



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:10 AM UTC

PDB ID : 9FSK / pdb_00009fsk
Title : Crystal structure of the HECT domain of Smurf1
Authors : Ostermann, N.
Deposited on : 2024-06-21
Resolution : 2.75 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) 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

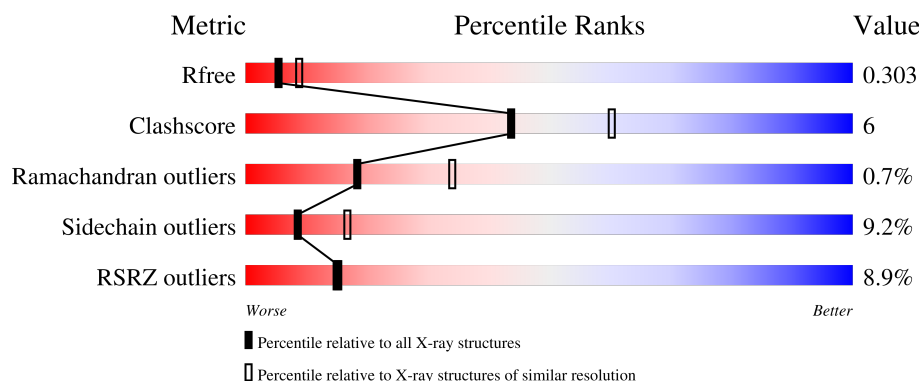
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

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 $\leq 5\%$. 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	377	5% 78% 20% ..
1	B	377	5% 76% 20% ..
1	C	377	10% 76% 18% ...
1	D	377	15% 75% 18% • 5%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12302 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 E3 ubiquitin-protein ligase SMURF1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	371	Total	C	N	O	S	0	0	0
			3060	1970	532	546	12			
1	B	371	Total	C	N	O	S	0	0	0
			3064	1973	532	547	12			
1	C	367	Total	C	N	O	S	0	0	0
			3019	1943	522	542	12			
1	D	358	Total	C	N	O	S	0	0	0
			2963	1910	513	528	12			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	375	GLY	-	expression tag	UNP Q9HCE7
A	376	PRO	-	expression tag	UNP Q9HCE7
B	375	GLY	-	expression tag	UNP Q9HCE7
B	376	PRO	-	expression tag	UNP Q9HCE7
C	375	GLY	-	expression tag	UNP Q9HCE7
C	376	PRO	-	expression tag	UNP Q9HCE7
D	375	GLY	-	expression tag	UNP Q9HCE7
D	376	PRO	-	expression tag	UNP Q9HCE7

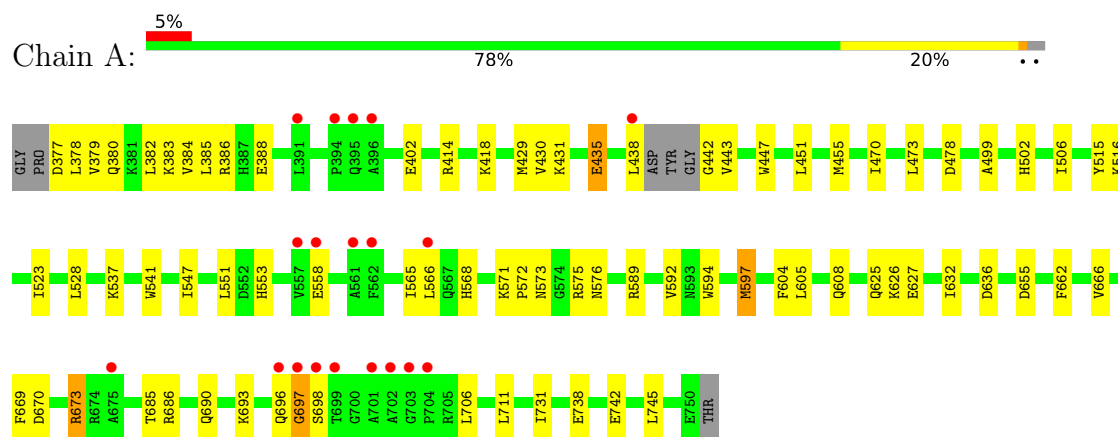
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	84	Total	O	0	0
			84	84		
2	B	50	Total	O	0	0
			50	50		
2	C	40	Total	O	0	0
			40	40		
2	D	22	Total	O	0	0
			22	22		

