



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:05 PM GMT

PDB ID : 4UWJ  
Title : Crystal structure of *Aspergillus fumigatus* N-myristoyl transferase in complex with myristoyl CoA and a capped pyrazole sulphonamide ligand  
Authors : Robinson, D.A.; Brand, S.; Norcross, N.R.; Thompson, S.; Harrison, J.R.; Smith, V.C.; Torrie, L.S.; McElroy, S.P.; Hallyburton, I.; Norval, S.; Stojanovski, L.; Simeons, F.R.C.; Frearson, J.A.; Brenk, R.; Fairlamb, A.H.; Ferguson, M.A.J.; Wyatt, P.G.; Gilbert, I.H.; Read, K.D.  
Deposited on : 2014-08-12  
Resolution : 1.70 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](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 (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

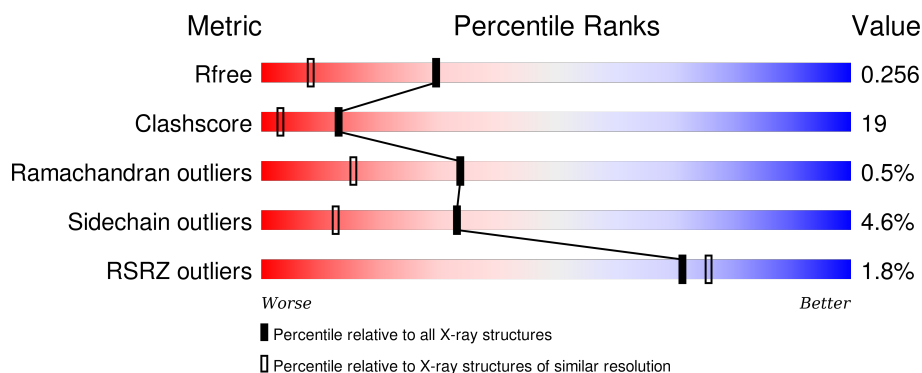
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

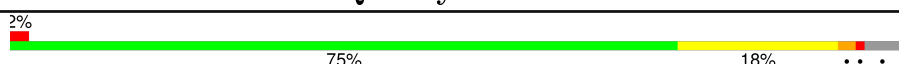
The reported resolution of this entry is 1.70 Å.

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	3190 (1.70-1.70)
Clashscore	102246	3585 (1.70-1.70)
Ramachandran outliers	100387	3527 (1.70-1.70)
Sidechain outliers	100360	3527 (1.70-1.70)
RSRZ outliers	91569	3200 (1.70-1.70)

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	407	

## 2 Entry composition [i](#)

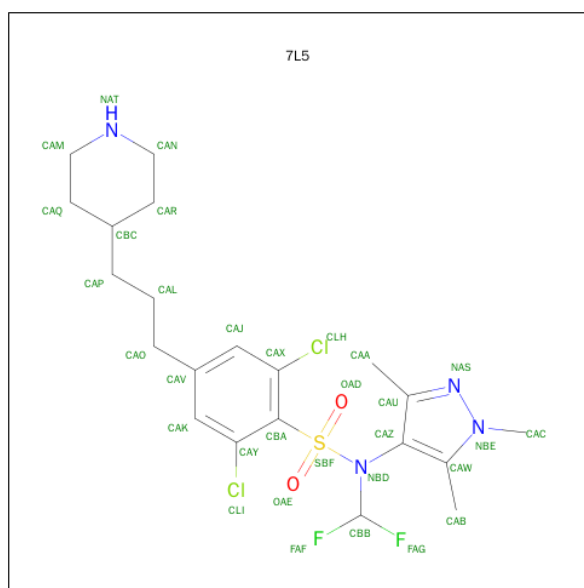
There are 4 unique types of molecules in this entry. The entry contains 3751 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 GLYCYLPEPTIDE N-TETRADECANOYLTRANSFERASE.

