



wwPDB X-ray Structure Validation Summary Report ⓘ

May 16, 2020 – 03:51 pm BST

PDB ID : 6KEA
Title : crystal structure of MBP-tagged REV7-IpaB complex
Authors : Wang, X.; Pernicone, N.; Pertz, L.; Hua, D.P.; Zhang, T.Q.; Listovsky, T.; Xie, W.
Deposited on : 2019-07-04
Resolution : 2.35 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 ⓘ symbol.

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	:	2.11
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

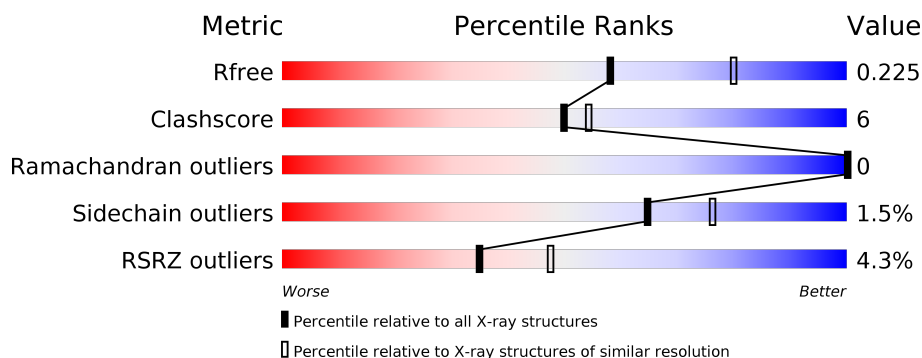
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

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 $\leq 5\%$. 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	631	<div> <div>2%</div> <div> <div></div> <div>82%</div> <div>10%</div> <div>8%</div> </div> </div>
1	B	631	<div> <div>%</div> <div> <div></div> <div>82%</div> <div>10%</div> <div>8%</div> </div> </div>
1	C	631	<div> <div>9%</div> <div> <div></div> <div>74%</div> <div>17%</div> <div>9%</div> </div> </div>
1	D	631	<div> <div>3%</div> <div> <div></div> <div>79%</div> <div>13%</div> <div>7%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 18392 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 Maltose-binding periplasmic protein, LINKER, hREV7, LINKER, Invasin IpaB, hREV3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	581	Total	C	N	O	S	0	0	0
			4520	2915	745	844	16			
1	B	582	Total	C	N	O	S	0	0	0
			4528	2921	746	845	16			
1	C	574	Total	C	N	O	S	0	0	0
			4471	2888	737	830	16			
1	D	584	Total	C	N	O	S	0	0	0
			4542	2929	750	847	16			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P0AEX9
A	83	ALA	ASP	engineered mutation	UNP P0AEX9
A	84	ALA	LYS	engineered mutation	UNP P0AEX9
A	173	ALA	GLU	engineered mutation	UNP P0AEX9
A	174	ALA	ASN	engineered mutation	UNP P0AEX9
A	240	ALA	LYS	engineered mutation	UNP P0AEX9
A	485	ALA	ARG	engineered mutation	UNP Q9UI95
B	1	MET	-	initiating methionine	UNP P0AEX9
B	83	ALA	ASP	engineered mutation	UNP P0AEX9
B	84	ALA	LYS	engineered mutation	UNP P0AEX9
B	173	ALA	GLU	engineered mutation	UNP P0AEX9
B	174	ALA	ASN	engineered mutation	UNP P0AEX9
B	240	ALA	LYS	engineered mutation	UNP P0AEX9
B	485	ALA	ARG	engineered mutation	UNP Q9UI95
C	1	MET	-	initiating methionine	UNP P0AEX9
C	83	ALA	ASP	engineered mutation	UNP P0AEX9
C	84	ALA	LYS	engineered mutation	UNP P0AEX9
C	173	ALA	GLU	engineered mutation	UNP P0AEX9
C	174	ALA	ASN	engineered mutation	UNP P0AEX9
C	240	ALA	LYS	engineered mutation	UNP P0AEX9

