



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 28, 2014 – 11:29 AM EDT

PDB ID : 3WUQ  
Title : Structure of the entire stalk region of the dynein motor domain  
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Deposited on : 2014-05-01  
Resolution : 3.50 Å(reported)

This is a full wwPDB validation 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/ValidationPDFNotes.html>

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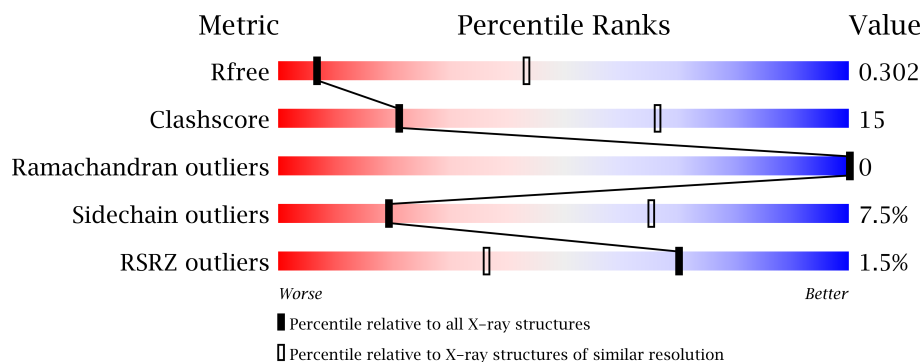
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.16 November 2013  
Xtriage (Phenix) : dev-1439  
EDS : stable23489  
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) : stable23489

# 1 Overall quality at a glance

The reported resolution of this entry is 3.50 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	1243 (3.70-3.30)
Clashscore	79885	1039 (3.66-3.34)
Ramachandran outliers	78287	1000 (3.66-3.34)
Sidechain outliers	78261	1000 (3.66-3.34)
RSRZ outliers	66119	1243 (3.70-3.30)

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. 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	283	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1962 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 Cytoplasmic dynein 1 heavy chain 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	263	1962	1228	340	382	12	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

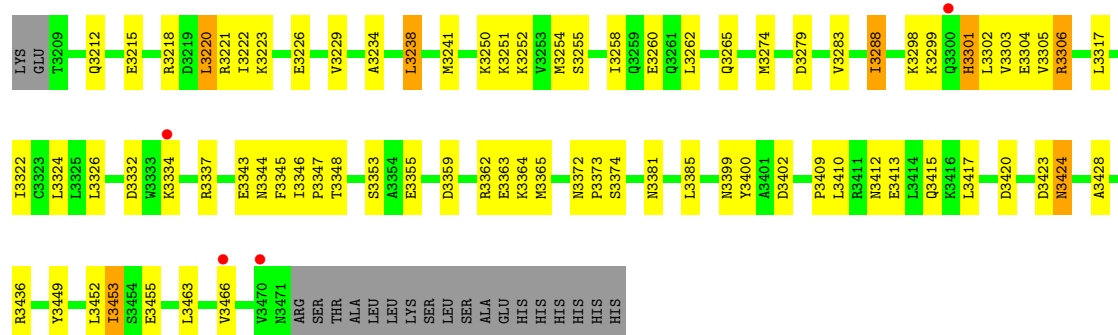
Chain	Residue	Modelled	Actual	Comment	Reference
A	3484	HIS	-	EXPRESSION TAG	UNP Q9JHU4
A	3485	HIS	-	EXPRESSION TAG	UNP Q9JHU4
A	3486	HIS	-	EXPRESSION TAG	UNP Q9JHU4
A	3487	HIS	-	EXPRESSION TAG	UNP Q9JHU4
A	3488	HIS	-	EXPRESSION TAG	UNP Q9JHU4
A	3489	HIS	-	EXPRESSION TAG	UNP Q9JHU4

### 3 Residue-property plots

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: Cytoplasmic dynein 1 heavy chain 1

Chain A: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	102.94Å 102.94Å 69.07Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.57 – 3.50 44.57 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.6 (44.57-3.50) 96.3 (44.57-3.50)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.95 (at 3.48Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, $R_{free}$	0.279 , 0.305 0.274 , 0.302	Depositor DCC
$R_{free}$ test set	530 reflections (9.92%)	DCC
Wilson B-factor (Å <sup>2</sup> )	106.6	Xtriage
Anisotropy	0.069	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 134.5	EDS
Estimated twinning fraction	0.048 for -h,-k,l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 5536 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	1962	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	172.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.60% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

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	0.30	0/1981	0.60	4/2678 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3305	VAL	CB-CA-C	-7.93	96.33	111.40
1	A	3220	LEU	CA-CB-CG	5.81	128.66	115.30
1	A	3455	GLU	CB-CA-C	-5.19	100.02	110.40
1	A	3305	VAL	N-CA-C	5.12	124.83	111.00

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	1962	0	1867	59	0
All	All	1962	0	1867	59	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 15.