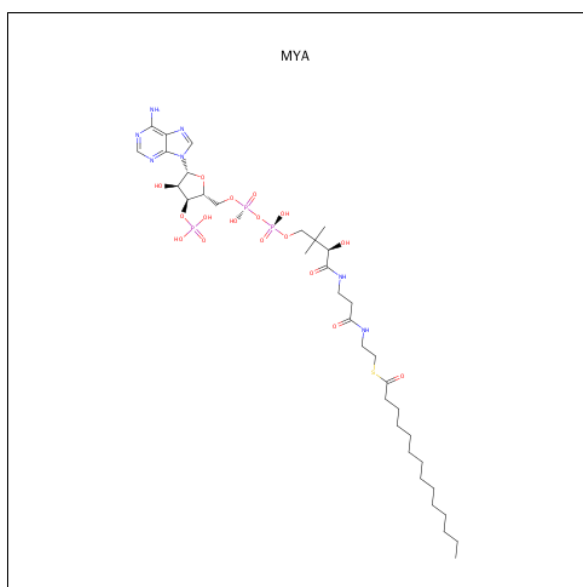
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	392	3188	2060	543	573	12	0	0	0

- Molecule 2 is 2,6-DICHLORO-N-(DIFLUOROMETHYL)-4-[3-(PIPERIDIN-4-YL)PROPYL]-N-(1,3,5-TRIMETHYL-1H-PYRAZOL-4-YL)BENZENESULFONAMIDE (three-letter code: 7L5) (formula: C<sub>21</sub>H<sub>28</sub>Cl<sub>2</sub>F<sub>2</sub>N<sub>4</sub>O<sub>2</sub>S).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
			Total	C	Cl	F	N	O	S		
2	A	1	32	21	2	2	4	2	1	0	0

- Molecule 3 is TETRADECANOYL-COA (three-letter code: MYA) (formula: C<sub>35</sub>H<sub>62</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	S	0	0
			63	35	7	17	3	1		

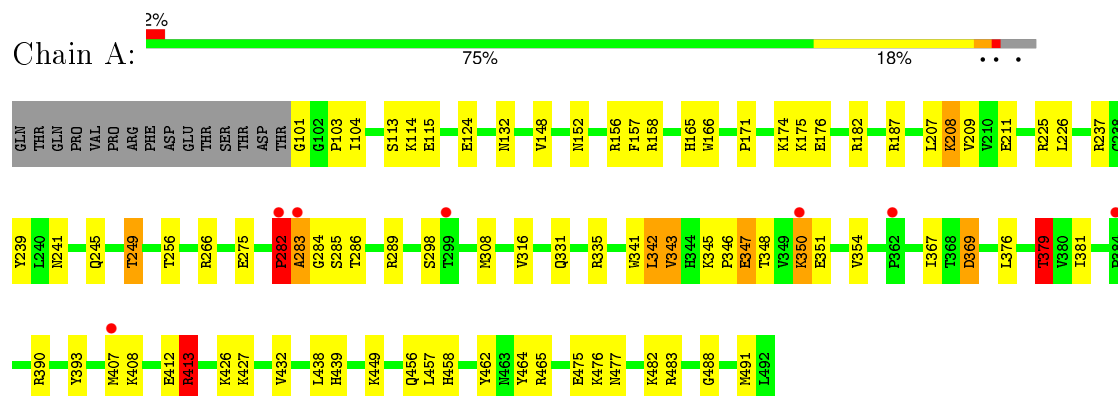
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	468	Total	O	0	0
			468	468		

### 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: GLYCYLPEPTIDE N-TETRADECANOYLTRANSFERASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	51.01Å 58.61Å 152.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.56 – 1.70 19.56 – 1.70	Depositor EDS
% Data completeness (in resolution range)	73.1 (19.56-1.70) 73.1 (19.56-1.70)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.83 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.194 , 0.257 0.198 , 0.256	Depositor DCC
$R_{free}$ test set	1901 reflections (5.36%)	DCC
Wilson B-factor (Å <sup>2</sup> )	19.1	Xtriage
Anisotropy	0.126	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 37.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 37375 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3751	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.64% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MYA, 7L5

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	1.09	2/3275 (0.1%)	1.02	8/4452 (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	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	432	VAL	CB-CG1	5.46	1.64	1.52
1	A	316	VAL	CB-CG2	5.11	1.63	1.52

