



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 01:07 pm BST

PDB ID : 3OTT
Title : Crystal Structure of the extracellular domain of the putative one component system BT4673 from B. thetaiotaomicron
Authors : Zhang, Z.; Liu, Q.; Hendrickson, W.A.
Deposited on : 2010-09-13
Resolution : 2.30 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

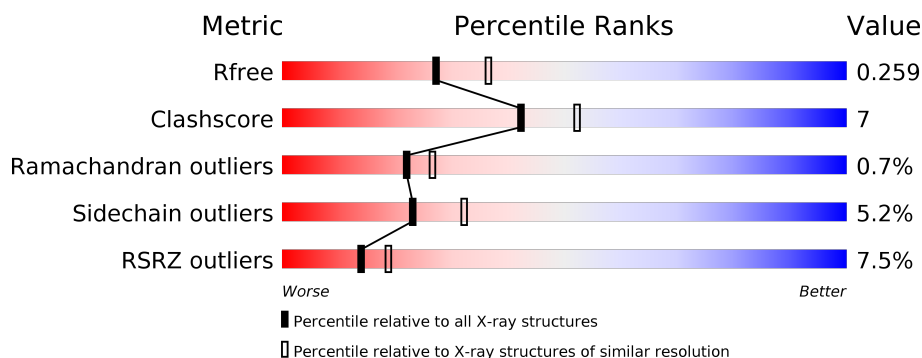
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 ≥ 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	758	<div> <div>11%</div> <div> <div></div> <div>79%</div> <div>16%</div> <div>• •</div> </div> </div>
1	B	758	<div> <div>4%</div> <div> <div></div> <div>82%</div> <div>14%</div> <div>• •</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12329 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.

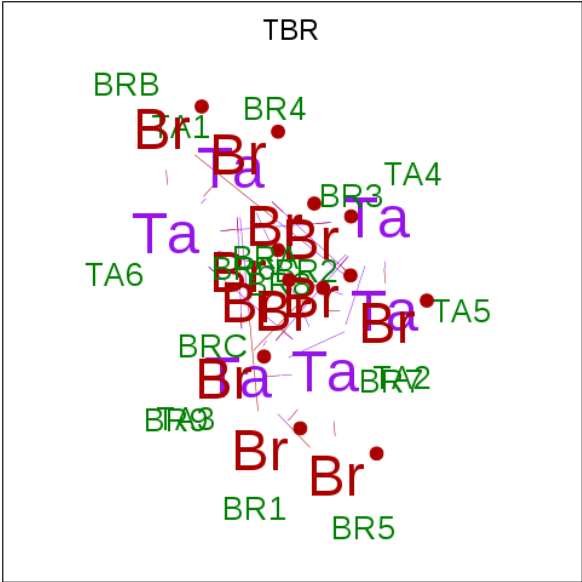
- Molecule 1 is a protein called Two-component system sensor histidine kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	737	Total	C	N	O	S	0	0	0
			6002	3810	1030	1145	17			
1	B	739	Total	C	N	O	S	0	2	0
			6011	3815	1028	1151	17			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	MET	-	expression tag	UNP Q89YQ8
A	29	GLU	-	expression tag	UNP Q89YQ8
A	778	LEU	-	expression tag	UNP Q89YQ8
A	779	GLU	-	expression tag	UNP Q89YQ8
A	780	HIS	-	expression tag	UNP Q89YQ8
A	781	HIS	-	expression tag	UNP Q89YQ8
A	782	HIS	-	expression tag	UNP Q89YQ8
A	783	HIS	-	expression tag	UNP Q89YQ8
A	784	HIS	-	expression tag	UNP Q89YQ8
A	785	HIS	-	expression tag	UNP Q89YQ8
B	28	MET	-	expression tag	UNP Q89YQ8
B	29	GLU	-	expression tag	UNP Q89YQ8
B	778	LEU	-	expression tag	UNP Q89YQ8
B	779	GLU	-	expression tag	UNP Q89YQ8
B	780	HIS	-	expression tag	UNP Q89YQ8
B	781	HIS	-	expression tag	UNP Q89YQ8
B	782	HIS	-	expression tag	UNP Q89YQ8
B	783	HIS	-	expression tag	UNP Q89YQ8
B	784	HIS	-	expression tag	UNP Q89YQ8
B	785	HIS	-	expression tag	UNP Q89YQ8

- Molecule 2 is HEXATANTALUM DODECABROMIDE (three-letter code: TBR) (formula: Br₁₂Ta₆).

