



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 5, 2016 – 01:56 PM EDT

PDB ID : 5I0I  
Title : Crystal structure of myosin X motor domain with 2IQ motifs in pre-powerstroke state  
Authors : Isabet, T.; Sweeney, H.L.; Houdusse, A.  
Deposited on : 2016-02-04  
Resolution : 3.15 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20027939  
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) : rb-20027939

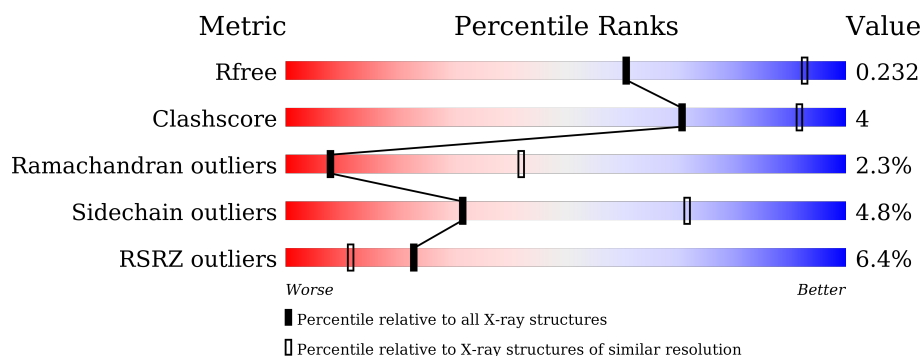
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.15 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	1112 (3.20-3.12)
Clashscore	102246	1249 (3.20-3.12)
Ramachandran outliers	100387	1222 (3.20-3.12)
Sidechain outliers	100360	1221 (3.20-3.12)
RSRZ outliers	91569	1117 (3.20-3.12)

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  $\geq 3$ , 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	791	<div> <div>4%</div> <div>88%</div> <div>9%</div> <div>...</div> </div>
1	B	791	<div> <div>6%</div> <div>90%</div> <div>9%</div> <div>..</div> </div>
2	C	145	<div> <div>5%</div> <div>74%</div> <div>20%</div> <div>5%</div> <div>.</div> </div>
3	E	145	<div> <div>3%</div> <div>74%</div> <div>23%</div> <div>..</div> </div>
4	G	43	<div> <div>35%</div> <div>67%</div> <div>28%</div> <div>5%</div> </div>
5	I	64	<div> <div>33%</div> <div>63%</div> <div>25%</div> <div>5%</div> <div>8%</div> </div>

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
10	SO4	A	907	-	-	-	X
10	SO4	A	908	-	-	-	X
6	MPO	B	901	-	-	-	X
8	VO4	A	903	-	-	X	-
8	VO4	B	904	-	-	X	-

## 2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 15350 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 Unconventional myosin-X.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	784	Total	C	N	O	S	0	0	0
			6203	3935	1071	1169	28			
1	B	784	Total	C	N	O	S	0	1	0
			6159	3907	1060	1164	28			

- Molecule 2 is a protein called Calmodulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	145	Total	C	N	O	S	0	0	0
			1086	666	170	242	8			

- Molecule 3 is a protein called Calmodulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	145	Total	C	N	O	S	0	0	0
			1024	625	162	228	9			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	19	ALA	PHE	conflict	UNP P62158

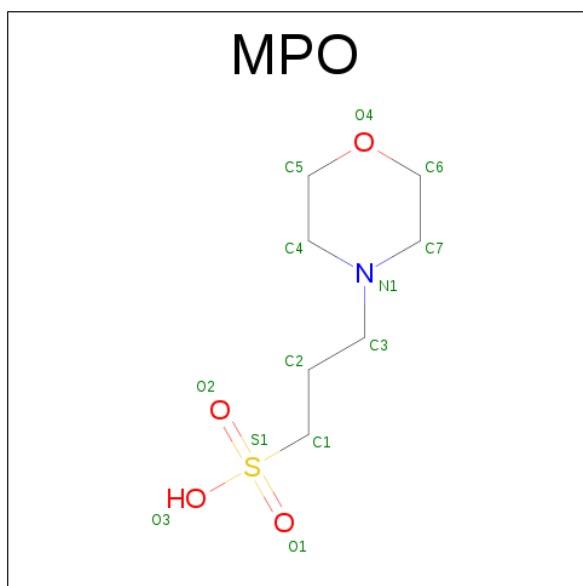
- Molecule 4 is a protein called Calmodulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	G	43	Total	C	N	O	S	0	0	0
			306	188	45	71	2			

- Molecule 5 is a protein called Calmodulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	I	59	Total	C	N	O	S	0	0	0
			424	254	68	99	3			

- Molecule 6 is 3[N-MORPHOLINO]PROPANE SULFONIC ACID (three-letter code: MPO) (formula: C<sub>7</sub>H<sub>15</sub>NO<sub>4</sub>S).