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	156	ARG	NE-CZ-NH1	9.07	124.83	120.30
1	A	413	ARG	NE-CZ-NH1	8.64	124.62	120.30
1	A	182	ARG	NE-CZ-NH2	-8.35	116.12	120.30
1	A	342	LEU	CB-CG-CD1	7.63	123.98	111.00
1	A	156	ARG	NE-CZ-NH2	-6.84	116.88	120.30
1	A	335	ARG	NE-CZ-NH2	-6.49	117.06	120.30
1	A	413	ARG	NE-CZ-NH2	-6.18	117.21	120.30
1	A	379	THR	N-CA-CB	5.38	120.53	110.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	282	PRO	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	3188	0	3170	120	0
2	A	32	0	28	4	0
3	A	63	0	58	0	0
4	A	468	0	0	86	0
All	All	3751	0	3256	124	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 19.

All (124) 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:348:THR:HB	4:A:2361:HOH:O	1.24	1.26
1:A:113:SER:HB2	4:A:2022:HOH:O	1.24	1.25
1:A:103:PRO:HD2	4:A:2007:HOH:O	1.12	1.24
1:A:187:ARG:CZ	4:A:2051:HOH:O	1.80	1.24
1:A:286:THR:HB	4:A:2288:HOH:O	1.40	1.19
1:A:124:GLU:CG	4:A:2049:HOH:O	1.89	1.18
1:A:465:ARG:HB2	4:A:2006:HOH:O	1.46	1.14
1:A:174:LYS:HE3	4:A:2139:HOH:O	1.46	1.13
1:A:249:THR:CG2	1:A:457:LEU:HD11	1.78	1.11
1:A:249:THR:HG23	1:A:457:LEU:HD11	1.25	1.08
1:A:354:VAL:HG23	4:A:2347:HOH:O	0.93	1.08
1:A:124:GLU:CD	4:A:2049:HOH:O	1.90	1.07
1:A:347:GLU:N	4:A:2357:HOH:O	1.85	1.07
1:A:124:GLU:CB	4:A:2049:HOH:O	2.01	1.06
1:A:124:GLU:HB2	4:A:2049:HOH:O	1.56	1.04
1:A:345:LYS:HG2	4:A:2349:HOH:O	0.83	0.99
1:A:376:LEU:HG	4:A:2116:HOH:O	0.80	0.98
1:A:465:ARG:CB	4:A:2006:HOH:O	2.04	0.96
1:A:275:GLU:CD	4:A:2277:HOH:O	2.10	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:245:GLN:HB2	4:A:2189:HOH:O	1.71	0.89
1:A:249:THR:HG23	1:A:457:LEU:CD1	2.02	0.88
1:A:104:ILE:HG12	4:A:2006:HOH:O	1.72	0.87
1:A:483:ARG:NH1	4:A:2455:HOH:O	1.94	0.87
1:A:282:PRO:HA	1:A:283:ALA:HB2	1.58	0.85
1:A:347:GLU:HB2	4:A:2357:HOH:O	1.78	0.83
1:A:158:ARG:HH11	1:A:379:THR:HG21	1.45	0.81
1:A:286:THR:HG23	1:A:289:ARG:H	1.46	0.80
1:A:284:GLY:HA2	4:A:2285:HOH:O	1.81	0.80
1:A:166:TRP:CZ2	4:A:2346:HOH:O	2.35	0.80
1:A:491:MET:CE	4:A:2193:HOH:O	2.31	0.79
1:A:124:GLU:OE2	4:A:2049:HOH:O	1.93	0.79