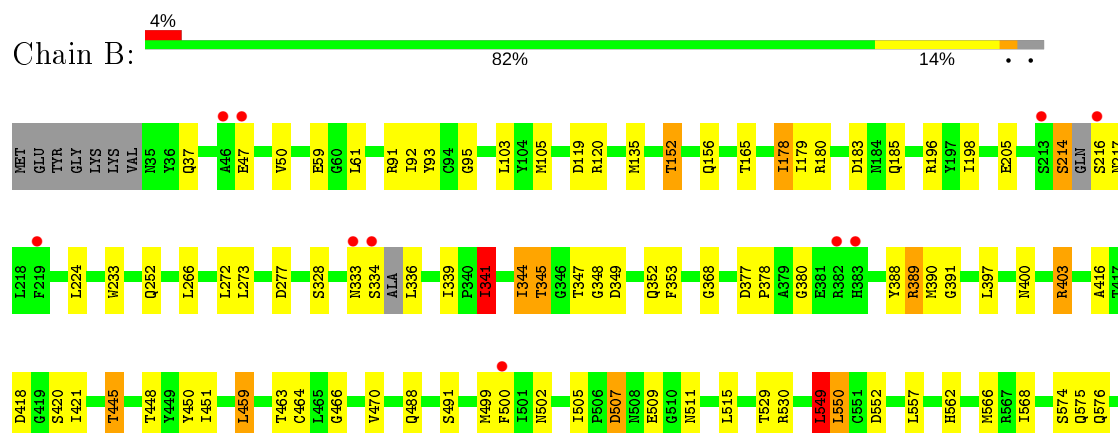
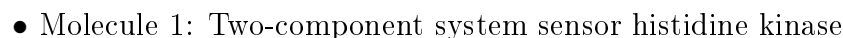


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	Br	Ta	0	0
			18	12	6		
2	B	1	Total	Br	Ta	0	0
			18	12	6		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	138	Total	O	0	0
			138	138		
3	B	142	Total	O	0	0
			142	142		

- Molecule 1: Two-component system sensor histidine kinase





4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	88.17Å 88.17Å 432.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.27 – 2.30 39.27 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.1 (39.27-2.30) 99.1 (39.27-2.30)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.93 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.195 , 0.253 0.204 , 0.259	Depositor DCC
R_{free} test set	3840 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	30.7	Xtriage
Anisotropy	0.275	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 38.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12329	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.38% 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, 0.333 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: TBR

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	0.85	2/6153 (0.0%)	0.85	9/8355 (0.1%)
1	B	0.99	0/6165	0.93	15/8372 (0.2%)
All	All	0.92	2/12318 (0.0%)	0.89	24/16727 (0.1%)

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
1	B	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	614	MET	C-N	5.98	1.47	1.34
1	A	573	GLU	C-N	5.61	1.47	1.34

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	403	ARG	NE-CZ-NH2	-13.49	113.55	120.30
1	B	403	ARG	NE-CZ-NH1	10.01	125.30	120.30
1	A	403	ARG	NE-CZ-NH2	-9.55	115.53	120.30
1	A	117	ARG	NE-CZ-NH2	-9.45	115.57	120.30
1	A	403	ARG	NE-CZ-NH1	8.98	124.79	120.30
1	A	133	ARG	NE-CZ-NH2	-7.62	116.49	120.30
1	B	341	ILE	CB-CA-C	-6.39	98.82	111.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	344	ILE	C-N-CA	6.38	137.65	121.70
1	A	267	ASP	CB-CG-OD2	-6.28	112.65	118.30
1	B	550	LEU	CA-CB-CG	6.21	129.59	115.30
1	B	180	ARG	NE-CZ-NH2	-6.14	117.23	120.30
1	B	549	LEU	CA-CB-CG	6.02	129.15	115.30
1	A	117	ARG	CG-CD-NE	-5.58	100.08	111.80
1	A	267	ASP	CB-CG-OD1	5.55	123.30	118.30
1	B	549	LEU	CB-CG-CD2	5.51	120.36	111.00
1	B	507	ASP	CB-CG-OD1	-5.49	113.36	118.30
1	B	552	ASP	CB-CG-OD1	5.45	123.20	118.30
1	B	664	LEU	CA-CB-CG	5.29	127.48	115.30
1	B	180	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	A	401	ARG	NE-CZ-NH1	5.19	122.90	120.30
1	B	507	ASP	CB-CA-C	-5.12	100.16	110.40
1	B	344	ILE	N-CA-C	5.08	124.71	111.00
1	A	401	ARG	NE-CZ-NH2	-5.03	117.78	120.30
1	B	344	ILE	CA-C-N	5.03	128.26	117.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	573	GLU	Mainchain
1	B	344	ILE	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	6002	0	5719	94	0
1	B	6011	0	5748	70	0
2	A	18	0	0	2	0
2	B	18	0	0	1	0
3	A	138	0	0	1	0
3	B	142	0	0	4	0
All	All	12329	0	11467	162	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 7.

