Full wwPDB X-ray Structure Validation Report ⓘ

Sep 9, 2023 – 09:38 PM EDT

PDB ID	:	4HL6
Title	:	YfdE from Escherichia coli
Authors	:	Mullins, E.A.; Sullivan, K.L.; Nyffeler, K.E.; Kappock, T.J.
Deposited on	:	2012-10-16
Resolution	:	2.12 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:

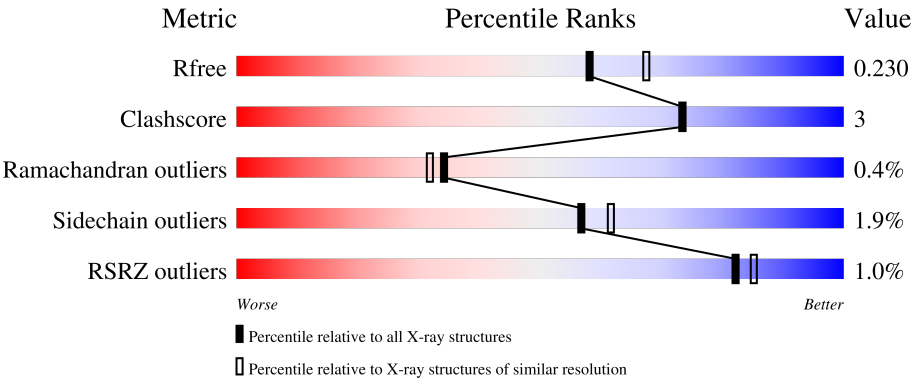
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.12 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	6241 (2.14-2.10)
Clashscore	141614	6778 (2.14-2.10)
Ramachandran outliers	138981	6705 (2.14-2.10)
Sidechain outliers	138945	6706 (2.14-2.10)
RSRZ outliers	127900	6112 (2.14-2.10)

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	401	83% 10% 6%
1	B	401	86% 8% 6%
1	C	401	. 84% 9% 6%
1	D	401	83% 9% 7%
1	E	401	. 86% 7% 7%

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Mol	Chain	Length	Quality of chain
1	F	401	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 18281 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 Uncharacterized protein YfdE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	375	Total	C	N	O	S	0	0	0
			2878	1826	493	539	20			
1	B	376	Total	C	N	O	S	0	0	0
			2884	1829	494	541	20			
1	C	375	Total	C	N	O	S	0	0	0
			2878	1826	493	539	20			
1	D	374	Total	C	N	O	S	0	0	0
			2871	1823	492	536	20			
1	E	374	Total	C	N	O	S	0	0	0
			2871	1823	492	536	20			
1	F	375	Total	C	N	O	S	0	0	0
			2878	1826	493	539	20			

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP P76518
A	-18	GLY	-	expression tag	UNP P76518
A	-17	SER	-	expression tag	UNP P76518
A	-16	SER	-	expression tag	UNP P76518
A	-15	HIS	-	expression tag	UNP P76518
A	-14	HIS	-	expression tag	UNP P76518
A	-13	HIS	-	expression tag	UNP P76518
A	-12	HIS	-	expression tag	UNP P76518
A	-11	HIS	-	expression tag	UNP P76518
A	-10	HIS	-	expression tag	UNP P76518
A	-9	SER	-	expression tag	UNP P76518
A	-8	SER	-	expression tag	UNP P76518
A	-7	GLY	-	expression tag	UNP P76518
A	-6	LEU	-	expression tag	UNP P76518
A	-5	VAL	-	expression tag	UNP P76518
A	-4	PRO	-	expression tag	UNP P76518
A	-3	ARG	-	expression tag	UNP P76518

