



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:55 PM GMT

PDB ID : 4QBD
Title : The first X-ray crystal structure of an insect muscle myosin. *Drosophila melanogaster*, skeletal muscle myosin II, an embryonic isoform, subfragment-1
Authors : Caldwell, J.T.; Bernstein, S.I.; Huxford, T.
Deposited on : 2014-05-07
Resolution : 2.23 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

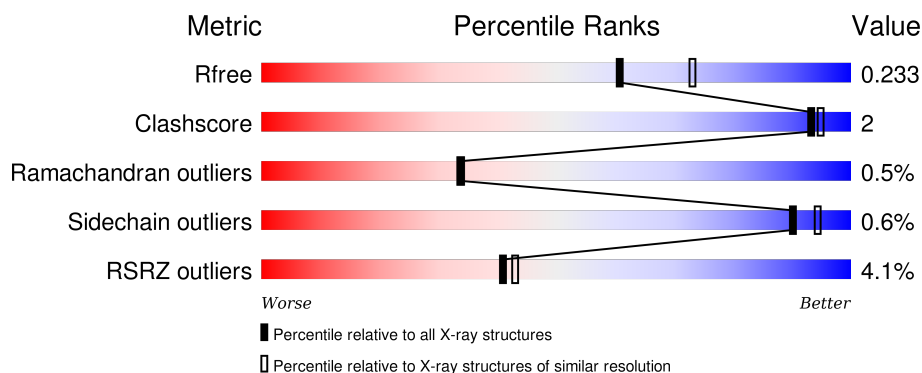
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.23 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	1611 (2.26-2.22)
Clashscore	102246	1764 (2.26-2.22)
Ramachandran outliers	100387	1724 (2.26-2.22)
Sidechain outliers	100360	1724 (2.26-2.22)
RSRZ outliers	91569	1616 (2.26-2.22)

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	818	<div> <div>5%</div> <div>92%</div> <div>• •</div> </div>
1	C	818	<div> <div>2%</div> <div>92%</div> <div>• 5%</div> </div>
2	B	155	<div> <div>8%</div> <div>97%</div> <div>• •</div> </div>
2	D	155	<div> <div>2%</div> <div>94%</div> <div>• • •</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 30727 atoms, of which 14681 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 Myosin heavy chain, muscle.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	786	Total	C	H	N	O	S	0	1	0
			12457	3988	6174	1085	1173	37			
1	C	778	Total	C	H	N	O	S	0	4	0
			12345	3962	6107	1075	1163	38			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	MET	-	EXPRESSION TAG	UNP P05661
A	-11	HIS	-	EXPRESSION TAG	UNP P05661
A	-10	HIS	-	EXPRESSION TAG	UNP P05661
A	-9	HIS	-	EXPRESSION TAG	UNP P05661
A	-8	HIS	-	EXPRESSION TAG	UNP P05661
A	-7	HIS	-	EXPRESSION TAG	UNP P05661
A	-6	HIS	-	EXPRESSION TAG	UNP P05661
A	-5	GLU	-	EXPRESSION TAG	UNP P05661
A	-4	ASN	-	EXPRESSION TAG	UNP P05661
A	-3	LEU	-	EXPRESSION TAG	UNP P05661
A	-2	TYR	-	EXPRESSION TAG	UNP P05661
A	-1	PHE	-	EXPRESSION TAG	UNP P05661
A	0	GLN	-	EXPRESSION TAG	UNP P05661
A	1	GLY	-	EXPRESSION TAG	UNP P05661
C	-12	MET	-	EXPRESSION TAG	UNP P05661
C	-11	HIS	-	EXPRESSION TAG	UNP P05661
C	-10	HIS	-	EXPRESSION TAG	UNP P05661
C	-9	HIS	-	EXPRESSION TAG	UNP P05661
C	-8	HIS	-	EXPRESSION TAG	UNP P05661
C	-7	HIS	-	EXPRESSION TAG	UNP P05661
C	-6	HIS	-	EXPRESSION TAG	UNP P05661
C	-5	GLU	-	EXPRESSION TAG	UNP P05661
C	-4	ASN	-	EXPRESSION TAG	UNP P05661
C	-3	LEU	-	EXPRESSION TAG	UNP P05661
C	-2	TYR	-	EXPRESSION TAG	UNP P05661

