



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:02 PM GMT

PDB ID : 1W9K
Title : DICTYOSTELIUM DISCOIDEUM MYOSIN II MOTOR DOMAIN S456E
WITH BOUND MGADP-BEFX
Authors : Morris, C.A.; Coureux, P.-D.; Wells, A.L.; Houdusse, A.; Sweeney, H.L.
Deposited on : 2004-10-13
Resolution : 2.05 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

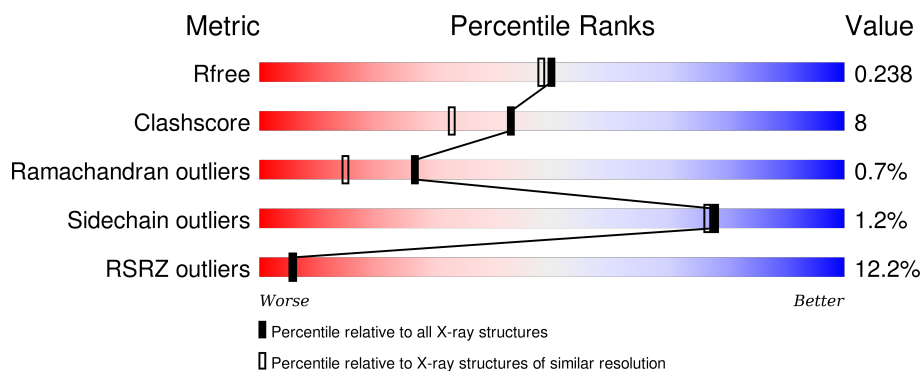
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	1192 (2.04-2.04)
Clashscore	102246	1269 (2.04-2.04)
Ramachandran outliers	100387	1258 (2.04-2.04)
Sidechain outliers	100360	1258 (2.04-2.04)
RSRZ outliers	91569	1194 (2.04-2.04)

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	770	

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
5	EDO	A	1761	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	EDO	A	1762	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6109 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 MYOSIN II HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	719	Total	C	N	O	S	0	7	0
			5612	3577	955	1064	16			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	443	GLU	GLN	CONFLICT	UNP P08799
A	456	GLU	SER	ENGINEERED MUTATION	UNP P08799
A	737	PHE	TYR	CONFLICT	UNP P08799

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

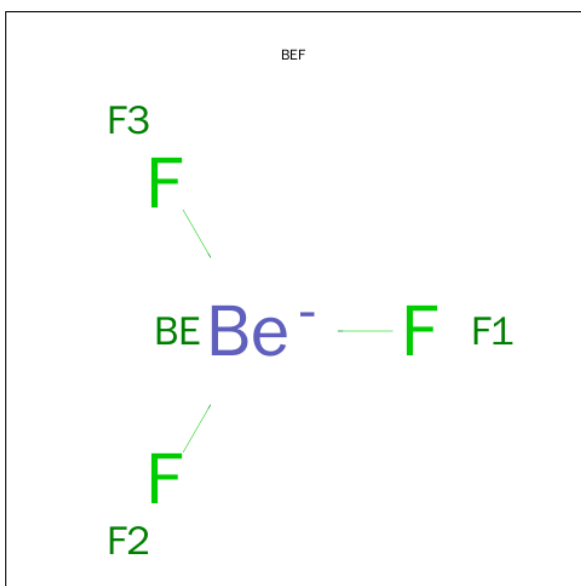
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



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

- Molecule 4 is BERYLLIUM TRIFLUORIDE ION (three-letter code: BEF) (formula: BeF₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	Be	F	0	0
			4	1	3		

