



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:44 AM GMT

PDB ID : 3MYH
Title : Insights into the Importance of Hydrogen Bonding in the Gamma-Phosphate Binding Pocket of Myosin: Structural and Functional Studies of Ser236
Authors : Frye, J.J.; Klenchin, V.A.; Bagshaw, C.R.; Rayment, I.
Deposited on : 2010-05-10
Resolution : 2.01 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

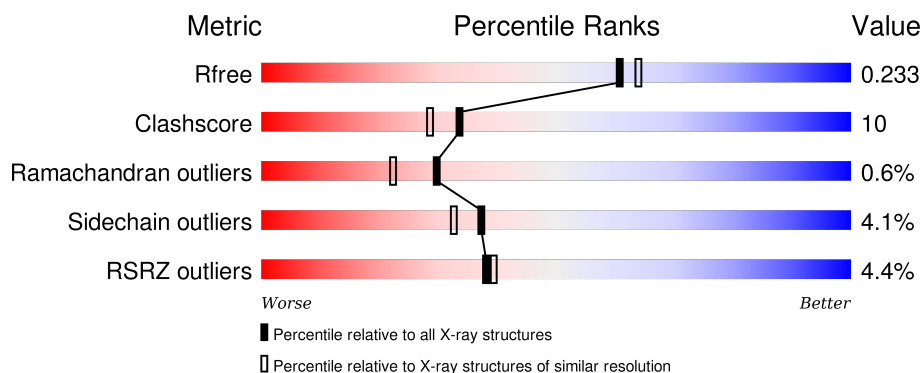
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.01 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	X	762	<div> <div>4%</div> <div>77%</div> <div>14%</div> <div>7%</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6046 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-2 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	X	708	Total	C	N	O	S	0	8	0
			5640	3595	958	1070	17			

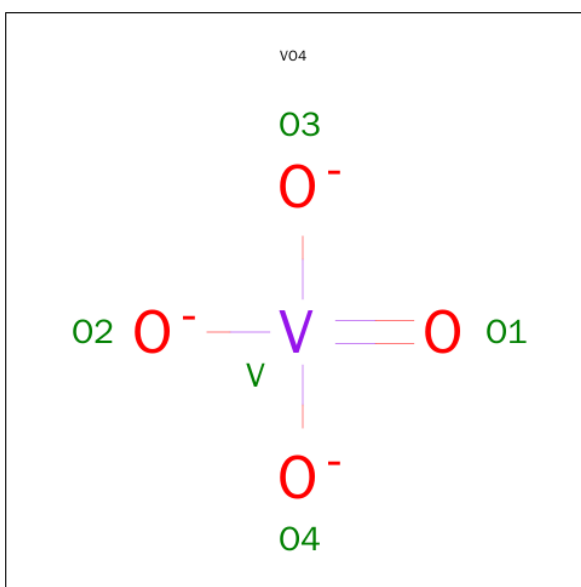
There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	1	GLY	-	EXPRESSION TAG	UNP P08799
X	236	ALA	SER	ENGINEERED MUTATION	UNP P08799
X	760	LEU	-	EXPRESSION TAG	UNP P08799
X	761	PRO	-	EXPRESSION TAG	UNP P08799
X	762	ASN	-	EXPRESSION TAG	UNP P08799

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

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

- Molecule 3 is VANADATE ION (three-letter code: VO4) (formula: O₄V).



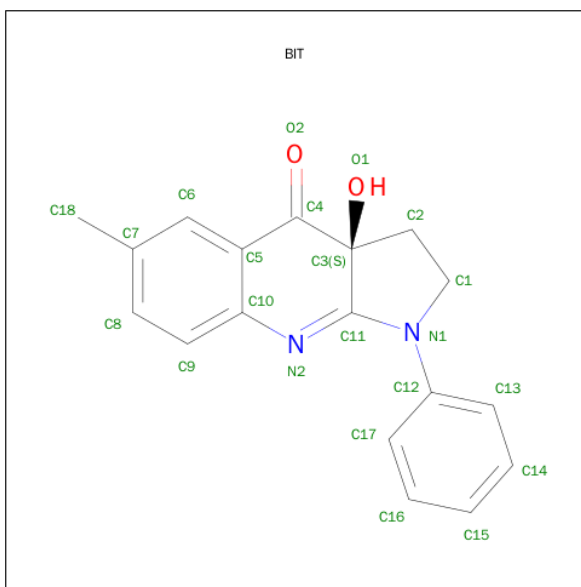
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	X	1	Total	O	V	0	0
			5	4	1		

