Full wwPDB X-ray Structure Validation Report (i)

May 29, 2020 – 06:57 am BST

PDB ID	:	5FIY
Title	:	crystal structure of coiled coil domain of PAWR
Authors	:	Tiruttani Subhramanyam, U.K.; Kubicek, J.; Eidhoff, U.B.; Labahn, J.
Deposited on	:	2015-10-03
Resolution	:	3.00 Å(reported)

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

|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

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 3.00 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	Percentile Ranks	Value
Rfree		0.312
Clashscore		3
Ramachandran outliers		0
Sidechain outliers		0
RSRZ outliers		5.1%

Worse ... *Better*

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
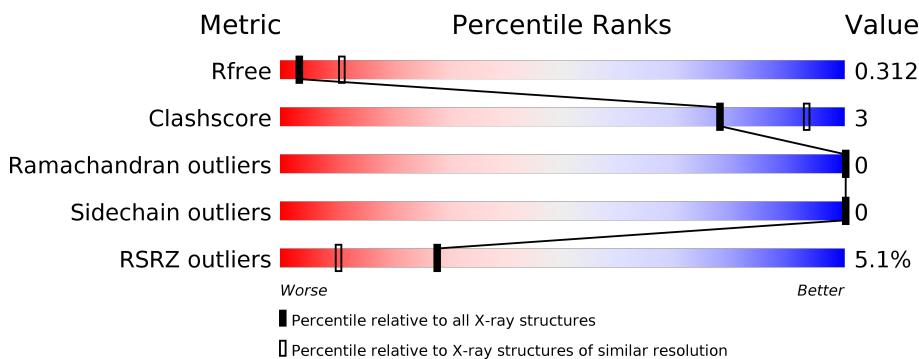
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 <=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	104	3% / 70% 5% 25%
1	B	104	70% 5% 25%
1	C	104	2% / 70% 5% 25%
1	D	104	2% / 66% 8% 26%
1	E	104	4% / 71% • 25%
1	F	104	7% / 34% 5% 62%
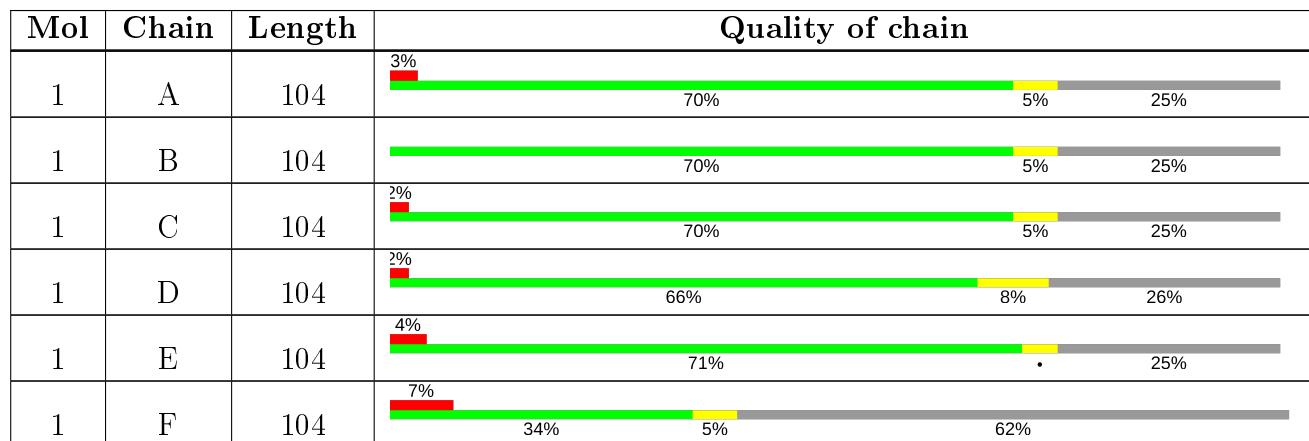
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Mol	Chain	Length	Quality of chain
1	G	104	5% · 34% · 5% · 62%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	K	D	403	-	-	-	X
2	K	F	401	-	-	-	X

