



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 12, 2021 – 08:42 AM EDT

PDB ID : 1Z26  
Title : Structure of Pyrococcus furiosus Argonaute with bound tungstate  
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Deposited on : 2005-03-07  
Resolution : 2.50 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.23.2  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.23.2

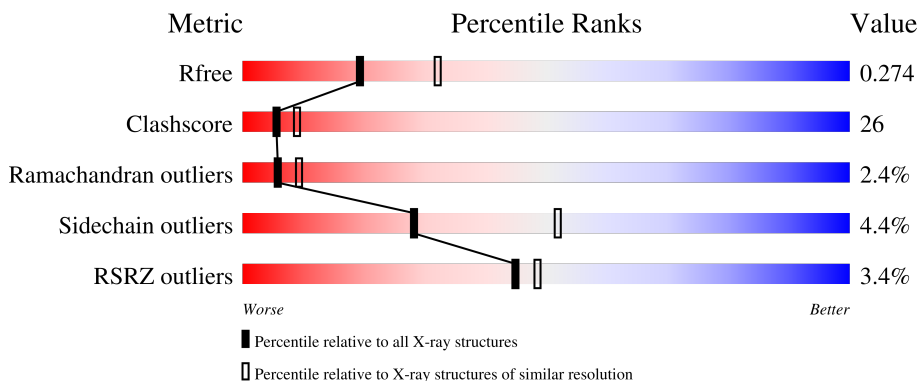
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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))
$R_{free}$	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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	771	

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
2	WO4	A	771	-	-	X	-

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<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
2	WO4	A	772	-	-	X	-
2	WO4	A	773	-	-	X	-

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6106 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.

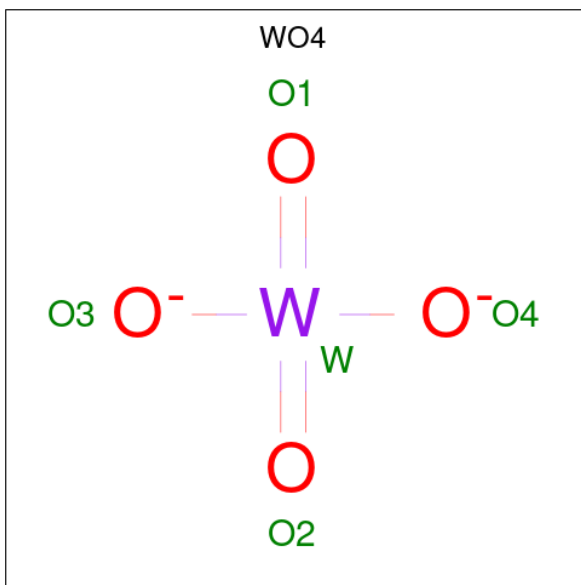
- Molecule 1 is a protein called Argonaute.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	716	5951	3872	985	1076	18	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	cloning artifact	UNP Q8U3D2
A	4	ILE	LYS	engineered mutation	UNP Q8U3D2

- Molecule 2 is TUNGSTATE(VI)ION (three-letter code: WO4) (formula: O<sub>4</sub>W).



