



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 11:04 PM UTC

PDB ID : 5MFC / pdb_00005mfc
Title : Designed armadillo repeat protein YIIIM5AII in complex with (KR)4-GFP
Authors : Hansen, S.; Kiefer, J.; Madhurantakam, C.; Mittl, P.; Plueckthun, A.
Deposited on : 2016-11-18
Resolution : 2.40 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
Mogul : 2022.3.0, CSD as543be (2022)
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

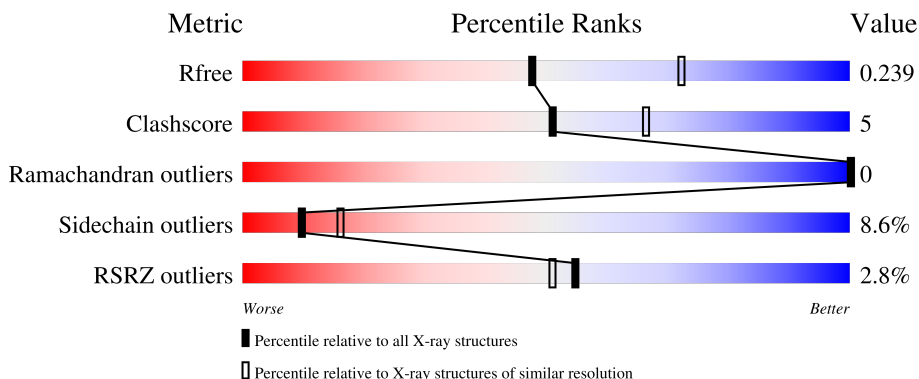
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	286	<div style="display: flex; align-items: center;"> <div style="width: 3%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 78%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 20%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: red;"></div> </div> <p style="text-align: center;">3% 78% 20% •</p>
1	C	286	<div style="display: flex; align-items: center;"> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 80%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 16%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: red;"></div> </div> <p style="text-align: center;">5% 80% 16% • •</p>
2	B	255	<div style="display: flex; align-items: center;"> <div style="width: 75%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 17%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: red;"></div> </div> <p style="text-align: center;">75% 17% • 5%</p>
2	D	255	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 71%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 21%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 1%; height: 10px; background-color: red;"></div> </div> <p style="text-align: center;">2% 71% 21% • 7%</p>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8151 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 YIIIM5AII.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	285	2111	1314	360	436	1	0	1	0
1	C	282	2108	1315	359	433	1	0	2	0

- Molecule 2 is a protein called (KR)4-Green fluorescent protein, Green fluorescent protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	241	1938	1224	344	364	6	0	0	0
2	D	238	1912	1208	338	360	6	0	0	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1030	ARG	SER	conflict	UNP A0A059PIQ0
B	1066	CRO	THR	chromophore	UNP A0A059PIQ0
B	1066	CRO	TYR	chromophore	UNP A0A059PIQ0
B	1066	CRO	GLY	chromophore	UNP A0A059PIQ0
B	1072	SER	ALA	conflict	UNP A0A059PIQ0
B	1080	ARG	GLN	conflict	UNP A0A059PIQ0
B	1206	VAL	ALA	conflict	UNP A0A059PIQ0
D	1030	ARG	SER	conflict	UNP A0A059PIQ0
D	1066	CRO	THR	chromophore	UNP A0A059PIQ0
D	1066	CRO	TYR	chromophore	UNP A0A059PIQ0
D	1066	CRO	GLY	chromophore	UNP A0A059PIQ0
D	1072	SER	ALA	conflict	UNP A0A059PIQ0
D	1080	ARG	GLN	conflict	UNP A0A059PIQ0
D	1206	VAL	ALA	conflict	UNP A0A059PIQ0

- Molecule 3 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 4 2 2	0	0

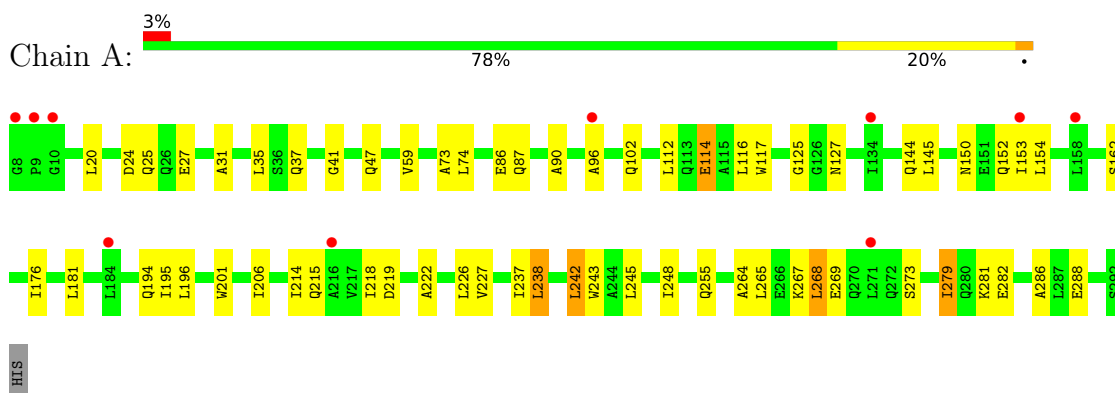
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	19	Total O 19 19	0	0
4	B	43	Total O 43 43	0	0
4	C	8	Total O 8 8	0	0
4	D	8	Total O 8 8	0	0

