



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 17, 2017 – 03:18 AM EDT

PDB ID : 5HK5
Title : Structure of the Grem2-GDF5 Inhibitory Complex
Authors : Nolan, K.; Thompson, T.B.; Read, R.J.
Deposited on : unknown
Resolution : 2.90 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
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20029824
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	rb-20029824

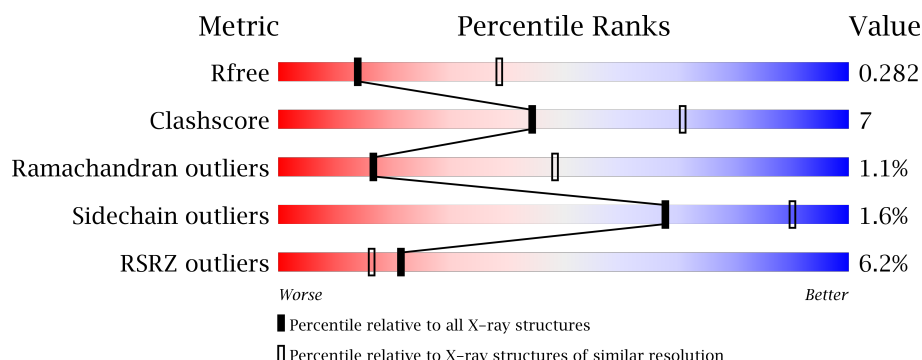
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	100719	1586 (2.90-2.90)
Clashscore	112137	1807 (2.90-2.90)
Ramachandran outliers	110173	1768 (2.90-2.90)
Sidechain outliers	110143	1770 (2.90-2.90)
RSRZ outliers	101464	1596 (2.90-2.90)

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	E	147	<div> <div>6%</div> <div> <div></div> <div>67%</div> <div>16%</div> <div>•</div> <div>13%</div> </div> </div>
1	F	147	<div> <div>9%</div> <div> <div></div> <div>71%</div> <div>15%</div> <div>•</div> <div>12%</div> </div> </div>
1	G	147	<div> <div>5%</div> <div> <div></div> <div>73%</div> <div>14%</div> <div>•</div> <div>12%</div> </div> </div>
1	H	147	<div> <div>12%</div> <div> <div></div> <div>62%</div> <div>18%</div> <div>••</div> <div>19%</div> </div> </div>
2	A	120	<div> <div>•%</div> <div> <div></div> <div>78%</div> <div>8%</div> <div>•</div> <div>13%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	B	120	<div><div><div></div><div></div><div></div></div><div><div>3%</div><div>74%</div><div>12%</div><div>•</div><div>13%</div></div></div>
2	C	120	<div><div><div></div><div></div><div></div></div><div><div>%</div><div>77%</div><div>11%</div><div></div><div>13%</div></div></div>
2	D	120	<div><div><div></div><div></div><div></div></div><div><div>4%</div><div>79%</div><div>8%</div><div></div><div>13%</div></div></div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7436 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 Gremlin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	128	Total	C	N	O	S	0	0	0
			1033	652	187	184	10			
1	F	129	Total	C	N	O	S	0	0	0
			1042	658	189	185	10			
1	G	129	Total	C	N	O	S	0	0	0
			1042	658	189	185	10			
1	H	119	Total	C	N	O	S	0	0	0
			972	611	178	173	10			

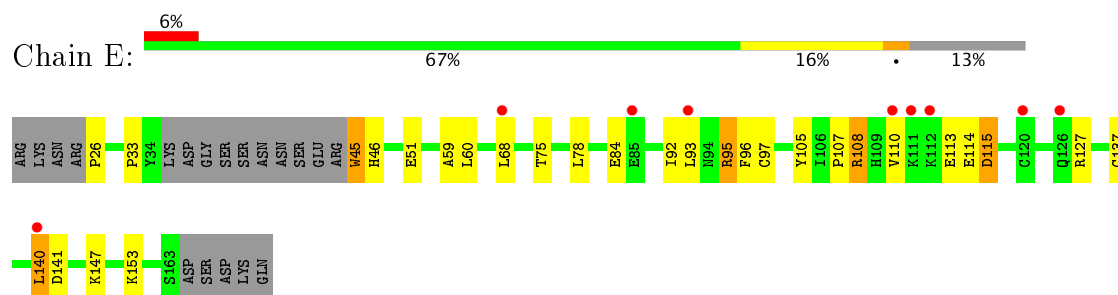
- Molecule 2 is a protein called Growth/differentiation factor 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	105	Total	C	N	O	S	0	0	0
			834	525	141	157	11			
2	B	105	Total	C	N	O	S	0	0	0
			834	525	141	157	11			
2	C	105	Total	C	N	O	S	0	1	0
			845	535	142	157	11			
2	D	105	Total	C	N	O	S	0	0	0
			834	525	141	157	11			