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

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

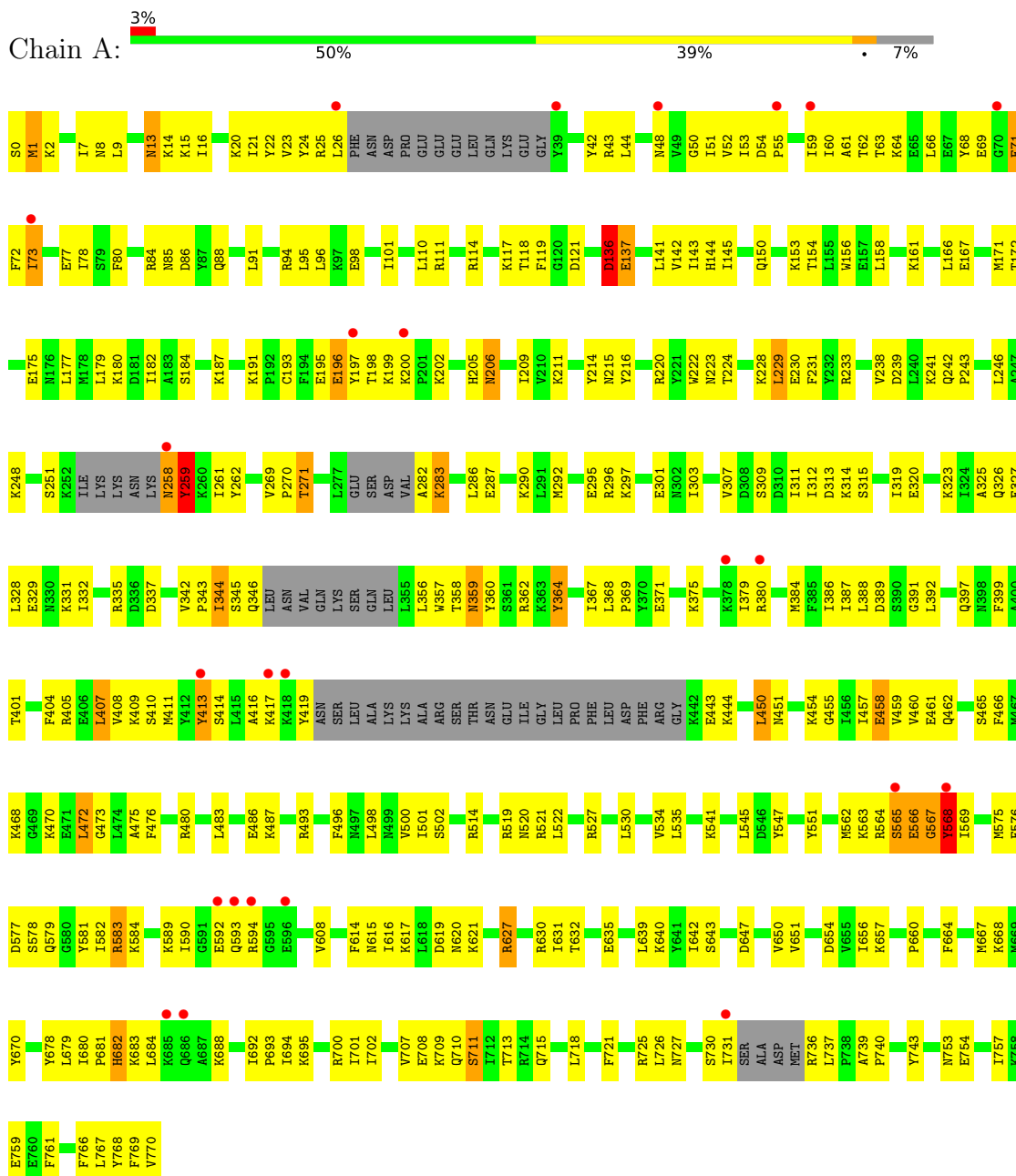
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	140	140	140	0	0

### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: Argonaute



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	69.10Å 103.50Å 73.22Å 90.00° 102.46° 90.00°	Depositor
Resolution (Å)	37.82 – 2.50 37.82 – 2.00	Depositor EDS
% Data completeness (in resolution range)	92.6 (37.82-2.50) 72.4 (37.82-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.97 (at 2.00Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.224 , 0.282 0.221 , 0.274	Depositor DCC
$R_{free}$ test set	1336 reflections (2.28%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	48.3	Xtrriage
Anisotropy	0.284	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 59.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6106	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	70.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.67% 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 [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: WO4

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	0.38	0/6067	0.62	0/8155

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

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	5951	0	6133	310	0
2	A	15	0	0	12	0
3	A	140	0	0	18	0
All	All	6106	0	6133	311	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 26.

