



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 07:55 AM GMT

PDB ID : 3CM2
Title : Crystal Structure of XIAP BIR3 domain in complex with a Smac-mimetic compound, Smac010
Authors : Cossu, F.; Mastrangelo, E.; Milani, M.
Deposited on : 2008-03-20
Resolution : 2.50 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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

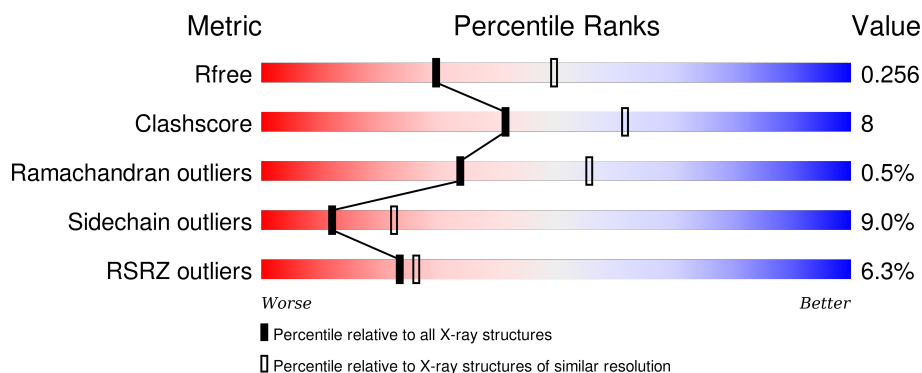
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	A	130	<div> <div>3%</div> <div>62%</div> <div>15%</div> <div>•</div> <div>21%</div> </div>
1	B	130	<div> <div>11%</div> <div>58%</div> <div>20%</div> <div>••</div> <div>21%</div> </div>
1	C	130	<div> <div>2%</div> <div>62%</div> <div>15%</div> <div>•</div> <div>22%</div> </div>
1	D	130	<div> <div>3%</div> <div>63%</div> <div>13%</div> <div>•</div> <div>22%</div> </div>
1	E	130	<div> <div>5%</div> <div>68%</div> <div>8%</div> <div>•</div> <div>22%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	130	
1	G	130	
1	H	130	
1	I	130	
1	J	130	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	X23	A	600	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8952 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 Baculoviral IAP repeat-containing protein 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	102	Total	C	N	O	S	0	0	0
			832	532	142	153	5			
1	A	103	Total	C	N	O	S	0	0	0
			838	535	143	155	5			
1	B	103	Total	C	N	O	S	0	0	0
			838	535	143	155	5			
1	C	102	Total	C	N	O	S	0	0	0
			831	531	142	153	5			
1	E	102	Total	C	N	O	S	0	0	0
			832	532	142	153	5			
1	F	103	Total	C	N	O	S	0	0	0
			838	535	143	155	5			
1	G	102	Total	C	N	O	S	0	0	0
			832	532	142	153	5			
1	H	102	Total	C	N	O	S	0	0	0
			832	532	142	153	5			
1	I	102	Total	C	N	O	S	0	0	0
			832	532	142	153	5			
1	J	103	Total	C	N	O	S	0	0	0
			839	536	143	155	5			

There are 140 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	227	MET	-	EXPRESSION TAG	UNP P98170
D	228	ALA	-	EXPRESSION TAG	UNP P98170
D	229	SER	-	EXPRESSION TAG	UNP P98170
D	230	MET	-	EXPRESSION TAG	UNP P98170
D	231	THR	-	EXPRESSION TAG	UNP P98170
D	232	GLY	-	EXPRESSION TAG	UNP P98170
D	233	GLY	-	EXPRESSION TAG	UNP P98170
D	234	GLN	-	EXPRESSION TAG	UNP P98170
D	235	GLN	-	EXPRESSION TAG	UNP P98170

