



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 3C3R
Title : ALIX BRO1 CHMP4C complex
Authors : McCullough, J.B.; Fisher, R.D.; Whitby, F.G.; Sundquist, W.I.; Hill, C.P.
Deposited on : 2008-01-28
Resolution : 2.02 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

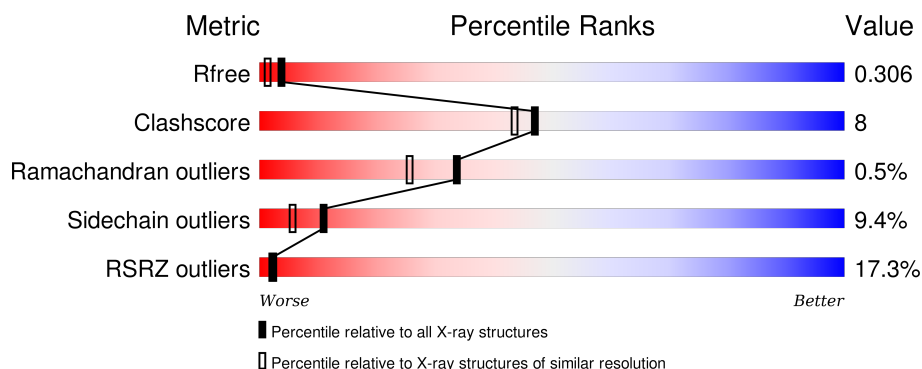
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.02 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	7858 (2.04-2.00)
Clashscore	102246	9060 (2.04-2.00)
Ramachandran outliers	100387	8952 (2.04-2.00)
Sidechain outliers	100360	8951 (2.04-2.00)
RSRZ outliers	91569	7873 (2.04-2.00)

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	380	
2	B	13	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2969 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 Programmed cell death 6-interacting protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	357	2803	1792	471	529	11	0	0	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	EXPRESSION TAG	UNP Q8WUM4
A	-19	HIS	-	EXPRESSION TAG	UNP Q8WUM4
A	-18	HIS	-	EXPRESSION TAG	UNP Q8WUM4
A	-17	HIS	-	EXPRESSION TAG	UNP Q8WUM4
A	-16	HIS	-	EXPRESSION TAG	UNP Q8WUM4
A	-15	HIS	-	EXPRESSION TAG	UNP Q8WUM4
A	-14	HIS	-	EXPRESSION TAG	UNP Q8WUM4
A	-13	HIS	-	EXPRESSION TAG	UNP Q8WUM4
A	-12	HIS	-	EXPRESSION TAG	UNP Q8WUM4
A	-11	HIS	-	EXPRESSION TAG	UNP Q8WUM4
A	-10	HIS	-	EXPRESSION TAG	UNP Q8WUM4
A	-9	SER	-	EXPRESSION TAG	UNP Q8WUM4
A	-8	GLY	-	EXPRESSION TAG	UNP Q8WUM4
A	-7	GLN	-	EXPRESSION TAG	UNP Q8WUM4
A	-6	ASN	-	EXPRESSION TAG	UNP Q8WUM4
A	-5	LEU	-	EXPRESSION TAG	UNP Q8WUM4
A	-4	TYR	-	EXPRESSION TAG	UNP Q8WUM4
A	-3	PHE	-	EXPRESSION TAG	UNP Q8WUM4
A	-2	GLN	-	EXPRESSION TAG	UNP Q8WUM4
A	-1	GLY	-	EXPRESSION TAG	UNP Q8WUM4
A	0	HIS	-	EXPRESSION TAG	UNP Q8WUM4

- Molecule 2 is a protein called Charged multivesicular body protein 4c peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	13	Total	C	N	O	0	0	0
			104	64	16	24			

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	55	Total	O	0	0
			55	55		
4	B	1	Total	O	0	0
			1	1		

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	120.91Å 62.40Å 76.35Å 90.00° 121.62° 90.00°	Depositor
Resolution (Å)	33.86 – 2.02 33.86 – 2.02	Depositor EDS
% Data completeness (in resolution range)	95.3 (33.86-2.02) 95.3 (33.86-2.02)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 2.03Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.243 , 0.288 0.259 , 0.306	Depositor DCC
R_{free} test set	2168 reflections (7.69%)	DCC
Wilson B-factor (Å ²)	47.9	Xtriage
Anisotropy	0.068	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 42.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 30373 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2969	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.02% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.75	0/2856	0.88	6/3854 (0.2%)
2	B	0.47	0/105	1.03	2/141 (1.4%)
All	All	0.74	0/2961	0.89	8/3995 (0.2%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	314	ASP	CB-CG-OD2	6.86	124.47	118.30
1	A	299	ASP	CB-CG-OD2	6.51	124.16	118.30
1	A	302	ASP	CB-CG-OD2	5.87	123.58	118.30
1	A	226	ASP	CB-CG-OD2	5.81	123.53	118.30
2	B	223	ASP	CB-CG-OD2	5.79	123.51	118.30
1	A	210	ASP	CB-CG-OD2	5.68	123.41	118.30
2	B	222	ASP	CB-CG-OD2	5.04	122.83	118.30
1	A	235	ASP	CB-CG-OD2	5.03	122.83	118.30

