



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 06:40 AM GMT

PDB ID : 4JD2
Title : Crystal structure of Bos taurus Arp2/3 complex binding with Mus musculus GMF
Authors : Nolen, B.J.; Luan, Q.
Deposited on : 2013-02-22
Resolution : 3.08 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

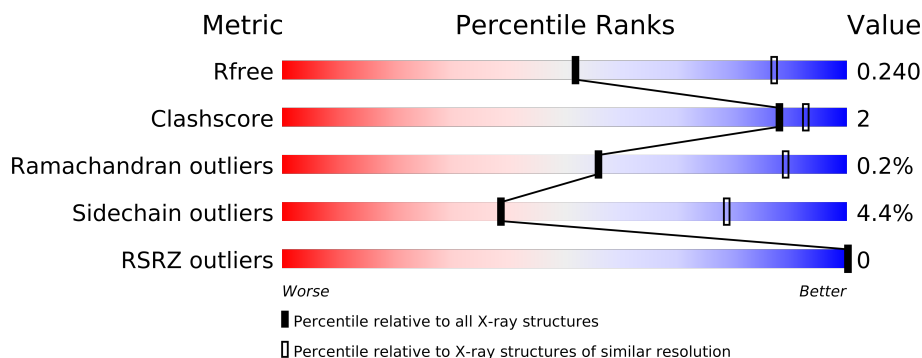
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 3.08 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}	66092	2204 (3.16-3.00)
Clashscore	79885	1061 (3.14-3.02)
Ramachandran outliers	78287	1025 (3.14-3.02)
Sidechain outliers	78261	1025 (3.14-3.02)
RSRZ outliers	66119	2206 (3.16-3.00)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	418	
2	B	394	
3	C	372	
4	D	300	
5	E	178	
6	F	168	
7	G	151	
8	H	142	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
9	CA	A	501	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
9	CA	B	501	-	X

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 16016 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Actin-related protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	398	Total	C	N	O	S	0	0	0
			3170	2034	531	591	14			

- Molecule 2 is a protein called Actin-related protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	377	Total	C	N	O	S	0	0	0
			2963	1898	507	542	16			

- Molecule 3 is a protein called Actin-related protein 2/3 complex subunit 1B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	342	Total	C	N	O	S	0	0	0
			2650	1681	464	486	19			

- Molecule 4 is a protein called Actin-related protein 2/3 complex subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	283	Total	C	N	O	S	0	0	0
			2280	1447	395	430	8			

- Molecule 5 is a protein called Actin-related protein 2/3 complex subunit 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	170	Total	C	N	O	S	0	0	0
			1350	869	225	247	9			

- Molecule 6 is a protein called Actin-related protein 2/3 complex subunit 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	166	Total	C	N	O	S	0	0	0
			1356	866	237	244	9			

- Molecule 7 is a protein called Actin-related protein 2/3 complex subunit 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	139	Total	C	N	O	S	0	0	0
			1041	650	183	205	3			

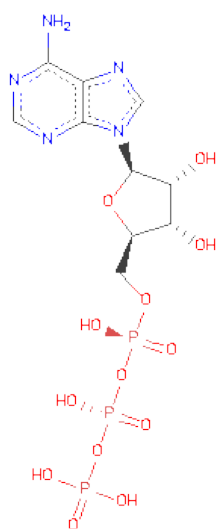
- Molecule 8 is a protein called Glia maturation factor gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	138	Total	C	N	O	S	0	0	0
			1116	713	188	208	7			

- Molecule 9 is CALCIUM ION (three-letter code: CA) (formula: Ca).

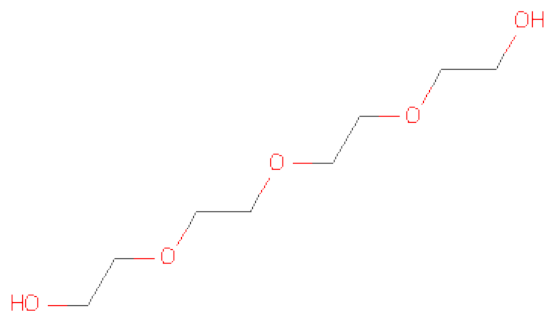
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	1	Total	Ca	0	0
			1	1		
9	A	1	Total	Ca	0	0
			1	1		

