Full wwPDB X-ray Structure Validation Report ⓘ

Feb 21, 2024 – 04:35 AM EST

PDB ID	:	4OD4
Title	:	Apo structure of a UbiA homolog from Aeropyrum pernix K1
Authors	:	Li, W.; Cheng, W.
Deposited on	:	2014-01-09
Resolution	:	3.30 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:

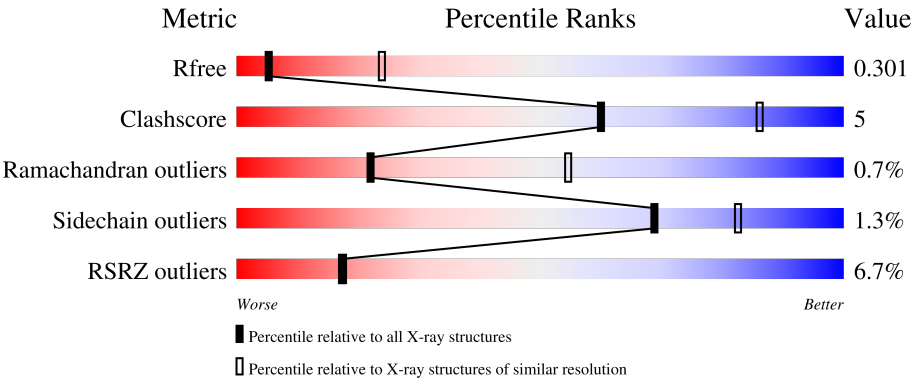
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 3.30 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	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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	303	5% 80% 11% 9%
1	B	303	8% 81% 9% 9%
1	C	303	2% 82% 9% 9%
1	D	303	4% 82% 9% 9%
1	E	303	8% 81% 10% 9%

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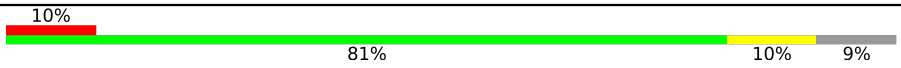
Mol	Chain	Length	Quality of chain
1	F	303	

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 12036 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 4-hydroxybenzoate octaprenyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	275	Total	C	N	O	S	0	0	0
			2006	1320	333	346	7			
1	B	275	Total	C	N	O	S	0	0	0
			2006	1320	333	346	7			
1	C	275	Total	C	N	O	S	0	0	0
			2006	1320	333	346	7			
1	D	275	Total	C	N	O	S	0	0	0
			2006	1320	333	346	7			
1	E	275	Total	C	N	O	S	0	0	0
			2006	1320	333	346	7			
1	F	275	Total	C	N	O	S	0	0	0
			2006	1320	333	346	7			

