



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 07:14 AM GMT

PDB ID : 1UFO
Title : Crystal Structure of TT1662 from *Thermus thermophilus*
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RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2003-06-03
Resolution : 1.60 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

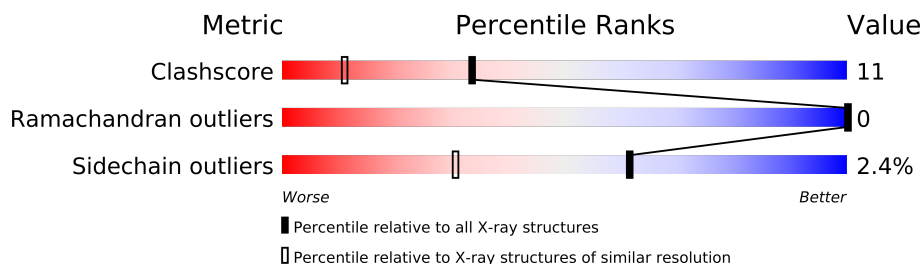
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.60 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))
Clashscore	79885	2199 (1.60-1.60)
Ramachandran outliers	78287	2126 (1.60-1.60)
Sidechain outliers	78261	2125 (1.60-1.60)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	238	
1	B	238	
1	C	238	
1	D	238	
1	E	238	
1	F	238	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12988 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 hypothetical protein TT1662.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	238	Total	C	N	O	Se	0	2	0
			1861	1197	343	317	4			
1	B	238	Total	C	N	O	Se	0	1	0
			1850	1191	339	316	4			
1	C	238	Total	C	N	O	Se	0	3	0
			1866	1203	341	318	4			
1	D	238	Total	C	N	O	Se	0	2	0
			1857	1195	340	318	4			
1	E	238	Total	C	N	O	Se	0	2	0
			1861	1197	343	317	4			
1	F	238	Total	C	N	O	Se	0	2	0
			1858	1197	340	317	4			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	319	Total	O	0	0
			319	319		
2	B	258	Total	O	0	0
			258	258		
2	C	327	Total	O	0	0
			327	327		
2	D	331	Total	O	0	0
			331	331		
2	E	299	Total	O	0	0
			299	299		
2	F	301	Total	O	0	0
			301	301		

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.

Note EDS was not executed.

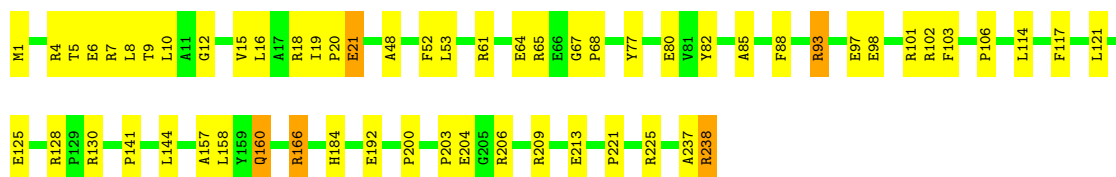
- Molecule 1: hypothetical protein TT1662

Chain A: 



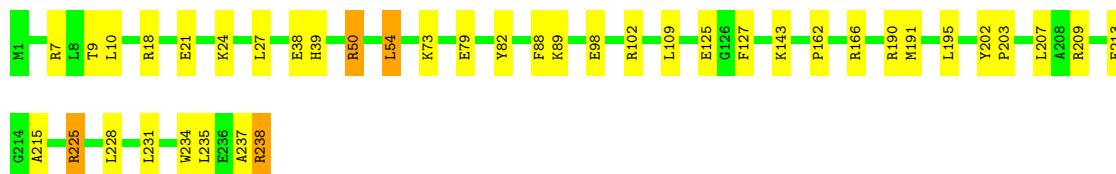
- Molecule 1: hypothetical protein TT1662

Chain B: 



- Molecule 1: hypothetical protein TT1662

Chain C: 



- Molecule 1: hypothetical protein TT1662

Chain D: 