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	2803	0	2828	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	104	0	92	5	0
3	A	6	0	8	0	0
4	A	55	0	0	4	0
4	B	1	0	0	0	0
All	All	2969	0	2928	44	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.

All (44) 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:19:LYS:HB3	1:A:20:PRO:HD3	1.68	0.76
1:A:337:LEU:HD21	2:B:228:LEU:HB3	1.68	0.74
1:A:147:LYS:NZ	2:B:231:TRP:O	2.21	0.69
1:A:78:ILE:HD11	1:A:355:PHE:CD1	2.28	0.69
1:A:129:ALA:O	1:A:133:GLN:HG3	1.94	0.66
1:A:74:GLN:HE21	1:A:78:ILE:HD13	1.61	0.66
1:A:91:LEU:O	1:A:114:ALA:HA	1.96	0.66
1:A:56:ARG:HG2	4:A:3599:HOH:O	1.97	0.64
1:A:337:LEU:CD2	2:B:228:LEU:HB3	2.27	0.64
1:A:163:ILE:O	1:A:167:VAL:HG22	1.98	0.64
1:A:101:LYS:H	1:A:101:LYS:HD3	1.63	0.63
1:A:216:LEU:HD21	1:A:337:LEU:HD13	1.82	0.61
1:A:216:LEU:CD2	1:A:337:LEU:HD13	2.35	0.56
1:A:357:LYS:HA	1:A:357:LYS:HE3	1.89	0.55
1:A:58:LEU:HD21	4:A:3585:HOH:O	2.06	0.54
1:A:71:TYR:CZ	1:A:75:ILE:HD11	2.42	0.54
1:A:284:ILE:HD12	1:A:297:VAL:HG22	1.90	0.54
1:A:158:GLY:HA2	1:A:340:SER:HB3	1.90	0.54
1:A:139:ASN:HD22	1:A:139:ASN:C	2.11	0.54
1:A:284:ILE:HD12	1:A:297:VAL:CG2	2.39	0.53
1:A:219:GLN:HG2	1:A:336:THR:HB	1.93	0.51
1:A:50:ARG:O	1:A:54:VAL:HG22	2.09	0.51
1:A:201:LEU:O	4:A:3557:HOH:O	2.19	0.51
1:A:150:ALA:O	1:A:154:GLN:HG3	2.14	0.48
1:A:59:ASP:HB3	1:A:64:ALA:HB2	1.96	0.47
1:A:162:HIS:O	1:A:166:THR:HB	2.15	0.47
1:A:212:ILE:HD11	2:B:221:GLU:HA	1.96	0.47
1:A:78:ILE:HG22	1:A:116:LEU:HD21	1.97	0.47
1:A:101:LYS:H	1:A:101:LYS:CD	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:231:CYS:HB2	1:A:242:PHE:HD1	1.80	0.46
1:A:56:ARG:CG	4:A:3599:HOH:O	2.59	0.45
1:A:292:ASP:OD2	1:A:292:ASP:N	2.48	0.45
1:A:15:VAL:HG12	1:A:17:LEU:HD23	1.99	0.44
1:A:24:PHE:HD2	1:A:82:PHE:HD2	1.66	0.44
1:A:335:ALA:HB1	2:B:225:ILE:HD11	2.00	0.43
1:A:96:LYS:HG3	1:A:110:LYS:HG2	1.99	0.42
1:A:59:ASP:OD1	1:A:61:HIS:HB2	2.19	0.42
1:A:12:THR:HB	1:A:95:TRP:CE3	2.55	0.42
1:A:73:ASP:OD1	1:A:346:PRO:HA	2.20	0.41
1:A:81:LYS:HE3	1:A:81:LYS:HA	2.03	0.41
1:A:69:LEU:HD23	1:A:127:CYS:SG	2.61	0.40
1:A:19:LYS:HB3	1:A:20:PRO:CD	2.46	0.40
1:A:10:LYS:NZ	1:A:96:LYS:O	2.55	0.40
1:A:199:PHE:CE1	1:A:338:VAL:HG23	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	355/380 (93%)	335 (94%)	18 (5%)	2 (1%)	30	21
2	B	11/13 (85%)	11 (100%)	0	0	100	100
All	All	366/393 (93%)	346 (94%)	18 (5%)	2 (0%)	34	26