1:A:187:ARG:NH2	4:A:2051:HOH:O	1.94	0.79
1:A:226:LEU:HD22	4:A:2201:HOH:O	1.83	0.78
1:A:158:ARG:HH11	1:A:379:THR:CG2	1.97	0.78
1:A:286:THR:HG21	4:A:2169:HOH:O	1.87	0.75
1:A:379:THR:HG23	4:A:2083:HOH:O	1.88	0.74
1:A:158:ARG:HD2	1:A:379:THR:HG22	1.70	0.72
1:A:456:GLN:HE22	1:A:477:ASN:HD21	1.35	0.71
1:A:187:ARG:NH1	4:A:2050:HOH:O	2.24	0.70
1:A:482:LYS:HD3	4:A:2448:HOH:O	1.91	0.70
1:A:483:ARG:NH1	4:A:2454:HOH:O	2.23	0.70
1:A:491:MET:HE2	4:A:2193:HOH:O	1.92	0.68
1:A:369:ASP:OD2	1:A:413:ARG:HD3	1.93	0.67
1:A:331:GLN:NE2	4:A:2165:HOH:O	2.27	0.67
1:A:488:GLY:O	4:A:2335:HOH:O	2.12	0.66
1:A:249:THR:HG21	4:A:2459:HOH:O	1.96	0.65
1:A:381:ILE:O	4:A:2388:HOH:O	2.13	0.65
1:A:283:ALA:H	1:A:285:SER:H	1.45	0.64
1:A:491:MET:HE1	4:A:2193:HOH:O	1.92	0.63
1:A:407:MET:HB3	4:A:2405:HOH:O	1.98	0.63
1:A:174:LYS:CE	4:A:2139:HOH:O	2.20	0.62
1:A:283:ALA:HA	4:A:2284:HOH:O	1.99	0.62
1:A:208:LYS:O	4:A:2189:HOH:O	2.16	0.62
1:A:103:PRO:CD	4:A:2007:HOH:O	1.95	0.62
1:A:350:LYS:HG3	4:A:2356:HOH:O	2.00	0.61
1:A:341:TRP:HE3	4:A:2346:HOH:O	1.84	0.60
1:A:475:GLU:CD	1:A:475:GLU:H	2.04	0.59
2:A:1493:7L5:CLH	2:A:1493:7L5:FAG	2.48	0.58
2:A:1493:7L5:CBA	4:A:2262:HOH:O	2.51	0.58
1:A:175:LYS:NZ	4:A:2141:HOH:O	1.93	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:286:THR:HG22	1:A:289:ARG:HG3	1.86	0.57
1:A:158:ARG:NH1	1:A:379:THR:HG21	2.17	0.56
1:A:157:PHE:CD1	1:A:376:LEU:HD21	2.40	0.56
1:A:225:ARG:HD2	4:A:2214:HOH:O	2.06	0.55
1:A:165:HIS:HE1	4:A:2121:HOH:O	1.90	0.55
1:A:282:PRO:CA	1:A:283:ALA:HB2	2.35	0.54
1:A:379:THR:HB	4:A:2114:HOH:O	2.07	0.54
1:A:132:ASN:HB2	4:A:2057:HOH:O	2.06	0.54
1:A:407:MET:HE3	4:A:2452:HOH:O	2.06	0.53
1:A:439:HIS:HD2	4:A:2401:HOH:O	1.91	0.53
1:A:458:HIS:HE1	4:A:2243:HOH:O	1.91	0.53
1:A:241:ASN:HB3	4:A:2138:HOH:O	2.09	0.53
1:A:104:ILE:CG1	4:A:2006:HOH:O	2.44	0.52
1:A:354:VAL:CG2	4:A:2347:HOH:O	1.82	0.52
1:A:114:LYS:HE3	4:A:2028:HOH:O	2.10	0.52
1:A:331:GLN:HG2	4:A:2165:HOH:O	2.10	0.52
1:A:282:PRO:O	1:A:285:SER:HB2	2.11	0.51
1:A:346:PRO:HG2	4:A:2357:HOH:O	2.10	0.51