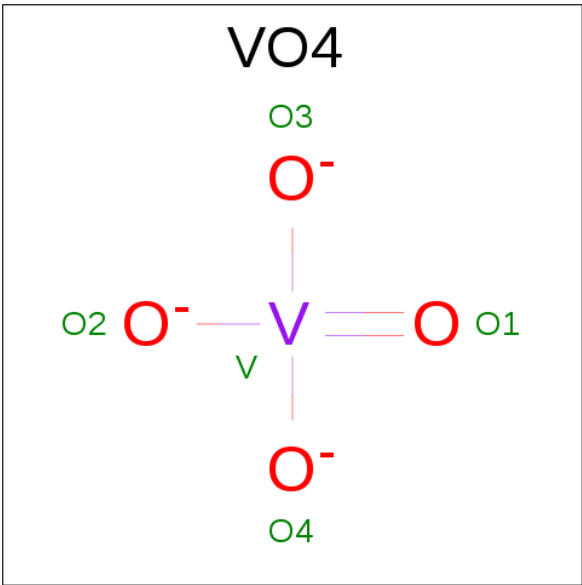


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	S	0	0
			13	7	1	4	1		
6	B	1	Total	C	N	O	S	0	0
			13	7	1	4	1		

- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

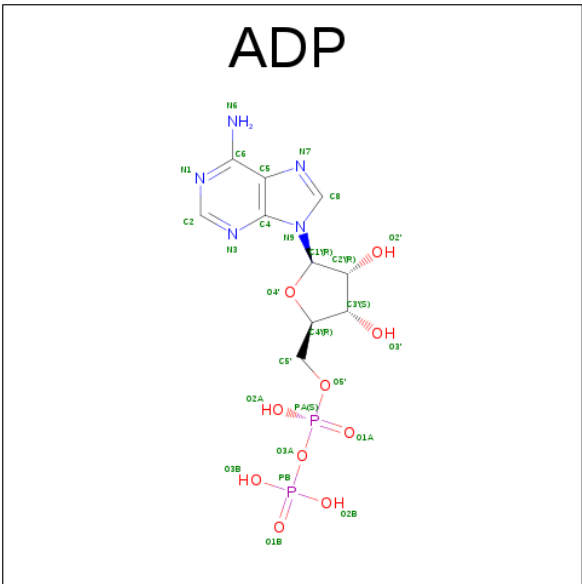
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total	Mg	0	0
			1	1		
7	A	1	Total	Mg	0	0
			1	1		

- Molecule 8 is VANADATE ION (three-letter code: VO4) (formula: O<sub>4</sub>V).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	O	V	0	0
			5	4	1		
8	B	1	Total	O	V	0	0
			5	4	1		

- Molecule 9 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>).



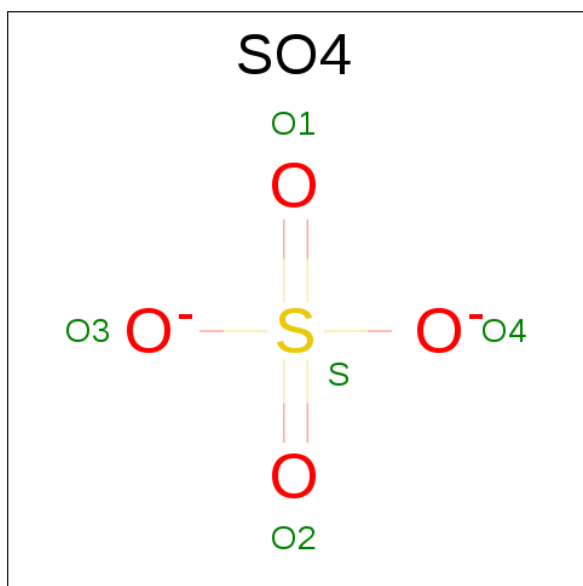
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	N	O	P	0
			27	10	5	10	2	