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Chain	Residue	Modelled	Actual	Comment	Reference
D	236	MET	-	EXPRESSION TAG	UNP P98170
D	237	GLY	-	EXPRESSION TAG	UNP P98170
D	238	ARG	-	EXPRESSION TAG	UNP P98170
D	239	GLY	-	EXPRESSION TAG	UNP P98170
D	240	SER	-	EXPRESSION TAG	UNP P98170
A	227	MET	-	EXPRESSION TAG	UNP P98170
A	228	ALA	-	EXPRESSION TAG	UNP P98170
A	229	SER	-	EXPRESSION TAG	UNP P98170
A	230	MET	-	EXPRESSION TAG	UNP P98170
A	231	THR	-	EXPRESSION TAG	UNP P98170
A	232	GLY	-	EXPRESSION TAG	UNP P98170
A	233	GLY	-	EXPRESSION TAG	UNP P98170
A	234	GLN	-	EXPRESSION TAG	UNP P98170
A	235	GLN	-	EXPRESSION TAG	UNP P98170
A	236	MET	-	EXPRESSION TAG	UNP P98170
A	237	GLY	-	EXPRESSION TAG	UNP P98170
A	238	ARG	-	EXPRESSION TAG	UNP P98170
A	239	GLY	-	EXPRESSION TAG	UNP P98170
A	240	SER	-	EXPRESSION TAG	UNP P98170
B	227	MET	-	EXPRESSION TAG	UNP P98170
B	228	ALA	-	EXPRESSION TAG	UNP P98170
B	229	SER	-	EXPRESSION TAG	UNP P98170
B	230	MET	-	EXPRESSION TAG	UNP P98170
B	231	THR	-	EXPRESSION TAG	UNP P98170
B	232	GLY	-	EXPRESSION TAG	UNP P98170
B	233	GLY	-	EXPRESSION TAG	UNP P98170
B	234	GLN	-	EXPRESSION TAG	UNP P98170
B	235	GLN	-	EXPRESSION TAG	UNP P98170
B	236	MET	-	EXPRESSION TAG	UNP P98170
B	237	GLY	-	EXPRESSION TAG	UNP P98170
B	238	ARG	-	EXPRESSION TAG	UNP P98170
B	239	GLY	-	EXPRESSION TAG	UNP P98170
B	240	SER	-	EXPRESSION TAG	UNP P98170
C	227	MET	-	EXPRESSION TAG	UNP P98170
C	228	ALA	-	EXPRESSION TAG	UNP P98170
C	229	SER	-	EXPRESSION TAG	UNP P98170
C	230	MET	-	EXPRESSION TAG	UNP P98170
C	231	THR	-	EXPRESSION TAG	UNP P98170
C	232	GLY	-	EXPRESSION TAG	UNP P98170
C	233	GLY	-	EXPRESSION TAG	UNP P98170
C	234	GLN	-	EXPRESSION TAG	UNP P98170
C	235	GLN	-	EXPRESSION TAG	UNP P98170

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Chain	Residue	Modelled	Actual	Comment	Reference
C	236	MET	-	EXPRESSION TAG	UNP P98170
C	237	GLY	-	EXPRESSION TAG	UNP P98170
C	238	ARG	-	EXPRESSION TAG	UNP P98170
C	239	GLY	-	EXPRESSION TAG	UNP P98170
C	240	SER	-	EXPRESSION TAG	UNP P98170
E	227	MET	-	EXPRESSION TAG	UNP P98170
E	228	ALA	-	EXPRESSION TAG	UNP P98170
E	229	SER	-	EXPRESSION TAG	UNP P98170
E	230	MET	-	EXPRESSION TAG	UNP P98170
E	231	THR	-	EXPRESSION TAG	UNP P98170
E	232	GLY	-	EXPRESSION TAG	UNP P98170
E	233	GLY	-	EXPRESSION TAG	UNP P98170
E	234	GLN	-	EXPRESSION TAG	UNP P98170
E	235	GLN	-	EXPRESSION TAG	UNP P98170
E	236	MET	-	EXPRESSION TAG	UNP P98170
E	237	GLY	-	EXPRESSION TAG	UNP P98170
E	238	ARG	-	EXPRESSION TAG	UNP P98170
E	239	GLY	-	EXPRESSION TAG	UNP P98170
E	240	SER	-	EXPRESSION TAG	UNP P98170
F	227	MET	-	EXPRESSION TAG	UNP P98170
F	228	ALA	-	EXPRESSION TAG	UNP P98170
F	229	SER	-	EXPRESSION TAG	UNP P98170
F	230	MET	-	EXPRESSION TAG	UNP P98170
F	231	THR	-	EXPRESSION TAG	UNP P98170
F	232	GLY	-	EXPRESSION TAG	UNP P98170
F	233	GLY	-	EXPRESSION TAG	UNP P98170
F	234	GLN	-	EXPRESSION TAG	UNP P98170
F	235	GLN	-	EXPRESSION TAG	UNP P98170
F	236	MET	-	EXPRESSION TAG	UNP P98170
F	237	GLY	-	EXPRESSION TAG	UNP P98170
F	238	ARG	-	EXPRESSION TAG	UNP P98170
F	239	GLY	-	EXPRESSION TAG	UNP P98170
F	240	SER	-	EXPRESSION TAG	UNP P98170
G	227	MET	-	EXPRESSION TAG	UNP P98170
G	228	ALA	-	EXPRESSION TAG	UNP P98170
G	229	SER	-	EXPRESSION TAG	UNP P98170
G	230	MET	-	EXPRESSION TAG	UNP P98170
G	231	THR	-	EXPRESSION TAG	UNP P98170
G	232	GLY	-	EXPRESSION TAG	UNP P98170
G	233	GLY	-	EXPRESSION TAG	UNP P98170
G	234	GLN	-	EXPRESSION TAG	UNP P98170
G	235	GLN	-	EXPRESSION TAG	UNP P98170

