-	expression tag	UNP A0A0F7JC72
B	-7	GLY	-	expression tag	UNP A0A0F7JC72
B	-6	LEU	-	expression tag	UNP A0A0F7JC72
B	-5	VAL	-	expression tag	UNP A0A0F7JC72
B	-4	PRO	-	expression tag	UNP A0A0F7JC72
B	-3	ARG	-	expression tag	UNP A0A0F7JC72
B	-2	GLY	-	expression tag	UNP A0A0F7JC72
B	-1	SER	-	expression tag	UNP A0A0F7JC72
B	0	HIS	-	expression tag	UNP A0A0F7JC72
D	-19	MET	-	initiating methionine	UNP A0A0F7JC72
D	-18	GLY	-	expression tag	UNP A0A0F7JC72
D	-17	SER	-	expression tag	UNP A0A0F7JC72
D	-16	SER	-	expression tag	UNP A0A0F7JC72
D	-15	HIS	-	expression tag	UNP A0A0F7JC72
D	-14	HIS	-	expression tag	UNP A0A0F7JC72
D	-13	HIS	-	expression tag	UNP A0A0F7JC72
D	-12	HIS	-	expression tag	UNP A0A0F7JC72
D	-11	HIS	-	expression tag	UNP A0A0F7JC72
D	-10	HIS	-	expression tag	UNP A0A0F7JC72
D	-9	SER	-	expression tag	UNP A0A0F7JC72
D	-8	SER	-	expression tag	UNP A0A0F7JC72
D	-7	GLY	-	expression tag	UNP A0A0F7JC72
D	-6	LEU	-	expression tag	UNP A0A0F7JC72
D	-5	VAL	-	expression tag	UNP A0A0F7JC72
D	-4	PRO	-	expression tag	UNP A0A0F7JC72
D	-3	ARG	-	expression tag	UNP A0A0F7JC72
D	-2	GLY	-	expression tag	UNP A0A0F7JC72
D	-1	SER	-	expression tag	UNP A0A0F7JC72
D	0	HIS	-	expression tag	UNP A0A0F7JC72
F	-19	MET	-	initiating methionine	UNP A0A0F7JC72
F	-18	GLY	-	expression tag	UNP A0A0F7JC72
F	-17	SER	-	expression tag	UNP A0A0F7JC72
F	-16	SER	-	expression tag	UNP A0A0F7JC72
F	-15	HIS	-	expression tag	UNP A0A0F7JC72
F	-14	HIS	-	expression tag	UNP A0A0F7JC72
F	-13	HIS	-	expression tag	UNP A0A0F7JC72

Continued on next page...

Continued from previous page...

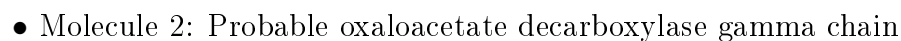
Chain	Residue	Modelled	Actual	Comment	Reference
F	-12	HIS	-	expression tag	UNP A0A0F7JC72
F	-11	HIS	-	expression tag	UNP A0A0F7JC72
F	-10	HIS	-	expression tag	UNP A0A0F7JC72
F	-9	SER	-	expression tag	UNP A0A0F7JC72
F	-8	SER	-	expression tag	UNP A0A0F7JC72
F	-7	GLY	-	expression tag	UNP A0A0F7JC72
F	-6	LEU	-	expression tag	UNP A0A0F7JC72
F	-5	VAL	-	expression tag	UNP A0A0F7JC72
F	-4	PRO	-	expression tag	UNP A0A0F7JC72
F	-3	ARG	-	expression tag	UNP A0A0F7JC72
F	-2	GLY	-	expression tag	UNP A0A0F7JC72
F	-1	SER	-	expression tag	UNP A0A0F7JC72
F	0	HIS	-	expression tag	UNP A0A0F7JC72

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.

- Chain A:
-
- 29% 75% 22%
- Chain A is a single chain with 104 residues. The residues are: MET, GLU, SER, LEU, ASN, ALA, LEU, LEU, GLN, GLY, MET, GLY, I13, M23, V26, S27, L28, L29, L30, L31, L32, L33, A34, P41, L45, P46, F49, L52, L55, H73, Q77, V105, M109, Y118, L123, A130, I131, A136, P137, L138, V139, I140, F141, M142, F150, L153, L154, T159, L160, L161, L162, T173, V174, L175, L178, M181, F188, A194, A195, I196, G201, A202, D203, G204, P205, T206, A207, L208, Y209, L210, L214, L219, A225, P234, Q237, M241, R242, R250, M254, L273, A283, A284, G288, P289, F290, C291, F292, V302, L305, V309, L314, L321, G322, A327, V330, A331, Q336, P337, L342, L343, L344, L345, L348, V358, N365, K371, L372, N373, P374, L375, L376, G377, S378, S382, A383, V384, A387, V390, S391, N392, G395, L396, D399, N402, F403, L405, P411, N412, S419, A422, A423, G424, V425, M426, A432, MET.