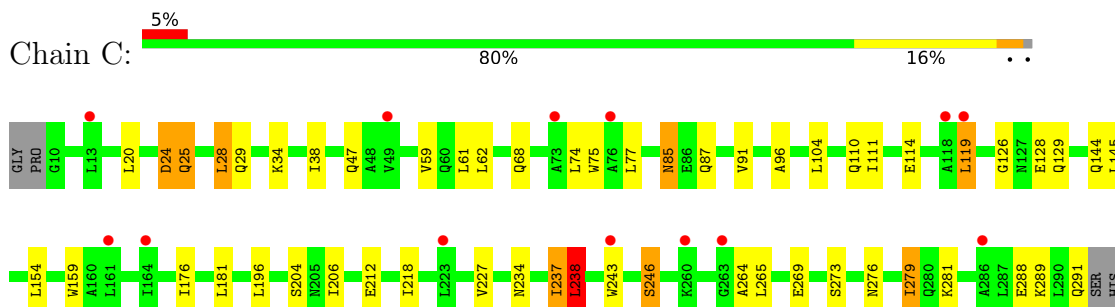
3 Residue-property plots [i](#)

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.

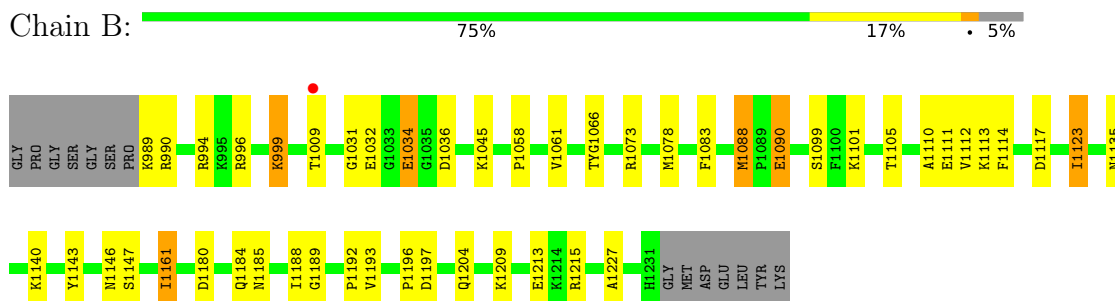
- Molecule 1: YIIIM5AII



- Molecule 1: YIIIM5AII

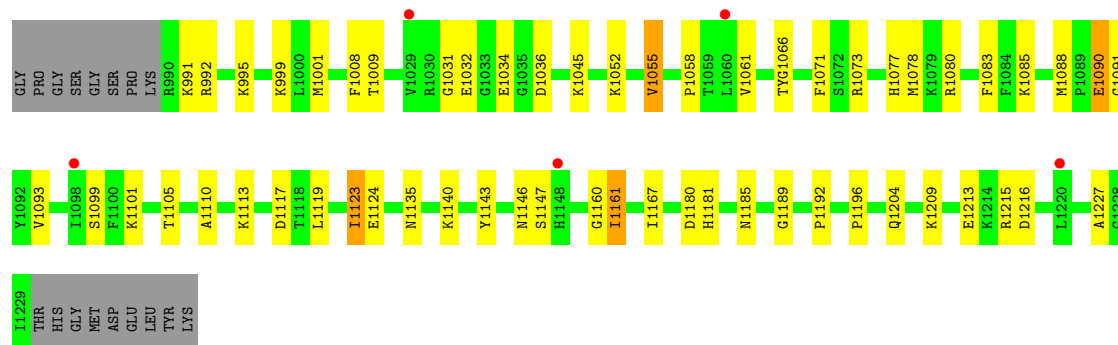


- Molecule 2: (KR)4-Green fluorescent protein, Green fluorescent protein



- Molecule 2: (KR)4-Green fluorescent protein, Green fluorescent protein





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	81.11Å 124.24Å 245.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.56 – 2.40 40.56 – 2.40	Depositor EDS
% Data completeness (in resolution range)	97.9 (40.56-2.40) 83.2 (40.56-2.40)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.19 (at 2.39Å)	Xtrriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.218 , 0.240 (Not available) , 0.239	Depositor DCC
R_{free} test set	2364 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	64.3	Xtrriage
Anisotropy	0.046	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 88.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8151	wwPDB-VP
Average B, all atoms (Å ²)	99.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.47% 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

