Full wwPDB X-ray Structure Validation Report ⓘ

Nov 7, 2014 – 02:17 PM EST

PDB ID	:	3HGM
Title	:	Universal Stress Protein TeaD from the TRAP transporter TeaABC of Halomonas elongata
Authors	:	Schweikhard, E.S.; Kuhlmann, S.I.; Ziegler, C.M.
Deposited on	:	2009-05-14
Resolution	:	1.90 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

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

MolProbity	:	4.02b-467
Mogul	:	1.16 November 2013
Xtriage (Phenix)	:	dev-1439
EDS	:	trunk24195
Percentile statistics	:	23426
Refmac	:	5.8.0049
CCP4	:	6.1.3
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk24195

1   Overall quality at a glance ⓘ

The reported resolution of this entry is 1.90 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	Percentile Ranks	Value
Rfree		0.253
Clashscore		3
Ramachandran outliers		0
Sidechain outliers		0.2%
RSRZ outliers		12.8%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
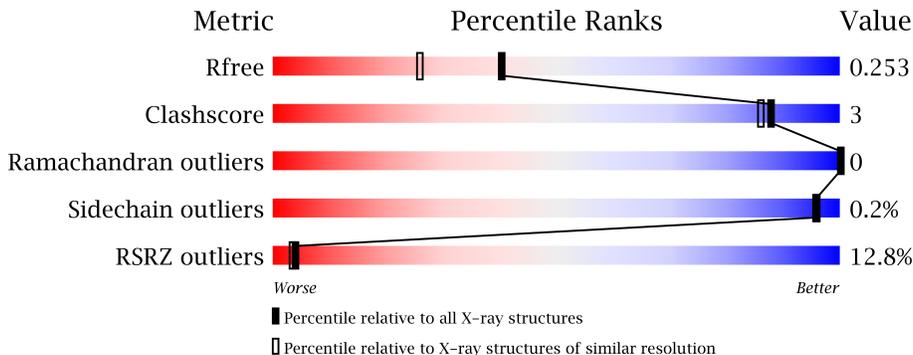
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	77520	4208 (1.90-1.90)
Clashscore	88313	4838 (1.90-1.90)
Ramachandran outliers	86584	4785 (1.90-1.90)
Cα geometry	86677	4778 (1.90-1.90)
Sidechain outliers	86556	4786 (1.90-1.90)
RSRZ outliers	77580	4210 (1.90-1.90)

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.

| Mol	Chain	Length	Quality of chain
1	A	147	
1	B	147	
1	C	147	
1	D	147	

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 4512 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 Universal Stress Protein TeaD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	147	Total	C	N	O	S	0	0	0
			1102	693	201	202	6			
1	B	147	Total	C	N	O	S	0	1	0
			1114	700	206	202	6			
1	C	135	Total	C	N	O	S	0	1	0
			1011	635	186	184	6			
1	D	141	Total	C	N	O	S	0	1	0
			1060	667	196	191	6			

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).
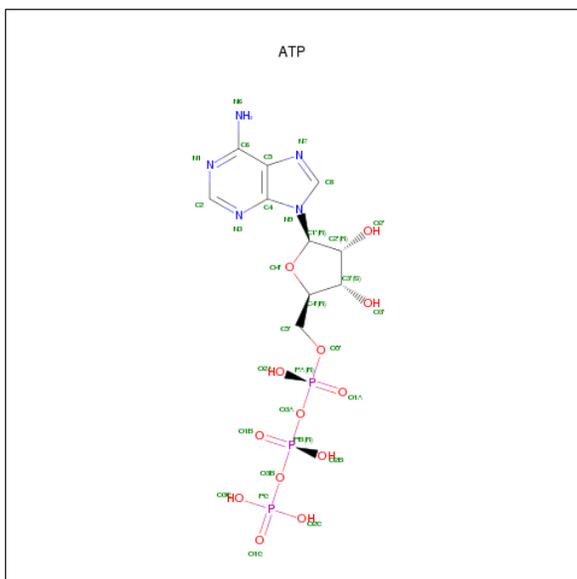
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	B	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total 31	C 10	N 5	O 13	P 3	0	0
2	D	1	Total 31	C 10	N 5	O 13	P 3	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Mg 1	0	0
3	A	1	Total 1	Mg 1	0	0
3	D	1	Total 1	Mg 1	0	0
3	C	1	Total 1	Mg 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	32	Total 32	O 32	0	0
4	B	29	Total 29	O 29	0	0
4	C	16	Total 17	O 17	0	1
4	D	19	Total 19	O 19	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Universal Stress Protein TeaD