All (311) 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:1:MET:HG3	1:A:2:LYS:H	1.15	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:CYS:HB3	1:A:202:LYS:HE3	1.38	1.05
1:A:454:LYS:HD2	1:A:454:LYS:H	1.23	1.02
1:A:62:THR:HG22	1:A:64:LYS:H	1.24	1.02
1:A:25:ARG:HB3	1:A:73:ILE:HG23	1.42	1.01
1:A:315:SER:HB3	3:A:873:HOH:O	1.70	0.91
1:A:371:GLU:HB2	1:A:541:LYS:HB2	1.54	0.90
1:A:386:ILE:HG21	1:A:401:THR:HG22	1.56	0.89
1:A:640:LYS:HD3	1:A:707:VAL:HG23	1.58	0.84
1:A:375:LYS:HE3	1:A:379:ILE:HD11	1.59	0.82
1:A:413:TYR:HD1	1:A:417:LYS:HG2	1.44	0.82
1:A:229:LEU:HD13	1:A:233:ARG:NH2	1.97	0.80
1:A:48:ASN:O	1:A:62:THR:HG23	1.82	0.79
1:A:193:CYS:HB3	1:A:202:LYS:CE	2.12	0.79
1:A:13:ASN:HD22	1:A:15:LYS:H	1.29	0.78
1:A:16:ILE:HB	1:A:311:ILE:HD11	1.67	0.77
1:A:144:HIS:HA	2:A:773:WO4:O3	1.84	0.77
1:A:1:MET:HG3	1:A:2:LYS:N	1.99	0.77
1:A:384:MET:HE2	1:A:408:VAL:HB	1.68	0.76
1:A:389:ASP:OD2	1:A:480:ARG:HG3	1.84	0.76
1:A:454:LYS:HD2	1:A:454:LYS:N	2.01	0.76
1:A:391:GLY:HA3	1:A:480:ARG:NH1	2.01	0.74
1:A:405:ARG:O	1:A:408:VAL:HG22	1.88	0.74
1:A:13:ASN:ND2	1:A:15:LYS:H	1.87	0.72
1:A:1:MET:CG	1:A:2:LYS:H	1.95	0.72
1:A:292:MET:SD	1:A:688:LYS:HG3	2.30	0.71
1:A:53:ILE:HD11	1:A:61:ALA:HB2	1.73	0.71
1:A:7:ILE:HD12	1:A:9:LEU:HD13	1.74	0.69
1:A:630:ARG:HH21	1:A:632:THR:HG22	1.57	0.69
1:A:62:THR:HG22	1:A:64:LYS:N	2.04	0.68
1:A:335:ARG:CZ	1:A:368:LEU:HD12	2.24	0.68
1:A:261:ILE:HD12	1:A:261:ILE:N	2.08	0.68
1:A:514:ARG:HD3	1:A:519:ARG:O	1.94	0.67
1:A:150:GLN:NE2	1:A:180:LYS:HE3	2.09	0.67
1:A:590:ILE:HD12	1:A:593:GLN:NE2	2.09	0.67
1:A:627:ARG:HG2	1:A:631:ILE:HD13	1.75	0.67
1:A:454:LYS:H	1:A:454:LYS:CD	2.00	0.67
1:A:51:ILE:HG13	1:A:91:LEU:HD13	1.78	0.66
1:A:239:ASP:O	1:A:242:GLN:HG2	1.97	0.65
1:A:25:ARG:HD2	1:A:73:ILE:HG21	1.78	0.65
1:A:632:THR:OG1	1:A:635:GLU:HG3	1.97	0.64
1:A:388:LEU:HD11	1:A:401:THR:CG2	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:211:LYS:HZ2	1:A:215:ASN:HB2	1.64	0.63
1:A:214:TYR:CE2	1:A:238:VAL:HG22	2.32	0.63
1:A:206:ASN:ND2	1:A:209:ILE:HG13	2.13	0.63
1:A:230:GLU:HA	1:A:233:ARG:NH1	2.15	0.62
1:A:501:ILE:HD12	1:A:768:TYR:HB2	1.81	0.62
1:A:150:GLN:HE22	1:A:180:LYS:HE3	1.64	0.62
1:A:290:LYS:N	3:A:832:HOH:O	2.27	0.62
1:A:579:GLN:NE2	1:A:581:TYR:HE2	1.97	0.62
1:A:743:TYR:HE1	1:A:770:VAL:HG11	1.64	0.61
1:A:375:LYS:HE2	1:A:761:PHE:HE1	1.65	0.61
1:A:24:TYR:HB2	1:A:60:ILE:HG12	1.81	0.61
1:A:608:VAL:CG2	1:A:642:ILE:HD11	2.30	0.61
1:A:309:SER:OG	1:A:311:ILE:HG22	2.01	0.60
1:A:721:PHE:O	1:A:725:ARG:HG2	2.02	0.60
1:A:62:THR:HG22	1:A:63:THR:N	2.17	0.60
1:A:229:LEU:HD22	1:A:233:ARG:NE	2.17	0.60
1:A:229:LEU:HD13	1:A:233:ARG:HH21	1.64	0.60
1:A:172:THR:HG22	1:A:486:GLU:OE2	2.02	0.59
1:A:343:PRO:O	1:A:345:SER:N	2.35	0.59
