wwPDB X-ray Structure Validation Summary Report (i)

Mar 24, 2022 – 12:31 pm GMT

PDB ID	:	6GWK
Title	:	The crystal structure of Hfq from Caulobacter crescentus
Authors	:	Santiago-Frangos, A.; Frohlich, K.S.; Jeliazkov, J.R.; Gray, J.R.; Luisi, B.F.; Woodson, S.A.; Hardwick, S.W.
Deposited on	:	2018-06-25
Resolution	:	2.15 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

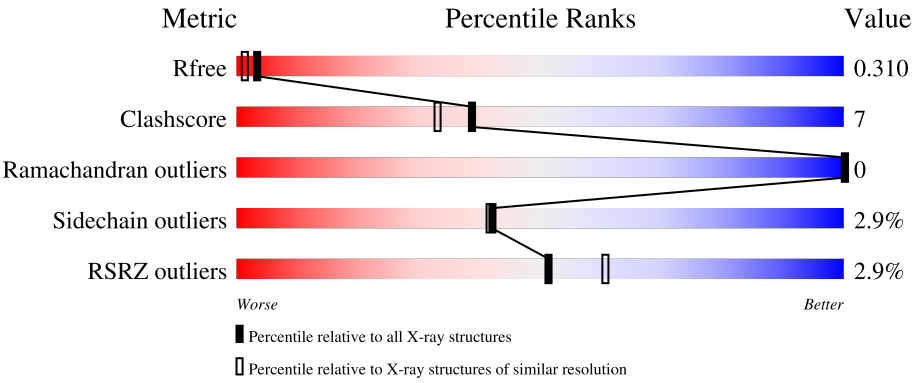
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.27
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

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 2.15 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	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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	82	70% 7% 23%
1	B	82	% 83% 11% 6%
1	C	82	2% 72% 11% • 16%
1	D	82	% 77% 17% 6%
1	E	82	71% 11% 18%

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Mol	Chain	Length	Quality of chain
1	F	82	2% 66% 17% 17%
1	G	82	6% 59% 18% 22%
1	H	82	9% 77% 13% 7%
1	I	82	5% 63% 12% 23%
1	J	82	% 80% 13% 6%
1	K	82	2% 57% 16% 27%
1	L	82	6% 54% 29% 15%
1	M	82	68% 10% 20%
1	N	82	% 87% 5% 7%
1	O	82	2% 70% 12% 17%
1	P	82	87% 7% 6%
1	Q	82	67% 7% 26%
1	R	82	72% 13% 13%
1	S	82	5% 50% 26% 24%
1	T	82	% 71% 13% 15%
1	U	82	2% 59% 17% 24%
1	V	82	2% 71% 22% 6%
1	W	82	% 56% 21% 23%
1	X	82	6% 68% 13% 18%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 12914 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 RNA-binding protein Hfq.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	63	Total	C	N	O	S	0	0	0
			482	313	83	84	2			
1	B	77	Total	C	N	O	S	0	0	0
			601	385	100	114	2			
1	C	69	Total	C	N	O	S	0	2	0
			542	356	91	93	2			
1	D	77	Total	C	N	O	S	0	3	0
			607	393	100	112	2			
1	E	67	Total	C	N	O	S	0	1	0
			522	337	91	92	2			
1	F	68	Total	C	N	O	S	0	1	0
			538	352	91	93	2			
1	G	64	Total	C	N	O	S	0	0	0
			476	311	80	83	2			
1	H	76	Total	C	N	O	S	0	0	0
			583	373	97	111	2			
1	I	63	Total	C	N	O	S	0	0	0
			484	314	85	83	2			
1	J	77	Total	C	N	O	S	0	0	0
			599	384	101	112	2			
1	K	60	Total	C	N	O	S	0	0	0
			465	302	81	81	1			
1	L	70	Total	C	N	O	S	0	2	0
			545	354	91	98	2			
1	M	66	Total	C	N	O	S	0	0	0
			511	329	89	91	2			
1	N	76	Total	C	N	O	S	0	0	0
			593	380	101	110	2			
1	O	68	Total	C	N	O	S	0	1	0
			537	352	90	93	2			
1	P	77	Total	C	N	O	S	0	0	0
			596	382	100	112	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	61	Total	C	N	O	S	4	2	0
			489	320	84	83	2			
1	R	71	Total	C	N	O	S	0	1	0
			559	361	97	99	2			
1	S	62	Total	C	N	O	S	0	0	0
			478	309	83	84	2			
1	T	70	Total	C	N	O	S	0	0	0
			532	344	86	100	2			
1	U	62	Total	C	N	O	S	0	0	0
			476	307	83	84	2			
1	V	77	Total	C	N	O	S	0	1	0
			600	387	100	111	2			
1	W	63	Total	C	N	O	S	0	0	0
			476	308	80	86	2			
1	X	67	Total	C	N	O	S	0	1	0
			513	335	85	91	2			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	7	Total	O	0	0
			7	7		
2	B	10	Total	O	0	0
			10	10		
2	C	4	Total	O	0	0
			4	4		
2	D	9	Total	O	0	0
			9	9		
2	E	6	Total	O	0	0
			6	6		
2	F	3	Total	O	0	0
			3	3		
2	G	3	Total	O	0	0
			3	3		
2	H	3	Total	O	0	0
			3	3		
2	I	3	Total	O	0	0
			3	3		
2	J	4	Total	O	0	0
			4	4		
2	K	2	Total	O	0	0
			2	2		