All (162) 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:616:ALA:HB2	3:A:799:HOH:O	1.47	1.14
1:A:107:THR:HG22	1:A:109:ASN:H	1.09	1.11
1:A:345:THR:HG23	1:A:385:ALA:HB3	1.15	1.08
1:A:166:ARG:HG3	1:A:166:ARG:HH11	1.15	1.05
1:A:345:THR:CG2	1:A:385:ALA:HB3	1.86	1.03
1:B:507:ASP:HB3	1:B:509:GLU:H	1.25	1.02
1:A:602:THR:HG22	1:A:605:GLY:O	1.65	0.96
1:B:502:ASN:HB2	1:B:515:LEU:HD12	1.51	0.89
1:B:333:ASN:HA	3:B:831:HOH:O	1.74	0.86
1:A:107:THR:HG22	1:A:109:ASN:N	1.90	0.84
1:A:420:SER:OG	1:A:445:THR:HG23	1.76	0.84
1:A:345:THR:HG23	1:A:385:ALA:CB	2.05	0.83
1:B:416:ALA:HB1	1:B:448:THR:HG22	1.62	0.82
1:A:166:ARG:HG3	1:A:166:ARG:NH1	1.94	0.81
1:B:732:LEU:O	1:B:733:LYS:CB	2.29	0.81
1:A:166:ARG:HH11	1:A:166:ARG:CG	1.95	0.79
1:A:331:ARG:NH1	1:A:713:ASP:OD1	2.16	0.79
1:A:47:GLU:HG3	1:A:68:LYS:HG3	1.65	0.76
1:A:346:GLY:HA2	1:A:347:THR:O	1.85	0.75
1:B:345:THR:HG22	1:B:347:THR:H	1.52	0.75
1:A:464:CYS:SG	1:A:464:CYS:O	2.44	0.75
1:A:513:TRP:CZ2	1:A:524:LYS:HD3	2.22	0.75
1:A:586:ASN:N	1:A:604:ASN:HD21	1.85	0.74
1:B:334:SER:HB2	1:B:336:LEU:N	2.04	0.73
1:B:152:THR:HG22	3:B:895:HOH:O	1.89	0.73
1:B:670:ILE:HD12	1:B:675:VAL:HG21	1.70	0.72
1:A:602:THR:HG23	1:A:604:ASN:H	1.56	0.71
1:A:565:VAL:HG21	1:A:609:ILE:HD13	1.74	0.70
1:B:732:LEU:O	1:B:733:LYS:HB2	1.92	0.69
1:A:420:SER:OG	1:A:445:THR:CG2	2.42	0.68
1:B:341:ILE:O	1:B:345:THR:HB	1.94	0.68
1:B:214:SER:HG	1:B:216:SER:N	1.90	0.68
1:A:525:ILE:HG12	1:A:532:VAL:HG22	1.77	0.66
1:B:119:ASP:OD2	1:B:676:SER:HB2	1.96	0.66
1:B:152:THR:HG21	3:B:6:HOH:O	1.98	0.64
1:B:566:MET:HE2	1:B:568:ILE:HD11	1.79	0.63
1:A:56:GLN:OE1	1:A:315:GLN:HG2	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:198:ILE:HD11	1:B:205:GLU:HB2	1.80	0.62
1:B:420:SER:OG	1:B:445:THR:HG23	1.98	0.62
1:A:463:THR:HG22	1:A:465:LEU:H	1.64	0.62
1:A:481:SER:O	1:A:483:GLN:N	2.33	0.62
1:A:602:THR:HG23	1:A:604:ASN:N	2.15	0.61
1:A:114:TYR:OH	1:A:119:ASP:OD1	2.18	0.61
1:A:166:ARG:NH1	1:A:166:ARG:CG	2.59	0.61
1:A:403:ARG:NH2	1:B:156:GLN:O	2.33	0.61
1:A:549:LEU:HD23	1:A:559:VAL:HG22	1.81	0.60
1:A:498:GLY:HA3	1:A:500:PHE:CE2	2.36	0.60
1:A:513:TRP:CE2	1:A:524:LYS:HD3	2.37	0.59
1:A:602:THR:HG22	1:A:605:GLY:H	1.68	0.59
1:B:334:SER:CB	1:B:336:LEU:N	2.66	0.59
1:A:565:VAL:HG21	1:A:609:ILE:CD1	2.31	0.59
1:B:95:GLY:HA2	1:B:135:MET:CE	2.32	0.58
1:B:566:MET:CE	1:B:568:ILE:HD11	2.32	0.58
1:A:568:ILE:HA	1:A:575:GLN:HB2	1.85	0.58
1:A:377:ASP:O	1:A:383:HIS:ND1	2.37	0.57