1:A:670:TYR:HA	1:A:678:TYR:O	2.01	0.59
1:A:375:LYS:HG2	1:A:379:ILE:HD11	1.84	0.59
1:A:651:VAL:HG22	1:A:701:ILE:CD1	2.33	0.59
1:A:297:LYS:O	1:A:301:GLU:HG3	2.03	0.58
1:A:701:ILE:CG2	1:A:708:GLU:HB2	2.33	0.58
1:A:323:LYS:HE2	1:A:667:MET:SD	2.43	0.58
1:A:375:LYS:HE2	1:A:761:PHE:CE1	2.38	0.58
1:A:229:LEU:HD22	1:A:233:ARG:CZ	2.33	0.58
1:A:563:LYS:HA	1:A:568:TYR:HA	1.86	0.58
1:A:392:LEU:HD23	1:A:480:ARG:HG2	1.86	0.58
1:A:198:THR:HG22	1:A:200:LYS:H	1.69	0.57
1:A:96:LEU:HD13	1:A:141:LEU:HD13	1.85	0.57
1:A:335:ARG:NE	1:A:368:LEU:HD12	2.20	0.57
1:A:680:ILE:HD11	1:A:693:PRO:HG3	1.86	0.57
1:A:292:MET:HB2	1:A:295:GLU:HG3	1.86	0.57
1:A:329:GLU:OE2	2:A:772:WO4:O4	2.23	0.57
1:A:640:LYS:HD3	1:A:707:VAL:CG2	2.30	0.57
1:A:683:LYS:O	1:A:684:LEU:HD23	2.04	0.57
1:A:13:ASN:HD22	1:A:14:LYS:N	2.02	0.56
1:A:701:ILE:HG22	1:A:708:GLU:HB2	1.87	0.56
1:A:193:CYS:SG	1:A:248:LYS:HG3	2.45	0.56
1:A:136:ASP:O	1:A:137:GLU:HG2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:375:LYS:CE	1:A:379:ILE:HD11	2.31	0.56
1:A:392:LEU:CD2	1:A:480:ARG:HG2	2.35	0.56
1:A:541:LYS:HG3	1:A:581:TYR:CD1	2.41	0.56
1:A:224:THR:O	1:A:228:LYS:HG3	2.05	0.56
1:A:451:ASN:O	1:A:487:LYS:HE2	2.06	0.56
1:A:179:LEU:HD23	1:A:270:PRO:HA	1.88	0.56
1:A:668:LYS:HD3	2:A:771:WO4:O3	2.05	0.56
1:A:13:ASN:ND2	1:A:15:LYS:HG2	2.21	0.56
1:A:167:GLU:O	1:A:171:MET:HG3	2.05	0.55
1:A:657:LYS:HB3	1:A:737:LEU:HD21	1.88	0.55
1:A:144:HIS:ND1	2:A:773:WO4:O2	2.39	0.55
1:A:408:VAL:O	1:A:411:MET:HB2	2.07	0.55
1:A:530:LEU:O	1:A:534:VAL:HG23	2.06	0.55
1:A:329:GLU:OE2	2:A:771:WO4:O2	2.25	0.55
1:A:679:LEU:O	1:A:681:PRO:HD3	2.07	0.55
1:A:214:TYR:CD2	1:A:238:VAL:HG22	2.42	0.55
1:A:66:LEU:HD13	1:A:66:LEU:O	2.07	0.55
1:A:80:PHE:CZ	1:A:88:GLN:HB3	2.42	0.54
1:A:287:GLU:C	3:A:832:HOH:O	2.44	0.54
1:A:156:TRP:CD1	1:A:161:LYS:HG2	2.41	0.54
1:A:296:ARG:HB3	2:A:773:WO4:O4	2.07	0.54
1:A:710:GLN:HG3	1:A:711:SER:H	1.71	0.54
1:A:753:ASN:O	1:A:754:GLU:HB2	2.07	0.54
1:A:94:ARG:HH12	1:A:98:GLU:HG2	1.73	0.54
1:A:329:GLU:CD	2:A:771:WO4:O3	2.46	0.54
1:A:362:ARG:HH21	1:A:520:ASN:HB2	1.72	0.54
1:A:22:TYR:HD1	1:A:77:GLU:HG2	1.73	0.54
1:A:416:ALA:HB1	1:A:419:TYR:HD1	1.72	0.54
1:A:42:TYR:CD1	1:A:52:VAL:HG21	2.42	0.54
1:A:166:LEU:HD23	1:A:167:GLU:N	2.21	0.54
1:A:296:ARG:NH1	2:A:773:WO4:O2	2.41	0.54
1:A:110:LEU:HB2	1:A:303:ILE:HD11	1.89	0.53
1:A:391:GLY:C	1:A:480:ARG:HD3	2.29	0.53
1:A:458:GLU:O	1:A:462:GLN:HG3	2.07	0.53
1:A:620:ASN:HA	1:A:647:ASP:O	2.08	0.53
1:A:20:LYS:HD3	1:A:77:GLU:OE2	2.09	0.53
1:A:13:ASN:O	1:A:16:ILE:HG22	2.09	0.53
1:A:101:ILE:HD13	1:A:312:ILE:HD13	1.90	0.52
1:A:158:LEU:HD23	1:A:158:LEU:O	2.09	0.52
1:A:342:VAL:HG13	1:A:343:PRO:HD2	1.90	0.52