There are 114 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MET	-	expression tag	UNP Q9YBM8
A	-17	GLY	-	expression tag	UNP Q9YBM8
A	-16	SER	-	expression tag	UNP Q9YBM8
A	-15	SER	-	expression tag	UNP Q9YBM8
A	-14	HIS	-	expression tag	UNP Q9YBM8
A	-13	HIS	-	expression tag	UNP Q9YBM8
A	-12	HIS	-	expression tag	UNP Q9YBM8
A	-11	HIS	-	expression tag	UNP Q9YBM8
A	-10	HIS	-	expression tag	UNP Q9YBM8
A	-9	HIS	-	expression tag	UNP Q9YBM8
A	-8	SER	-	expression tag	UNP Q9YBM8
A	-7	SER	-	expression tag	UNP Q9YBM8
A	-6	GLY	-	expression tag	UNP Q9YBM8
A	-5	LEU	-	expression tag	UNP Q9YBM8
A	-4	VAL	-	expression tag	UNP Q9YBM8
A	-3	PRO	-	expression tag	UNP Q9YBM8
A	-2	ALA	-	expression tag	UNP Q9YBM8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q9YBM8
A	0	SER	-	expression tag	UNP Q9YBM8
B	-18	MET	-	expression tag	UNP Q9YBM8
B	-17	GLY	-	expression tag	UNP Q9YBM8
B	-16	SER	-	expression tag	UNP Q9YBM8
B	-15	SER	-	expression tag	UNP Q9YBM8
B	-14	HIS	-	expression tag	UNP Q9YBM8
B	-13	HIS	-	expression tag	UNP Q9YBM8
B	-12	HIS	-	expression tag	UNP Q9YBM8
B	-11	HIS	-	expression tag	UNP Q9YBM8
B	-10	HIS	-	expression tag	UNP Q9YBM8
B	-9	HIS	-	expression tag	UNP Q9YBM8
B	-8	SER	-	expression tag	UNP Q9YBM8
B	-7	SER	-	expression tag	UNP Q9YBM8
B	-6	GLY	-	expression tag	UNP Q9YBM8
B	-5	LEU	-	expression tag	UNP Q9YBM8
B	-4	VAL	-	expression tag	UNP Q9YBM8
B	-3	PRO	-	expression tag	UNP Q9YBM8
B	-2	ALA	-	expression tag	UNP Q9YBM8
B	-1	GLY	-	expression tag	UNP Q9YBM8
B	0	SER	-	expression tag	UNP Q9YBM8
C	-18	MET	-	expression tag	UNP Q9YBM8
C	-17	GLY	-	expression tag	UNP Q9YBM8
C	-16	SER	-	expression tag	UNP Q9YBM8
C	-15	SER	-	expression tag	UNP Q9YBM8
C	-14	HIS	-	expression tag	UNP Q9YBM8
C	-13	HIS	-	expression tag	UNP Q9YBM8
C	-12	HIS	-	expression tag	UNP Q9YBM8
C	-11	HIS	-	expression tag	UNP Q9YBM8
C	-10	HIS	-	expression tag	UNP Q9YBM8
C	-9	HIS	-	expression tag	UNP Q9YBM8
C	-8	SER	-	expression tag	UNP Q9YBM8
C	-7	SER	-	expression tag	UNP Q9YBM8
C	-6	GLY	-	expression tag	UNP Q9YBM8
C	-5	LEU	-	expression tag	UNP Q9YBM8
C	-4	VAL	-	expression tag	UNP Q9YBM8
C	-3	PRO	-	expression tag	UNP Q9YBM8
C	-2	ALA	-	expression tag	UNP Q9YBM8
C	-1	GLY	-	expression tag	UNP Q9YBM8
C	0	SER	-	expression tag	UNP Q9YBM8
D	-18	MET	-	expression tag	UNP Q9YBM8
D	-17	GLY	-	expression tag	UNP Q9YBM8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	expression tag	UNP Q9YBM8
D	-15	SER	-	expression tag	UNP Q9YBM8
D	-14	HIS	-	expression tag	UNP Q9YBM8
D	-13	HIS	-	expression tag	UNP Q9YBM8
D	-12	HIS	-	expression tag	UNP Q9YBM8
D	-11	HIS	-	expression tag	UNP Q9YBM8
D	-10	HIS	-	expression tag	UNP Q9YBM8
D	-9	HIS	-	expression tag	UNP Q9YBM8
D	-8	SER	-	expression tag	UNP Q9YBM8
D	-7	SER	-	expression tag	UNP Q9YBM8
D	-6	GLY	-	expression tag	UNP Q9YBM8
D	-5	LEU	-	expression tag	UNP Q9YBM8
D	-4	VAL	-	expression tag	UNP Q9YBM8
D	-3	PRO	-	expression tag	UNP Q9YBM8
D	-2	ALA	-	expression tag	UNP Q9YBM8
D	-1	GLY	-	expression tag	UNP Q9YBM8
D	0	SER	-	expression tag	UNP Q9YBM8
E	-18	MET	-	expression tag	UNP Q9YBM8
E	-17	GLY	-	expression tag	UNP Q9YBM8
E	-16	SER	-	expression tag	UNP Q9YBM8
E	-15	SER	-	expression tag	UNP Q9YBM8
E	-14	HIS	-	expression tag	UNP Q9YBM8
E	-13	HIS	-	expression tag	UNP Q9YBM8
E	-12	HIS	-	expression tag	UNP Q9YBM8
E	-11	HIS	-	expression tag	UNP Q9YBM8
E	-10	HIS	-	expression tag	UNP Q9YBM8
E	-9	HIS	-	expression tag	UNP Q9YBM8
E	-8	SER	-	expression tag	UNP Q9YBM8
E	-7	SER	-	expression tag	UNP Q9YBM8
E	-6	GLY	-	expression tag	UNP Q9YBM8
E	-5	LEU	-	expression tag	UNP Q9YBM8
E	-4	VAL	-	expression tag	UNP Q9YBM8
E	-3	PRO	-	expression tag	UNP Q9YBM8
E	-2	ALA	-	expression tag	UNP Q9YBM8
E	-1	GLY	-	expression tag	UNP Q9YBM8
E	0	SER	-	expression tag	UNP Q9YBM8
F	-18	MET	-	expression tag	UNP Q9YBM8
F	-17	GLY	-	expression tag	UNP Q9YBM8
F	-16	SER	-	expression tag	UNP Q9YBM8
F	-15	SER	-	expression tag	UNP Q9YBM8
F	-14	HIS	-	expression tag	UNP Q9YBM8
F	-13	HIS	-	expression tag	UNP Q9YBM8