1:B:416:ALA:CB	1:B:448:THR:HG22	2.34	0.56
1:A:107:THR:CG2	1:A:109:ASN:H	2.01	0.56
1:A:500:PHE:O	1:A:517:TYR:HB3	2.06	0.55
1:A:602:THR:CG2	1:A:605:GLY:H	2.19	0.55
1:A:784:HIS:O	1:A:785:HIS:HB2	2.07	0.54
1:B:352:GLN:O	1:B:368:GLY:HA3	2.08	0.54
1:A:451:ILE:HD11	1:A:459:LEU:HG	1.89	0.54
1:A:315:GLN:HG3	2:A:1:TBR:BRC	2.64	0.53
1:A:97:ILE:HG12	1:A:103:LEU:HD23	1.90	0.53
1:A:119:ASP:OD2	1:A:676:SER:HB2	2.08	0.53
1:A:505:ILE:HG21	1:A:551:CYS:HB2	1.92	0.52
1:B:689:THR:HG22	1:B:691:SER:H	1.75	0.52
1:A:470:VAL:HB	1:A:488:GLN:HB2	1.92	0.52
1:B:591:MET:CE	1:B:598:ILE:HD11	2.40	0.52
1:A:544:LYS:H	1:A:544:LYS:HD2	1.75	0.51
1:A:159:LYS:HE2	1:B:587:GLU:OE2	2.11	0.51
1:A:96:VAL:HG12	1:A:135:MET:HE3	1.91	0.51
1:A:96:VAL:HG12	1:A:135:MET:CE	2.41	0.50
1:A:104:TYR:O	1:A:135:MET:HE1	2.10	0.50
1:B:389:ARG:HB2	1:B:400:ASN:OD1	2.10	0.50
1:B:463:THR:HG22	1:B:464:CYS:O	2.11	0.50
1:B:507:ASP:HB2	1:B:511:ASN:H	1.77	0.49
1:A:44:LEU:HD23	1:A:78:THR:HG21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:502:ASN:HB2	1:B:515:LEU:CD1	2.33	0.49
1:B:224:LEU:HD21	1:B:266:LEU:HG	1.95	0.49
1:A:97:ILE:HG12	1:A:103:LEU:CD2	2.42	0.49
1:A:251:LYS:NZ	1:A:286:ASP:OD1	2.43	0.48
1:A:449:TYR:CE1	1:A:464:CYS:HB2	2.48	0.48
1:A:408:ASP:HB2	1:A:453:GLU:OE2	2.13	0.48
1:B:47:GLU:HG3	1:B:47:GLU:O	2.13	0.48
1:B:732:LEU:O	1:B:733:LYS:HB3	2.10	0.48
1:B:347:THR:HG22	1:B:349:ASP:H	1.79	0.48
1:A:566:MET:CE	1:A:568:ILE:HD11	2.44	0.47
1:A:565:VAL:CG2	1:A:609:ILE:HD13	2.43	0.47
1:B:185:GLN:NE2	1:B:196:ARG:HD2	2.29	0.47
1:A:303:LEU:HD11	1:A:308:ILE:HD11	1.97	0.47
1:A:540:LEU:HD11	1:A:566:MET:HE2	1.97	0.47
1:A:516:LEU:HB3	1:A:519:ASN:HB3	1.95	0.47
1:A:142:LEU:HD13	1:A:144:LEU:HD21	1.97	0.47
1:B:403:ARG:HD2	1:B:418:ASP:OD1	2.15	0.47
1:A:733:LYS:HB2	1:A:736:ILE:HD12	1.97	0.47
1:B:529:THR:O	1:B:530:ARG:HB2	2.15	0.47
1:B:591:MET:HE2	1:B:598:ILE:HD11	1.96	0.47
1:A:640:LEU:HD12	1:A:640:LEU:N	2.30	0.46
1:B:59:GLU:HA	2:B:2:TBR:BR8	2.71	0.46
1:A:353:PHE:O	1:A:628:SER:HB2	2.15	0.46
1:A:603:THR:O	1:A:625:ARG:HG2	2.16	0.46
1:B:591:MET:HB3	1:B:598:ILE:HD11	1.98	0.46
1:B:50:VAL:HG11	1:B:91[A]:ARG:HH21	1.81	0.46
1:A:577:SER:O	1:A:578:ILE:HG23	2.16	0.46
1:B:763:SER:OG	1:B:764:ASN:N	2.49	0.46
1:A:550:LEU:HD12	1:A:550:LEU:O	2.15	0.46
1:B:421:ILE:HG22	1:B:448:THR:HG21	1.98	0.46
1:B:669:TYR:HB2	1:B:702:SER:HB2	1.97	0.46
1:A:107:THR:CG2	1:A:108:ASP:N	2.78	0.46
1:B:463:THR:HG22	1:B:466:GLY:H	1.81	0.46