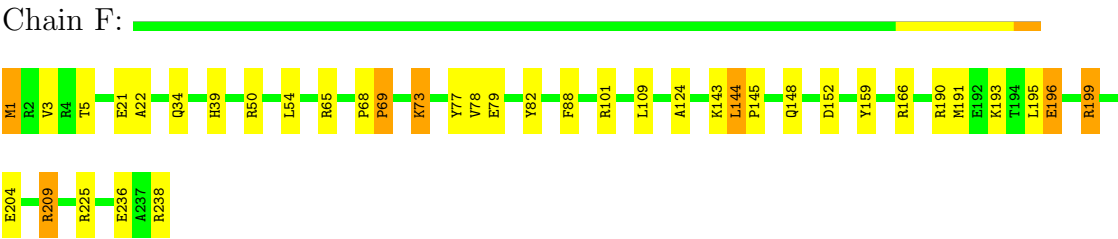


- Molecule 1: hypothetical protein TT1662

Chain E: 



● Molecule 1: hypothetical protein TT1662



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	129.86Å 129.86Å 70.12Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	21.99 – 1.60	Depositor
% Data completeness (in resolution range)	99.7 (21.99-1.60)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.170 , 0.207	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	12988	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

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	1.08	1/1906 (0.1%)	1.10	5/2575 (0.2%)
1	B	1.11	1/1895 (0.1%)	1.11	5/2561 (0.2%)
1	C	1.16	2/1911 (0.1%)	1.12	5/2583 (0.2%)
1	D	1.12	6/1902 (0.3%)	1.07	5/2571 (0.2%)
1	E	1.07	2/1906 (0.1%)	1.06	4/2575 (0.2%)
1	F	1.10	2/1903 (0.1%)	1.09	10/2573 (0.4%)
All	All	1.11	14/11423 (0.1%)	1.09	34/15438 (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
1	B	0	2
1	C	0	1
1	D	0	1
1	F	0	2
All	All	0	7

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	192	GLU	CD-OE1	7.70	1.34	1.25
1	F	196	GLU	CD-OE2	6.70	1.33	1.25
1	D	204	GLU	CB-CG	6.52	1.64	1.52
1	B	160	GLN	CG-CD	5.92	1.64	1.51
1	D	204	GLU	CG-CD	5.83	1.60	1.51
1	D	66	GLU	CB-CG	5.73	1.63	1.52
1	C	234	TRP	CG-CD1	5.71	1.44	1.36
1	E	234	TRP	CG-CD1	5.64	1.44	1.36
1	F	79	GLU	CB-CG	-5.61	1.41	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	77	TYR	CD1-CE1	5.33	1.47	1.39
1	E	196	GLU	CG-CD	5.25	1.59	1.51
1	A	66	GLU	CG-CD	5.13	1.59	1.51
1	D	204	GLU	CD-OE2	5.11	1.31	1.25
1	C	79	GLU	CB-CG	-5.07	1.42	1.52

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	225	ARG	NE-CZ-NH2	9.13	124.87	120.30
1	D	199	ARG	NE-CZ-NH2	-8.95	115.82	120.30
1	E	206	ARG	NE-CZ-NH1	-8.03	116.28	120.30
1	B	128	ARG	NE-CZ-NH1	-7.50	116.55	120.30
1	E	101	ARG	NE-CZ-NH1	-7.25	116.68	120.30
1	E	225	ARG	NE-CZ-NH1	-7.18	116.71	120.30
1	A	225	ARG	NE-CZ-NH1	-6.82	116.89	120.30
1	B	225	ARG	NE-CZ-NH2	6.60	123.60	120.30
1	B	166	ARG	NE-CZ-NH2	-6.53	117.04	120.30
1	A	7	ARG	NE-CZ-NH1	-6.52	117.04	120.30
1	D	65	ARG	NE-CZ-NH1	-6.43	117.09	120.30
1	B	65	ARG	NE-CZ-NH1	-6.36	117.12	120.30
1	F	199	ARG	NE-CZ-NH2	-6.31	117.14	120.30
1	C	225	ARG	NE-CZ-NH1	-6.23	117.18	120.30
1	C	231	LEU	CB-CG-CD1	-6.07	100.69	111.00
1	C	18	ARG	NE-CZ-NH1	-6.02	117.29	120.30
1	C	88	PHE	CB-CG-CD1	-5.99	116.61	120.80
1	A	190	ARG	NE-CZ-NH1	-5.89	117.35	120.30
1	D	93	ARG	NE-CZ-NH2	5.75	123.18	120.30
1	C	50	ARG	NE-CZ-NH2	-5.75	117.43	120.30
1	F	65	ARG	NE-CZ-NH1	-5.72	117.44	120.30
1	A	61	ARG	NE-CZ-NH1	-5.68	117.46	120.30
1	F	225	ARG	NE-CZ-NH1	-5.46	117.57	120.30
1	D	195	LEU	CB-CG-CD2	5.41	120.19	111.00
1	F	225	ARG	NE-CZ-NH2	5.26	122.93	120.30
1	F	109[A]	LEU	CB-CG-CD2	-5.25	102.07	111.00
1	F	109[B]	LEU	CB-CG-CD2	-5.25	102.07	111.00
1	F	209	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	B	225	ARG	NE-CZ-NH1	-5.19	117.70	120.30
1	F	152	ASP	CB-CG-OD1	-5.19	113.63	118.30
1	E	50	ARG	NE-CZ-NH2	-5.13	117.73	120.30
1	F	191	MSE	CG-SE-CE	-5.13	87.62	98.90
1	F	88	PHE	CB-CG-CD1	5.11	124.38	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	225	ARG	NE-CZ-NH1	-5.00	117.80	120.30

