



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:22 PM GMT

PDB ID : 1K0F
Title : Crystal structure of Zn(II)-free T. pallidum TroA
Authors : Lee, Y.H.; Dorwart, M.R.; Hazlett, K.R.; Deka, R.K.; Norgard, M.V.; Radolf, J.D.; Hasemann, C.A.
Deposited on : 2001-09-19
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
A user guide is available at
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

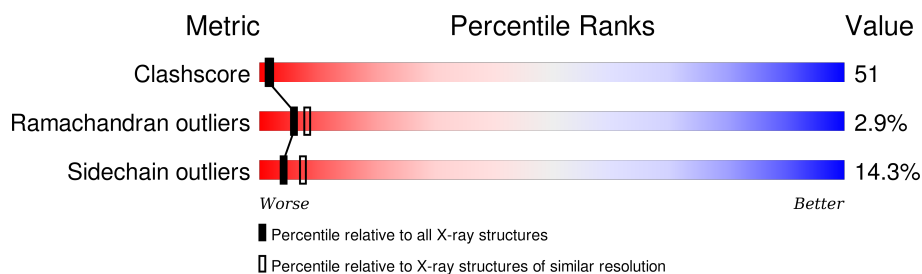
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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))
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	277	<div> <div></div> <div>35%</div> <div>54%</div> <div>11%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2166 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 Periplasmic zinc-binding protein troA.

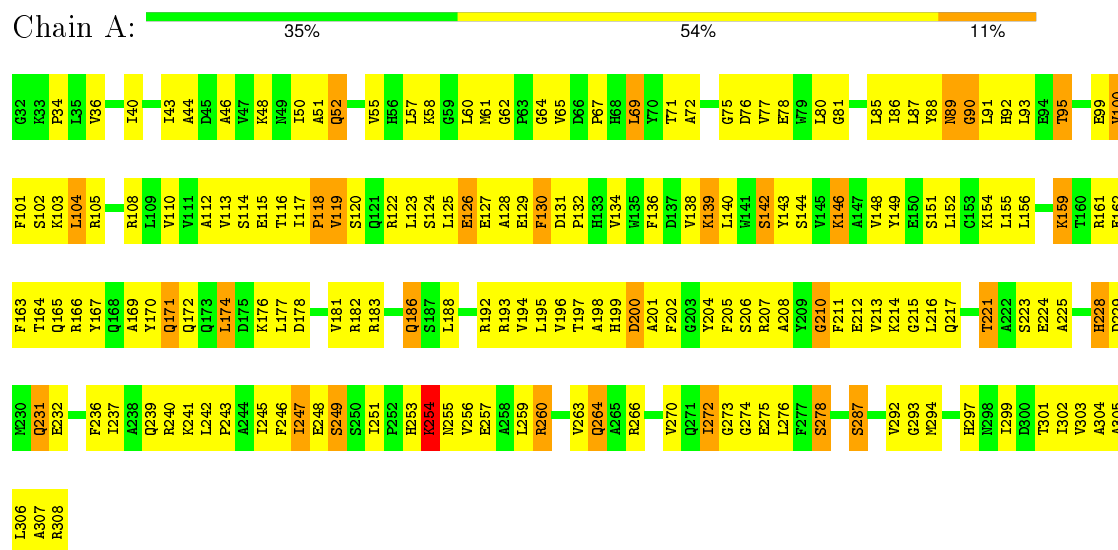
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	277	Total	C	N	O	S	0	0	0
			2138	1358	372	401	7			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	28	Total	O	0	0
			28	28		

Note EDS was not executed.

- Molecule 1: Periplasmic zinc-binding protein troA



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	117.36Å 38.35Å 104.47Å 90.00° 104.11° 90.00°	Depositor
Resolution (Å)	30.00 – 2.50	Depositor
% Data completeness (in resolution range)	(Not available) (30.00-2.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.208 , 0.253	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2166	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0/2181	0.63	2/2954 (0.1%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	90	GLY	N-CA-C	-5.60	99.10	113.10
1	A	272	ILE	N-CA-C	-5.50	96.14	111.00

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	2138	0	2133	217	0
2	A	28	0	0	33	1
All	All	2166	0	2133	217	1

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 51.