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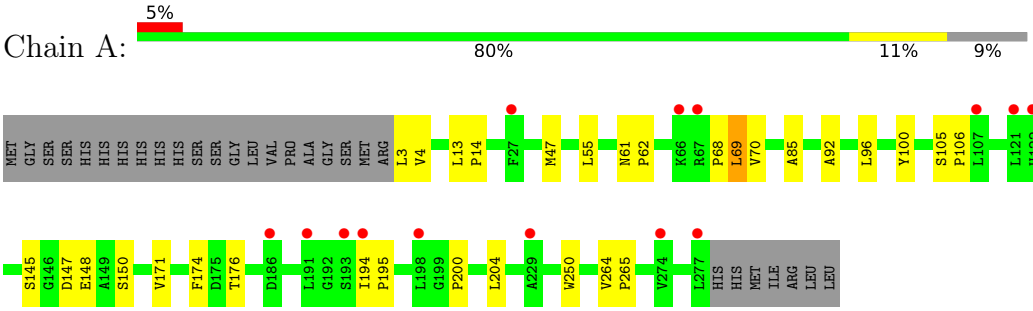
Chain	Residue	Modelled	Actual	Comment	Reference
F	-12	HIS	-	expression tag	UNP Q9YBM8
F	-11	HIS	-	expression tag	UNP Q9YBM8
F	-10	HIS	-	expression tag	UNP Q9YBM8
F	-9	HIS	-	expression tag	UNP Q9YBM8
F	-8	SER	-	expression tag	UNP Q9YBM8
F	-7	SER	-	expression tag	UNP Q9YBM8
F	-6	GLY	-	expression tag	UNP Q9YBM8
F	-5	LEU	-	expression tag	UNP Q9YBM8
F	-4	VAL	-	expression tag	UNP Q9YBM8
F	-3	PRO	-	expression tag	UNP Q9YBM8
F	-2	ALA	-	expression tag	UNP Q9YBM8
F	-1	GLY	-	expression tag	UNP Q9YBM8
F	0	SER	-	expression tag	UNP Q9YBM8

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.

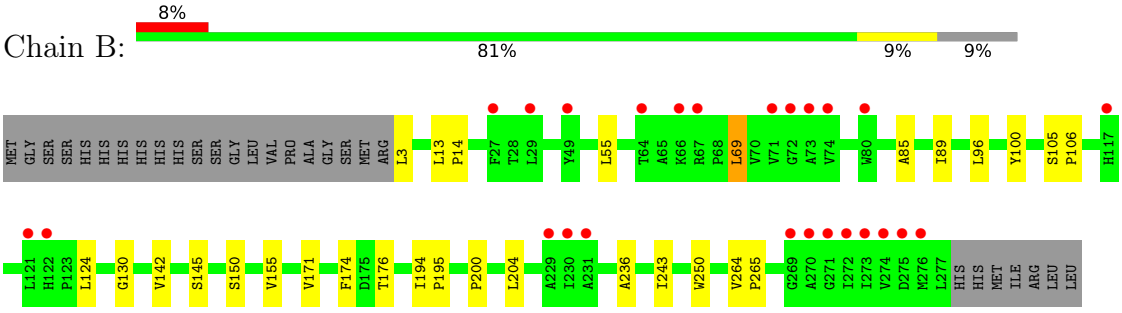
• Molecule 1: 4-hydroxybenzoate octaprenyltransferase

Chain A:



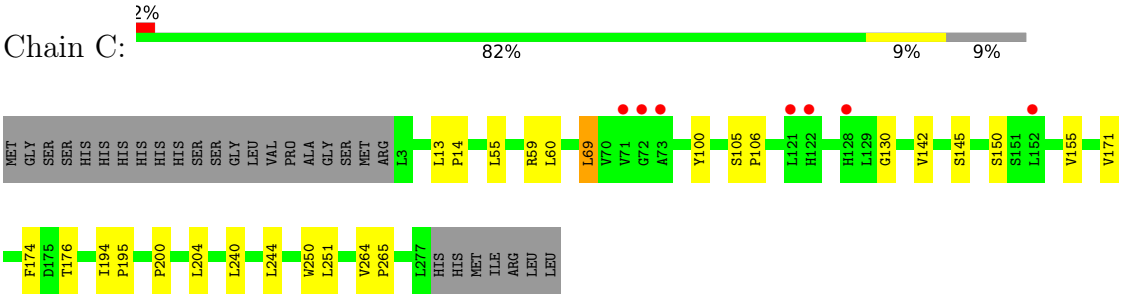
• Molecule 1: 4-hydroxybenzoate octaprenyltransferase

