



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:06 AM GMT

PDB ID : 2PEM
Title : Crystal structure of RbcX in complex with substrate
Authors : Saschenbrecker, S.; Bracher, A.; Vasudeva Rao, K.; Vasudeva Rao, B.; Hartl, F.U.; Hayer-Hartl, M.
Deposited on : 2007-04-03
Resolution : 2.95 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

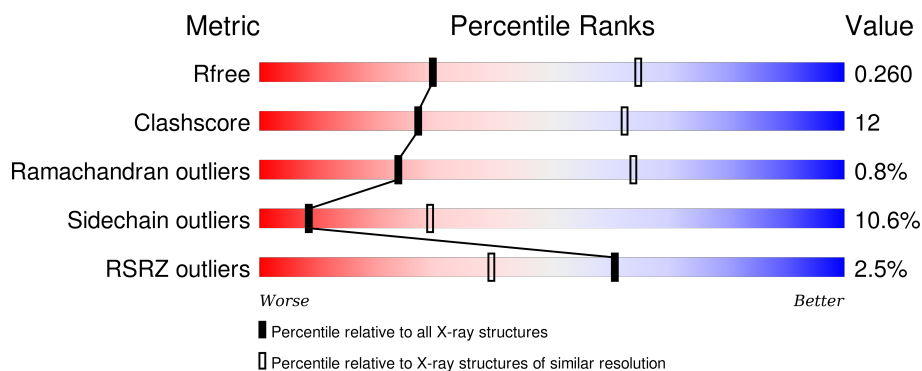
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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	2184 (3.00-2.92)
Clashscore	102246	2552 (3.00-2.92)
Ramachandran outliers	100387	2468 (3.00-2.92)
Sidechain outliers	100360	2471 (3.00-2.92)
RSRZ outliers	91569	2201 (3.00-2.92)

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 $\leq 5\%$. 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	134	<div> <div>51%</div> <div>27%</div> <div>•</div> <div>18%</div> </div>
1	B	134	<div> <div>66%</div> <div>13%</div> <div>• •</div> <div>17%</div> </div>
1	C	134	<div> <div>54%</div> <div>23%</div> <div>5%</div> <div>18%</div> </div>
1	D	134	<div> <div>60%</div> <div>19%</div> <div>•</div> <div>19%</div> </div>
1	E	134	<div> <div>5%</div> <div>68%</div> <div>14%</div> <div>•</div> <div>16%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	134	<div><div><div></div><div></div><div></div><div></div></div><div>2%59%20%18%</div></div>
2	R	7	<div><div><div></div><div></div><div></div><div></div></div><div>29%71%14%14%</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5232 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 ORF134.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	110	Total	C	N	O	S	0	0	0
			871	553	153	162	3			
1	B	111	Total	C	N	O	S	0	0	0
			883	560	155	165	3			
1	C	110	Total	C	N	O	S	0	0	0
			866	549	150	163	4			
1	D	108	Total	C	N	O	S	0	0	0
			850	540	147	160	3			
1	E	112	Total	C	N	O	S	0	0	0
			829	526	148	152	3			
1	F	110	Total	C	N	O	S	0	0	0
			862	548	150	161	3			

- Molecule 2 is a protein called RbcL.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	R	7	Total	C	N	O	0	0	0
			55	38	7	10			

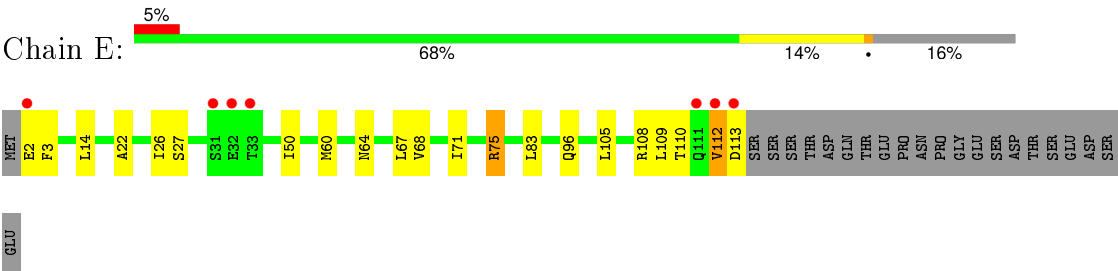
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	6	Total	O	0	0
			6	6		
3	B	3	Total	O	0	0
			3	3		
3	C	5	Total	O	0	0
			5	5		
3	D	2	Total	O	0	0
			2	2		