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P76518
A	-1	SER	-	expression tag	UNP P76518
A	0	HIS	-	expression tag	UNP P76518
B	-19	MET	-	expression tag	UNP P76518
B	-18	GLY	-	expression tag	UNP P76518
B	-17	SER	-	expression tag	UNP P76518
B	-16	SER	-	expression tag	UNP P76518
B	-15	HIS	-	expression tag	UNP P76518
B	-14	HIS	-	expression tag	UNP P76518
B	-13	HIS	-	expression tag	UNP P76518
B	-12	HIS	-	expression tag	UNP P76518
B	-11	HIS	-	expression tag	UNP P76518
B	-10	HIS	-	expression tag	UNP P76518
B	-9	SER	-	expression tag	UNP P76518
B	-8	SER	-	expression tag	UNP P76518
B	-7	GLY	-	expression tag	UNP P76518
B	-6	LEU	-	expression tag	UNP P76518
B	-5	VAL	-	expression tag	UNP P76518
B	-4	PRO	-	expression tag	UNP P76518
B	-3	ARG	-	expression tag	UNP P76518
B	-2	GLY	-	expression tag	UNP P76518
B	-1	SER	-	expression tag	UNP P76518
B	0	HIS	-	expression tag	UNP P76518
C	-19	MET	-	expression tag	UNP P76518
C	-18	GLY	-	expression tag	UNP P76518
C	-17	SER	-	expression tag	UNP P76518
C	-16	SER	-	expression tag	UNP P76518
C	-15	HIS	-	expression tag	UNP P76518
C	-14	HIS	-	expression tag	UNP P76518
C	-13	HIS	-	expression tag	UNP P76518
C	-12	HIS	-	expression tag	UNP P76518
C	-11	HIS	-	expression tag	UNP P76518
C	-10	HIS	-	expression tag	UNP P76518
C	-9	SER	-	expression tag	UNP P76518
C	-8	SER	-	expression tag	UNP P76518
C	-7	GLY	-	expression tag	UNP P76518
C	-6	LEU	-	expression tag	UNP P76518
C	-5	VAL	-	expression tag	UNP P76518
C	-4	PRO	-	expression tag	UNP P76518
C	-3	ARG	-	expression tag	UNP P76518
C	-2	GLY	-	expression tag	UNP P76518
C	-1	SER	-	expression tag	UNP P76518

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Chain	Residue	Modelled	Actual	Comment	Reference
C	0	HIS	-	expression tag	UNP P76518
D	-19	MET	-	expression tag	UNP P76518
D	-18	GLY	-	expression tag	UNP P76518
D	-17	SER	-	expression tag	UNP P76518
D	-16	SER	-	expression tag	UNP P76518
D	-15	HIS	-	expression tag	UNP P76518
D	-14	HIS	-	expression tag	UNP P76518
D	-13	HIS	-	expression tag	UNP P76518
D	-12	HIS	-	expression tag	UNP P76518
D	-11	HIS	-	expression tag	UNP P76518
D	-10	HIS	-	expression tag	UNP P76518
D	-9	SER	-	expression tag	UNP P76518
D	-8	SER	-	expression tag	UNP P76518
D	-7	GLY	-	expression tag	UNP P76518
D	-6	LEU	-	expression tag	UNP P76518
D	-5	VAL	-	expression tag	UNP P76518
D	-4	PRO	-	expression tag	UNP P76518
D	-3	ARG	-	expression tag	UNP P76518
D	-2	GLY	-	expression tag	UNP P76518
D	-1	SER	-	expression tag	UNP P76518
D	0	HIS	-	expression tag	UNP P76518
E	-19	MET	-	expression tag	UNP P76518
E	-18	GLY	-	expression tag	UNP P76518
E	-17	SER	-	expression tag	UNP P76518
E	-16	SER	-	expression tag	UNP P76518
E	-15	HIS	-	expression tag	UNP P76518
E	-14	HIS	-	expression tag	UNP P76518
E	-13	HIS	-	expression tag	UNP P76518
E	-12	HIS	-	expression tag	UNP P76518
E	-11	HIS	-	expression tag	UNP P76518
E	-10	HIS	-	expression tag	UNP P76518
E	-9	SER	-	expression tag	UNP P76518
E	-8	SER	-	expression tag	UNP P76518
E	-7	GLY	-	expression tag	UNP P76518
E	-6	LEU	-	expression tag	UNP P76518
E	-5	VAL	-	expression tag	UNP P76518
E	-4	PRO	-	expression tag	UNP P76518
E	-3	ARG	-	expression tag	UNP P76518
E	-2	GLY	-	expression tag	UNP P76518
E	-1	SER	-	expression tag	UNP P76518
E	0	HIS	-	expression tag	UNP P76518
F	-19	MET	-	expression tag	UNP P76518