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	82	TYR	Sidechain
1	B	77	TYR	Sidechain
1	B	82	TYR	Sidechain
1	C	82	TYR	Sidechain
1	D	82	TYR	Sidechain
1	F	77	TYR	Sidechain
1	F	82	TYR	Sidechain

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	1861	0	1905	45	0
1	B	1850	0	1893	72	0
1	C	1866	0	1913	47	0
1	D	1857	0	1899	24	0
1	E	1861	0	1905	32	0
1	F	1858	0	1904	36	0
2	A	319	0	0	24	0
2	B	258	0	0	16	0
2	C	327	0	0	12	0
2	D	331	0	0	11	0
2	E	299	0	0	12	0
2	F	301	0	0	15	0
All	All	12988	0	11419	249	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 11.

All (249) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:238:ARG:H	1:C:238:ARG:CD	1.49	1.26
1:C:238:ARG:N	1:C:238:ARG:HD2	1.38	1.19
1:C:10[A]:LEU:HD12	1:C:98:GLU:HG3	1.32	1.09
1:A:73:LYS:HE2	2:A:497:HOH:O	1.53	1.08
1:F:166:ARG:HD2	2:F:425:HOH:O	1.54	1.07
1:F:1:MSE:HE1	1:F:22:ALA:H	1.05	1.06
1:F:1:MSE:HE1	1:F:22:ALA:N	1.79	0.98
1:F:1:MSE:CE	1:F:22:ALA:H	1.76	0.97
1:A:143:LYS:HG3	2:A:326:HOH:O	1.77	0.84
1:C:10[A]:LEU:HD13	1:C:102:ARG:NH2	1.96	0.81
1:C:10[A]:LEU:HD12	1:C:98:GLU:CG	2.11	0.80
1:D:166:ARG:HD2	2:D:361:HOH:O	1.81	0.79
1:B:157:ALA:HA	1:B:160:GLN:CD	2.02	0.79
1:C:10[A]:LEU:CD1	1:C:98:GLU:HG3	2.13	0.78
1:B:16:LEU:CG	1:B:18:ARG:HH12	1.97	0.77
1:B:221:PRO:HG2	2:B:360:HOH:O	1.85	0.77
1:A:7:ARG:HD3	2:A:483:HOH:O	1.82	0.77
1:A:18:ARG:HG2	1:A:18:ARG:HH11	1.50	0.76
1:F:68:PRO:HD2	2:F:299:HOH:O	1.86	0.76
1:A:18:ARG:HG2	1:A:18:ARG:NH1	2.02	0.75
1:B:158[B]:LEU:O	1:B:158[B]:LEU:HD12	1.86	0.75
1:F:195:LEU:CD1	1:F:209:ARG:HD3	2.18	0.74
1:D:1:MSE:N	2:D:565:HOH:O	2.21	0.73
1:B:157:ALA:O	1:B:160:GLN:HG2	1.88	0.72
1:E:225:ARG:NH1	1:F:236:GLU:OE1	2.20	0.72
1:C:238:ARG:H	1:C:238:ARG:HD2	0.61	0.71
1:D:101:ARG:HD3	2:D:356:HOH:O	1.90	0.71
1:F:1:MSE:HB3	2:F:429:HOH:O	1.91	0.70
1:A:4:ARG:NH2	1:A:6:GLU:OE1	2.24	0.70
1:B:117:PHE:HZ	1:B:158[B]:LEU:HD13	1.59	0.68
1:B:16:LEU:CD1	1:B:18:ARG:HH12	2.08	0.67
1:A:206:ARG:HD2	2:A:543:HOH:O	1.93	0.67
1:B:16:LEU:HG	1:B:18:ARG:HH12	1.59	0.66
1:B:8:LEU:HD13	1:B:103:PHE:HZ	1.61	0.66
1:B:1:MSE:SE	1:B:20:PRO:HB2	2.46	0.66