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Chain	Residue	Modelled	Actual	Comment	Reference
G	236	MET	-	EXPRESSION TAG	UNP P98170
G	237	GLY	-	EXPRESSION TAG	UNP P98170
G	238	ARG	-	EXPRESSION TAG	UNP P98170
G	239	GLY	-	EXPRESSION TAG	UNP P98170
G	240	SER	-	EXPRESSION TAG	UNP P98170
H	227	MET	-	EXPRESSION TAG	UNP P98170
H	228	ALA	-	EXPRESSION TAG	UNP P98170
H	229	SER	-	EXPRESSION TAG	UNP P98170
H	230	MET	-	EXPRESSION TAG	UNP P98170
H	231	THR	-	EXPRESSION TAG	UNP P98170
H	232	GLY	-	EXPRESSION TAG	UNP P98170
H	233	GLY	-	EXPRESSION TAG	UNP P98170
H	234	GLN	-	EXPRESSION TAG	UNP P98170
H	235	GLN	-	EXPRESSION TAG	UNP P98170
H	236	MET	-	EXPRESSION TAG	UNP P98170
H	237	GLY	-	EXPRESSION TAG	UNP P98170
H	238	ARG	-	EXPRESSION TAG	UNP P98170
H	239	GLY	-	EXPRESSION TAG	UNP P98170
H	240	SER	-	EXPRESSION TAG	UNP P98170
I	227	MET	-	EXPRESSION TAG	UNP P98170
I	228	ALA	-	EXPRESSION TAG	UNP P98170
I	229	SER	-	EXPRESSION TAG	UNP P98170
I	230	MET	-	EXPRESSION TAG	UNP P98170
I	231	THR	-	EXPRESSION TAG	UNP P98170
I	232	GLY	-	EXPRESSION TAG	UNP P98170
I	233	GLY	-	EXPRESSION TAG	UNP P98170
I	234	GLN	-	EXPRESSION TAG	UNP P98170
I	235	GLN	-	EXPRESSION TAG	UNP P98170
I	236	MET	-	EXPRESSION TAG	UNP P98170
I	237	GLY	-	EXPRESSION TAG	UNP P98170
I	238	ARG	-	EXPRESSION TAG	UNP P98170
I	239	GLY	-	EXPRESSION TAG	UNP P98170
I	240	SER	-	EXPRESSION TAG	UNP P98170
J	227	MET	-	EXPRESSION TAG	UNP P98170
J	228	ALA	-	EXPRESSION TAG	UNP P98170
J	229	SER	-	EXPRESSION TAG	UNP P98170
J	230	MET	-	EXPRESSION TAG	UNP P98170
J	231	THR	-	EXPRESSION TAG	UNP P98170
J	232	GLY	-	EXPRESSION TAG	UNP P98170
J	233	GLY	-	EXPRESSION TAG	UNP P98170
J	234	GLN	-	EXPRESSION TAG	UNP P98170
J	235	GLN	-	EXPRESSION TAG	UNP P98170

