WORLDWIDE wwPDB PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 03:44 PM GMT

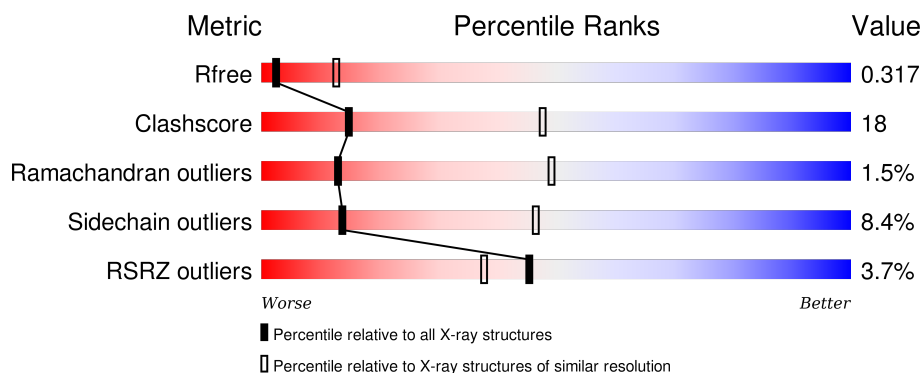|		
PDB ID	:	4DAY
Title	:	Crystal structure of the RMI core complex with MM2 peptide from FANCM
Authors	:	Hoadley, K.A.; Keck, J.L.
Deposited on	:	2012-01-13
Resolution	:	3.30 Å(reported)

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}	91344	2060 (3.40-3.20)
Clashscore	102246	1058 (3.38-3.22)
Ramachandran outliers	100387	1038 (3.38-3.22)
Sidechain outliers	100360	1037 (3.38-3.22)
RSRZ outliers	91569	2070 (3.40-3.20)

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. 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	157	
2	B	150	
3	C	37	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2098 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 RecQ-mediated genome instability protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	144	Total	C	N	O	S	0	0	0
			1121	723	178	211	9			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	469	GLY	-	EXPRESSION TAG	UNP Q9H9A7
A	470	SER	-	EXPRESSION TAG	UNP Q9H9A7
A	471	HIS	-	EXPRESSION TAG	UNP Q9H9A7
A	472	MET	-	EXPRESSION TAG	UNP Q9H9A7

- Molecule 2 is a protein called RecQ-mediated genome instability protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	113	Total	C	N	O	S	0	0	0
			882	548	167	158	9			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	GLY	-	EXPRESSION TAG	UNP Q96E14
B	-1	SER	-	EXPRESSION TAG	UNP Q96E14
B	0	HIS	-	EXPRESSION TAG	UNP Q96E14

- Molecule 3 is a protein called Fanconi anemia group M protein.

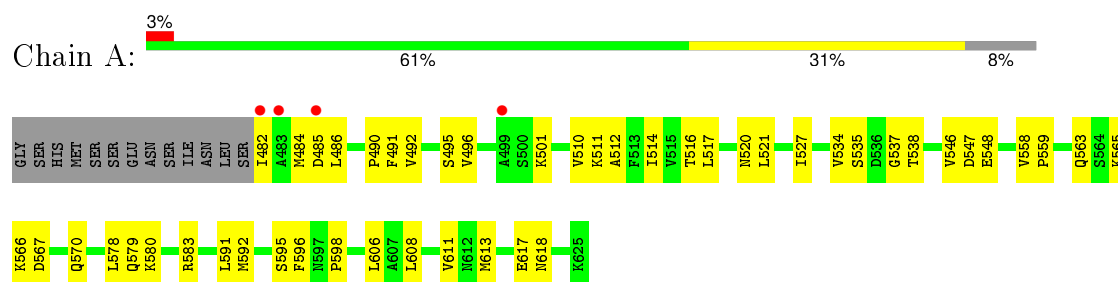| Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	12	Total	C	N	O	S	0	0	0
			95	64	12	18	1			

There are 3 discrepancies between the modelled and reference sequences:

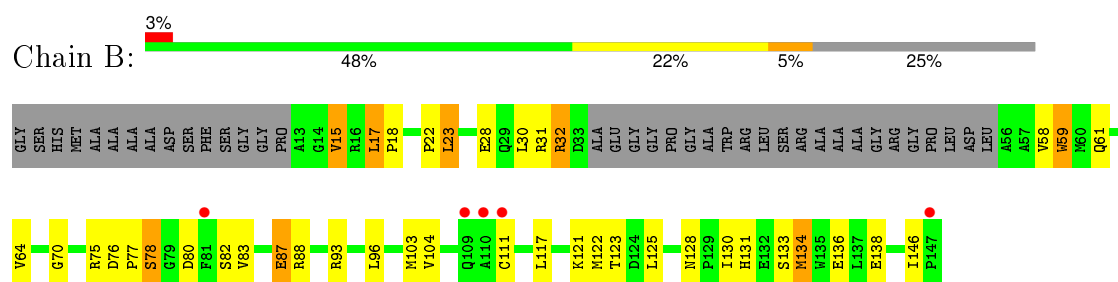| Chain	Residue	Modelled	Actual	Comment	Reference
C	1215	GLY	-	EXPRESSION TAG	UNP Q8IYD8
C	1216	HIS	-	EXPRESSION TAG	UNP Q8IYD8
C	1217	MET	-	EXPRESSION TAG	UNP Q8IYD8

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.
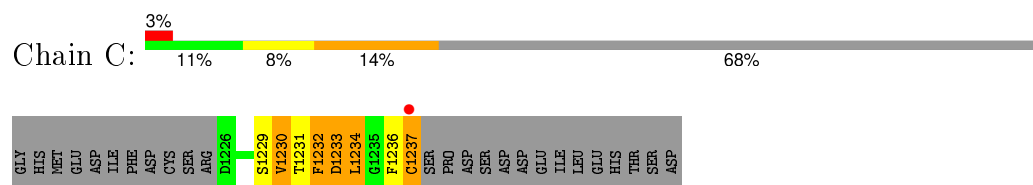
- Molecule 1: RecQ-mediated genome instability protein 1

- Molecule 2: RecQ-mediated genome instability protein 2

- Molecule 3: Fanconi anemia group M protein

4   Data and refinement statistics (i)

Property	Value	Source
Space group	I 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	75.31Å 96.44Å 99.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.30 48.22 – 3.29	Depositor EDS
% Data completeness (in resolution range)	99.7 (50.00-3.30) 99.1 (48.22-3.29)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.30 (at 3.25Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.216 , 0.325 0.210 , 0.317	Depositor DCC
R_{free} test set	270 reflections (5.03%)	DCC
Wilson B-factor (Å^2)	89.1	Xtriage
Anisotropy	0.173	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 60.8	EDS
Estimated twinning fraction	0.001 for -h,-l,-k	Xtriage
L-test for twinning[2]	$< |L| > = 0.48, < L^2 > = 0.32$	Xtriage
Outliers	0 of 5686 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	2098	wwPDB-VP
Average B, all atoms (Å^2)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.46% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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	0.48	0/1139	0.65	0/1538
2	B	0.53	0/899	0.68	0/1215
3	C	0.69	0/97	0.92	0/130
All	All	0.51	0/2135	0.68	0/2883

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	1121	0	1170	44	0
2	B	882	0	894	28	0
3	C	95	0	85	20	0
All	All	2098	0	2149	75	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 18.

