Full wwPDB X-ray Structure Validation Report ⓘ

May 23, 2020 – 08:04 pm BST

PDB ID	:	5I7D
Title	:	Crystal Structure of srGAP2 F-BARx WT Form-2
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Deposited on	:	2016-02-17
Resolution	:	3.95 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 ⓘ symbol.

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

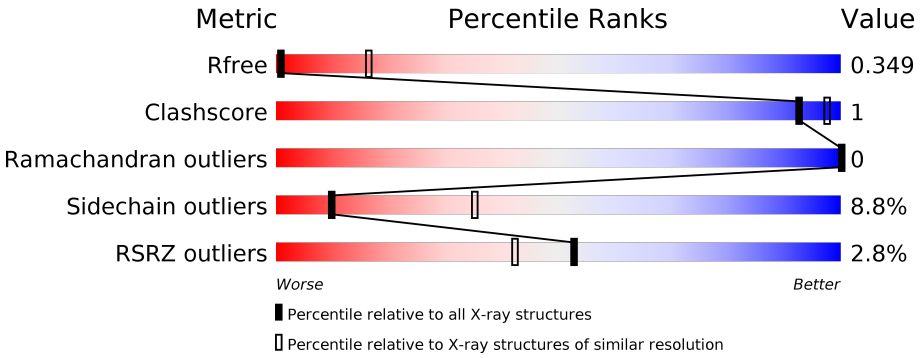
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.95 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}	130704	1025 (4.22-3.70)
Clashscore	141614	1085 (4.22-3.70)
Ramachandran outliers	138981	1047 (4.22-3.70)
Sidechain outliers	138945	1039 (4.22-3.70)
RSRZ outliers	127900	1013 (4.28-3.64)

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	484	3% 75% 9% • 15%
1	B	484	% 74% 10% • 15%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6714 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 SLIT-ROBO Rho GTPase-activating protein 2.

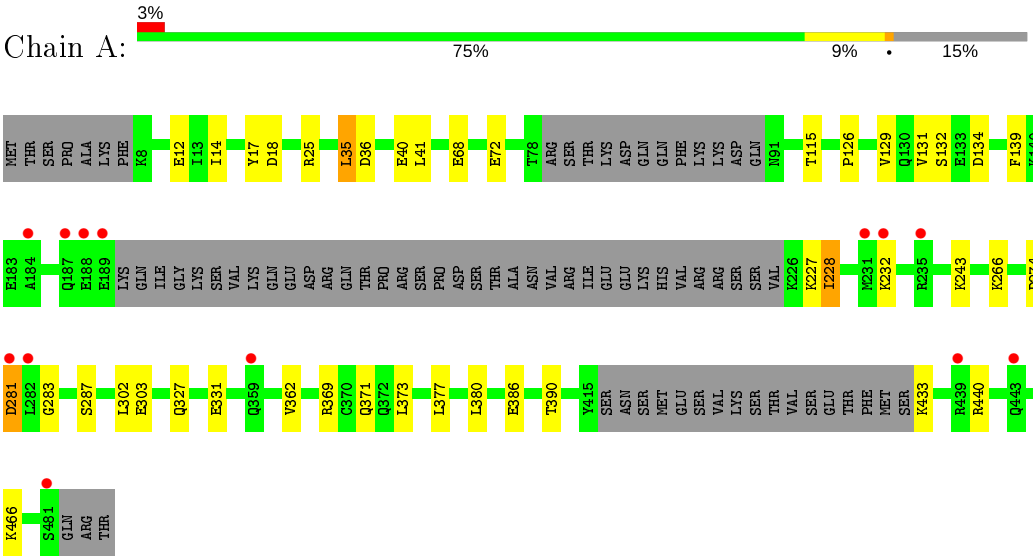
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	409	Total	C	N	O	S	0	1	0
			3357	2100	579	656	22			
1	B	409	Total	C	N	O	S	0	1	0
			3357	2100	579	656	22			

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 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.