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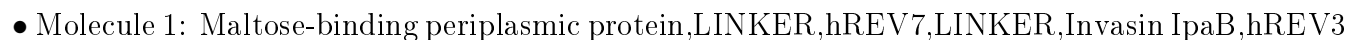
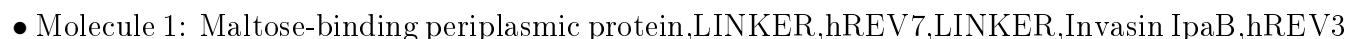
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Chain	Residue	Modelled	Actual	Comment	Reference
C	485	ALA	ARG	engineered mutation	UNP Q9UI95
D	1	MET	-	initiating methionine	UNP P0AEX9
D	83	ALA	ASP	engineered mutation	UNP P0AEX9
D	84	ALA	LYS	engineered mutation	UNP P0AEX9
D	173	ALA	GLU	engineered mutation	UNP P0AEX9
D	174	ALA	ASN	engineered mutation	UNP P0AEX9
D	240	ALA	LYS	engineered mutation	UNP P0AEX9
D	485	ALA	ARG	engineered mutation	UNP Q9UI95

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	130	Total O 130 130	0	0
2	B	113	Total O 113 113	0	0
2	C	31	Total O 31 31	0	0
2	D	57	Total O 57 57	0	0

- Molecule 1: Maltose-binding periplasmic protein, LINKER, hREV7, LINKER, Invasin IpaB, hREV3





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.83Å 146.71Å 102.47Å 90.00° 116.58° 90.00°	Depositor
Resolution (Å)	29.91 – 2.35 29.90 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.91-2.35) 97.5 (29.90-2.35)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.65 (at 2.36Å)	Xtriage
Refinement program	PHENIX 1.14-3260	Depositor
R, R_{free}	0.192 , 0.226 0.191 , 0.225	Depositor DCC
R_{free} test set	4849 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	43.1	Xtriage
Anisotropy	0.686	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 29.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.065 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	18392	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.26% 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, 0.333 respectively for untwinned datasets, and 0.375, 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	0.45	0/4626	0.58	0/6293
1	B	0.44	0/4634	0.58	0/6304
1	C	0.34	0/4575	0.49	0/6223
1	D	0.39	0/4649	0.53	0/6325
All	All	0.41	0/18484	0.55	0/25145

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	4520	0	4534	38	0
1	B	4528	0	4545	52	0
1	C	4471	0	4489	65	0
1	D	4542	0	4558	58	0
2	A	130	0	0	11	0
2	B	113	0	0	12	0
2	C	31	0	0	7	0
2	D	57	0	0	3	0
All	All	18392	0	18126	211	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 6.

The worst 5 of 211 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:B:355:ARG:HH11	1:B:355:ARG:HA	1.25	1.01
1:B:176:LYS:HD3	1:B:469:LEU:HD11	1.60	0.82
1:B:4:GLU:HB2	1:B:7:LYS:HE2	1.64	0.80
1:B:355:ARG:NH1	1:B:355:ARG:HA	2.00	0.75
1:A:551:LYS:NZ	2:A:708:HOH:O	2.20	0.74

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	577/631 (91%)	561 (97%)	16 (3%)	0	100	100
1	B	578/631 (92%)	565 (98%)	13 (2%)	0	100	100
1	C	567/631 (90%)	552 (97%)	15 (3%)	0	100	100
1	D	580/631 (92%)	564 (97%)	16 (3%)	0	100	100
All	All	2302/2524 (91%)	2242 (97%)	60 (3%)	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	480/518 (93%)	477 (99%)	3 (1%)	86	93
1	B	481/518 (93%)	472 (98%)	9 (2%)	57	68
1	C	474/518 (92%)	465 (98%)	9 (2%)	57	68
1	D	483/518 (93%)	476 (99%)	7 (1%)	67	78
All	All	1918/2072 (93%)	1890 (98%)	28 (2%)	65	76

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	37	THR
1	C	300	LEU
1	D	416	SER
1	C	139	GLU
1	C	276	LEU

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

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 carbohydrates 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 [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	581/631 (92%)	-0.12	14 (2%) 59 68	27, 42, 80, 103	0
1	B	582/631 (92%)	-0.14	6 (1%) 82 88	31, 45, 72, 109	0
1	C	574/631 (90%)	0.45	59 (10%) 6 10	42, 67, 117, 128	0
1	D	584/631 (92%)	0.09	21 (3%) 42 55	32, 54, 93, 129	0
All	All	2321/2524 (91%)	0.07	100 (4%) 35 47	27, 51, 102, 129	0

The worst 5 of 100 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	53	ALA	6.9
1	A	55	GLY	5.9
1	C	28	PHE	5.7
1	B	543	HIS	5.4
1	A	54	THR	5.1

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.