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	PHE	-	EXPRESSION TAG	UNP P05661
C	0	GLN	-	EXPRESSION TAG	UNP P05661
C	1	GLY	-	EXPRESSION TAG	UNP P05661

- Molecule 2 is a protein called Myosin light chain alkali.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	154	Total	C	H	N	O	S	0	4	0
			2446	781	1211	194	252	8			
2	D	151	Total	C	H	N	O	S	0	2	0
			2402	766	1189	192	247	8			

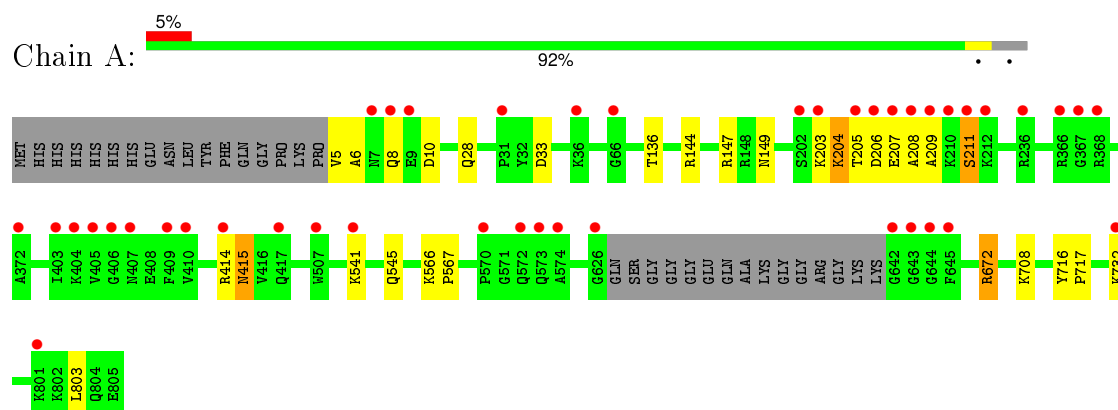
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	437	Total	O	0	0
			437	437		
3	B	54	Total	O	0	0
			54	54		
3	C	484	Total	O	0	0
			484	484		
3	D	102	Total	O	0	0
			102	102		

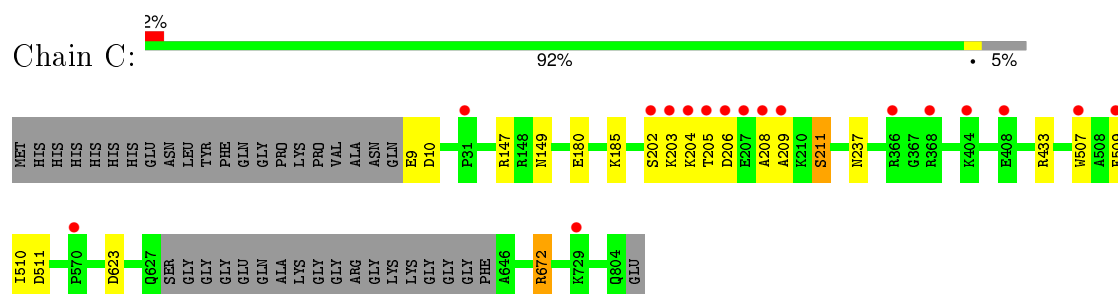
3 Residue-property plots [i](#)

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.