All (59) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:3238:LEU:HD12	1:A:3241:MET:CE	1.85	1.06
1:A:3413:GLU:O	1:A:3417:LEU:HD12	1.68	0.92
1:A:3220:LEU:HD21	1:A:3466:VAL:HG21	1.60	0.83
1:A:3413:GLU:O	1:A:3417:LEU:CD1	2.27	0.82
1:A:3417:LEU:O	1:A:3420:ASP:OD1	1.98	0.80
1:A:3353:SER:OG	1:A:3355:GLU:OE1	2.03	0.75
1:A:3238:LEU:HD12	1:A:3241:MET:HE3	1.70	0.74
1:A:3220:LEU:HD11	1:A:3466:VAL:HG23	1.70	0.74
1:A:3220:LEU:HD21	1:A:3466:VAL:CG2	2.19	0.71
1:A:3346:ILE:HB	1:A:3347:PRO:HD3	1.73	0.70
1:A:3238:LEU:HD12	1:A:3241:MET:HE2	1.77	0.65
1:A:3238:LEU:CD1	1:A:3241:MET:CE	2.71	0.62
1:A:3420:ASP:HA	1:A:3423:ASP:HB2	1.82	0.62
1:A:3265:GLN:NE2	1:A:3420:ASP:OD1	2.33	0.61
1:A:3223:LYS:HB3	1:A:3463:LEU:HD11	1.82	0.60
1:A:3301:HIS:HA	1:A:3304:GLU:HB2	1.83	0.59
1:A:3324:LEU:HD23	1:A:3365:MET:HE2	1.83	0.59
1:A:3212:GLN:HA	1:A:3215:GLU:HG2	1.83	0.59
1:A:3344:ASN:O	1:A:3348:THR:HG23	2.00	0.59
1:A:3413:GLU:OE2	1:A:3417:LEU:HD11	2.02	0.59
1:A:3234:ALA:HB1	1:A:3449:TYR:CE1	2.39	0.57
1:A:3303:VAL:HA	1:A:3306:ARG:HB3	1.85	0.57
1:A:3409:PRO:HA	1:A:3412:ASN:ND2	2.20	0.56
1:A:3298:LYS:HB2	1:A:3301:HIS:CE1	2.42	0.55
1:A:3372:ASN:OD1	1:A:3374:SER:OG	2.15	0.54
1:A:3220:LEU:HD11	1:A:3466:VAL:CG2	2.39	0.52
1:A:3332:ASP:OD1	1:A:3332:ASP:N	2.42	0.51
1:A:3362:ARG:HG3	1:A:3363:GLU:N	2.25	0.51
1:A:3381:ASN:OD1	1:A:3385:LEU:HA	2.10	0.51
1:A:3345:PHE:O	1:A:3348:THR:OG1	2.16	0.50
1:A:3234:ALA:HB2	1:A:3452:LEU:HD22	1.92	0.50
1:A:3359:ASP:O	1:A:3362:ARG:NE	2.45	0.50
1:A:3410:LEU:O	1:A:3413:GLU:HB3	2.12	0.49
1:A:3322:ILE:HG23	1:A:3326:LEU:HD13	1.95	0.49
1:A:3413:GLU:CD	1:A:3417:LEU:HD11	2.34	0.48
1:A:3265:GLN:NE2	1:A:3420:ASP:CG	2.67	0.48
1:A:3234:ALA:HB1	1:A:3449:TYR:HE1	1.77	0.47
1:A:3324:LEU:HD11	1:A:3364:LYS:HD3	1.96	0.46
1:A:3417:LEU:HA	1:A:3420:ASP:OD1	2.15	0.45
1:A:3238:LEU:HD12	1:A:3241:MET:HE1	1.86	0.45
1:A:3258:ILE:HG21	1:A:3428:ALA:HB2	1.98	0.45
1:A:3262:LEU:HD12	1:A:3262:LEU:HA	1.73	0.45
1:A:3299:LYS:O	1:A:3303:VAL:HG22	2.18	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:3417:LEU:HD12	1:A:3417:LEU:N	2.32	0.44
1:A:3218:ARG:O	1:A:3222:ILE:HG12	2.18	0.44
1:A:3359:ASP:HB3	1:A:3362:ARG:CZ	2.49	0.43
1:A:3252:LYS:O	1:A:3255:SER:HB3	2.19	0.43
1:A:3299:LYS:HA	1:A:3302:LEU:HD12	2.01	0.43
1:A:3372:ASN:HA	1:A:3373:PRO:HD3	1.75	0.43
1:A:3262:LEU:HD13	1:A:3424:ASN:HB3	2.00	0.43
1:A:3283:VAL:HG21	1:A:3400:TYR:HA	2.01	0.42
1:A:3453:ILE:HD12	1:A:3453:ILE:HA	1.68	0.42
1:A:3226:GLU:O	1:A:3229:VAL:HB	2.19	0.42
1:A:3334:LYS:O	1:A:3337:ARG:HG2	2.20	0.42
1:A:3250:LYS:O	1:A:3254:MET:HG3	2.21	0.41
1:A:3420:ASP:O	1:A:3424:ASN:HB2	2.20	0.41
1:A:3288:ILE:H	1:A:3288:ILE:HG13	1.54	0.41
1:A:3399:ASN:O	1:A:3402:ASP:HB2	2.21	0.41
1:A:3218:ARG:O	1:A:3221:ARG:HB3	2.22	0.40

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	261/283 (92%)	234 (90%)	27 (10%)	0	100	100

There are no Ramachandran outliers to report.

### 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	186/249 (75%)	172 (92%)	14 (8%)	19 65

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3238	LEU
1	A	3251	LYS
1	A	3260	GLU
1	A	3274	MET
1	A	3279	ASP
1	A	3288	ILE
1	A	3301	HIS
1	A	3306	ARG
1	A	3317	LEU
1	A	3343	GLU
1	A	3415	GLN
1	A	3424	ASN
1	A	3436	ARG
1	A	3453	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3265	GLN

### 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 ⓘ

There are no ligands in this entry.

## 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, 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	263/283 (92%)	-0.02	4 (1%) 70 36	53, 153, 358, 472	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3334	LYS	2.5
1	A	3300	GLN	2.2
1	A	3470	VAL	2.0
1	A	3466	VAL	2.0

### 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 ⓘ

There are no ligands in this entry.

### 6.5 Other polymers ⓘ

There are no such residues in this entry.