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3958 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 PRKC APOPTOSIS WT1 REGULATOR PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	78	Total	C	N	O	Se	0	1	0
			653	399	113	138	3			
1	B	78	Total	C	N	O	Se	0	2	0
			660	400	115	142	3			
1	C	78	Total	C	N	O	Se	0	2	0
			660	400	115	142	3			
1	D	77	Total	C	N	O	Se	0	2	0
			651	394	113	141	3			
1	E	78	Total	C	N	O	Se	0	2	0
			648	393	113	139	3			
1	F	40	Total	C	N	O	Se	0	0	0
			323	195	58	68	2			
1	G	40	Total	C	N	O	Se	0	0	0
			318	193	58	65	2			

There are 77 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	229	ALA	-	expression tag	UNP Q62627
A	230	SER	-	expression tag	UNP Q62627
A	231	TRP	-	expression tag	UNP Q62627
A	232	SER	-	expression tag	UNP Q62627
A	233	HIS	-	expression tag	UNP Q62627
A	234	PRO	-	expression tag	UNP Q62627
A	235	GLN	-	expression tag	UNP Q62627
A	236	PHE	-	expression tag	UNP Q62627
A	237	GLU	-	expression tag	UNP Q62627
A	238	LYS	-	expression tag	UNP Q62627
A	239	ALA	-	expression tag	UNP Q62627
B	229	ALA	-	expression tag	UNP Q62627
B	230	SER	-	expression tag	UNP Q62627
B	231	TRP	-	expression tag	UNP Q62627
B	232	SER	-	expression tag	UNP Q62627

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Chain	Residue	Modelled	Actual	Comment	Reference
B	233	HIS	-	expression tag	UNP Q62627
B	234	PRO	-	expression tag	UNP Q62627
B	235	GLN	-	expression tag	UNP Q62627
B	236	PHE	-	expression tag	UNP Q62627
B	237	GLU	-	expression tag	UNP Q62627
B	238	LYS	-	expression tag	UNP Q62627
B	239	ALA	-	expression tag	UNP Q62627
C	229	ALA	-	expression tag	UNP Q62627
C	230	SER	-	expression tag	UNP Q62627
C	231	TRP	-	expression tag	UNP Q62627
C	232	SER	-	expression tag	UNP Q62627
C	233	HIS	-	expression tag	UNP Q62627
C	234	PRO	-	expression tag	UNP Q62627
C	235	GLN	-	expression tag	UNP Q62627
C	236	PHE	-	expression tag	UNP Q62627
C	237	GLU	-	expression tag	UNP Q62627
C	238	LYS	-	expression tag	UNP Q62627
C	239	ALA	-	expression tag	UNP Q62627
D	229	ALA	-	expression tag	UNP Q62627
D	230	SER	-	expression tag	UNP Q62627
D	231	TRP	-	expression tag	UNP Q62627
D	232	SER	-	expression tag	UNP Q62627
D	233	HIS	-	expression tag	UNP Q62627
D	234	PRO	-	expression tag	UNP Q62627
D	235	GLN	-	expression tag	UNP Q62627
D	236	PHE	-	expression tag	UNP Q62627
D	237	GLU	-	expression tag	UNP Q62627
D	238	LYS	-	expression tag	UNP Q62627
D	239	ALA	-	expression tag	UNP Q62627
E	229	ALA	-	expression tag	UNP Q62627
E	230	SER	-	expression tag	UNP Q62627
E	231	TRP	-	expression tag	UNP Q62627
E	232	SER	-	expression tag	UNP Q62627
E	233	HIS	-	expression tag	UNP Q62627
E	234	PRO	-	expression tag	UNP Q62627
E	235	GLN	-	expression tag	UNP Q62627
E	236	PHE	-	expression tag	UNP Q62627
E	237	GLU	-	expression tag	UNP Q62627
E	238	LYS	-	expression tag	UNP Q62627
E	239	ALA	-	expression tag	UNP Q62627
F	229	ALA	-	expression tag	UNP Q62627
F	230	SER	-	expression tag	UNP Q62627

