Full wwPDB X-ray Structure Validation Report (i)

Mar 10, 2026 – 09:02 AM UTC

PDB ID	:	5FI1 / pdb_00005fi1
Title	:	Crystal Structure of the P-Rex1 DH/PH tandem in complex with Cdc42
Authors	:	Cash, J.N.; Tesmer, J.J.G.
Deposited on	:	2015-12-22
Resolution	:	3.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

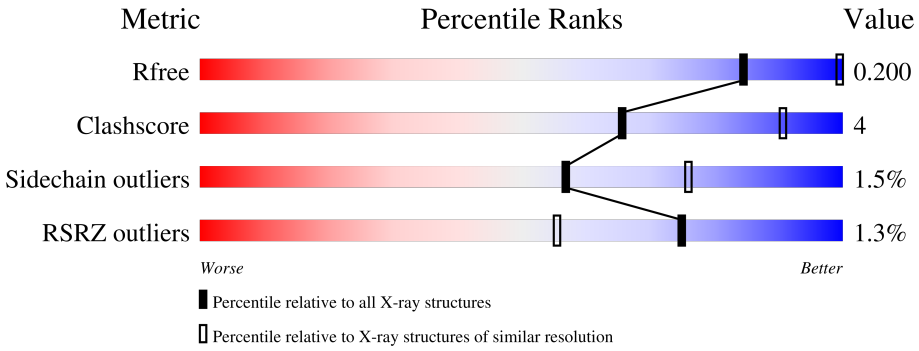
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

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 3.20 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}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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 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	374	2% 81% 10% • 8%
2	B	194	81% 11% 7%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4194 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 Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein,Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	344	Total	C	N	O	S	0	0	0
			2788	1767	490	516	15			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q8TCU6
A	-1	GLU	-	expression tag	UNP Q8TCU6
A	0	PHE	-	expression tag	UNP Q8TCU6

- Molecule 2 is a protein called Cell division control protein 42 homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	180	Total	C	N	O	S	0	0	0
			1406	907	223	269	7			

There are 3 discrepancies between the modelled and reference sequences:

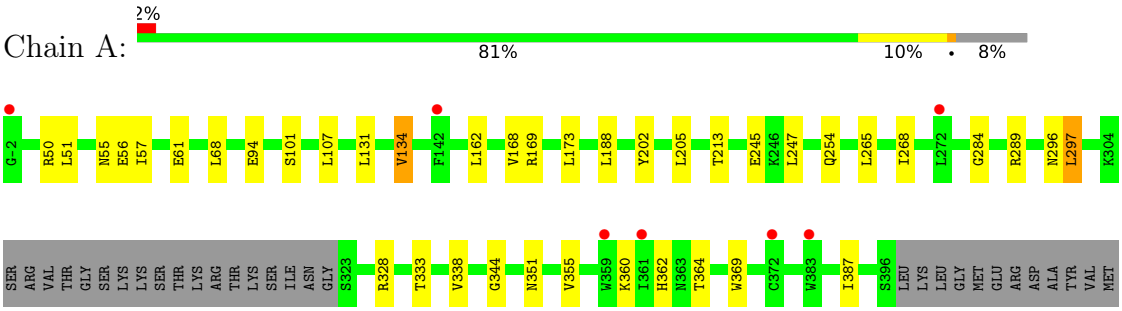
Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	GLY	-	expression tag	UNP P60953
B	-1	GLU	-	expression tag	UNP P60953
B	0	PHE	-	expression tag	UNP P60953

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.

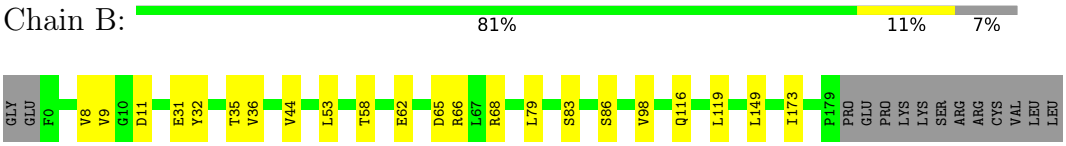
• Molecule 1: Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein,Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein

Chain A:



• Molecule 2: Cell division control protein 42 homolog

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	67.31Å 95.91Å 277.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.12 – 3.20 43.12 – 3.20	Depositor EDS
% Data completeness (in resolution range)	81.2 (43.12-3.20) 77.2 (43.12-3.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.41 (at 3.19Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.205 , 0.198 0.216 , 0.200	Depositor DCC
R_{free} test set	607 reflections (3.99%)	wwPDB-VP
Wilson B-factor (Å^2)	79.5	Xtriage
Anisotropy	0.659	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 69.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4194	wwPDB-VP
Average B, all atoms (Å^2)	124.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.32% of the height of the origin peak. No significant pseudotranslation is detected.*