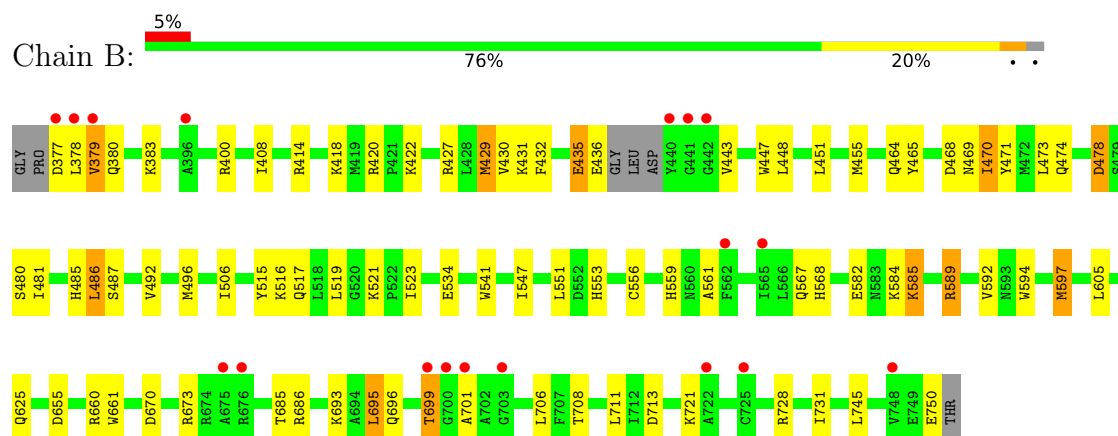
3 Residue-property plots [i](#)

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.

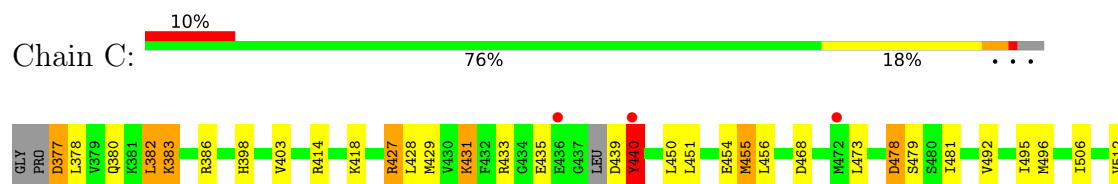
- Molecule 1: E3 ubiquitin-protein ligase SMURF1

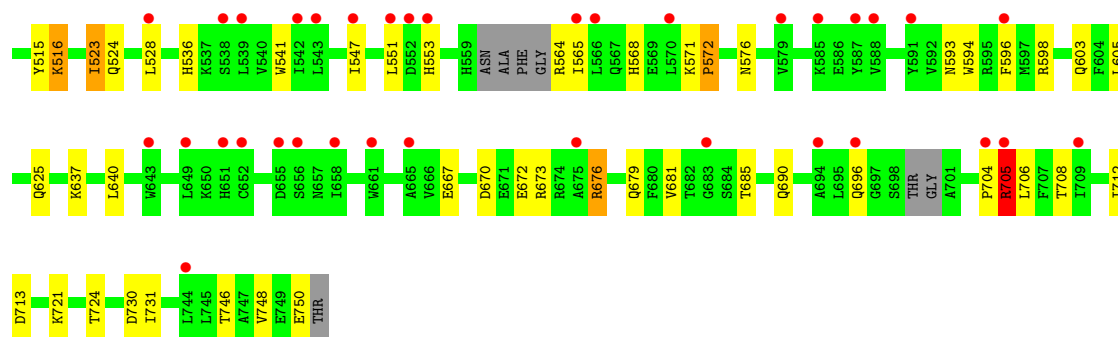


- Molecule 1: E3 ubiquitin-protein ligase SMURF1

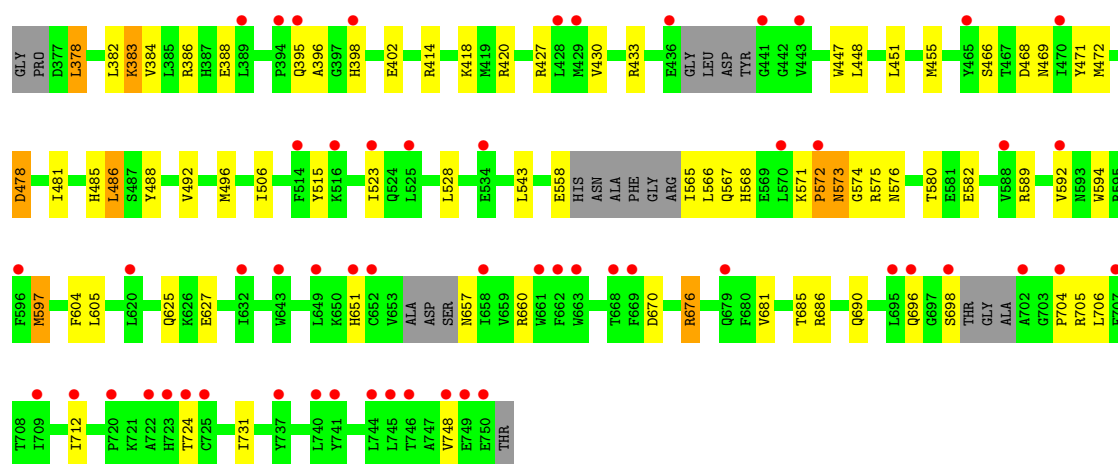
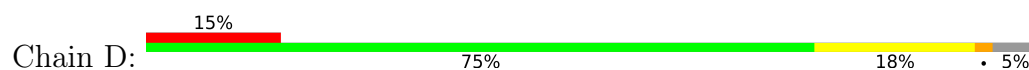