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0

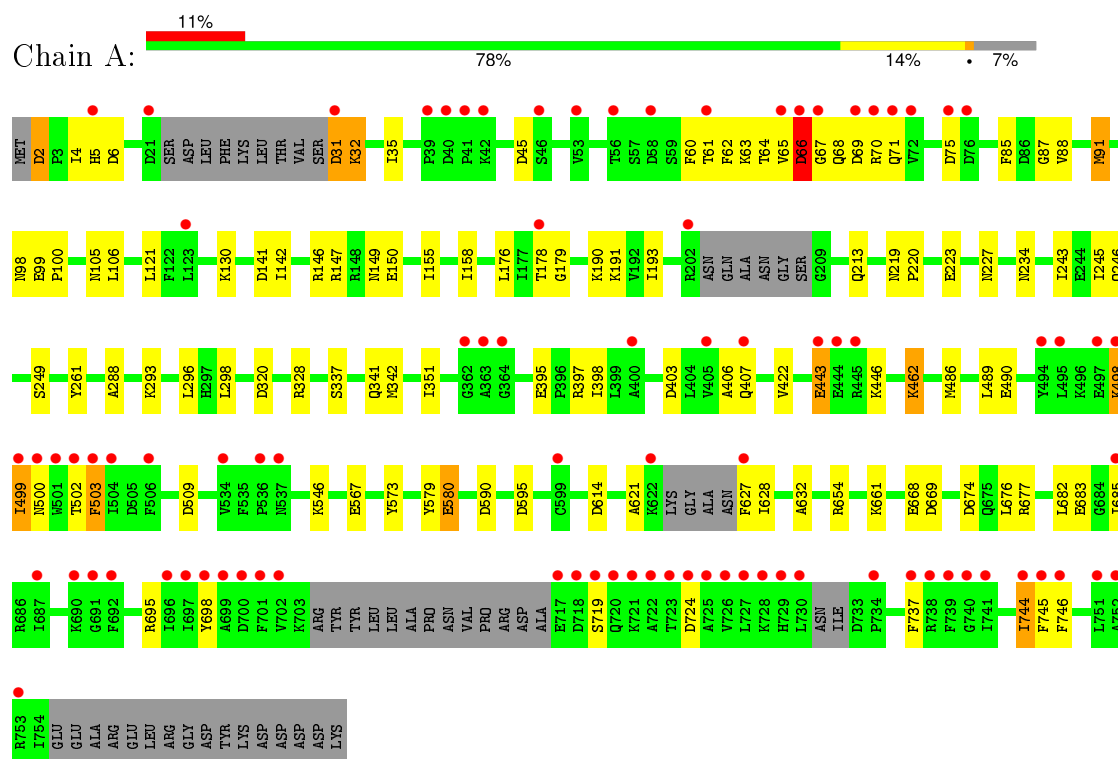
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	437	Total O 437 437	0	0

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 ($\text{RSRZ} > 2$). 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 II HEAVY CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	104.70 Å 179.43 Å 54.15 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.05 37.64 – 2.05	Depositor EDS
% Data completeness (in resolution range)	98.1 (40.00-2.05) 98.1 (37.64-2.05)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.08 (at 2.05 Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.198 , 0.232 0.207 , 0.238	Depositor DCC
R_{free} test set	3179 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	26.3	Xtriage
Anisotropy	0.247	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 58.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 63788 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6109	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.71% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, BEF, EDO, 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	0.49	2/5745 (0.0%)	0.75	19/7774 (0.2%)

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	1	0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	621	ALA	CA-C	5.35	1.66	1.52
1	A	91	MET	CG-SD	-5.11	1.67	1.81

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	443	GLU	N-CA-C	6.69	129.07	111.00
1	A	320	ASP	CB-CG-OD2	6.04	123.74	118.30
1	A	724	ASP	CB-CG-OD2	5.77	123.49	118.30
1	A	66	ASP	CB-CG-OD2	5.72	123.45	118.30
1	A	674	ASP	CB-CG-OD2	5.65	123.39	118.30
1	A	621	ALA	N-CA-C	5.38	125.52	111.00
1	A	509	ASP	CB-CG-OD2	5.36	123.12	118.30
1	A	69	ASP	CB-CG-OD2	5.36	123.12	118.30
1	A	75	ASP	CB-CG-OD2	5.34	123.11	118.30
1	A	31	ASP	CB-CG-OD2	5.34	123.11	118.30
1	A	595	ASP	CB-CG-OD2	5.29	123.06	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	6	ASP	CB-CG-OD2	5.29	123.06	118.30
1	A	590	ASP	CB-CG-OD2	5.23	123.01	118.30
1	A	669	ASP	CB-CG-OD2	5.16	122.95	118.30
1	A	403	ASP	CB-CG-OD2	5.15	122.94	118.30
1	A	2	ASP	CB-CG-OD2	5.15	122.93	118.30
1	A	141	ASP	CB-CG-OD2	5.13	122.92	118.30
1	A	614	ASP	CB-CG-OD2	5.12	122.91	118.30
1	A	45	ASP	CB-CG-OD2	5.07	122.87	118.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	443	GLU	CA