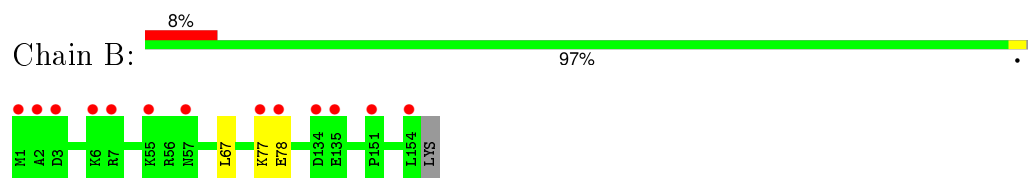
- Molecule 1: Myosin heavy chain, muscle



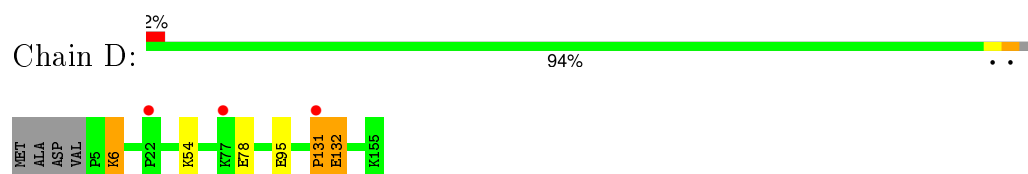
- Molecule 1: Myosin heavy chain, muscle



- Molecule 2: Myosin light chain alkali



- Molecule 2: Myosin light chain alkali



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	108.55Å 148.58Å 148.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	105.12 – 2.23 105.12 – 2.23	Depositor EDS
% Data completeness (in resolution range)	98.8 (105.12-2.23) 98.8 (105.12-2.23)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.22Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.9_1675)	Depositor
R, R_{free}	0.189 , 0.224 0.203 , 0.233	Depositor DCC
R_{free} test set	5836 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	30.4	Xtriage
Anisotropy	0.300	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 41.4	EDS
Estimated twinning fraction	0.014 for -h,l,k	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 116642 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	30727	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.71% 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](#)

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	0.23	0/6411	0.39	0/8629
1	C	0.23	0/6377	0.39	0/8584
2	B	0.22	0/1268	0.38	0/1708
2	D	0.22	0/1235	0.41	0/1660
All	All	0.23	0/15291	0.39	0/20581

There are no bond length outliers.

There are no bond angle outliers.

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	6283	6174	6255	26	0
1	C	6238	6107	6223	24	0
2	B	1235	1211	1215	2	0
2	D	1213	1189	1190	4	0
3	A	437	0	0	3	0
3	B	54	0	0	0	0
3	C	484	0	0	2	0
3	D	102	0	0	2	0
All	All	16046	14681	14883	56	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 2.