All (75) 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:520:ASN:HD22	3:C:1229:SER:HB3	1.32	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:520:ASN:HD22	3:C:1229:SER:CB	1.83	0.90
1:A:521:LEU:H	3:C:1229:SER:HA	1.37	0.87
1:A:580:LYS:HG2	1:A:583:ARG:HH12	1.40	0.86
2:B:103:MET:HG3	2:B:123:THR:HB	1.69	0.74
1:A:520:ASN:ND2	3:C:1229:SER:HB3	2.04	0.71
1:A:595:SER:HB2	1:A:606:LEU:HD11	1.73	0.71
1:A:527:ILE:HA	1:A:558:VAL:HG21	1.74	0.70
1:A:592:MET:HG2	1:A:608:LEU:HD23	1.74	0.69
3:C:1229:SER:HB2	3:C:1231:THR:HG23	1.74	0.69
1:A:538:THR:HG22	2:B:146:ILE:HD11	1.79	0.65
2:B:121:LYS:HG2	2:B:122:MET:N	2.12	0.65
3:C:1233:ASP:OD2	3:C:1233:ASP:N	2.30	0.65
1:A:484:MET:HE3	1:A:486:LEU:HD12	1.81	0.62
2:B:103:MET:HB3	2:B:125:LEU:HD11	1.84	0.60
2:B:70:GLY:HA3	2:B:87:GLU:HG2	1.84	0.59
1:A:558:VAL:HB	1:A:559:PRO:HD3	1.85	0.59
1:A:567:ASP:HB3	1:A:570:GLN:HG2	1.85	0.58
2:B:121:LYS:HG2	2:B:122:MET:H	1.69	0.57
1:A:516:THR:HG21	2:B:15:VAL:HG21	1.86	0.57
2:B:121:LYS:HB2	3:C:1234:LEU:HD22	1.86	0.56
1:A:546:VAL:CG1	1:A:548:GLU:HB2	2.35	0.56
1:A:485:ASP:HB2	1:A:496:VAL:HG11	1.87	0.56
1:A:527:ILE:CA	1:A:558:VAL:HG21	2.36	0.56
3:C:1230:VAL:O	3:C:1230:VAL:HG23	2.06	0.55
2:B:22:PRO:HB2	2:B:59:TRP:HB2	1.88	0.55
2:B:76:ASP:HB2	2:B:77:PRO:HD3	1.89	0.54
1:A:546:VAL:HG12	1:A:548:GLU:HB2	1.89	0.54
3:C:1229:SER:O	3:C:1231:THR:N	2.42	0.53
1:A:517:LEU:HD12	3:C:1231:THR:HA	1.89	0.53
3:C:1229:SER:HB2	3:C:1231:THR:CG2	2.38	0.53
2:B:28:GLU:H	2:B:78:SER:HG	1.56	0.52
2:B:17:LEU:HB2	2:B:18:PRO:HD2	1.93	0.51
1:A:514:ILE:HA	1:A:534:VAL:HG12	1.92	0.51
2:B:61:GLN:O	2:B:76:ASP:HB3	2.11	0.51
3:C:1236:PHE:O	3:C:1237:CYS:HB2	2.11	0.51
1:A:495:SER:HB3	1:A:538:THR:HB	1.92	0.51
1:A:592:MET:HG2	1:A:608:LEU:CD2	2.41	0.50
2:B:128:ASN:HB3	2:B:131:HIS:CD2	2.47	0.50
1:A:580:LYS:HG2	1:A:583:ARG:NH1	2.18	0.49
1:A:596:PHE:CE2	1:A:598:PRO:HA	2.47	0.49
1:A:591:LEU:HG	1:A:611:VAL:HG12	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:64:VAL:HG21	2:B:96:LEU:HD11	1.94	0.49
1:A:520:ASN:HA	3:C:1229:SER:HB3	1.95	0.49
2:B:59:TRP:C	2:B:59:TRP:CD1	2.85	0.49
2:B:83:VAL:HG12	2:B:117:LEU:HB2	1.95	0.48
1:A:563:GLN:C	1:A:565:LYS:H	2.17	0.48
2:B:23:LEU:H	2:B:58:VAL:HA	1.78	0.47
2:B:76:ASP:HB2	2:B:77:PRO:CD	2.45	0.47
2:B:75:ARG:HG3	2:B:80:ASP:OD1	2.15	0.47
1:A:583:ARG:HD2	2:B:93:ARG:CZ	2.47	0.45
1:A:520:ASN:HA	3:C:1229:SER:CB	2.46	0.45
2:B:121:LYS:HB2	3:C:1234:LEU:CD2	2.47	0.45
1:A:613:MET:O	1:A:617:GLU:HG2	2.17	0.45
1:A:517:LEU:HD12	3:C:1232:PHE:H	1.82	0.45
1:A:537:GLY:HA2	2:B:22:PRO:O	2.17	0.45
2:B:130:ILE:CG2	2:B:134:MET:HG3	2.47	0.44
2:B:15:VAL:HG23	2:B:17:LEU:HD23	1.99	0.44
1:A:510:VAL:O	1:A:591:LEU:HA	2.18	0.44
1:A:565:LYS:O	1:A:566:LYS:C	2.56	0.43
3:C:1229:SER:O	3:C:1231:THR:HG23	2.18	0.43
1:A:578:LEU:HG	3:C:1230:VAL:CG1	2.49	0.43
1:A:563:GLN:C	1:A:565:LYS:N	2.71	0.43
2:B:28:GLU:HG2	2:B:32:ARG:HG3	2.01	0.42
1:A:511:LYS:HB2	1:A:591:LEU:HD23	2.02	0.42
1:A:520:ASN:ND2	3:C:1229:SER:CB	2.65	0.42
1:A:618:ASN:HA	1:A:618:ASN:HD22	1.69	0.42
1:A:578:LEU:HD12	1:A:578:LEU:HA	1.87	0.41
2:B:31:ARG:NH2	2:B:32:ARG:CZ	2.83	0.41
1:A:490:PRO:HG2	1:A:491:PHE:CD2	2.55	0.41
1:A:491:PHE:HB3	1:A:591:LEU:HD22	2.01	0.41
1:A:485:ASP:O	1:A:492:VAL:HG11	2.20	0.41
1:A:517:LEU:HD12	3:C:1232:PHE:N	2.36	0.41
1:A:512:ALA:HB1	1:A:535:SER:O	2.21	0.40
2:B:104:VAL:HG22	2:B:122:MET:HG3	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	142/157 (90%)	126 (89%)	16 (11%)	0	100	100
2	B	109/150 (73%)	103 (94%)	3 (3%)	3 (3%)	6	34
3	C	10/37 (27%)	7 (70%)	2 (20%)	1 (10%)	1	5
All	All	261/344 (76%)	236 (90%)	21 (8%)	4 (2%)	13	49