All (217) 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:34:PRO:HG3	1:A:156:LEU:HD21	1.22	1.10
1:A:214:LYS:HE2	2:A:329:HOH:O	1.65	0.96
1:A:149:TYR:HD2	2:A:325:HOH:O	1.53	0.92
1:A:247:ILE:HG13	1:A:275:GLU:HA	1.53	0.91
1:A:224:GLU:HB2	2:A:319:HOH:O	1.72	0.90
1:A:123:LEU:HD21	1:A:207:ARG:HD3	1.50	0.90
1:A:118:PRO:HD2	2:A:310:HOH:O	1.73	0.87
1:A:260:ARG:HD2	1:A:264:GLN:HE22	1.38	0.86
1:A:125:LEU:HB2	1:A:129:GLU:HB3	1.59	0.84
1:A:101:PHE:O	1:A:105:ARG:HG3	1.78	0.83
1:A:287:SER:O	1:A:293:GLY:HA3	1.80	0.82
1:A:216:LEU:HD13	1:A:259:LEU:HD22	1.63	0.80
1:A:149:TYR:CD2	2:A:325:HOH:O	2.30	0.79
1:A:177:LEU:HD22	1:A:292:VAL:HA	1.64	0.78
1:A:247:ILE:HD12	1:A:275:GLU:HG3	1.65	0.78
1:A:146:LYS:HA	2:A:325:HOH:O	1.83	0.77
1:A:34:PRO:HG3	1:A:156:LEU:CD2	2.11	0.76
1:A:117:ILE:HA	2:A:310:HOH:O	1.86	0.75
1:A:138:VAL:HB	1:A:178:ASP:HB2	1.67	0.75
1:A:231:GLN:HG3	1:A:266:ARG:NH2	2.01	0.75
1:A:245:ILE:HG23	1:A:270:VAL:HG21	1.70	0.74
1:A:299:ILE:O	1:A:303:VAL:HG22	1.88	0.74
1:A:51:ALA:HA	1:A:163:PHE:CE1	2.23	0.73
1:A:228:HIS:O	1:A:232:GLU:HG3	1.88	0.73
1:A:52:GLN:HG3	1:A:166:ARG:CZ	2.19	0.73
1:A:105:ARG:HG2	1:A:110:VAL:HG11	1.73	0.71
1:A:260:ARG:HG2	1:A:270:VAL:HG13	1.74	0.70
1:A:131:ASP:HB3	1:A:204:TYR:HE2	1.57	0.69
1:A:194:VAL:HG13	1:A:212:GLU:HG2	1.74	0.69
1:A:131:ASP:HB3	1:A:204:TYR:CE2	2.28	0.69
1:A:247:ILE:HG12	1:A:272:ILE:HG23	1.75	0.68
1:A:161:ARG:HG3	1:A:161:ARG:HH11	1.57	0.68
1:A:186:GLN:HG2	2:A:324:HOH:O	1.92	0.68
1:A:231:GLN:HG3	1:A:266:ARG:HH22	1.58	0.68
1:A:91:LEU:O	1:A:132:PRO:HB3	1.94	0.67
1:A:50:ILE:HG21	2:A:332:HOH:O	1.93	0.66
1:A:254:LYS:HB2	2:A:327:HOH:O	1.94	0.66
1:A:237:ILE:HG23	1:A:242:LEU:HB2	1.78	0.66
1:A:259:LEU:O	1:A:263:VAL:HG23	1.96	0.65
1:A:260:ARG:CZ	1:A:260:ARG:HB3	2.26	0.65
1:A:192:ARG:HD3	1:A:306:LEU:O	1.97	0.65
1:A:119:VAL:HG13	1:A:130:PHE:CZ	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:216:LEU:O	1:A:225:ALA:HB2	1.97	0.65
1:A:62:GLY:O	1:A:65:VAL:HB	1.98	0.64
1:A:61:MET:HB3	1:A:65:VAL:HG11	1.79	0.64
1:A:217:GLN:NE2	1:A:221:THR:HG22	2.12	0.64
1:A:88:TYR:O	1:A:112:ALA:HA	1.98	0.63
1:A:236:PHE:CZ	2:A:318:HOH:O	2.50	0.63
1:A:52:GLN:HG3	1:A:166:ARG:NE	2.13	0.63
1:A:206:SER:HB2	1:A:211:PHE:O	1.98	0.63
1:A:194:VAL:HA	1:A:212:GLU:HB3	1.80	0.63
1:A:246:PHE:CZ	1:A:302:ILE:HA	2.33	0.62
1:A:246:PHE:HE2	1:A:301:THR:HG22	1.65	0.62