1:B:4:ARG:NH1	2:B:425:HOH:O	2.21	0.66
1:E:143:LYS:HE3	2:E:501:HOH:O	1.95	0.66
1:B:121:LEU:HD21	1:B:158[A]:LEU:HD22	1.77	0.65
1:C:9:THR:O	1:C:10[B]:LEU:HD23	1.96	0.65
1:D:192:GLU:HG3	2:D:282:HOH:O	1.95	0.65
1:A:143:LYS:NZ	2:A:471:HOH:O	2.26	0.65
1:B:16:LEU:HD21	1:B:18:ARG:HH22	1.62	0.65
1:B:160:GLN:HG3	2:B:381:HOH:O	1.96	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:8:LEU:CD1	1:B:103:PHE:HZ	2.08	0.65
1:F:1:MSE:HE3	1:F:21:GLU:HG2	1.79	0.65
1:C:7:ARG:NH2	2:C:562:HOH:O	2.30	0.65
1:E:24:LYS:NZ	1:E:24:LYS:HB3	2.12	0.64
1:D:195:LEU:HD13	1:D:207:LEU:HD21	1.80	0.64
1:F:50:ARG:NH1	2:F:401:HOH:O	2.31	0.64
1:F:101:ARG:NH2	2:F:490:HOH:O	2.31	0.64
1:C:166:ARG:HD2	2:C:357:HOH:O	1.98	0.64
1:B:61:ARG:NH2	1:B:68:PRO:O	2.29	0.64
1:B:213:GLU:HG2	2:B:364:HOH:O	1.98	0.64
1:A:199:ARG:HB2	2:A:493:HOH:O	1.97	0.63
1:E:76:ARG:NH2	1:E:151:GLU:OE2	2.31	0.63
1:D:2:ARG:HB3	2:D:367:HOH:O	1.97	0.63
1:B:101:ARG:NH1	2:B:436:HOH:O	2.32	0.63
1:B:16:LEU:HD11	1:B:18:ARG:HH12	1.64	0.62
1:B:61:ARG:NE	1:B:68:PRO:O	2.31	0.62
1:A:209:ARG:NH1	1:B:213:GLU:OE1	2.31	0.62
1:F:143:LYS:HG3	1:F:190:ARG:NH1	2.13	0.62
1:F:1:MSE:HE2	1:F:21:GLU:N	2.15	0.62
1:D:192:GLU:CG	2:D:282:HOH:O	2.47	0.61
1:C:10[B]:LEU:CD2	1:C:102:ARG:CZ	2.78	0.60
1:B:5:THR:HG23	1:B:18:ARG:NH1	2.17	0.60
1:A:10:LEU:HD23	1:A:102:ARG:NH1	2.17	0.59
1:C:238:ARG:NE	2:C:521:HOH:O	2.34	0.59
1:F:1:MSE:CE	1:F:21:GLU:HG2	2.32	0.59
1:A:202:TYR:HB3	2:A:340:HOH:O	2.01	0.59
1:F:143:LYS:CG	1:F:190:ARG:NH1	2.65	0.59
1:B:157:ALA:HA	1:B:160:GLN:CG	2.32	0.59
1:B:158[B]:LEU:HD12	1:B:158[B]:LEU:C	2.23	0.59
1:B:157:ALA:HA	1:B:160:GLN:HG2	1.85	0.59
1:A:202:TYR:C	2:A:426:HOH:O	2.42	0.58
1:B:238:ARG:NH1	1:B:238:ARG:HG2	2.18	0.58
1:E:125:GLU:HG3	2:E:264:HOH:O	2.03	0.58
1:E:143:LYS:NZ	1:E:143:LYS:CB	2.65	0.58
1:C:10[B]:LEU:HD22	1:C:102:ARG:NH2	2.17	0.58
1:F:73:LYS:HE3	2:F:393:HOH:O	2.04	0.58
1:A:206:ARG:HD2	2:A:418:HOH:O	2.04	0.58
1:E:4:ARG:HD3	1:E:6:GLU:OE2	2.04	0.57
1:B:10:LEU:HD22	1:B:98:GLU:HG2	1.86	0.57
1:A:146:GLN:HG3	2:A:413:HOH:O	2.04	0.57
1:D:125:GLU:HG3	2:D:492:HOH:O	2.04	0.57