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	5612	0	5409	90	1
2	A	1	0	0	0	0
3	A	27	0	12	0	0
4	A	4	0	0	0	0
5	A	28	0	42	7	0
6	A	437	0	0	11	0
All	All	6109	0	5463	91	1

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 (91) 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:654:ARG:NH1	6:A:2400:HOH:O	1.93	1.00
1:A:498:LYS:O	1:A:499:ILE:HG13	1.67	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:498:LYS:C	1:A:499:ILE:HG13	1.95	0.86
1:A:744:ILE:HD12	1:A:746:PHE:CE2	2.11	0.86
5:A:1763:EDO:H12	6:A:2174:HOH:O	1.76	0.84
1:A:628:ILE:HG12	1:A:632:ALA:HB3	1.59	0.82
1:A:142:ILE:HD11	5:A:1761:EDO:H21	1.59	0.82
1:A:744:ILE:HD12	1:A:746:PHE:CZ	2.13	0.82
1:A:219:ASN:HB3	1:A:220:PRO:HD3	1.61	0.81
1:A:193[B]:ILE:HD13	5:A:1760:EDO:H22	1.63	0.80
1:A:178[A]:THR:HG22	1:A:179:GLY:N	1.97	0.79
1:A:147:ARG:NH1	1:A:149:ASN:OD1	2.21	0.74
1:A:178[A]:THR:HG22	1:A:179:GLY:H	1.54	0.73
1:A:627:PHE:HB2	6:A:2371:HOH:O	1.91	0.70
1:A:261:TYR:CG	5:A:1764:EDO:H12	2.27	0.69
1:A:219:ASN:HD22	5:A:1760:EDO:HO1	1.41	0.68
1:A:31:ASP:O	1:A:32:LYS:CB	2.42	0.67
1:A:31:ASP:O	1:A:32:LYS:HG3	1.95	0.66
1:A:580:GLU:OE2	6:A:2340:HOH:O	2.13	0.66
1:A:31:ASP:O	1:A:32:LYS:CG	2.43	0.66
1:A:685:ILE:HB	6:A:2421:HOH:O	1.95	0.66
1:A:498:LYS:O	1:A:499:ILE:CG1	2.44	0.64
1:A:35:ILE:HD11	1:A:62:PHE:CD2	2.32	0.64
1:A:628:ILE:HD11	1:A:632:ALA:HB1	1.81	0.63
1:A:87:GLY:H	1:A:105:ASN:ND2	1.97	0.63
1:A:178[A]:THR:CG2	1:A:179:GLY:H	2.12	0.63
1:A:342:MET:HE3	1:A:342:MET:HA	1.82	0.61
1:A:580:GLU:HG3	6:A:2342:HOH:O	2.00	0.61
1:A:121:LEU:HD12	1:A:486:MET:SD	2.42	0.60
1:A:31:ASP:O	1:A:32:LYS:HB2	2.03	0.58
1:A:328:ARG:HD2	6:A:2210:HOH:O	2.03	0.58
1:A:546:LYS:NZ	6:A:2304:HOH:O	2.34	0.58
1:A:342:MET:CE	1:A:342:MET:HA	2.33	0.57
1:A:147:ARG:NH2	1:A:150:GLU:OE2	2.37	0.56
1:A:573:TYR:OH	1:A:683:GLU:OE2	2.24	0.56
1:A:628:ILE:CG1	1:A:632:ALA:HB3	2.33	0.54
1:A:66:ASP:OD1	1:A:66:ASP:N	2.36	0.54
1:A:219:ASN:HB3	1:A:220:PRO:CD	2.35	0.53
1:A:85:PHE:O	1:A:88[A]:VAL:HG13	2.09	0.53
1:A:397:ARG:HA	1:A:406:ALA:HA	1.91	0.53
1:A:744:ILE:HD13	1:A:744:ILE:C	2.29	0.52
1:A:191:LYS:HA	1:A:191:LYS:HE2	1.90	0.52