Chain A:
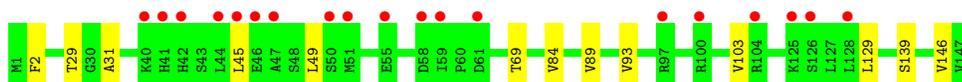
- Molecule 1: Universal Stress Protein TeaD

Chain B:

- Molecule 1: Universal Stress Protein TeaD

Chain C:
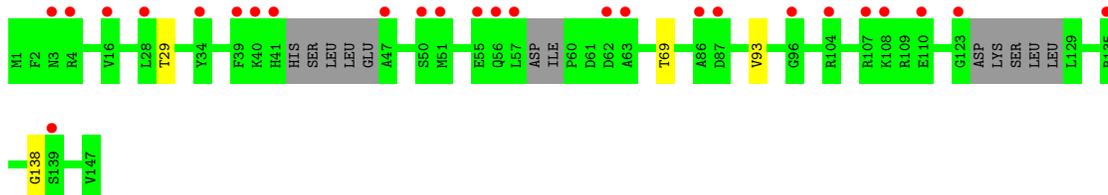
- Molecule 1: Universal Stress Protein TeaD

Chain D:
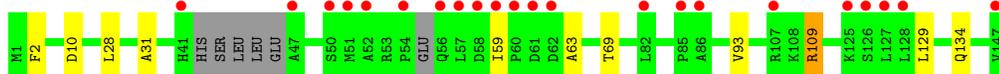
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	74.05Å 74.65Å 97.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.90 48.50 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (20.00-1.90) 99.9 (48.50-1.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	2.16 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.218 , 0.251 0.222 , 0.253	Depositor DCC
R_{free} test set	2167 reflections (5.04%)	DCC
Wilson B-factor (Å^2)	32.5	Xtriage
Anisotropy	0.388	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 38.7	EDS
Estimated twinning fraction	0.023 for k,h,-l	Xtriage
L-test for twinning [2]	$<\lvert L\rvert> = 0.48$, $<L^2> = 0.31$	Xtriage
Outliers	0 of 43018 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4512	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.36% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $<\lvert L\rvert>$, $<L^2>$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$|Z|$>5	RMSZ	#$|Z|$>5
1	A	0.30	0/1116	0.48	0/1504
1	B	0.31	0/1134	0.47	0/1528
1	C	0.29	0/1024	0.47	0/1374
1	D	0.30	0/1074	0.48	0/1443
All	All	0.30	0/4348	0.48	0/5849

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1102	0	1156	7	0
1	B	1114	0	1171	10	0
1	C	1011	0	1059	3	0
1	D	1060	0	1121	10	0
2	A	31	0	12	0	0
2	B	31	0	12	1	0
2	C	31	0	12	0	0
2	D	31	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	32	0	0	0	0
4	B	29	0	0	0	0
4	C	17	0	0	0	0
4	D	19	0	0	0	0
All	All	4512	0	4555	26	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 3.

All (26) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:46:GLU:HA	1:B:49:LEU:HD22	1.81	0.62
1:A:29:THR:HG22	1:B:28:LEU:HD21	1.90	0.54
1:B:69:THR:HA	1:B:93:VAL:HG21	1.89	0.53
1:C:29:THR:HG22	1:D:28:LEU:HD21	1.90	0.53
1:B:2:PHE:O	1:B:31:ALA:HB2	2.09	0.52
1:D:129:LEU:HD12	1:D:134:GLN:HB2	1.92	0.51
1:D:59:ILE:HG22	1:D:63:ALA:HB3	1.94	0.49
1:B:57:LEU:HG	1:D:59:ILE:HD13	1.95	0.49
1:D:2:PHE:O	1:D:31:ALA:HB2	2.13	0.48
1:A:69:THR:HA	1:A:93:VAL:HG21	1.97	0.47
1:C:69:THR:HA	1:C:93:VAL:HG21	1.96	0.46
1:D:59:ILE:CG2	1:D:63:ALA:HB3	2.44	0.46
1:D:10:ASP:HB3	2:D:148:ATP:C5	2.51	0.46
1:D:69:THR:HA	1:D:93:VAL:HG21	1.97	0.46
1:A:84:VAL:HG11	1:A:89:VAL:HG22	1.98	0.46
1:C:138:GLY:HA2	1:D:129:LEU:HD23	2.00	0.43
1:A:103:VAL:HG21	1:A:139:SER:OG	2.19	0.43
1:B:67:TYR:CZ	1:B:71:ILE:HD11	2.54	0.43
1:B:128:LEU:O	1:B:128:LEU:HD12	2.19	0.41
1:D:109:ARG:HD3	1:D:109:ARG:HA	1.80	0.41
1:A:129:LEU:HD11	1:A:146:VAL:HG11	2.03	0.41
1:B:44:LEU:HD11	1:B:97:ARG:CZ	2.51	0.41
1:A:2:PHE:O	1:A:31:ALA:HB2	2.20	0.41
1:B:103:VAL:HG21	1:B:139:SER:OG	2.21	0.41
1:B:10:ASP:HB3	2:B:148:ATP:C5	2.56	0.41
1:A:45:LEU:O	1:A:49:LEU:HD13	2.20	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	145/147 (99%)	143 (99%)	2 (1%)	0	100	100
1	B	147/147 (100%)	147 (100%)	0	0	100	100
1	C	128/147 (87%)	125 (98%)	3 (2%)	0	100	100
1	D	136/147 (92%)	135 (99%)	1 (1%)	0	100	100
All	All	556/588 (95%)	550 (99%)	6 (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	117/117 (100%)	117 (100%)	0	100	100
1	B	118/117 (101%)	118 (100%)	0	100	100
1	C	106/117 (91%)	106 (100%)	0	100	100
1	D	112/117 (96%)	111 (99%)	1 (1%)	86	86
All	All	453/468 (97%)	452 (100%)	1 (0%)	96	96