1:F:195:LEU:HD12	1:F:209:ARG:HD3	1.87	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:143:LYS:HE3	1:A:190:ARG:HD3	1.86	0.56
1:E:143:LYS:HB3	1:E:143:LYS:NZ	2.21	0.56
1:A:205:GLY:N	2:A:426:HOH:O	2.39	0.56
1:E:151:GLU:HB3	2:E:454:HOH:O	2.06	0.55
1:B:16:LEU:HG	1:B:18:ARG:NH1	2.22	0.55
1:C:213:GLU:HG2	2:C:459:HOH:O	2.07	0.55
1:E:143:LYS:NZ	2:E:397:HOH:O	2.40	0.55
1:B:48:ALA:HA	1:B:52:PHE:O	2.06	0.55
1:B:158[A]:LEU:HD23	2:B:367:HOH:O	2.07	0.55
1:A:202:TYR:CE2	1:A:207[B]:LEU:HD13	2.42	0.55
1:D:195:LEU:O	1:D:199:ARG:HG3	2.07	0.54
1:C:89:LYS:NZ	1:C:125:GLU:OE2	2.38	0.54
1:B:125:GLU:HG3	2:B:314:HOH:O	2.07	0.54
1:A:206:ARG:CZ	2:A:543:HOH:O	2.56	0.53
1:F:193:LYS:NZ	2:F:338:HOH:O	2.40	0.53
1:A:207[A]:LEU:HD23	2:A:493:HOH:O	2.08	0.53
1:B:4:ARG:NH2	1:B:6:GLU:OE1	2.41	0.53
1:C:21:GLU:HG3	2:C:460:HOH:O	2.07	0.53
1:B:19:ILE:HA	1:B:53:LEU:HD13	1.90	0.53
1:E:166:ARG:HG2	1:E:166:ARG:HH21	1.72	0.53
1:E:166:ARG:NE	2:E:445:HOH:O	2.40	0.53
1:F:39:HIS:HB3	2:F:394:HOH:O	2.08	0.53
1:B:166:ARG:HD2	2:B:419:HOH:O	2.08	0.53
1:B:184:HIS:ND1	2:B:338:HOH:O	2.28	0.53
1:E:143:LYS:HB3	1:E:143:LYS:HZ3	1.74	0.53
1:B:238:ARG:HG2	1:B:238:ARG:HH11	1.74	0.53
1:F:196:GLU:CD	2:F:375:HOH:O	2.47	0.53
1:E:146:GLN:N	1:E:146:GLN:OE1	2.42	0.53
1:F:1:MSE:HE2	1:F:21:GLU:H	1.74	0.52
1:C:191:MSE:O	1:C:195[A]:LEU:HD23	2.09	0.52
1:A:145:PRO:HD2	1:A:148:GLN:HG3	1.91	0.52
1:B:97:GLU:HG2	2:B:321:HOH:O	2.10	0.52
1:B:85:ALA:HB2	1:B:114:LEU:HD11	1.91	0.52
1:A:73:LYS:NZ	2:A:489:HOH:O	2.43	0.52
1:B:192:GLU:OE1	1:B:209:ARG:NH2	2.41	0.52
1:C:225:ARG:NH1	1:D:236:GLU:OE1	2.37	0.52
1:F:78:VAL:HG21	1:F:144[A]:LEU:HD23	1.91	0.52
1:B:61:ARG:HH12	1:B:80:GLU:CD	2.13	0.51
1:A:209:ARG:NE	1:B:213:GLU:OE1	2.43	0.51
1:C:10[A]:LEU:HD13	1:C:102:ARG:CZ	2.41	0.51
1:E:143:LYS:O	1:E:145:PRO:HD3	2.11	0.51
1:F:143:LYS:HE3	2:F:419:HOH:O	2.08	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:166:ARG:NH1	2:C:343:HOH:O	2.43	0.51
1:C:109[B]:LEU:HD11	1:C:127:PHE:CE2	2.46	0.51
1:E:24:LYS:HZ2	1:E:24:LYS:HB3	1.75	0.51
1:B:166:ARG:NH1	2:B:273:HOH:O	2.36	0.51
1:C:215:ALA:N	1:D:204:GLU:OE1	2.44	0.50