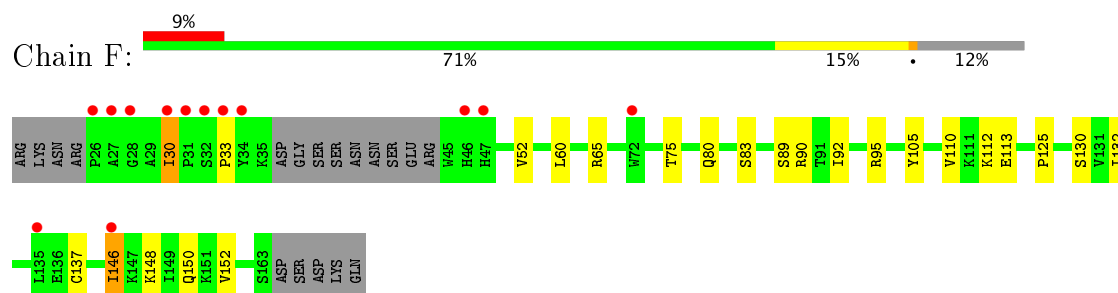
3 Residue-property plots [i](#)

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.

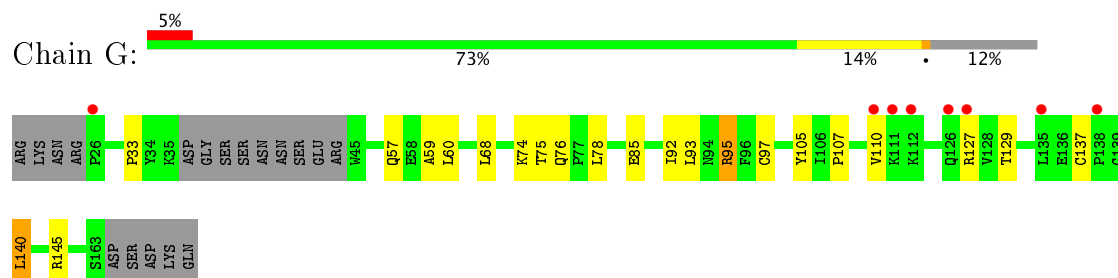
- Molecule 1: Gremlin-2



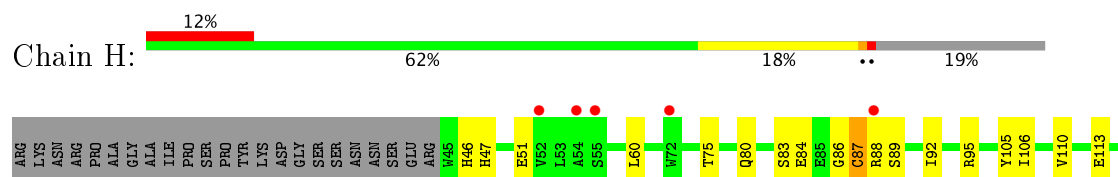
- Molecule 1: Gremlin-2

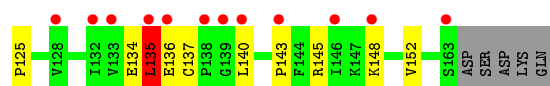


- Molecule 1: Gremlin-2

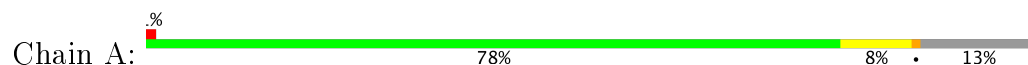


- Molecule 1: Gremlin-2





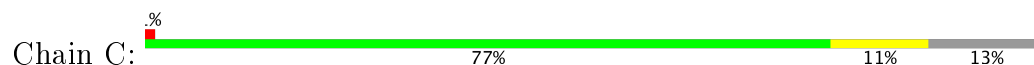
- Molecule 2: Growth/differentiation factor 5



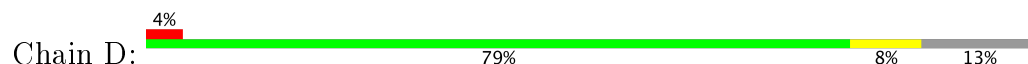
- Molecule 2: Growth/differentiation factor 5



- Molecule 2: Growth/differentiation factor 5



- Molecule 2: Growth/differentiation factor 5



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 2 21	Depositor
Cell constants a, b, c, α , β , γ	114.72Å 125.79Å 125.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.55 – 2.90 50.52 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.2 (50.55-2.90) 99.2 (50.52-2.90)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.8.0124	Depositor
R, R_{free}	0.261 , 0.282 0.262 , 0.282	Depositor DCC
R_{free} test set	2113 reflections (5.44%)	DCC
Wilson B-factor (Å ²)	51.9	Xtriage
Anisotropy	0.173	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 1.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.467 for -h,l,k	Xtriage
Reported twinning fraction	0.517 for H, K, L 0.483 for -H, L, K	Depositor
Outliers	6 of 40921 reflections (0.015%)	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7436	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 56.46 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.7298e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