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 10 is SULFATE ION (three-letter code: SO<sub>4</sub>) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	O	S	0	0
			5	4	1		
10	A	1	Total	O	S	0	0
			5	4	1		
10	A	1	Total	O	S	0	0
			5	4	1		
10	A	1	Total	O	S	0	0
			5	4	1		
10	B	1	Total	O	S	0	0
			5	4	1		
10	C	1	Total	O	S	0	0
			5	4	1		
10	E	1	Total	O	S	0	0
			5	4	1		

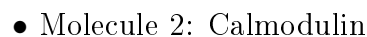
- Molecule 11 is water.

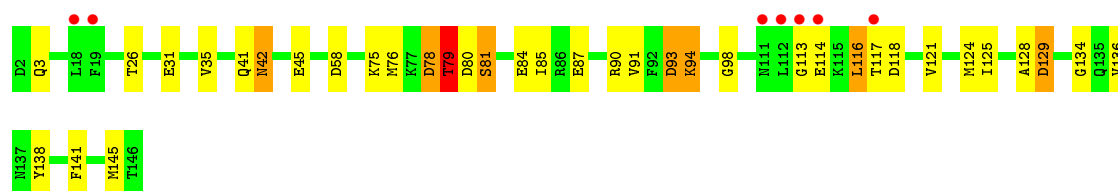
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	11	Total 11	O 11	0	0
11	B	5	Total 5	O 5	0	0



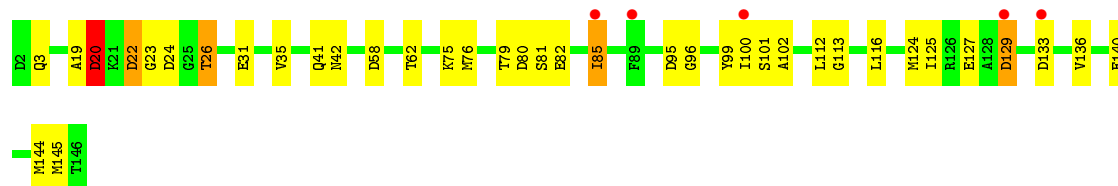
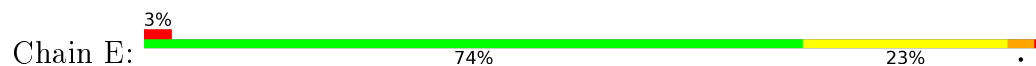


- Molecule 1: Unconventional myosin-X





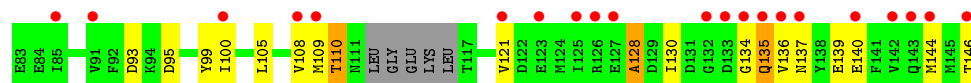
• Molecule 3: Calmodulin



• Molecule 4: Calmodulin



• Molecule 5: Calmodulin



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	113.95Å 173.41Å 178.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.53 – 3.15 49.53 – 3.15	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.53-3.15) 99.9 (49.53-3.15)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.19 (at 3.12Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, $R_{free}$	0.192 , 0.218 0.205 , 0.232	Depositor DCC
$R_{free}$ test set	3074 reflections (5.23%)	DCC
Wilson B-factor (Å <sup>2</sup> )	103.7	Xtriage
Anisotropy	0.102	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 86.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.006 for -h,l,k	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	15350	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	126.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.91% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: VO4, MPO, MG, SO4, ADP

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	0.54	0/6330	0.74	10/8571 (0.1%)
1	B	0.48	0/6286	0.70	2/8519 (0.0%)
2	C	0.51	0/1098	0.80	1/1486 (0.1%)
3	E	0.58	0/1032	0.84	0/1401
4	G	0.60	0/307	0.86	0/417
5	I	0.54	0/425	0.74	0/576
All	All	0.52	0/15478	0.74	13/20970 (0.1%)

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	A	0	1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	179	GLN	C-N-CA	9.10	144.44	121.70
2	C	78	ASP	C-N-CA	6.96	139.10	121.70
1	A	52	GLN	C-N-CA	6.69	138.44	121.70
1	A	299	THR	C-N-CA	6.26	137.35	121.70
1	A	15	GLU	C-N-CA	6.13	137.02	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	52	GLN	Peptide

