W O R L D W I D E
wwPDB
PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

May 17, 2020 – 05:31 am BST

PDB ID	:	3CL3
Title	:	Crystal Structure of a vFLIP-IKKgamma complex: Insights into viral activation of the IKK signalosome
Authors	:	Bagneris, C.; Ageichik, A.V.; Cronin, N.; Boshoff, C.; Waksman, G.; Barrett, T.
Deposited on	:	2008-03-18
Resolution	:	3.20 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 (i) symbol.

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

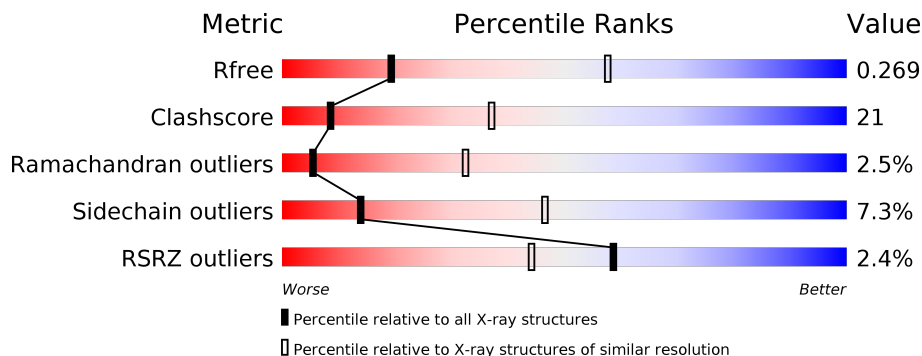|		
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 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	Percentile Ranks	Value
Rfree		0.269
Clashscore		21
Ramachandran outliers		2.5%
Sidechain outliers		7.3%
RSRZ outliers		2.4%

Worse   *Better*

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (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 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	183	51% 37% 5% • 6%
1	B	183	2% 52% 34% • 10%
2	D	130	2% 27% 18% • 55%
2	E	130	4% 33% 11% • 55%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3477 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 ORF K13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	172	Total	C	N	O	S	0	0	0
			1341	854	233	246	8			
1	B	165	Total	C	N	O	S	0	0	0
			1264	806	218	231	9			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP P88961
A	-3	ALA	-	expression tag	UNP P88961
A	-2	MET	-	expression tag	UNP P88961
A	-1	GLY	-	expression tag	UNP P88961
A	0	SER	-	expression tag	UNP P88961
B	-4	GLY	-	expression tag	UNP P88961
B	-3	ALA	-	expression tag	UNP P88961
B	-2	MET	-	expression tag	UNP P88961
B	-1	GLY	-	expression tag	UNP P88961
B	0	SER	-	expression tag	UNP P88961

- Molecule 2 is a protein called NF-kappa-B essential modulator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	59	Total	C	N	O	S	0	0	0
			452	276	89	85	2			
2	E	58	Total	C	N	O	S	0	0	0
			420	260	74	84	2			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	143	GLY	-	expression tag	UNP Q9Y6K9
D	144	HIS	-	expression tag	UNP Q9Y6K9

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| Chain	Residue	Modelled	Actual	Comment	Reference
D	145	MET	-	expression tag	UNP Q9Y6K9
D	146	ALA	-	expression tag	UNP Q9Y6K9
D	147	SER	-	expression tag	UNP Q9Y6K9
D	148	GLY	-	expression tag	UNP Q9Y6K9
D	149	SER	-	expression tag	UNP Q9Y6K9
E	143	GLY	-	expression tag	UNP Q9Y6K9
E	144	HIS	-	expression tag	UNP Q9Y6K9
E	145	MET	-	expression tag	UNP Q9Y6K9
E	146	ALA	-	expression tag	UNP Q9Y6K9
E	147	SER	-	expression tag	UNP Q9Y6K9
E	148	GLY	-	expression tag	UNP Q9Y6K9
E	149	SER	-	expression tag	UNP Q9Y6K9