1:D:6:GLU:HB2	2:D:456:HOH:O	2.10	0.50
1:E:7:ARG:HG2	2:E:466:HOH:O	2.11	0.50
1:B:121:LEU:HD21	1:B:158[A]:LEU:CD2	2.41	0.50
1:A:206:ARG:NH1	2:A:379:HOH:O	2.45	0.50
1:B:19:ILE:HG23	1:B:19:ILE:O	2.12	0.50
1:B:237:ALA:O	1:B:238:ARG:O	2.30	0.49
1:A:202:TYR:CD2	1:A:207[B]:LEU:HD13	2.48	0.49
1:A:202:TYR:HB2	1:A:207[B]:LEU:HD22	1.93	0.49
1:A:3:VAL:CG1	1:A:18:ARG:HG3	2.42	0.49
1:B:106:PRO:HB3	1:B:130:ARG:HH21	1.78	0.49
1:C:238:ARG:N	1:C:238:ARG:CD	2.24	0.49
1:C:10[B]:LEU:CD2	1:C:102:ARG:NH2	2.76	0.49
1:B:16:LEU:HD11	1:B:18:ARG:NH1	2.28	0.49
1:C:195[B]:LEU:HD23	1:C:209:ARG:CZ	2.43	0.48
1:B:117:PHE:HZ	1:B:158[B]:LEU:CD1	2.24	0.48
1:C:10[B]:LEU:HD22	1:C:102:ARG:CZ	2.43	0.48
1:C:27:LEU:HB3	1:C:54:LEU:HD12	1.96	0.48
1:E:61:ARG:O	1:E:69:PRO:HG3	2.13	0.47
1:D:69:PRO:HD3	2:D:348:HOH:O	2.12	0.47
1:C:10[A]:LEU:CD1	1:C:102:ARG:CZ	2.92	0.47
1:C:9:THR:C	1:C:10[B]:LEU:HD23	2.35	0.47
1:C:24:LYS:HE3	1:C:235:LEU:CD2	2.43	0.47
1:B:160:GLN:CG	2:B:381:HOH:O	2.59	0.47
1:F:204:GLU:OE1	2:F:368:HOH:O	2.20	0.47
1:A:18:ARG:CG	1:A:18:ARG:NH1	2.73	0.47
1:D:2:ARG:HD3	1:D:2:ARG:HA	1.44	0.47
1:F:34:GLN:OE1	1:F:69:PRO:HG3	2.14	0.47
1:F:5:THR:HG21	2:F:498:HOH:O	2.14	0.47
1:B:19:ILE:HA	1:B:53:LEU:CD1	2.45	0.47
1:A:108:PHE:CD2	1:A:231:LEU:HD22	2.50	0.47
1:D:5:THR:O	1:D:5:THR:HG23	2.15	0.46
1:E:24:LYS:NZ	1:E:24:LYS:CB	2.78	0.46
1:C:166:ARG:CZ	2:C:443:HOH:O	2.63	0.46
1:C:195[B]:LEU:HD21	1:C:209:ARG:HB3	1.98	0.46
1:B:192:GLU:OE1	2:B:300:HOH:O	2.21	0.46
1:B:238:ARG:OXT	1:B:238:ARG:HG3	2.16	0.46
1:C:39:HIS:CD2	2:C:415:HOH:O	2.67	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:205:GLY:C	2:A:340:HOH:O	2.55	0.46
1:B:238:ARG:CG	1:B:238:ARG:HH11	2.26	0.46
1:C:50:ARG:HG3	1:C:228:LEU:HD21	1.98	0.46
1:B:7:ARG:NH2	1:B:64:GLU:OE2	2.44	0.46
1:B:5:THR:HG23	1:B:18:ARG:CZ	2.46	0.46
1:F:195:LEU:HD11	1:F:209:ARG:HD3	1.97	0.46
1:A:206:ARG:HG2	1:A:234:TRP:CH2	2.50	0.46
1:B:61:ARG:CZ	1:B:68:PRO:O	2.64	0.46
1:D:184:HIS:ND1	2:D:363:HOH:O	2.28	0.46
1:B:12:GLY:HA2	2:B:349:HOH:O	2.15	0.46
1:E:79:GLU:HG2	2:E:412:HOH:O	2.16	0.46
1:D:140:PHE:CE2	1:D:193:LYS:HE2	2.50	0.46