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-18	GLY	-	expression tag	UNP P76518
F	-17	SER	-	expression tag	UNP P76518
F	-16	SER	-	expression tag	UNP P76518
F	-15	HIS	-	expression tag	UNP P76518
F	-14	HIS	-	expression tag	UNP P76518
F	-13	HIS	-	expression tag	UNP P76518
F	-12	HIS	-	expression tag	UNP P76518
F	-11	HIS	-	expression tag	UNP P76518
F	-10	HIS	-	expression tag	UNP P76518
F	-9	SER	-	expression tag	UNP P76518
F	-8	SER	-	expression tag	UNP P76518
F	-7	GLY	-	expression tag	UNP P76518
F	-6	LEU	-	expression tag	UNP P76518
F	-5	VAL	-	expression tag	UNP P76518
F	-4	PRO	-	expression tag	UNP P76518
F	-3	ARG	-	expression tag	UNP P76518
F	-2	GLY	-	expression tag	UNP P76518
F	-1	SER	-	expression tag	UNP P76518
F	0	HIS	-	expression tag	UNP P76518

- Molecule 2 is water.

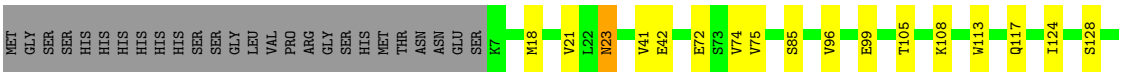
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	185	Total	O	0	0
			185	185		
2	B	226	Total	O	0	0
			226	226		
2	C	203	Total	O	0	0
			203	203		
2	D	173	Total	O	0	0
			173	173		
2	E	118	Total	O	0	0
			118	118		
2	F	116	Total	O	0	0
			116	116		

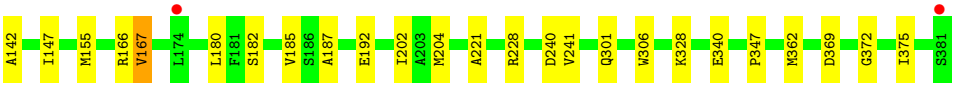
3 Residue-property plots (i)

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: Uncharacterized protein YfdE

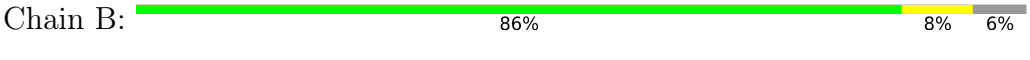
Chain A:

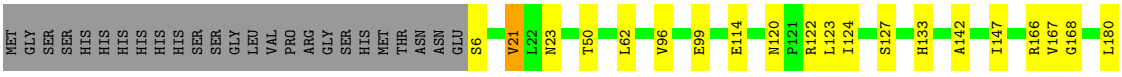




• Molecule 1: Uncharacterized protein YfdE

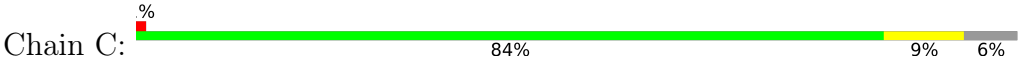
Chain B:

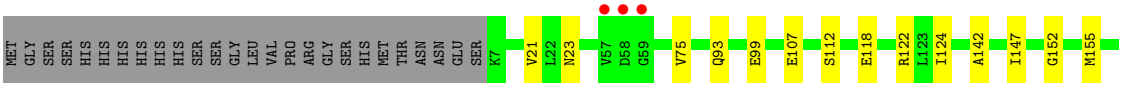


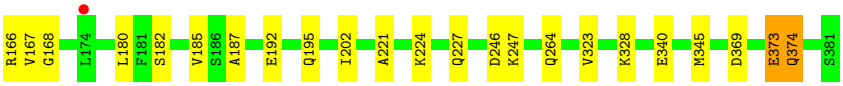


• Molecule 1: Uncharacterized protein YfdE

Chain C:

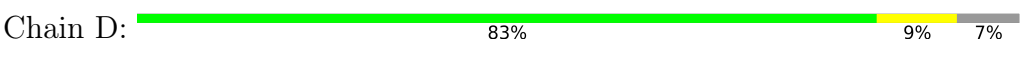


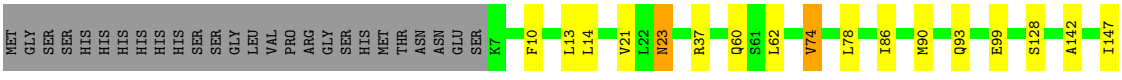


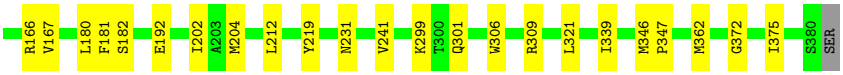


• Molecule 1: Uncharacterized protein YfdE

Chain D:

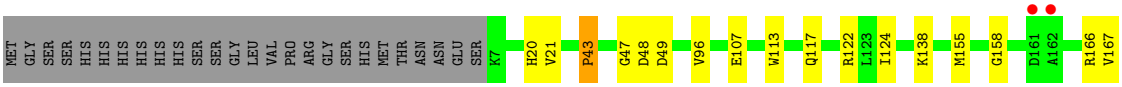


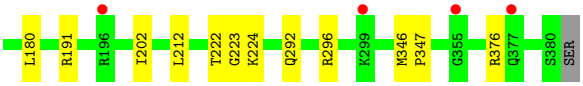




• Molecule 1: Uncharacterized protein YfdE

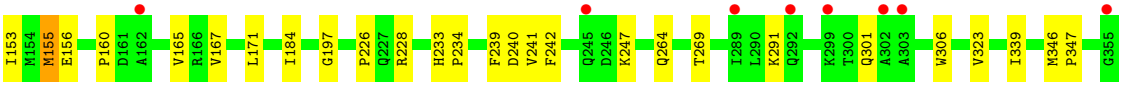
Chain E:





• Molecule 1: Uncharacterized protein YfdE

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	111.42Å 79.53Å 276.19Å 90.00° 99.95° 90.00°	Depositor
Resolution (Å)	42.48 – 2.12 43.81 – 2.12	Depositor EDS
% Data completeness (in resolution range)	79.7 (42.48-2.12) 76.1 (43.81-2.12)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	2.16 (at 2.12Å)	Xtriage
Refinement program	PHENIX 1.7.3_928	Depositor
R, R_{free}	0.189 , 0.236 0.185 , 0.230	Depositor DCC
R_{free} test set	5456 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	23.9	Xtriage
Anisotropy	0.677	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 36.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.014 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	18281	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.51% 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	0.24	0/2943	0.42	0/3990
1	B	0.24	0/2949	0.42	0/3998
1	C	0.24	0/2943	0.42	0/3990
1	D	0.24	0/2936	0.42	0/3982
1	E	0.23	0/2936	0.42	0/3982
1	F	0.23	0/2943	0.41	0/3990
All	All	0.24	0/17650	0.42	0/23932

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	2878	0	2858	26	0
1	B	2884	0	2863	17	0
1	C	2878	0	2858	22	0
1	D	2871	0	2853	27	0
1	E	2871	0	2853	13	0
1	F	2878	0	2858	26	0
2	A	185	0	0	1	0
2	B	226	0	0	0	0
2	C	203	0	0	1	0
2	D	173	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	118	0	0	2	0
2	F	116	0	0	2	0
All	All	18281	0	17143	115	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 3.