- Molecule 1: E3 ubiquitin-protein ligase SMURF1





● Molecule 1: E3 ubiquitin-protein ligase SMURF1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	170.16Å 74.32Å 161.06Å 90.00° 111.93° 90.00°	Depositor
Resolution (Å)	78.92 – 2.75 78.92 – 2.75	Depositor EDS
% Data completeness (in resolution range)	98.9 (78.92-2.75) 98.9 (78.92-2.75)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.20 (at 2.73Å)	Xtriage
Refinement program	BUSTER 2.11.8	Depositor
R, R_{free}	0.248 , 0.301 0.244 , 0.303	Depositor DCC
R_{free} test set	2419 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	51.0	Xtriage
Anisotropy	0.528	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 67.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	12302	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.83% 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	0.82	0/3137	1.18	9/4242 (0.2%)
1	B	0.78	1/3142 (0.0%)	1.16	6/4249 (0.1%)
1	C	0.72	1/3094 (0.0%)	1.10	5/4183 (0.1%)
1	D	0.72	0/3035	1.10	2/4099 (0.0%)
All	All	0.76	2/12408 (0.0%)	1.13	22/16773 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	701	ALA	CA-C	7.28	1.62	1.52
1	C	455	MET	SD-CE	-5.98	1.64	1.79

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	636	ASP	CA-CB-CG	6.84	119.44	112.60
1	B	378	LEU	N-CA-C	6.81	118.36	111.07
1	A	670	ASP	CA-CB-CG	6.61	119.21	112.60
1	A	443	VAL	N-CA-C	6.43	117.11	108.11
1	B	695	LEU	CA-C-N	6.08	133.16	121.54

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	3060	0	3043	33	0
1	B	3064	0	3041	45	0
1	C	3019	0	2971	35	0
1	D	2963	0	2941	37	0
2	A	84	0	0	2	0
2	B	50	0	0	1	0
2	C	40	0	0	2	0
2	D	22	0	0	0	0
All	All	12302	0	11996	147	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 147 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:573:ASN:HD21	1:A:576:ASN:ND2	1.59	1.00
1:D:580:THR:HB	1:D:582:GLU:HG2	1.45	0.97
1:A:573:ASN:HD21	1:A:576:ASN:HD22	0.92	0.91
1:B:464:GLN:NE2	1:B:474:GLN:HE21	1.67	0.91
1:D:398:HIS:NE2	1:D:427:ARG:NH1	2.29	0.80

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	367/377 (97%)	345 (94%)	21 (6%)	1 (0%)	36 56
1	B	367/377 (97%)	339 (92%)	24 (6%)	4 (1%)	11 22
1	C	359/377 (95%)	340 (95%)	16 (4%)	3 (1%)	16 30
1	D	348/377 (92%)	324 (93%)	22 (6%)	2 (1%)	21 38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1441/1508 (96%)	1348 (94%)	83 (6%)	10 (1%)	18	34

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	697	GLY
1	B	696	GLN
1	C	705	ARG
1	B	435	GLU
1	C	440	TYR

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	334/338 (99%)	308 (92%)	26 (8%)	11	21
1	B	334/338 (99%)	300 (90%)	34 (10%)	7	14
1	C	327/338 (97%)	293 (90%)	34 (10%)	7	13
1	D	324/338 (96%)	297 (92%)	27 (8%)	10	19
All	All	1319/1352 (98%)	1198 (91%)	121 (9%)	8	17

5 of 121 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	713	ASP
1	D	573	ASN
1	C	468	ASP
1	D	567	GLN
1	D	698	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	482	ASN
1	C	696	GLN
1	C	504	HIS
1	C	625	GLN
1	D	393	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 oligosaccharides 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	371/377 (98%)	0.40	19 (5%) 33 33	26, 47, 81, 97	0
1	B	371/377 (98%)	0.68	18 (4%) 35 34	30, 61, 93, 108	0
1	C	367/377 (97%)	0.82	38 (10%) 11 11	27, 72, 128, 138	0
1	D	358/377 (94%)	1.09	56 (15%) 5 4	38, 83, 145, 163	0
All	All	1467/1508 (97%)	0.75	131 (8%) 15 15	26, 63, 126, 163	0

The worst 5 of 131 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	748	VAL	4.7
1	C	539	LEU	4.4
1	B	675	ALA	4.3
1	A	704	PRO	4.1
1	D	652	CYS	3.9

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 oligosaccharides 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.