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Chain	Residue	Modelled	Actual	Comment	Reference
F	231	TRP	-	expression tag	UNP Q62627
F	232	SER	-	expression tag	UNP Q62627
F	233	HIS	-	expression tag	UNP Q62627
F	234	PRO	-	expression tag	UNP Q62627
F	235	GLN	-	expression tag	UNP Q62627
F	236	PHE	-	expression tag	UNP Q62627
F	237	GLU	-	expression tag	UNP Q62627
F	238	LYS	-	expression tag	UNP Q62627
F	239	ALA	-	expression tag	UNP Q62627
G	229	ALA	-	expression tag	UNP Q62627
G	230	SER	-	expression tag	UNP Q62627
G	231	TRP	-	expression tag	UNP Q62627
G	232	SER	-	expression tag	UNP Q62627
G	233	HIS	-	expression tag	UNP Q62627
G	234	PRO	-	expression tag	UNP Q62627
G	235	GLN	-	expression tag	UNP Q62627
G	236	PHE	-	expression tag	UNP Q62627
G	237	GLU	-	expression tag	UNP Q62627
G	238	LYS	-	expression tag	UNP Q62627
G	239	ALA	-	expression tag	UNP Q62627

- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	3	Total 3	K 3	0	0
2	E	3	Total 3	K 3	0	0
2	B	3	Total 3	K 3	0	0
2	C	4	Total 4	K 4	0	0
2	A	3	Total 3	K 3	0	0
2	F	2	Total 2	K 2	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	7	Total 7	O 7	0	0

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| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	7	Total 7	O 7	0	0
3	C	4	Total 4	O 4	0	0
3	D	2	Total 2	O 2	0	0
3	E	5	Total 5	O 5	0	0
3	G	2	Total 2	O 2	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA 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: PRKC APOPTOSIS WT1 REGULATOR PROTEIN
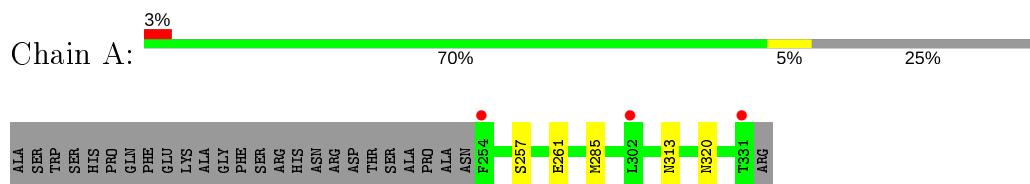
- Molecule 1: PRKC APOPTOSIS WT1 REGULATOR PROTEIN

- Molecule 1: PRKC APOPTOSIS WT1 REGULATOR PROTEIN


- Molecule 1: PRKC APOPTOSIS WT1 REGULATOR PROTEIN

- Molecule 1: PRKC APOPTOSIS WT1 REGULATOR PROTEIN

- Molecule 1: PRKC APOPTOSIS WT1 REGULATOR PROTEIN

Chain F:

• **Molecule 1: PRKC APOPTOSIS WT1 REGULATOR PROTEIN**

Chain G:
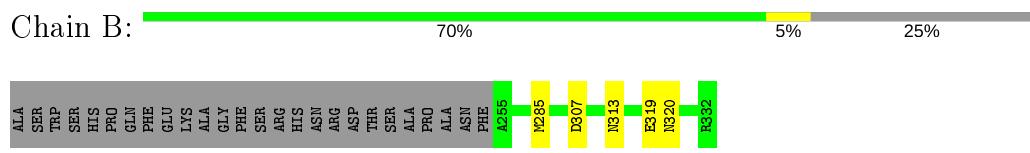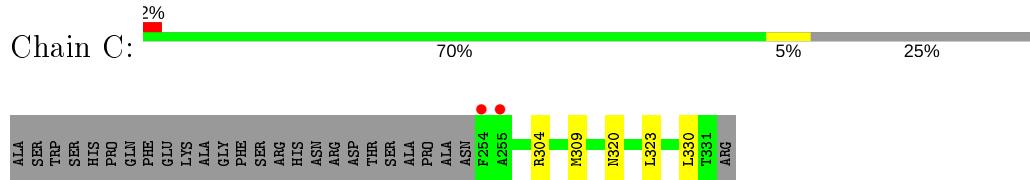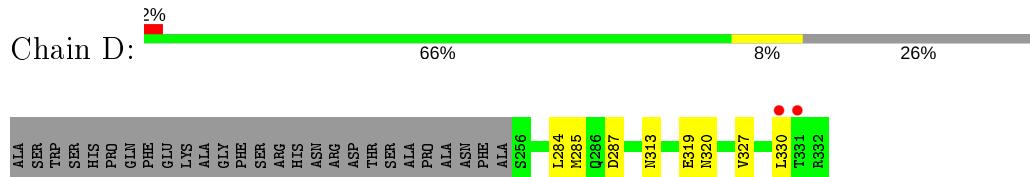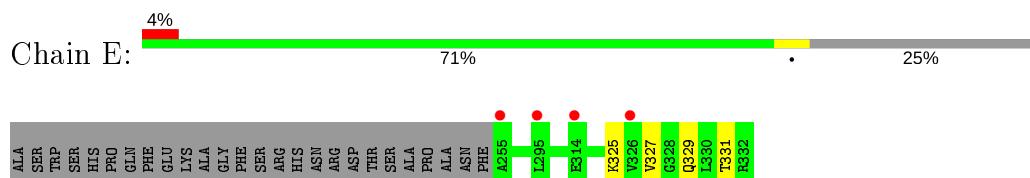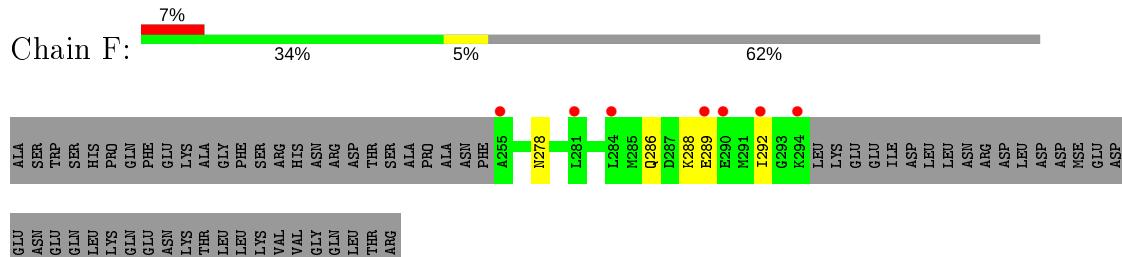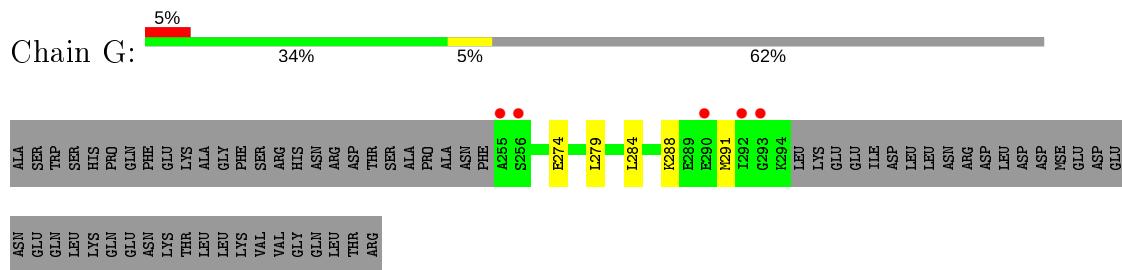
4　Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	114.99Å　114.99Å　121.81Å 90.00°　　90.00°　　90.00°	Depositor
Resolution (Å)	41.81　−　3.00	Depositor
	41.81　−　3.00	EDS
% Data completeness	99.7 (41.81-3.00)	Depositor
(in resolution range)	99.6 (41.81-3.00)	EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.43 (at 3.01Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.245　,　0.294	Depositor
	0.269　,　0.312	DCC
R_{free} test set	1646 reflections (9.76%)	wwPDB-VP
Wilson B-factor (Å^2)	74.0	Xtriage
Anisotropy	0.480	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 74.9	EDS
L-test for twinning[2]	$< |L| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	3958	wwPDB-VP
Average B, all atoms (Å^2)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.03% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: K