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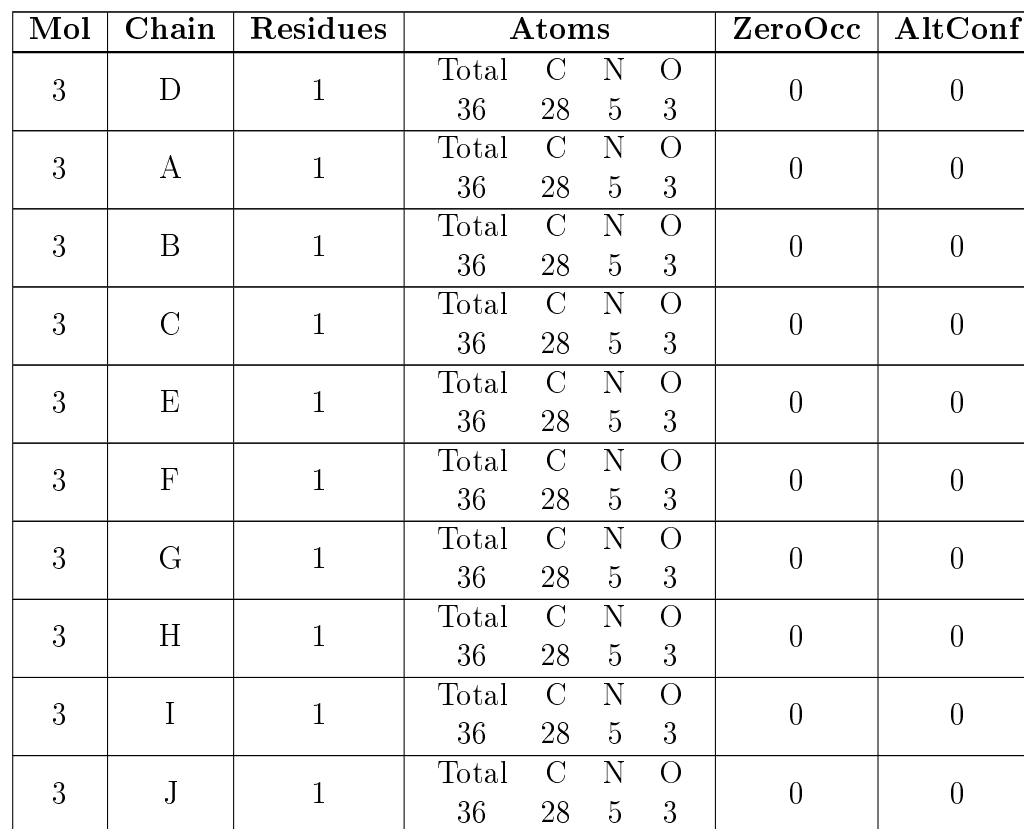
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Chain	Residue	Modelled	Actual	Comment	Reference
J	236	MET	-	EXPRESSION TAG	UNP P98170
J	237	GLY	-	EXPRESSION TAG	UNP P98170
J	238	ARG	-	EXPRESSION TAG	UNP P98170
J	239	GLY	-	EXPRESSION TAG	UNP P98170
J	240	SER	-	EXPRESSION TAG	UNP P98170

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	1	Total Zn 1 1	0	0
2	J	1	Total Zn 1 1	0	0
2	D	1	Total Zn 1 1	0	0
2	E	1	Total Zn 1 1	0	0
2	H	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0
2	I	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0
2	A	1	Total Zn 1 1	0	0
2	F	1	Total Zn 1 1	0	0

- Molecule 3 is (3S,6S,7R,9AS)-6-([(2S)-2-AMINO BUTANOYL]AMINO)-7-(AMINOMETHYL)-N-(DIPHENYLMETHYL)-5-OXOOCTAHYDRO-1H-PYRROLO[1,2-A]AZEPINE-3-CARBOXAMIDE (three-letter code: X23) (formula: C₂₈H₃₇N₅O₃).



- | Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|------------------|---------|---------|
| 4 | A | 20 | Total O
20 20 | 0 | 0 |
| 4 | B | 23 | Total O
23 23 | 0 | 0 |



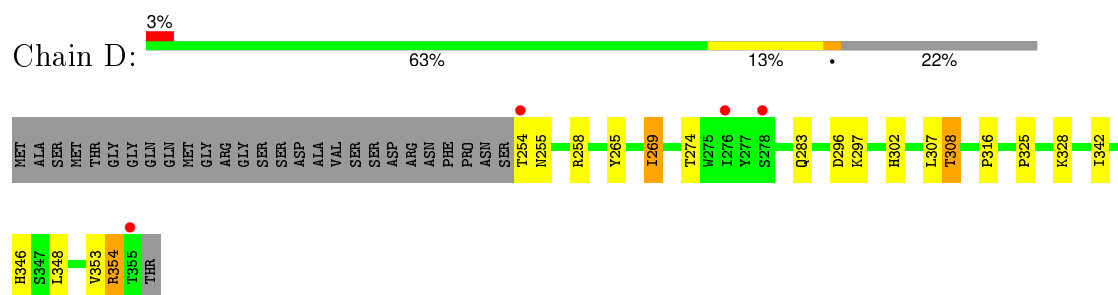
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	22	Total 22	O 22	0	0
4	D	23	Total 23	O 23	0	0
4	E	33	Total 33	O 33	0	0
4	F	24	Total 24	O 24	0	0
4	G	18	Total 18	O 18	0	0
4	H	27	Total 27	O 27	0	0
4	I	29	Total 29	O 29	0	0
4	J	19	Total 19	O 19	0	0

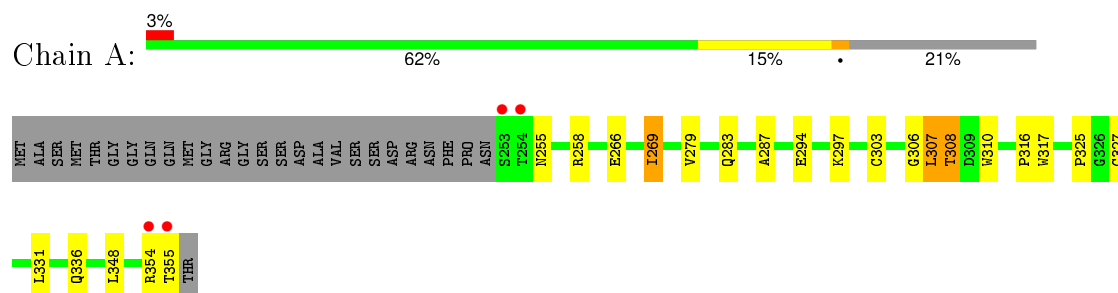
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

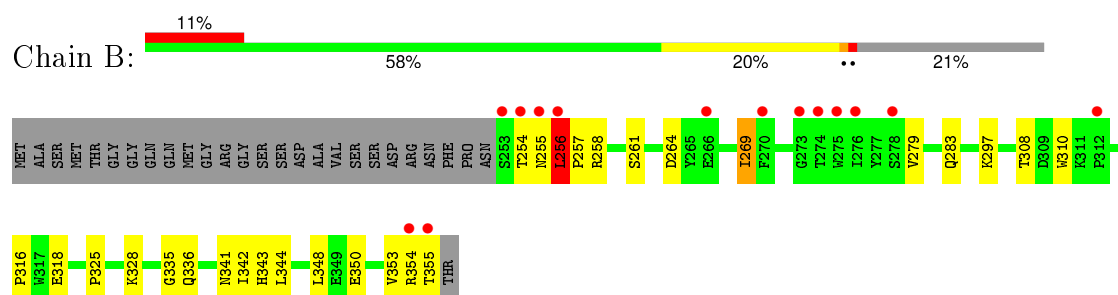
- Molecule 1: Baculoviral IAP repeat-containing protein 4



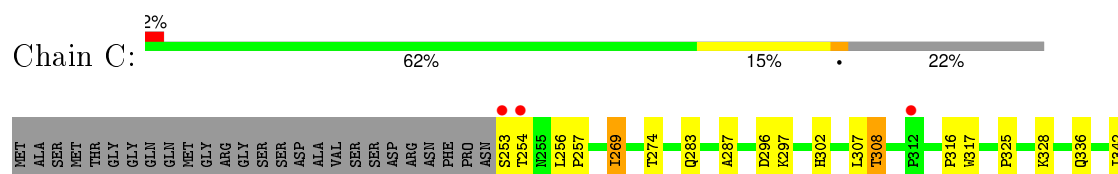
- Molecule 1: Baculoviral IAP repeat-containing protein 4