1:A:744:ILE:HD13	1:A:745:PHE:N	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:GLU:OE1	1:A:677:ARG:NH2	2.43	0.52
1:A:142:ILE:CD1	5:A:1761:EDO:H21	2.34	0.51
1:A:176:LEU:HD12	1:A:176:LEU:N	2.26	0.51
1:A:490:GLU:HB3	1:A:503:PHE:CE1	2.46	0.51
1:A:246:GLN:HG2	1:A:446:LYS:HD2	1.93	0.51
1:A:462:LYS:HD3	1:A:462:LYS:H	1.76	0.50
1:A:351:ILE:HG23	1:A:422:VAL:HG13	1.94	0.50
1:A:147:ARG:CZ	1:A:150:GLU:OE2	2.61	0.49
1:A:87:GLY:H	1:A:105:ASN:HD21	1.60	0.49
1:A:193[B]:ILE:HD11	1:A:243:ILE:HD13	1.95	0.48
1:A:91:MET:HE1	1:A:106:LEU:HG	1.94	0.48
1:A:63:LYS:HA	1:A:68:GLN:O	2.12	0.48
1:A:490:GLU:HB3	1:A:503:PHE:HE1	1.78	0.48
1:A:261:TYR:CB	5:A:1764:EDO:H12	2.44	0.47
1:A:190:LYS:HE3	1:A:223:GLU:OE2	2.13	0.47
1:A:60:PHE:O	1:A:71:GLN:HA	2.13	0.47
1:A:121:LEU:CD1	1:A:486:MET:SD	3.03	0.47
1:A:4:ILE:HD12	1:A:146:ARG:NE	2.29	0.47
1:A:737:PHE:HA	1:A:745:PHE:O	2.15	0.46
1:A:98:ASN:OD1	1:A:100:PRO:HG2	2.15	0.46
1:A:2:ASP:OD2	1:A:5:HIS:HD2	1.99	0.46
1:A:193[A]:ILE:HD12	1:A:245:ILE:HD11	1.99	0.44
1:A:178[A]:THR:CG2	1:A:179:GLY:N	2.63	0.44
1:A:4:ILE:HD12	1:A:146:ARG:CZ	2.47	0.44
1:A:676:LEU:HB3	1:A:682:LEU:HG	2.00	0.44
1:A:155:ILE:O	1:A:158:ILE:HG22	2.18	0.43
1:A:91:MET:CE	1:A:106:LEU:HG	2.49	0.43
1:A:567:GLU:HA	1:A:579:TYR:O	2.19	0.43
1:A:398:ILE:HG12	1:A:407:GLN:HG2	2.00	0.43
1:A:661:LYS:NZ	1:A:668:GLU:OE2	2.47	0.43
1:A:234:ASN:ND2	6:A:2154:HOH:O	2.52	0.42
1:A:130:LYS:HE2	6:A:2081:HOH:O	2.18	0.42
1:A:99:GLU:N	1:A:100:PRO:HD2	2.35	0.42
1:A:695:ARG:HG2	1:A:745:PHE:CD2	2.55	0.42
1:A:64:THR:OG1	1:A:66:ASP:OD1	2.30	0.42
1:A:288:ALA:O	1:A:293:LYS:HE3	2.19	0.42
1:A:698:TYR:HB3	1:A:719:SER:CB	2.49	0.42
1:A:489:LEU:HD11	6:A:2270:HOH:O	2.18	0.42
1:A:61:THR:HA	1:A:70:ARG:O	2.20	0.42
1:A:65:VAL:C	1:A:67:GLY:H	2.24	0.41
1:A:296:LEU:HB2	1:A:298:LEU:HG	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:395:GLU:HA	1:A:407:GLN:O	2.20	0.41
1:A:337:SER:O	1:A:341:GLN:HG3	2.20	0.41
1:A:4:ILE:CD1	1:A:146:ARG:NE	2.84	0.41
1:A:223:GLU:O	1:A:227:ASN:HB2	2.21	0.41
1:A:498:LYS:C	1:A:499:ILE:CG1	2.75	0.40
1:A:503:PHE:N	1:A:503:PHE:CD2	2.90	0.40
1:A:31:ASP:OD1	1:A:32:LYS:N	2.52	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:249:SER:OG	1:A:580:GLU:OE1[1_554]	2.19	0.01