## 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	6203	0	5954	49	0
1	B	6159	0	5853	32	0
2	C	1086	0	955	17	0
3	E	1024	0	869	17	0
4	G	306	0	257	3	0
5	I	424	0	347	8	0
6	A	13	0	14	0	0
6	B	13	0	14	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
8	A	5	0	0	3	0
8	B	5	0	0	3	0
9	A	27	0	12	1	0
9	B	27	0	12	0	0
10	A	25	0	0	0	0
10	B	5	0	0	0	0
10	C	5	0	0	0	0
10	E	5	0	0	0	0
11	A	11	0	0	0	0
11	B	5	0	0	0	0
All	All	15350	0	14287	129	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 4.

The worst 5 of 129 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:607:ARG:HH11	1:A:607:ARG:HG3	1.11	1.15
3:E:80:ASP:HA	3:E:81:SER:N	1.74	1.02
3:E:22:ASP:HB2	3:E:23:GLY:HA3	1.46	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:191:SER:HB3	1:B:195:ARG:HB2	1.52	0.89
1:A:65:VAL:HG11	1:A:70:SER:HB2	1.53	0.88

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	782/791 (99%)	738 (94%)	29 (4%)	15 (2%)	10	48
1	B	783/791 (99%)	735 (94%)	37 (5%)	11 (1%)	14	55
2	C	143/145 (99%)	124 (87%)	13 (9%)	6 (4%)	3	24
3	E	141/145 (97%)	122 (86%)	13 (9%)	6 (4%)	3	23
4	G	41/43 (95%)	32 (78%)	4 (10%)	5 (12%)	0	2
5	I	55/64 (86%)	50 (91%)	4 (7%)	1 (2%)	11	49
All	All	1945/1979 (98%)	1801 (93%)	100 (5%)	44 (2%)	8	42

5 of 44 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	60	THR
1	A	63	GLU
1	A	180	GLN
1	A	192	CYS
1	A	295	VAL

### 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	657/704 (93%)	633 (96%)	24 (4%)	41	78
1	B	644/704 (92%)	628 (98%)	16 (2%)	55	85
2	C	111/125 (89%)	99 (89%)	12 (11%)	8	32
3	E	97/124 (78%)	85 (88%)	12 (12%)	6	26
4	G	29/37 (78%)	23 (79%)	6 (21%)	1	7
5	I	40/55 (73%)	34 (85%)	6 (15%)	3	17
All	All	1578/1749 (90%)	1502 (95%)	76 (5%)	31	71

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	676	ARG
2	C	42	ASN
5	I	95	ASP
1	B	753	VAL
1	B	771	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	40	GLN
1	B	46	GLN
2	C	42	ASN
1	A	773	GLN
2	C	107	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 16 ligands modelled in this entry, 2 are monoatomic - leaving 14 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	$\# Z  > 2$
6	MPO	A	901	-	13,13,13	1.09	1 (7%)	16,17,17	0.36	0
8	VO4	A	903	9,7	1,4,4	1.10	0	0,6,6	0.00	-
9	ADP	A	904	8,7	24,29,29	0.97	1 (4%)	23,45,45	0.88	2 (8%)
10	SO4	A	905	-	4,4,4	0.53	0	6,6,6	0.55	0
10	SO4	A	906	-	4,4,4	0.35	0	6,6,6	0.27	0
10	SO4	A	907	-	4,4,4	0.26	0	6,6,6	0.28	0
10	SO4	A	908	-	4,4,4	0.15	0	6,6,6	0.16	0
10	SO4	A	909	-	4,4,4	0.28	0	6,6,6	0.13	0
6	MPO	B	901	-	13,13,13	0.97	1 (7%)	16,17,17	1.03	1 (6%)
9	ADP	B	903	8,7	24,29,29	0.77	1 (4%)	23,45,45	0.83	0
8	VO4	B	904	9,7	1,4,4	0.83	0	0,6,6	0.00	-
10	SO4	B	905	-	4,4,4	0.28	0	6,6,6	0.31	0
10	SO4	C	201	-	4,4,4	0.16	0	6,6,6	0.28	0
10	SO4	E	201	-	4,4,4	0.21	0	6,6,6	0.23	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
6	MPO	A	901	-	-	0/7/15/15	0/1/1/1
8	VO4	A	903	9,7	-	0/0/0/0	0/0/0/0
9	ADP	A	904	8,7	-	0/12/32/32	0/3/3/3
10	SO4	A	905	-	-	0/0/0/0	0/0/0/0
10	SO4	A	906	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	SO4	A	907	-	-	0/0/0/0	0/0/0/0
10	SO4	A	908	-	-	0/0/0/0	0/0/0/0
10	SO4	A	909	-	-	0/0/0/0	0/0/0/0
6	MPO	B	901	-	-	0/7/15/15	0/1/1/1
9	ADP	B	903	8,7	-	0/12/32/32	0/3/3/3
8	VO4	B	904	9,7	-	0/0/0/0	0/0/0/0
10	SO4	B	905	-	-	0/0/0/0	0/0/0/0
10	SO4	C	201	-	-	0/0/0/0	0/0/0/0
10	SO4	E	201	-	-	0/0/0/0	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	901	MPO	C1-S1	-3.91	1.71	1.77
9	A	904	ADP	PB-O3B	-3.40	1.43	1.54
6	B	901	MPO	C1-S1	-3.27	1.72	1.77
9	B	903	ADP	PB-O3B	-2.59	1.45	1.54