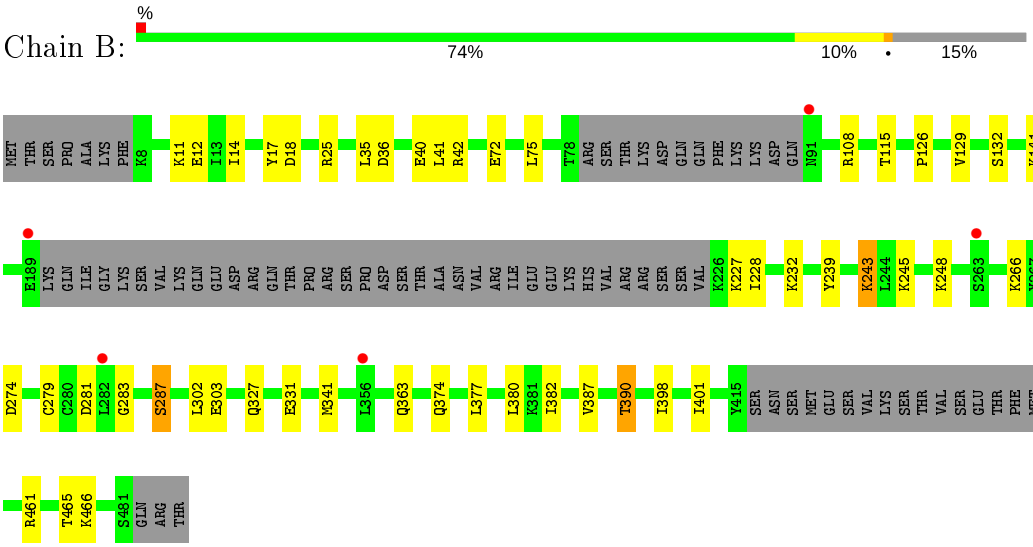
- Molecule 1: SLIT-ROBO Rho GTPase-activating protein 2

Chain A:



- Molecule 1: SLIT-ROBO Rho GTPase-activating protein 2

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	120.90Å 49.93Å 234.08Å 90.00° 102.57° 90.00°	Depositor
Resolution (Å)	46.39 – 3.95 46.39 – 3.94	Depositor EDS
% Data completeness (in resolution range)	98.3 (46.39-3.95) 98.3 (46.39-3.94)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.46 (at 4.00Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.277 , 0.349 0.283 , 0.349	Depositor DCC
R_{free} test set	615 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	163.7	Xtriage
Anisotropy	0.440	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 136.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.26$	Xtriage
Estimated twinning fraction	0.076 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	6714	wwPDB-VP
Average B, all atoms (Å^2)	196.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.68% 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	0.39	0/3398	0.58	0/4549
1	B	0.38	0/3398	0.58	0/4549
All	All	0.39	0/6796	0.58	0/9098

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

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	3357	0	3365	8	0
1	B	3357	0	3365	12	0
All	All	6714	0	6730	20	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 1.

All (20) 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:387:VAL:N	1:B:390:THR:HG1	1.96	0.64
1:A:68:GLU:O	1:A:72:GLU:HB2	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:281:ASP:C	1:A:283:GLY:H	2.15	0.50
1:B:281:ASP:C	1:B:283:GLY:H	2.16	0.49
1:B:72:GLU:HA	1:B:75:LEU:HB2	1.96	0.48
1:B:374:GLN:HA	1:B:377:LEU:HD12	1.97	0.47
1:B:283:GLY:O	1:B:287:SER:HB2	2.14	0.47
1:B:327:GLN:O	1:B:331:GLU:HG2	2.16	0.45
1:B:42:ARG:HH12	1:B:279:CYS:HB2	1.82	0.44
1:B:398:ILE:HA	1:B:401:ILE:HD12	2.00	0.43
1:A:131:VAL:HA	1:A:134:ASP:HB2	2.00	0.43
1:A:369:ARG:HG2	1:A:373:LEU:HD13	2.00	0.43
1:B:126:PRO:HA	1:B:129:VAL:HG22	1.99	0.43
1:B:239:TYR:O	1:B:243:LYS:HB2	2.19	0.42
1:B:11:LYS:HA	1:B:14:ILE:HG22	2.01	0.42
1:A:126:PRO:HA	1:A:129:VAL:HG22	2.01	0.42
1:A:327:GLN:O	1:A:331:GLU:HG2	2.20	0.42
1:A:228:ILE:H	1:A:228:ILE:HG13	1.57	0.41
1:A:35:LEU:HB3	1:A:139:PHE:HE1	1.85	0.41
1:B:245:LYS:HA	1:B:248:LYS:HE3	2.03	0.41