5.1 Standard geometry

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

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	0.89	0/2134	1.48	17/2907 (0.6%)
1	C	0.87	0/2132	1.51	14/2905 (0.5%)
2	B	0.84	1/1955 (0.1%)	1.24	9/2631 (0.3%)
2	D	0.76	0/1928	1.24	11/2595 (0.4%)
All	All	0.84	1/8149 (0.0%)	1.38	51/11038 (0.5%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1088	MET	SD-CE	-9.10	1.56	1.79

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1034	GLU	CA-C-N	7.77	126.94	121.65
2	B	1034	GLU	C-N-CA	7.77	126.94	121.65
2	D	1055	VAL	N-CA-CB	-7.68	103.42	111.64
1	A	73	ALA	CA-C-N	7.11	129.81	120.28
1	A	73	ALA	C-N-CA	7.11	129.81	120.28

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	2111	0	2115	19	0
1	C	2108	0	2109	23	0
2	B	1938	0	1920	22	0
2	D	1912	0	1893	29	0
3	B	4	0	3	1	0
4	A	19	0	0	2	0
4	B	43	0	0	0	0
4	C	8	0	0	0	0
4	D	8	0	0	0	0
All	All	8151	0	8040	84	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 5.

The worst 5 of 84 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:D:1088:MET:HE1	2:D:1113:LYS:HA	1.58	0.84
2:B:1088:MET:HE1	2:B:1113:LYS:HA	1.62	0.82
1:A:242:LEU:HD11	1:A:282:GLU:HB3	1.62	0.81
2:D:1078:MET:HE1	2:D:1227:ALA:HA	1.70	0.73
1:C:126:GLY:H	1:C:129:GLN:HE21	1.34	0.73

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	284/286 (99%)	278 (98%)	6 (2%)	0	100	100
1	C	282/286 (99%)	277 (98%)	5 (2%)	0	100	100
2	B	236/255 (92%)	234 (99%)	2 (1%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	233/255 (91%)	230 (99%)	3 (1%)	0	100	100
All	All	1035/1082 (96%)	1019 (98%)	16 (2%)	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	224/224 (100%)	200 (89%)	24 (11%)	6	10
1	C	223/224 (100%)	198 (89%)	25 (11%)	6	9
2	B	211/221 (96%)	197 (93%)	14 (7%)	15	26
2	D	208/221 (94%)	196 (94%)	12 (6%)	18	32
All	All	866/890 (97%)	791 (91%)	75 (9%)	10	16

5 of 75 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	269	GLU
2	D	1123	ILE
1	C	279	ILE
2	D	999	LYS
2	B	989	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	71	GLN
1	C	152	GLN
1	C	129	GLN
1	C	197	GLN
1	A	255	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](#)

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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
2	CRO	D	1066	2	22,23,24	1.51	3 (13%)	30,32,34	2.18	6 (20%)
2	CRO	B	1066	2	22,23,24	1.38	2 (9%)	30,32,34	2.47	7 (23%)

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
2	CRO	D	1066	2	-	0/12/31/32	0/2/2/2
2	CRO	B	1066	2	-	0/12/31/32	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1066	CRO	C1-N2	4.25	1.38	1.32
2	B	1066	CRO	C1-N2	3.87	1.37	1.32
2	D	1066	CRO	C1-N3	3.05	1.42	1.37
2	B	1066	CRO	C1-N3	2.79	1.41	1.37
2	D	1066	CRO	CG2-CB2	2.05	1.50	1.46

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1066	CRO	O2-C2-CA2	-9.65	124.86	131.02
2	D	1066	CRO	O2-C2-CA2	-7.59	126.18	131.02

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1066	CRO	CA2-N2-C1	5.27	109.92	105.80
2	D	1066	CRO	CA2-N2-C1	5.01	109.72	105.80
2	B	1066	CRO	C2-CA2-N2	-3.49	106.45	108.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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	ACT	B	1301	-	3,3,3	1.60	1 (33%)	3,3,3	1.09	0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1301	ACT	CH3-C	2.57	1.59	1.49

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1301	ACT	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 [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	285/286 (99%)	0.52	10 (3%) 47 43	35, 85, 202, 219	1 (0%)
1	C	282/286 (98%)	0.67	13 (4%) 37 33	35, 105, 194, 206	2 (0%)
2	B	240/255 (94%)	0.21	1 (0%) 88 86	49, 70, 103, 186	0
2	D	237/255 (92%)	0.50	5 (2%) 63 59	64, 102, 142, 164	0
All	All	1044/1082 (96%)	0.48	29 (2%) 55 51	35, 92, 184, 219	3 (0%)

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	119	LEU	3.6
1	A	158	LEU	3.4
1	A	8	GLY	3.2
1	C	164	ILE	3.2
2	D	1148	HIS	3.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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. 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	B-factors(Å ²)	Q<0.9
2	CRO	D	1066	22/23	0.90	0.16	71,79,84,87	0
2	CRO	B	1066	22/23	0.94	0.10	54,56,58,61	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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. 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	B-factors(\AA^2)	Q<0.9
3	ACT	B	1301	4/4	0.87	0.09	52,61,61,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.