All (115) 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:A:192:GLU:HG2	1:B:192:GLU:HG2	1.53	0.90
1:A:74:VAL:HG12	1:A:372:GLY:HA2	1.60	0.81
1:D:74:VAL:HG12	1:D:372:GLY:HA2	1.66	0.77
1:F:156:GLU:OE2	2:F:441:HOH:O	2.09	0.70
1:D:339:ILE:HD12	1:D:362:MET:HG3	1.75	0.68
1:B:122:ARG:NH1	1:B:195:GLN:OE1	2.27	0.66
1:A:105:THR:HA	1:A:108:LYS:HE3	1.77	0.66
1:C:93:GLN:NE2	2:C:516:HOH:O	2.27	0.66
1:D:147:ILE:HG13	1:D:204:MET:HE2	1.79	0.63
1:A:328:LYS:NZ	1:B:219:TYR:OH	2.33	0.62
1:C:192:GLU:HG3	1:D:192:GLU:HG2	1.81	0.62
1:D:142:ALA:HB1	1:D:147:ILE:HD11	1.81	0.61
1:C:182:SER:HB3	1:D:182:SER:HB3	1.81	0.61
1:F:86:ILE:HD13	1:F:376:ARG:HG2	1.81	0.61
1:C:122:ARG:NH1	1:C:195:GLN:OE1	2.37	0.58
1:C:221:ALA:HB2	1:D:62:LEU:HD22	1.87	0.57
1:B:142:ALA:HB1	1:B:147:ILE:HD11	1.87	0.57
1:F:121:PRO:O	1:F:197:GLY:N	2.36	0.56
1:A:185:VAL:HG22	1:B:185:VAL:HG12	1.87	0.56
1:C:124:ILE:HD12	1:C:187:ALA:HB1	1.86	0.56
1:A:347:PRO:HG3	1:B:216:LEU:HD23	1.89	0.54
1:A:142:ALA:HB1	1:A:147:ILE:HD11	1.90	0.53
1:C:224:LYS:O	1:C:227:GLN:NE2	2.42	0.53
1:F:167:VAL:HG21	1:F:171:LEU:HB2	1.90	0.53
1:C:340:GLU:HB3	1:C:345:MET:SD	2.49	0.53
1:E:96:VAL:HG22	1:E:124:ILE:HB	1.92	0.51
1:E:346:MET:HB2	1:E:347:PRO:HD2	1.92	0.51
1:B:124:ILE:HD12	1:B:187:ALA:HB1	1.91	0.51
1:F:339:ILE:HD12	1:F:362:MET:HG3	1.91	0.51
1:D:74:VAL:HG11	1:D:375:ILE:HB	1.93	0.51
1:C:107:GLU:HG3	1:C:112:SER:HB3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:127:SER:HG	1:B:133:HIS:CE1	2.29	0.50
1:E:376:ARG:NH1	2:E:504:HOH:O	2.42	0.50
1:F:74:VAL:HG13	1:F:372:GLY:HA2	1.94	0.50
1:C:142:ALA:HB1	1:C:147:ILE:HD11	1.94	0.49
1:F:160:PRO:HA	1:F:228:ARG:HB3	1.95	0.49
1:A:23:ASN:HD21	1:A:128:SER:HG	1.58	0.49
1:A:74:VAL:HG13	1:A:375:ILE:HD12	1.95	0.48
1:B:240:ASP:OD1	1:B:241:VAL:N	2.42	0.48
1:F:346:MET:HB2	1:F:347:PRO:HD2	1.95	0.48
1:F:29:GLN:NE2	1:F:33:ASN:OD1	2.40	0.47
1:C:166:ARG:HG2	1:C:167:VAL:O	2.15	0.47
1:C:182:SER:HB2	1:D:181:PHE:HE2	1.79	0.47
1:D:180:LEU:HA	1:D:202:ILE:HG13	1.96	0.47
1:E:180:LEU:HA	1:E:202:ILE:HG13	1.95	0.47
1:A:166:ARG:HG2	1:A:167:VAL:O	2.15	0.47
1:A:221:ALA:HB2	1:B:62:LEU:HD12	1.97	0.47
1:D:23:ASN:ND2	1:D:128:SER:OG	2.40	0.47
1:E:158:GLY:HA2	1:F:165:VAL:HG11	1.97	0.46
1:B:166:ARG:HG2	1:B:167:VAL:O	2.15	0.46
1:C:328:LYS:NZ	1:D:219:TYR:OH	2.26	0.46
1:D:166:ARG:HG2	1:D:167:VAL:O	2.16	0.46
1:A:369:ASP:OD2	1:A:372:GLY:HA3	2.16	0.45
1:C:152:GLY:HA2	1:D:321:LEU:O	2.16	0.45
1:F:16:ILE:HG12	1:F:94:ALA:HB2	1.99	0.45
1:C:75:VAL:HG23	1:C:369:ASP:HB2	1.99	0.45
1:F:372:GLY:O	1:F:376:ARG:HB2	2.17	0.45
1:C:182:SER:HB2	1:D:181:PHE:CE2	2.51	0.45
1:C:182:SER:HA	1:C:185:VAL:HG22	1.99	0.45
1:D:74:VAL:HG13	1:D:375:ILE:HD12	1.98	0.45
1:E:166:ARG:HG2	1:E:167:VAL:O	2.16	0.45
1:E:212:LEU:HD13	1:F:323:VAL:HG13	1.99	0.44