1:A:413:TYR:CD1	1:A:417:LYS:HG2	2.34	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:LEU:HD11	1:A:68:TYR:HB2	1.92	0.52
1:A:197:TYR:CD1	1:A:562:MET:HA	2.44	0.52
1:A:303:ILE:O	1:A:307:VAL:HG23	2.10	0.52
1:A:450:LEU:HB3	1:A:483:LEU:HD21	1.92	0.52
1:A:13:ASN:HD22	1:A:13:ASN:C	2.13	0.52
1:A:328:LEU:O	1:A:721:PHE:HE2	1.92	0.52
1:A:50:GLY:HA3	1:A:62:THR:HA	1.90	0.52
1:A:410:SER:O	1:A:414:SER:HB2	2.10	0.51
1:A:639:LEU:HA	1:A:642:ILE:HG22	1.92	0.51
1:A:614:PHE:O	1:A:615:ASN:HB2	2.10	0.51
1:A:700:ARG:NH1	1:A:700:ARG:HG3	2.25	0.51
1:A:408:VAL:HG12	1:A:476:PHE:CE2	2.46	0.51
1:A:94:ARG:HD3	3:A:874:HOH:O	2.11	0.51
1:A:335:ARG:HG3	1:A:368:LEU:HB3	1.93	0.51
1:A:576:PHE:HA	1:A:581:TYR:O	2.11	0.51
1:A:121:ASP:OD1	1:A:153:LYS:HE3	2.10	0.50
1:A:640:LYS:O	1:A:643:SER:HB3	2.11	0.50
1:A:66:LEU:HD11	1:A:68:TYR:HB3	1.94	0.50
1:A:356:LEU:HB3	1:A:359:ASN:ND2	2.26	0.50
1:A:656:ILE:HB	1:A:695:LYS:HB3	1.94	0.50
1:A:369:PRO:HG2	1:A:414:SER:O	2.11	0.50
1:A:53:ILE:CD1	1:A:61:ALA:HB2	2.40	0.50
1:A:94:ARG:NH1	1:A:98:GLU:HG2	2.27	0.50
1:A:177:LEU:HD11	1:A:270:PRO:HB3	1.93	0.50
1:A:229:LEU:O	1:A:233:ARG:HG3	2.12	0.50
1:A:145:ILE:N	2:A:773:WO4:O2	2.45	0.49
1:A:319:ILE:HG12	1:A:320:GLU:N	2.26	0.49
1:A:66:LEU:HD13	1:A:66:LEU:C	2.33	0.49
1:A:191:LYS:HB3	3:A:885:HOH:O	2.11	0.49
1:A:357:TRP:CE2	1:A:358:THR:HG23	2.48	0.49
1:A:327:GLU:C	1:A:329:GLU:H	2.14	0.49
1:A:577:ASP:OD1	1:A:577:ASP:C	2.50	0.49
1:A:767:LEU:HD22	1:A:770:VAL:HG21	1.94	0.49
1:A:417:LYS:O	1:A:417:LYS:HD3	2.11	0.49
1:A:337:ASP:HB3	1:A:417:LYS:HZ2	1.78	0.49
1:A:694:ILE:HD11	1:A:736:ARG:O	2.12	0.49
1:A:700:ARG:HG3	1:A:700:ARG:HH11	1.77	0.49
1:A:239:ASP:OD2	1:A:241:LYS:HB2	2.13	0.49
1:A:84:ARG:HG2	1:A:85:ASN:N	2.27	0.48
1:A:582:ILE:HG22	3:A:784:HOH:O	2.14	0.48
1:A:642:ILE:HG12	1:A:642:ILE:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:562:MET:O	1:A:569:ILE:N	2.46	0.48
1:A:364:TYR:CE1	1:A:407:LEU:HG	2.49	0.48
1:A:575:MET:HE1	1:A:616:ILE:HG13	1.95	0.47
1:A:202:LYS:HD2	1:A:246:LEU:HD23	1.96	0.47
1:A:205:HIS:CE1	1:A:243:PRO:HB3	2.49	0.47
1:A:389:ASP:OD1	1:A:480:ARG:NH1	2.46	0.47
1:A:487:LYS:HE3	3:A:787:HOH:O	2.13	0.47
1:A:639:LEU:HA	1:A:642:ILE:CG2	2.43	0.47
1:A:1:MET:CG	1:A:2:LYS:N	2.68	0.47
1:A:388:LEU:HD13	1:A:397:GLN:HB3	1.95	0.47
1:A:0:SER:OG	1:A:325:ALA:HA	2.14	0.47
1:A:8:ASN:HB3	1:A:664:PHE:CZ	2.50	0.47
1:A:408:VAL:HG23	1:A:409:LYS:N	2.30	0.47
1:A:564:ARG:O	1:A:565:SER:C	2.53	0.47
1:A:727:ASN:ND2	1:A:730:SER:H	2.12	0.47
1:A:346:GLN:N	1:A:346:GLN:OE1	2.48	0.47
1:A:473:GLY:O	1:A:500:VAL:HA	2.15	0.47
1:A:541:LYS:HD2	1:A:541:LYS:N	2.30	0.47
1:A:62:THR:CG2	1:A:63:THR:N	2.77	0.47
1:A:384:MET:CE	1:A:408:VAL:HB	2.39	0.47
1:A:388:LEU:HD11	1:A:401:THR:HG23	1.94	0.47
1:A:25:ARG:HB3	1:A:73:ILE:CG2	2.28	0.47