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	0/650	0.43	0/860
1	B	0.31	0/656	0.47	0/868
1	C	0.30	0/656	0.46	0/868
1	D	0.32	0/647	0.46	0/857
1	E	0.29	0/644	0.47	0/855
1	F	0.27	0/320	0.48	0/421
1	G	0.21	0/315	0.43	0/415
All	All	0.30	0/3888	0.46	0/5144

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 (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	653	0	654	5	0
1	B	660	0	664	5	0
1	C	660	0	664	6	0
1	D	651	0	648	7	0
1	E	648	0	637	2	0
1	F	323	0	324	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	318	0	317	5	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
2	C	4	0	0	0	0
2	D	3	0	0	0	0
2	E	3	0	0	0	0
2	F	2	0	0	0	0
3	A	7	0	0	0	0
3	B	7	0	0	0	0
3	C	4	0	0	0	0
3	D	2	0	0	0	0
3	E	5	0	0	0	0
3	G	2	0	0	0	0
All	All	3958	0	3908	23	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 (23) 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:F:278:ASN:ND2	1:G:274:GLU:OE2	2.27	0.67
1:A:320:ASN:ND2	1:B:320:ASN:OD1	2.22	0.67
1:G:284:LEU:HG	1:G:288:LYS:HE2	1.78	0.66
1:F:286:GLN:HA	1:F:289:GLU:HB2	1.82	0.61
1:G:284:LEU:O	1:G:288:LYS:HG2	2.03	0.58
1:A:320:ASN:HD21	1:B:319[B]:GLU:HG2	1.69	0.56
1:F:288:LYS:O	1:F:292:ILE:HG13	2.06	0.55
1:A:257:SER:O	1:A:261:GLU:HG2	2.09	0.53
1:F:292:ILE:HD13	1:G:291:MSE:HG2	1.90	0.53
1:E:325:LYS:O	1:E:329:GLN:HG3	2.13	0.49
1:C:323:LEU:HD22	1:D:327:VAL:HG21	1.94	0.49
1:C:320:ASN:OD1	1:D:320:ASN:ND2	2.32	0.47
1:A:313:ASN:ND2	1:B:313:ASN:OD1	2.48	0.47
1:G:279:LEU:HA	1:G:279:LEU:HD23	1.82	0.46
1:C:309:MSE:HE1	1:D:313:ASN:HB2	1.98	0.44
1:C:330:LEU:HD13	1:D:330:LEU:O	2.17	0.44
1:C:320:ASN:ND2	1:D:319[B]:GLU:HG2	2.33	0.43
1:B:285:MSE:HB2	1:B:285:MSE:HE2	1.95	0.43
1:D:284:LEU:O	1:D:287:ASP:HB2	2.20	0.42
1:A:285:MSE:HB2	1:A:285:MSE:HE2	1.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:327:VAL:O	1:E:331:THR:HG23	2.21	0.41
1:D:285:MSE:HE2	1:D:285:MSE:HB2	1.98	0.41
1:B:307:ASP:HB3	1:C:304:ARG:NH1	2.35	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	77/104 (74%)	76 (99%)	1 (1%)	0	100	100
1	B	78/104 (75%)	78 (100%)	0	0	100	100
1	C	78/104 (75%)	78 (100%)	0	0	100	100
1	D	77/104 (74%)	77 (100%)	0	0	100	100
1	E	78/104 (75%)	78 (100%)	0	0	100	100
1	F	38/104 (36%)	37 (97%)	1 (3%)	0	100	100
1	G	38/104 (36%)	38 (100%)	0	0	100	100
All	All	464/728 (64%)	462 (100%)	2 (0%)	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	74/93 (80%)	74 (100%)	0	100	100
1	B	76/93 (82%)	76 (100%)	0	100	100
1	C	76/93 (82%)	76 (100%)	0	100	100
1	D	75/93 (81%)	75 (100%)	0	100	100
1	E	72/93 (77%)	72 (100%)	0	100	100
1	F	36/93 (39%)	36 (100%)	0	100	100
1	G	34/93 (37%)	34 (100%)	0	100	100
All	All	443/651 (68%)	443 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some 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 carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 18 ligands modelled in this entry, 18 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 (i)