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	E	0.68	0/1057	0.95	5/1424 (0.4%)
1	F	0.65	0/1066	0.88	1/1435 (0.1%)
1	G	0.61	0/1066	0.86	2/1435 (0.1%)
1	H	0.68	0/993	0.97	2/1336 (0.1%)
2	A	0.50	0/856	0.78	1/1163 (0.1%)
2	B	0.51	0/856	0.78	1/1163 (0.1%)
2	C	0.54	0/872	0.77	1/1186 (0.1%)
2	D	0.54	0/856	0.75	1/1163 (0.1%)
All	All	0.60	0/7622	0.85	14/10305 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	H	0	2

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	60	LEU	CA-CB-CG	7.06	131.54	115.30
1	E	68	LEU	CB-CG-CD2	6.88	122.69	111.00
1	G	68	LEU	CB-CG-CD2	6.85	122.64	111.00
1	E	140	LEU	CA-CB-CG	6.46	130.16	115.30
2	B	120	ARG	NE-CZ-NH2	-6.24	117.18	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	134	GLU	Peptide
1	H	135	LEU	Peptide

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	E	1033	0	1032	23	0
1	F	1042	0	1045	19	1
1	G	1042	0	1045	23	0
1	H	972	0	973	21	0
2	A	834	0	796	8	1
2	B	834	0	796	29	0
2	C	845	0	806	7	0
2	D	834	0	796	6	0
All	All	7436	0	7289	110	1

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 7.

The worst 5 of 110 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:60:LEU:HD11	2:B:118:GLY:CA	1.31	1.61
2:B:60:LEU:CD1	2:B:118:GLY:CA	2.09	1.31
2:B:60:LEU:CD1	2:B:118:GLY:HA2	1.61	1.29
2:B:56:LEU:HD21	2:B:62:PRO:HG3	1.27	1.15
2:B:60:LEU:HD21	2:B:119:CYS:N	1.69	1.07

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:90:ARG:NH1	2:A:53:GLU:OE1[4_785]	1.96	0.24

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	E	124/147 (84%)	111 (90%)	9 (7%)	4 (3%)	5	19
1	F	125/147 (85%)	115 (92%)	10 (8%)	0	100	100
1	G	125/147 (85%)	115 (92%)	9 (7%)	1 (1%)	22	57
1	H	117/147 (80%)	102 (87%)	12 (10%)	3 (3%)	6	24
2	A	103/120 (86%)	102 (99%)	1 (1%)	0	100	100
2	B	103/120 (86%)	99 (96%)	2 (2%)	2 (2%)	9	33
2	C	104/120 (87%)	103 (99%)	1 (1%)	0	100	100
2	D	103/120 (86%)	102 (99%)	1 (1%)	0	100	100
All	All	904/1068 (85%)	849 (94%)	45 (5%)	10 (1%)	17	48

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	113	GLU
2	B	58	SER
1	H	88	ARG
2	B	59	HIS
1	G	85	GLU

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	E	119/137 (87%)	117 (98%)	2 (2%)	66	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	120/137 (88%)	117 (98%)	3 (2%)	53	83
1	G	120/137 (88%)	118 (98%)	2 (2%)	66	89
1	H	113/137 (82%)	108 (96%)	5 (4%)	33	67
2	A	96/108 (89%)	96 (100%)	0	100	100
2	B	96/108 (89%)	95 (99%)	1 (1%)	80	95
2	C	97/108 (90%)	96 (99%)	1 (1%)	80	95
2	D	96/108 (89%)	96 (100%)	0	100	100
All	All	857/980 (87%)	843 (98%)	14 (2%)	68	90

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	140	LEU
1	H	47	HIS
1	H	148	LYS
1	G	137	CYS
1	H	137	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	126	GLN
1	E	154	HIS
1	G	76	GLN
2	A	108	GLN
2	B	59	HIS

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 [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 ⓘ

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, 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	E	128/147 (87%)	0.75	9 (7%) 17 12	12, 34, 63, 103	0
1	F	129/147 (87%)	1.21	13 (10%) 8 5	13, 38, 80, 99	0
1	G	129/147 (87%)	0.77	8 (6%) 21 16	16, 32, 71, 97	0
1	H	119/147 (80%)	1.02	17 (14%) 3 2	17, 39, 71, 84	0
2	A	105/120 (87%)	0.85	1 (0%) 82 81	12, 26, 54, 75	0
2	B	105/120 (87%)	0.67	3 (2%) 52 46	15, 32, 60, 90	0
2	C	105/120 (87%)	0.77	1 (0%) 82 81	13, 28, 48, 84	0
2	D	105/120 (87%)	0.70	5 (4%) 31 27	19, 30, 52, 77	0
All	All	925/1068 (86%)	0.85	57 (6%) 21 16	12, 32, 66, 103	0

The worst 5 of 57 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	33	PRO	8.3
1	F	32	SER	7.4
1	F	28	GLY	7.3
1	F	26	PRO	7.2
1	G	110	VAL	6.8

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 [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.