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	X	1	Total	C	N	O	P	
			27	10	5	10	2	

- Molecule 5 is (-)-1-PHENYL-1,2,3,4-TETRAHYDRO-4-HYDROXYPYRROLO[2,3-B]-7-M ETHYLQUINOLIN-4-ONE (three-letter code: BIT) (formula: $C_{18}H_{16}N_2O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	X	1	Total	C	N	O	0	0
			22	18	2	2		

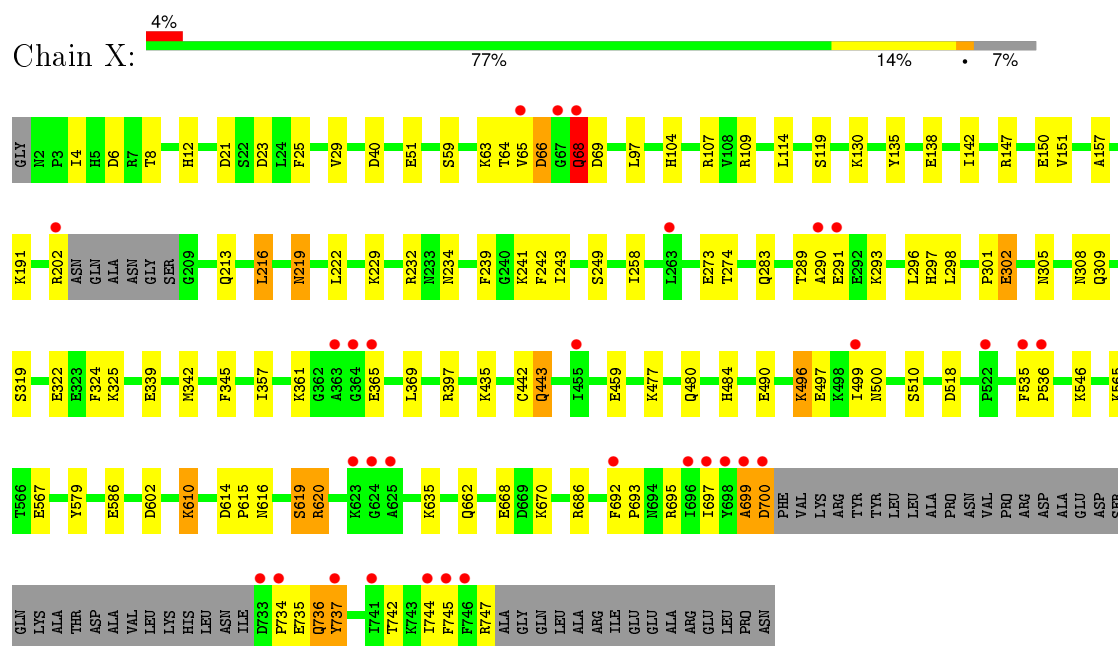
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	X	351	Total	O	0	0
			351	351		

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-2 heavy chain



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	88.43 Å 146.44 Å 153.76 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.62 – 2.01 35.61 – 2.01	Depositor EDS
% Data completeness (in resolution range)	96.7 (35.62-2.01) 96.7 (35.61-2.01)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.76 (at 2.01 Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.189 , 0.240 0.184 , 0.233	Depositor DCC
R_{free} test set	3262 reflections (5.35%)	DCC
Wilson B-factor (Å ²)	23.7	Xtriage
Anisotropy	0.200	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 53.8	EDS
Estimated twinning fraction	0.016 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.023 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 64269 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6046	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% 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: VO4, MG, BIT, 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	X	1.11	6/5774 (0.1%)	0.94	3/7799 (0.0%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	X	668	GLU	CG-CD	6.83	1.62	1.51
1	X	242	PHE	CE2-CZ	6.11	1.49	1.37
1	X	586	GLU	CG-CD	5.46	1.60	1.51
1	X	157	ALA	CA-CB	5.41	1.63	1.52
1	X	119	SER	CB-OG	-5.30	1.35	1.42
1	X	239	PHE	CE1-CZ	5.05	1.47	1.37