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	714/770 (93%)	695 (97%)	14 (2%)	5 (1%)	26	15

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	32	LYS
1	A	499	ILE
1	A	500	ASN
1	A	443	GLU
1	A	498	LYS

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	587/673 (87%)	580 (99%)	7 (1%)	78	76

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	ASP
1	A	213	GLN
1	A	462	LYS
1	A	502	THR
1	A	503	PHE
1	A	580	GLU
1	A	744	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	HIS
1	A	105	ASN
1	A	219	ASN
1	A	234	ASN
1	A	283	GLN
1	A	329	GLN
1	A	439	ASN
1	A	532	GLN
1	A	594	GLN
1	A	662	GLN

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 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 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$
3	ADP	A	1756	2,4	22,29,29	1.65	2 (9%)	27,45,45	2.48	6 (22%)
4	BEF	A	1757	3,2	0,3,3	0.00	-	0,3,3	0.00	-
5	EDO	A	1758	-	3,3,3	0.34	0	2,2,2	0.56	0
5	EDO	A	1759	-	3,3,3	0.29	0	2,2,2	0.50	0
5	EDO	A	1760	-	3,3,3	0.39	0	2,2,2	0.13	0
5	EDO	A	1761	-	3,3,3	0.32	0	2,2,2	0.45	0
5	EDO	A	1762	-	3,3,3	0.37	0	2,2,2	0.19	0
5	EDO	A	1763	-	3,3,3	0.29	0	2,2,2	0.43	0
5	EDO	A	1764	-	3,3,3	0.25	0	2,2,2	0.07	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	ADP	A	1756	2,4	-	0/12/32/32	0/3/3/3
4	BEF	A	1757	3,2	-	0/0/0/0	0/0/0/0
5	EDO	A	1758	-	-	0/1/1/1	0/0/0/0
5	EDO	A	1759	-	-	0/1/1/1	0/0/0/0
5	EDO	A	1760	-	-	0/1/1/1	0/0/0/0
5	EDO	A	1761	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	A	1762	-	-	0/1/1/1	0/0/0/0
5	EDO	A	1763	-	-	0/1/1/1	0/0/0/0
5	EDO	A	1764	-	-	0/1/1/1	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1756	ADP	PB-O1B	3.16	1.61	1.51
3	A	1756	ADP	C8-N7	5.42	1.45	1.34

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1756	ADP	N3-C2-N1	-9.51	121.62	128.89
3	A	1756	ADP	C2'-C1'-N9	-4.60	107.26	114.29
3	A	1756	ADP	C1'-N9-C4	-4.54	120.09	126.94
3	A	1756	ADP	O3B-PB-O2B	2.17	115.64	107.38
3	A	1756	ADP	C4'-O4'-C1'	2.25	112.19	109.72
3	A	1756	ADP	O3B-PB-O1B	2.28	117.91	110.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1760	EDO	2	0
5	A	1761	EDO	2	0
5	A	1763	EDO	1	0
5	A	1764	EDO	2	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