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	34	GLU
1	A	31	SER

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	299/320 (93%)	270 (90%)	29 (10%)	10	5
2	B	10/10 (100%)	10 (100%)	0	100	100
All	All	309/330 (94%)	280 (91%)	29 (9%)	11	6

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	LEU
1	A	28	THR
1	A	56	ARG
1	A	78	ILE
1	A	79	GLU
1	A	81	LYS
1	A	84	PHE
1	A	86	GLU
1	A	87	ASN
1	A	90	CYS
1	A	101	LYS
1	A	139	ASN
1	A	142	ASN
1	A	146	LEU
1	A	165	GLU
1	A	167	VAL
1	A	174	GLU
1	A	176	THR
1	A	182	ASP
1	A	184	VAL
1	A	228	PHE
1	A	296	ASN
1	A	297	VAL
1	A	298	LYS
1	A	337	LEU
1	A	338	VAL
1	A	339	LYS

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Mol	Chain	Res	Type
1	A	356	GLU
1	A	357	LYS

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

Mol	Chain	Res	Type
1	A	87	ASN
1	A	133	GLN
1	A	139	ASN
1	A	219	GLN
1	A	296	ASN

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](#)

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	GOL	A	3545	-	5,5,5	0.35	0	5,5,5	0.34	0

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	GOL	A	3545	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	357/380 (93%)	1.10	61 (17%) 2 2	17, 30, 64, 76	0
2	B	13/13 (100%)	1.55	3 (23%) 1 1	36, 40, 51, 52	0
All	All	370/393 (94%)	1.12	64 (17%) 2 2	17, 30, 64, 76	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	85	SER	10.5
1	A	83	PRO	9.5
1	A	105	PHE	8.4
1	A	84	PHE	7.8
1	A	107	GLY	7.4
1	A	106	GLY	7.0
1	A	28	THR	6.7
1	A	86	GLU	6.5
1	A	21	LEU	6.3
1	A	30	PRO	6.2
1	A	90	CYS	6.1
1	A	31	SER	5.9
1	A	25	ILE	5.7
1	A	103	SER	5.5
1	A	34	GLU	5.3
1	A	33	GLY	5.3
1	A	29	TYR	5.1
1	A	88	GLN	5.0
1	A	57	PRO	4.8
1	A	32	GLY	4.8
1	A	24	PHE	4.7
1	A	39	TYR	4.5
1	A	37	ALA	4.3
1	A	89	ILE	4.3

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Mol	Chain	Res	Type	RSRZ
1	A	35	GLU	4.0
1	A	356	GLU	4.0
1	A	108	SER	3.9
1	A	82	PHE	3.8
1	A	58	LEU	3.7
1	A	81	LYS	3.5
1	A	350	LYS	3.4
1	A	22	VAL	3.3
1	A	357	LYS	3.3
2	B	221	GLU	3.3
1	A	124	LEU	3.2
1	A	20	PRO	3.2
1	A	40	CYS	3.1
1	A	27	GLN	3.0
1	A	192	LEU	3.0
1	A	2	ALA	3.0
1	A	104	LEU	2.9
2	B	233	THR	2.9
1	A	358	MET	2.9
1	A	36	GLN	2.8
2	B	230	ALA	2.7
1	A	172	SER	2.7
1	A	60	LYS	2.6
1	A	123	VAL	2.5
1	A	190	ILE	2.5
1	A	193	ALA	2.5
1	A	91	LEU	2.5
1	A	191	MET	2.5
1	A	61	HIS	2.4
1	A	195	ALA	2.4
1	A	102	GLY	2.4
1	A	198	VAL	2.3
1	A	125	PHE	2.3
1	A	200	PHE	2.3
1	A	41	ARG	2.2
1	A	217	ALA	2.2
1	A	127	CYS	2.1
1	A	87	ASN	2.1
1	A	78	ILE	2.1
1	A	173	ARG	2.0

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](#)

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(\AA^2)	Q<0.9
3	GOL	A	3545	6/6	0.70	0.21	1.92	85,85,86,86	0

6.5 Other polymers [i](#)

There are no such residues in this entry.