1:A:236:PHE:CE2	2:A:318:HOH:O	2.52	0.62
1:A:123:LEU:HD21	1:A:207:ARG:CD	2.28	0.61
1:A:196:VAL:HG22	1:A:214:LYS:HB2	1.83	0.60
1:A:89:ASN:HD22	1:A:93:LEU:HB2	1.66	0.60
1:A:272:ILE:O	1:A:272:ILE:HG22	2.01	0.60
1:A:195:LEU:O	1:A:213:VAL:HA	2.03	0.59
1:A:51:ALA:HB2	1:A:152:LEU:HD13	1.84	0.59
1:A:257:GLU:CG	2:A:316:HOH:O	2.49	0.59
1:A:57:LEU:HD12	1:A:58:LYS:N	2.17	0.59
1:A:117:ILE:HG22	1:A:122:ARG:HG2	1.85	0.59
1:A:119:VAL:HA	1:A:122:ARG:CD	2.33	0.59
1:A:118:PRO:O	1:A:120:SER:N	2.35	0.59
1:A:199:HIS:HE1	1:A:278:SER:HB2	1.68	0.59
1:A:99:GLU:HG3	1:A:103:LYS:NZ	2.18	0.59
1:A:257:GLU:HG2	2:A:316:HOH:O	2.02	0.58
1:A:260:ARG:HD2	1:A:264:GLN:NE2	2.14	0.58
1:A:245:ILE:HD12	1:A:256:VAL:HG13	1.84	0.57
1:A:134:VAL:HG12	1:A:204:TYR:CE1	2.39	0.57
1:A:192:ARG:O	1:A:306:LEU:HD13	2.05	0.57
1:A:194:VAL:HG22	1:A:212:GLU:HB3	1.85	0.57
1:A:61:MET:HB3	1:A:65:VAL:CG1	2.35	0.57
1:A:125:LEU:HG	2:A:330:HOH:O	2.04	0.57
1:A:91:LEU:H	1:A:115:GLU:CD	2.08	0.57
1:A:246:PHE:CE2	1:A:301:THR:HG22	2.40	0.56
1:A:260:ARG:HG2	1:A:270:VAL:CG1	2.35	0.56
1:A:131:ASP:CB	1:A:204:TYR:HE2	2.18	0.56
1:A:92:HIS:NE2	1:A:95:THR:HG22	2.20	0.56
1:A:181:VAL:HG13	1:A:299:ILE:HD13	1.87	0.56
1:A:197:THR:HG22	1:A:246:PHE:HB2	1.88	0.55
1:A:246:PHE:HB3	1:A:276:LEU:HG	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:257:GLU:CD	2:A:316:HOH:O	2.45	0.55
1:A:303:VAL:HG23	2:A:322:HOH:O	2.05	0.55
1:A:242:LEU:HA	2:A:315:HOH:O	2.06	0.55
1:A:149:TYR:CE1	1:A:164:THR:HA	2.42	0.55
1:A:164:THR:O	1:A:167:TYR:HB3	2.06	0.55
1:A:177:LEU:CD2	1:A:292:VAL:HA	2.37	0.55
1:A:138:VAL:CB	1:A:178:ASP:HB2	2.36	0.54
1:A:40:ILE:HG22	1:A:67:PRO:HG3	1.89	0.54
1:A:260:ARG:HG3	1:A:272:ILE:CD1	2.38	0.54
1:A:138:VAL:CG1	1:A:178:ASP:HB2	2.38	0.54
1:A:253:HIS:O	1:A:255:ASN:N	2.41	0.54
1:A:247:ILE:HG12	1:A:272:ILE:CG2	2.37	0.53
1:A:113:VAL:HG23	1:A:114:SER:N	2.23	0.53
1:A:188:LEU:HD12	1:A:307:ALA:HB2	1.91	0.53
1:A:144:SER:O	1:A:148:VAL:HG23	2.09	0.53
1:A:64:GLY:HA2	1:A:249:SER:O	2.09	0.53
1:A:90:GLY:HA3	1:A:112:ALA:HB1	1.89	0.53
1:A:161:ARG:HG3	1:A:161:ARG:NH1	2.23	0.53
1:A:126:GLU:C	1:A:128:ALA:H	2.13	0.53
1:A:138:VAL:HG11	1:A:174:LEU:O	2.09	0.52
1:A:188:LEU:CD1	1:A:307:ALA:HB2	2.39	0.52
1:A:172:GLN:HB3	2:A:313:HOH:O	2.09	0.52
1:A:50:ILE:CG2	2:A:332:HOH:O	2.55	0.52
1:A:114:SER:C	1:A:116:THR:H	2.13	0.52
1:A:138:VAL:HB	1:A:178:ASP:CB	2.38	0.52
1:A:236:PHE:CE1	2:A:318:HOH:O	2.63	0.52