- Molecule 10 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
10	B	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 11 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C₈H₁₈O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	B	1	Total	C	O	0	0
			13	8	5		
11	F	1	Total	C	O	0	0
			13	8	5		

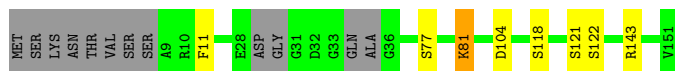
- Molecule 6: Actin-related protein 2/3 complex subunit 4

Chain F: 



- Molecule 7: Actin-related protein 2/3 complex subunit 5

Chain G: 



- Molecule 8: Glia maturation factor gamma

Chain H: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	231.54Å 231.54Å 109.74Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	35.82 – 3.08 35.82 – 3.08	Depositor EDS
% Data completeness (in resolution range)	97.6 (35.82-3.08) 97.6 (35.82-3.08)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.69 (at 3.06Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.209 , 0.248 0.207 , 0.240	Depositor DCC
R_{free} test set	3097 reflections (5.37%)	DCC
Wilson B-factor (Å ²)	72.8	Xtriage
Anisotropy	0.163	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 37.4	EDS
Estimated twinning fraction	0.019 for h,-h-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	1 of 60819 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	16016	wwPDB-VP
Average B, all atoms (Å ²)	96.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.24% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, PG4, ATP

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	0.35	0/3251	0.55	0/4413
2	B	0.35	0/3023	0.61	0/4093
3	C	0.35	0/2719	0.57	0/3692
4	D	0.34	0/2329	0.54	0/3146
5	E	0.33	0/1381	0.49	0/1863
6	F	0.38	0/1378	0.59	0/1849
7	G	0.36	0/1052	0.57	0/1415
8	H	0.34	0/1137	0.55	0/1536
All	All	0.35	0/16270	0.56	0/22007

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3170	0	0	3	0
2	B	2963	0	0	11	0
3	C	2650	0	0	8	0
4	D	2280	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	1350	0	0	4	0
6	F	1356	0	0	5	0
7	G	1041	0	0	5	0
8	H	1116	0	0	2	0
9	A	1	0	0	0	0
9	B	1	0	0	0	0
10	A	31	0	0	0	0
10	B	31	0	0	1	0
11	B	13	0	0	1	0
11	F	13	0	0	0	0
All	All	16016	0	0	39	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 2.

All (39) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:G:77:SER:O	7:G:81:LYS:CD	2.36	0.74
2:B:322:LYS:NZ	11:B:503:PG4:O3	2.25	0.69
3:C:144:THR:OG1	6:F:28:GLN:NE2	2.30	0.64
5:E:37:LYS:CG	5:E:38:ASP:N	2.61	0.62
7:G:81:LYS:CE	7:G:81:LYS:CA	2.82	0.58
4:D:212:THR:O	4:D:213:ASP:OD1	2.24	0.55
3:C:123:CYS:SG	3:C:134:CYS:CB	2.96	0.54
2:B:388:LYS:CD	2:B:388:LYS:N	2.70	0.53
8:H:79:ASP:OD1	8:H:80:GLY:N	2.40	0.53
2:B:381:LYS:CB	2:B:382:GLY:CA	2.87	0.53
7:G:81:LYS:N	7:G:81:LYS:CE	2.72	0.52
5:E:110:GLY:CA	5:E:111:PHE:C	2.78	0.52
4:D:265:ARG:NH1	6:F:145:GLU:OE2	2.43	0.52
3:C:369:LEU:C	3:C:370:LYS:CD	2.79	0.52
4:D:202:HIS:O	4:D:220:ILE:O	2.30	0.49
5:E:111:PHE:O	5:E:113:LEU:N	2.47	0.48
7:G:118:SER:O	7:G:121:SER:N	2.46	0.48
2:B:6:ARG:CB	2:B:7:LYS:CA	2.93	0.47
1:A:274:GLU:N	1:A:274:GLU:OE1	2.48	0.47
1:A:354:SER:CB	1:A:355:GLY:CA	2.93	0.47
4:D:32:GLU:OE2	4:D:44:HIS:NE2	2.48	0.47
2:B:4:GLN:N	2:B:6:ARG:O	2.47	0.46
6:F:163:GLU:O	6:F:167:ASN:ND2	2.48	0.46
2:B:345:GLU:OE2	8:H:124:ARG:NH1	2.48	0.46
6:F:38:VAL:O	6:F:41:ARG:NH1	2.48	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:43:ASP:OD1	5:E:143:ARG:NH1	2.49	0.46
2:B:382:GLY:O	2:B:384:ARG:CA	2.65	0.45
3:C:370:LYS:N	3:C:370:LYS:CD	2.80	0.45
7:G:104:ASP:OD2	7:G:143:ARG:NE	2.49	0.45
2:B:19:LYS:NZ	10:B:502:ATP:O1B	2.50	0.44
2:B:8:VAL:CG1	2:B:9:VAL:N	2.81	0.44
3:C:110:LYS:NZ	3:C:177:GLU:OE1	2.50	0.43
3:C:257:SER:OG	3:C:372:VAL:N	2.51	0.43
2:B:385:VAL:O	2:B:385:VAL:CG1	2.67	0.42
1:A:18:LYS:N	1:A:18:LYS:CD	2.82	0.42
3:C:110:LYS:NZ	3:C:171:ALA:O	2.53	0.41
3:C:67:ILE:O	3:C:79:TRP:N	2.53	0.41
6:F:98:ALA:O	6:F:101:PHE:O	2.38	0.41
2:B:388:LYS:CA	2:B:388:LYS:CE	2.98	0.41