1:A:18:MET:HG2	1:A:41:VAL:HB	1.98	0.44
1:F:155:MET:HG3	1:F:226:PRO:HG3	1.99	0.44
1:C:155:MET:HG3	1:D:321:LEU:O	2.17	0.44
1:E:222:THR:OG1	1:E:223:GLY:N	2.48	0.44
1:D:231:ASN:HB3	1:D:241:VAL:HG13	1.99	0.44
1:F:301:GLN:HB2	1:F:306:TRP:CE2	2.53	0.44
1:D:299:LYS:HB3	1:D:299:LYS:HE2	1.67	0.44
1:E:138:LYS:NZ	2:E:463:HOH:O	2.50	0.44
1:F:31:LEU:HD11	1:F:184:ILE:HG21	1.99	0.44
1:F:228:ARG:N	2:F:441:HOH:O	2.37	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:373:GLU:HG3	1:C:374:GLN:N	2.32	0.44
1:E:122:ARG:O	1:E:191:ARG:NH1	2.47	0.44
1:C:323:VAL:HG13	1:D:212:LEU:HD13	1.99	0.43
1:A:124:ILE:HD12	1:A:187:ALA:HB1	2.00	0.43
1:D:86:ILE:O	1:D:90:MET:HG3	2.17	0.43
1:F:233:HIS:HB2	1:F:239:PHE:CD2	2.54	0.43
1:A:42:GLU:O	1:A:75:VAL:HA	2.18	0.43
1:B:180:LEU:HA	1:B:202:ILE:HG13	2.00	0.43
1:D:10:PHE:O	1:D:13:LEU:HB2	2.18	0.43
1:E:43:PRO:HD2	1:E:47:GLY:HA2	2.01	0.43
1:B:96:VAL:HG22	1:B:124:ILE:HB	2.00	0.43
1:F:69:HIS:HA	1:F:365:ALA:HA	2.00	0.43
1:B:147:ILE:HG13	1:B:204:MET:HE1	2.01	0.43
1:A:113:TRP:O	1:A:117:GLN:HG3	2.19	0.42
1:C:180:LEU:HA	1:C:202:ILE:HG13	2.00	0.42
1:D:301:GLN:HB2	1:D:306:TRP:NE1	2.34	0.42
1:F:247:LYS:HE2	1:F:247:LYS:HB3	1.77	0.42
1:F:242:PHE:CE2	1:F:291:LYS:HG3	2.54	0.42
1:A:301:GLN:HB2	1:A:306:TRP:NE1	2.35	0.42
1:A:128:SER:HB2	1:A:180:LEU:HD22	2.02	0.42
1:D:93:GLN:NE2	2:D:521:HOH:O	2.52	0.42
1:A:180:LEU:HA	1:A:202:ILE:HG13	2.01	0.42
1:A:182:SER:HA	1:A:185:VAL:HG12	2.02	0.42
1:B:6:SER:HB3	1:B:355:GLY:O	2.19	0.42
1:C:246:ASP:OD1	1:C:247:LYS:N	2.50	0.42
1:F:240:ASP:OD1	1:F:241:VAL:N	2.46	0.42
1:A:147:ILE:HG13	1:A:204:MET:HE2	2.01	0.42
1:B:21:VAL:HA	1:B:50:THR:HG23	2.02	0.41
1:F:9:PRO:HD3	1:F:356:CYS:SG	2.60	0.41
1:E:48:ASP:OD1	1:E:49:ASP:N	2.53	0.41
1:D:23:ASN:HD21	1:D:128:SER:HG	1.64	0.41
1:B:120:ASN:HB3	1:B:123:LEU:HB2	2.03	0.41
1:D:14:LEU:HD13	1:D:37:ARG:HD3	2.03	0.41
1:A:72:GLU:OE2	1:A:375:ILE:HD11	2.21	0.41
1:F:21:VAL:HA	1:F:50:THR:HG23	2.02	0.41
1:F:233:HIS:CG	1:F:234:PRO:HD2	2.55	0.41
1:A:75:VAL:HG22	1:A:369:ASP:OD2	2.21	0.41
1:A:166:ARG:NH1	2:A:422:HOH:O	2.47	0.41
1:D:346:MET:HB2	1:D:347:PRO:HD2	2.03	0.41
1:F:107:GLU:HG3	1:F:108:LYS:N	2.36	0.40
1:A:240:ASP:OD1	1:A:241:VAL:N	2.48	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:113:TRP:O	1:E:117:GLN:HG3	2.22	0.40
1:A:96:VAL:HG22	1:A:124:ILE:HB	2.03	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	373/401 (93%)	360 (96%)	11 (3%)	2 (0%)	29	25
1	B	374/401 (93%)	365 (98%)	7 (2%)	2 (0%)	29	25
1	C	373/401 (93%)	361 (97%)	9 (2%)	3 (1%)	19	14
1	D	372/401 (93%)	362 (97%)	9 (2%)	1 (0%)	41	40
1	E	372/401 (93%)	350 (94%)	21 (6%)	1 (0%)	41	40
1	F	373/401 (93%)	361 (97%)	11 (3%)	1 (0%)	41	40
All	All	2237/2406 (93%)	2159 (96%)	68 (3%)	10 (0%)	34	32