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	396/484 (82%)	380 (96%)	16 (4%)	0	100	100
1	B	396/484 (82%)	379 (96%)	17 (4%)	0	100	100
All	All	792/968 (82%)	759 (96%)	33 (4%)	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	377/448 (84%)	342 (91%)	35 (9%)	9 32
1	B	377/448 (84%)	344 (91%)	33 (9%)	10 35
All	All	754/896 (84%)	686 (91%)	68 (9%)	10 34

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	GLU
1	A	14	ILE
1	A	17	TYR
1	A	18	ASP
1	A	25	ARG
1	A	35	LEU
1	A	36	ASP
1	A	40	GLU
1	A	41	LEU
1	A	115	THR
1	A	132	SER
1	A	141	LYS
1	A	181	LEU
1	A	227	LYS
1	A	228	ILE
1	A	232	LYS
1	A	243	LYS
1	A	266	LYS
1	A	274	ASP
1	A	275	LEU
1	A	281	ASP
1	A	287	SER
1	A	302	LEU
1	A	303[A]	GLU
1	A	303[B]	GLU
1	A	362	VAL
1	A	371	GLN

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Mol	Chain	Res	Type
1	A	377	LEU
1	A	380	LEU
1	A	386	GLU
1	A	390	THR
1	A	433	LYS
1	A	440	ARG
1	A	461	ARG
1	A	466	LYS
1	B	12	GLU
1	B	17	TYR
1	B	18	ASP
1	B	25	ARG
1	B	35	LEU
1	B	36	ASP
1	B	40	GLU
1	B	41	LEU
1	B	108	ARG
1	B	115	THR
1	B	132	SER
1	B	141	LYS
1	B	181	LEU
1	B	183	GLU
1	B	227	LYS
1	B	228	ILE
1	B	232	LYS
1	B	243	LYS
1	B	266	LYS
1	B	274	ASP
1	B	287	SER
1	B	302	LEU
1	B	303[A]	GLU
1	B	303[B]	GLU
1	B	341	MET
1	B	363	GLN
1	B	380	LEU
1	B	382	ILE
1	B	390	THR
1	B	440	ARG
1	B	461	ARG
1	B	465	THR
1	B	466	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	GLN
1	A	236	GLN
1	A	304	GLN
1	B	31	GLN
1	B	236	GLN
1	B	304	GLN

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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	3
1	A	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	281:ASP	C	282:LEU	N	5.21
1	B	281:ASP	C	282:LEU	N	5.10
1	A	386:GLU	C	387:VAL	N	3.42
1	B	386:GLU	C	387:VAL	N	3.06
1	A	319:ASN	C	320:LEU	N	3.04
1	B	361:PRO	C	362:VAL	N	2.93

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	409/484 (84%)	0.20	16 (3%) 39 31	130, 190, 295, 362	0
1	B	409/484 (84%)	0.02	7 (1%) 70 60	125, 180, 278, 319	0
All	All	818/968 (84%)	0.11	23 (2%) 53 42	125, 185, 290, 362	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	481	SER	7.4
1	A	282	LEU	4.7
1	A	281	ASP	4.4
1	B	91	ASN	3.7
1	A	231	MET	3.2
1	A	443	GLN	3.1
1	B	282	LEU	3.0
1	A	188	GLU	2.8
1	A	235	ARG	2.8
1	B	268	TYR	2.6
1	B	356	LEU	2.6
1	A	184	ALA	2.5
1	A	187	GLN	2.5
1	B	263	SER	2.3
1	A	359	GLN	2.3
1	B	189	GLU	2.3
1	A	189	GLU	2.3
1	A	439	ARG	2.2
1	A	232	LYS	2.2
1	A	278	GLN	2.2
1	A	447	GLU	2.2
1	A	182	LYS	2.1
1	B	272	LEU	2.1

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

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.