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	392/418 (94%)	372 (95%)	20 (5%)	0	100	100
2	B	373/394 (95%)	348 (93%)	24 (6%)	1 (0%)	50	85
3	C	338/372 (91%)	318 (94%)	20 (6%)	0	100	100
4	D	281/300 (94%)	266 (95%)	15 (5%)	0	100	100
5	E	162/178 (91%)	149 (92%)	12 (7%)	1 (1%)	33	77
6	F	164/168 (98%)	157 (96%)	7 (4%)	0	100	100
7	G	133/151 (88%)	124 (93%)	8 (6%)	1 (1%)	27	72
8	H	136/142 (96%)	130 (96%)	6 (4%)	0	100	100
All	All	1979/2123 (93%)	1864 (94%)	112 (6%)	3 (0%)	56	89

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	385	VAL
7	G	11	PHE
5	E	16	ILE

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	342/363 (94%)	323 (94%)	19 (6%)	30	70
2	B	315/345 (91%)	297 (94%)	18 (6%)	29	69
3	C	289/313 (92%)	281 (97%)	8 (3%)	56	89
4	D	247/264 (94%)	239 (97%)	8 (3%)	51	87
5	E	141/159 (89%)	133 (94%)	8 (6%)	29	69
6	F	151/155 (97%)	145 (96%)	6 (4%)	42	83
7	G	109/123 (89%)	107 (98%)	2 (2%)	71	93
8	H	123/134 (92%)	117 (95%)	6 (5%)	35	76
All	All	1717/1856 (92%)	1642 (96%)	75 (4%)	39	79

All (75) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LEU
1	A	62	ILE
1	A	68	GLU
1	A	143	VAL
1	A	191	LYS
1	A	192	HIS
1	A	230	ARG
1	A	257	THR
1	A	265	LYS
1	A	268	SER
1	A	289	ASN
1	A	297	SER
1	A	335	LEU
1	A	353	LEU
1	A	369	THR

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Mol	Chain	Res	Type
1	A	371	HIS
1	A	398	LYS
1	A	414	PHE
1	A	416	VAL
2	B	4	GLN
2	B	9	VAL
2	B	10	VAL
2	B	19	LYS
2	B	182	LEU
2	B	183	ASP
2	B	198	LEU
2	B	200	ARG
2	B	281	LEU
2	B	295	SER
2	B	299	LYS
2	B	320	GLU
2	B	333	ASP
2	B	337	LEU
2	B	361	LEU
2	B	367	ASP
2	B	386	LEU
2	B	388	LYS
3	C	8	VAL
3	C	21	THR
3	C	90	LEU
3	C	107	ASN
3	C	161	SER
3	C	175	GLU
3	C	183	THR
3	C	284	ARG
4	D	82	SER
4	D	106	LYS
4	D	116	LEU
4	D	157	LYS
4	D	199	LEU
4	D	213	ASP
4	D	265	ARG
4	D	281	ARG
5	E	62	ASN
5	E	82	LEU
5	E	95	MET
5	E	98	LEU