- Chain C:
-
- 4% 75% 21%
- Legend:
- MET
 - GLU
 - SER
 - LEU
 - ASN
 - ALA
 - LEU
 - LEU
 - GLY
 - MET
 - GLY
 - L13
 - M23
 - V26
 - S27
 - L28
 - L29
 - L30
 - L31
 - V32
 - L33
 - F39
 - F49
 - L52
 - N55
 - V91
 - V105
 - M109
 - A130
 - I131
 - A136
 - V139
 - I140
 - F141
 - M142
 - G143
 - F150
 - G161
 - P162
 - L163
 - L164
 - T169
 - L160
 - F182

- 



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	107.47Å 198.08Å 241.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.19 – 4.40 42.19 – 4.40	Depositor EDS
% Data completeness (in resolution range)	99.4 (42.19-4.40) 99.8 (42.19-4.40)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.77 (at 4.45Å)	Xtriage
Refinement program	PHENIX (1.13 _2998: ???)	Depositor
R, R_{free}	0.310 , 0.336 0.310 , 0.335	Depositor DCC
R_{free} test set	805 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	174.1	Xtriage
Anisotropy	0.543	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.22 , 112.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	10122	wwPDB-VP
Average B, all atoms (Å ²)	244.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.41% 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

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	0.27	0/3105	0.48	0/4222
1	C	0.26	0/3105	0.50	0/4222
1	E	0.26	0/3105	0.47	0/4222
2	B	0.29	0/326	0.45	0/437
2	D	0.28	0/326	0.43	0/437
2	F	0.29	0/326	0.36	0/437
All	All	0.27	0/10293	0.47	0/13977

There are no bond length outliers.

There are no bond angle outliers.