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	40	ASP	CB-CG-OD1	5.46	123.22	118.30
1	X	397	ARG	NE-CZ-NH1	-5.32	117.64	120.30
1	X	216	LEU	CB-CG-CD1	5.04	119.57	111.00

There are no chirality outliers.

There are no planarity outliers.

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	X	5640	0	5512	115	0
2	X	1	0	0	0	0
3	X	5	0	0	0	0
4	X	27	0	12	0	0
5	X	22	0	16	0	0
6	X	351	0	0	21	1
All	All	6046	0	5540	115	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 10.

All (115) 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:X:480[B]:GLN:NE2	1:X:510:SER:HB2	1.11	1.38
1:X:480[B]:GLN:NE2	1:X:510:SER:CB	1.96	1.27
1:X:342[B]:MET:CE	6:X:1052:HOH:O	1.83	1.24
1:X:342[B]:MET:HE1	6:X:1052:HOH:O	1.43	1.11
1:X:480[B]:GLN:HE22	1:X:510:SER:N	1.52	1.07
1:X:297:HIS:CE1	6:X:991:HOH:O	2.13	0.99
1:X:480[B]:GLN:NE2	1:X:510:SER:H	1.63	0.97
1:X:289:THR:HG21	1:X:291:GLU:OE1	1.66	0.95
1:X:480[B]:GLN:HE22	1:X:510:SER:H	0.92	0.90
1:X:219:ASN:ND2	6:X:1047:HOH:O	1.95	0.90
1:X:130:LYS:HE2	6:X:1104:HOH:O	1.71	0.89
1:X:480[B]:GLN:HE21	1:X:510:SER:CB	1.67	0.88
1:X:289:THR:HG22	1:X:290:ALA:H	1.41	0.85
1:X:565:LYS:HE3	6:X:941:HOH:O	1.76	0.84
1:X:480[B]:GLN:HE22	1:X:510:SER:CB	1.73	0.84
1:X:51:GLU:H	1:X:63[B]:LYS:HD2	1.43	0.84
1:X:51:GLU:H	1:X:63[B]:LYS:CD	1.91	0.83
1:X:480[B]:GLN:HE22	1:X:510:SER:CA	1.92	0.83
1:X:289:THR:CG2	1:X:291:GLU:OE1	2.26	0.82
1:X:443:GLN:HA	1:X:443:GLN:OE1	1.80	0.80
1:X:319:SER:HB3	1:X:322:GLU:HG3	1.63	0.79
1:X:342[B]:MET:HE3	6:X:1052:HOH:O	1.63	0.79
1:X:319:SER:CB	1:X:322:GLU:HG3	2.13	0.78
1:X:610:LYS:HG3	6:X:1117:HOH:O	1.84	0.76
1:X:232:ARG:NH1	6:X:955:HOH:O	2.15	0.76
1:X:616:ASN:HB3	6:X:1114:HOH:O	1.85	0.76
1:X:319:SER:OG	1:X:322:GLU:HG2	1.85	0.75
1:X:319:SER:OG	1:X:322:GLU:CG	2.35	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:699:ALA:CA	1:X:700:ASP:HB2	2.18	0.74
1:X:620:ARG:HH11	1:X:620:ARG:HG3	1.53	0.73