3 Residue-property plots ⓘ

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.
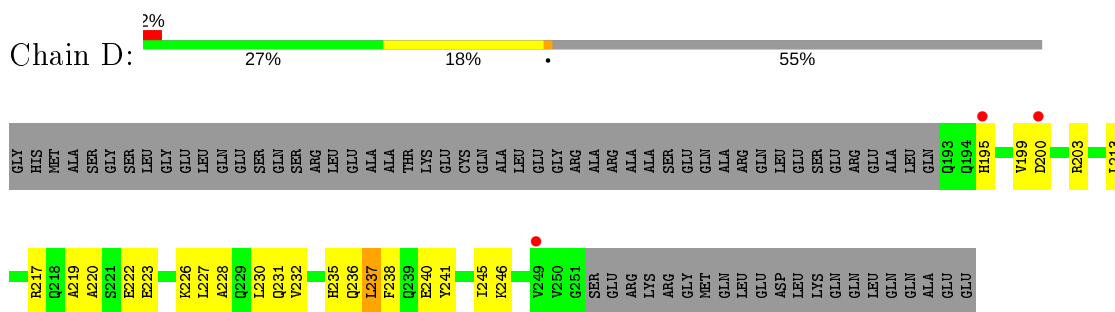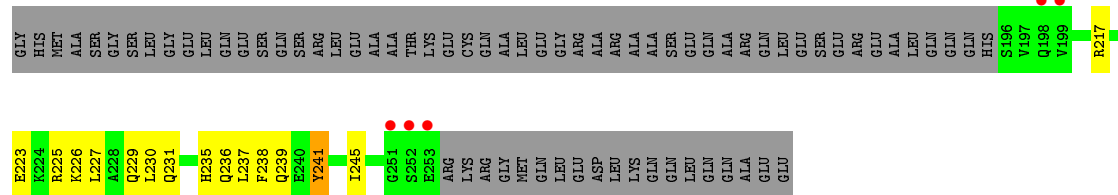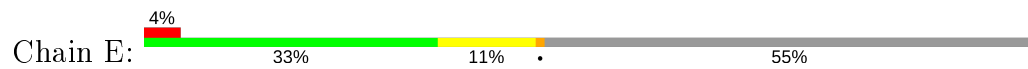
- Molecule 1: ORF K13
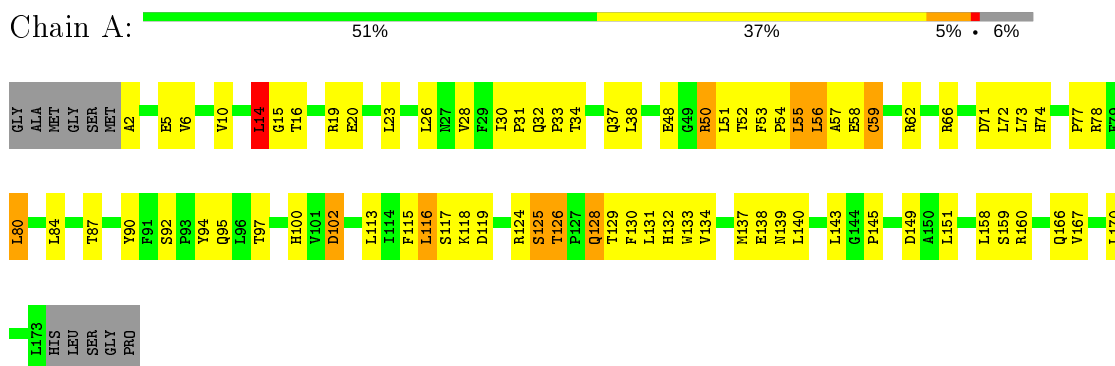
- Molecule 1: ORF K13
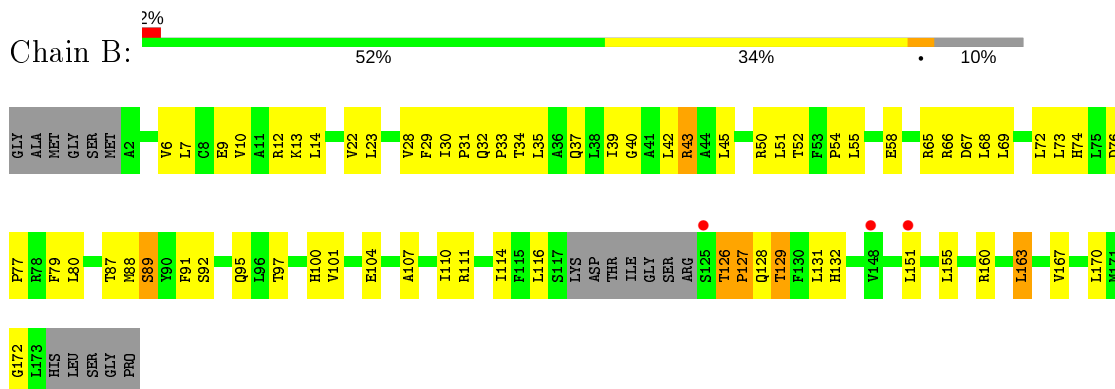
- Molecule 2: NF-kappa-B essential modulator