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	3054	0	3293	63	0
1	C	3054	0	3293	68	0
1	E	3054	0	3293	57	0
2	B	320	0	336	4	0
2	D	320	0	336	13	0
2	F	320	0	336	7	0
All	All	10122	0	10887	187	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 (187) 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:259:THR:HG22	1:C:260:VAL:HG23	1.64	0.80
1:C:365:ASN:HD22	1:C:371:LYS:HB3	1.49	0.77
1:C:258:ARG:HH22	2:D:34:ARG:HG2	1.53	0.74
1:E:426:MET:HG2	2:F:14:LEU:HD11	1.70	0.73
1:E:365:ASN:HD22	1:E:371:LYS:HB3	1.54	0.73
1:C:150:PHE:HB3	1:C:154:LEU:HD13	1.72	0.71
1:A:162:LEU:HD23	1:A:377:GLY:HA2	1.71	0.71
1:E:383:ALA:HB3	1:E:387:ALA:HB2	1.77	0.66
1:A:365:ASN:HD22	1:A:371:LYS:HB3	1.61	0.66
1:A:373:ASN:HD21	1:A:375:LEU:HD12	1.62	0.64
1:A:376:ILE:HG22	1:A:411:PRO:HG2	1.81	0.63
1:C:140:ILE:HA	1:C:314:ILE:HD12	1.82	0.61
1:C:173:THR:HG23	1:C:345:LEU:HB3	1.83	0.60
1:E:264:GLU:HB2	2:F:40:VAL:HG21	1.83	0.60
1:E:376:ILE:HG22	1:E:411:PRO:HG2	1.83	0.60
1:C:171:PHE:HB3	2:D:15:MET:HG3	1.84	0.60
1:C:142:MET:HB2	1:C:289:MET:HG3	1.83	0.60
1:A:159:THR:HA	1:A:162:LEU:HD13	1.83	0.60
1:C:421:ILE:HG22	2:D:22:VAL:HG22	1.83	0.60
1:A:292:PHE:HB2	1:E:49:PHE:CE2	2.36	0.60
2:F:26:LEU:HD23	2:F:29:LEU:HD12	1.85	0.59
1:E:181:ASN:ND2	1:E:188:PHE:O	2.36	0.59
1:C:302:VAL:HB	1:C:305:LEU:HB2	1.84	0.59
1:C:234:PRO:HA	1:C:390:VAL:HG21	1.85	0.58
1:A:399:ASP:HB3	1:A:402:ASN:HB2	1.85	0.58
1:C:426:MET:HG2	2:D:14:LEU:HD11	1.84	0.58
1:C:373:ASN:HD21	1:C:375:LEU:HD12	1.68	0.58
1:E:425:VAL:HG21	2:F:18:GLY:HA2	1.86	0.58
1:C:29:LEU:O	1:C:33:LEU:HB2	2.04	0.58
1:E:309:VAL:O	1:E:314:ILE:HG12	2.03	0.58
1:A:181:ASN:ND2	1:A:188:PHE:O	2.37	0.57
1:A:178:LEU:HD13	2:B:8:LEU:HA	1.86	0.57
1:A:273:LEU:HD13	1:A:288:GLY:HA2	1.87	0.57
1:A:49:PHE:CE2	1:C:292:PHE:HB2	2.40	0.57
1:A:28:LEU:HD12	1:A:52:LEU:HD21	1.87	0.57
1:C:309:VAL:O	1:C:314:ILE:HG12	2.05	0.57
1:C:188:PHE:HB3	1:C:193:ALA:HB2	1.87	0.56
1:A:203:ASP:HB3	1:A:206:THR:HG22	1.87	0.56
1:E:141:PHE:CE2	1:E:290:PHE:HB2	2.41	0.56
1:C:28:LEU:HD12	1:C:52:LEU:HD21	1.87	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:MET:HB3	1:A:55:ASN:ND2	2.21	0.55
1:A:375:LEU:HD13	1:A:395:GLY:HA2	1.89	0.55
1:E:302:VAL:HB	1:E:305:LEU:HB2	1.88	0.55
1:C:201:GLY:O	1:C:382:SER:OG	2.22	0.55
1:E:140:ILE:HA	1:E:314:ILE:HD12	1.88	0.54
1:C:140:ILE:HD12	1:C:321:LEU:HD13	1.90	0.53
1:C:237:GLN:NE2	1:C:378:SER:OG	2.41	0.53
1:E:311:ASN:O	1:E:315:ASN:ND2	2.41	0.53
1:A:383:ALA:HB3	1:A:387:ALA:HB2	1.90	0.53
1:C:181:ASN:ND2	1:C:188:PHE:O	2.42	0.53
1:C:23:MET:HA	1:C:26:VAL:HG12	1.90	0.53
1:E:46:PRO:HB2	1:E:322:GLY:HA3	1.91	0.53
1:C:376:ILE:HG22	1:C:411:PRO:HG2	1.91	0.53
1:E:159:THR:HA	1:E:162:LEU:HD13	1.91	0.52
1:C:242:ARG:HA	1:C:250:ARG:HH22	1.74	0.52
1:A:130:ALA:HB1	1:A:136:ALA:HB2	1.92	0.52
1:E:34:ALA:HB2	1:E:44:LEU:HD23	1.93	0.51
1:A:159:THR:HB	1:A:411:PRO:HG3	1.92	0.51
1:C:254:MET:SD	1:C:407:HIS:NE2	2.82	0.51
1:E:162:LEU:HD23	1:E:377:GLY:HA2	1.91	0.51
1:A:140:ILE:HA	1:A:314:ILE:HD12	1.93	0.51