Chain B:



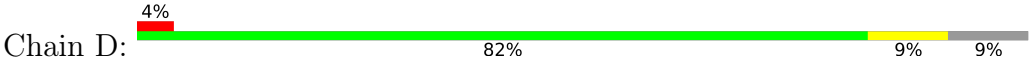
• Molecule 1: 4-hydroxybenzoate octaprenyltransferase

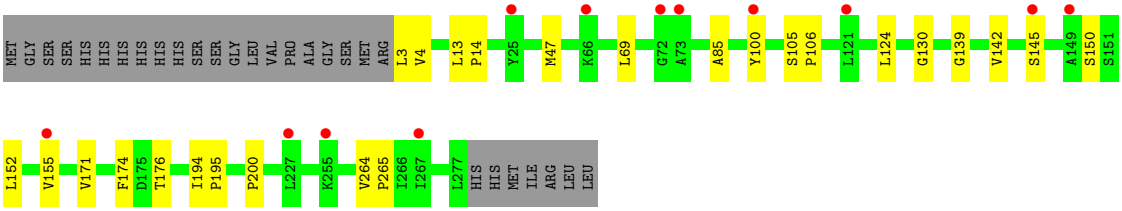
Chain C:



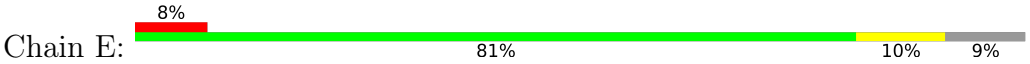
• Molecule 1: 4-hydroxybenzoate octaprenyltransferase

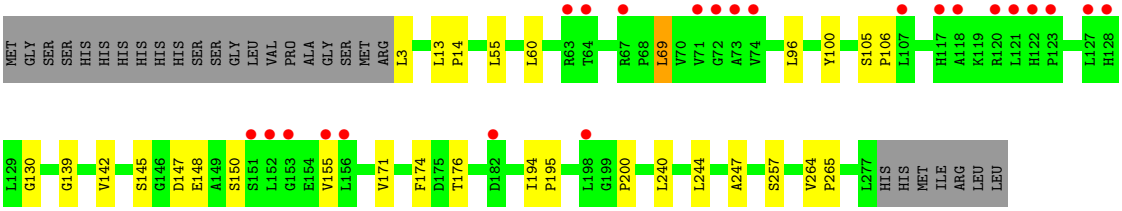
Chain D:



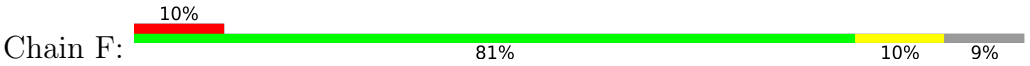


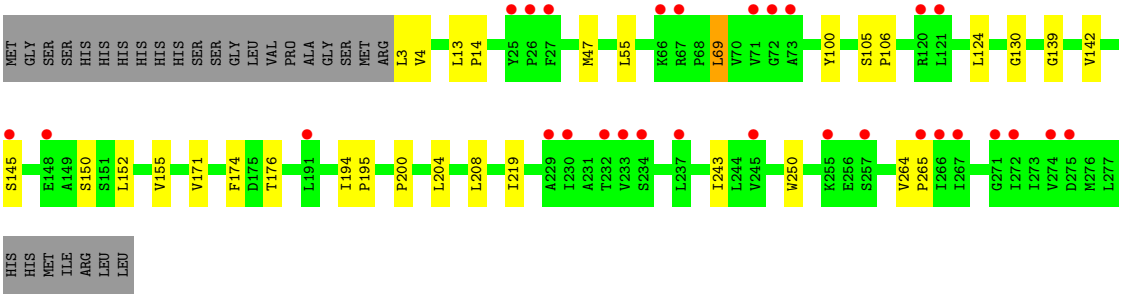
• Molecule 1: 4-hydroxybenzoate octaprenyltransferase