1:A:577:ASP:OD2	1:A:583:ARG:HD2	2.14	0.47
1:A:619:ASP:O	1:A:621:LYS:HG2	2.15	0.47
1:A:53:ILE:CG1	1:A:61:ALA:HB2	2.45	0.46
1:A:314:LYS:HG3	3:A:873:HOH:O	2.14	0.46
1:A:683:LYS:NZ	3:A:852:HOH:O	2.47	0.46
1:A:713:THR:HB	3:A:810:HOH:O	2.14	0.46
1:A:399:PHE:HE1	1:A:520:ASN:C	2.18	0.46
1:A:472:LEU:HD23	1:A:473:GLY:N	2.31	0.46
1:A:21:ILE:HB	1:A:78:ILE:CG2	2.45	0.46
1:A:329:GLU:OE1	2:A:772:WO4:O2	2.33	0.46
1:A:472:LEU:HD23	1:A:473:GLY:H	1.80	0.46
1:A:718:LEU:HD23	1:A:718:LEU:O	2.15	0.46
1:A:21:ILE:HB	1:A:78:ILE:HG22	1.97	0.46
1:A:545:LEU:HG	1:A:547:TYR:HB3	1.96	0.46
1:A:193:CYS:CB	1:A:202:LYS:HE3	2.27	0.46
1:A:389:ASP:CG	1:A:480:ARG:NH1	2.69	0.46
1:A:22:TYR:CD1	1:A:77:GLU:HG2	2.50	0.46
1:A:261:ILE:HG22	1:A:262:TYR:N	2.31	0.46
1:A:630:ARG:HG3	1:A:654:ASP:OD2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:282:ALA:O	1:A:283:LYS:C	2.53	0.46
1:A:326:GLN:HG2	1:A:326:GLN:O	2.17	0.45
1:A:567:GLY:O	1:A:589:LYS:HE2	2.17	0.45
1:A:84:ARG:HG2	1:A:84:ARG:HH11	1.82	0.45
1:A:455:GLY:O	1:A:459:VAL:HG23	2.15	0.45
1:A:367:ILE:O	1:A:369:PRO:HD3	2.15	0.45
1:A:617:LYS:HA	3:A:912:HOH:O	2.16	0.45
1:A:171:MET:HG2	1:A:199:LYS:O	2.17	0.45
1:A:493:ARG:HD2	3:A:881:HOH:O	2.16	0.45
1:A:404:PHE:O	1:A:408:VAL:HG13	2.16	0.45
1:A:457:ILE:O	1:A:461:GLU:HG3	2.17	0.45
1:A:143:ILE:O	2:A:773:WO4:O3	2.35	0.45
1:A:69:GLU:N	1:A:69:GLU:OE1	2.50	0.44
1:A:95:LEU:HD23	1:A:95:LEU:HA	1.84	0.44
1:A:568:TYR:OH	1:A:592:GLU:HG3	2.17	0.44
1:A:13:ASN:CG	1:A:15:LYS:HG2	2.37	0.44
1:A:150:GLN:HB2	1:A:271:THR:HG23	1.99	0.44
1:A:551:TYR:O	1:A:578:SER:HB3	2.17	0.44
1:A:708:GLU:O	1:A:709:LYS:C	2.56	0.44
1:A:759:GLU:HG3	3:A:854:HOH:O	2.17	0.44
1:A:175:GLU:HG2	3:A:825:HOH:O	2.18	0.44
1:A:387:ILE:CD1	1:A:475:ALA:HB1	2.48	0.44
1:A:404:PHE:CD1	1:A:476:PHE:HB3	2.52	0.44
1:A:739:ALA:HB3	1:A:740:PRO:HD3	1.99	0.44
1:A:668:LYS:HE3	1:A:668:LYS:HB2	1.74	0.44
1:A:682:HIS:HD2	1:A:725:ARG:NH1	2.15	0.44
1:A:577:ASP:OD1	1:A:579:GLN:N	2.50	0.44
1:A:222:TRP:CD1	1:A:231:PHE:HD1	2.36	0.43
1:A:71:GLU:HG3	3:A:846:HOH:O	2.18	0.43
1:A:328:LEU:HD23	1:A:331:LYS:HE2	2.01	0.43
1:A:627:ARG:HG2	1:A:631:ILE:CD1	2.47	0.43
1:A:725:ARG:HA	1:A:725:ARG:HH11	1.84	0.43
1:A:73:ILE:O	1:A:73:ILE:HG12	2.19	0.43
1:A:259:TYR:C	1:A:259:TYR:CD2	2.92	0.43
1:A:344:ILE:O	1:A:344:ILE:HG22	2.18	0.43
1:A:389:ASP:HB2	1:A:450:LEU:HD22	2.00	0.43
1:A:564:ARG:HE	1:A:564:ARG:HB3	1.64	0.43
1:A:23:VAL:HG12	1:A:24:TYR:N	2.34	0.43
1:A:465:SER:O	1:A:468:LYS:HG2	2.18	0.43
1:A:117:LYS:HD3	1:A:119:PHE:CZ	2.54	0.43
1:A:286:LEU:O	1:A:290:LYS:HG2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:460:VAL:HG13	1:A:498:LEU:HD11	2.00	0.43
1:A:667:MET:HA	1:A:683:LYS:HG2	2.00	0.43
1:A:743:TYR:CE1	1:A:770:VAL:HG11	2.50	0.43