- Molecule 1: Baculoviral IAP repeat-containing protein 4



- Molecule 1: Baculoviral IAP repeat-containing protein 4

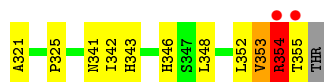




- Molecule 1: Baculoviral IAP repeat-containing protein 4



- Molecule 1: Baculoviral IAP repeat-containing protein 4



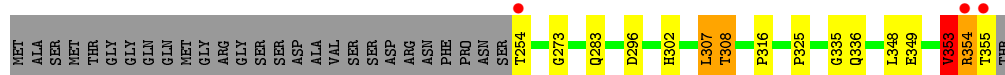
- Molecule 1: Baculoviral IAP repeat-containing protein 4



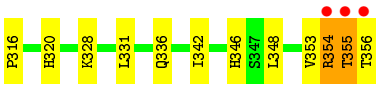
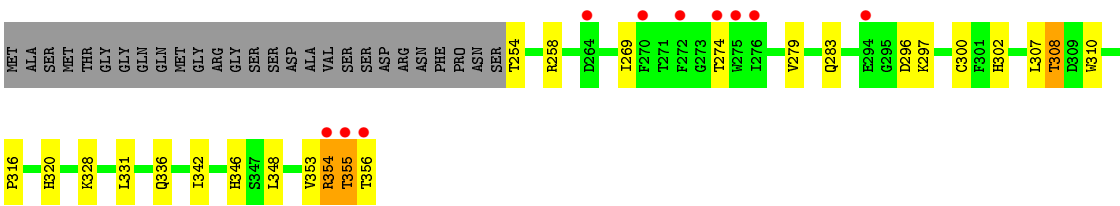
- Molecule 1: Baculoviral IAP repeat-containing protein 4



- Molecule 1: Baculoviral IAP repeat-containing protein 4



- Molecule 1: Baculoviral IAP repeat-containing protein 4



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	77.53Å 108.35Å 225.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.50 39.05 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.9 (40.00-2.50) 99.9 (39.05-2.50)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.27 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.221 , 0.264 0.217 , 0.256	Depositor DCC
R_{free} test set	3376 reflections (5.35%)	DCC
Wilson B-factor (Å ²)	50.0	Xtriage
Anisotropy	0.215	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 49.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	3 of 66464 reflections (0.005%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8952	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.57% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, X23

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	0.42	0/864	0.56	0/1171
1	B	0.40	0/864	0.54	0/1171
1	C	0.41	0/857	0.55	0/1161
1	D	0.44	0/858	0.56	0/1163
1	E	0.44	0/858	0.55	0/1163
1	F	0.40	0/864	0.55	0/1171
1	G	0.41	0/858	0.54	0/1163
1	H	0.43	0/858	0.58	0/1163
1	I	0.40	0/858	0.53	0/1163
1	J	0.41	0/865	0.54	0/1173
All	All	0.42	0/8604	0.55	0/11662

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	B	0	1
1	C	0	1
1	F	0	1
1	I	0	1
1	J	1	1
All	All	1	5

There are no bond length outliers.

There are no bond angle outliers.

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	J	355	THR	CB

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	255	ASN	Peptide
1	C	253	SER	Peptide
1	F	354	ARG	Peptide
1	I	353	VAL	Peptide
1	J	354	ARG	Peptide

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	838	0	787	18	0
1	B	838	0	786	35	0
1	C	831	0	779	15	0
1	D	832	0	782	19	0
1	E	832	0	781	8	0
1	F	838	0	787	14	0
1	G	832	0	781	6	0
1	H	832	0	781	23	0
1	I	832	0	781	11	0
1	J	839	0	789	17	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
3	A	36	0	37	0	0
3	B	36	0	37	0	0
3	C	36	0	36	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	36	0	36	0	0
3	E	36	0	37	0	0
3	F	36	0	37	0	0
3	G	36	0	37	1	0
3	H	36	0	37	2	0
3	I	36	0	37	1	0
3	J	36	0	37	0	0
4	A	20	0	0	0	0
4	B	23	0	0	0	0
4	C	22	0	0	0	0
4	D	23	0	0	1	0
4	E	33	0	0	0	0
4	F	24	0	0	0	0
4	G	18	0	0	0	0
4	H	27	0	0	0	0
4	I	29	0	0	1	0
4	J	19	0	0	0	0
All	All	8952	0	8202	143	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 8.