1:X:480[B]:GLN:NE2	1:X:510:SER:CA	2.51	0.71
1:X:97:LEU:CD2	1:X:686:ARG:HG2	2.20	0.71
1:X:297:HIS:ND1	6:X:991:HOH:O	2.20	0.71
1:X:289:THR:HG22	1:X:290:ALA:N	2.06	0.69
1:X:202:ARG:HH11	1:X:202:ARG:HG2	1.58	0.69
1:X:443:GLN:CA	1:X:443:GLN:OE1	2.41	0.68
1:X:442:CYS:O	1:X:443:GLN:OE1	2.10	0.68
1:X:480[B]:GLN:NE2	1:X:510:SER:N	2.29	0.67
1:X:499:ILE:O	1:X:500:ASN:O	2.13	0.65
1:X:692:PHE:CZ	1:X:747:ARG:NH1	2.65	0.65
1:X:615:PRO:O	1:X:619:SER:HB2	1.98	0.63
1:X:222:LEU:HD11	1:X:258:ILE:HD13	1.81	0.62
1:X:51:GLU:N	1:X:63[B]:LYS:HD2	2.13	0.62
1:X:620:ARG:HH11	1:X:620:ARG:CG	2.13	0.60
1:X:357:ILE:HG23	1:X:369:LEU:HD11	1.84	0.60
1:X:442:CYS:C	1:X:443:GLN:OE1	2.40	0.60
1:X:64:THR:OG1	1:X:68:GLN:HG3	2.02	0.60
1:X:234:ASN:H	1:X:662:GLN:HE22	1.48	0.60
1:X:490:GLU:HA	1:X:490:GLU:OE1	2.01	0.60
1:X:699:ALA:CA	1:X:700:ASP:CB	2.80	0.59
1:X:319:SER:OG	1:X:322:GLU:HG3	2.02	0.59
1:X:241:LYS:CE	1:X:243:ILE:HD11	2.33	0.58
1:X:138:GLU:O	1:X:142:ILE:HG13	2.04	0.58
1:X:130:LYS:CE	6:X:1104:HOH:O	2.42	0.57
1:X:241:LYS:HE2	1:X:243:ILE:HD11	1.88	0.56
1:X:297:HIS:HE1	6:X:1056:HOH:O	1.88	0.55
1:X:104:HIS:ND1	1:X:107[A]:ARG:NH1	2.54	0.54
1:X:735:GLU:HB2	1:X:736:GLN:NE2	2.23	0.54
1:X:97:LEU:HD23	1:X:686:ARG:HG2	1.89	0.54
1:X:480[B]:GLN:HE21	1:X:510:SER:HB2	0.72	0.54
1:X:614:ASP:OD1	1:X:614:ASP:C	2.46	0.53
1:X:620:ARG:NH1	1:X:620:ARG:HG3	2.16	0.53
1:X:662:GLN:NE2	6:X:1011:HOH:O	2.28	0.52
1:X:301:PRO:HD2	1:X:302[B]:GLU:OE2	2.10	0.51
1:X:567:GLU:HA	1:X:579:TYR:O	2.11	0.51
1:X:4:ILE:O	1:X:12:HIS:NE2	2.43	0.51
1:X:496:LYS:O	1:X:496:LYS:HG3	2.10	0.51
1:X:97:LEU:CD2	1:X:686:ARG:CG	2.88	0.51
1:X:296:LEU:HD11	1:X:342[A]:MET:HE1	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:567:GLU:OE2	6:X:1009:HOH:O	2.19	0.50
1:X:97:LEU:HD23	1:X:686:ARG:NE	2.26	0.50
1:X:293:LYS:CD	6:X:1048:HOH:O	2.60	0.50
1:X:499:ILE:O	1:X:500:ASN:HB2	2.12	0.50