1:E:206:ARG:CD	2:E:536:HOH:O	2.63	0.45
1:C:166:ARG:NE	2:C:443:HOH:O	2.49	0.45
1:F:39:HIS:ND1	2:F:394:HOH:O	2.26	0.45
1:C:24:LYS:HE3	1:C:235:LEU:HD23	1.97	0.45
2:C:459:HOH:O	1:D:209:ARG:HG2	2.16	0.45
1:E:166:ARG:CD	2:E:445:HOH:O	2.64	0.45
1:C:237:ALA:HA	1:C:238:ARG:NH1	2.31	0.45
1:A:143:LYS:HE3	1:A:190:ARG:CD	2.46	0.45
1:C:195[A]:LEU:HD22	1:C:195[A]:LEU:N	2.31	0.45
1:F:238:ARG:NH2	2:F:388:HOH:O	2.49	0.45
1:B:200:PRO:HG3	1:C:38:GLU:HG2	1.98	0.45
1:F:145:PRO:HD2	1:F:148:GLN:HG3	1.97	0.45
1:F:124:ALA:HB1	1:F:166:ARG:HE	1.81	0.45
1:A:143:LYS:HE2	2:A:456:HOH:O	2.17	0.45
1:F:195:LEU:O	1:F:199:ARG:HG3	2.16	0.45
1:A:202:TYR:CZ	1:A:207[B]:LEU:HD13	2.51	0.45
1:A:205:GLY:CA	2:A:340:HOH:O	2.64	0.45
1:A:146:GLN:NE2	2:A:462:HOH:O	2.37	0.45
1:D:18:ARG:NH1	2:D:278:HOH:O	2.49	0.44
1:F:143:LYS:HG2	1:F:190:ARG:NH1	2.32	0.44
1:E:4:ARG:CD	1:E:6:GLU:OE2	2.65	0.44
1:C:125:GLU:HG3	2:C:300:HOH:O	2.17	0.44
1:B:9:THR:O	1:B:102:ARG:NH2	2.51	0.44
1:E:205:GLY:O	1:E:206:ARG:HB2	2.17	0.44
1:A:190:ARG:HD2	1:A:190:ARG:HA	1.80	0.44
1:E:4:ARG:HH11	1:E:6:GLU:CG	2.31	0.44
1:C:191:MSE:SE	1:C:195[A]:LEU:HD23	2.68	0.44
1:A:73:LYS:CE	2:A:487:HOH:O	2.66	0.44
1:F:144[B]:LEU:HD21	1:F:159:TYR:CZ	2.53	0.43
1:E:206:ARG:HG2	1:E:206:ARG:HH11	1.83	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:18:ARG:HD3	1:D:54:LEU:HD12	2.00	0.43
1:E:94:ARG:NH2	2:E:355:HOH:O	2.44	0.43
1:A:175:LEU:HB3	1:A:207[B]:LEU:HD12	2.00	0.43
1:B:93:ARG:NH2	1:B:97:GLU:OE2	2.52	0.43
1:B:67:GLY:HA3	1:B:68:PRO:HA	1.71	0.43
1:B:8:LEU:HD13	1:B:103:PHE:CZ	2.47	0.43
1:D:160:GLN:HG2	1:D:161:ALA:N	2.32	0.43
1:B:98:GLU:O	1:B:101:ARG:N	2.51	0.43
1:A:206:ARG:CD	2:A:543:HOH:O	2.59	0.43
1:E:143:LYS:HZ2	1:E:143:LYS:HB2	1.84	0.43
1:F:238:ARG:NH1	2:F:482:HOH:O	2.46	0.43
1:C:190:ARG:HA	1:C:190:ARG:HD2	1.76	0.43
1:E:130[A]:ARG:HD2	2:E:333:HOH:O	2.19	0.42
1:E:206:ARG:HH11	1:E:206:ARG:CG	2.30	0.42
1:A:209:ARG:NH2	2:B:300:HOH:O	2.46	0.42
1:E:206:ARG:HD2	2:E:536:HOH:O	2.18	0.42
1:F:209:ARG:HH21	1:F:209:ARG:HD2	1.66	0.42
1:E:24:LYS:HG2	1:E:51:GLY:O	2.19	0.42
1:A:202:TYR:CB	1:A:207[B]:LEU:HD22	2.49	0.42