All (56) 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:C:204:LYS:HB3	1:C:205:THR:HA	1.51	0.90
1:C:204:LYS:HD3	1:C:209:ALA:CB	2.12	0.79
1:A:204:LYS:HD2	1:A:207:GLU:HA	1.64	0.79
1:C:204:LYS:HD3	1:C:209:ALA:HB3	1.64	0.78
1:A:203:LYS:HB2	1:A:205:THR:HG23	1.66	0.78
1:A:204:LYS:HD3	1:A:209:ALA:HB3	1.67	0.76
1:C:204:LYS:HD2	1:C:206:ASP:O	1.90	0.72
1:C:202:SER:HB2	1:C:203:LYS:C	2.15	0.66
1:C:202:SER:N	1:C:203:LYS:O	2.28	0.66
1:C:507:TRP:CZ2	1:C:509:PHE:HB2	2.31	0.66
1:A:203:LYS:HB2	1:A:205:THR:CG2	2.27	0.64
1:A:28:GLN:NE2	3:A:914:HOH:O	2.30	0.64
1:A:204:LYS:HB3	1:A:205:THR:HA	1.83	0.59
1:A:414:ARG:O	1:A:415:ASN:ND2	2.36	0.58
1:C:147:ARG:NH1	1:C:149:ASN:OD1	2.37	0.57
1:A:204:LYS:N	1:A:205:THR:OG1	2.35	0.57
1:C:202:SER:HB2	1:C:203:LYS:CB	2.35	0.57
1:C:203:LYS:HB3	1:C:205:THR:OG1	2.04	0.57
1:C:507:TRP:CE2	1:C:509:PHE:HB2	2.40	0.57
1:A:10:ASP:OD1	1:A:10:ASP:N	2.38	0.56
1:A:204:LYS:HD3	1:A:209:ALA:CB	2.34	0.55
1:A:566:LYS:HG3	1:A:567:PRO:HD2	1.92	0.51
1:A:672:ARG:NH2	3:A:972:HOH:O	2.43	0.51
1:C:9:GLU:N	3:C:1136:HOH:O	2.44	0.50
1:A:204:LYS:HD2	1:A:206:ASP:O	2.12	0.50
1:C:202:SER:HB2	1:C:203:LYS:CA	2.42	0.50
1:A:5:VAL:HG13	1:A:6:ALA:H	1.77	0.49
1:A:203:LYS:CB	1:A:205:THR:HG23	2.41	0.49
1:C:204:LYS:HB3	1:C:205:THR:CA	2.34	0.49
1:A:204:LYS:CB	1:A:205:THR:HA	2.44	0.47
1:A:208:ALA:HA	1:A:209:ALA:C	2.35	0.47
2:B:77:LYS:CG	2:B:78[A]:GLU:HA	2.45	0.46
1:C:202:SER:HB2	1:C:204:LYS:N	2.30	0.46
1:C:208:ALA:HA	1:C:209:ALA:C	2.36	0.46
2:B:77:LYS:CG	2:B:78[B]:GLU:HA	2.46	0.45
1:C:672:ARG:NH2	3:C:1034:HOH:O	2.49	0.45
1:C:204:LYS:CB	1:C:205:THR:HA	2.31	0.45
1:A:545:GLN:OE1	1:A:545:GLN:N	2.49	0.45
1:A:208:ALA:HB2	1:A:211:SER:HB2	1.98	0.44
2:D:6:LYS:NZ	3:D:283:HOH:O	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:54:LYS:NZ	3:D:259:HOH:O	2.48	0.44
1:A:203:LYS:O	1:A:204:LYS:HB2	2.17	0.44
1:C:202:SER:HB2	1:C:205:THR:OG1	2.18	0.43
1:A:716:TYR:N	1:A:717:PRO:HD2	2.34	0.43
1:C:180:GLU:OE1	1:C:237[A]:ASN:ND2	2.47	0.43
1:C:433[B]:ARG:NH1	1:C:623:ASP:OD2	2.51	0.43
1:A:144:ARG:NH2	3:A:1244:HOH:O	2.46	0.43
2:D:131:PRO:O	2:D:132:GLU:HB3	2.19	0.42
1:C:203:LYS:HB3	1:C:204:LYS:H	1.61	0.41
1:A:8:GLN:HG3	1:A:136:THR:HG22	2.03	0.41
1:A:672:ARG:HD2	1:A:672:ARG:HA	1.98	0.41
1:C:202:SER:CB	1:C:203:LYS:HB2	2.51	0.41
2:D:131:PRO:O	2:D:132:GLU:CB	2.69	0.40
1:A:5:VAL:HG13	1:A:6:ALA:N	2.37	0.40
1:C:510:ILE:HG22	1:C:511:ASP:N	2.36	0.40
1:A:147:ARG:NH1	1:A:149:ASN:OD1	2.54	0.40

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	783/818 (96%)	751 (96%)	28 (4%)	4 (0%)	34	34
1	C	778/818 (95%)	758 (97%)	18 (2%)	2 (0%)	46	51
2	B	156/155 (101%)	154 (99%)	2 (1%)	0	100	100
2	D	151/155 (97%)	143 (95%)	4 (3%)	4 (3%)	7	2
All	All	1868/1946 (96%)	1806 (97%)	52 (3%)	10 (0%)	34	34

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	732	LYS
2	D	132	GLU
1	A	204	LYS
1	C	211	SER
2	D	6	LYS
1	A	211	SER
1	C	10	ASP
2	D	131	PRO
1	A	33	ASP
2	D	95	GLU