1:A:416:ALA:HB1	1:A:448:THR:HG22	1.98	0.45
1:B:388:TYR:HB3	1:B:397:LEU:HG	1.97	0.45
1:A:341:ILE:HG13	1:A:644:ASP:C	2.37	0.45
1:A:550:LEU:HD12	1:A:550:LEU:C	2.36	0.45
1:B:470:VAL:HB	1:B:488:GLN:HB2	1.97	0.45
1:A:421:ILE:HG22	1:A:448:THR:HG21	1.97	0.45
1:A:152:THR:HG23	1:A:163:PHE:HE1	1.82	0.45
1:A:557:LEU:HD13	1:A:570:PRO:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:347:THR:HG22	1:B:348:GLY:N	2.32	0.45
1:B:380:GLY:HA2	3:B:819:HOH:O	2.16	0.45
1:B:451:ILE:HD11	1:B:459:LEU:HG	1.98	0.45
1:B:515:LEU:HD13	1:B:515:LEU:C	2.38	0.44
1:B:764:ASN:C	1:B:766:PRO:HD3	2.38	0.44
1:B:92:ILE:HG23	1:B:105:MET:HB3	1.98	0.44
1:A:59:GLU:HA	2:A:1:TBR:BR1	2.72	0.44
1:A:716:ASN:CG	1:A:755:LYS:HE3	2.38	0.44
1:A:565:VAL:HG22	1:A:578:ILE:HD11	1.99	0.44
1:B:658:GLN:HA	1:B:659:PRO:HD2	1.77	0.44
1:A:544:LYS:N	1:A:544:LYS:HD2	2.34	0.43
1:B:591:MET:CE	1:B:598:ILE:CD1	2.96	0.43
1:A:47:GLU:CG	1:A:48:ALA:N	2.81	0.43
1:A:345:THR:O	1:A:347:THR:HB	2.19	0.43
1:A:382:ARG:O	1:A:384:ASP:N	2.47	0.43
1:B:562:HIS:NE2	1:B:587:GLU:HG2	2.34	0.42
1:B:119:ASP:OD2	1:B:677:PRO:HD2	2.19	0.42
1:A:376:THR:O	1:A:383:HIS:HA	2.18	0.42
1:A:463:THR:HG22	1:A:464:CYS:N	2.34	0.42
1:B:421:ILE:CG2	1:B:448:THR:HG21	2.50	0.42
1:A:586:ASN:N	1:A:604:ASN:ND2	2.61	0.42
1:A:754:SER:OG	1:A:766:PRO:HB3	2.19	0.42
1:A:459:LEU:HD12	1:A:459:LEU:HA	1.87	0.42
1:A:669:TYR:HB2	1:A:702:SER:HB2	2.01	0.42
1:B:397:LEU:HD23	1:B:397:LEU:HA	1.87	0.42
1:B:178:ILE:HG13	1:B:179:ILE:N	2.34	0.42
1:A:307:ILE:HB	1:A:324:ASP:HB2	2.00	0.42
1:B:95:GLY:HA2	1:B:135:MET:HE1	2.02	0.42
1:A:209:LEU:HB2	1:A:218:LEU:HD21	2.02	0.41
1:B:390:MET:HE3	1:B:391:GLY:H	1.84	0.41
1:A:569:ASN:H	1:A:575:GLN:HG2	1.85	0.41
1:B:353:PHE:O	1:B:628:SER:HB2	2.21	0.41
1:B:505:ILE:HG13	1:B:549:LEU:HD13	2.02	0.41
1:B:91[A]:ARG:HD3	1:B:93:TYR:CE1	2.56	0.41
1:A:705:LEU:C	1:A:705:LEU:HD12	2.41	0.41
1:B:233:TRP:CE2	1:B:272:LEU:HG	2.56	0.40
1:B:591:MET:HE2	1:B:598:ILE:CD1	2.51	0.40
1:B:377:ASP:HA	1:B:378:PRO:HD2	1.88	0.40
1:B:390:MET:CE	1:B:391:GLY:N	2.84	0.40
1:A:451:ILE:CD1	1:A:459:LEU:HG	2.50	0.40
1:B:491:SER:HB2	1:B:499:MET:SD	2.61	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:451:ILE:HD11	1:A:459:LEU:CG	2.50	0.40
1:A:74:ASP:OD1	1:A:74:ASP:C	2.57	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	723/758 (95%)	677 (94%)	38 (5%)	8 (1%)	14	15
1	B	731/758 (96%)	698 (96%)	31 (4%)	2 (0%)	41	50
All	All	1454/1516 (96%)	1375 (95%)	69 (5%)	10 (1%)	22	26