The worst 5 of 143 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:256:LEU:CB	1:B:257:PRO:HD3	1.59	1.29
1:B:256:LEU:HB3	1:B:257:PRO:HD3	1.15	1.11
1:D:354:ARG:HG2	1:D:354:ARG:O	1.48	1.04
1:B:297:LYS:HG2	1:B:308:THR:CG2	1.94	0.96
1:B:354:ARG:H	1:B:355:THR:HA	1.31	0.95

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	101/130 (78%)	97 (96%)	4 (4%)	0	100	100
1	B	101/130 (78%)	90 (89%)	10 (10%)	1 (1%)	19	34
1	C	100/130 (77%)	97 (97%)	3 (3%)	0	100	100
1	D	100/130 (77%)	96 (96%)	4 (4%)	0	100	100
1	E	100/130 (77%)	99 (99%)	1 (1%)	0	100	100
1	F	101/130 (78%)	94 (93%)	7 (7%)	0	100	100
1	G	100/130 (77%)	95 (95%)	4 (4%)	1 (1%)	19	34
1	H	100/130 (77%)	94 (94%)	5 (5%)	1 (1%)	19	34
1	I	100/130 (77%)	95 (95%)	3 (3%)	2 (2%)	9	15
1	J	101/130 (78%)	98 (97%)	3 (3%)	0	100	100
All	All	1004/1300 (77%)	955 (95%)	44 (4%)	5 (0%)	34	55

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	273	GLY
1	I	353	VAL
1	B	256	LEU
1	H	353	VAL
1	I	273	GLY

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	88/109 (81%)	83 (94%)	5 (6%)	25	46
1	B	88/109 (81%)	80 (91%)	8 (9%)	12	22
1	C	87/109 (80%)	81 (93%)	6 (7%)	19	35
1	D	87/109 (80%)	79 (91%)	8 (9%)	11	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	87/109 (80%)	80 (92%)	7 (8%)	15	28
1	F	88/109 (81%)	73 (83%)	15 (17%)	2	4
1	G	87/109 (80%)	78 (90%)	9 (10%)	9	17
1	H	87/109 (80%)	79 (91%)	8 (9%)	11	21
1	I	87/109 (80%)	82 (94%)	5 (6%)	25	46
1	J	88/109 (81%)	80 (91%)	8 (9%)	12	22
All	All	874/1090 (80%)	795 (91%)	79 (9%)	12	22

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	256	LEU
1	F	309	ASP
1	J	269	ILE
1	F	258	ARG
1	F	286	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	336	GLN
1	F	255	ASN
1	J	341	ASN
1	E	343	HIS
1	F	343	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 20 ligands modelled in this entry, 10 are monoatomic - leaving 10 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	X23	A	600	-	37,39,39	0.66	0	44,54,54	1.94	10 (22%)
3	X23	B	600	-	37,39,39	0.73	0	44,54,54	1.88	12 (27%)
3	X23	C	600	-	37,39,39	0.64	0	44,54,54	2.14	13 (29%)
3	X23	D	600	-	37,39,39	1.00	2 (5%)	44,54,54	2.06	12 (27%)
3	X23	E	600	-	37,39,39	0.70	1 (2%)	44,54,54	1.93	12 (27%)
3	X23	F	600	-	37,39,39	0.75	1 (2%)	44,54,54	1.82	8 (18%)
3	X23	G	600	-	37,39,39	0.69	0	44,54,54	1.78	8 (18%)
3	X23	H	600	-	37,39,39	0.85	2 (5%)	44,54,54	1.95	10 (22%)
3	X23	I	600	-	37,39,39	0.89	3 (8%)	44,54,54	1.82	9 (20%)
3	X23	J	600	-	37,39,39	0.74	0	44,54,54	1.83	9 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	X23	A	600	-	-	0/28/58/58	0/4/4/4
3	X23	B	600	-	-	0/28/58/58	0/4/4/4
3	X23	C	600	-	-	0/28/58/58	0/4/4/4
3	X23	D	600	-	-	0/28/58/58	0/4/4/4
3	X23	E	600	-	-	0/28/58/58	0/4/4/4
3	X23	F	600	-	-	0/28/58/58	0/4/4/4
3	X23	G	600	-	-	0/28/58/58	0/4/4/4
3	X23	H	600	-	-	0/28/58/58	0/4/4/4
3	X23	I	600	-	-	0/28/58/58	0/4/4/4
3	X23	J	600	-	-	0/28/58/58	0/4/4/4