1:E:159:THR:HB	1:E:411:PRO:HG3	1.93	0.51
2:D:26:LEU:HD23	2:D:29:LEU:HD12	1.93	0.51
1:C:141:PHE:CE2	1:C:290:PHE:HB2	2.47	0.50
1:E:345:LEU:HD23	1:E:348:ILE:HD11	1.92	0.50
1:C:190:LEU:HB2	2:D:7:LEU:HD22	1.93	0.50
1:C:131:ILE:HD11	1:C:219:LEU:HD21	1.93	0.50
1:E:373:ASN:HD21	1:E:375:LEU:HD12	1.75	0.50
1:A:396:LEU:HD21	1:A:403:PHE:CD1	2.47	0.50
1:C:130:ALA:HB1	1:C:136:ALA:HB2	1.94	0.49
1:C:425:VAL:HG21	2:D:18:GLY:HA2	1.94	0.49
1:C:273:LEU:HD13	1:C:288:GLY:HA2	1.94	0.49
1:E:28:LEU:HD12	1:E:52:LEU:HD21	1.94	0.49
1:A:140:ILE:HD12	1:A:321:LEU:HD13	1.94	0.49
1:C:375:LEU:HD13	1:C:395:GLY:HA2	1.93	0.49
1:A:254:MET:HG3	1:A:376:ILE:HD11	1.94	0.49
1:E:29:LEU:O	1:E:33:LEU:HB2	2.12	0.49
1:E:87:CYS:SG	1:E:88:ALA:N	2.84	0.48
1:A:283:ALA:HB2	1:A:424:GLY:HA3	1.94	0.48
1:C:49:PHE:CE2	1:E:292:PHE:HB2	2.48	0.48
1:A:150:PHE:HB3	1:A:154:LEU:HD13	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:THR:HG23	1:A:345:LEU:HB3	1.96	0.48
1:C:241:MET:O	1:C:250:ARG:NH2	2.45	0.48
1:A:309:VAL:O	1:A:314:ILE:HG12	2.12	0.48
1:A:208:ILE:HD13	1:A:321:LEU:HD21	1.96	0.48
1:A:336:GLN:NE2	1:A:337:PRO:HD2	2.29	0.47
1:A:31:LEU:HD11	1:A:52:LEU:HD11	1.96	0.47
1:C:23:MET:HB3	1:C:55:ASN:ND2	2.29	0.47
1:C:272:LEU:HD13	2:D:29:LEU:HD11	1.95	0.47
1:C:392:ASN:ND2	1:C:405:LEU:HB2	2.30	0.47
1:A:396:LEU:HD21	1:A:403:PHE:HD1	1.80	0.47
1:A:34:ALA:O	1:A:41:PRO:HB3	2.14	0.47
1:A:399:ASP:HB3	1:A:402:ASN:CB	2.44	0.47
1:A:392:ASN:ND2	1:A:405:LEU:HB2	2.30	0.47
1:C:345:LEU:HD23	1:C:348:ILE:HD11	1.97	0.47
1:A:105:VAL:O	1:A:109:MET:HG2	2.15	0.46
1:E:242:ARG:HA	1:E:250:ARG:NH2	2.31	0.46
1:C:365:ASN:ND2	1:C:371:LYS:HB3	2.26	0.46
1:A:345:LEU:HD23	1:A:348:ILE:HD11	1.98	0.46
1:C:39:PHE:HD1	1:C:231:ALA:HB3	1.81	0.46
1:E:275:LEU:HD11	2:F:28:LEU:HD13	1.96	0.46
1:A:302:VAL:HB	1:A:305:LEU:HB2	1.98	0.46
1:A:141:PHE:CE2	1:A:290:PHE:HB2	2.51	0.46
1:E:271:VAL:HG11	2:F:32:ALA:HB1	1.98	0.46
1:E:273:LEU:HD13	1:E:288:GLY:HA2	1.97	0.46
1:C:143:GLY:HA3	1:C:314:ILE:HG13	1.98	0.46
1:A:123:LEU:HB3	1:A:327:ALA:HB2	1.97	0.45
1:C:304:ARG:HG3	1:C:305:LEU:HD12	1.98	0.45
1:E:180:LEU:HD23	1:E:188:PHE:CE2	2.52	0.45
1:C:260:VAL:HG12	1:C:261:SER:H	1.81	0.45
1:C:174:VAL:HG11	2:D:14:LEU:HD23	1.98	0.45
1:E:23:MET:HA	1:E:26:VAL:HG12	1.97	0.45
1:E:203:ASP:HB3	1:E:206:THR:HG22	1.98	0.45
1:A:131:ILE:HD11	1:A:219:LEU:HD21	1.98	0.45
1:A:29:LEU:O	1:A:33:LEU:HB2	2.16	0.45
1:C:31:LEU:HD11	1:C:52:LEU:HD11	1.98	0.45
1:E:393:LYS:O	1:E:397:GLU:HG2	2.16	0.44
1:A:178:LEU:CD2	2:B:11:GLY:HA3	2.46	0.44
1:C:263:ARG:HB2	2:D:40:VAL:HG11	1.99	0.44
1:E:85:LEU:HD21	1:E:109:MET:HG3	1.99	0.44
1:E:102:LEU:HB2	1:E:105:VAL:HG23	2.00	0.44
1:E:153:LEU:HD21	1:E:160:LEU:HD21	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:196:ILE:HG12	1:E:342:ILE:HG12	1.98	0.44
1:C:153:LEU:HD21	1:C:160:LEU:HD21	2.00	0.44
1:E:123:LEU:HB3	1:E:327:ALA:HB2	1.99	0.44
1:E:143:GLY:HA3	1:E:314:ILE:HG13	2.00	0.44
1:E:375:LEU:HD13	1:E:395:GLY:HA2	2.00	0.44
2:B:26:LEU:HD23	2:B:29:LEU:HD12	2.00	0.44