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	109	ARG

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

Mol	Chain	Res	Type
1	C	56	GLN
1	C	122	ASN

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 ⓘ

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

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	ATP	A	148	3	33,33,33	1.09	2 (6%)	52,52,52	1.79	8 (15%)
2	ATP	B	148	3	33,33,33	1.15	2 (6%)	52,52,52	1.82	8 (15%)
2	ATP	C	148	3	33,33,33	1.07	3 (9%)	52,52,52	1.97	9 (17%)
2	ATP	D	148	3	33,33,33	1.03	2 (6%)	52,52,52	1.93	7 (13%)

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	ATP	A	148	3	-	0/22/38/38	0/3/3/3
2	ATP	B	148	3	-	0/22/38/38	0/3/3/3
2	ATP	C	148	3	-	0/22/38/38	0/3/3/3
2	ATP	D	148	3	-	0/22/38/38	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	148	ATP	C4-N9	-3.45	1.32	1.37
2	B	148	ATP	C4-N9	-3.27	1.33	1.37
2	B	148	ATP	C5-C4	3.19	1.47	1.40
2	C	148	ATP	C5-C4	3.11	1.47	1.40
2	D	148	ATP	C4-N9	-2.99	1.33	1.37
2	A	148	ATP	C5-C4	2.97	1.47	1.40
2	D	148	ATP	C5-C4	2.80	1.46	1.40
2	C	148	ATP	C4-N9	-2.76	1.33	1.37
2	C	148	ATP	O4'-C1'	2.05	1.43	1.41

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	148	ATP	C5-C4-N3	-7.34	118.82	125.98
2	D	148	ATP	C5-C4-N3	-7.12	119.03	125.98
2	D	148	ATP	N3-C2-N1	-7.02	122.72	128.89
2	B	148	ATP	C5-C4-N3	-6.77	119.38	125.98
2	C	148	ATP	N3-C2-N1	-6.72	122.98	128.89
2	A	148	ATP	N3-C2-N1	-6.47	123.20	128.89
2	B	148	ATP	N3-C2-N1	-6.28	123.37	128.89
2	A	148	ATP	C5-C4-N3	-6.12	120.01	125.98
2	D	148	ATP	N3-C4-N9	5.84	135.41	125.39
2	C	148	ATP	N3-C4-N9	5.73	135.22	125.39
2	B	148	ATP	N3-C4-N9	5.45	134.74	125.39
2	A	148	ATP	N3-C4-N9	4.86	133.72	125.39
2	A	148	ATP	PB-O3B-PG	-2.85	124.05	131.93
2	C	148	ATP	PB-O3B-PG	-2.77	124.26	131.93
2	C	148	ATP	C2-N3-C4	2.73	121.12	113.27
2	D	148	ATP	C2-N3-C4	2.71	121.07	113.27
2	A	148	ATP	C4-C5-N7	-2.71	106.80	109.41
2	D	148	ATP	C8-N9-C4	2.55	109.03	106.96
2	C	148	ATP	C4-C5-N7	-2.44	107.05	109.41
2	B	148	ATP	C2-N3-C4	2.44	120.29	113.27
2	A	148	ATP	C2-N3-C4	2.41	120.22	113.27
2	B	148	ATP	PB-O3B-PG	-2.32	125.50	131.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	148	ATP	C8-N9-C4	2.30	108.83	106.96
2	B	148	ATP	C4-C5-N7	-2.30	107.19	109.41
2	B	148	ATP	C8-N9-C4	2.29	108.82	106.96
2	C	148	ATP	C8-N9-C4	2.28	108.81	106.96
2	C	148	ATP	PA-O3A-PB	-2.26	125.67	131.93
2	D	148	ATP	PB-O3B-PG	-2.14	126.02	131.93
2	D	148	ATP	C4-C5-N7	-2.05	107.43	109.41
2	C	148	ATP	O3G-PG-O2G	2.04	115.03	107.38
2	A	148	ATP	C2-N1-C6	2.03	122.37	118.76
2	B	148	ATP	C2-N1-C6	2.02	122.36	118.76