1:A:14:LYS:C	1:A:16:ILE:N	2.72	0.43
1:A:193:CYS:HB3	1:A:202:LYS:NZ	2.34	0.43
1:A:25:ARG:O	1:A:72:PHE:HA	2.19	0.42
1:A:564:ARG:O	1:A:566:GLU:N	2.52	0.42
1:A:14:LYS:C	1:A:16:ILE:H	2.22	0.42
1:A:25:ARG:HD2	1:A:73:ILE:CG2	2.47	0.42
1:A:757:ILE:O	1:A:757:ILE:HG22	2.19	0.42
1:A:375:LYS:HE3	1:A:379:ILE:CD1	2.41	0.42
1:A:444:LYS:HD2	1:A:466:PHE:CE1	2.54	0.42
1:A:692:ILE:HG21	1:A:736:ARG:HH11	1.85	0.42
1:A:725:ARG:CZ	3:A:848:HOH:O	2.66	0.42
1:A:197:TYR:HH	1:A:568:TYR:HE2	1.65	0.42
1:A:375:LYS:O	1:A:379:ILE:HG13	2.19	0.42
1:A:389:ASP:CA	1:A:450:LEU:HD22	2.48	0.42
1:A:567:GLY:O	1:A:568:TYR:CB	2.68	0.42
1:A:136:ASP:O	1:A:137:GLU:CG	2.67	0.42
1:A:650:VAL:HB	1:A:702:ILE:HB	2.02	0.42
1:A:187:LYS:HE2	3:A:903:HOH:O	2.19	0.42
1:A:198:THR:HG22	1:A:199:LYS:N	2.33	0.42
1:A:177:LEU:HD11	1:A:270:PRO:CB	2.49	0.42
1:A:195:GLU:O	1:A:196:GLU:C	2.57	0.42
1:A:51:ILE:CD1	1:A:61:ALA:HB3	2.50	0.42
1:A:230:GLU:HA	1:A:233:ARG:HH11	1.81	0.42
1:A:496:PHE:CE2	1:A:768:TYR:CE1	3.08	0.42
1:A:651:VAL:HG22	1:A:701:ILE:HD12	2.02	0.42
1:A:337:ASP:HB3	1:A:417:LYS:NZ	2.34	0.42
1:A:743:TYR:CD1	1:A:770:VAL:HG21	2.55	0.42
1:A:9:LEU:HG	1:A:142:VAL:HG22	2.01	0.42
1:A:24:TYR:CE2	1:A:66:LEU:HB2	2.55	0.42
1:A:54:ASP:HB2	1:A:59:ILE:HD12	2.02	0.42
1:A:769:PHE:CE1	1:A:770:VAL:HG23	2.55	0.42
1:A:154:THR:HG22	1:A:182:ILE:HD11	2.02	0.41
1:A:111:ARG:HA	1:A:114:ARG:O	2.20	0.41
1:A:211:LYS:NZ	1:A:215:ASN:HB2	2.32	0.41
1:A:214:TYR:CZ	1:A:238:VAL:HG22	2.56	0.41
1:A:411:MET:O	1:A:414:SER:HB3	2.20	0.41
1:A:248:LYS:HZ1	1:A:258:ASN:N	2.18	0.41
1:A:329:GLU:CG	1:A:725:ARG:HH21	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:54:ASP:CB	1:A:59:ILE:HD12	2.50	0.41
1:A:84:ARG:HD3	1:A:86:ASP:OD2	2.20	0.41
1:A:182:ILE:HD13	1:A:269:VAL:HG13	2.01	0.41
1:A:387:ILE:HD13	1:A:475:ALA:HB1	2.02	0.41
1:A:475:ALA:HB3	1:A:502:SER:HB3	2.03	0.41
1:A:22:TYR:HD2	1:A:64:LYS:O	2.04	0.41
1:A:391:GLY:CA	1:A:480:ARG:NH1	2.78	0.41
1:A:731:ILE:HG21	3:A:842:HOH:O	2.21	0.41
1:A:25:ARG:HG2	1:A:26:LEU:N	2.36	0.41
1:A:184:SER:O	1:A:187:LYS:HD2	2.20	0.41
2:A:771:WO4:O2	2:A:772:WO4:O4	2.38	0.41
1:A:389:ASP:CB	1:A:450:LEU:HD22	2.50	0.41
1:A:408:VAL:HA	1:A:411:MET:HB2	2.02	0.41
1:A:761:PHE:HB3	1:A:766:PHE:HB2	2.03	0.41
1:A:575:MET:HE1	1:A:584:LYS:HG2	2.03	0.40
1:A:136:ASP:C	1:A:137:GLU:HG2	2.40	0.40
1:A:48:ASN:HB3	1:A:62:THR:CG2	2.52	0.40
1:A:216:TYR:O	1:A:220:ARG:HB3	2.21	0.40
1:A:332:ILE:HD13	1:A:726:LEU:HD23	2.03	0.40
1:A:389:ASP:OD2	1:A:480:ARG:NH1	2.53	0.40
1:A:358:THR:C	1:A:360:TYR:H	2.25	0.40
1:A:388:LEU:HD11	1:A:401:THR:HG21	2.01	0.40
1:A:521:ARG:HG3	1:A:527:ARG:NH2	2.37	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	702/771 (91%)	625 (89%)	60 (8%)	17 (2%)	<b>6</b> <b>9</b>