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	600	X23	CBA-NBJ	-2.79	1.32	1.35
3	H	600	X23	CBA-NBJ	-2.30	1.32	1.35
3	E	600	X23	CBA-NBJ	-2.24	1.32	1.35
3	F	600	X23	CBA-NBJ	-2.08	1.32	1.35
3	I	600	X23	CBA-NBJ	-2.01	1.33	1.35

The worst 5 of 103 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	600	X23	CBI-CAZ-NAW	-4.30	106.98	116.64
3	E	600	X23	CBI-CAZ-NAW	-3.84	108.02	116.64
3	H	600	X23	CBI-CAZ-NAW	-3.66	108.42	116.64
3	D	600	X23	CBI-CAZ-NAW	-3.63	108.48	116.64
3	B	600	X23	CBI-CAZ-NAW	-3.53	108.71	116.64

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	600	X23	3	0
3	G	600	X23	1	0
3	H	600	X23	2	0
3	I	600	X23	1	0

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	A	103/130 (79%)	0.26	4 (3%) 43 48	28, 48, 71, 90	1 (0%)
1	B	103/130 (79%)	0.60	14 (13%) 4 4	28, 54, 86, 97	1 (0%)
1	C	102/130 (78%)	0.21	3 (2%) 55 60	28, 45, 69, 92	1 (0%)
1	D	102/130 (78%)	0.17	4 (3%) 43 48	25, 42, 66, 89	1 (0%)
1	E	102/130 (78%)	0.24	6 (5%) 26 29	26, 42, 67, 94	1 (0%)
1	F	103/130 (79%)	0.51	12 (11%) 6 6	29, 54, 78, 94	1 (0%)
1	G	102/130 (78%)	0.48	7 (6%) 20 22	31, 50, 75, 88	1 (0%)
1	H	102/130 (78%)	0.35	2 (1%) 68 72	28, 46, 71, 88	1 (0%)
1	I	102/130 (78%)	0.28	3 (2%) 55 60	30, 48, 70, 93	1 (0%)
1	J	103/130 (79%)	0.55	10 (9%) 10 10	34, 53, 77, 105	1 (0%)
All	All	1024/1300 (78%)	0.37	65 (6%) 23 26	25, 49, 78, 105	10 (0%)

The worst 5 of 65 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	356	THR	7.7
1	I	355	THR	7.3
1	G	355	THR	5.9
1	B	274	THR	5.8
1	F	355	THR	5.8

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 ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	X23	A	600	36/36	0.93	0.18	2.09	46,53,61,62	0
3	X23	G	600	36/36	0.92	0.18	1.11	47,53,62,63	0
3	X23	J	600	36/36	0.91	0.18	0.92	48,55,62,62	0
3	X23	F	600	36/36	0.94	0.16	0.72	45,55,61,61	0
3	X23	H	600	36/36	0.92	0.18	0.64	38,49,55,58	0
3	X23	I	600	36/36	0.94	0.16	0.49	40,51,54,55	0
3	X23	E	600	36/36	0.93	0.17	0.46	38,49,53,55	0
3	X23	C	600	36/36	0.94	0.17	0.33	39,47,52,63	0
3	X23	B	600	36/36	0.92	0.16	0.13	45,49,55,58	0
2	ZN	D	502	1/1	1.00	0.14	-0.08	30,30,30,30	0
2	ZN	H	502	1/1	0.99	0.14	-0.16	38,38,38,38	0
3	X23	D	600	36/36	0.95	0.15	-0.27	35,42,47,51	0
2	ZN	B	502	1/1	0.99	0.14	-0.41	38,38,38,38	0
2	ZN	C	502	1/1	1.00	0.14	-0.41	30,30,30,30	0
2	ZN	J	502	1/1	0.99	0.13	-0.67	38,38,38,38	0
2	ZN	A	502	1/1	0.99	0.13	-0.73	33,33,33,33	0
2	ZN	F	502	1/1	1.00	0.11	-0.96	39,39,39,39	0
2	ZN	I	502	1/1	1.00	0.12	-	38,38,38,38	0
2	ZN	G	502	1/1	1.00	0.13	-	36,36,36,36	0
2	ZN	E	502	1/1	1.00	0.14	-	32,32,32,32	0

6.5 Other polymers ⓘ

There are no such residues in this entry.