• Molecule 1: 4-hydroxybenzoate octaprenyltransferase





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	70.09Å 123.07Å 423.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.78 – 3.30 49.78 – 3.30	Depositor EDS
% Data completeness (in resolution range)	99.2 (49.78-3.30) 99.2 (49.78-3.30)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.69 (at 3.33Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.272 , 0.303 0.273 , 0.301	Depositor DCC
R_{free} test set	2824 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	108.9	Xtriage
Anisotropy	0.575	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 64.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.85	EDS
Total number of atoms	12036	wwPDB-VP
Average B, all atoms (Å^2)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.93% 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	0.29	0/2050	0.45	0/2809
1	B	0.29	0/2050	0.45	0/2809
1	C	0.30	0/2050	0.46	0/2809
1	D	0.29	0/2050	0.45	0/2809
1	E	0.29	0/2050	0.45	0/2809
1	F	0.29	0/2050	0.45	0/2809
All	All	0.29	0/12300	0.45	0/16854

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	2006	0	2089	19	0
1	B	2006	0	2089	27	0
1	C	2006	0	2089	34	0
1	D	2006	0	2089	13	0
1	E	2006	0	2089	30	0
1	F	2006	0	2089	21	0
All	All	12036	0	12534	113	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 5.

All (113) 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:59:ARG:CB	1:E:60:LEU:HD22	2.18	0.73
1:C:59:ARG:HD3	1:E:60:LEU:HD22	1.72	0.71
1:C:59:ARG:CD	1:E:60:LEU:HD22	2.23	0.69
1:C:59:ARG:HB3	1:E:60:LEU:CD2	2.24	0.67
1:C:59:ARG:HB3	1:E:60:LEU:HD22	1.76	0.66
1:E:247:ALA:HB1	1:F:219:ILE:HD11	1.79	0.63
1:B:243:ILE:CG1	1:C:244:LEU:HD11	2.31	0.61
1:B:243:ILE:HG21	1:C:244:LEU:HD11	1.84	0.58
1:B:243:ILE:CG2	1:C:244:LEU:HD11	2.32	0.58
1:A:85:ALA:HB1	1:B:96:LEU:HD21	1.88	0.56
1:C:59:ARG:CB	1:E:60:LEU:CD2	2.83	0.55
1:C:130:GLY:HA2	1:C:171:VAL:HG21	1.88	0.55
1:E:130:GLY:HA2	1:E:171:VAL:HG21	1.88	0.55
1:B:130:GLY:HA2	1:B:171:VAL:HG21	1.87	0.55
1:D:130:GLY:HA2	1:D:171:VAL:HG21	1.88	0.55
1:E:244:LEU:HD11	1:F:243:ILE:HD12	1.88	0.55
1:C:264:VAL:HB	1:C:265:PRO:HD3	1.89	0.54
1:B:243:ILE:O	1:C:240:LEU:HD21	2.08	0.54
1:F:130:GLY:HA2	1:F:171:VAL:HG21	1.90	0.54
1:B:243:ILE:HD12	1:C:244:LEU:HD11	1.90	0.54
1:A:130:GLY:HA2	1:A:171:VAL:HG21	1.88	0.53
1:B:130:GLY:HA2	1:B:171:VAL:CG2	2.39	0.52
1:B:243:ILE:HG13	1:C:244:LEU:HD11	1.91	0.52
1:D:264:VAL:HB	1:D:265:PRO:HD3	1.92	0.52
1:F:264:VAL:HB	1:F:265:PRO:HD3	1.92	0.52
1:C:130:GLY:HA2	1:C:171:VAL:CG2	2.40	0.52
1:E:130:GLY:HA2	1:E:171:VAL:CG2	2.40	0.51
1:A:130:GLY:HA2	1:A:171:VAL:CG2	2.40	0.50
1:A:264:VAL:HB	1:A:265:PRO:HD3	1.93	0.50
1:D:130:GLY:HA2	1:D:171:VAL:CG2	2.41	0.50
1:E:264:VAL:HB	1:E:265:PRO:HD3	1.93	0.50
1:C:176:THR:HG23	1:C:194:ILE:CG2	2.42	0.50
1:F:130:GLY:HA2	1:F:171:VAL:CG2	2.41	0.50
1:E:100:TYR:OH	1:E:150:SER:O	2.30	0.50
1:B:264:VAL:HB	1:B:265:PRO:HD3	1.94	0.50
1:A:100:TYR:OH	1:A:150:SER:O	2.30	0.50
1:D:100:TYR:OH	1:D:150:SER:O	2.31	0.49
1:F:100:TYR:OH	1:F:150:SER:O	2.30	0.49
1:E:244:LEU:HD11	1:F:243:ILE:CD1	2.41	0.49
1:C:60:LEU:HD21	1:E:60:LEU:HD11	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:60:LEU:HD23	1:E:60:LEU:N	2.28	0.49
1:F:176:THR:HG23	1:F:194:ILE:CG2	2.43	0.48
1:C:100:TYR:OH	1:C:150:SER:O	2.32	0.48
1:A:171:VAL:HA	1:A:174:PHE:CE2	2.49	0.48