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	681/705 (97%)	676 (99%)	5 (1%)	88	93
1	C	679/705 (96%)	676 (100%)	3 (0%)	93	96
2	B	137/135 (102%)	136 (99%)	1 (1%)	88	93
2	D	134/135 (99%)	133 (99%)	1 (1%)	88	93
All	All	1631/1680 (97%)	1621 (99%)	10 (1%)	90	94

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	415	ASN
1	A	541	LYS
1	A	672	ARG
1	A	708	LYS
1	A	803	LEU
2	B	67	LEU
1	C	185	LYS
1	C	211	SER
1	C	672	ARG
2	D	78	GLU

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

such sidechains identified.

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 ⓘ

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	786/818 (96%)	0.28	43 (5%) 29 30	20, 34, 72, 137	0
1	C	778/818 (95%)	0.07	17 (2%) 65 68	18, 29, 58, 112	0
2	B	154/155 (99%)	0.31	13 (8%) 14 14	30, 44, 72, 95	0
2	D	151/155 (97%)	0.01	3 (1%) 68 70	21, 30, 51, 75	0
All	All	1869/1946 (96%)	0.17	76 (4%) 41 43	18, 32, 66, 137	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	642	GLY	9.7
1	A	643	GLY	8.9
1	C	206	ASP	8.7
1	A	407	ASN	8.1
1	A	7	ASN	8.0
1	A	572	GLN	7.9
1	A	8	GLN	7.3
1	A	367	GLY	7.1
1	C	209	ALA	6.4
1	A	405	VAL	6.3
1	A	210	LYS	6.2
1	A	645	PHE	6.2
2	B	2	ALA	6.0
1	A	206	ASP	5.7
1	A	202	SER	5.7
1	A	205	THR	5.7
2	B	1	MET	5.5
1	C	205	THR	5.4
1	A	368	ARG	5.3
1	A	209	ALA	5.0
1	A	207	GLU	4.9

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Mol	Chain	Res	Type	RSRZ
1	C	507	TRP	4.9
1	C	509	PHE	4.9
1	C	202	SER	4.8
1	A	211	SER	4.7
1	A	404	LYS	4.3
1	C	208	ALA	4.3
1	A	203	LYS	4.2
1	C	204	LYS	4.0
1	A	570	PRO	3.9
1	A	573	GLN	3.9
1	A	574	ALA	3.7
1	C	207	GLU	3.7
1	A	212	LYS	3.5
1	A	732	LYS	3.5
1	A	644	GLY	3.4
1	A	403	ILE	3.3
1	A	9	GLU	3.3
1	C	404	LYS	3.1
2	B	55	LYS	3.1
2	B	135	GLU	3.0
1	C	31	PRO	2.9
1	A	507	TRP	2.8
2	B	3	ASP	2.8
1	A	31	PRO	2.8
1	C	729	LYS	2.7
1	C	203	LYS	2.7
2	D	131	PRO	2.7
2	B	57	ASN	2.7
2	B	77	LYS	2.7
2	D	77	LYS	2.6
1	A	414	ARG	2.5
1	A	406	GLY	2.5
1	A	541	LYS	2.5
1	C	366	ARG	2.4
1	A	208	ALA	2.3
2	B	154	LEU	2.3
1	A	410	VAL	2.3
1	A	409	PHE	2.3
2	B	78[A]	GLU	2.3
2	B	134	ASP	2.3
1	A	236	ARG	2.2
1	C	570	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	7	ARG	2.2
1	A	626	GLY	2.2
1	A	36	LYS	2.2
1	A	417	GLN	2.1
2	B	151	PRO	2.1
1	A	372	ALA	2.1
2	B	6	LYS	2.1
1	A	366	ARG	2.1
1	C	368	ARG	2.1
1	C	408	GLU	2.0
2	D	22	PRO	2.0
1	A	66	GLY	2.0
1	A	801	LYS	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.