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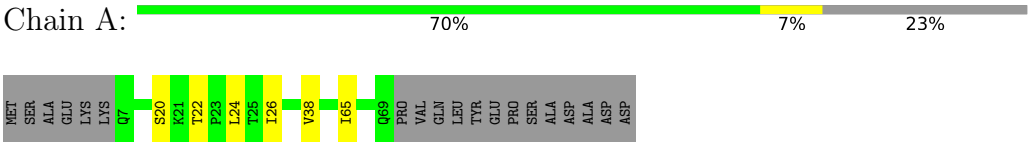
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	L	3	Total O 3 3	0	0
2	M	10	Total O 10 10	0	0
2	N	5	Total O 5 5	0	0
2	O	7	Total O 7 7	0	0
2	P	10	Total O 10 10	0	0
2	Q	3	Total O 3 3	0	0
2	R	5	Total O 5 5	0	0
2	S	3	Total O 3 3	0	0
2	T	1	Total O 1 1	0	0
2	U	3	Total O 3 3	0	0
2	V	2	Total O 2 2	0	0
2	W	3	Total O 3 3	0	0
2	X	1	Total O 1 1	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

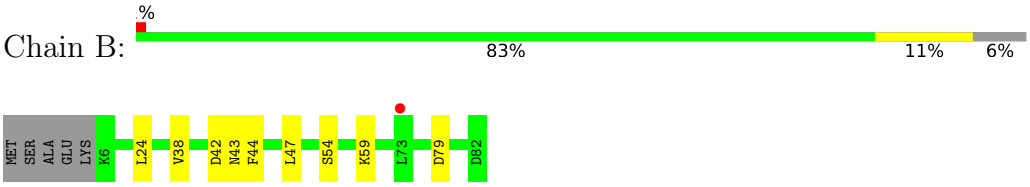
• Molecule 1: RNA-binding protein Hfq

Chain A:



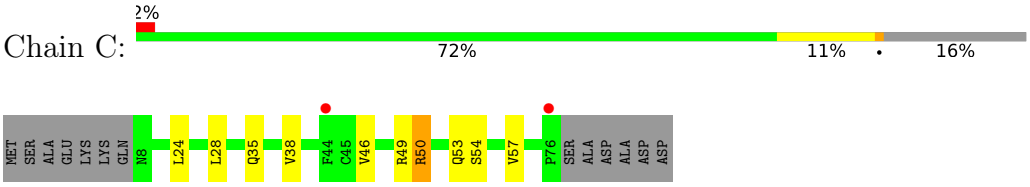
• Molecule 1: RNA-binding protein Hfq

Chain B:



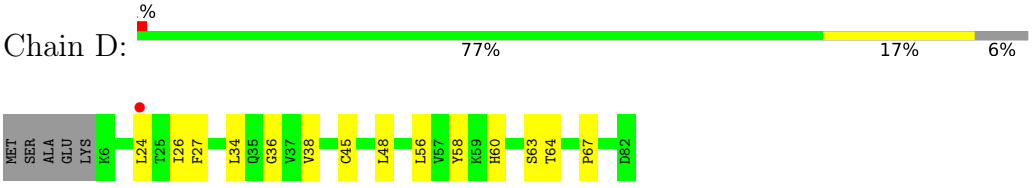
• Molecule 1: RNA-binding protein Hfq

Chain C:



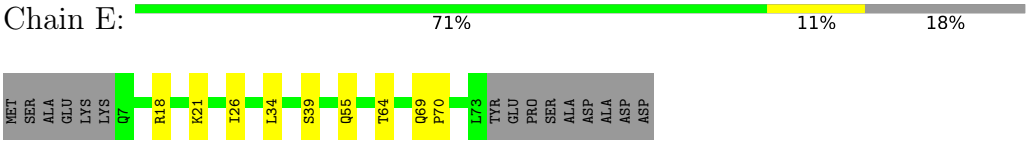
• Molecule 1: RNA-binding protein Hfq

Chain D:



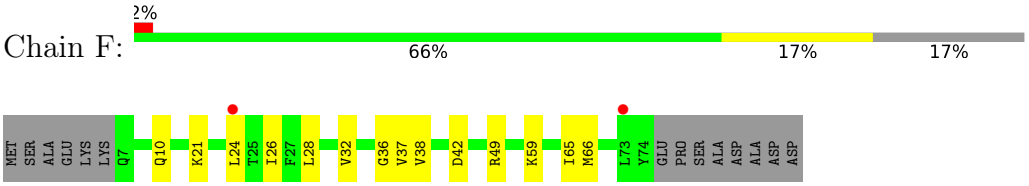
• Molecule 1: RNA-binding protein Hfq

Chain E:



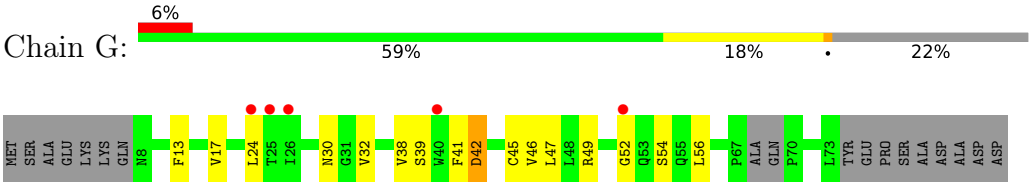
• Molecule 1: RNA-binding protein Hfq

Chain F:



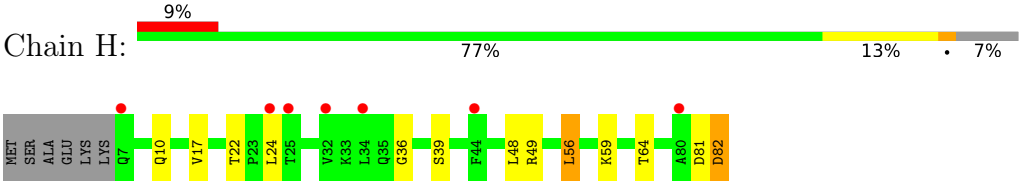
• Molecule 1: RNA-binding protein Hfq

Chain G:



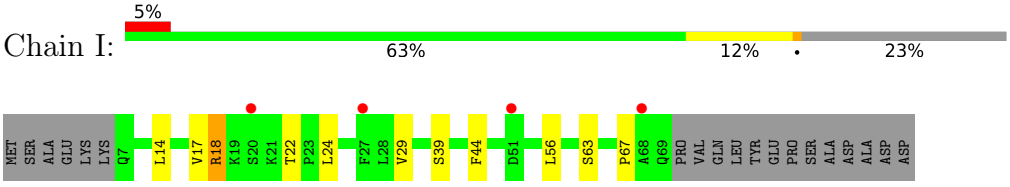
• Molecule 1: RNA-binding protein Hfq

Chain H:



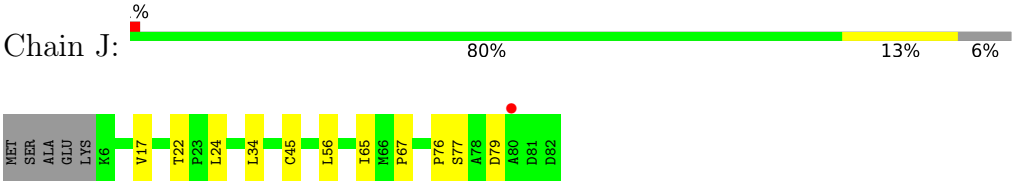
• Molecule 1: RNA-binding protein Hfq

Chain I:



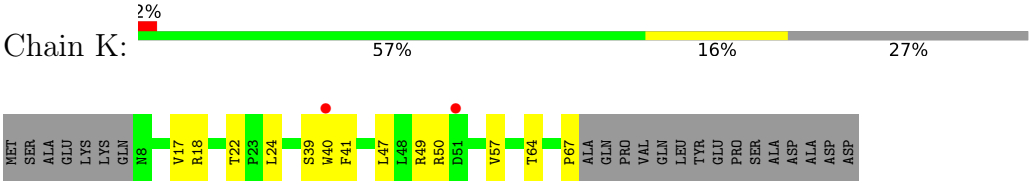
• Molecule 1: RNA-binding protein Hfq

Chain J:



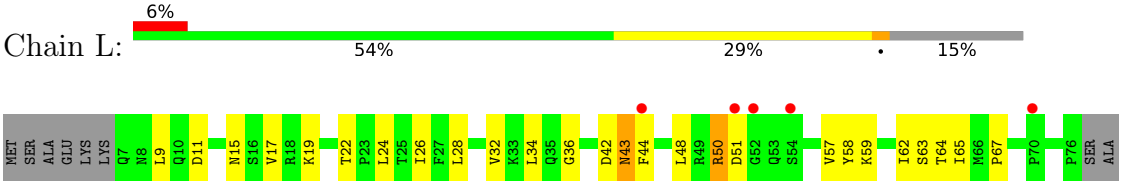
• Molecule 1: RNA-binding protein Hfq

Chain K:



• Molecule 1: RNA-binding protein Hfq

Chain L:

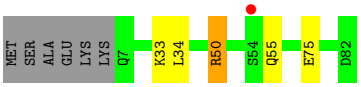


• Molecule 1: RNA-binding protein Hfq

Chain M:

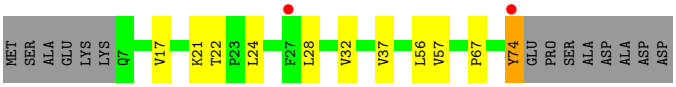
• Molecule 1: RNA-binding protein Hfq

Chain N:



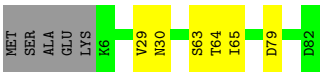
• Molecule 1: RNA-binding protein Hfq

Chain O:



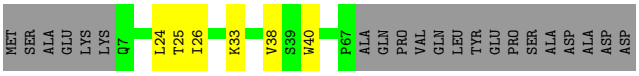
• Molecule 1: RNA-binding protein Hfq

Chain P:



• Molecule 1: RNA-binding protein Hfq

Chain Q:

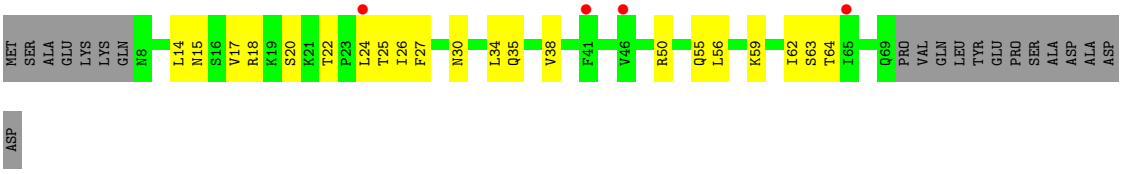


• Molecule 1: RNA-binding protein Hfq

Chain R:

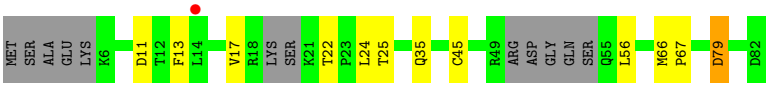
• Molecule 1: RNA-binding protein Hfq

Chain S:



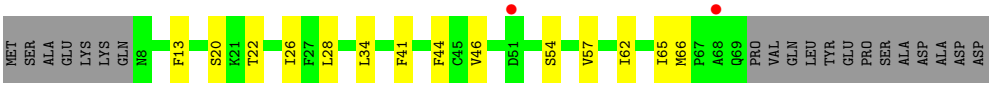
• Molecule 1: RNA-binding protein Hfq

Chain T:



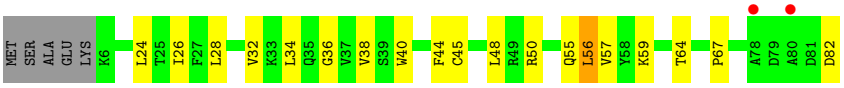
• Molecule 1: RNA-binding protein Hfq

Chain U:



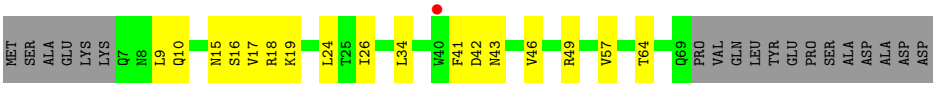
• Molecule 1: RNA-binding protein Hfq

Chain V:



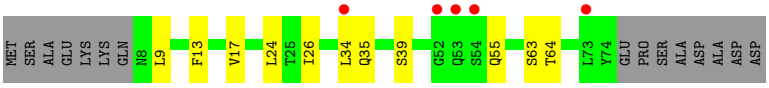
• Molecule 1: RNA-binding protein Hfq

Chain W:



• Molecule 1: RNA-binding protein Hfq

Chain X:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α, β, γ	97.32Å 97.32Å 203.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	87.81 – 2.15 87.81 – 2.15	Depositor EDS
% Data completeness (in resolution range)	97.8 (87.81-2.15) 97.8 (87.81-2.15)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.93 (at 2.14Å)	Xtriage
Refinement program	PHENIX dev_3112	Depositor
R, R_{free}	0.278 , 0.305 0.286 , 0.310	Depositor DCC
R_{free} test set	4990 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	38.1	Xtriage
Anisotropy	0.094	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	0.248 for h,-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	12914	wwPDB-VP
Average B, all atoms (Å^2)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 71.68 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.5170e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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	0.25	0/491	0.40	0/668
1	B	0.27	0/613	0.45	0/835
1	C	0.26	0/560	0.43	0/764
1	D	0.26	0/628	0.44	0/856
1	E	0.27	0/535	0.43	0/728
1	F	0.26	0/552	0.46	0/751
1	G	0.28	0/485	0.45	0/660
1	H	0.27	0/595	0.53	0/812
1	I	0.35	0/493	0.53	0/670
1	J	0.26	0/611	0.45	0/832
1	K	0.25	0/474	0.46	0/645
1	L	0.25	0/562	0.44	0/767
1	M	0.26	0/521	0.44	0/709
1	N	0.26	0/605	0.42	0/824
1	O	0.27	0/552	0.44	0/751
1	P	0.26	0/608	0.43	0/829
1	Q	0.25	0/504	0.43	0/684
1	R	0.26	0/573	0.43	0/779
1	S	0.26	0/487	0.44	0/662
1	T	0.26	0/542	0.44	0/740
1	U	0.26	0/485	0.40	0/661
1	V	0.28	0/615	0.50	1/838 (0.1%)
1	W	0.26	0/485	0.46	0/662
1	X	0.25	0/527	0.42	0/720
All	All	0.27	0/13103	0.45	1/17847 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	V	56	LEU	CB-CG-CD1	-5.33	101.94	111.00

There are no chirality outliers.

There are no planarity outliers.