All (17) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	A	251	SER
1	A	283	LYS
1	A	344	ILE
1	A	1	MET
1	A	71	GLU
1	A	137	GLU
1	A	55	PRO
1	A	136	ASP
1	A	196	GLU
1	A	259	TYR
1	A	380	ARG
1	A	565	SER
1	A	206	ASN
1	A	359	ASN
1	A	568	TYR
1	A	594	ARG
1	A	567	GLY

### 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	658/707 (93%)	629 (96%)	29 (4%)	28 52

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ASN
1	A	43	ARG
1	A	73	ILE
1	A	118	THR
1	A	136	ASP
1	A	223	ASN
1	A	229	LEU
1	A	258	ASN
1	A	259	TYR
1	A	271	THR

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Mol	Chain	Res	Type
1	A	313	ASP
1	A	364	TYR
1	A	407	LEU
1	A	413	TYR
1	A	443	GLU
1	A	450	LEU
1	A	458	GLU
1	A	470	LYS
1	A	472	LEU
1	A	522	LEU
1	A	535	LEU
1	A	566	GLU
1	A	568	TYR
1	A	583	ARG
1	A	627	ARG
1	A	660	PRO
1	A	682	HIS
1	A	711	SER
1	A	715	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	ASN
1	A	57	ASN
1	A	150	GLN
1	A	205	HIS
1	A	215	ASN
1	A	223	ASN
1	A	258	ASN
1	A	359	ASN
1	A	550	ASN
1	A	579	GLN
1	A	682	HIS
1	A	727	ASN

### 5.3.3 RNA

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

3 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	WO4	A	772	2,1	2,4,4	0.73	0	-		
2	WO4	A	773	-	2,4,4	0.77	0	-		
2	WO4	A	771	2,1	2,4,4	0.61	0	-		

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	772	WO4	3	0
2	A	773	WO4	6	0
2	A	771	WO4	4	0

## 5.7 Other polymers [i](#)

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	716/771 (92%)	-0.25	24 (3%) 45 48	32, 64, 120, 166	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	413	TYR	4.7
1	A	73	ILE	4.3
1	A	731	ILE	3.9
1	A	59	ILE	3.7
1	A	378	LYS	3.7
1	A	686	GLN	3.6
1	A	593	GLN	3.5
1	A	592	GLU	3.3
1	A	568	TYR	3.2
1	A	258	ASN	3.2
1	A	594	ARG	3.2
1	A	197	TYR	2.9
1	A	685	LYS	2.8
1	A	39	TYR	2.7
1	A	48	ASN	2.7
1	A	55	PRO	2.5
1	A	596	GLU	2.4
1	A	200	LYS	2.3
1	A	380	ARG	2.3
1	A	418	LYS	2.2
1	A	565	SER	2.1
1	A	70	GLY	2.1
1	A	26	LEU	2.1
1	A	417	LYS	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 monosaccharides 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. 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	B-factors(Å <sup>2</sup> )	Q<0.9
2	WO4	A	771	5/5	0.98	0.17	57,57,57,57	5
2	WO4	A	772	5/5	0.99	0.14	62,62,62,62	5
2	WO4	A	773	5/5	0.99	0.27	89,89,89,89	5

## 6.5 Other polymers [i](#)

There are no such residues in this entry.