[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	0.28	0/2837	0.71	2/3823 (0.1%)
2	B	0.30	0/1438	0.77	0/1958
All	All	0.29	0/4275	0.73	2/5781 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	101	SER	CB-CA-C	-5.59	110.11	116.54
1	A	297	LEU	N-CA-C	5.29	116.88	108.79

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	2788	0	2814	22	0
2	B	1406	0	1421	12	0
All	All	4194	0	4235	32	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 4.

All (32) 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)
2:B:44:VAL:HG21	2:B:173:ILE:HD13	1.69	0.75
1:A:284:GLY:HA2	1:A:351:ASN:HD21	1.51	0.73
1:A:50:ARG:NH1	1:A:213:THR:OG1	2.31	0.64
1:A:61:GLU:OE1	1:A:202:TYR:OH	2.15	0.63
2:B:53:LEU:HD22	2:B:173:ILE:HD11	1.86	0.56
1:A:56:GLU:OE2	2:B:32:TYR:OH	2.15	0.56
1:A:297:LEU:HA	1:A:333:THR:HG23	1.88	0.55
1:A:202:TYR:HA	1:A:205:LEU:HD12	1.87	0.54
1:A:254:GLN:HG3	1:A:265:LEU:HD12	1.91	0.53
2:B:83:SER:HB3	2:B:86:SER:HB3	1.94	0.49
1:A:162:LEU:HB3	1:A:168:VAL:HG11	1.94	0.49
1:A:51:LEU:O	1:A:55:ASN:ND2	2.41	0.47
2:B:62:GLU:O	2:B:68:ARG:NH1	2.48	0.47
1:A:362:HIS:CE1	1:A:364:THR:HG22	2.51	0.46
2:B:9:VAL:HG12	2:B:58:THR:HG21	1.97	0.46
1:A:245:GLU:OE1	2:B:66:ARG:NH1	2.41	0.45
2:B:98:VAL:HG21	2:B:149:LEU:HD13	1.97	0.45
1:A:289:ARG:HE	1:A:328:ARG:HG2	1.82	0.44
2:B:35:THR:HG23	2:B:36:VAL:HG23	1.99	0.44
1:A:131:LEU:O	1:A:134:VAL:HG22	2.18	0.44
1:A:169:ARG:O	1:A:173:LEU:HG	2.19	0.43
1:A:362:HIS:HB2	1:A:369:TRP:CZ3	2.55	0.42
2:B:8:VAL:HG22	2:B:79:LEU:HD12	2.00	0.42
1:A:57:ILE:HG12	1:A:205:LEU:HD22	2.01	0.42
1:A:268:ILE:O	1:A:296:ASN:ND2	2.50	0.42
1:A:68:LEU:HB2	1:A:107:LEU:HD13	2.02	0.42
1:A:338:VAL:HG21	1:A:387:ILE:HD13	2.02	0.41
2:B:116:GLN:HB3	2:B:119:LEU:HD12	2.02	0.41
1:A:131:LEU:HD23	1:A:131:LEU:HA	1.91	0.41
1:A:360:LYS:HE2	1:A:369:TRP:CE3	2.56	0.41
2:B:65:ASP:OD1	2:B:65:ASP:N	2.54	0.41
1:A:344:GLY:N	1:A:355:VAL:O	2.50	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

There are no protein backbone outliers to report in this entry.

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	246/332 (74%)	242 (98%)	4 (2%)	55 75
2	B	160/173 (92%)	158 (99%)	2 (1%)	61 78
All	All	406/505 (80%)	400 (98%)	6 (2%)	57 76

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	94	GLU
1	A	134	VAL
1	A	188	LEU
1	A	247	LEU
2	B	11	ASP
2	B	31	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	133	ASN
1	A	351	ASN

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 oligosaccharides 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	344/374 (91%)	-0.24	7 (2%) 65 45	64, 106, 224, 248	0
2	B	180/194 (92%)	-0.27	0 100 100	71, 103, 159, 198	0
All	All	524/568 (92%)	-0.25	7 (1%) 75 55	64, 104, 215, 248	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	359	TRP	2.9
1	A	372	CYS	2.9
1	A	361	ILE	2.8
1	A	383	TRP	2.6
1	A	272	LEU	2.4
1	A	142	PHE	2.3
1	A	-2	GLY	2.3

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 oligosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.