1:A:195:LEU:N	1:A:212:GLU:O	2.43	0.52
1:A:88:TYR:OH	1:A:105:ARG:NH1	2.43	0.51
1:A:43:ILE:HG21	1:A:87:LEU:HB3	1.92	0.51
1:A:123:LEU:HD23	1:A:207:ARG:NH1	2.26	0.51
1:A:46:ALA:HA	1:A:170:TYR:CE2	2.46	0.51
1:A:155:LEU:O	1:A:156:LEU:HD23	2.11	0.50
1:A:52:GLN:HG3	1:A:166:ARG:CD	2.41	0.50
1:A:119:VAL:HA	1:A:122:ARG:NE	2.27	0.50
1:A:80:LEU:HD22	1:A:86:ILE:HD13	1.94	0.50
1:A:50:ILE:O	1:A:166:ARG:HD2	2.12	0.50
1:A:196:VAL:HA	1:A:214:LYS:O	2.12	0.50
1:A:183:ARG:O	1:A:186:GLN:HB2	2.11	0.50
1:A:90:GLY:HA3	1:A:115:GLU:CG	2.41	0.50
1:A:188:LEU:HD21	1:A:306:LEU:HB3	1.93	0.50
1:A:246:PHE:CZ	1:A:305:ALA:HB3	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:ARG:HD3	1:A:210:GLY:O	2.11	0.49
1:A:36:VAL:HG22	1:A:85:LEU:HD23	1.95	0.49
1:A:202:PHE:HB3	1:A:205:PHE:HB3	1.95	0.49
1:A:260:ARG:HH11	1:A:272:ILE:HD13	1.78	0.48
1:A:247:ILE:HG13	1:A:275:GLU:CA	2.34	0.48
1:A:171:GLN:O	1:A:174:LEU:HB2	2.12	0.48
1:A:236:PHE:CD2	2:A:318:HOH:O	2.67	0.48
1:A:217:GLN:OE1	1:A:221:THR:HA	2.14	0.48
1:A:118:PRO:O	1:A:119:VAL:C	2.51	0.48
1:A:248:GLU:HA	1:A:276:LEU:O	2.14	0.48
1:A:119:VAL:HG13	1:A:130:PHE:HZ	1.78	0.48
1:A:60:LEU:HD22	1:A:76:ASP:OD1	2.14	0.48
1:A:166:ARG:O	1:A:169:ALA:HB3	2.14	0.47
1:A:92:HIS:CE1	1:A:95:THR:HG22	2.50	0.47
1:A:140:LEU:HG	1:A:140:LEU:O	2.14	0.47
1:A:101:PHE:C	1:A:105:ARG:HG3	2.34	0.47
1:A:246:PHE:CE2	1:A:302:ILE:HA	2.50	0.46
1:A:143:TYR:CG	2:A:310:HOH:O	2.67	0.46
1:A:198:ALA:HB3	1:A:248:GLU:CD	2.35	0.46
1:A:243:PRO:CD	2:A:315:HOH:O	2.63	0.46
1:A:221:THR:HG21	1:A:251:ILE:CG1	2.45	0.46
1:A:44:ALA:O	1:A:48:LYS:HG3	2.16	0.46
1:A:90:GLY:CA	1:A:112:ALA:HB1	2.44	0.46
1:A:85:LEU:CD2	1:A:152:LEU:HD23	2.45	0.46
1:A:169:ALA:O	1:A:172:GLN:N	2.48	0.46
1:A:276:LEU:HD13	1:A:302:ILE:HD11	1.98	0.46
1:A:124:SER:OG	1:A:127:GLU:HA	2.16	0.46
1:A:52:GLN:CG	1:A:166:ARG:HD3	2.45	0.46
1:A:243:PRO:HD3	2:A:315:HOH:O	2.16	0.45
1:A:119:VAL:O	1:A:122:ARG:HG3	2.16	0.45
1:A:240:ARG:HG3	2:A:318:HOH:O	2.16	0.45
1:A:195:LEU:HD11	1:A:197:THR:HG23	1.99	0.45
1:A:119:VAL:HA	1:A:122:ARG:HG3	1.97	0.45
1:A:163:PHE:HB3	2:A:332:HOH:O	2.15	0.45
1:A:307:ALA:O	1:A:308:ARG:HG3	2.16	0.45
1:A:117:ILE:CG2	1:A:122:ARG:HG2	2.47	0.45
1:A:88:TYR:CZ	1:A:112:ALA:HB2	2.52	0.45
1:A:91:LEU:HD23	1:A:115:GLU:OE1	2.16	0.45
1:A:197:THR:O	1:A:215:GLY:HA2	2.17	0.44
1:A:117:ILE:O	1:A:118:PRO:C	2.55	0.44