1:E:176:THR:HG23	1:E:194:ILE:CG2	2.44	0.47
1:F:171:VAL:HA	1:F:174:PHE:CE2	2.50	0.47
1:B:243:ILE:CD1	1:C:244:LEU:HD11	2.43	0.47
1:B:176:THR:HG23	1:B:194:ILE:CG2	2.45	0.47
1:B:171:VAL:HA	1:B:174:PHE:CE2	2.49	0.47
1:C:244:LEU:HD12	1:C:244:LEU:N	2.29	0.47
1:B:243:ILE:HG13	1:C:244:LEU:CG	2.45	0.47
1:B:100:TYR:OH	1:B:150:SER:O	2.32	0.46
1:B:243:ILE:HG13	1:C:244:LEU:HG	1.97	0.46
1:C:59:ARG:HH11	1:E:60:LEU:HB3	1.79	0.46
1:E:171:VAL:HA	1:E:174:PHE:CE2	2.50	0.46
1:A:176:THR:HG23	1:A:194:ILE:CG2	2.46	0.46
1:D:171:VAL:HA	1:D:174:PHE:CE2	2.50	0.46
1:D:176:THR:HG23	1:D:194:ILE:CG2	2.45	0.46
1:C:171:VAL:HA	1:C:174:PHE:CE2	2.52	0.45
1:A:4:VAL:HG23	1:A:47:MET:SD	2.57	0.44
1:B:243:ILE:HG13	1:C:244:LEU:CD1	2.48	0.44
1:E:240:LEU:HD12	1:F:208:LEU:HD11	1.99	0.44
1:B:13:LEU:N	1:B:14:PRO:CD	2.80	0.44
1:E:105:SER:N	1:E:106:PRO:HD2	2.33	0.44
1:F:55:LEU:HD13	1:F:69:LEU:HD13	1.99	0.44
1:D:105:SER:N	1:D:106:PRO:HD2	2.33	0.43
1:E:147:ASP:HA	1:E:148:GLU:HA	1.85	0.43
1:A:92:ALA:HB1	1:B:89:ILE:CG2	2.48	0.43
1:C:55:LEU:HD13	1:C:69:LEU:HD13	2.01	0.43
1:F:105:SER:N	1:F:106:PRO:HD2	2.34	0.43
1:A:55:LEU:HD13	1:A:69:LEU:HD13	2.01	0.43
1:D:4:VAL:HG23	1:D:47:MET:SD	2.59	0.42
1:A:204:LEU:HB3	1:A:250:TRP:CZ2	2.53	0.42
1:B:105:SER:N	1:B:106:PRO:HD2	2.34	0.42
1:C:105:SER:N	1:C:106:PRO:HD2	2.34	0.42
1:D:85:ALA:HB1	1:E:96:LEU:HD21	2.01	0.42
1:A:96:LEU:HD21	1:B:85:ALA:HB1	2.02	0.42
1:B:204:LEU:HB3	1:B:250:TRP:CZ2	2.55	0.42
1:B:236:ALA:HB2	1:C:251:LEU:HD13	2.02	0.42
1:D:13:LEU:N	1:D:14:PRO:CD	2.82	0.42
1:A:194:ILE:N	1:A:195:PRO:HD2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243:ILE:HG21	1:C:244:LEU:CD1	2.49	0.42
1:E:13:LEU:N	1:E:14:PRO:CD	2.83	0.42
1:F:152:LEU:HA	1:F:155:VAL:HG12	2.02	0.42
1:C:13:LEU:N	1:C:14:PRO:CD	2.83	0.41
1:C:204:LEU:HB3	1:C:250:TRP:CZ2	2.55	0.41
1:F:204:LEU:HB3	1:F:250:TRP:CZ2	2.55	0.41
1:B:55:LEU:HD13	1:B:69:LEU:HD13	2.02	0.41
1:C:142:VAL:HG12	1:C:155:VAL:HG22	2.03	0.41
1:F:194:ILE:N	1:F:195:PRO:HD2	2.35	0.41
1:D:194:ILE:N	1:D:195:PRO:HD2	2.36	0.41
1:F:13:LEU:N	1:F:14:PRO:CD	2.83	0.41
1:B:194:ILE:N	1:B:195:PRO:HD2	2.36	0.41
1:C:194:ILE:N	1:C:195:PRO:HD2	2.35	0.41
1:E:240:LEU:CD2	1:F:243:ILE:HG23	2.50	0.41
1:A:105:SER:N	1:A:106:PRO:HD2	2.35	0.41
1:D:139:GLY:HA2	1:D:142:VAL:HG22	2.03	0.41
1:E:244:LEU:HD11	1:F:243:ILE:HG13	2.03	0.41
1:F:4:VAL:HG23	1:F:47:MET:SD	2.61	0.41
1:F:142:VAL:HG12	1:F:155:VAL:HG22	2.03	0.41
1:A:61:ASN:HA	1:A:62:PRO:HD3	1.99	0.41
1:E:139:GLY:HA2	1:E:142:VAL:HG22	2.03	0.41
1:A:147:ASP:HA	1:A:148:GLU:HA	1.85	0.40
1:D:152:LEU:HA	1:D:155:VAL:HG12	2.03	0.40
1:A:13:LEU:HB2	1:A:14:PRO:HD3	2.03	0.40
1:A:68:PRO:C	1:A:70:VAL:H	2.24	0.40
1:B:142:VAL:HG12	1:B:155:VAL:HG22	2.04	0.40
1:E:55:LEU:HD13	1:E:69:LEU:HD13	2.04	0.40
1:E:194:ILE:N	1:E:195:PRO:HD2	2.36	0.40
1:A:13:LEU:N	1:A:14:PRO:CD	2.85	0.40
1:C:60:LEU:HD23	1:E:60:LEU:HD21	2.02	0.40
1:E:142:VAL:HG12	1:E:155:VAL:HG22	2.04	0.40
1:F:139:GLY:HA2	1:F:142:VAL:HG22	2.02	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	273/303 (90%)	252 (92%)	19 (7%)	2 (1%)	22	54
1	B	273/303 (90%)	252 (92%)	19 (7%)	2 (1%)	22	54
1	C	273/303 (90%)	251 (92%)	20 (7%)	2 (1%)	22	54
1	D	273/303 (90%)	252 (92%)	19 (7%)	2 (1%)	22	54
1	E	273/303 (90%)	251 (92%)	20 (7%)	2 (1%)	22	54
1	F	273/303 (90%)	252 (92%)	19 (7%)	2 (1%)	22	54
All	All	1638/1818 (90%)	1510 (92%)	116 (7%)	12 (1%)	22	54