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	482	0	477	5	0
1	B	601	0	590	5	0
1	C	542	0	548	6	0
1	D	607	0	609	13	0
1	E	522	0	525	8	0
1	F	538	0	550	11	0
1	G	476	0	454	12	0
1	H	583	0	563	13	0
1	I	484	0	486	12	0
1	J	599	0	590	8	0
1	K	465	0	466	7	0
1	L	545	0	550	17	0
1	M	511	0	507	9	0
1	N	593	0	587	3	0
1	O	537	0	534	9	0
1	P	596	0	584	4	0
1	Q	489	0	510	6	0
1	R	559	0	568	8	0
1	S	478	0	472	14	0
1	T	532	0	503	8	0
1	U	476	0	471	9	0
1	V	600	0	595	16	0
1	W	476	0	462	12	0
1	X	513	0	502	6	0
2	A	7	0	0	0	0
2	B	10	0	0	0	0
2	C	4	0	0	0	0
2	D	9	0	0	0	0
2	E	6	0	0	1	0
2	F	3	0	0	0	0
2	G	3	0	0	1	0
2	H	3	0	0	0	0
2	I	3	0	0	0	0
2	J	4	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	K	2	0	0	0	0
2	L	3	0	0	0	0
2	M	10	0	0	0	0
2	N	5	0	0	0	0
2	O	7	0	0	1	0
2	P	10	0	0	1	0
2	Q	3	0	0	0	0
2	R	5	0	0	0	0
2	S	3	0	0	1	0
2	T	1	0	0	0	0
2	U	3	0	0	0	0
2	V	2	0	0	0	0
2	W	3	0	0	0	0
2	X	1	0	0	0	0
All	All	12914	0	12703	190	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 7.

The worst 5 of 190 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:I:17:VAL:HG21	1:I:24:LEU:HD21	1.51	0.92
1:T:45:CYS:HB3	1:T:56:LEU:HD11	1.58	0.86
1:J:76:PRO:O	2:J:101:HOH:O	1.95	0.83
1:W:17:VAL:HG21	1:W:24:LEU:HD21	1.61	0.80
1:G:13:PHE:CZ	1:H:56:LEU:HD11	2.16	0.80

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	61/82 (74%)	60 (98%)	1 (2%)	0	100	100
1	B	75/82 (92%)	72 (96%)	3 (4%)	0	100	100
1	C	69/82 (84%)	66 (96%)	3 (4%)	0	100	100
1	D	78/82 (95%)	72 (92%)	6 (8%)	0	100	100
1	E	66/82 (80%)	63 (96%)	3 (4%)	0	100	100
1	F	67/82 (82%)	64 (96%)	3 (4%)	0	100	100
1	G	60/82 (73%)	57 (95%)	3 (5%)	0	100	100
1	H	74/82 (90%)	66 (89%)	8 (11%)	0	100	100
1	I	61/82 (74%)	59 (97%)	2 (3%)	0	100	100
1	J	75/82 (92%)	71 (95%)	4 (5%)	0	100	100
1	K	58/82 (71%)	56 (97%)	2 (3%)	0	100	100
1	L	70/82 (85%)	66 (94%)	4 (6%)	0	100	100
1	M	64/82 (78%)	63 (98%)	1 (2%)	0	100	100
1	N	74/82 (90%)	71 (96%)	3 (4%)	0	100	100
1	O	67/82 (82%)	64 (96%)	3 (4%)	0	100	100
1	P	75/82 (92%)	72 (96%)	3 (4%)	0	100	100
1	Q	61/82 (74%)	58 (95%)	3 (5%)	0	100	100
1	R	70/82 (85%)	65 (93%)	5 (7%)	0	100	100
1	S	60/82 (73%)	57 (95%)	3 (5%)	0	100	100
1	T	64/82 (78%)	61 (95%)	3 (5%)	0	100	100
1	U	60/82 (73%)	57 (95%)	3 (5%)	0	100	100
1	V	76/82 (93%)	71 (93%)	5 (7%)	0	100	100
1	W	61/82 (74%)	59 (97%)	2 (3%)	0	100	100
1	X	66/82 (80%)	61 (92%)	5 (8%)	0	100	100
All	All	1612/1968 (82%)	1531 (95%)	81 (5%)	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	51/74 (69%)	51 (100%)	0	100	100
1	B	67/74 (90%)	66 (98%)	1 (2%)	65	69
1	C	60/74 (81%)	58 (97%)	2 (3%)	38	37
1	D	68/74 (92%)	68 (100%)	0	100	100
1	E	58/74 (78%)	58 (100%)	0	100	100
1	F	60/74 (81%)	59 (98%)	1 (2%)	60	65
1	G	48/74 (65%)	46 (96%)	2 (4%)	30	28
1	H	64/74 (86%)	62 (97%)	2 (3%)	40	39
1	I	52/74 (70%)	50 (96%)	2 (4%)	33	31
1	J	66/74 (89%)	66 (100%)	0	100	100
1	K	51/74 (69%)	47 (92%)	4 (8%)	12	7
1	L	62/74 (84%)	57 (92%)	5 (8%)	11	7
1	M	56/74 (76%)	54 (96%)	2 (4%)	35	33
1	N	66/74 (89%)	64 (97%)	2 (3%)	41	40
1	O	58/74 (78%)	57 (98%)	1 (2%)	60	65
1	P	66/74 (89%)	65 (98%)	1 (2%)	65	69
1	Q	56/74 (76%)	56 (100%)	0	100	100
1	R	63/74 (85%)	59 (94%)	4 (6%)	18	13
1	S	51/74 (69%)	49 (96%)	2 (4%)	32	30
1	T	57/74 (77%)	54 (95%)	3 (5%)	22	19
1	U	52/74 (70%)	51 (98%)	1 (2%)	57	61
1	V	66/74 (89%)	65 (98%)	1 (2%)	65	69
1	W	51/74 (69%)	49 (96%)	2 (4%)	32	30
1	X	55/74 (74%)	50 (91%)	5 (9%)	9	5
All	All	1404/1776 (79%)	1361 (97%)	43 (3%)	42	39