1:X:339:GLU:OE1	1:X:342[B]:MET:HE2	2.11	0.49
1:X:51:GLU:N	1:X:63[B]:LYS:CD	2.71	0.49
1:X:736:GLN:HA	1:X:737:TYR:CB	2.42	0.49
1:X:289:THR:HG21	1:X:291:GLU:CD	2.33	0.49
1:X:305[B]:ASN:ND2	6:X:966:HOH:O	2.46	0.49
1:X:518:ASP:OD2	1:X:635:LYS:HD2	2.12	0.48
1:X:435:LYS:NZ	6:X:1114:HOH:O	2.45	0.48
1:X:66:ASP:OD1	1:X:66:ASP:N	2.39	0.48
1:X:234:ASN:ND2	6:X:837:HOH:O	2.47	0.48
1:X:697:ILE:HA	1:X:742:THR:O	2.14	0.48
1:X:147:ARG:HB2	1:X:150:GLU:HG3	1.96	0.47
1:X:535:PHE:HD1	1:X:536:PRO:HD2	1.79	0.47
1:X:51:GLU:H	1:X:63[B]:LYS:CE	2.28	0.47
1:X:63[A]:LYS:HG2	1:X:69:ASP:OD1	2.15	0.46
1:X:322:GLU:OE2	1:X:325:LYS:NZ	2.49	0.45
1:X:283:GLN:HB3	1:X:324:PHE:HB2	1.99	0.45
1:X:499:ILE:O	1:X:500:ASN:C	2.53	0.45
1:X:693:PRO:HD2	1:X:747:ARG:HA	1.99	0.44
1:X:21:ASP:OD1	1:X:23:ASP:HB2	2.18	0.44
1:X:6:ASP:OD1	1:X:8:THR:OG1	2.30	0.43
1:X:202:ARG:HG2	1:X:202:ARG:NH1	2.29	0.43
1:X:342[A]:MET:HE3	1:X:345:PHE:HB2	1.99	0.43
1:X:65:VAL:HG22	6:X:1045:HOH:O	2.18	0.43
1:X:296:LEU:HB2	1:X:298:LEU:HG	1.99	0.43
1:X:229:LYS:HG3	1:X:234:ASN:HD22	1.84	0.43
1:X:109:ARG:HB3	1:X:114:LEU:HB2	2.00	0.43
1:X:66:ASP:OD2	1:X:68:GLN:OE1	2.36	0.42
1:X:635:LYS:HB3	1:X:635:LYS:HE3	1.46	0.42
1:X:497:GLU:HG3	1:X:745:PHE:CZ	2.54	0.42
1:X:308:ASN:OD1	1:X:309:GLN:NE2	2.52	0.42
1:X:97:LEU:HD23	1:X:686:ARG:CG	2.49	0.42
1:X:289:THR:HG22	1:X:291:GLU:OE1	2.15	0.42
1:X:610:LYS:HE2	1:X:614:ASP:HB2	2.03	0.41
1:X:65:VAL:HG23	1:X:66:ASP:OD1	2.20	0.41
1:X:66:ASP:OD2	1:X:68:GLN:CG	2.69	0.41
1:X:135:TYR:CG	1:X:191:LYS:HE2	2.55	0.41
1:X:25:PHE:O	1:X:29:VAL:HG22	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:273:GLU:HG2	1:X:274:THR:HG23	2.02	0.41
1:X:459:GLU:HA	6:X:955:HOH:O	2.21	0.41
1:X:339:GLU:OE1	1:X:342[B]:MET:CE	2.69	0.41
1:X:477:LYS:HB3	1:X:477:LYS:HE3	1.90	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)
6:X:888:HOH:O	6:X:951:HOH:O[3_655]	2.02	0.18