1:A:209:VAL:HA	4:A:2189:HOH:O	2.11	0.51
1:A:426:LYS:HE3	4:A:2267:HOH:O	2.11	0.50
1:A:286:THR:HG22	1:A:289:ARG:CG	2.42	0.50
1:A:101:GLY:N	4:A:2003:HOH:O	2.44	0.49
1:A:256:THR:HA	4:A:2251:HOH:O	2.12	0.49
1:A:465:ARG:HB3	4:A:2006:HOH:O	1.90	0.49
1:A:286:THR:CB	4:A:2288:HOH:O	2.23	0.48
1:A:376:LEU:CD2	4:A:2116:HOH:O	2.27	0.48
1:A:175:LYS:CE	4:A:2141:HOH:O	2.50	0.48
1:A:148:VAL:HB	1:A:157:PHE:HD2	1.78	0.47
1:A:308:MET:O	4:A:2318:HOH:O	2.20	0.47
1:A:408:LYS:O	1:A:412:GLU:HG3	2.14	0.46
1:A:211:GLU:HG2	1:A:491:MET:HE3	1.97	0.46
1:A:427:LYS:HE2	4:A:2421:HOH:O	2.16	0.46
1:A:350:LYS:HD3	1:A:350:LYS:N	2.31	0.45
1:A:331:GLN:CD	4:A:2165:HOH:O	2.52	0.45
1:A:101:GLY:N	4:A:2004:HOH:O	2.50	0.45
1:A:331:GLN:CG	4:A:2165:HOH:O	2.64	0.45
1:A:350:LYS:HD3	1:A:350:LYS:H	1.82	0.45
1:A:347:GLU:CB	4:A:2357:HOH:O	2.49	0.45
1:A:341:TRP:HB3	4:A:2346:HOH:O	2.16	0.45
1:A:286:THR:CG2	1:A:289:ARG:HG3	2.47	0.44
1:A:239:TYR:HH	1:A:462:TYR:HH	1.61	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:390:ARG:HG3	4:A:2272:HOH:O	2.16	0.44
1:A:449:LYS:HE2	4:A:2299:HOH:O	2.18	0.43
1:A:286:THR:CG2	1:A:289:ARG:H	2.24	0.43
2:A:1493:7L5:CAX	2:A:1493:7L5:HAB3	2.47	0.43
1:A:176:GLU:O	1:A:237:ARG:HD3	2.19	0.43
1:A:187:ARG:NE	4:A:2051:HOH:O	2.24	0.42
1:A:283:ALA:N	1:A:285:SER:H	2.14	0.42
1:A:456:GLN:HE22	1:A:477:ASN:ND2	2.10	0.42
1:A:152:ASN:OD1	4:A:2099:HOH:O	2.22	0.42
1:A:148:VAL:HB	1:A:157:PHE:CD2	2.54	0.42
1:A:158:ARG:HH11	1:A:379:THR:HG22	1.81	0.42
1:A:347:GLU:CA	4:A:2357:HOH:O	2.52	0.41
2:A:1493:7L5:OAD	2:A:1493:7L5:CLI	2.75	0.41
1:A:284:GLY:CA	4:A:2285:HOH:O	2.52	0.41
1:A:115:GLU:HB2	4:A:2023:HOH:O	2.21	0.41
1:A:376:LEU:HB3	1:A:393:TYR:CE1	2.56	0.41
1:A:390:ARG:HD2	4:A:2218:HOH:O	2.20	0.41
1:A:343:VAL:HA	4:A:2348:HOH:O	2.21	0.41
1:A:249:THR:CG2	4:A:2459:HOH:O	2.61	0.40
1:A:249:THR:HG21	1:A:457:LEU:HD21	2.02	0.40
1:A:207:LEU:HD21	1:A:464:TYR:CE1	2.56	0.40
1:A:241:ASN:ND2	4:A:2224:HOH:O	2.54	0.40
1:A:249:THR:HG23	1:A:457:LEU:CG	2.48	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	390/407 (96%)	376 (96%)	12 (3%)	2 (0%)	34 15