- Molecule 2: NF-kappa-B essential modulator

Chain E:

4%

33%   11%   •   55%

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	145.67Å 145.67Å 101.54Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 3.20 36.42 – 3.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (30.00-3.20) 100.0 (36.42-3.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$<I/\sigma(I)>$ [1]	3.01 (at 3.18Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.261 , 0.287 0.241 , 0.269	Depositor DCC
R_{free} test set	1065 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å^2)	86.0	Xtriage
Anisotropy	0.577	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 56.5	EDS
L-test for twinning[2]	$<|L|> = 0.48, <L^2> = 0.31$	Xtriage
Estimated twinning fraction	0.034 for -h,-k,l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	3477	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 3.76% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 (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	0.50	0/1365	0.68	0/1854
1	B	0.48	0/1286	0.65	1/1748 (0.1%)
2	D	0.47	0/457	0.56	0/613
2	E	0.56	0/424	0.58	0/573
All	All	0.50	0/3532	0.64	1/4788 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	126	THR	C-N-CD	-6.42	106.47	120.60

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	1341	0	1332	54	0
1	B	1264	0	1236	65	0
2	D	452	0	416	16	0
2	E	420	0	368	12	0
All	All	3477	0	3352	141	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 21.

The worst 5 of 141 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:87:THR:HG22	1:B:88:MET:H	1.28	0.97
1:B:129:THR:HG23	1:B:132:HIS:HB2	1.50	0.93
1:B:14:LEU:HD21	1:B:22:VAL:HG21	1.51	0.91
1:A:117:SER:O	1:A:119:ASP:N	2.06	0.88
1:A:50:ARG:HH11	1:A:50:ARG:HB3	1.41	0.83

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	170/183 (93%)	144 (85%)	20 (12%)	6 (4%)	3	24
1	B	161/183 (88%)	136 (84%)	20 (12%)	5 (3%)	4	26
2	D	57/130 (44%)	57 (100%)	0	0	100	100
2	E	56/130 (43%)	50 (89%)	6 (11%)	0	100	100
All	All	444/626 (71%)	387 (87%)	46 (10%)	11 (2%)	5	32

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	14	LEU
1	A	118	LYS
1	A	125	SER
1	B	127	PRO
1	A	116	LEU

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	144/160 (90%)	128 (89%)	16 (11%)	6	25
1	B	133/160 (83%)	130 (98%)	3 (2%)	50	78
2	D	42/107 (39%)	39 (93%)	3 (7%)	14	47
2	E	37/107 (35%)	33 (89%)	4 (11%)	6	27
All	All	356/534 (67%)	330 (93%)	26 (7%)	14	46

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	113	LEU
1	A	143	LEU
2	E	237	LEU
1	A	116	LEU
1	A	128	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	95	GLN
1	B	132	HIS
2	D	235	HIS
1	B	37	GLN
2	D	231	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 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 (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(Å²)	Q<0.9
1	A	172/183 (93%)	-0.39	0	100	100	39, 60, 79, 96	0
1	B	165/183 (90%)	-0.17	3 (1%)	68	55	40, 71, 113, 128	0
2	D	59/130 (45%)	-0.10	3 (5%)	28	16	36, 70, 124, 129	0
2	E	58/130 (44%)	0.34	5 (8%)	10	5	31, 79, 125, 134	0
All	All	454/626 (72%)	-0.18	11 (2%)	59	44	31, 66, 116, 134	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	252	SER	3.6
2	E	251	GLY	3.1
1	B	125	SER	3.1
1	B	151	LEU	3.0
2	E	198	GLN	3.0

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.