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	69	LEU
1	A	69	LEU
1	B	69	LEU
1	C	69	LEU
1	D	69	LEU
1	E	69	LEU
1	B	200	PRO
1	C	200	PRO
1	E	200	PRO
1	A	200	PRO
1	D	200	PRO
1	F	200	PRO

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	199/227 (88%)	196 (98%)	3 (2%)	65	81
1	B	199/227 (88%)	196 (98%)	3 (2%)	65	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	C	199/227 (88%)	198 (100%)	1 (0%)	88 93
1	D	199/227 (88%)	196 (98%)	3 (2%)	65 81
1	E	199/227 (88%)	196 (98%)	3 (2%)	65 81
1	F	199/227 (88%)	196 (98%)	3 (2%)	65 81
All	All	1194/1362 (88%)	1178 (99%)	16 (1%)	69 82

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	124	LEU
1	A	145	SER
1	B	3	LEU
1	B	124	LEU
1	B	145	SER
1	C	145	SER
1	D	3	LEU
1	D	124	LEU
1	D	145	SER
1	E	3	LEU
1	E	145	SER
1	E	257	SER
1	F	3	LEU
1	F	124	LEU
1	F	145	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	ASN
1	A	246	GLN
1	B	50	ASN
1	B	246	GLN
1	C	50	ASN
1	C	246	GLN
1	D	50	ASN
1	D	246	GLN
1	E	50	ASN
1	E	246	GLN
1	F	50	ASN

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Mol	Chain	Res	Type
1	F	246	GLN