1:C:229:TYR:CD1	1:C:232:LEU:HD12	2.52	0.44
1:C:241:MET:SD	1:C:358:VAL:HG11	2.56	0.44
1:C:383:ALA:HB3	1:C:387:ALA:HB2	1.99	0.44
1:A:422:ALA:HA	1:A:425:VAL:HG12	2.00	0.44
1:C:242:ARG:HA	1:C:250:ARG:NH2	2.33	0.44
1:A:234:PRO:HA	1:A:390:VAL:HG21	2.00	0.44
1:E:336:GLN:NE2	1:E:337:PRO:HD2	2.33	0.44
1:A:284:ALA:HB2	1:E:56:ILE:HG21	2.00	0.43
1:E:33:LEU:HG	1:E:39:PHE:CE2	2.52	0.43
1:A:225:ALA:HB2	1:A:343:LEU:HD23	1.99	0.43
1:C:258:ARG:HG3	1:C:259:THR:H	1.83	0.43
1:C:311:ASN:O	1:C:315:ASN:ND2	2.51	0.43
1:A:23:MET:HG3	1:A:331:ALA:HA	2.00	0.43
1:A:178:LEU:HD21	2:B:11:GLY:HA3	2.00	0.43
1:C:162:LEU:HD23	1:C:377:GLY:HA2	2.00	0.43
1:E:140:ILE:HD12	1:E:321:LEU:HD13	2.01	0.43
1:A:175:LEU:HA	1:A:178:LEU:HG	2.00	0.43
1:A:23:MET:HA	1:A:26:VAL:HG12	2.00	0.43
1:A:194:ALA:HB1	1:A:426:MET:HE2	2.00	0.43
1:A:242:ARG:HA	1:A:250:ARG:NH2	2.34	0.42
1:E:47:ILE:HG12	1:E:325:VAL:HB	2.00	0.42
1:C:139:VAL:HG11	1:C:317:VAL:HG21	2.00	0.42
1:E:234:PRO:HA	1:E:390:VAL:HG21	2.02	0.42
1:A:174:VAL:O	1:A:178:LEU:HG	2.20	0.42
1:E:23:MET:HG3	1:E:331:ALA:HA	2.00	0.42
1:C:229:TYR:OH	1:C:343:LEU:O	2.28	0.42
1:E:144:VAL:O	1:E:148:THR:OG1	2.27	0.42
1:A:330:VAL:HG22	1:A:331:ALA:H	1.84	0.42
1:C:178:LEU:HD13	2:D:7:LEU:O	2.20	0.42
1:E:308:THR:O	1:E:313:LEU:N	2.52	0.42
1:E:330:VAL:HG22	1:E:331:ALA:H	1.85	0.42
1:E:225:ALA:HB2	1:E:343:LEU:HD23	2.01	0.42
1:C:178:LEU:HD22	2:D:7:LEU:HB3	2.02	0.42
1:C:210:LEU:HD21	1:C:214:LEU:HD22	2.01	0.42
1:A:46:PRO:HB2	1:A:322:GLY:HA3	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:210:LEU:HD21	1:A:214:LEU:HD22	2.03	0.41
1:E:105:VAL:O	1:E:109:MET:HG2	2.18	0.41
1:C:105:VAL:O	1:C:109:MET:HG2	2.21	0.41
1:A:138:LEU:HB3	1:A:289:MET:HG2	2.02	0.41
1:A:196:ILE:HG12	1:A:342:ILE:HG12	2.01	0.41
1:E:182:TYR:CG	2:F:8:LEU:HD11	2.55	0.41
1:A:142:MET:HB2	1:A:289:MET:HG3	2.03	0.41
1:E:180:LEU:HD21	1:E:186:ILE:HD11	2.02	0.41
1:E:304:ARG:HG3	1:E:305:LEU:HD12	2.02	0.41
1:C:259:THR:OG1	2:D:37:SER:HB2	2.21	0.41
1:E:198:ILE:HG13	1:E:210:LEU:HD22	2.03	0.41
1:A:45:LEU:HB3	1:A:46:PRO:HD3	2.03	0.41
1:C:159:THR:HA	1:C:162:LEU:HD13	2.03	0.41
1:A:153:LEU:HD21	1:A:160:LEU:HD21	2.02	0.41
1:C:203:ASP:HB3	1:C:206:THR:HG22	2.02	0.41
1:A:237:GLN:NE2	1:A:378:SER:OG	2.54	0.40
1:C:177:ALA:O	1:C:188:PHE:HD2	2.04	0.40
1:C:237:GLN:O	1:C:241:MET:HG2	2.21	0.40
1:E:23:MET:HB3	1:E:55:ASN:ND2	2.36	0.40
1:C:254:MET:SD	1:C:376:ILE:HD11	2.60	0.40
1:C:384:VAL:HA	1:C:385:PRO:HA	1.75	0.40
1:E:242:ARG:HA	1:E:250:ARG:HH22	1.85	0.40
1:A:241:MET:SD	1:A:358:VAL:HG11	2.61	0.40
1:A:384:VAL:HA	1:A:412:ASN:HD21	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	418/433 (96%)	399 (96%)	19 (4%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	418/433 (96%)	396 (95%)	20 (5%)	2 (0%)	29	68
1	E	418/433 (96%)	399 (96%)	19 (4%)	0	100	100
2	B	40/104 (38%)	40 (100%)	0	0	100	100
2	D	40/104 (38%)	40 (100%)	0	0	100	100
2	F	40/104 (38%)	40 (100%)	0	0	100	100
All	All	1374/1611 (85%)	1314 (96%)	58 (4%)	2 (0%)	51	85