1:A:186:GLN:CG	2:A:324:HOH:O	2.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:213:VAL:O	1:A:214:LYS:HG2	2.17	0.44
1:A:57:LEU:HD12	1:A:58:LYS:H	1.82	0.44
1:A:174:LEU:O	1:A:177:LEU:HB3	2.18	0.44
1:A:303:VAL:HG23	1:A:304:ALA:N	2.32	0.44
1:A:99:GLU:HG3	1:A:103:LYS:HZ3	1.82	0.44
1:A:253:HIS:CD2	2:A:312:HOH:O	2.70	0.44
1:A:274:GLY:HA3	1:A:301:THR:CG2	2.48	0.44
1:A:275:GLU:O	1:A:297:HIS:NE2	2.46	0.44
1:A:77:VAL:HG22	1:A:100:VAL:HG11	1.99	0.44
1:A:253:HIS:HA	2:A:309:HOH:O	2.17	0.43
1:A:253:HIS:C	1:A:255:ASN:N	2.72	0.43
1:A:143:TYR:CE1	2:A:310:HOH:O	2.70	0.43
1:A:65:VAL:O	1:A:67:PRO:HD3	2.18	0.43
1:A:221:THR:HG21	1:A:251:ILE:HG12	2.00	0.43
1:A:102:SER:HA	1:A:105:ARG:HD3	2.00	0.43
1:A:246:PHE:N	1:A:246:PHE:CD1	2.87	0.43
1:A:99:GLU:O	1:A:103:LYS:HD2	2.19	0.43
1:A:93:LEU:HB2	1:A:132:PRO:HB2	2.01	0.43
1:A:199:HIS:CE1	1:A:201:ALA:HB2	2.53	0.42
1:A:80:LEU:HD22	1:A:86:ILE:CD1	2.48	0.42
1:A:221:THR:C	1:A:223:SER:H	2.22	0.42
1:A:125:LEU:HB2	1:A:129:GLU:CB	2.40	0.42
1:A:126:GLU:HA	1:A:126:GLU:OE2	2.20	0.42
1:A:146:LYS:HG2	2:A:325:HOH:O	2.18	0.42
1:A:105:ARG:HG2	1:A:110:VAL:CG1	2.47	0.42
1:A:159:LYS:HD2	1:A:162:GLU:CD	2.40	0.42
1:A:146:LYS:NZ	2:A:320:HOH:O	2.53	0.42
1:A:51:ALA:HB1	1:A:55:VAL:HG13	2.02	0.42
1:A:123:LEU:CD2	1:A:207:ARG:NH1	2.83	0.42
1:A:114:SER:C	1:A:116:THR:N	2.73	0.42
1:A:92:HIS:CG	1:A:92:HIS:O	2.70	0.41
1:A:75:GLY:O	1:A:78:GLU:HB3	2.20	0.41
1:A:196:VAL:HG11	1:A:237:ILE:HD11	2.01	0.41
1:A:119:VAL:HA	1:A:122:ARG:CG	2.51	0.41
1:A:85:LEU:CB	1:A:155:LEU:HD22	2.50	0.41
1:A:118:PRO:C	1:A:120:SER:N	2.73	0.41
1:A:228:HIS:ND1	1:A:229:ASP:N	2.69	0.41
1:A:72:ALA:HB3	1:A:77:VAL:HG23	2.03	0.41
1:A:81:GLY:O	1:A:108:ARG:NH2	2.54	0.41
1:A:243:PRO:HG2	1:A:306:LEU:CD2	2.51	0.41
1:A:134:VAL:C	1:A:136:PHE:H	2.24	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:ILE:HG22	1:A:67:PRO:CG	2.49	0.41
1:A:104:LEU:HD23	1:A:108:ARG:HD2	2.03	0.41
1:A:90:GLY:HA3	1:A:115:GLU:HG2	2.02	0.41
1:A:134:VAL:HG12	1:A:204:TYR:CZ	2.56	0.40
1:A:69:LEU:HD11	1:A:221:THR:HB	2.02	0.40
1:A:292:VAL:HG12	1:A:293:GLY:N	2.36	0.40
1:A:139:LYS:O	1:A:142:SER:OG	2.37	0.40
1:A:202:PHE:O	1:A:205:PHE:HB3	2.22	0.40
1:A:34:PRO:CG	1:A:156:LEU:HD11	2.52	0.40
1:A:131:ASP:CG	1:A:204:TYR:HE2	2.25	0.40
1:A:182:ARG:NH2	1:A:208:ALA:O	2.54	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:327:HOH:O	2:A:327:HOH:O[2_655]	2.04	0.16