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	283	ALA
1	A	282	PRO

### 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	346/364 (95%)	330 (95%)	16 (5%)	33 12

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	171	PRO
1	A	208	LYS
1	A	249	THR
1	A	266	ARG
1	A	298	SER
1	A	342	LEU
1	A	343	VAL
1	A	347	GLU
1	A	350	LYS
1	A	351	GLU
1	A	367	ILE
1	A	369	ASP
1	A	379	THR
1	A	413	ARG
1	A	438	LEU
1	A	476	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	165	HIS
1	A	241	ASN
1	A	419	ASN
1	A	439	HIS

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Mol	Chain	Res	Type
1	A	447	GLN
1	A	458	HIS
1	A	477	ASN

### 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 ⓘ

2 ligands are modelled in this entry.

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	$\# Z  > 2$
2	7L5	A	1493	-	31,34,34	3.90	10 (32%)	33,50,50	2.42	15 (45%)
3	MYA	A	1494	-	53,65,65	1.05	3 (5%)	65,91,91	2.11	12 (18%)

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
2	7L5	A	1493	-	-	0/18/34/34	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MYA	A	1494	-	-	0/59/80/80	0/3/3/3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1493	7L5	NAS-NBE	-12.30	1.24	1.37
2	A	1493	7L5	CAW-NBE	-2.12	1.34	1.37
2	A	1493	7L5	FAG-CBB	2.31	1.37	1.34
2	A	1493	7L5	FAF-CBB	2.61	1.37	1.34
2	A	1493	7L5	CAA-CAU	2.70	1.55	1.50
3	A	1494	MYA	C2A-N3A	2.77	1.37	1.32
2	A	1493	7L5	CAB-CAW	3.01	1.56	1.49
3	A	1494	MYA	P3X-O9A	3.13	1.61	1.51
3	A	1494	MYA	O10-C10	3.43	1.49	1.42
2	A	1493	7L5	OAE-SBF	4.52	1.49	1.43
2	A	1493	7L5	OAD-SBF	5.12	1.50	1.43
2	A	1493	7L5	CAC-NBE	8.41	1.56	1.46
2	A	1493	7L5	SBF-NBD	12.56	1.81	1.65

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1494	MYA	N3A-C2A-N1A	-10.78	120.64	128.89
2	A	1493	7L5	CAW-CAZ-CAU	-5.09	104.07	107.56
2	A	1493	7L5	OAE-SBF-OAD	-3.99	112.58	119.47
3	A	1494	MYA	C2X-C1X-N9A	-3.31	109.23	114.29
3	A	1494	MYA	C1X-N9A-C4A	-3.09	122.27	126.94
2	A	1493	7L5	CAC-NBE-CAW	-2.97	124.03	128.84
2	A	1493	7L5	CAK-CAY-CBA	-2.78	117.99	121.36
3	A	1494	MYA	P2A-O3A-P1A	-2.43	125.91	132.73
3	A	1494	MYA	C6-C7-N8	-2.36	106.71	111.88
2	A	1493	7L5	CAP-CBC-CAQ	-2.30	107.22	112.10
2	A	1493	7L5	CAR-CAN-NAT	-2.23	106.67	110.46
2	A	1493	7L5	CAP-CBC-CAR	-2.08	107.69	112.10
3	A	1494	MYA	O5-C5-C6	-2.07	118.42	121.98
3	A	1494	MYA	C2X-C3X-C4X	-2.01	99.52	103.29
2	A	1493	7L5	OAE-SBF-NBD	2.39	109.11	106.46
2	A	1493	7L5	CAQ-CAM-NAT	2.46	114.63	110.46
2	A	1493	7L5	CBA-CAX-CLH	2.66	123.52	121.55
2	A	1493	7L5	CAC-NBE-NAS	3.06	123.14	118.05
2	A	1493	7L5	CBA-CAY-CLI	3.13	123.87	121.55
3	A	1494	MYA	C7-N8-C9	3.17	128.80	122.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1494	MYA	C2A-N1A-C6A	3.28	124.63	118.77
3	A	1494	MYA	C2-S1-C2M	3.47	105.42	100.40
3	A	1494	MYA	C3-N4-C5	4.01	130.67	122.79
2	A	1493	7L5	OAD-SBF-NBD	4.05	110.95	106.46
2	A	1493	7L5	CAZ-NBD-SBF	4.29	126.37	116.86
2	A	1493	7L5	CAU-NAS-NBE	4.89	108.69	104.34
3	A	1494	MYA	O2M-C2M-C3M	5.96	119.94	109.05

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1493	7L5	4	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 [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	392/407 (96%)	-0.09	7 (1%) 71 76	11, 18, 32, 43	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	350	LYS	3.1
1	A	362	PRO	2.9
1	A	283	ALA	2.6
1	A	282	PRO	2.6
1	A	407	MET	2.5
1	A	299	THR	2.4
1	A	384	PRO	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, 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( $\text{\AA}^2$ )	Q<0.9
2	7L5	A	1493	32/32	0.91	0.10	1.42	20,26,42,48	0
3	MYA	A	1494	63/63	0.95	0.09	0.64	10,15,33,42	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.