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	719/770 (93%)	0.62	88 (12%) 5 6	17, 33, 80, 89	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	701	PHE	8.1
1	A	723	THR	7.8
1	A	502	THR	7.2
1	A	65	VAL	7.1
1	A	685	ILE	6.4
1	A	725	ALA	6.4
1	A	534	VAL	6.2
1	A	722	ALA	6.1
1	A	745	PHE	6.0
1	A	717	GLU	6.0
1	A	503	PHE	6.0
1	A	727	LEU	6.0
1	A	698	TYR	5.9
1	A	67	GLY	5.7
1	A	501	TRP	5.4
1	A	739	PHE	5.3
1	A	751	LEU	5.2
1	A	494	TYR	5.1
1	A	66	ASP	5.0
1	A	499	ILE	5.0
1	A	721	LYS	4.7
1	A	718	ASP	4.7
1	A	699	ALA	4.5
1	A	746	PHE	4.5
1	A	444	GLU	4.4
1	A	71	GLN	4.4
1	A	726	VAL	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	692	PHE	4.2
1	A	400	ALA	4.2
1	A	752	ALA	4.2
1	A	744	ILE	4.2
1	A	56	THR	4.2
1	A	741	ILE	4.1
1	A	504	ILE	4.1
1	A	719	SER	4.0
1	A	536	PRO	4.0
1	A	53	VAL	3.9
1	A	696	ILE	3.8
1	A	41	PRO	3.7
1	A	730	LEU	3.7
1	A	740	GLY	3.7
1	A	443	GLU	3.7
1	A	729	HIS	3.7
1	A	700	ASP	3.6
1	A	5	HIS	3.6
1	A	58	ASP	3.6
1	A	75	ASP	3.5
1	A	31	ASP	3.5
1	A	697	ILE	3.4
1	A	627	PHE	3.3
1	A	69	ASP	3.2
1	A	39	PRO	3.2
1	A	70	ARG	3.2
1	A	738	ARG	3.2
1	A	537	ASN	3.2
1	A	728	LYS	3.2
1	A	734	PRO	3.2
1	A	495	LEU	3.2
1	A	362	GLY	3.2
1	A	720	GLN	3.1
1	A	445	ARG	3.1
1	A	500	ASN	3.1
1	A	702	VAL	3.0
1	A	622	LYS	2.8
1	A	497	GLU	2.8
1	A	76	ASP	2.7
1	A	599	CYS	2.7
1	A	202	ARG	2.7
1	A	61	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	506	PHE	2.6
1	A	753	ARG	2.6
1	A	364	GLY	2.5
1	A	21	ASP	2.5
1	A	691	GLY	2.4
1	A	690	LYS	2.4
1	A	72	VAL	2.3
1	A	46	SER	2.2
1	A	498	LYS	2.2
1	A	123	LEU	2.2
1	A	737	PHE	2.2
1	A	42	LYS	2.2
1	A	687	ILE	2.1
1	A	724	ASP	2.1
1	A	405	VAL	2.1
1	A	363	ALA	2.1
1	A	40	ASP	2.0
1	A	178[A]	THR	2.0
1	A	407	GLN	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(Å ²)	Q<0.9
5	EDO	A	1762	4/4	0.93	0.17	5.69	25,38,42,46	0
5	EDO	A	1761	4/4	0.89	0.27	3.99	45,51,52,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	EDO	A	1763	4/4	0.90	0.17	1.20	54,55,57,57	0
5	EDO	A	1759	4/4	0.92	0.15	0.82	40,42,43,44	0
5	EDO	A	1760	4/4	0.91	0.15	0.80	36,38,38,38	0
5	EDO	A	1764	4/4	0.99	0.18	0.47	21,21,23,24	0
2	MG	A	1755	1/1	0.98	0.16	0.00	20,20,20,20	0
5	EDO	A	1758	4/4	0.95	0.17	-0.04	29,36,37,41	0
3	ADP	A	1756	27/27	0.99	0.12	-0.82	15,20,23,24	0
4	BEF	A	1757	4/4	0.94	0.13	-0.95	17,19,21,21	0

6.5 Other polymers [i](#)

There are no such residues in this entry.