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	384	ASP
1	A	482	GLY
1	A	656	THR
1	A	347	THR
1	A	439	ASN
1	B	345	THR
1	B	733	LYS
1	A	465	LEU
1	A	101	THR
1	A	377	ASP

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	658/676 (97%)	623 (95%)	35 (5%)	22	31
1	B	660/676 (98%)	626 (95%)	34 (5%)	23	32
All	All	1318/1352 (98%)	1249 (95%)	69 (5%)	23	32

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	142	LEU
1	A	303	LEU
1	A	345	THR
1	A	377	ASP
1	A	382	ARG
1	A	445	THR
1	A	450	TYR
1	A	465	LEU
1	A	475	LYS
1	A	478	GLN
1	A	479	SER
1	A	497	SER
1	A	500	PHE
1	A	501	ILE
1	A	507	ASP
1	A	524	LYS
1	A	533	THR
1	A	544	LYS
1	A	549	LEU
1	A	550	LEU
1	A	557	LEU
1	A	566	MET
1	A	568	ILE
1	A	573	GLU
1	A	576	GLN
1	A	596	ASN
1	A	598	ILE
1	A	615	ASP
1	A	665	LEU
1	A	725	MET
1	A	727	LYS
1	A	756	LEU
1	A	759	ASP

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Mol	Chain	Res	Type
1	A	779	GLU
1	A	785	HIS
1	B	37	GLN
1	B	61	LEU
1	B	103	LEU
1	B	120	ARG
1	B	152	THR
1	B	165	THR
1	B	178	ILE
1	B	183	ASP
1	B	214	SER
1	B	217	ASN
1	B	252	GLN
1	B	273	LEU
1	B	277	ASP
1	B	328	SER
1	B	339	ILE
1	B	341	ILE
1	B	389	ARG
1	B	445	THR
1	B	450	TYR
1	B	459	LEU
1	B	500	PHE
1	B	549	LEU
1	B	550	LEU
1	B	557	LEU
1	B	574	SER
1	B	575	GLN
1	B	576	GLN
1	B	592	THR
1	B	606	LEU
1	B	665	LEU
1	B	680	ARG
1	B	734	SER
1	B	751	LEU
1	B	759	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	242	GLN
1	B	185	GLN

5.3.3 RNA [i](#)

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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	TBR	A	1	-	0,36,36	0.00	-	-		
2	TBR	B	2	-	0,36,36	0.00	-	-		