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	901	MPO	O1-S1-C1	-3.06	104.70	106.87
9	A	904	ADP	O3'-C3'-C4'	2.34	118.00	111.01
9	A	904	ADP	O3'-C3'-C2'	2.47	119.83	111.86

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	903	VO4	3	0
9	A	904	ADP	1	0
8	B	904	VO4	3	0

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	E	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	80:ASP	C	81:SER	N	3.33

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	784/791 (99%)	0.06	28 (3%)	46	29	62, 88, 196, 246	3 (0%)
1	B	784/791 (99%)	0.21	50 (6%)	23	11	79, 121, 232, 258	6 (0%)
2	C	145/145 (100%)	0.04	7 (4%)	34	20	109, 153, 217, 228	0
3	E	145/145 (100%)	0.02	5 (3%)	49	32	88, 144, 211, 234	0
4	G	43/43 (100%)	1.83	15 (34%)	0	0	191, 215, 230, 238	0
5	I	59/64 (92%)	1.56	21 (35%)	0	0	165, 214, 248, 253	0
All	All	1960/1979 (99%)	0.20	126 (6%)	23	11	62, 116, 225, 258	9 (0%)

The worst 5 of 126 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	29	GLU	9.4
1	B	28	ALA	9.3
1	B	3	ASN	8.1
1	B	31	ILE	7.8
1	A	600	LEU	7.6

### 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

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
10	SO4	A	908	5/5	0.64	0.40	5.10	217,217,217,218	0
10	SO4	A	907	5/5	0.83	0.44	3.22	168,168,171,172	0
6	MPO	B	901	13/13	0.75	0.36	3.09	163,167,188,190	0
10	SO4	E	201	5/5	0.86	0.26	1.29	171,171,172,173	0
7	MG	B	902	1/1	0.96	0.25	1.04	101,101,101,101	0
10	SO4	C	201	5/5	0.92	0.22	1.00	181,182,182,182	0
6	MPO	A	901	13/13	0.80	0.25	0.98	132,139,176,178	0
10	SO4	B	905	5/5	0.85	0.30	0.71	159,160,161,161	0
10	SO4	A	905	5/5	0.94	0.28	0.38	121,122,123,124	0
9	ADP	A	904	27/27	0.98	0.21	0.16	69,78,85,87	0
10	SO4	A	906	5/5	0.82	0.24	0.15	144,148,149,150	0
8	VO4	B	904	5/5	0.99	0.23	0.11	109,110,111,111	0
9	ADP	B	903	27/27	0.97	0.21	-0.04	103,119,126,129	0
7	MG	A	902	1/1	0.99	0.19	-0.57	69,69,69,69	0
8	VO4	A	903	5/5	0.99	0.18	-0.73	72,75,77,77	0
10	SO4	A	909	5/5	0.64	0.83	-	191,192,193,193	0

## 6.5 Other polymers

There are no such residues in this entry.