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	87	GLU
2	B	111	CYS
2	B	138	GLU
3	C	1230	VAL

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	131/143 (92%)	127 (97%)	4 (3%)	47	79
2	B	97/117 (83%)	85 (88%)	12 (12%)	6	25
3	C	11/35 (31%)	7 (64%)	4 (36%)	0	1
All	All	239/295 (81%)	219 (92%)	20 (8%)	14	46

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	482	ILE
1	A	501	LYS
1	A	547	ASP
1	A	579	GLN
2	B	15	VAL
2	B	17	LEU
2	B	23	LEU
2	B	30	LEU
2	B	32	ARG
2	B	59	TRP
2	B	78	SER
2	B	82	SER
2	B	88	ARG
2	B	133	SER
2	B	134	MET
2	B	136	GLU
3	C	1232	PHE
3	C	1233	ASP
3	C	1234	LEU
3	C	1237	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	520	ASN
1	A	618	ASN
2	B	29	GLN
2	B	131	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å²)	Q<0.9
1	A	144/157 (91%)	0.12	4 (2%)	56	50	66, 88, 118, 140	0
2	B	113/150 (75%)	0.43	5 (4%)	38	31	70, 91, 125, 143	0
3	C	12/37 (32%)	0.47	1 (8%)	14	11	82, 89, 109, 114	0
All	All	269/344 (78%)	0.27	10 (3%)	45	38	66, 89, 122, 143	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	111	CYS	5.3
2	B	109	GLN	4.5
2	B	110	ALA	4.3
2	B	147	PRO	3.4
3	C	1237	CYS	3.0
1	A	482	ILE	2.9
1	A	485	ASP	2.6
1	A	483	ALA	2.1
1	A	499	ALA	2.1
2	B	81	PHE	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates 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.