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	275/303 (90%)	-0.02	14 (5%) 28 26	33, 67, 112, 135	0
1	B	275/303 (90%)	0.14	25 (9%) 9 9	26, 61, 111, 140	0
1	C	275/303 (90%)	-0.15	7 (2%) 57 54	37, 69, 128, 161	0
1	D	275/303 (90%)	0.05	12 (4%) 34 33	38, 70, 110, 145	0
1	E	275/303 (90%)	0.18	23 (8%) 11 10	44, 83, 139, 191	0
1	F	275/303 (90%)	0.30	29 (10%) 6 6	41, 72, 127, 169	0
All	All	1650/1818 (90%)	0.09	110 (6%) 17 17	26, 70, 122, 191	0

All (110) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	121	LEU	5.6
1	D	145	SER	5.4
1	E	63	ARG	5.4
1	E	122	HIS	5.0
1	F	66	LYS	4.9
1	B	121	LEU	4.8
1	F	230	ILE	4.6
1	B	66	LYS	4.5
1	C	72	GLY	4.4
1	E	152	LEU	4.4
1	B	230	ILE	4.4
1	A	121	LEU	4.4
1	F	274	VAL	4.3
1	E	64	THR	4.2
1	D	73	ALA	4.1
1	E	74	VAL	4.1
1	E	72	GLY	4.0
1	B	117	HIS	3.9
1	E	71	VAL	3.9

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Mol	Chain	Res	Type	RSRZ
1	F	229	ALA	3.8
1	B	74	VAL	3.8
1	F	71	VAL	3.7
1	A	274	VAL	3.7
1	E	151	SER	3.6
1	F	245	VAL	3.6
1	A	122	HIS	3.6
1	E	117	HIS	3.5
1	F	145	SER	3.4
1	F	232	THR	3.4
1	B	27	PHE	3.4
1	B	274	VAL	3.3
1	D	66	LYS	3.3
1	B	229	ALA	3.2
1	A	66	LYS	3.2
1	D	227	LEU	3.1
1	F	25	TYR	3.0
1	F	73	ALA	3.0
1	B	270	ALA	3.0
1	B	73	ALA	3.0
1	F	121	LEU	3.0
1	B	272	ILE	3.0
1	D	155	VAL	3.0
1	B	276	MET	3.0
1	B	71	VAL	2.9
1	F	148	GLU	2.9
1	B	271	GLY	2.9
1	D	72	GLY	2.9
1	F	191	LEU	2.9
1	E	120	ARG	2.9
1	B	273	ILE	2.8
1	F	275	ASP	2.8
1	E	128	HIS	2.7
1	F	233	VAL	2.6
1	F	266	ILE	2.6
1	F	26	PRO	2.6
1	A	277	LEU	2.6
1	C	71	VAL	2.6
1	E	73	ALA	2.6
1	A	191	LEU	2.6
1	B	29	LEU	2.6
1	E	182	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
1	F	234	SER	2.5
1	E	67	ARG	2.5
1	B	64	THR	2.5
1	D	255	LYS	2.5
1	F	267	ILE	2.5
1	E	198	LEU	2.5
1	E	155	VAL	2.5
1	D	149	ALA	2.5
1	E	123	PRO	2.5
1	F	120	ARG	2.4
1	C	128	HIS	2.4
1	B	67	ARG	2.4
1	F	265	PRO	2.4
1	F	257	SER	2.4
1	D	25	TYR	2.4
1	C	122	HIS	2.3
1	E	153	GLY	2.3
1	B	275	ASP	2.3
1	B	269	GLY	2.3
1	F	27	PHE	2.3
1	F	237	LEU	2.3
1	F	255	LYS	2.3
1	C	152	LEU	2.3
1	A	186	ASP	2.3
1	A	107	LEU	2.3
1	C	121	LEU	2.3
1	B	80	TRP	2.2
1	B	72	GLY	2.2
1	B	122	HIS	2.2
1	D	121	LEU	2.2
1	E	107	LEU	2.2
1	E	156	LEU	2.2
1	F	272	ILE	2.2
1	F	72	GLY	2.2
1	A	198	LEU	2.2
1	E	118	ALA	2.2
1	A	194	ILE	2.2
1	F	271	GLY	2.2
1	B	49	TYR	2.1
1	B	231	ALA	2.1
1	D	267	ILE	2.1
1	A	27	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	100	TYR	2.1
1	F	67	ARG	2.1
1	A	67	ARG	2.0
1	A	193	SER	2.0
1	E	127	LEU	2.0
1	C	73	ALA	2.0
1	A	229	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.