6.1 Protein, DNA and RNA chains (i)

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	75/104 (72%)	0.03	3 (4%) 38	15	28, 66, 95, 106	0
1	B	75/104 (72%)	-0.02	0 100	100	28, 62, 87, 103	0
1	C	75/104 (72%)	0.01	2 (2%) 54	26	39, 66, 96, 121	0
1	D	74/104 (71%)	0.09	2 (2%) 54	26	37, 72, 114, 120	0
1	E	75/104 (72%)	0.26	4 (5%) 26	10	25, 91, 123, 128	0
1	F	38/104 (36%)	0.66	7 (18%) 1	0	65, 100, 149, 155	0
1	G	38/104 (36%)	0.37	5 (13%) 3	1	64, 101, 147, 155	0
All	All	450/728 (61%)	0.15	23 (5%) 28	10	25, 74, 123, 155	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	255	ALA	10.6
1	C	254	PHE	4.1
1	G	293	GLY	3.9
1	G	256	SER	3.6
1	C	255	ALA	3.4
1	F	289	GLU	3.2
1	E	326	VAL	2.8
1	E	295	LEU	2.8
1	G	290	GLU	2.8
1	G	292	ILE	2.7
1	G	255	ALA	2.6
1	D	331	THR	2.6
1	F	292	ILE	2.6
1	F	290	GLU	2.6
1	F	284	LEU	2.6
1	F	255	ALA	2.5
1	A	254	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	331	THR	2.3
1	A	302	LEU	2.2
1	F	294	LYS	2.2
1	D	330	LEU	2.2
1	E	314	GLU	2.1
1	F	281	LEU	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 carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	K	F	401	1/1	0.49	0.43	194,194,194,194	0
2	K	D	403	1/1	0.79	0.73	202,202,202,202	0
2	K	C	402	1/1	0.84	0.18	112,112,112,112	0
2	K	B	402	1/1	0.89	0.26	103,103,103,103	0
2	K	F	402	1/1	0.90	0.31	94,94,94,94	0
2	K	C	404	1/1	0.91	0.39	86,86,86,86	0
2	K	D	402	1/1	0.92	0.25	103,103,103,103	0
2	K	A	402	1/1	0.92	0.29	73,73,73,73	0
2	K	E	402	1/1	0.93	0.22	117,117,117,117	0
2	K	A	401	1/1	0.95	0.19	92,92,92,92	0
2	K	E	401	1/1	0.95	0.46	87,87,87,87	0
2	K	A	403	1/1	0.97	0.40	69,69,69,69	0
2	K	D	401	1/1	0.97	0.28	85,85,85,85	0
2	K	B	403	1/1	0.97	0.28	62,62,62,62	0
2	K	C	403	1/1	0.98	0.41	75,75,75,75	0
2	K	E	403	1/1	0.98	0.41	56,56,56,56	0
2	K	C	401	1/1	0.98	0.36	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	K	B	401	1/1	0.99	0.25	60,60,60,60	0

6.5 Other polymers (i)

There are no such residues in this entry.