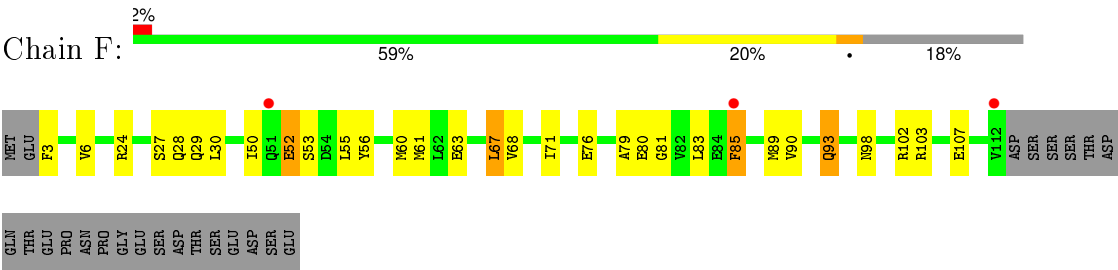
- Molecule 1: ORF134



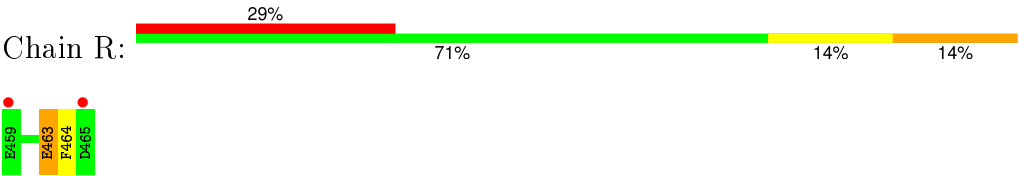
● Molecule 1: ORF134



● Molecule 1: ORF134



● Molecule 2: RbcL



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	93.21Å 93.21Å 412.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.95 19.94 – 2.95	Depositor EDS
% Data completeness (in resolution range)	95.6 (20.00-2.95) 95.6 (19.94-2.95)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 2.93Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.235 , 0.264 0.229 , 0.260	Depositor DCC
R_{free} test set	1913 reflections (5.35%)	DCC
Wilson B-factor (Å ²)	77.0	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 37.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 37701 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5232	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.60	0/883	0.72	0/1194
1	B	0.54	0/895	0.70	1/1210 (0.1%)
1	C	0.62	0/878	0.70	0/1189
1	D	0.64	0/862	0.70	0/1166
1	E	0.48	0/841	0.61	0/1145
1	F	0.52	0/874	0.64	0/1184
2	R	0.51	0/56	0.66	0/73
All	All	0.57	0/5289	0.68	1/7161 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	105	LEU	CA-CB-CG	5.30	127.49	115.30

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	871	0	880	41	0
1	B	883	0	892	16	0
1	C	866	0	866	34	0
1	D	850	0	849	19	0
1	E	829	0	780	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	862	0	856	25	0
2	R	55	0	40	2	0
3	A	6	0	0	1	0
3	B	3	0	0	0	0
3	C	5	0	0	0	0
3	D	2	0	0	0	0
All	All	5232	0	5163	125	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 12.

The worst 5 of 125 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:E:112:VAL:HG12	1:E:113:ASP:H	1.14	1.09
1:C:33:THR:HG23	1:C:34:ASN:HD22	1.23	1.03
1:F:60:MET:HE2	1:F:68:VAL:HG22	1.41	0.97
1:F:52:GLU:HG2	1:F:55:LEU:HD22	1.61	0.81
1:D:37:GLN:HE22	1:D:64:ASN:HD21	1.30	0.79

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	108/134 (81%)	100 (93%)	8 (7%)	0	100	100
1	B	109/134 (81%)	98 (90%)	10 (9%)	1 (1%)	21	61
1	C	108/134 (81%)	103 (95%)	5 (5%)	0	100	100
1	D	106/134 (79%)	99 (93%)	6 (6%)	1 (1%)	21	61
1	E	110/134 (82%)	99 (90%)	9 (8%)	2 (2%)	11	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	108/134 (81%)	100 (93%)	7 (6%)	1 (1%)	21	61
2	R	5/7 (71%)	5 (100%)	0	0	100	100
All	All	654/811 (81%)	604 (92%)	45 (7%)	5 (1%)	24	64

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	29	GLN
1	E	75	ARG
1	E	112	VAL
1	B	62	LEU
1	D	108	ARG

5.3.2 Protein sidechains ⓘ

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	94/123 (76%)	82 (87%)	12 (13%)	5	21
1	B	95/123 (77%)	83 (87%)	12 (13%)	5	22
1	C	93/123 (76%)	81 (87%)	12 (13%)	5	21
1	D	91/123 (74%)	86 (94%)	5 (6%)	27	64
1	E	79/123 (64%)	72 (91%)	7 (9%)	12	39
1	F	91/123 (74%)	83 (91%)	8 (9%)	12	40
2	R	4/7 (57%)	2 (50%)	2 (50%)	0	0
All	All	547/745 (73%)	489 (89%)	58 (11%)	8	29

5 of 58 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	21	GLN
1	C	75	ARG
1	F	67	LEU

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Mol	Chain	Res	Type
1	C	27	SER
1	C	61	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	34	ASN
1	C	93	GLN
1	D	37	GLN
1	C	21	GLN
1	D	93	GLN

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 [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	110/134 (82%)	-0.28	2 (1%) 71 51	42, 57, 85, 95	0
1	B	111/134 (82%)	-0.10	2 (1%) 71 51	52, 71, 94, 99	0
1	C	110/134 (82%)	-0.38	1 (0%) 85 70	48, 62, 86, 94	0
1	D	108/134 (80%)	-0.16	0 100 100	49, 61, 76, 90	0
1	E	112/134 (83%)	0.06	7 (6%) 23 12	70, 90, 124, 126	0
1	F	110/134 (82%)	-0.09	3 (2%) 58 37	56, 79, 91, 102	0
2	R	7/7 (100%)	1.05	2 (28%) 1 0	90, 93, 97, 98	0
All	All	668/811 (82%)	-0.14	17 (2%) 61 39	42, 69, 100, 126	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	113	ASP	4.5
1	E	112	VAL	3.7
1	F	112	VAL	3.7
1	E	111	GLN	3.7
2	R	459	GLU	3.4

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

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.