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	21	VAL
1	B	21	VAL
1	A	228	ARG
1	C	21	VAL
1	C	23	ASN
1	D	21	VAL
1	E	21	VAL
1	F	21	VAL
1	C	168	GLY
1	B	168	GLY

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	311/334 (93%)	304 (98%)	7 (2%)	50	53
1	B	312/334 (93%)	308 (99%)	4 (1%)	69	74
1	C	311/334 (93%)	306 (98%)	5 (2%)	62	68
1	D	310/334 (93%)	304 (98%)	6 (2%)	57	61
1	E	310/334 (93%)	303 (98%)	7 (2%)	50	53
1	F	311/334 (93%)	304 (98%)	7 (2%)	50	53
All	All	1865/2004 (93%)	1829 (98%)	36 (2%)	57	61

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	ASN
1	A	85	SER
1	A	99	GLU
1	A	155	MET
1	A	167	VAL
1	A	340	GLU
1	A	362	MET
1	B	23	ASN
1	B	99	GLU
1	B	114	GLU
1	B	362	MET
1	C	99	GLU
1	C	118	GLU
1	C	264	GLN
1	C	373	GLU
1	C	374	GLN
1	D	23	ASN
1	D	60	GLN
1	D	74	VAL
1	D	78	LEU
1	D	99	GLU
1	D	309	ARG

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Mol	Chain	Res	Type
1	E	20	HIS
1	E	43	PRO
1	E	107	GLU
1	E	155	MET
1	E	224	LYS
1	E	292	GLN
1	E	296	ARG
1	F	20	HIS
1	F	60	GLN
1	F	107	GLU
1	F	153	ILE
1	F	155	MET
1	F	264	GLN
1	F	269	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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, 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	375/401 (93%)	-0.13	2 (0%) 91 92	19, 29, 47, 66	0
1	B	376/401 (93%)	-0.23	0 100 100	17, 26, 41, 59	0
1	C	375/401 (93%)	-0.23	4 (1%) 80 84	18, 28, 44, 62	0
1	D	374/401 (93%)	-0.14	0 100 100	20, 30, 48, 60	0
1	E	374/401 (93%)	-0.00	6 (1%) 72 76	19, 34, 52, 72	0
1	F	375/401 (93%)	0.21	11 (2%) 51 57	20, 38, 59, 74	0
All	All	2249/2406 (93%)	-0.09	23 (1%) 82 85	17, 30, 51, 74	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	381	SER	5.3
1	F	381	SER	4.0
1	C	59	GLY	3.6
1	E	196	ARG	3.3
1	F	245	GLN	3.2
1	F	355	GLY	3.2
1	F	302	ALA	3.1
1	E	161	ASP	2.7
1	C	174	LEU	2.6
1	F	292	GLN	2.5
1	C	58	ASP	2.4
1	F	289	ILE	2.4
1	C	57	VAL	2.4
1	E	162	ALA	2.4
1	F	162	ALA	2.4
1	E	377	GLN	2.3
1	E	299	LYS	2.2
1	E	355	GLY	2.1
1	F	303	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	F	114	GLU	2.1
1	F	299	LYS	2.1
1	A	174	LEU	2.1
1	F	121	PRO	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

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

6.3 Carbohydrates (i)

There are no 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.