1:B:8:LEU:CD1	1:B:103:PHE:CZ	2.95	0.42
1:D:10:LEU:HB2	1:D:15:VAL:HG21	2.01	0.42
1:B:157:ALA:C	1:B:160:GLN:HG2	2.40	0.42
1:A:206:ARG:NE	2:A:543:HOH:O	2.52	0.41
1:A:205:GLY:HA2	2:A:340:HOH:O	2.18	0.41
1:B:5:THR:HG23	1:B:16:LEU:HD11	2.02	0.41
1:A:199:ARG:CB	2:A:493:HOH:O	2.64	0.41
1:C:195[A]:LEU:CD1	1:C:207:LEU:HD11	2.50	0.41
1:B:21:GLU:HG2	1:B:21:GLU:H	1.61	0.41
1:B:157:ALA:HA	1:B:160:GLN:OE1	2.21	0.41
1:B:141:PRO:HD3	1:B:158[B]:LEU:HD11	2.03	0.41
1:B:8:LEU:HB3	1:B:102:ARG:NH1	2.36	0.41
1:B:19:ILE:HD13	2:B:425:HOH:O	2.21	0.41
1:C:21:GLU:CG	2:C:460:HOH:O	2.66	0.41
1:C:202:TYR:N	1:C:203:PRO:CD	2.84	0.41
1:C:109[B]:LEU:HD11	1:C:127:PHE:HE2	1.85	0.40
1:C:225:ARG:HH12	1:D:236:GLU:CD	2.23	0.40
1:B:203:PRO:HB2	1:B:206:ARG:HD3	2.04	0.40
1:D:107:LEU:HD23	1:D:107:LEU:C	2.42	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	238/238 (100%)	234 (98%)	4 (2%)	0	100	100
1	B	237/238 (100%)	232 (98%)	5 (2%)	0	100	100
1	C	239/238 (100%)	237 (99%)	2 (1%)	0	100	100
1	D	238/238 (100%)	236 (99%)	2 (1%)	0	100	100
1	E	238/238 (100%)	236 (99%)	2 (1%)	0	100	100
1	F	238/238 (100%)	234 (98%)	4 (2%)	0	100	100
All	All	1428/1428 (100%)	1409 (99%)	19 (1%)	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	185/179 (103%)	183 (99%)	2 (1%)	84	67
1	B	184/179 (103%)	177 (96%)	7 (4%)	44	15
1	C	186/179 (104%)	181 (97%)	5 (3%)	57	26
1	D	185/179 (103%)	182 (98%)	3 (2%)	75	50
1	E	185/179 (103%)	182 (98%)	3 (2%)	75	50
1	F	185/179 (103%)	178 (96%)	7 (4%)	44	15
All	All	1110/1074 (103%)	1083 (98%)	27 (2%)	61	31

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	ARG
1	A	209	ARG
1	B	15	VAL
1	B	21	GLU
1	B	88	PHE
1	B	93	ARG
1	B	144	LEU
1	B	204	GLU
1	B	238	ARG
1	C	54	LEU
1	C	73	LYS
1	C	143	LYS
1	C	162	PRO
1	C	238	ARG
1	D	88	PHE
1	D	160	GLN
1	D	204	GLU
1	E	4	ARG
1	E	24	LYS
1	E	88	PHE
1	F	1	MSE
1	F	3	VAL
1	F	54	LEU
1	F	69	PRO
1	F	73	LYS
1	F	144[A]	LEU
1	F	144[B]	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	GLN
1	A	201	HIS
1	E	160	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

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.