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	R	63[B]	SER
1	V	82	ASP
1	S	50	ARG
1	T	67	PRO

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Mol	Chain	Res	Type
1	W	49	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	O	43	ASN
1	R	72	GLN
1	S	55	GLN
1	S	35	GLN
1	M	10	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	63/82 (76%)	-0.18	0 100 100	21, 44, 59, 79	0
1	B	77/82 (93%)	-0.01	1 (1%) 77 82	17, 43, 65, 84	0
1	C	69/82 (84%)	-0.06	2 (2%) 51 61	14, 40, 68, 89	0
1	D	77/82 (93%)	-0.11	1 (1%) 77 82	14, 39, 62, 81	0
1	E	67/82 (81%)	-0.04	0 100 100	19, 44, 66, 76	0
1	F	68/82 (82%)	0.03	2 (2%) 51 61	18, 41, 76, 96	0
1	G	64/82 (78%)	0.51	5 (7%) 13 18	38, 78, 98, 114	0
1	H	76/82 (92%)	0.48	7 (9%) 9 13	47, 69, 89, 100	0
1	I	63/82 (76%)	0.24	4 (6%) 20 27	39, 60, 81, 90	0
1	J	77/82 (93%)	0.01	1 (1%) 77 82	30, 50, 91, 104	0
1	K	60/82 (73%)	0.16	2 (3%) 46 55	42, 62, 80, 96	0
1	L	70/82 (85%)	0.37	5 (7%) 16 22	42, 65, 97, 124	0
1	M	66/82 (80%)	0.15	0 100 100	30, 52, 69, 89	0
1	N	76/82 (92%)	0.01	1 (1%) 77 82	28, 47, 66, 74	0
1	O	68/82 (82%)	0.20	2 (2%) 51 61	30, 48, 77, 92	0
1	P	77/82 (93%)	0.05	0 100 100	26, 42, 67, 86	0
1	Q	61/82 (74%)	0.02	0 100 100	30, 44, 61, 94	0
1	R	71/82 (86%)	0.02	0 100 100	25, 44, 73, 87	0
1	S	62/82 (75%)	0.40	4 (6%) 18 25	33, 72, 88, 95	0
1	T	70/82 (85%)	0.43	1 (1%) 75 80	40, 69, 89, 106	0
1	U	62/82 (75%)	0.07	2 (3%) 47 56	39, 58, 76, 90	0
1	V	77/82 (93%)	0.06	2 (2%) 56 64	38, 56, 84, 101	0
1	W	63/82 (76%)	0.14	1 (1%) 72 77	36, 61, 79, 91	0
1	X	67/82 (81%)	0.39	5 (7%) 14 19	42, 68, 92, 102	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
All	All	1651/1968 (83%)	0.14	48 (2%) 51 61	14, 53, 86, 124	0

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	O	74	TYR	5.1
1	L	54	SER	4.9
1	L	44	PHE	3.9
1	H	44	PHE	3.7
1	T	14	LEU	3.3

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.