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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, 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(Å²)	Q<0.9
1	A	147/147 (100%)	0.96	19 (12%)	4	3	26, 35, 50, 60	1 (0%)
1	B	147/147 (100%)	0.81	6 (4%)	34	35	26, 34, 45, 53	0
1	C	135/147 (91%)	0.95	26 (19%)	1	1	26, 35, 43, 47	1 (0%)
1	D	141/147 (95%)	0.98	22 (15%)	2	2	26, 34, 47, 53	3 (2%)
All	All	570/588 (96%)	0.93	73 (12%)	4	3	26, 35, 47, 60	5 (0%)

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	45	LEU	6.3
1	D	128	LEU	6.0
1	D	127	LEU	5.4
1	A	51	MET	5.1
1	A	44	LEU	4.7
1	D	51	MET	4.6
1	A	128	LEU	4.4
1	A	58	ASP	4.3
1	D	54	PRO	4.2
1	A	61	ASP	4.1
1	C	47	ALA	4.1
1	D	125	LYS	4.1
1	C	28	LEU	4.1
1	A	47	ALA	4.0
1	C	86	ALA	3.9
1	D	59	ILE	3.9
1	C	55	GLU	3.8
1	A	42	HIS	3.8
1	C	57	LEU	3.7
1	D	47	ALA	3.5
1	C	108	LYS	3.3

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Mol	Chain	Res	Type	RSRZ
1	D	50	SER	3.3
1	D	61	ASP	3.2
1	B	44	LEU	3.2
1	D	86	ALA	3.2
1	C	51	MET	3.1
1	C	41	HIS	2.9
1	A	59	ILE	2.9
1	D	52	ALA	2.8
1	C	56	GLN	2.8
1	D	60	PRO	2.8
1	C	107	ARG	2.7
1	A	46	GLU	2.7
1	B	104[A]	ARG	2.6
1	C	40	LYS	2.6
1	D	56	GLN	2.6
1	C	87	ASP	2.5
1	C	39	PHE	2.5
1	C	63	ALA	2.5
1	D	58	ASP	2.5
1	C	104	ARG	2.5
1	C	135	ARG	2.4
1	C	62[A]	ASP	2.4
1	B	128	LEU	2.4
1	D	82	LEU	2.4
1	D	126	SER	2.4
1	D	57	LEU	2.4
1	D	62	ASP	2.4
1	D	147	VAL	2.4
1	A	100	ARG	2.3
1	C	110	GLU	2.3
1	C	123	GLY	2.3
1	B	47	ALA	2.3
1	A	125	LYS	2.3
1	A	41	HIS	2.2
1	C	96	GLY	2.2
1	A	97	ARG	2.2
1	C	34	TYR	2.2
1	D	85	PRO	2.1
1	A	40	LYS	2.1
1	A	126	SER	2.1
1	C	16	VAL	2.1
1	A	55	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	50	SER	2.1
1	D	107	ARG	2.1
1	C	139	SER	2.1
1	C	4	ARG	2.1
1	C	50	SER	2.1
1	B	7	VAL	2.1
1	A	104	ARG	2.0
1	D	41	HIS	2.0
1	B	35	ILE	2.0
1	C	3	ASN	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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, 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	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	ATP	D	148	31/31	0.15	0.55	30,32,49,50	0
2	ATP	B	148	31/31	0.17	0.21	29,32,46,48	0
2	ATP	A	148	31/31	0.14	-0.16	28,34,51,53	0
3	MG	C	149	1/1	0.15	-0.27	60,60,60,60	0
2	ATP	C	148	31/31	0.13	-0.35	38,44,62,63	0
3	MG	A	149	1/1	0.11	-1.74	44,44,44,44	0
3	MG	B	149	1/1	0.14	-2.02	46,46,46,46	0
3	MG	D	149	1/1	0.09	-2.28	44,44,44,44	0

6.5 Other polymers ⓘ

There are no such residues in this entry.