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	275/277 (99%)	226 (82%)	41 (15%)	8 (3%)	6 8

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	95	THR
1	A	119	VAL
1	A	254	LYS
1	A	273	GLY
1	A	200	ASP

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Mol	Chain	Res	Type
1	A	89	ASN
1	A	210	GLY
1	A	118	PRO

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	223/223 (100%)	191 (86%)	32 (14%)	4 7

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	GLN
1	A	69	LEU
1	A	71	THR
1	A	100	VAL
1	A	104	LEU
1	A	126	GLU
1	A	130	PHE
1	A	139	LYS
1	A	142	SER
1	A	146	LYS
1	A	151	SER
1	A	154	LYS
1	A	159	LYS
1	A	165	GLN
1	A	171	GLN
1	A	174	LEU
1	A	176	LYS
1	A	186	GLN
1	A	200	ASP
1	A	221	THR
1	A	228	HIS
1	A	231	GLN
1	A	239	GLN

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Mol	Chain	Res	Type
1	A	241	LYS
1	A	247	ILE
1	A	249	SER
1	A	254	LYS
1	A	260	ARG
1	A	264	GLN
1	A	278	SER
1	A	287	SER
1	A	294	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	GLN
1	A	68	HIS
1	A	168	GLN
1	A	217	GLN
1	A	239	GLN
1	A	264	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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.