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Mol	Chain	Res	Type
5	E	130	ARG
5	E	144	LEU
5	E	145	CYS
5	E	152	GLN
6	F	57	GLU
6	F	68	ASN
6	F	89	LYS
6	F	104	LEU
6	F	128	LYS
6	F	165	LEU
7	G	81	LYS
7	G	122	SER
8	H	15	LYS
8	H	38	LYS
8	H	41	GLN
8	H	52	ILE
8	H	124	ARG
8	H	129	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains 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 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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$
10	ATP	A	502	9	33,33,33	1.16	2 (6%)	52,52,52	1.72	9 (17%)
10	ATP	B	502	9	33,33,33	1.06	2 (6%)	52,52,52	1.69	8 (15%)
11	PG4	B	503	-	12,12,12	0.71	0	11,11,11	0.61	0
11	PG4	F	201	-	12,12,12	0.58	0	11,11,11	0.19	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
10	ATP	A	502	9	-	0/22/38/38	0/1/3/3
10	ATP	B	502	9	-	0/22/38/38	0/1/3/3
11	PG4	B	503	-	-	0/10/10/10	0/0/0/0
11	PG4	F	201	-	-	0/10/10/10	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	B	502	ATP	C4-N9	-3.43	1.32	1.37
10	A	502	ATP	C4-N9	-3.24	1.33	1.37
10	A	502	ATP	C5-C4	2.96	1.47	1.40
10	B	502	ATP	C5-C4	2.66	1.46	1.40

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	502	ATP	N3-C2-N1	-5.31	124.27	128.71
10	B	502	ATP	N3-C2-N1	-5.22	124.34	128.71
10	A	502	ATP	N3-C4-N9	4.97	134.40	125.43
10	B	502	ATP	N3-C4-N9	4.96	134.39	125.43
10	A	502	ATP	O4'-C1'-N9	4.78	112.89	108.44
10	A	502	ATP	C4-C5-N7	-3.97	106.12	109.52
10	B	502	ATP	PA-O3A-PB	-3.58	121.19	131.68
10	B	502	ATP	PB-O3B-PG	-3.30	122.01	131.68
10	A	502	ATP	C5-C4-N3	-3.20	118.74	125.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	B	502	ATP	C8-N9-C4	3.17	109.32	106.90
10	B	502	ATP	C4-C5-N7	-2.97	106.98	109.52
10	B	502	ATP	C5-C4-N3	-2.79	119.63	125.70
10	A	502	ATP	PB-O3B-PG	-2.78	123.54	131.68
10	A	502	ATP	PA-O3A-PB	-2.55	124.21	131.68
10	A	502	ATP	C2-N3-C4	2.25	120.41	114.01
10	A	502	ATP	O4'-C1'-C2'	-2.07	103.61	106.77
10	B	502	ATP	O2G-PG-O1G	2.01	117.01	110.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	398/418 (95%)	-0.29	0 100 100	57, 83, 126, 163	0
2	B	377/394 (95%)	-0.30	0 100 100	53, 92, 141, 160	0
3	C	342/372 (91%)	-0.29	0 100 100	56, 75, 113, 143	0
4	D	283/300 (94%)	-0.18	0 100 100	61, 97, 142, 162	0
5	E	170/178 (95%)	-0.05	0 100 100	94, 145, 183, 200	0
6	F	166/168 (98%)	-0.39	0 100 100	52, 69, 94, 109	0
7	G	139/151 (92%)	-0.24	0 100 100	62, 98, 131, 155	0
8	H	138/142 (97%)	-0.18	0 100 100	82, 120, 164, 186	0
All	All	2013/2123 (94%)	-0.25	0 100 100	52, 90, 154, 200	0

There are no RSRZ outliers to report.

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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
9	CA	A	501	1/1	0.33	14.46	64,64,64,64	0
9	CA	B	501	1/1	0.39	5.91	77,77,77,77	0
11	PG4	B	503	13/13	0.25	1.12	83,100,104,104	0
11	PG4	F	201	13/13	0.21	0.55	93,97,99,101	0
10	ATP	A	502	31/31	0.16	-0.35	60,71,82,84	0
10	ATP	B	502	31/31	0.17	-0.44	66,71,90,95	0

6.5 Other polymers ⓘ

There are no such residues in this entry.