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	X	710/762 (93%)	688 (97%)	18 (2%)	4 (1%)	30	22

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	X	734	PRO
1	X	68	GLN
1	X	699	ALA
1	X	737	TYR

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	X	600/664 (90%)	574 (96%)	26 (4%)	35	30

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	X	59	SER
1	X	66	ASP
1	X	68	GLN
1	X	151	VAL
1	X	213	GLN
1	X	216	LEU
1	X	219	ASN
1	X	249	SER
1	X	302[A]	GLU
1	X	302[B]	GLU
1	X	361	LYS
1	X	365	GLU
1	X	443	GLN
1	X	484[A]	HIS
1	X	484[B]	HIS
1	X	496	LYS
1	X	546	LYS
1	X	602	ASP
1	X	610	LYS
1	X	619	SER
1	X	620	ARG
1	X	670	LYS
1	X	695	ARG
1	X	700	ASP
1	X	736	GLN
1	X	744	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	X	68	GLN
1	X	219	ASN
1	X	234	ASN
1	X	283	GLN
1	X	329	GLN

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Mol	Chain	Res	Type
1	X	500	ASN
1	X	532	GLN
1	X	582	GLN
1	X	606	ASN
1	X	662	GLN
1	X	736	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 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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	$\# Z > 2$
5	BIT	X	800	-	23,25,25	2.55	7 (30%)	27,38,38	2.27	8 (29%)
3	VO4	X	998	2,4	1,4,4	2.88	1 (100%)	0,6,6	0.00	-
4	ADP	X	999	3,2	22,29,29	1.23	2 (9%)	27,45,45	2.50	6 (22%)

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
5	BIT	X	800	-	-	0/4/34/34	0/3/4/4
3	VO4	X	998	2,4	-	0/0/0/0	0/0/0/0
4	ADP	X	999	3,2	-	0/12/32/32	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	X	800	BIT	C5-C4	-3.29	1.43	1.48
5	X	800	BIT	C14-C13	2.20	1.43	1.38
5	X	800	BIT	O1-C3	2.29	1.46	1.42
5	X	800	BIT	C13-C12	2.32	1.43	1.39
5	X	800	BIT	C16-C15	2.52	1.44	1.38
5	X	800	BIT	C1-N1	2.57	1.51	1.47
4	X	999	ADP	C5-C4	2.63	1.46	1.40
3	X	998	VO4	O1-V	2.88	1.82	1.63
4	X	999	ADP	O4'-C1'	3.83	1.46	1.41
5	X	800	BIT	C11-N2	9.62	1.40	1.28

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	X	999	ADP	N3-C2-N1	-10.72	120.69	128.89
5	X	800	BIT	C13-C12-N1	-3.66	114.75	120.17
5	X	800	BIT	C9-C8-C7	-3.50	116.68	121.39
4	X	999	ADP	C4'-O4'-C1'	-2.55	106.92	109.72
4	X	999	ADP	C2'-C1'-N9	-2.21	110.91	114.29
4	X	999	ADP	C4-C5-N7	-2.03	107.61	109.48
5	X	800	BIT	C6-C5-C4	2.01	122.72	118.87
5	X	800	BIT	C8-C7-C6	2.79	122.54	117.95
5	X	800	BIT	C9-C10-C5	2.93	122.69	119.19
4	X	999	ADP	C2-N1-C6	3.16	124.41	118.77
4	X	999	ADP	O2B-PB-O1B	3.44	121.65	110.58
5	X	800	BIT	C16-C17-C12	3.68	124.69	119.69
5	X	800	BIT	C10-N2-C11	5.16	124.77	116.03
5	X	800	BIT	C17-C12-N1	5.25	127.93	120.17

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	X	708/762 (92%)	-0.02	31 (4%) 38 39	11, 25, 50, 81	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	X	67	GLY	5.2
1	X	734	PRO	5.1
1	X	697	ILE	4.9
1	X	65	VAL	4.4
1	X	696	ILE	4.3
1	X	733	ASP	3.8
1	X	699	ALA	3.7
1	X	698	TYR	3.5
1	X	536	PRO	3.4
1	X	745	PHE	3.3
1	X	291	GLU	3.1
1	X	365	GLU	2.8
1	X	741	ILE	2.7
1	X	623	LYS	2.6
1	X	263	LEU	2.6
1	X	692	PHE	2.5
1	X	68	GLN	2.5
1	X	624	GLY	2.5
1	X	744	ILE	2.5
1	X	625	ALA	2.4
1	X	737	TYR	2.4
1	X	535	PHE	2.4
1	X	499	ILE	2.4
1	X	746	PHE	2.3
1	X	363	ALA	2.3
1	X	290	ALA	2.3
1	X	202	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	X	455	ILE	2.2
1	X	364	GLY	2.2
1	X	522	PRO	2.2
1	X	700	ASP	2.1

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	VO4	X	998	5/5	1.00	0.18	0.62	13,13,15,16	0
5	BIT	X	800	22/22	0.98	0.16	0.14	12,16,18,19	0
4	ADP	X	999	27/27	0.99	0.11	-0.55	12,16,20,21	0
2	MG	X	997	1/1	0.99	0.09	-1.23	12,12,12,12	0

6.5 Other polymers [i](#)

There are no such residues in this entry.