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	259	THR
1	C	260	VAL

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	317/327 (97%)	316 (100%)	1 (0%)	92	95
1	C	317/327 (97%)	316 (100%)	1 (0%)	92	95
1	E	317/327 (97%)	316 (100%)	1 (0%)	92	95
2	B	31/78 (40%)	31 (100%)	0	100	100
2	D	31/78 (40%)	31 (100%)	0	100	100
2	F	31/78 (40%)	31 (100%)	0	100	100
All	All	1044/1215 (86%)	1041 (100%)	3 (0%)	92	95

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	LEU
1	C	33	LEU
1	E	33	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	336	GLN
1	E	72	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](#)

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, 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	420/433 (96%)	-0.12	10 (2%) 59 49	161, 212, 260, 290	0
1	C	420/433 (96%)	-0.04	17 (4%) 38 31	182, 258, 343, 387	0
1	E	420/433 (96%)	-0.10	13 (3%) 49 39	163, 223, 332, 386	0
2	B	42/104 (40%)	0.49	2 (4%) 30 26	263, 286, 357, 375	0
2	D	42/104 (40%)	0.40	1 (2%) 59 49	306, 323, 371, 417	0
2	F	42/104 (40%)	0.08	0 100 100	267, 283, 314, 332	0
All	All	1386/1611 (86%)	-0.05	43 (3%) 49 39	161, 233, 336, 417	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	256	GLN	5.8
1	C	406	MET	4.5
1	E	370	ASN	4.3
1	C	370	ASN	4.3
1	C	260	VAL	4.0
1	A	203	ASP	3.9
1	E	256	GLN	3.7
1	C	259	THR	3.4
1	A	382	SER	3.3
1	C	257	LEU	3.2
1	E	258	ARG	2.9
1	E	257	LEU	2.9
1	E	91	VAL	2.8
1	A	77	GLN	2.7
2	B	13	THR	2.7
1	E	95	LYS	2.7
1	C	258	ARG	2.7
1	A	204	GLY	2.6
1	A	73	HIS	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	E	66	LEU	2.6
1	A	419	SER	2.5
1	C	405	LEU	2.5
1	C	394	VAL	2.5
1	A	118	TYR	2.5
1	C	403	PHE	2.4
1	C	91	VAL	2.4
1	C	393	LYS	2.4
1	C	401	GLN	2.4
1	C	407	HIS	2.4
1	E	253	ARG	2.3
1	E	15	HIS	2.3
1	A	202	ALA	2.3
1	A	201	GLY	2.2
1	A	205	PRO	2.2
1	C	253	ARG	2.2
1	E	163	GLY	2.2
1	E	401	GLN	2.2
1	C	151	GLY	2.2
2	D	17	LEU	2.1
1	E	255	VAL	2.1
1	C	332	ASP	2.1
2	B	2	THR	2.0
1	E	382	SER	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.