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.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	TBR	2	0
2	B	2	TBR	1	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	737/758 (97%)	0.55	83 (11%) 5 7	12, 33, 91, 120	6 (0%)
1	B	739/758 (97%)	0.26	27 (3%) 41 48	10, 24, 47, 83	0
All	All	1476/1516 (97%)	0.40	110 (7%) 14 19	10, 27, 80, 120	6 (0%)

All (110) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	585	ASN	6.2
1	B	333	ASN	6.2
1	B	584	SER	6.0
1	A	427	ALA	5.6
1	A	497	SER	5.5
1	A	499	MET	5.4
1	B	583	PHE	5.2
1	A	478	GLN	4.9
1	A	379	ALA	4.6
1	A	785	HIS	4.6
1	A	538	ASP	4.4
1	A	380	GLY	4.4
1	A	534	LYS	4.4
1	B	582	SER	4.3
1	B	655	ALA	4.2
1	A	615	ASP	4.1
1	A	616	ALA	4.0
1	A	382	ARG	4.0
1	A	535	LEU	4.0
1	A	537	ALA	4.0
1	A	345	THR	3.8
1	A	625	ARG	3.8
1	A	482	GLY	3.8
1	A	539	GLU	3.8

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Mol	Chain	Res	Type	RSRZ
1	B	758	ARG	3.8
1	A	533	THR	3.7
1	A	575	GLN	3.7
1	B	216	SER	3.7
1	A	493	HIS	3.7
1	A	443	TYR	3.7
1	A	165	THR	3.7
1	A	623	ASN	3.6
1	A	480	THR	3.5
1	A	510	GLY	3.4
1	B	759	ASP	3.3
1	B	765	ARG	3.3
1	B	581	GLY	3.3
1	A	511	ASN	3.2
1	A	523	ASP	3.2
1	A	617	ARG	3.2
1	A	569	ASN	3.2
1	A	385	ALA	3.2
1	A	614	MET	3.2
1	A	655	ALA	3.2
1	A	455	THR	3.1
1	A	383	HIS	3.1
1	A	597	SER	3.1
1	B	383	HIS	3.0
1	B	334	SER	3.0
1	A	500	PHE	3.0
1	A	529	THR	3.0
1	A	477	MET	3.0
1	A	570	PRO	2.9
1	B	636	ASP	2.9
1	B	653	LEU	2.9
1	A	395	TYR	2.9
1	A	612	LYS	2.8
1	B	382	ARG	2.8
1	A	495	GLY	2.8
1	A	522	ILE	2.8
1	A	494	ASN	2.8
1	B	760	GLY	2.8
1	A	544	LYS	2.7
1	A	574	SER	2.7
1	A	472	ASP	2.7
1	B	681	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	384	ASP	2.7
1	A	568	ILE	2.7
1	A	622	THR	2.6
1	B	652	ASN	2.6
1	A	565	VAL	2.6
1	B	620	ASN	2.6
1	A	490	TYR	2.5
1	A	394	THR	2.5
1	A	540	LEU	2.5
1	A	439	ASN	2.4
1	B	500	PHE	2.4
1	A	166	ARG	2.4
1	A	607	TRP	2.3
1	A	381	GLU	2.3
1	B	47	GLU	2.3
1	A	483	GLN	2.3
1	A	746	TYR	2.3
1	A	656	THR	2.3
1	A	475	LYS	2.3
1	A	507	ASP	2.2
1	B	219	PHE	2.2
1	A	758	ARG	2.2
1	A	474	HIS	2.2
1	A	377	ASP	2.2
1	A	521	GLY	2.2
1	B	619	GLN	2.2
1	A	509	GLU	2.2
1	B	213	SER	2.2
1	A	167	ARG	2.1
1	A	513	TRP	2.1
1	A	437	VAL	2.1
1	A	517	TYR	2.1
1	A	520	LYS	2.1
1	A	782	HIS	2.1
1	B	761	GLN	2.1
1	A	496	LEU	2.1
1	A	531	GLU	2.0
1	A	530	ARG	2.0
1	A	604	ASN	2.0
1	A	567	ARG	2.0
1	A	516	LEU	2.0
1	A	127	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	168	ASN	2.0
1	B	46	ALA	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. 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	B-factors(\AA^2)	Q<0.9
2	TBR	A	1	18/18	0.84	0.24	44,51,54,56	18
2	TBR	B	2	18/18	0.89	0.18	30,40,44,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.